Genome Survey Sequence and Characterization of Simple Sequence Repeat (SSR) Markers in *Mesona chinensis* Benth (Chinese Mesona)

Zhao Zheng [1,2,#], Nannan Zhang [1,#], Zhenghui Huang [1,2], Qiaoying Zeng [1], Yonghong Huang [1] and Yongwen Qi [1,2,*]

[1] Guangdong sugarcane Genetic Improvement Engineering Center，Guangdong Provincial Bioengineering Institute (Guangzhou Sugarcane Industry Research Institute), Guangzhou 510316, China；

[2] Zhongkai University of Agriculture and Engineering, Guangzhou 510225, China

* Correspondence: yongwen2001@163.com; Tel.: +86 20 84168434 (F.L.)

[#] These authors contributed equally to this work

Authors list

Zhao Zheng

Email: 13710053962@163.com

Affiliation:

Guangdong Sugarcane Genetic Improvement Engineering Center，Guangdong Provincial Bioengineering Institute (Guangzhou Sugarcane Industry Research Institute), Guangzhou 510316, China；

Zhongkai University of Agriculture and Engineering, Guangzhou 510225, China

Nannan Zhang

Email: zhangnn23@mail2.sysu.edu.cn

Affiliation:

Guangdong Sugarcane Genetic Improvement Engineering Center，Guangdong Provincial Bioengineering Institute (Guangzhou Sugarcane Industry Research Institute), Guangzhou 510316, China；

Zhenghui Huang

Email: hzh85501@foxmail.com

Affiliation:

Guangdong Sugarcane Genetic Improvement Engineering Center，Guangdong Provincial Bioengineering Institute (Guangzhou Sugarcane Industry Research Institute), Guangzhou 510316, China；

Zhongkai University of Agriculture and Engineering, Guangzhou 510225, China

Qiaoying Zeng

Email: zengqiaoying123@163.com

Affiliation:

Guangdong Sugarcane Genetic Improvement Engineering Center，Guangdong Provincial Bioengineering Institute (Guangzhou Sugarcane Industry Research Institute), Guangzhou 510316, China；

Yonghong Huang

Email: bear20081013@126.com

Affiliation:
Guangdong Sugarcane Genetic Improvement Engineering Center, Guangdong Provincial Bioengineering Institute (Guangzhou Sugarcane Industry Research Institute), Guangzhou 510316, China；

Yongwen Qi

Email: yongwen2001@163.com
Affiliation:
Guangdong Sugarcane Genetic Improvement Engineering Center, Guangdong Provincial Bioengineering Institute (Guangzhou Sugarcane Industry Research Institute), Guangzhou 510316, China；
Zhongkai University of Agriculture and Engineering, Guangzhou 510225, China

Supplementary Table 1. The predict genome size of *Mesona chinensis* Benth with different tools.

Software	Kmer size	Genome size (bp)
GenomeScope2	21	1258798638
GenomeScope2	23	1258743939
GenomeScope2	25	1258153982
GenomeScope2	27	1257443508
FindGSE	21	1387232711
FindGSE	23	1406061078
FindGSE	25	1384082434
FindGSE	27	1403375561
MGSE	-	1346321495
Gce	21	2196260000
Gce	23	2180150000
Gce	25	2128670000
Gce	27	2219320000

Supplementary Table 2. Details of all the SSR markers that identified from *Mesona chinensis* Benth

ID	SSR nr.	SSR type	SSR	size	start	end	FORWARD PRIMER1 (5'-3')
scaffold61_15.9	1	p2	(AT)9	18	1483	1500	AACGAATTGAAATGAATTCTACG
scaffold84_14.4	1	p2	(TA)9	18	50	67	CGAACGCTCCAAATTAGAATG
scaffold124_12.6	1	p2	(AT)7	14	277	290	GGCTATAGGTCAACGGACCA
scaffold127_13.5	1	p2	(TA)9	18	132	149	CTGAGCTTCAGAGCCCAGTT
scaffold219_12.9	1	p2	(TA)8	16	644	659	TGAATTCATAACCTTCCCATTCA
scaffold343_12.1	1	p2	(CT)11	22	423	444	GCTCCACCTCCAAACAAGAG
scaffold367_15.0	1	p2	(AT)6	12	15141	15152	CTGGAGCAGCATCCAAAGTT
scaffold407_11.5	1	p2	(AT)9	18	47	64	TGTGTTGTGTGGAATAAAAAGTTTG
scaffold441_16.0	1	p2	(CT)6	12	694	705	TCTTCGTTTCTGGTCTGCCT
scaffold452_15.0	1	p2	(AT)10	20	48	67	TGCAGCAATGGTTGTGATTT
scaffold509_17.8	1	p2	(AT)6	12	183	194	CGAGACACTTGGCAACTTCA
scaffold549_11.1	1	p2	(AC)6	12	65	76	CCCTCGACACACACTCACAT
scaffold642_16.5	1	p2	(TC)6	12	301	312	TAAATCATCAGCCCACGTCA
scaffold820_12.7	1	p2	(AT)9	18	375	392	CAGTAATCATGCGCGAAAAA
scaffold851_10.9	1	p2	(AG)6	12	302	313	TGACCGGAAGGTATGAACAA
scaffold900_11.1	1	p2	(TA)7	14	523	536	TCGCTGACATCATCTTATGGA
scaffold909_11.1	1	p2	(GA)6	12	532	543	CAAGGGTTCAAGCATTGGAG
scaffold914_14.0	1	p2	(GA)7	14	586	599	AAGCATTTGAGGGGTTTTCC
scaffold992_13.1	1	p2	(GC)6	12	61	72	CGGGGACACATAAACCTCAC
scaffold1174_17.5	1	p2	(CT)6	12	54	65	TTCCCCTTTGCCCTCTATTT
scaffold1268_20.1	1	p2	(GA)7	14	75	88	CCCACTGATTTGTGTGAGGA
scaffold1316_13.6	1	p2	(AG)8	16	52	67	AGTTTTCATGGATGGATGCC
scaffold1359_13.2	1	p2	(AT)7	14	694	707	TCCAAGTTTTTACCCCACCA
scaffold1398_10.7	1	p2	(TA)6	12	54	65	TGACCATATCTCGGTTTAGCA
scaffold1420_11.1	1	p2	(TC)6	12	695	706	TTTTAATGGGCGGTTATGGA
scaffold1450_12.4	1	p2	(AG)7	14	263	276	GACATATCGTCGATCGGCTT
scaffold1683_20.2	1	p2	(AT)6	12	107	118	GGGTGGATGACTTTGGTGTT
scaffold1739_11.1	1	p2	(CT)6	12	44	55	TCTAACCCAAACCCAAACCC
scaffold2019_12.7	1	p2	(TA)6	12	94	105	TTTCGTCCCGAAATTTTGTT
scaffold2112_11.2	1	p2	(TA)9	18	209	226	GACAACCTTCGGCTTGAAAA
scaffold2138_14.4	1	p2	(CT)6	12	185	196	AACTTGGCCCCTAAGCTTGT
scaffold2197_15.4	1	p2	(TA)7	14	52	65	CCATCTATAGCGGTTAGCGTG
scaffold2272_15.8	1	p2	(TA)6	12	54	65	CCCACTTAGGAACATTTAGGGA
scaffold2610_13.8	1	p2	(AT)10	20	401	420	TTGATACCTCCTCCCACGAC
scaffold2693_15.1	1	p2	(AT)8	16	375	390	GTTAGCGGAGTGAATGAGGG
scaffold2696_12.8	1	p2	(CT)7	14	104	117	AATTGATCATGGCTTCTGGC
scaffold2789_10.8	1	p2	(TC)6	12	208	219	GGGAGTTTGACACCTAAAGCC
scaffold2800_12.0	1	p2	(AT)6	12	388	399	ACAGGCTCTTTGGAAGACGA
scaffold2816_18.4	1	p2	(TA)9	18	100	117	TGGTTATTACTGGAACGCGA
scaffold2829_15.3	1	p2	(CT)7	14	2222	2235	ACAGGTCCCTGAAACAAACG
scaffold2857_14.5	1	p2	(TC)6	12	2399	2410	ACGTGAAGGCTGGGACATAC
scaffold2889_11.2	1	p2	(AT)6	12	54	65	ATTTGACATCTAATACCCAACTATTTT
scaffold3055_12.9	1	p2	(CT)10	20	266	285	TTTATTGCAGGCGCTCTCTT
scaffold3064_11.0	1	p2	(TG)6	12	54	65	GGATACCCTCTCAAACCCTAGT
scaffold3164_15.8	1	p2	(TC)7	14	209	222	GGGGCGTGACAAGTTATGTT
scaffold3415_18.4	1	p2	(GA)7	14	1148	1161	ATCAAACAGCTGAGGCTCGT
scaffold3600_10.3	1	p2	(GA)6	12	106	117	TGATGAAGGTCCAAATGCAA
scaffold3641_11.1	1	p2	(AT)6	12	54	65	AATTCTAACCATCTTCTTTTGCC
scaffold3739_12.5	1	p2	(TA)7	14	238	251	ATCCTCCCACCCCACTTAAC
scaffold3746_15.6	1	p2	(GA)6	12	490	501	AGAAAAGGGGAGAGAGCAGG
scaffold3844_17.5	1	p2	(TC)6	12	139	150	GACTGTTCGAGCTTATCCGC
scaffold3968_15.2	1	p2	(AT)6	12	417	428	CACGTACTGGCCTAAATAATGTCA
scaffold4045_13.5	1	p2	(AT)10	20	818	837	GAGAGCATGAAGAATGAACCC
scaffold4135_23.5	1	p2	(AG)6	12	54	65	TGGTGAGATTTGTGGTTTGG
scaffold4211_12.1	1	p2	(AT)6	12	176	187	TCGGTCGAAACCGAATAAAC

scaffold4517_11.1	1	p2	(TA)8	16	485	500	ATTGGCAAAATATCACCGGA
scaffold4547_12.1	1	p2	(AT)6	12	55	66	CAATAATTTTGTTTCCCACCAA
scaffold4626_12.8	1	p2	(AC)7	14	236	249	AAGTCCACCACGATGTCCTC
scaffold4628_13.4	1	p2	(TA)9	18	1079	1096	TTTCACAAACCACGTTGACA
scaffold4661_18.0	1	p2	(CT)7	14	341	354	CCCTAACTCGACCCAGATCA
scaffold4751_14.3	1	p2	(TC)8	16	1454	1469	GCTGAGTTTTGAGGATTGGG
scaffold4790_16.1	1	p2	(AG)6	12	3258	3269	CGCTAAGATGGAGTTTTCGG
scaffold4808_11.4	1	p2	(TC)6	12	34	45	GGGATGCCATTCGTTAGTCC
scaffold5156_12.2	1	p2	(AT)7	14	1019	1032	TGGAAGATTAAGAGGCCCAA
scaffold5238_13.0	1	p2	(TC)6	12	48	59	CCCCTTTGTCAACTTAGGCA
scaffold5329_11.0	1	p2	(AT)6	12	587	598	ATTCCTAGGCGGCATTCTGT
scaffold5553_14.7	1	p2	(TG)10	20	302	321	CGGTGGAGTGGTTTCACAGT
scaffold5614_15.9	1	p2	(TA)8	16	1933	1948	CAGAGGATCCAAATCCGAAG
scaffold5636_13.9	1	p2	(AT)6	12	54	65	GCTACCTTATTGATCCATTCCTC
scaffold5978_13.4	1	p2	(AC)8	16	42	57	GCATGAAATTGTGTATTTTGGTG
scaffold6020_16.6	1	p2	(GA)8	16	2628	2643	TGCCATGCACAGTTTTTCTC
scaffold6052_11.1	1	p2	(CT)8	16	52	67	TCTCTCTTTTTGGTTGGTGGA
scaffold6064_14.9	1	p2	(TA)8	16	1004	1019	TGTGAATTGGGTATGTGAATCAT
scaffold6255_13.3	1	p2	(AT)7	14	756	769	TGCAATCTCAGCCACTCATT
scaffold6310_14.4	1	p2	(TG)7	14	4263	4276	TGGTCGTTGACACGACAGAT
scaffold6349_13.7	1	p2	(AT)7	14	466	479	TGCAAGAATGGGTTTTTGAAT
scaffold6381_11.9	1	p2	(AT)7	14	250	263	TTTCGTGTTGCCATTGATCT
scaffold6512_15.5	1	p2	(AG)9	18	231	248	GAGCACTCGAAAAGTAGCGG
scaffold6602_12.8	1	p2	(TA)6	12	95	106	CGAGGAGAACCTTGGAGTGA
scaffold6618_10.5	1	p2	(AG)6	12	54	65	TGAGTTTCAATTGCGTAGTCAAA
scaffold6619_15.4	1	p2	(AG)6	12	415	426	TCACAGACGGAGAGAGACACA
scaffold6738_16.2	1	p2	(AT)7	14	1345	1358	TCTCATTCTCCATCAGCCAA
scaffold6920_13.8	1	p2	(TA)6	12	156	167	TATTTTGGACGATTTTGCCC
scaffold6952_14.0	1	p2	(CT)6	12	493	504	TCGTCCGCTGCAGTAATATG
scaffold7013_13.2	1	p2	(TA)7	14	550	563	TGTCTTGCAGGCAATTCATAA
scaffold7196_16.8	1	p2	(TA)6	12	627	638	ACGGAAATGACCCTCATTCA
scaffold7245_14.4	1	p2	(TA)6	12	239	250	CCGATCCCACCTTGTTTTTA
scaffold7348_15.5	1	p2	(TA)8	16	380	395	TTCATTTGCCTAAAATGCCC
scaffold7671_15.8	1	p2	(CT)6	12	1325	1336	AAGGTGAACTCAAACGGCTC
scaffold7698_16.2	1	p2	(GA)7	14	1656	1669	ACAACTGGTTTCATCCGTGG
scaffold7781_16.5	1	p2	(TA)6	12	1023	1034	CTTGTTCAGCGTCACAAGGA
scaffold7789_12.7	1	p2	(TA)6	12	151	162	CAGATATTACGGTTGGCGCT
scaffold7795_12.6	1	p2	(TG)6	12	54	65	TGGAAATTAGACGATTTACACAAAA
scaffold7872_13.4	1	p2	(TA)8	16	1620	1635	ATTGGACACAACCCACACCT
scaffold7881_14.8	1	p2	(AT)6	12	1056	1067	CCTCTCTTTCCCCTCCATTC
scaffold7900_13.9	1	p2	(AG)9	18	71	88	AAAAGGTGGTGGTGGTGTTC
scaffold7903_15.7	1	p2	(AG)7	14	316	329	GTTCTGCCCTCCTTTTCCTC
scaffold7944_15.0	1	p2	(AG)6	12	466	477	ATTCCCCCAAAACCGAATAA
scaffold7956_13.3	1	p2	(TA)9	18	266	283	ACTAGATCACTCGGCCAACC
scaffold8351_16.2	1	p2	(AG)6	12	55	66	TGGAAATTCATCCACGTTCA
scaffold8352_11.8	1	p2	(TA)7	14	76	89	GCATACATGAATGGATGTGATTT
scaffold8401_11.5	1	p2	(AG)6	12	157	168	TTGGGCTCGAGTGAAAAGAT
scaffold8559_13.9	1	p2	(GA)6	12	265	276	TCCCAAACTTCGTGTGTGTT
scaffold8644_10.7	1	p2	(AC)8	16	47	62	GAAAAGCTTGGCCATTCAAC
scaffold8647_13.5	1	p2	(TA)6	12	831	842	CCCCCTTAATTACTTTGTCACG
scaffold9000_15.0	1	p2	(TC)6	12	1431	1442	GAAACCCGCTGTTTGGTTTA
scaffold9015_16.4	1	p2	(AG)6	12	78	89	TTTTGTTTGTTCCCAGGTTG
scaffold9063_17.2	1	p2	(TC)8	16	5059	5074	GCCCATTATGGAATCTCACG
scaffold9386_16.2	1	p2	(TA)6	12	398	409	ACTTTGAATCACAGCCGTCC
scaffold9656_15.1	1	p2	(CT)7	14	53	66	AAACAACAATTCATCAAATATCCG
scaffold9734_14.4	1	p2	(CT)6	12	273	284	ACTTTGCATCCCAGTCAGGA
scaffold9750_14.4	1	p2	(AG)9	18	2311	2328	TCCTGCATATTTGAGGTCCC
scaffold9825_15.2	1	p2	(AG)7	14	639	652	TCACCGGAGAAGCTTAGGAA

scaffold9930_12.2	1	p2	(TC)6	12	154	165	GGCTGCGATTTGTACTCTCC
scaffold9955_16.7	1	p2	(GT)8	16	2157	2172	GCAAATGTAGCACGCAGAAA
scaffold10006_19.5	1	p2	(TA)6	12	725	736	TTGTGCACTTCATATCGCGT
scaffold10021_17.7	1	p2	(TC)7	14	53	66	AAGTGAGAATGATGAGGGCG
scaffold10026_12.8	1	p2	(GA)7	14	674	687	TTCCTTTAGGCCATCCACAG
scaffold10202_18.3	1	p2	(TA)9	18	102	119	CACTGACATCCATCCATTGC
scaffold10504_12.8	1	p2	(AT)6	12	745	756	GATAGTATGCCAATTTTTCGTGA
scaffold10505_13.1	1	p2	(AT)9	18	391	408	TGGCACATTATTGGTCTCTCA
scaffold10509_11.7	1	p2	(AT)7	14	209	222	CGTACGTGTGTGTGTGCATT
scaffold10556_13.4	1	p2	(AG)6	12	1050	1061	AGAAGAGCAAATGGTGGTGG
scaffold10610_13.9	1	p2	(GA)6	12	103	114	CGAATTTGGTGTTGGAATTG
scaffold10725_10.5	1	p2	(TA)9	18	442	459	CAACGGTTGTCATTGTTTCCT
scaffold10927_11.0	1	p2	(GT)6	12	950	961	AACATTTCGTGGCCTTGATT
scaffold11109_15.2	1	p2	(AT)8	16	205	220	CGGCCGGAATATCTAAAGTG
scaffold11245_15.3	1	p2	(AT)6	12	100	111	AATATTGGATGTCTTGCGGC
scaffold11632_13.4	1	p2	(GT)6	12	147	158	TTCCCAAATTTTGATTCCGA
scaffold12076_16.0	1	p2	(TC)7	14	212	225	TTGCTTTCCAAAAAGTTGTACG
scaffold12338_19.0	1	p2	(TA)7	14	185	198	CGTGGTTCGGGTATTCACTT
scaffold12523_15.6	1	p2	(TC)7	14	1289	1302	CAATTTCCATGTTCCGCTCT
scaffold12579_14.6	1	p2	(TC)9	18	54	71	CATCCCAAACTCTCTCGCTC
scaffold12584_13.1	1	p2	(GA)9	18	194	211	CAACATTCCCCTCAACACCT
scaffold12609_15.7	1	p2	(TC)7	14	53	66	CGTCGATCCTTCCTCATCTC
scaffold12818_12.8	1	p2	(TC)6	12	406	417	TGCACTTGAGTTGCTTTTGC
scaffold12829_13.2	1	p2	(CT)6	12	190	201	CAATAACCCTTGGCTCGAAA
scaffold13262_12.2	1	p2	(CT)9	18	641	658	TCTTTATTTCCACCCCCTCC
scaffold13418_14.1	1	p2	(TC)6	12	461	472	TCTTCCCCAAATTGGTTTCC
scaffold13611_11.1	1	p2	(CT)6	12	250	261	CGTTGTTTGCTTCCAATTCA
scaffold13755_15.4	1	p2	(AT)7	14	1110	1123	AACGGACGTGTTTTGGCTAC
scaffold13867_12.0	1	p2	(GT)7	14	53	66	TCTGTGCTCTCTTTCTCAGTCG
scaffold14014_13.2	1	p2	(CT)6	12	257	268	TTCACCACCTAAAGAAGGGC
scaffold14047_13.9	1	p2	(TC)7	14	53	66	TTGGGAGGATTTTCTCTTGC
scaffold14058_10.3	1	p2	(CA)6	12	339	350	TTCCTTCATCTGTCACGTCG
scaffold14070_14.4	1	p2	(TA)9	18	542	559	TTATGAAATTCCGACGAGCA
scaffold14173_11.4	1	p2	(GA)9	18	641	658	TGACGAGAGCAGAGCAGAGA
scaffold14271_15.7	1	p2	(GA)6	12	63	74	TGTCCTGTTGAGGTGGAACA
scaffold14290_16.7	1	p2	(TA)6	12	1980	1991	TCCCACGTAACGAATTTTCC
scaffold14393_18.3	1	p2	(GA)7	14	1373	1386	ACAAAAAGCAGCACAACGTG
scaffold14571_15.9	1	p2	(TA)8	16	328	343	ACTGTCCTCTTAGACCGCCA
scaffold14576_13.7	1	p2	(AT)6	12	737	748	GATCGGCACGATAAGGACAC
scaffold14583_17.9	1	p2	(AT)7	14	696	709	TGGTAGGCGAACTCGTAACC
scaffold14676_12.1	1	p2	(AT)7	14	320	333	GTTGCCACCAATGTGTTTCA
scaffold14735_14.1	1	p2	(CT)6	12	1641	1652	TCAATGTTTTGCGTTTCCAA
scaffold14770_13.8	1	p2	(AT)6	12	138	149	AACAATGCAAGTGATATTCATCG
scaffold14976_15.1	1	p2	(CT)6	12	167	178	GAGCTTGCACTCAGAGAGCTT
scaffold15213_14.6	1	p2	(AG)7	14	53	66	GTGACCCTATGACGCCAAGT
scaffold15319_15.4	1	p2	(TA)6	12	942	953	TCCCGCTTCATAGCAAATTC
scaffold15396_15.5	1	p2	(AG)8	16	1941	1956	ATAAGGGTTTGTGCTCCGTG
scaffold15494_19.2	1	p2	(CT)8	16	580	595	AGTGCGTGCTTGTTTCAATG
scaffold15586_14.3	1	p2	(TA)6	12	533	544	TGGCGTTTGATATTTGAGAAGA
scaffold15592_15.7	1	p2	(TG)7	14	1084	1097	TTTCCACACCACGTCAGCTA
scaffold15604_13.1	1	p2	(TC)7	14	636	649	CGGTTGTGATAACGATGACG
scaffold15653_13.1	1	p2	(TG)6	12	251	262	CGTGTTCTTCACTCATCCCA
scaffold15658_16.5	1	p2	(AT)6	12	1223	1234	GCACTGAAACGCCAAAAGAT
scaffold15744_15.0	1	p2	(TC)6	12	108	119	CTCCCCAAACCCACTATCAC
scaffold15796_16.2	1	p2	(CA)6	12	2254	2265	GGCATGAAGGAAACCAAAGA
scaffold16102_19.0	1	p2	(AG)7	14	1097	1110	GTGACTGTGAGGGAGTGGGT
scaffold16183_16.3	1	p2	(AG)6	12	42	53	GATGAACTCTCTTGGGTGGG
scaffold16380_14.5	1	p2	(AG)8	16	2267	2282	AGAATGGCACAGACTCCAGAA

scaffold16415_18.1	1	p2	(GA)6	12	298	309	TCCGACTTACCACCACACAA
scaffold16429_15.3	1	p2	(GA)7	14	54	67	AACCCAGAAGAAAGACAGCAA
scaffold16490_10.1	1	p2	(AT)9	18	714	731	AGACTCATGCGGCTCTTGAT
scaffold16617_19.7	1	p2	(TA)6	12	510	521	TCTGTCGATCAACACCACAAA
scaffold16628_13.0	1	p2	(AT)8	16	712	727	TCGAGTGAGCATTTTGGATG
scaffold16695_15.3	1	p2	(CT)9	18	460	477	CCTCCAAATCTAACCCCTCC
scaffold16976_13.7	1	p2	(GA)7	14	665	678	AAACACACACACCGTCTCCA
scaffold16993_17.1	1	p2	(TA)6	12	145	156	CGTGCATTCCTACCCTATTTG
scaffold17025_17.7	1	p2	(TC)6	12	106	117	TCTCATTCACGCTTTTCAGC
scaffold17035_13.6	1	p2	(CT)6	12	2315	2326	AAGGAGTCCTCTCAGTTTCATCA
scaffold17725_11.1	1	p2	(AG)6	12	277	288	CCTTGAAGACAATGAAATTTTGG
scaffold17815_12.7	1	p2	(AG)6	12	146	157	TGTTATCCTTTGTGAGCCCC
scaffold17887_14.0	1	p2	(GC)6	12	210	221	GTTCAAGTCCGGCTCTTCAG
scaffold17896_15.4	1	p2	(TC)6	12	128	139	GATTTGCACCTTCCACGAAT
scaffold17935_10.1	1	p2	(AT)7	14	185	198	GTCGGAACACTTCGTGTTGA
scaffold18182_11.5	1	p2	(TA)7	14	184	197	ACACATTTTTCTTTTGGGCG
scaffold18195_18.3	1	p2	(GA)7	14	54	67	CATGAGAGAGAGGGCTGGAA
scaffold18226_11.3	1	p2	(CT)6	12	75	86	CCCCCAAAGTTATGGTGAAA
scaffold18386_13.8	1	p2	(GT)6	12	109	120	AGTGCACGTCAGAGTTGGC
scaffold18474_15.9	1	p2	(TA)7	14	400	413	CAATCAATCTCAGCCGTTTG
scaffold18527_15.1	1	p2	(AT)8	16	105	120	AAACATTTTACCACATGATTAAGACC
scaffold18576_15.8	1	p2	(TA)6	12	477	488	ACCAATTGCCCATCTGCTAC
scaffold18624_12.6	1	p2	(AT)8	16	2083	2098	CACCAAACTGATTAAAATCCCAA
scaffold18640_12.5	1	p2	(TA)7	14	54	67	GGTTTCACGTCGGAATATTGA
scaffold18659_17.0	1	p2	(AT)6	12	1468	1479	TCCGAATATGAAATCGGGTT
scaffold18668_12.8	1	p2	(TG)7	14	1222	1235	TCGAGAAGTTGTTTGTCTCAACA
scaffold18787_12.1	1	p2	(CA)6	12	208	219	GGTCCCCTCCTAACTTTGCT
scaffold18794_15.1	1	p2	(TG)6	12	461	472	CCCCGAGGAAGCTAGAAAAA
scaffold19150_15.0	1	p2	(TC)6	12	109	120	TAATCCACTCCCACTTTCCG
scaffold19158_15.9	1	p2	(GA)6	12	56	67	CGGGCAGAGAGAGAGAACC
scaffold19324_12.0	1	p2	(AG)11	22	374	395	GGGTGGGTTTGGAGAAGAGT
scaffold19347_14.4	1	p2	(AT)7	14	416	429	GGACATTCCGTGGAGTTTGA
scaffold19477_14.8	1	p2	(CT)6	12	314	325	GTCACGTCAGCAAACCATTG
scaffold19491_14.8	1	p2	(AT)6	12	1301	1312	GAGATAGGGGTTGGGGTGTT
scaffold19757_16.2	1	p2	(TC)10	20	102	121	ACGTTGGACCTGAAAGAGCA
scaffold19937_15.1	1	p2	(TA)6	12	195	206	AACCTTAACAAAATGAATCATCAAA
scaffold19974_18.0	1	p2	(AT)6	12	81	92	TTCCAACTCCATTTGCAATACT
scaffold20002_17.4	1	p2	(TA)7	14	152	165	AAAGCCTACCTTGCTTCCGT
scaffold20074_13.5	1	p2	(GA)8	16	172	187	GGAGAAACTTGCTTCTTGGC
scaffold20104_13.2	1	p2	(TA)10	20	1093	1112	GATCCACATGCATGAAATCG
scaffold20185_15.1	1	p2	(AG)6	12	570	581	AATAACAAATGGCCACGGAA
scaffold20444_16.2	1	p2	(AC)6	12	322	333	CAAAGGAAGGGCAGAAACAA
scaffold20565_11.9	1	p2	(GA)9	18	486	503	TGCATTCCTTTCCAGTCTCA
scaffold20626_15.3	1	p2	(AT)6	12	1201	1212	CCGTTCCGTTCCATAAATGA
scaffold20660_14.1	1	p2	(AG)7	14	900	913	CAGGCCAACTCCTATCTGGA
scaffold20704_12.8	1	p2	(TC)6	12	182	193	TAAAAATGGGAGATGAGGCG
scaffold20825_11.7	1	p2	(TA)7	14	729	742	TTTTAATTCATTACTCATATTTGCATC
scaffold20936_12.9	1	p2	(CT)6	12	46	57	CTCTCTCCTGCGTCTCTCTCA
scaffold21030_12.2	1	p2	(AT)9	18	831	848	TGCTATTGAAAATGATCCCACA
scaffold21236_14.6	1	p2	(AG)7	14	1914	1927	CAAGACCTACCGAGCTTCTGA
scaffold21289_15.3	1	p2	(TA)6	12	3727	3738	TCGAAGGGGATTTTATGTGG
scaffold21314_13.4	1	p2	(TA)8	16	151	166	TAGAAATGGGATACGGACGG
scaffold21318_16.3	1	p2	(CT)6	12	2654	2665	TTTGACAGACAAATCGCTCG
scaffold21423_10.9	1	p2	(TA)10	20	111	130	CGCAGATCTAATGGTCCAGA
scaffold21430_13.6	1	p2	(TA)8	16	105	120	GCACCACAAACATGTCACAA
scaffold21500_15.1	1	p2	(TA)7	14	326	339	CGGATTGTAAATCGGGAGAA
scaffold21518_14.4	1	p2	(TA)7	14	313	326	TCTTCGTCGTACAACTCGTCA
scaffold21688_15.8	1	p2	(GA)9	18	536	553	ATGCCCATTCCAAAACACAC

scaffold21713_11.3	1	p2	(AG)7	14	54	67	CGCCTTTTCACCTCAAATTC
scaffold21799_14.1	1	p2	(AT)7	14	143	156	GCTACTTCCGACTCTCTCGC
scaffold21832_12.9	1	p2	(TA)8	16	1049	1064	TCTTCCACGATCTCCCATACA
scaffold21974_19.3	1	p2	(TC)6	12	55	66	TGCTAATCAGAAACTTGGAGCA
scaffold22095_13.0	1	p2	(AT)9	18	6948	6965	CATGGTTTGAGACGGATTGA
scaffold22126_16.2	1	p2	(GA)6	12	267	278	GATATTGACGGTTGGTTGGC
scaffold22303_17.6	1	p2	(AG)7	14	510	523	ACGCAAGCGATATGGAAAAG
scaffold22306_11.5	1	p2	(CG)6	12	52	63	CATGGGTGGTATGGTGTGG
scaffold22391_13.0	1	p2	(GA)6	12	86	97	GATCGGTGAGGAGATGAAGG
scaffold22631_14.2	1	p2	(AT)8	16	1517	1532	AAGTTGGCTAGGTGGCCTCT
scaffold22751_13.1	1	p2	(AT)6	12	54	65	TTTACGTGTTAAGCCTTGGGA
scaffold22868_14.3	1	p2	(AG)11	22	168	189	ATGCGTGTGTGTCTGCATGT
scaffold23028_10.7	1	p2	(CT)6	12	24	35	CTTCTCTTCCACATCCGGTA
scaffold23082_15.0	1	p2	(CT)6	12	100	111	TTCGATGTTGTAACGGAGACA
scaffold23170_14.8	1	p2	(TC)7	14	52	65	TGGCTCTCACACTCACTCTCA
scaffold23350_12.1	1	p2	(TC)6	12	737	748	TCGATCGATAATAACGCTTTCA
scaffold23417_14.4	1	p2	(AG)9	18	240	257	AGATTCCGTCCGATTTAGCA
scaffold23575_15.8	1	p2	(GA)6	12	3568	3579	CTTCCCACATGTCGTTCCTT
scaffold23652_15.3	1	p2	(TC)6	12	664	675	GTGGGTGCAGTTGGATTACC
scaffold23713_17.6	1	p2	(AG)6	12	1626	1637	GCTGCGAAGAACACAATCAA
scaffold23732_15.9	1	p2	(TC)8	16	315	330	TGTGGAAACAAGTGCAGAGG
scaffold23750_12.1	1	p2	(AG)6	12	151	162	TCGAAACAGAAAATCCGAGG
scaffold23881_16.2	1	p2	(TA)6	12	56	67	GGGGCGTGACAATATCCTAA
scaffold23894_10.3	1	p2	(TA)7	14	107	120	GTCGCTTGAATTGCGACATA
scaffold23961_11.5	1	p2	(TC)6	12	271	282	ATGTGGTCCCAAACTCTCCA
scaffold23963_13.3	1	p2	(TA)6	12	875	886	CCGGCTCTGGGTACAGATTA
scaffold24071_10.1	1	p2	(CT)7	14	47	60	CACTCACTCTCACTAGCCGC
scaffold24205_16.1	1	p2	(TC)7	14	54	67	ACGCATTCAAAGCTGAAGAT
scaffold24355_15.5	1	p2	(TC)8	16	3453	3468	AGACTGGGGAATGGCTTCTT
scaffold24430_13.8	1	p2	(TA)9	18	325	342	TTGGGAATTCAAAATGATTCG
scaffold24613_13.4	1	p2	(AG)6	12	162	173	ACTCGCATTAATGAGCCGTC
scaffold24667_14.6	1	p2	(AC)7	14	3151	3164	TTTGTCAACTTCCCTCACCC
scaffold24685_16.0	1	p2	(AC)8	16	1605	1620	AGCACTGTGAGACTGAGGCA
scaffold24712_11.9	1	p2	(TA)7	14	84	97	AAGGCATCAAAGTTGTCGAT
scaffold24832_10.0	1	p2	(TC)6	12	77	88	CGAGGGCATTATGGGAAGT
scaffold24883_15.3	1	p2	(CT)10	20	194	213	AATGATAATCTTCGCCGTGG
scaffold24945_16.0	1	p2	(TA)7	14	90	103	GCAATAAATCCACGTACAGGAAA
scaffold24992_12.5	1	p2	(TA)9	18	276	293	AAAACACCTCCTTAGGTGCAAA
scaffold25112_16.3	1	p2	(TC)7	14	54	67	GGAAATGAAAGGCCAAGTCA
scaffold25265_10.5	1	p2	(TA)6	12	334	345	CGAAGAACACACACTTTTGGG
scaffold25281_11.2	1	p2	(AT)7	14	54	67	ATCACCAACTGGCGAGAAAT
scaffold25398_17.5	1	p2	(CT)6	12	499	510	ACCCTATCTGCCCCAATACC
scaffold25401_17.5	1	p2	(CT)6	12	71	82	CAAATGGCCAAGAAAGTTTACA
scaffold25421_14.5	1	p2	(CT)6	12	56	67	GGGGACTTTTCACTTTTGGC
scaffold25507_12.4	1	p2	(GA)6	12	107	118	TGAAGAATTCCCTTGGGTTG
scaffold25519_19.2	1	p2	(AG)7	14	192	205	TTTCTAACGATGATGGAAAAACAA
scaffold25718_12.1	1	p2	(AT)7	14	564	577	TCAATGGTTTTGGTTTGTTCC
scaffold25729_16.1	1	p2	(CA)6	12	2978	2989	ATTTCACCTGCAGAAACGCT
scaffold25792_13.9	1	p2	(GA)10	20	1178	1197	TTGGCCTTTCTTGATTGTCA
scaffold25870_21.8	1	p2	(TC)7	14	496	509	TCCACTTAGGTTGGCTTTGC
scaffold25893_16.0	1	p2	(AT)6	12	6106	6117	TTTCTCTTCACACGTTTGGATT
scaffold26018_11.9	1	p2	(GA)6	12	297	308	AGACAAGAGCCGAAAAGTCG
scaffold26053_16.5	1	p2	(CT)6	12	38	49	ACTCTATAGCAAGATCTCACGCA
scaffold26077_14.0	1	p2	(AT)8	16	3308	3323	ACATGATTCGTCGGGTCTTC
scaffold26197_13.9	1	p2	(TA)8	16	464	479	CACATTAAGAGGAGGTATCATTTGAA
scaffold26225_17.2	1	p2	(TC)6	12	270	281	AAGTTGGGCTAAGTGGAGGG
scaffold26343_18.6	1	p2	(GA)6	12	914	925	AGTAGTTCCGGTCGGGTGAT
scaffold26943_13.7	1	p2	(TC)7	14	538	551	CTGTTAGGCCCATGTCGTTT

scaffold27238_15.1	1	p2	(TA)8	16	779	794	TATGTTGGACCAAAAAGCCC
scaffold27243_17.9	1	p2	(CT)8	16	507	522	CGTTGTTTCCTCACACCCTT
scaffold27244_13.3	1	p2	(AT)6	12	50	61	CATTTCATTTCAGGAGCTTCG
scaffold27248_10.3	1	p2	(AT)7	14	309	322	TCCATTTTTATCTTCTCTATCTTCCC
scaffold27280_11.3	1	p2	(AC)6	12	328	339	GGCAGCAATCAATTGGAAAT
scaffold27421_16.2	1	p2	(TA)9	18	290	307	AGATCATCACGTAAACGGGG
scaffold27545_16.5	1	p2	(AT)7	14	355	368	ACAGCTTACACCGTTGAGCA
scaffold27709_16.3	1	p2	(GA)6	12	517	528	GAGCAAGGAGAAGTTCGTGG
scaffold27756_17.8	1	p2	(AT)12	24	1058	1081	GGTGAACATTGGGAGCAAAT
scaffold28165_11.9	1	p2	(TA)7	14	340	353	ACCGATTGTTGCATTTTAAGTT
scaffold28175_14.2	1	p2	(AT)6	12	824	835	AAGTTGTGTCCCCCCAACACT
scaffold28277_17.2	1	p2	(AG)6	12	55	66	TGTATTTAATTGAATGCTAGAGAGAG
scaffold28322_13.6	1	p2	(GT)6	12	55	66	GGGTAACTTGGTTCTGTAACCG
scaffold28370_12.0	1	p2	(TC)6	12	55	66	CCCACTAACCCTTCATCACC
scaffold28421_10.0	1	p2	(TC)6	12	285	296	TGTGGAATATTGTCCCGGAT
scaffold28565_10.2	1	p2	(TA)9	18	102	119	CTTAGCCGAGAAGAACCGTG
scaffold28616_10.2	1	p2	(TA)6	12	55	66	CTCCAAATGATAAAATCGTGG
scaffold28682_12.6	1	p2	(TA)6	12	408	419	AGTCTTCACAAGCGGGTGTC
scaffold28700_12.6	1	p2	(TA)8	16	1029	1044	TCAATTTGTGTCTTATAAATTAAATGC
scaffold28762_11.4	1	p2	(TA)6	12	185	196	TTCCCTAGGATGAAAACTTGC
scaffold28851_15.9	1	p2	(AT)6	12	55	66	CGAACGGTTGGAATATCTAAAG
scaffold28911_16.2	1	p2	(CT)7	14	781	794	CAAAACCCAAATCCCCTTTT
scaffold29014_12.6	1	p2	(TA)6	12	55	66	AGTTATGCGTATTGTTACCTTCATT
scaffold29070_10.9	1	p2	(GA)7	14	147	160	CTTTGCGACGTAATTCCCAT
scaffold29112_15.1	1	p2	(CT)6	12	461	472	TGTATCAGTCACCACCTCCACT
scaffold29162_11.8	1	p2	(AT)8	16	106	121	TTGTGCCTTTTATTTGAGTAAGACA
scaffold29163_13.4	1	p2	(AT)8	16	488	503	TTCAGCCTTTTTCATGTGGA
scaffold29164_10.9	1	p2	(TA)6	12	126	137	GCTTGTAATTTTTGGCTGGC
scaffold29178_12.8	1	p2	(TA)10	20	74	93	CGGGTTATTACCTGATTGCG
scaffold29216_14.0	1	p2	(CT)6	12	280	291	ACCAACCCATCAAGAATCCA
scaffold29242_16.6	1	p2	(CA)7	14	149	162	AAACGAAAAAGCCGAAACTG
scaffold29377_19.5	1	p2	(GA)6	12	55	66	TCAAGATGAGGAATGAAAAAGAGA
scaffold29487_13.1	1	p2	(TA)7	14	54	67	GGAAATAAGGAGGTGTTATGAAAGG
scaffold29563_10.8	1	p2	(GA)6	12	55	66	GGTGATGGTTGGTGTTGATG
scaffold29678_12.7	1	p2	(AG)6	12	55	66	AGGGGGAAGAGGTTGAAGAC
scaffold29824_16.7	1	p2	(AG)6	12	213	224	TTTGATAGAGCCGGATTTGG
scaffold29880_16.2	1	p2	(AT)9	18	1913	1930	CGAAGTTTGCATTTTAAGATGAGTT
scaffold30087_15.1	1	p2	(AT)8	16	626	641	TGTTTTGTCTTTGTGGTGCG
scaffold30637_10.1	1	p2	(AT)10	20	50	69	TGGTTACTGTTACGTATGCCAA
scaffold30666_11.8	1	p2	(CT)9	18	569	586	TAACCGTTGTTTTCCCCTCC
scaffold30669_16.5	1	p2	(CT)7	14	1482	1495	ACCATCAAGGTCAAACCTGC
scaffold30692_17.7	1	p2	(AT)9	18	1571	1588	GCTGTTGTGTTGGCATTAGC
scaffold30807_14.9	1	p2	(AT)9	18	349	366	AATGGGGACATCTGGTGTGT
scaffold30864_10.4	1	p2	(AT)6	12	254	265	AGGGAGAAGATGAGGAGGGA
scaffold30982_16.9	1	p2	(AT)6	12	3530	3541	CGCCGTTTCACCATTTTATT
scaffold30986_16.9	1	p2	(TA)7	14	3593	3606	GGGCCCACATTAGCTGTCT
scaffold31055_16.3	1	p2	(CT)9	18	5870	5887	AATTTAGTCGGCCGGATTTT
scaffold31144_12.9	1	p2	(AT)9	18	103	120	TTGAACCGTGTTACCCTTCC
scaffold31172_13.2	1	p2	(TA)7	14	489	502	GATTCTCCAAATCTGACGGC
scaffold31482_14.2	1	p2	(TA)8	16	2153	2168	TTTTCCCCAAAACACCTCTG
scaffold31497_16.4	1	p2	(TG)7	14	843	856	TCTTCTCCAACCCACAAACC
scaffold31576_15.2	1	p2	(AT)6	12	55	66	TCCTAACAACAAAAGATAAAGTCAAC
scaffold31729_17.7	1	p2	(CT)9	18	196	213	ACCACCACCACCTCAACATT
scaffold31755_12.2	1	p2	(GT)9	18	103	120	TCTGCGGTACATCCAAATGA
scaffold31756_16.4	1	p2	(CT)7	14	202	215	TCACACTCACTCTCACTAGCTGC
scaffold31788_15.6	1	p2	(TC)7	14	492	505	AGATGTTCCCAGAGTGGTGG
scaffold31824_14.6	1	p2	(TA)8	16	485	500	ATTACCTCCACGCCGAGAG
scaffold31917_14.4	1	p2	(TC)8	16	1963	1978	GTTGGAAAATGGTGGAATGG

scaffold32086_13.9	1	p2	(TC)9	18	493	510	TGCACCCCAAGATGGTAAAC
scaffold32184_12.1	1	p2	(TA)7	14	488	501	GCTTGCTGAGTTGGCATGTA
scaffold32321_10.7	1	p2	(TA)12	24	482	505	ATTTCGAAGATCAACGGACG
scaffold32385_13.2	1	p2	(TA)10	20	770	789	AAAAATGTGCATGCAACTGA
scaffold32440_15.7	1	p2	(CT)7	14	63	76	TCTCTCTTTTTGGTTGGTGGA
scaffold32447_13.2	1	p2	(AT)6	12	203	214	GAGGTTTTGGGAGAAGGAGG
scaffold32610_11.9	1	p2	(TG)8	16	821	836	TCAGTGCTGAACGTGTCAAA
scaffold32640_17.1	1	p2	(AT)7	14	302	315	CGGTCTACCAGTCCGTGAAT
scaffold32686_10.9	1	p2	(AT)10	20	48	67	AGTGTTTTGACATGATTACTCGTC
scaffold32799_13.2	1	p2	(TA)12	24	1740	1763	AAATATCGGCCGTCAGATTG
scaffold32886_15.2	1	p2	(TC)9	18	95	112	ACTGCAGAAAAATTCACGCC
scaffold33031_10.2	1	p2	(CT)6	12	119	130	ACACATGGCCACTAACACCA
scaffold33109_14.7	1	p2	(TA)6	12	1223	1234	TTTGTTCTCGTTCAAACCCC
scaffold33135_11.2	1	p2	(CA)6	12	55	66	CTCTCACACACGCAGTTAGACA
scaffold33204_15.2	1	p2	(AT)9	18	3309	3326	ATTTAATGTCCCACCCCGAG
scaffold33339_13.1	1	p2	(TA)8	16	2780	2795	CTCGCCGCTTAAAATTGTGT
scaffold33458_10.0	1	p2	(AT)7	14	230	243	TTCTTGGCATCCAGTTCCTT
scaffold33501_18.8	1	p2	(TA)7	14	52	65	AAGGGGGTTATTAGTGGATCA
scaffold33588_14.5	1	p2	(AT)6	12	995	1006	TTGGTGTTATGGATTGTGTGA
scaffold33613_14.8	1	p2	(TA)6	12	55	66	ACTATGTGCCCTCGCCAATA
scaffold34095_15.5	1	p2	(AG)7	14	215	228	CTGAACATTGCCTGCTTGAA
scaffold34230_15.7	1	p2	(TC)13	26	510	535	AGCCTCACTGCAGCTGTCTA
scaffold34316_18.1	1	p2	(TA)6	12	55	66	TCGTCATTTATACAAAAACAATTCC
scaffold34388_14.5	1	p2	(TA)9	18	163	180	CCCCTCGTATGCACTCAACT
scaffold34491_19.2	1	p2	(GA)8	16	216	231	CACCATCATCCTCAGAGCAA
scaffold34494_17.0	1	p2	(TA)8	16	623	638	CGTGAATGAAAGTGATTGCG
scaffold34497_12.4	1	p2	(TA)6	12	91	102	AGATTTGGGCAGTGTGGTGT
scaffold34548_16.8	1	p2	(CA)7	14	38	51	GCGAATCGAACGAATCTGA
scaffold34600_12.6	1	p2	(AT)8	16	2999	3014	AACACCTCCTTATTTCCTAACTTCA
scaffold34616_11.1	1	p2	(CT)6	12	284	295	CTCTCAGCTCTTTTGCCTGG
scaffold34701_10.7	1	p2	(AG)6	12	219	230	TGTTCGTTGGTGGAGTTGAG
scaffold34734_14.6	1	p2	(GA)6	12	55	66	GTCGGAAAAGCTTGGATGAA
scaffold34894_11.4	1	p2	(TC)6	12	47	58	TCTTTTGGTAGGTGAATGTATTGAA
scaffold35174_11.2	1	p2	(AC)6	12	219	230	TCGTGTCAGAAATCGTCAGC
scaffold35218_15.9	1	p2	(AT)8	16	540	555	TCGCCTTGTTTAGGAGAGGA
scaffold35323_14.5	1	p2	(CT)6	12	215	226	ATATGGCAATGGGACCAAGA
scaffold35350_13.8	1	p2	(GA)7	14	460	473	TTCATCAACATGCAGCCATT
scaffold35374_12.7	1	p2	(AT)6	12	75	86	GGTGCTTGGTGAAGGAAGTG
scaffold35399_14.9	1	p2	(AT)10	20	283	302	TGCAGTTGAGATGTCCTTGC
scaffold35412_13.8	1	p2	(AT)6	12	2772	2783	ACATGGGCCAAATGAGAGAC
scaffold35419_14.1	1	p2	(CT)8	16	3146	3161	TTTTCAAGGAGGGGTGAATG
scaffold35439_10.6	1	p2	(AT)7	14	271	284	TATGGATTATCACCGGATCG
scaffold35482_20.2	1	p2	(GA)6	12	191	202	TAAATGGCAGTGTGGGTTGA
scaffold35966_10.2	1	p2	(AT)6	12	181	192	TCAACAAAATTCTAAAATTGCAGG
scaffold36081_12.6	1	p2	(TA)8	16	40	55	CGGATTTAAGGGTTATTACCTGAT
scaffold36127_11.0	1	p2	(TC)7	14	252	265	GAACACGAGAGGAAGAACGC
scaffold36213_15.1	1	p2	(TA)9	18	341	358	GGCGAATGATGTTTCTAGGG
scaffold36244_16.4	1	p2	(AG)9	18	293	310	CGCATTATGGTTATGCGAAA
scaffold36295_13.7	1	p2	(AT)7	14	1698	1711	AACGGTTTGAGCCTATTGAGT
scaffold36339_12.6	1	p2	(GT)6	12	445	456	CTTGGAAGAAAAACCCCACA
scaffold36392_21.6	1	p2	(AT)8	16	622	637	CTATTCGAATGCGAGGGAAA
scaffold36445_15.4	1	p2	(TA)6	12	1273	1284	CATTCCAACCTCCTAATCAAGAA
scaffold36447_15.7	1	p2	(AC)9	18	1076	1093	AATGTCGCCATCATATTTTGC
scaffold36452_14.7	1	p2	(TA)7	14	684	697	GCTCATTCTGCTTCTTCCGT
scaffold36489_15.8	1	p2	(TA)6	12	1083	1094	GAGTTCGATCTGGAACCTCG
scaffold36504_15.6	1	p2	(AG)6	12	1477	1488	CTTGACCGCAAGAAAGGTTC
scaffold36545_14.3	1	p2	(TA)8	16	1789	1804	TTCGGGCTAAACGAGTCAAT
scaffold36548_14.1	1	p2	(TA)9	18	654	671	GGGCACTCAACCCTTCAATA

scaffold36648_10.7	1	p2	(GT)8	16	50	65	AGGATGTAAATACGGTCTGTGC
scaffold36658_13.4	1	p2	(GA)6	12	569	580	CGTTCATTCGTATTGGGCTT
scaffold36735_11.1	1	p2	(AT)6	12	218	229	AAGTGACGACTCACGACCCT
scaffold36905_16.0	1	p2	(TA)7	14	1210	1223	TGTATGGTCTCCTTCCCTTTG
scaffold37028_13.0	1	p2	(TC)6	12	376	387	CTCCAACACCTCCAACTTGC
scaffold37093_16.9	1	p2	(AT)6	12	143	154	TCTTTAGCCCAAGTTGTATCCAT
scaffold37106_10.5	1	p2	(CT)10	20	112	131	AAAAATGGCGATGAAACCAG
scaffold37279_16.1	1	p2	(TA)6	12	54	65	TGAGCTGTTATGCGTTTTGA
scaffold37396_11.8	1	p2	(CA)6	12	137	148	GAACACCGGATTTACGTGGT
scaffold37402_11.1	1	p2	(CT)7	14	351	364	TAAGCAATGAGCGAAAAGCA
scaffold37499_11.9	1	p2	(GA)6	12	56	67	GTTAAGTAACCGGAGAGGCG
scaffold37527_15.9	1	p2	(GA)8	16	539	554	TCAGAAATTGTAGTCGCCCA
scaffold37548_13.2	1	p2	(AT)6	12	93	104	TTGGAACTTGAGCAACTGGA
scaffold37569_11.9	1	p2	(GA)11	22	969	990	TCTGGGGTTTCAGGTAGTCG
scaffold37624_15.6	1	p2	(AT)7	14	1029	1042	ATAGGGGCATATTCAGGTGC
scaffold37664_12.5	1	p2	(AC)6	12	56	67	AGAGGTAGAAGCACTTGTGTGG
scaffold37683_12.8	1	p2	(TA)6	12	226	237	AGGGCAACATTCGTCAAAAA
scaffold37761_10.4	1	p2	(AT)6	12	220	231	CGCACGTCGAGAATTGAATA
scaffold37815_13.5	1	p2	(GA)7	14	160	173	CGGGTTTTAGTGGAGAACGA
scaffold37878_10.9	1	p2	(AT)6	12	145	156	GCCACCCTTAAGTGATTTCG
scaffold37889_13.4	1	p2	(AT)6	12	574	585	GCTGCGAAAAAGGTCATCAT
scaffold37905_14.1	1	p2	(AG)8	16	1601	1616	GCTTACTCCCACCGATGTTC
scaffold37935_15.4	1	p2	(TA)9	18	371	388	CACATGCATGCTCGTACTCA
scaffold38074_13.9	1	p2	(AT)8	16	576	591	TCCTTTTTGTCTTTCATTCGG
scaffold38219_16.5	1	p2	(CT)6	12	626	637	GAAGGGAAACCGGTTAGGAC
scaffold38234_12.2	1	p2	(TC)9	18	635	652	TCAGCCGGAGAAACTCATCT
scaffold38307_15.4	1	p2	(GA)7	14	2060	2073	CAGCGCAGATAACAATTGGA
scaffold38377_17.6	1	p2	(AT)6	12	56	67	ACACTCGACAATTTGGGAGG
scaffold38415_16.6	1	p2	(TG)6	12	82	93	TGCTTTTCAACTTAGAATTCAATCA
scaffold38622_10.0	1	p2	(GT)7	14	300	313	GTGAGCTGAAGCGAGCTGAT
scaffold38717_15.0	1	p2	(AT)6	12	56	67	AAAACTATAGGTGTTTGGTAAACGTC
scaffold38766_16.9	1	p2	(AG)7	14	39	52	CAATTACAATGTTTATCCAATCCC
scaffold38991_10.0	1	p2	(CA)6	12	56	67	CAGGATCTCATCGGAACCAT
scaffold39087_13.1	1	p2	(AC)7	14	816	829	TTTCCGATTCTCAATTCCCA
scaffold39139_16.8	1	p2	(TA)8	16	857	872	TTGTGCATGCGGACTATGTT
scaffold39253_17.1	1	p2	(AG)7	14	612	625	GCAGCGTCGTTCTTCAGAG
scaffold39351_20.9	1	p2	(CT)6	12	56	67	AATCTCACAAACCCACACCC
scaffold39404_10.6	1	p2	(TC)6	12	56	67	TGGTCACTTACACAGCAATCAA
scaffold39519_18.2	1	p2	(CT)6	12	281	292	CTCGTCAACTGCTCGGTACA
scaffold39522_18.4	1	p2	(TA)6	12	142	153	TGCAGTAGGTTGTAGGTACTAAAATA
scaffold39545_12.3	1	p2	(AT)6	12	125	136	TGAATTTGGGTCATGAATTTTG
scaffold39578_13.5	1	p2	(TA)6	12	1046	1057	GGATTTTCTCGATTGCCAGA
scaffold39580_10.9	1	p2	(TA)8	16	130	145	GTGGCTAGATGCAAGCCTTT
scaffold39635_12.6	1	p2	(TA)7	14	406	419	GGGCAGTAAGTTGAGTCCGA
scaffold39779_14.2	1	p2	(AT)7	14	341	354	TTGATTGGTTGTTGGGCATA
scaffold39902_11.9	1	p2	(TA)8	16	1373	1388	GGCTTACCCCTGCACTTATG
scaffold40050_12.7	1	p2	(AG)6	12	56	67	TCGCACTAAAGCAGAACGAA
scaffold40145_11.0	1	p2	(GC)7	14	869	882	TCAGCCCAGCCCAATATTAC
scaffold40299_10.4	1	p2	(TA)9	18	104	121	CCCCTATTTTTGGAGGGAAA
scaffold40302_14.9	1	p2	(AT)7	14	3753	3766	GCACCACCATCTTCTTCGAT
scaffold40385_16.2	1	p2	(AC)6	12	1606	1617	CAGCAACCTGAAAGCATGTG
scaffold40409_17.2	1	p2	(TA)6	12	204	215	TTAAGGGGCGGTATCATTTG
scaffold40443_15.1	1	p2	(AT)6	12	967	978	AATTTGGTGGATGGGACAAA
scaffold40508_17.2	1	p2	(AG)8	16	1050	1065	CATGCAATGCGATGTGTTTT
scaffold40511_12.5	1	p2	(TC)8	16	1435	1450	GCCACCTCAGAAGATGGAAG
scaffold40583_10.0	1	p2	(CA)8	16	54	69	CAATTCATAAAATACATAGAAAGGTG
scaffold40611_13.6	1	p2	(AT)6	12	83	94	CCCCATCAACACACACATACACA
scaffold40637_16.6	1	p2	(TC)6	12	39	50	CAAACCCCATCACCAACTCT

scaffold40681_13.1	1	p2	(TA)6	12	81	92	GAAGTTTTCGGCCTTTTGAA
scaffold40726_11.4	1	p2	(CA)7	14	913	926	TTCAGGCAATACCAGTTCCC
scaffold40747_16.6	1	p2	(AG)6	12	37	48	GAAGAACAATTACAATGTTTATCCAA
scaffold40752_20.5	1	p2	(AT)8	16	655	670	TGTTTGCAATTATTTCGTGG
scaffold40921_19.5	1	p2	(AT)6	12	56	67	TGCATCAAGTTCTCTTCTCTAATTTT
scaffold40926_10.3	1	p2	(AT)6	12	129	140	TTGAACCGATGAAACTAAAATCAA
scaffold40985_14.7	1	p2	(TC)6	12	308	319	GTTGGAAGTGCGAATGTTCA
scaffold41039_18.8	1	p2	(AG)8	16	2884	2899	AGAATGGGGAAGCTCCAACT
scaffold41047_10.5	1	p2	(AT)6	12	176	187	AGTTGAACCTCGAACCGTTG
scaffold41081_15.8	1	p2	(TA)6	12	690	701	AATCATTGTGCGCATGTGTT
scaffold41215_13.5	1	p2	(TA)6	12	2325	2336	CTAGGCCCAAGGTAGTGGTG
scaffold41519_16.8	1	p2	(AC)6	12	2182	2193	ACGTGTTCAAGGTTGAAGGG
scaffold41908_11.3	1	p2	(CA)6	12	462	473	AAAGGCATCTGAGCCGTTAC
scaffold41963_12.2	1	p2	(AG)6	12	151	162	TCGGCTGGGGTAGTAATTTG
scaffold41965_17.8	1	p2	(GA)7	14	195	208	CCGAGATAGGAGCAAGCACT
scaffold41971_15.8	1	p2	(GA)8	16	234	249	GGGAAGAAAAACGACGAGAG
scaffold41989_15.1	1	p2	(TC)8	16	1837	1852	GTTTCCCAAAGCCACAAAAA
scaffold42065_17.4	1	p2	(CT)8	16	971	986	AAAATGAGGAAATCCCTCGG
scaffold42288_20.7	1	p2	(TC)6	12	156	167	CTCCAACACCTCCAACTTGC
scaffold42290_16.0	1	p2	(CT)8	16	2188	2203	ATTTCCTGCCCCAAATTACC
scaffold42291_10.7	1	p2	(AT)6	12	210	221	TGAAACTCCATCAAAACCTCTTT
scaffold42364_11.5	1	p2	(AC)7	14	74	87	GGCAGCAATCAATTGGAAAT
scaffold42625_17.2	1	p2	(GA)6	12	1056	1067	AGATTGGAGCGAAGAGTGGA
scaffold42762_12.4	1	p2	(AG)6	12	67	78	TGTTTTGTAATTTCCCATGTTTG
scaffold42948_16.5	1	p2	(CT)8	16	54	69	TCAATTTTCTCAAGAAACCTCC
scaffold43012_12.3	1	p2	(AT)6	12	259	270	AGAAACGCATCGTTTTCTGG
scaffold43292_10.5	1	p2	(AT)6	12	56	67	CCGATACGGTATAATTTCCAAAA
scaffold43398_15.6	1	p2	(TC)6	12	235	246	ATAACCCCACCATCCTAGCC
scaffold43419_13.8	1	p2	(AG)6	12	521	532	AGGCAACTTGGTGGAGAAGA
scaffold43445_16.4	1	p2	(TC)6	12	2766	2777	TTTCAGTTTCGCCATTTTCC
scaffold43964_12.6	1	p2	(TC)8	16	188	203	AAACAAGCCAATAAAGGCCA
scaffold43975_15.8	1	p2	(CT)6	12	1805	1816	GGCTAGATGCAGTGGACCAT
scaffold44077_15.7	1	p2	(TA)6	12	591	602	AGGATGGTGATGTTGAAGCC
scaffold44096_12.8	1	p2	(TA)10	20	474	493	GTATACACGGTCCGGTTTGG
scaffold44104_11.2	1	p2	(AT)10	20	463	482	GTGCGTGTGTATGCTGAGGT
scaffold44276_13.6	1	p2	(TA)6	12	1524	1535	CCTATATCAGCGGCCAAAAA
scaffold44489_16.4	1	p2	(TG)6	12	240	251	TGCATTCATGTACTCAGCCC
scaffold44540_13.3	1	p2	(TA)6	12	393	404	CCATGGAGTCCAATCTACCG
scaffold44589_12.4	1	p2	(AT)9	18	313	330	TGCAACAAATATCTGCACACG
scaffold44611_10.8	1	p2	(AG)6	12	94	105	TTCTGTTCATCATCTTCGTCCT
scaffold44613_13.9	1	p2	(GA)8	16	724	739	TCAGCTTGCAAAAGAGAGGA
scaffold44759_10.9	1	p2	(CT)6	12	38	49	CACTCTCCCTCTTTCTCTCTCG
scaffold44771_13.8	1	p2	(CT)6	12	82	93	TCGAAATCGTAATAATCGGACA
scaffold44778_13.4	1	p2	(CT)7	14	169	182	CTTCATTTCCCTTCCCCTTC
scaffold45060_11.2	1	p2	(TC)8	16	54	69	TGTTCTCATTCGTTTGCTCTAA
scaffold45274_10.4	1	p2	(GT)6	12	56	67	TTGTCTGCGGTAATGCTTTG
scaffold45337_10.2	1	p2	(AG)6	12	512	523	GTTAAAATGTGTGCCGGCTT
scaffold45611_10.7	1	p2	(GA)8	16	54	69	TGGAGTTGGAGTTGAGAGGAG
scaffold45757_15.2	1	p2	(AT)6	12	208	219	GCCTTCAATTTTATACCCGAGA
scaffold45982_15.6	1	p2	(TC)6	12	444	455	CTTGGTAAGCGGAGAGAACG
scaffold46113_15.5	1	p2	(GT)6	12	220	231	GCCTAACGTGGCTCTGATGT
scaffold46130_12.1	1	p2	(CT)6	12	56	67	AGCCTTCTAGCATCTCTTGCTC
scaffold46265_13.7	1	p2	(TC)6	12	936	947	CATTCTCTGCCTGTGTCTGC
scaffold46398_13.1	1	p2	(CA)9	18	1121	1138	ACTGGTTTCGACAAAATGGC
scaffold46882_17.0	1	p2	(TG)6	12	1177	1188	TTCGCAAGAACAACGACAAC
scaffold47031_12.8	1	p2	(AT)10	20	306	325	TTGATAAATAGTGCAATCCCAAC
scaffold47072_15.7	1	p2	(AT)6	12	56	67	GATTGTCTAAAACGTAAAGCTTGATT
scaffold47105_15.4	1	p2	(TA)6	12	94	105	GGGACAAAAACCGAAGGAAT

scaffold47160_11.4	1	p2	(TC)6	12	1030	1041	CGAAATTCCACCGACTCAAC
scaffold47168_16.1	1	p2	(AG)6	12	232	243	ATCTTGGGGAATGTGTGCAT
scaffold47242_15.0	1	p2	(TA)7	14	3783	3796	TCCGTAGACCTTCCAACCAC
scaffold47262_12.7	1	p2	(TA)8	16	353	368	CATGGATATGTGGAAGCACG
scaffold47301_13.3	1	p2	(TC)7	14	2153	2166	GGTGCCCATTCTGTTCACTT
scaffold47469_14.1	1	p2	(TA)6	12	267	278	TGAAAGAAAGAGAAAAGGAATTTTT
scaffold47593_14.0	1	p2	(TG)7	14	364	377	CAGTGGATCGTTCTGCTTCA
scaffold47614_13.4	1	p2	(AT)11	22	766	787	TTGATTGCAATAAGCAAATTTTTA
scaffold47664_15.2	1	p2	(AT)6	12	603	614	TCGCGGATATCAATTATCAACA
scaffold47763_14.3	1	p2	(TA)8	16	824	839	TTCTGTAATCGAGTTCAAGAGAGAGA
scaffold47947_14.6	1	p2	(AT)6	12	145	156	GCAAGGTGAGGAAGGAAGAA
scaffold48158_13.7	1	p2	(GA)6	12	449	460	CGAGGAATGAAATCGATGGT
scaffold48249_13.1	1	p2	(TA)8	16	157	172	GCAAACCCGTGTTCTTCAAT
scaffold48356_14.3	1	p2	(GA)10	20	371	390	GCCTGCAGACAGACAAACAA
scaffold48387_14.9	1	p2	(TC)7	14	272	285	TGCCATGGATATGATTGTTGA
scaffold48402_20.5	1	p2	(AT)7	14	713	726	GCATAAATTCATCTGAACAAGGG
scaffold48491_13.6	1	p2	(TA)10	20	331	350	GGATGAACGTCGGTCGTATT
scaffold48501_12.6	1	p2	(AT)10	20	1202	1221	GAATGTCATTGTTCGGACCC
scaffold48671_14.0	1	p2	(GA)8	16	723	738	CCGGTTTTGTTGACGAACTT
scaffold48765_14.5	1	p2	(AG)7	14	286	299	AAGCAAAAGAGTCAGCCGAA
scaffold48824_12.3	1	p2	(CT)6	12	463	474	CCGCATGTCATGTTATTGGA
scaffold48828_15.0	1	p2	(TA)6	12	1142	1153	CAAAAATACCCCGAAAACCC
scaffold48859_10.0	1	p2	(AT)8	16	74	89	AATCTCCCACTTGGGCAAC
scaffold48975_17.7	1	p2	(AG)6	12	318	329	CCGGGTTCAAGTTCCTATCA
scaffold48987_14.8	1	p2	(TA)6	12	919	930	ATGCCAGTCTTGAGCCAGAT
scaffold49021_16.1	1	p2	(TA)11	22	1350	1371	GGTCTTTTACTTTTCAGACAACGA
scaffold49032_10.2	1	p2	(CT)7	14	1189	1202	GAGTCGAGCCGAGTAGTTGC
scaffold49325_14.3	1	p2	(AT)9	18	953	970	AAGTTCGAGCGGAGTTTCAA
scaffold49339_10.5	1	p2	(AT)10	20	334	353	GCATTCATGCAGCATTCAAC
scaffold49375_12.4	1	p2	(GA)7	14	874	887	GGGAGAGATGCGTCAGAAGA
scaffold49397_15.6	1	p2	(AG)6	12	1245	1256	CTTCCCAAAGTCATTTCCCA
scaffold49410_16.5	1	p2	(AG)6	12	2347	2358	CGAGGATCCGAGGATACAGA
scaffold49414_13.9	1	p2	(AT)7	14	164	177	GCCATATGTGGAAACCTTCCT
scaffold49582_14.7	1	p2	(AT)7	14	767	780	GTCACGCCCCGACTATCTTA
scaffold49596_10.9	1	p2	(TA)7	14	224	237	CCCAATTTGCCCTTATATGC
scaffold49789_17.1	1	p2	(CT)7	14	446	459	TCTGTTGTTGGCAGTTCTCG
scaffold49842_17.5	1	p2	(AT)6	12	664	675	TGGGGGTCTGTCAAAAATTC
scaffold49899_14.7	1	p2	(AT)6	12	821	832	TCGATTTCGTGGAGATTGAA
scaffold49910_11.0	1	p2	(CA)6	12	131	142	GTGAAACCCCCAATTGTGTC
scaffold49957_14.6	1	p2	(GT)7	14	2299	2312	GCGTTTGACATCCTCAACCT
scaffold50057_16.6	1	p2	(TC)6	12	589	600	ATGGTTCGCCATAAAAATGC
scaffold50117_10.2	1	p2	(AT)6	12	317	328	TGATAGTGGGTTGGGTGTCA
scaffold50215_14.7	1	p2	(TA)7	14	51	64	CCCACTTTTGGGTTATTACCTG
scaffold50337_17.1	1	p2	(TC)7	14	2396	2409	TACGTGGATTTGACAGTGGC
scaffold50406_14.4	1	p2	(GA)6	12	489	500	GAGAGAGGAAGAGGGATGGG
scaffold50603_15.1	1	p2	(CT)10	20	221	240	TGTCCAAGCAAAATTGACGA
scaffold50898_10.7	1	p2	(AG)7	14	53	66	AAAGCTCAAAATGAAGAGGGC
scaffold50982_12.0	1	p2	(CT)6	12	157	168	CGCGACACCTCTAGAACACA
scaffold51119_15.4	1	p2	(TG)6	12	1145	1156	GGGAGGAAATTTTGAGGCTT
scaffold51332_14.1	1	p2	(TA)10	20	1017	1036	TCATAGTTTTCATTTGGACACCTC
scaffold51539_13.8	1	p2	(CT)8	16	380	395	CATAAGCCTACGAGCCCAAA
scaffold51591_12.0	1	p2	(AT)7	14	178	191	CCGAAAACCAAACCGAATTA
scaffold51800_11.1	1	p2	(CA)6	12	49	60	TTTTGGAGAATTTTCTCTTGCTC
scaffold51817_15.4	1	p2	(AG)6	12	378	389	TGTTTGAGTTAGCAGCCAGG
scaffold51942_11.2	1	p2	(TA)9	18	655	672	ACAAATTTGCCCTCGTATGC
scaffold52146_11.1	1	p2	(CT)6	12	295	306	CTGCATGGAGACTTGCATCA
scaffold52335_14.7	1	p2	(AT)6	12	1456	1467	TGCATAAACCTGCATACCCA
scaffold52435_13.4	1	p2	(AC)7	14	382	395	AAAAATCGTGCATTTTTGGC

scaffold52523_10.0	1	p2	(AT)10	20	288	307	CAATATCCCAATGTTTGAATCG
scaffold52705_12.4	1	p2	(TA)8	16	260	275	TCACCAAAAGGAGGGGTTATC
scaffold52807_13.4	1	p2	(AT)7	14	814	827	TTGGGCCTGAATGGACTTTA
scaffold52845_19.2	1	p2	(TC)6	12	1114	1125	GGAGGAGATGGAGACAGTCG
scaffold52868_16.5	1	p2	(AG)6	12	131	142	ACGTCGTCTCAAAGGGTGTC
scaffold52894_16.0	1	p2	(AT)6	12	263	274	GCTGGATATTTGGGCTTGAA
scaffold53005_15.6	1	p2	(AG)7	14	110	123	AAATGCTCGCTCTCACACCT
scaffold53126_14.0	1	p2	(TA)9	18	845	862	CGCGTCCCTTTTTACATGAT
scaffold53272_15.5	1	p2	(CT)6	12	577	588	TCCAGACTCAACCGGGTACT
scaffold53274_11.5	1	p2	(TA)10	20	100	119	TCAGATCTGCGCTGAAAATAAA
scaffold53345_15.8	1	p2	(CT)6	12	1388	1399	CACATGCACACACGTGATTC
scaffold53462_12.0	1	p2	(AT)8	16	704	719	ATGGAAACAATCACATCGCA
scaffold53484_14.4	1	p2	(TC)8	16	2474	2489	CTTGGCCAGCTCTAGGAATG
scaffold53634_15.9	1	p2	(TC)8	16	432	447	TGCATGGTAGTTGGGTGGTA
scaffold53859_10.3	1	p2	(TA)9	18	181	198	ACACATTTTTCTTTTGGGCG
scaffold54193_11.0	1	p2	(AT)10	20	513	532	GACTTCGTGGCGGTATTCTC
scaffold54246_20.6	1	p2	(AC)6	12	99	110	TGTCTCCATTTGTGTGTGTGT
scaffold54270_17.0	1	p2	(AG)8	16	125	140	ACCGACCTCCACTTCAACAC
scaffold54349_10.7	1	p2	(AT)7	14	184	197	TGGCCTATGAAGGAAAATGC
scaffold54599_14.6	1	p2	(AT)6	12	514	525	TTGCTAACCAACTACGTTGAGA
scaffold54716_14.5	1	p2	(AG)7	14	3513	3526	AAATGGGCAGACATACTCGG
scaffold54783_15.3	1	p2	(AG)6	12	131	142	ACACGCCTTTATCCGATGAG
scaffold54940_10.3	1	p2	(AG)6	12	53	64	AACAATTACAATGTTTGTGAAATCAA
scaffold54960_10.7	1	p2	(AG)6	12	492	503	TGTACCTCTCGCTGCTCTGA
scaffold55381_17.5	1	p2	(GA)9	18	6557	6574	GCAATGGCAAACCATTACCT
scaffold55384_10.4	1	p2	(CG)6	12	86	97	GGGTCCAGTCAATGAAACGA
scaffold55500_14.1	1	p2	(AT)6	12	1384	1395	CGGTGAAGATAAATTGCACGTA
scaffold55533_15.9	1	p2	(GA)6	12	918	929	AACACAATGGCGGGAATAAG
scaffold55771_11.4	1	p2	(GA)6	12	67	78	GAAACACGCAACGCAAGTAG
scaffold55892_15.1	1	p2	(TA)9	18	312	329	CCATCCAGCGCTATAAAATCA
scaffold55951_15.6	1	p2	(TC)6	12	200	211	TGCCATTTTGAGACCAGACA
scaffold56133_17.7	1	p2	(AT)7	14	194	207	GGTTGTAATGAGGCTTTCGG
scaffold56254_10.5	1	p2	(TA)8	16	50	65	AAGGGGAGTATCACTTGAATGC
scaffold56284_15.4	1	p2	(GA)6	12	2560	2571	AGCTGGAAAAGGCTATGCAA
scaffold56303_13.8	1	p2	(GA)6	12	2106	2117	GGGCTACTTCCCAACACAAA
scaffold56673_16.3	1	p2	(AT)9	18	271	288	CAACACGAATGTGCTGATGA
scaffold56746_16.8	1	p2	(TG)7	14	869	882	CACGGGTCTTCATCCATTTT
scaffold56794_14.0	1	p2	(GA)6	12	576	587	GAGCAAGAGAAAATTCTCCCAA
scaffold56796_16.6	1	p2	(GT)8	16	1219	1234	TGAAAGTGCCAACTTACGGA
scaffold56807_12.9	1	p2	(GA)6	12	3585	3596	TTTTTGCCCCAATCCATTTA
scaffold56831_16.5	1	p2	(TC)8	16	986	1001	CCAACCTTGTCGGAACAGTC
scaffold56849_16.0	1	p2	(TG)8	16	513	528	TGTCCAGCACATCAAAGCTC
scaffold57139_14.2	1	p2	(TG)6	12	482	493	ATGCAGGTTAGCGACGTTTT
scaffold57167_13.7	1	p2	(AG)6	12	95	106	TTCTGTTCATCATCTTCGTCCT
scaffold57169_11.1	1	p2	(CT)6	12	253	264	TCTTTTCCAGCCTGCAACTT
scaffold57170_11.3	1	p2	(GA)7	14	109	122	CATCAACTCTGATGCGGAGA
scaffold57258_12.2	1	p2	(AT)7	14	109	122	TCTTATCTCATCAACCGCCA
scaffold57325_15.2	1	p2	(TC)6	12	152	163	CAATCCCAATTGTAGCCTGC
scaffold57488_11.2	1	p2	(GA)9	18	291	308	TGCTGAGACATAGCGGACAC
scaffold57547_16.3	1	p2	(AG)6	12	57	68	AAAGAAGAACTAAAGCTTCGGAAA
scaffold57611_11.2	1	p2	(CT)6	12	63	74	TGTGAACACAGCCTCACCTT
scaffold57798_17.3	1	p2	(AG)9	18	1909	1926	CAGCCATGGATCAGCAGTAA
scaffold57902_19.1	1	p2	(AT)6	12	109	120	TCAGAAAAGTTCGAGCGTGA
scaffold58112_16.5	1	p2	(AT)6	12	521	532	ATCACCAACTGGCGAGAAAT
scaffold58242_13.0	1	p2	(AT)7	14	55	68	TGGACGTGGAACAATTACGA
scaffold58399_10.7	1	p2	(GA)7	14	252	265	AAGGTGTAGATCTGGCGGTG
scaffold58401_15.6	1	p2	(CT)6	12	949	960	GGCTCAGATTTTCCCAATCA
scaffold58491_13.2	1	p2	(TA)8	16	108	123	TGGTGTAAAAAGGGGTTGATG

scaffold58561_10.2	1	p2	(AT)6	12	66	77	TAACGACACGAACGGTTTTG
scaffold58654_13.7	1	p2	(CT)8	16	95	110	TTTGCACAAATTCGTTTAGGC
scaffold58657_16.1	1	p2	(AT)6	12	3245	3256	CTTGCGATCGTTTCTGTCAC
scaffold58720_12.9	1	p2	(TA)6	12	241	252	TTTCTTTTGTCAATGGAGCATCT
scaffold58853_15.1	1	p2	(GA)6	12	418	429	TGCAATAACAAATTTGGGAAA
scaffold58861_15.5	1	p2	(TG)7	14	2513	2526	ATGAGGCTGCTTTGCAAGTT
scaffold58925_16.1	1	p2	(GA)8	16	361	376	AAATGCGAGAGTGGTACGCT
scaffold59114_16.1	1	p2	(AC)6	12	4337	4348	GATTTCCCAACCCCAGTTCT
scaffold59129_14.6	1	p2	(TC)10	20	3160	3179	CAACTTTCTGCCCATCCATT
scaffold59205_10.3	1	p2	(AG)6	12	111	122	TGACTAAGCACAAGAGACGAAGA
scaffold59218_16.9	1	p2	(TC)6	12	611	622	ACATACCCTGTTCCTCGTGC
scaffold59358_11.6	1	p2	(TA)7	14	271	284	ATACCCTTGCATGCACAACA
scaffold59589_13.1	1	p2	(CT)8	16	405	420	GATGCATCAAGTCGACAATCA
scaffold59673_16.0	1	p2	(AG)6	12	1258	1269	GATGTCCCCATTGAGACTCG
scaffold59807_17.8	1	p2	(TC)6	12	231	242	TAGAATCCGATGTATGGCCC
scaffold60005_12.4	1	p2	(TA)6	12	523	534	CACCTGAAGGCGAAAAAGAG
scaffold60017_15.9	1	p2	(GA)7	14	326	339	ACATACTCCACCAACTCGGC
scaffold60137_10.7	1	p2	(TA)7	14	45	58	TTTCCAAGTCACCTTCCATT
scaffold60211_16.2	1	p2	(CT)6	12	297	308	CCAAAGGGGCTGCAATACTA
scaffold60282_10.4	1	p2	(TA)8	16	48	63	ACCATATTTAAGGGTTATCACCTG
scaffold60545_10.7	1	p2	(AT)6	12	119	130	AGCACGAATCACACAGCAAC
scaffold60673_17.7	1	p2	(AG)6	12	195	206	TCCCCATGTATATTGCCGTT
scaffold61001_14.0	1	p2	(TC)10	20	51	70	ACTGAGCCCTGATTTGGAAG
scaffold61042_16.3	1	p2	(AG)7	14	1474	1487	ATTTGGTATCAGAGCCACGG
scaffold61066_14.9	1	p2	(AG)6	12	2747	2758	TCTTTCAACCTGAATTGCCC
scaffold61119_11.3	1	p2	(AT)6	12	811	822	AGCTATCAAGCACCGGAAAA
scaffold61168_16.1	1	p2	(AT)7	14	272	285	CGGGTTCCCACATTTAACAA
scaffold61186_14.6	1	p2	(GA)7	14	87	100	TTTTATCAAGCGCAACCTCC
scaffold61355_10.3	1	p2	(TA)8	16	157	172	TTGTCGTATGCTGTCCGAAA
scaffold61357_10.3	1	p2	(TG)9	18	808	825	GGGATAGTACCTGATCATCTCCA
scaffold61549_14.2	1	p2	(TA)11	22	1125	1146	GCAGCCTTCTTGTCTCCTGT
scaffold61642_11.3	1	p2	(AT)8	16	648	663	CCGCCTGATTTGTTTCTCAT
scaffold61826_13.1	1	p2	(TA)6	12	807	818	CAAAGCATAAACATCCCAGC
scaffold61843_13.7	1	p2	(GA)9	18	441	458	TGATGGCATTCATCGTCAGT
scaffold61977_12.5	1	p2	(TA)9	18	82	99	ACGCCCCAGATTGTTTCTTA
scaffold62095_18.0	1	p2	(AT)9	18	245	262	GGGGAGATGTTCCTTTAGTCG
scaffold62187_11.9	1	p2	(AT)8	16	315	330	ACTTATTTGCATTGGGCCAC
scaffold62244_12.1	1	p2	(TG)7	14	143	156	CATTCGTACCCCAAACTTGC
scaffold62265_14.2	1	p2	(TA)7	14	936	949	AAACTCGACTGCCCCTTTTT
scaffold62278_16.9	1	p2	(TC)6	12	432	443	CATCACTCTGAGCCTCTCCC
scaffold62317_10.1	1	p2	(CA)7	14	183	196	TCGTGCGGTCAATGATTTTA
scaffold62360_14.3	1	p2	(TC)6	12	153	164	GGATTCAGTTGCTTCAAGAGC
scaffold62374_17.7	1	p2	(CT)7	14	265	278	CAATATTACAATGGGCAAGAGAG
scaffold62410_15.1	1	p2	(TG)6	12	3061	3072	TGGAATGCTTCTTTCTTGGG
scaffold62431_14.7	1	p2	(TA)6	12	443	454	GATCGACGTCCCAGATTTGT
scaffold62474_12.3	1	p2	(TC)6	12	732	743	CTCGTCTCCTCCACTTCCTG
scaffold62639_13.4	1	p2	(AC)6	12	83	94	AAAGAACAAAATGACACGAAGAA
scaffold63015_14.5	1	p2	(AT)10	20	638	657	AATGGTTCGGTTCCAGTTTC
scaffold63163_14.9	1	p2	(AG)7	14	65	78	TTTTGTGATTTCCCATGTTTG
scaffold63191_13.9	1	p2	(GT)6	12	2778	2789	CTCTCAACACTTCAACGGGAG
scaffold63399_14.7	1	p2	(AT)9	18	405	422	CCCGGCAACTTCTCAAATAA
scaffold63424_15.7	1	p2	(TA)8	16	3194	3209	CTGCAACAGCATAGTGGCAT
scaffold63688_13.4	1	p2	(TA)6	12	504	515	AGGAAATTGGGGGAAAATTG
scaffold63740_11.3	1	p2	(AG)7	14	272	285	CTCTTCCCATTTTCCCAACA
scaffold63772_16.0	1	p2	(GA)12	24	7241	7264	TCTCTCTGCAGGGGAGTCAC
scaffold63886_10.5	1	p2	(TA)6	12	371	382	CGAAGGAGACTGGAACCGTA
scaffold63970_14.3	1	p2	(AT)8	16	442	457	GGGCCCCTAGTCTGTCTCTT
scaffold64133_13.7	1	p2	(TC)6	12	254	265	ACCTAAACCCAAAACCCCAC

scaffold64202_15.3	1	p2	(AT)8	16	161	176	TGTCAACATTCAATCACAGCC
scaffold64267_10.4	1	p2	(AT)9	18	204	221	TCCCACCACTGGTTTCTTTC
scaffold64348_14.7	1	p2	(TA)7	14	391	404	TGAATCCCATCGATCCATTT
scaffold64461_13.7	1	p2	(AG)7	14	1082	1095	GGCTCTTCTCTGTCCGCTAA
scaffold64467_17.4	1	p2	(AG)6	12	2396	2407	GGTCACAGAGGTCGTCCCTA
scaffold64917_14.6	1	p2	(TA)6	12	1852	1863	GCTTGGTTTGCAGTCTCCTC
scaffold65164_13.0	1	p2	(AT)6	12	192	203	TTCTGAACGTGCAACTCGTC
scaffold65248_18.0	1	p2	(AG)6	12	806	817	TCCCTTACCAACATTCACGA
scaffold65405_10.6	1	p2	(AT)7	14	65	78	TCAAAAGCAAGAAAATGTGATTTC
scaffold65470_13.6	1	p2	(AG)6	12	1578	1589	CCACAAGCATTGCAGAGAGA
scaffold65495_10.5	1	p2	(AG)6	12	207	218	GGGGTTAATGATTGGTGTCG
scaffold65564_11.2	1	p2	(TC)6	12	23	34	ATACCACTCGTTAATCCGGC
scaffold65574_16.3	1	p2	(AG)6	12	3495	3506	AGAGGGAGTTTCCGGAGAGA
scaffold65640_17.7	1	p2	(TA)6	12	425	436	TGGTTCAATGGGTTATTCGAC
scaffold65643_19.0	1	p2	(TA)9	18	107	124	GTGCATCAACTTATGCCAAA
scaffold65647_12.9	1	p2	(AT)10	20	105	124	TGAAGTTAGGAAATAAGGAGGTGTT
scaffold65648_11.0	1	p2	(AT)9	18	564	581	ACGCGATTTCACTCACAACA
scaffold65649_15.9	1	p2	(AT)7	14	111	124	ATGATGGGCACATGGATTTT
scaffold65650_13.3	1	p2	(AT)7	14	174	187	GGTGTTGGATGGAAAATGCT
scaffold65651_15.9	1	p2	(AT)6	12	113	124	CGCTTTGGGACAGCAATTAG
scaffold65760_10.7	1	p2	(CA)7	14	379	392	ACTCCATCGATATTCACCGC
scaffold65783_10.2	1	p2	(AG)6	12	1582	1593	ATCCGCCATTGTTGAAACTC
scaffold65975_15.9	1	p2	(TC)12	24	43	66	CTTAGGCCACCACAAAGGAA
scaffold65986_16.2	1	p2	(TC)6	12	590	601	TTTCCCTCTCCTCCTCCATT
scaffold66008_15.3	1	p2	(GA)8	16	1590	1605	GACCAATTCGGTTTGGTGAC
scaffold66195_16.6	1	p2	(TA)6	12	2846	2857	CACGTGTCATCTTCTTCAGCA
scaffold66342_17.4	1	p2	(GA)6	12	837	848	GGTGGTGCAATGGGTAAAAC
scaffold66411_11.7	1	p2	(AT)7	14	139	152	ATTTTCAATCTCCGGGCTCT
scaffold66442_15.5	1	p2	(TA)6	12	1324	1335	CTTGGACCAGATTGTCCCTC
scaffold66569_11.9	1	p2	(GA)7	14	470	483	GCTGGAGCAGGTCTCTTGTC
scaffold66707_14.1	1	p2	(TA)6	12	181	192	GGGGAAGTGTGATGTTTGGT
scaffold66711_14.1	1	p2	(AT)9	18	467	484	AAGTAGGGTTGGGGTGCATA
scaffold66715_13.9	1	p2	(TA)9	18	1017	1034	GGGTACGGGTTGAGACAAAA
scaffold66757_11.4	1	p2	(TA)13	26	420	445	TGAAAATAAAAATGGAGTGATGTGA
scaffold66776_11.3	1	p2	(AG)7	14	147	160	TTTTACGAGATGGAAGAAGCTG
scaffold66851_10.1	1	p2	(TA)10	20	63	82	GCGAAATTCATGTTGACCCT
scaffold66911_10.3	1	p2	(AT)8	16	447	462	GAAATGCAAGGATTTCCCAA
scaffold66914_12.1	1	p2	(TA)7	14	93	106	GGCATTGCTAGAGCCATTGA
scaffold66961_21.4	1	p2	(AT)10	20	164	183	CCCTCGGATGCTAGTGTTTC
scaffold67058_10.3	1	p2	(TA)8	16	390	405	ATGCTAACTCCCCTTCCCAT
scaffold67350_12.3	1	p2	(AT)8	16	127	142	CCTCCGAACTCATGGTGTTT
scaffold67562_10.8	1	p2	(TA)10	20	693	712	GATGGGAATGGGAGGTATGA
scaffold67614_11.4	1	p2	(AG)7	14	113	126	AAAAGAGAGGGATGGGGAGA
scaffold67678_17.9	1	p2	(AG)6	12	1919	1930	TTGTGGCAGTCAGTGAGGAG
scaffold67698_13.4	1	p2	(GA)8	16	523	538	AGGATTCCAGCCACATGAAC
scaffold67727_11.1	1	p2	(AT)8	16	341	356	TGGGCTAATCATTCTCAGCA
scaffold67751_15.6	1	p2	(AG)7	14	2186	2199	GTCCTCTTTCTTCGCCTCCT
scaffold68014_16.6	1	p2	(GA)6	12	791	802	GTTCCGAATGCGAGTTTGTT
scaffold68050_11.4	1	p2	(TA)9	18	84	101	ATCAACCGCCTGATTTGTTC
scaffold68147_12.1	1	p2	(AG)6	12	141	152	GAATGAGTTTGCCGTGTTGA
scaffold68232_10.3	1	p2	(TA)6	12	86	97	TTGGTGCGATATTTTGTTCG
scaffold68284_15.2	1	p2	(AG)7	14	283	296	CAATCTCAACCCAAACCCAT
scaffold68324_10.7	1	p2	(AC)7	14	38	51	GAAAAGCTTGGCCATTCAAC
scaffold68365_16.8	1	p2	(TC)7	14	1529	1542	AGCTATGATGCTGATGCGTG
scaffold68439_13.4	1	p2	(GA)8	16	374	389	GTTTTTCCACCGAATCAAGC
scaffold68509_16.6	1	p2	(CT)6	12	529	540	TGCTGCTAATTATCCCTCCAA
scaffold68725_11.5	1	p2	(CT)8	16	178	193	ATGATTGGCTAGACATCGCC
scaffold68785_14.4	1	p2	(AT)6	12	58	69	TTCATCCATTTTGCACCTGA

scaffold68837_16.2	1	p2	(GA)6	12	206	217	ATTTTGATCCTTGTGGCCTG
scaffold68883_15.6	1	p2	(AG)7	14	675	688	GATGGTAGAAGAAGCGCAGC
scaffold68889_13.6	1	p2	(AT)9	18	697	714	TGGATGGCTAAGACAACAACA
scaffold68919_15.6	1	p2	(AG)6	12	221	232	CACGTCAAATCCTCCCAAAT
scaffold68965_13.2	1	p2	(TA)6	12	1542	1553	CTACAGCTCTATCCCGTCGC
scaffold69138_13.4	1	p2	(TC)6	12	67	78	ATTTGCAAGTTCCAGCGATT
scaffold69210_18.3	1	p2	(GA)6	12	1063	1074	GTCGAGGCGTAAGTTTGAGC
scaffold69241_13.5	1	p2	(AG)8	16	109	124	AGCCAGGGCTTTTATCATGT
scaffold69326_15.6	1	p2	(TC)6	12	2664	2675	ATCAGGAGACAACGGAGTGG
scaffold69338_14.5	1	p2	(CT)6	12	112	123	GCTTCATAGCATCTCTTGCTCA
scaffold69450_10.7	1	p2	(GA)6	12	134	145	GGTAAGCAGACTGCCAGGAC
scaffold69456_16.5	1	p2	(TA)7	14	2708	2721	TGTGGCTGAATTTGACGATG
scaffold69613_14.8	1	p2	(TA)7	14	49	62	GCACACAAGTTATTGGTTTCTATTTG
scaffold69649_14.2	1	p2	(GA)7	14	873	886	ACGGGCGATAGTAAGAGGGT
scaffold69713_10.2	1	p2	(TA)9	18	194	211	ATTTCGAAGATCAACGGACG
scaffold69879_10.8	1	p2	(TA)8	16	109	124	AATTGAGCCTTTACAAACTCTCTACA
scaffold70086_15.6	1	p2	(TC)6	12	2737	2748	GAGTTACCGCTTGCTCCTTG
scaffold70201_13.9	1	p2	(AT)10	20	246	265	TGCGATGTCTATGTGACGGT
scaffold70478_13.3	1	p2	(GA)6	12	208	219	AAGTCGGACTCTTGTTCGGA
scaffold70516_10.1	1	p2	(GA)6	12	199	210	TTCATCCTCCCTCATTTTCG
scaffold70547_16.7	1	p2	(CT)6	12	1487	1498	GGTGTCTACACGGTCCTCCT
scaffold70648_17.1	1	p2	(GA)8	16	698	713	AGAAAGGTGGGCATGAATTG
scaffold70700_15.4	1	p2	(AT)10	20	1874	1893	ACATCCATCTCAAAACAATATCAA
scaffold70754_15.3	1	p2	(AG)7	14	3082	3095	GCAGTTTGGCATCAGAGTCA
scaffold70765_14.9	1	p2	(GA)7	14	1269	1282	TGTGACAGAGCTGAAATGGG
scaffold70908_12.0	1	p2	(TC)6	12	326	337	GTTTCGTTTTGTTGCGGATT
scaffold71009_11.3	1	p2	(CT)6	12	833	844	CAACTGCTTCCGCATCTGTA
scaffold71097_11.0	1	p2	(TC)7	14	126	139	TTGCTTCAATGCAAGCTGTC
scaffold71188_15.8	1	p2	(AT)7	14	2060	2073	CCCCCTAACATTTTCCCACT
scaffold71421_10.6	1	p2	(TC)8	16	238	253	CAGCCCGGTACAGAAGGTAA
scaffold71441_17.3	1	p2	(AG)6	12	390	401	TGCAAAGGCTGAAGATCTGA
scaffold71536_14.5	1	p2	(TA)6	12	837	848	TTGTTTTCTCTTTTGCATAATCAAT
scaffold71577_13.5	1	p2	(GA)7	14	293	306	CGTGCTTGGCTTGGAGTAGT
scaffold71803_14.6	1	p2	(GT)6	12	474	485	TATGAGCCCGCACATTATCA
scaffold71837_15.2	1	p2	(TA)6	12	1309	1320	TTTTGTGCCTTCATTATGCC
scaffold71942_17.3	1	p2	(TA)8	16	989	1004	TTGGAAGGTATGTGAAATTTGG
scaffold71983_11.7	1	p2	(AT)6	12	172	183	ATCTTGGCAAGGCTCTGAAA
scaffold72090_10.4	1	p2	(TA)7	14	111	124	TCTGTTACTCTATCTGCATGCTCTG
scaffold72103_12.0	1	p2	(AT)6	12	301	312	AAAGGGAGTTGCAGTCAGGA
scaffold72139_15.3	1	p2	(CT)6	12	240	251	ACTTCTCCCCCTCTCTCTCG
scaffold72250_15.6	1	p2	(CT)6	12	65	76	CATACTCACGCATTCCCAGA
scaffold72400_10.0	1	p2	(TA)9	18	150	167	AAAGCCTACCTTGCTTCCGT
scaffold72443_13.1	1	p2	(CT)6	12	222	233	AGGATATCCCACGCCTCTTT
scaffold72497_12.9	1	p2	(TA)9	18	292	309	GACCGAACCGAAACTGGTAA
scaffold72610_14.2	1	p2	(TA)10	20	79	98	ATTTTGCAAGATCCAAGGGA
scaffold72933_12.5	1	p2	(AT)8	16	504	519	CAAACATTTATCTTGCACTTGG
scaffold72943_20.0	1	p2	(GA)6	12	113	124	ACAGCAGGGTGTTTGTGTGA
scaffold73058_16.7	1	p2	(AT)9	18	949	966	ACTCGCGTCTCTCATCCATT
scaffold73241_12.4	1	p2	(TA)8	16	786	801	GGGAGTATCACTGGAATGCG
scaffold73261_15.6	1	p2	(GA)7	14	407	420	TAACGACGCATAAAGAGGCA
scaffold73330_13.1	1	p2	(TA)7	14	314	327	CAGTCGCTGTTTCACCATTG
scaffold73359_14.6	1	p2	(AG)8	16	537	552	CCGCCATTAACTGCCATAGT
scaffold73547_18.4	1	p2	(TC)6	12	178	189	AAGGTTCACCAAACTACGCAA
scaffold73577_15.8	1	p2	(AG)9	18	433	450	CGTGGTTCAGCCATTTTGAT
scaffold73627_15.8	1	p2	(CT)7	14	1062	1075	AAAGAAGCGCGCTAAATCAG
scaffold73645_10.6	1	p2	(GA)6	12	82	93	GAACCAGAGGAGAAATAGGGAGA
scaffold73653_13.7	1	p2	(TA)11	22	182	203	TGACCACTTTTTACGGATTTGA
scaffold73752_15.2	1	p2	(CT)7	14	629	642	TTCTTTTGAACCAGGCAACC

scaffold73766_15.0	1	p2	(CT)7	14	3631	3644	CCAATCATGCTGGTTTTTCA
scaffold73768_16.2	1	p2	(GT)9	18	694	711	ATGCAACCAGATTCAAAGGG
scaffold73777_13.6	1	p2	(AT)9	18	556	573	AAATTGCAAAACCCAACTAAGC
scaffold74002_13.1	1	p2	(AT)6	12	185	196	AAGGTTTGGCTTGACCTTGA
scaffold74026_10.3	1	p2	(TC)8	16	182	197	GGAAATGACACCCAAACCAC
scaffold74468_12.1	1	p2	(TA)7	14	179	192	TCTCCACTCTCTTCTCTCTCCC
scaffold74505_17.1	1	p2	(AT)7	14	52	65	ACCATATTTAAGGGTTATCACCTG
scaffold74655_15.5	1	p2	(TA)7	14	223	236	TAACTCAAAATCTTGCCCCG
scaffold74691_15.7	1	p2	(AT)8	16	362	377	ATGCACGCCCTTAATATTGC
scaffold74821_12.4	1	p2	(TA)10	20	418	437	CAAGCCATGAGCCTTTGATT
scaffold74999_11.6	1	p2	(TA)8	16	174	189	AAAAATGGGGGAAATTTGATT
scaffold75004_11.1	1	p2	(AT)7	14	1663	1676	AAACCGTCCAAAATCGTATCC
scaffold75110_14.4	1	p2	(GA)6	12	1538	1549	TAGTGGCCATTCTTCAGGCT
scaffold75161_14.5	1	p2	(AT)8	16	1743	1758	CGTTTCGCAAATTAATCGGT
scaffold75322_12.4	1	p2	(GA)6	12	99	110	GTTAATGTGGATTGTGGGGG
scaffold75331_13.8	1	p2	(AT)6	12	1185	1196	CAATGAAACCAAACCATCCA
scaffold75332_16.5	1	p2	(TC)9	18	5652	5669	ATATGCCAATTTGGTTCCGA
scaffold75351_10.9	1	p2	(TA)9	18	349	366	TGCACTTTAAGAGGTGGTTGC
scaffold75530_10.9	1	p2	(TA)10	20	212	231	TCGAAAATCAAAGGCACACA
scaffold75602_15.4	1	p2	(AG)11	22	4802	4823	ATCGGAACGCTCATCAAATC
scaffold75683_15.9	1	p2	(AG)6	12	835	846	GCATTTGTCCCGTATGGCTA
scaffold75870_16.1	1	p2	(AC)6	12	1135	1146	CCCTCTTGATGGATTTTTGA
scaffold75920_13.8	1	p2	(CT)9	18	1794	1811	TTGGCAGACTACTTTGTGGG
scaffold75965_12.1	1	p2	(AT)9	18	619	636	CATTTATTTCTGCCCCTCCA
scaffold76005_15.8	1	p2	(TA)8	16	383	398	TGACATTAGACCTACCAGCACG
scaffold76059_16.4	1	p2	(TA)8	16	729	744	TCGCTGGTTTTGTAGTCGTG
scaffold76061_12.2	1	p2	(TC)6	12	31	42	ATTCTGTCGGATAGGTGCGT
scaffold76151_14.4	1	p2	(AG)6	12	1746	1757	TCATTTGGTTTGCAGTCAGC
scaffold76276_18.4	1	p2	(TA)11	22	42	63	GCGTTTTGACGATATATAGTGTTTTG
scaffold76979_11.3	1	p2	(TA)11	22	316	337	AATCAATCTTTGAAACCGGC
scaffold77023_14.2	1	p2	(TA)9	18	380	397	CTCTAACAAATGCCAGCCGT
scaffold77310_12.3	1	p2	(CT)6	12	297	308	TTTAACTAGCGTCGTTGCCC
scaffold77357_12.1	1	p2	(CA)7	14	197	210	GCTTCACTCACTCACGCAGA
scaffold77360_14.8	1	p2	(CT)6	12	2075	2086	CACTGCTCTCTTTTCCTCGG
scaffold77455_15.9	1	p2	(AG)6	12	312	323	TGATTTCGATGGTTTTGGGT
scaffold77486_15.2	1	p2	(CT)8	16	856	871	GGCACACCTGTATACCCCAC
scaffold77561_15.4	1	p2	(TG)6	12	1481	1492	TTGATGCACCCTCTTTTTCC
scaffold77651_14.8	1	p2	(TA)8	16	241	256	AAAATCGACCGCACATTTTA
scaffold77708_13.1	1	p2	(TC)6	12	708	719	CCCTAACTCGACCCAGATCA
scaffold77732_13.0	1	p2	(TA)6	12	170	181	CGTTGTCCTGAGCACGTTAG
scaffold77796_12.0	1	p2	(AT)6	12	635	646	ATCGTGGGAGAGAGAGATCG
scaffold78146_15.2	1	p2	(TA)6	12	805	816	TTCAATCATCTCAAGGCGAC
scaffold78188_14.5	1	p2	(GA)6	12	52	63	TGATGAAGTTGGGTGTTGGA
scaffold78227_10.1	1	p2	(AT)7	14	136	149	CCTAAAATTGAACGAAACTCGAA
scaffold78392_10.0	1	p2	(AC)8	16	276	291	TAGCCCCTTTGAGACCATTG
scaffold78396_13.6	1	p2	(AG)6	12	661	672	TCCAGTGTTGCTCTTGCATC
scaffold78453_13.0	1	p2	(TG)6	12	349	360	TTCCGATGGAATGCATTTTT
scaffold78461_10.9	1	p2	(TA)7	14	211	224	AGGCACATGCCAAACTTTTC
scaffold78530_17.2	1	p2	(TC)6	12	139	150	TCCCAGTTCAACTCTTTCTCG
scaffold78563_12.0	1	p2	(AG)6	12	345	356	GTGTGGGTTCCTCTCGTGTT
scaffold78622_17.0	1	p2	(TC)6	12	357	368	TTCCACTAGGGGTACCAAAATG
scaffold78859_10.5	1	p2	(AG)6	12	102	113	AAAGCCAATCGAGTCTTGGA
scaffold78947_15.0	1	p2	(GA)8	16	85	100	GGATGGGGCTGTGATTGTAG
scaffold79075_14.2	1	p2	(AT)6	12	298	309	CAATTCCGAACCGAATAAGC
scaffold79112_10.0	1	p2	(AT)10	20	45	64	CGAATAGAGTGATGAGCCAAC
scaffold79127_20.0	1	p2	(TC)6	12	96	107	GCAACGGAATACCACTCGTT
scaffold79379_15.8	1	p2	(CT)6	12	2695	2706	ACACCATACCCAAAAGCCTG
scaffold79413_19.3	1	p2	(TC)6	12	556	567	TCTCAATCATGCGATCCAAA

scaffold79543_13.0	1	p2	(AT)9	18	323	340	GGAAGCGCAATTAATACGGA
scaffold79547_20.3	1	p2	(TA)8	16	158	173	ACGATTTTGCCCTTGTATGC
scaffold79728_13.6	1	p2	(TA)6	12	185	196	CACGATAAGGGATGGATTCAC
scaffold79739_13.7	1	p2	(AG)6	12	1235	1246	ACGAGGGAGTGATCAAGTGG
scaffold80293_13.2	1	p2	(GT)8	16	166	181	TGTTCAAATGATTTTGGGGG
scaffold80295_13.1	1	p2	(AC)6	12	143	154	ACTCTCAGCCACGCACTCTC
scaffold80667_14.1	1	p2	(TA)7	14	1762	1775	CGCGCCTTGCCTAATAATAA
scaffold80688_13.0	1	p2	(AT)6	12	244	255	TAATCGTTGCTGGAGCGTC
scaffold80703_16.5	1	p2	(AT)6	12	153	164	ACAGCCATCGCTCAACCTAC
scaffold80711_14.1	1	p2	(TA)9	18	284	301	TCATGGGATCAGTTTCAATCC
scaffold80726_11.0	1	p2	(AG)7	14	247	260	ACTGTGCTGCTGGAAAATTG
scaffold80753_12.9	1	p2	(CT)7	14	80	93	ACAAATGACCAAGGAGGAGTT
scaffold80774_12.7	1	p2	(TA)6	12	201	212	TGGATTGTATGTGTCCCCAG
scaffold80812_13.9	1	p2	(TA)9	18	190	207	GTTATGTGGCCCGAATGACT
scaffold81113_22.3	1	p2	(AG)7	14	50	63	TCCCATGTTTGTAATTATTGTAGGG
scaffold81146_18.6	1	p2	(CT)7	14	3436	3449	CAGGGACGGGCATGTTACTA
scaffold81182_18.9	1	p2	(TA)6	12	593	604	TTCACGACCCTGTATGTCCA
scaffold81228_11.2	1	p2	(TA)6	12	494	505	CCTTATTTGATGCACGGACC
scaffold81275_18.3	1	p2	(GA)6	12	476	487	AGAAGTCTGCGAAGGTCAGC
scaffold81313_15.2	1	p2	(AG)8	16	272	287	GCCAACTATGAGACATGCGA
scaffold81406_13.5	1	p2	(TA)7	14	484	497	GCGTGACGCACAGTTTCTTA
scaffold81510_16.9	1	p2	(TA)7	14	844	857	CTGATGTCAATTTCCATATCCA
scaffold81530_18.7	1	p2	(TC)6	12	964	975	ATTCAGGCATATGCTTTGGC
scaffold81719_15.3	1	p2	(GA)6	12	4130	4141	GGGTTTGGTTGGAGACGTAA
scaffold81773_10.9	1	p2	(TC)6	12	215	226	GAGTTCGTCAAACCTCCCAA
scaffold81873_14.1	1	p2	(TC)6	12	39	50	GGCAACGGAATACCATTTGT
scaffold81933_15.9	1	p2	(AC)6	12	1686	1697	AGATGCTCCCTCTCCCATCT
scaffold82011_15.6	1	p2	(AG)7	14	2392	2405	TCCAAGGGAAAGTGTTCAAGA
scaffold82102_14.1	1	p2	(TC)6	12	1070	1081	AAGGAGGGGCAAAGAAAAGA
scaffold82158_17.4	1	p2	(TC)6	12	113	124	TCAAACACTAGCCTTTGCCTC
scaffold82302_16.3	1	p2	(CT)6	12	89	100	AACAAACACCTGGGACCACT
scaffold82381_15.2	1	p2	(AT)6	12	343	354	TGAAGAGTACAACTTACACCCCA
scaffold82405_14.2	1	p2	(AC)10	20	472	491	CGAAAGCTGAAGAGCGAGAT
scaffold82466_10.0	1	p2	(AT)6	12	560	571	GACTACTGGTCGGGGAACAA
scaffold82718_17.8	1	p2	(CT)6	12	56	67	CATGTGGCCTAACTTGACACA
scaffold82736_14.0	1	p2	(CT)7	14	381	394	ATCAAACGCTTTGTTTTCCG
scaffold82741_10.0	1	p2	(AT)6	12	422	433	AATTCCATGCACAGTGACCA
scaffold82925_14.9	1	p2	(AG)8	16	284	299	CAATCTCAACCCAAACCCAT
scaffold83013_17.1	1	p2	(CT)7	14	80	93	GTTCTCACCGGAGTTGGTTC
scaffold83070_11.6	1	p2	(TA)7	14	185	198	TCCCACTAAAATTTTCCCGTT
scaffold83254_16.4	1	p2	(AC)6	12	1418	1429	TTGATGCTGCAAGAAGCCTA
scaffold83389_10.0	1	p2	(AG)6	12	139	150	GCATGCTAGTGCCTGTTGTG
scaffold83423_13.2	1	p2	(AG)6	12	931	942	TCAAAAGAAGAGGCTGGCAT
scaffold83586_14.3	1	p2	(AG)8	16	380	395	AGGAAGGAGGCAGAGAGGAC
scaffold83612_16.1	1	p2	(TA)6	12	308	319	TGAAATGGTGATTTGAGGGG
scaffold83641_13.7	1	p2	(GT)9	18	695	712	AATGGATCTATAGAGCGCCG
scaffold83653_16.9	1	p2	(TA)6	12	219	230	GCCTAGTGAGGAGTTCACGG
scaffold83790_14.6	1	p2	(AT)10	20	2162	2181	TCTCAAAACCACAACAAACCC
scaffold84019_13.5	1	p2	(AT)7	14	544	557	CGACTACTCAATCATCCAACCA
scaffold84188_14.7	1	p2	(GA)6	12	680	691	TCCAAGATTGAAGTCGCAGA
scaffold84201_13.9	1	p2	(TA)10	20	191	210	CTCCCTCAATCAAACCTTCG
scaffold84225_13.9	1	p2	(AC)11	22	2421	2442	CCGTGGTTGATCCAGAGAAT
scaffold84249_17.6	1	p2	(TA)6	12	80	91	GGGGAAAATTTGCAAGATGA
scaffold84367_16.1	1	p2	(AG)10	20	4252	4271	CGTCCGTGTTCTATTGCAGA
scaffold84561_12.1	1	p2	(AT)7	14	443	456	TCATCTGCTGAAAGGAGGGT
scaffold84577_10.1	1	p2	(TC)6	12	100	111	ATCGGCGAATTTATCTGCAA
scaffold84595_11.8	1	p2	(AT)11	22	699	720	CAGGTGCAGGGAAGAAATGT
scaffold84671_16.8	1	p2	(GA)7	14	1871	1884	CAACCAGACCCCTACCAAGA

scaffold84675_10.7	1	p2	(TA)8	16	72	87	ATGGGAAGAGGGGGTATGAG
scaffold85082_13.5	1	p2	(AC)6	12	401	412	TAGAGCCAACCAAATGGTCC
scaffold85248_14.4	1	p2	(TA)9	18	237	254	TTAGGGTTTAAAATCGCGCA
scaffold85249_10.0	1	p2	(TA)8	16	131	146	CGTTGAGCCGAATGTGTTTA
scaffold85335_13.8	1	p2	(AG)6	12	1079	1090	ATTCACGTCCACGTTTCTCC
scaffold85607_14.8	1	p2	(AG)6	12	45	56	CCTTTCCTAACAGTTTGGCATC
scaffold85613_14.5	1	p2	(AG)7	14	112	125	CGCCATTCTCTCTCCACTCT
scaffold85756_13.2	1	p2	(AT)6	12	286	297	GCGTGTTCTTGGTGTTCTTG
scaffold86034_10.8	1	p2	(GA)10	20	238	257	AATCGCAAATCACACCATGA
scaffold86089_11.0	1	p2	(CT)9	18	129	146	TTGCTTCAATGCAAGCTGTC
scaffold86147_14.0	1	p2	(GA)8	16	1072	1087	TGACTCGCCGTAGAATCCTT
scaffold86450_17.3	1	p2	(TG)7	14	2655	2668	AGGCCTCTCACATCTTCACC
scaffold86573_11.2	1	p2	(AG)7	14	190	203	GATATTGACGGTTGGTTGGC
scaffold86741_16.1	1	p2	(TA)6	12	94	105	AATGAACCAAGTCATTGCAGC
scaffold86750_10.6	1	p2	(AT)6	12	169	180	AGTGAAGCCAAGCCAAAAGA
scaffold86829_14.3	1	p2	(TA)7	14	553	566	AGGTTGGAGGGAATGGAGAG
scaffold86867_10.4	1	p2	(AT)11	22	55	76	AAATACCATTTCATTTTGTAAACTCTT
scaffold86965_15.3	1	p2	(CT)8	16	3590	3605	AAAAACATGGAGCAACGACA
scaffold87030_13.0	1	p2	(GA)6	12	35	46	CACGAGTGAAGAAAGGGAGAG
scaffold87093_14.4	1	p2	(TC)6	12	913	924	TTGATTGATCGACAGCATCC
scaffold87127_17.6	1	p2	(AC)6	12	1051	1062	TGGGATTAATTTCCACCATGA
scaffold87146_10.6	1	p2	(TC)6	12	60	71	TCAAATCATAGTCTTTCCTCGTTTC
scaffold87264_15.1	1	p2	(TA)9	18	47	64	TGAAGTTAGGAAATAAGGAGGTGTT
scaffold87358_13.9	1	p2	(TC)6	12	866	877	TCCCACAAATCGCATAAACA
scaffold87503_11.0	1	p2	(GT)9	18	214	231	GAAATTTCGCTAAGTCGAGAATAA
scaffold87510_15.6	1	p2	(CT)9	18	2258	2275	AGGGACAGCTGTGGACTCTG
scaffold87547_12.3	1	p2	(TA)6	12	365	376	TTGTCGTGGTTCGGTATTCA
scaffold87549_19.0	1	p2	(TG)7	14	181	194	GCATTTATGTGTCAGCCCCT
scaffold87635_17.8	1	p2	(CT)6	12	365	376	TGGTGAACGTGTTTTGTTGC
scaffold87819_17.1	1	p2	(CT)7	14	148	161	TTTGTTGGCTAACAGGTCCC
scaffold87836_15.3	1	p2	(AG)6	12	232	243	TGTTCGTTGGTGGAGTTGAG
scaffold87992_12.1	1	p2	(AT)6	12	138	149	CATCCTAAAGATAAGAATGGTAATCA
scaffold88024_14.1	1	p2	(TC)7	14	294	307	GGCAAACATGAATTCGTTCC
scaffold88025_14.0	1	p2	(GA)6	12	114	125	TGGGAGAAGTTGGTGAATTTG
scaffold88033_10.2	1	p2	(TA)6	12	250	261	CTTTCTCCCCCGTAAATTCC
scaffold88052_12.9	1	p2	(TA)10	20	99	118	GCCCTTGATTTCCAAGATCC
scaffold88060_10.7	1	p2	(TC)6	12	111	122	CCTCCATCCTTACTCCACCA
scaffold88373_19.1	1	p2	(TA)6	12	334	345	TGAGTTTTGAATTCGGACCC
scaffold88663_15.0	1	p2	(AG)6	12	619	630	AGACAGCAATACCAGGGGTG
scaffold88725_13.9	1	p2	(GA)7	14	2448	2461	GAAGGTAACGTCGCTGAAGG
scaffold88735_15.0	1	p2	(AG)6	12	449	460	ACCGACTTCTGCACCATTTC
scaffold88775_12.0	1	p2	(TA)8	16	158	173	TCGGTTCTTGCTCCATTACC
scaffold88848_10.1	1	p2	(TC)8	16	119	134	TTTTTCTTTCCACAAACCCC
scaffold88855_15.6	1	p2	(TC)6	12	114	125	CAGGAAGGGAAAAGCATCTG
scaffold88921_11.0	1	p2	(TG)8	16	647	662	GGTAGGAAATTTTTGGCTAAGTGA
scaffold88926_15.0	1	p2	(AC)6	12	2077	2088	GGGTTTGAAATTTTGAATGCTT
scaffold88990_16.1	1	p2	(TA)8	16	574	589	CCTTGAAAATCTGAGCGTCC
scaffold89043_10.5	1	p2	(TA)7	14	329	342	GATTTGGCTAGGAATGGCAA
scaffold89126_17.5	1	p2	(GA)8	16	308	323	TCGTCCGAACACATTGAAGA
scaffold89226_16.9	1	p2	(CT)7	14	109	122	GTACTCGGACGGGATCTTGA
scaffold89596_15.0	1	p2	(TC)9	18	2078	2095	TAGGGCAGATTTATGCCAGG
scaffold89612_12.1	1	p2	(TC)6	12	190	201	CACGTCTCGTGTTTCTTCCA
scaffold89630_13.7	1	p2	(GA)6	12	67	78	CGAGTGGTTGTGAGGTGAGT
scaffold89631_11.9	1	p2	(TC)6	12	529	540	TCGCACAAATGATAGCGAAT
scaffold89673_14.1	1	p2	(TA)6	12	1348	1359	TGAACCACCTCTGCAAACAA
scaffold89677_12.5	1	p2	(TC)9	18	249	266	TGCATAAGACACCTAGCCCA
scaffold89747_16.3	1	p2	(GT)6	12	368	379	AGCAATATTGGTGGGACGAG
scaffold89787_12.3	1	p2	(TC)6	12	770	781	TCATCTCCATCCCCCAATAA

scaffold89854_12.9	1	p2	(AT)7	14	564	577	CCTGGGTTTAAAAATGCGAA
scaffold90114_10.9	1	p2	(TA)7	14	461	474	TGCAAATCTGGATCCTTCGT
scaffold90191_11.0	1	p2	(TA)9	18	258	275	AAACTTGAGCAGTCAGTTCGATT
scaffold90198_11.7	1	p2	(GA)6	12	205	216	TCTCCACCAGATCATCACCA
scaffold90221_15.6	1	p2	(AC)9	18	3195	3212	CTCCAACCTCCCTGTACTGC
scaffold90289_17.0	1	p2	(GA)6	12	1907	1918	TAGTTGGAGGGAATGCTTCG
scaffold90295_19.0	1	p2	(AT)8	16	380	395	TGGCTCCTGAATCTCACAGA
scaffold90477_14.5	1	p2	(TA)7	14	145	158	TCACACAGAATCCCTGTTGC
scaffold90480_20.7	1	p2	(AG)7	14	56	69	ATAAATATCAGGTGTTTTCTGAGTTG
scaffold90540_16.9	1	p2	(AT)6	12	53	64	CCCTTTTAGGCTCAAATCTCTTT
scaffold90609_12.5	1	p2	(AT)9	18	355	372	TTTTCGCCTCCCACTAAAAA
scaffold90611_10.6	1	p2	(TA)8	16	329	344	TTTTTGCCACCTATGCACAA
scaffold90630_11.6	1	p2	(AT)9	18	65	82	TCGGCCAGAGAGAAAAAGAA
scaffold90656_22.4	1	p2	(TC)7	14	144	157	AGTGCGTTTGCAGAGCTTTT
scaffold90675_16.7	1	p2	(AT)8	16	131	146	TCATGATATTTTTCCTAAATTTTCCTT
scaffold90762_10.9	1	p2	(AT)7	14	142	155	CTCACCGTGGACGTAGATCA
scaffold90841_16.8	1	p2	(AG)9	18	1248	1265	AGCGGCAGACGTTTCTAGTC
scaffold90872_11.4	1	p2	(TA)8	16	531	546	CGGAGATGAGGATGCTTAGG
scaffold91053_15.4	1	p2	(CT)6	12	24	35	CCACAAACCGAGCTCACC
scaffold91226_20.8	1	p2	(AT)9	18	225	242	CATGGATAGAGCGTGCAATG
scaffold91237_10.8	1	p2	(AT)10	20	218	237	TCCGTCGGTGATTCAAGAGT
scaffold91306_10.8	1	p2	(CA)7	14	155	168	ATTCCCGGGCTGAGATAGTT
scaffold91539_12.7	1	p2	(AT)9	18	46	63	AAGGAACAAATGAGAATGTTAGTGC
scaffold91625_11.1	1	p2	(CT)6	12	93	104	GGGATTTGGGACGATTTTCT
scaffold92324_14.2	1	p2	(AT)8	16	567	582	GTAACGCGCGAATGCTACTT
scaffold92325_16.1	1	p2	(TC)9	18	30	47	GGTGTTCTTGGCAACAGGTC
scaffold92365_10.7	1	p2	(TA)6	12	83	94	TCAGTTTCGAGTTATGAAGTTAGGAA
scaffold92386_15.5	1	p2	(TG)9	18	1971	1988	GTGGATTGAAGCATGAGCCT
scaffold92435_14.6	1	p2	(GA)6	12	238	249	ATGGGGCTGTGGTTGTAGAG
scaffold92521_11.7	1	p2	(TA)6	12	474	485	AGTGACTCACCTGAAACGCC
scaffold92650_14.7	1	p2	(AG)8	16	581	596	CACCTGCAACAGAGGAGTCA
scaffold92855_10.4	1	p2	(TA)6	12	186	197	TCACATCAATTTTCACACCCA
scaffold92942_14.4	1	p2	(AT)8	16	297	312	CCTGTTGCATCAATCAATGG
scaffold92968_11.7	1	p2	(GA)6	12	530	541	TGCAAGCATCAAACAACACA
scaffold93104_17.3	1	p2	(AT)8	16	247	262	ATGAGACAGTCCGGGATTTG
scaffold93263_13.9	1	p2	(TC)6	12	429	440	ACCTTACCCAACCCACTTCC
scaffold93321_15.8	1	p2	(AG)7	14	688	701	ATTCATTCCCACCAGAATGC
scaffold93480_10.8	1	p2	(TG)6	12	142	153	ACGTCTTGATGTCGAAACCC
scaffold93632_13.3	1	p2	(AG)6	12	934	945	CTAGGGTTAGCATGCTTGGG
scaffold93749_11.5	1	p2	(AT)7	14	312	325	TCAACCGCCAGGATTATTTC
scaffold93774_19.0	1	p2	(GA)6	12	302	313	CGTGGTTCGATCGTAAATGA
scaffold93780_11.7	1	p2	(TA)7	14	210	223	ACCCCACCTTTCTTGGATTC
scaffold93792_20.9	1	p2	(AG)6	12	516	527	GGTGGAGTGTTGGAAAAGGA
scaffold93947_13.8	1	p2	(TG)6	12	620	631	GCGTACATTTGCCCCTAAGA
scaffold93967_16.1	1	p2	(AT)7	14	250	263	ATCCAGGTTCGGTTTCAATG
scaffold94001_16.5	1	p2	(AT)7	14	242	255	TTGACTTGGGCTTTGCATTA
scaffold94218_15.7	1	p2	(TA)8	16	286	301	CTCTTGTAACAAAACCCCATGT
scaffold94308_10.5	1	p2	(CT)7	14	178	191	TATGGGGTGAGTGGGCTAAG
scaffold94373_15.2	1	p2	(CT)7	14	442	455	CCAATGGAGAACCCTTTGTC
scaffold94724_15.3	1	p2	(CA)6	12	3862	3873	CCAAGTCAATTCCTAGTGCG
scaffold94884_10.2	1	p2	(CT)8	16	415	430	TTGACTTGTGACCCTCTCCC
scaffold95089_18.1	1	p2	(CA)6	12	213	224	CATACCAAGTCCCAGGGAGA
scaffold95093_14.8	1	p2	(TC)6	12	400	411	TGAGACTGCCTTCGTCACAC
scaffold95133_15.2	1	p2	(GA)6	12	651	662	TGCTTCACTGCAAAACAAGG
scaffold95134_12.5	1	p2	(CT)6	12	78	89	CAAATGGCCGAGAGAGAGTT
scaffold95302_15.1	1	p2	(TC)6	12	1143	1154	CCCCACAGATATCCCACCTA
scaffold95343_12.1	1	p2	(TA)6	12	698	709	TCATCATTCGACTTCCATGC
scaffold95449_16.8	1	p2	(AT)7	14	79	92	AATCTCCATGTTCAGGACTTCA

scaffold95502_16.0	1	p2	(AT)6	12	3670	3681	TGTGACACCAATGTGATGGA
scaffold95592_14.0	1	p2	(TA)6	12	518	529	GCAAAGTGTGCGGTCAAAT
scaffold95628_14.2	1	p2	(TA)7	14	112	125	GAAGGAGCAATGAGAGGTGC
scaffold95630_14.4	1	p2	(AT)8	16	111	126	AATCTTCATAAGTGGAGGGGC
scaffold95669_14.9	1	p2	(AT)8	16	1027	1042	CAAAACGTCCGTATCGACAA
scaffold95717_10.8	1	p2	(AG)6	12	231	242	TGAAGATTTTCATGGTGGATTC
scaffold95781_13.6	1	p2	(CT)7	14	616	629	ATGTTTCAATGACACGTGGG
scaffold95826_18.3	1	p2	(TG)7	14	266	279	CTGGGTCTGGTGTTGTTGTG
scaffold95907_12.2	1	p2	(AG)6	12	1333	1344	TTACATTTTTCTGGCTCCCAA
scaffold96034_14.8	1	p2	(TA)9	18	71	88	TCAGTTTCGAGTTATGAAGTTAGGAA
scaffold96357_15.2	1	p2	(TC)10	20	4238	4257	TCATCATCGTGCTTTCCTTG
scaffold96416_14.0	1	p2	(AG)6	12	232	243	ACCATCATCGTCATCCACCT
scaffold96508_17.0	1	p2	(CT)7	14	2597	2610	CAACAAAAAGCTCGCAATCA
scaffold96755_16.6	1	p2	(AT)8	16	1512	1527	TTCATGCTGAGGTGTTGTCG
scaffold96796_15.4	1	p2	(CT)6	12	1670	1681	GGCTGAACCATTCACCTGAT
scaffold96934_17.3	1	p2	(AT)7	14	1280	1293	TTATATTTGGTCGGTGGGGA
scaffold97005_14.6	1	p2	(CT)7	14	441	454	CCTTCATTTTATCGGCTCCA
scaffold97045_10.2	1	p2	(AT)9	18	680	697	ATTGGTGACGAGAGAGTGGG
scaffold97071_12.4	1	p2	(AT)6	12	58	69	TTGCAATTAGTGCATACAATGATAA
scaffold97146_10.5	1	p2	(TA)10	20	176	195	ATCGCAAATAAAACAACCGC
scaffold97172_17.7	1	p2	(AT)7	14	1995	2008	ATTGCCCCCATCATAACAAA
scaffold97502_13.9	1	p2	(TC)6	12	114	125	CTGATTCGCACAAATGATCG
scaffold97673_12.0	1	p2	(AT)12	24	236	259	GACGTGTGTGTGATTGAGGG
scaffold97704_13.0	1	p2	(TA)13	26	417	442	TGGTTATTACTCGAACGCGA
scaffold97943_12.0	1	p2	(AG)6	12	275	286	GACCGTGTAGGAAGGCTGAG
scaffold98089_12.9	1	p2	(AC)8	16	316	331	TTCTAGGCACAAAACCCACC
scaffold98248_13.8	1	p2	(CT)6	12	204	215	AATGGCAGATTTGAAGACGG
scaffold98287_15.2	1	p2	(AT)8	16	400	415	GCCAACATCAACTGCGAGTA
scaffold98322_16.2	1	p2	(AT)6	12	928	939	GTTCAAGAAAGCCGTGGAAG
scaffold98487_12.0	1	p2	(AT)6	12	309	320	CATCCTCATAACCCCCACAC
scaffold98557_14.8	1	p2	(AT)6	12	2293	2304	CTTAAGACCCGATGCCTTTG
scaffold98577_13.9	1	p2	(AG)6	12	1016	1027	TTCTCTATCAATCGGCTGGG
scaffold98867_15.7	1	p2	(GA)7	14	488	501	AAACCACCCCGTCTTTTCTT
scaffold98871_13.8	1	p2	(AG)7	14	270	283	TCCTTTCCATCTTCCCTCCT
scaffold99059_14.3	1	p2	(CA)6	12	1933	1944	AAATGAGACAAATGTGGGGG
scaffold99064_15.8	1	p2	(TC)6	12	1078	1089	AATCTTGTGCACTGTGTGCC
scaffold99164_15.5	1	p2	(CA)6	12	1410	1421	GCGGCATCATCTTCTCTCTC
scaffold99432_16.3	1	p2	(CT)8	16	550	565	CGTCCGTCCCATAAACAACT
scaffold99434_15.6	1	p2	(AT)6	12	4425	4436	TCCGTACAACTAACATCCTCCC
scaffold99474_16.4	1	p2	(GA)8	16	176	191	GGCCTGATTTGCAATACTGTG
scaffold99531_15.1	1	p2	(CT)6	12	698	709	ACCCTCAAGCATCAGCATTC
scaffold99667_14.1	1	p2	(TC)9	18	2024	2041	CTACCTTAGGCCAACCCACA
scaffold99668_12.1	1	p2	(TG)6	12	341	352	GATTTTGCACGAAGCAATGA
scaffold99774_13.8	1	p2	(AG)6	12	394	405	TGAAAATGGGTACCACACACA
scaffold99932_15.6	1	p2	(CT)6	12	1455	1466	GCGCTACATGCTTTGTGAAT
scaffold100046_12.	1	p2	(TA)10	20	328	347	GCAGGTTCGAAGTAGGGTGT
scaffold100151_15.	1	p2	(AT)9	18	3923	3940	ATCTTTTGCGATGCCTCAAG
scaffold100153_13.	1	p2	(TA)6	12	399	410	CCCCTTTGAGCTTTTTAGCC
scaffold100162_13.	1	p2	(TA)7	14	171	184	CGATTGGGCCTATCCTATCA
scaffold100272_11.	1	p2	(AG)6	12	79	90	GGATTTTCGAAATTTTCTCGC
scaffold100288_16.	1	p2	(AT)8	16	457	472	GCGAAACAATGATCGCATTA
scaffold100746_10.	1	p2	(AT)8	16	463	478	CTTTTTCGGGTTTGGACGTA
scaffold100776_13.	1	p2	(AG)6	12	65	76	ACAATACAACTGTCGAGCTGAA
scaffold100999_13.	1	p2	(CA)7	14	295	308	GGCCCACGATGGTTATTAAA
scaffold101406_11.	1	p2	(AT)7	14	450	463	TGGAATTCAATGGCAGATGA
scaffold101547_12.	1	p2	(TA)6	12	378	389	AACCGTGTGTACAACAATAGCAA
scaffold101660_12.	1	p2	(GA)10	20	95	114	CCTCTCCTCTCAACTTGCTTG
scaffold101684_13.	1	p2	(TG)9	18	99	116	TAATTGGCCCTTGATCTCCA

scaffold101705_13.2	1	p2	(CT)7	14	126	139	GCATCTCTTGCTCTCTCGTTG
scaffold101726_19.2	1	p2	(GA)9	18	1618	1635	GCAGAAGGAACTGATGGCTC
scaffold101865_18.1	1	p2	(TC)6	12	668	679	CCCTCAAACCTACTGTCGGA
scaffold101888_19.2	1	p2	(GA)7	14	559	572	CCCAATTCTAGCAGCAGAGC
scaffold102077_17.4	1	p2	(AT)8	16	234	249	CTCTTGACTTCTGATCCGGC
scaffold102318_10.6	1	p2	(CA)7	14	337	350	CCTTATGAAAAACGTTGGGG
scaffold102497_12.0	1	p2	(AT)7	14	64	77	GAGCCTCGGATTTCCTGTTT
scaffold102773_14.2	1	p2	(AG)6	12	300	311	CTAGGGTTAGCATGCTTGGG
scaffold102849_12.5	1	p2	(AT)7	14	258	271	ACGGATGCATTCGACATTTA
scaffold102891_15.1	1	p2	(AG)6	12	109	120	ACTGAATTTGGGGTTGTTGG
scaffold103040_11.3	1	p2	(AT)7	14	241	254	GGATTGGGCTTTGAGAATGA
scaffold103208_12.6	1	p2	(TA)6	12	326	337	CTTTTTGCCCTCGTATGCTC
scaffold103262_10.7	1	p2	(TC)7	14	43	56	CAGAAATTGCCTTGGTTGTTC
scaffold103433_12.3	1	p2	(TA)7	14	365	378	TTGACGCTGAAGTTAATGCAA
scaffold103583_13.6	1	p2	(CT)6	12	162	173	GGTCTTCTAGCCTCTCTCGCT
scaffold103610_17.8	1	p2	(TA)9	18	349	366	CGAATCGCATTGCTATCATC
scaffold103622_10.9	1	p2	(TC)6	12	183	194	TTACTTTCCGTTTTGGGACG
scaffold103869_16.7	1	p2	(CT)6	12	357	368	GAAACACTTTCACCTCCCCA
scaffold104571_10.1	1	p2	(CT)7	14	174	187	GGCAAACAGGTCCCTAAACA
scaffold104583_13.6	1	p2	(TC)6	12	1378	1389	ATGGGATAGCACTTTTGCCA
scaffold104709_11.5	1	p2	(TA)9	18	43	60	CGGATTTAAGGGTTATTACCTGAT
scaffold104722_11.0	1	p2	(AT)6	12	612	623	TTCTCCTCCCCTTAGCTTCC
scaffold104808_15.6	1	p2	(CT)6	12	226	237	CGTCGAAAGGGAAAGAAACA
scaffold104827_14.3	1	p2	(AT)6	12	254	265	TTTTGGGGTACATGCCACTT
scaffold104838_12.2	1	p2	(CT)8	16	675	690	CACAAAATGGATCGAAACGA
scaffold105003_13.3	1	p2	(GT)6	12	760	771	AAAAGCGTTATGCGTCGAGT
scaffold105045_11.7	1	p2	(GT)6	12	202	213	TTCCACAACTGCAATTTACTGTG
scaffold105151_16.4	1	p2	(CT)6	12	355	366	AGGATTGGAAGCAGTGCCTA
scaffold105170_17.4	1	p2	(AG)8	16	3103	3118	GAGACACGTTGGGTCTGGTT
scaffold105173_15.0	1	p2	(GA)6	12	2248	2259	CACAACAGGAGGAGGCACTT
scaffold105290_16.1	1	p2	(CT)9	18	1011	1028	CCAAGATTGAGGTCCGTTTC
scaffold105314_16.2	1	p2	(AG)6	12	4149	4160	TATTCCCAATCTGGGCACTC
scaffold105325_13.7	1	p2	(AT)6	12	287	298	GGACGCACCAGATTGTTTTT
scaffold105496_12.8	1	p2	(TA)7	14	176	189	TTTGACATCAACGGATGGAA
scaffold105518_16.2	1	p2	(AT)6	12	105	116	GAAAGTGGCTTTGATGGAGA
scaffold105585_11.9	1	p2	(TA)6	12	218	229	TGCAATATGTTTATTTCGGGA
scaffold105617_13.7	1	p2	(AT)6	12	139	150	CCACATTTTTCCCGACTGTT
scaffold105757_15.5	1	p2	(TG)7	14	174	187	GCCTGAATGTAATGCCGAAA
scaffold105937_13.6	1	p2	(TC)7	14	97	110	CCCCTTTGTCAACTTAGGCA
scaffold106235_14.3	1	p2	(CT)7	14	806	819	CAGCTTTCGGCTTCTTCTTG
scaffold106473_13.2	1	p2	(AG)10	20	179	198	GGAAATCCCGTACGCTATCA
scaffold106474_15.5	1	p2	(AG)6	12	2320	2331	TAAGCAATACACGCACAGGG
scaffold106499_16.3	1	p2	(TA)8	16	1052	1067	TGATATGCAAGAATTGTCACCC
scaffold106528_20.0	1	p2	(TC)7	14	764	777	GGCCTCAGCAGCTTCTCTAC
scaffold106593_10.7	1	p2	(TA)6	12	327	338	CGTGCGACCAAATGTGACT
scaffold106603_15.4	1	p2	(AT)6	12	4496	4507	TGTAGGCTTTGGTTTCCATTG
scaffold106633_16.4	1	p2	(AG)8	16	746	761	TGGTGTCTTGATTGAGCGAG
scaffold106666_13.5	1	p2	(GA)6	12	31	42	GAAGATGGAGTAGAGAGAGAGATTT
scaffold106678_12.0	1	p2	(TA)6	12	466	477	CATTTCAACCCACCATCTCC
scaffold106707_13.4	1	p2	(GT)7	14	257	270	GAACCGGATTTAGAGCAATCA
scaffold106769_13.9	1	p2	(TA)9	18	639	656	GAACAAATCTGGGCCATCAG
scaffold106778_18.3	1	p2	(TA)6	12	351	362	GGTGTGGTGGGGACATTTTA
scaffold106974_15.5	1	p2	(CT)7	14	1596	1609	ACACCCATTGCTGTGTGAGA
scaffold107088_13.0	1	p2	(AT)6	12	1588	1599	ATCCAACACCGCATCTTCTC
scaffold107115_12.5	1	p2	(TG)6	12	90	101	AGACTAGAACGTAGACCTGGCA
scaffold107221_12.7	1	p2	(AT)6	12	188	199	CAATTTAGCCCGAAATGAGC
scaffold107252_16.7	1	p2	(TA)6	12	4607	4618	GAGGTGGCGCTCTGCTATAC
scaffold107257_14.9	1	p2	(TA)7	14	750	763	TCAACAATCTCAAACTGCAACC

scaffold107337_15.4	1	p2	(TA)6	12	310	321	ACAACCTGGGTATCCCAAAA
scaffold107459_15.5	1	p2	(AT)8	16	285	300	ACGGAATTGAATTTGGGACA
scaffold107504_10.1	1	p2	(AT)12	24	458	481	CATGCCAAGTGGTGTGATCT
scaffold107603_10.1	1	p2	(AT)6	12	102	113	GCTTGGTGAAGGAAGTGAGG
scaffold107689_12.5	1	p2	(AG)6	12	204	215	GAAACGACGGGAAGATGAAA
scaffold107806_11.7	1	p2	(AC)6	12	155	166	GCGCAGATCTAATGGTCCAG
scaffold107931_15.4	1	p2	(GA)11	22	2966	2987	ACCGGAGAGTGGTGGTGTAG
scaffold108279_15.4	1	p2	(TA)6	12	222	233	CCGAATGATGTGCATTTTTG
scaffold108368_11.0	1	p2	(TA)6	12	92	103	ACATTCAGGCCTTTTGAACA
scaffold108577_20.9	1	p2	(AT)6	12	108	119	TTCTAACTCCATTTGTAATAGTAAGG
scaffold108710_15.7	1	p2	(AT)8	16	141	156	AGAAAGGAGATGGAGCGTGA
scaffold108812_10.5	1	p2	(GA)6	12	160	171	GGGTGATGAGGCTTGAAGAA
scaffold108860_14.0	1	p2	(AT)11	22	2438	2459	CATGCATGCAAAACTGAGGT
scaffold109050_14.4	1	p2	(AC)7	14	1232	1245	TGGGTGGAACTTCTTGCTTT
scaffold109061_17.0	1	p2	(AT)8	16	1609	1624	TTTCAAACGAATTGCAGCAG
scaffold109161_15.9	1	p2	(AG)7	14	2428	2441	AGCTGGTAGCCATTCTCCTG
scaffold109174_17.6	1	p2	(AG)8	16	327	342	TGCCTGAAAATGTCTGCAAG
scaffold109379_14.4	1	p2	(AT)7	14	233	246	CTCGTTCCCAAGCCTCCTAT
scaffold109456_15.4	1	p2	(CG)6	12	2690	2701	CACTGGGTTATTCCAATCCG
scaffold109463_16.4	1	p2	(TC)10	20	753	772	ATTAAATCCCCCGAAGAAGC
scaffold109545_14.2	1	p2	(TA)13	26	412	437	TGGGATATCGTCTAACCAGCA
scaffold109557_15.4	1	p2	(GC)6	12	125	136	GCAAATCCCAAAACCGAATA
scaffold109834_20.1	1	p2	(CT)6	12	459	470	ATCGAAAAGAGGTGAGCGAA
scaffold110045_10.5	1	p2	(AG)7	14	365	378	GACCGCGAAGTTTACATGGT
scaffold110087_15.8	1	p2	(CT)7	14	299	312	ACCAACCCAACCCATTATCA
scaffold110177_14.0	1	p2	(AC)7	14	1182	1195	GGCAGGTCATGTGTATGTGG
scaffold110178_10.9	1	p2	(TC)7	14	86	99	TGAAATGCCTCCGGTTAGTC
scaffold110196_15.5	1	p2	(AG)6	12	272	283	TTGGTTTGTTGCTTGATTGC
scaffold110232_13.7	1	p2	(AT)6	12	175	186	CCTTCTCCACCACCACTTTG
scaffold110245_15.4	1	p2	(AT)7	14	114	127	CCAGGTGAGCTAGCCCATAA
scaffold110366_15.5	1	p2	(GA)6	12	652	663	GGTGTGTGGAAGGAAGGTGT
scaffold110486_12.6	1	p2	(AC)7	14	277	290	AAATTCCATGGCCTTTCACA
scaffold110519_10.9	1	p2	(GT)9	18	389	406	GAGTGTGTGTCGTGGGTGTC
scaffold110535_14.8	1	p2	(CT)6	12	2021	2032	GGGATTTCAGCGACGATTTA
scaffold110711_12.6	1	p2	(AT)6	12	375	386	AGAGGAGGGCTTCAACATGA
scaffold110847_12.0	1	p2	(CT)6	12	163	174	CAAAGGATCGAAAAACGAGG
scaffold110891_10.4	1	p2	(TC)8	16	371	386	TAATGTGGAACCATAGGGGC
scaffold111070_16.3	1	p2	(AG)6	12	113	124	ACCTATCGTCTCCTCCCGAT
scaffold111248_15.1	1	p2	(CT)7	14	35	48	GCCTCTTCTCTGCTAAAAGCC
scaffold111277_14.2	1	p2	(TG)7	14	226	239	TGAAAAGATTTGAAAAACATTCAAC
scaffold111400_11.6	1	p2	(CA)6	12	260	271	CTCTCGCCATCTTCGACACT
scaffold111409_20.9	1	p2	(CT)6	12	306	317	TAGGCATGGCCTCAACTACC
scaffold111442_16.6	1	p2	(GA)6	12	114	125	GATGGAACGGGGATTTGTTA
scaffold111456_15.9	1	p2	(GA)6	12	458	469	TCGAGCATAAACACATCCCC
scaffold111468_21.7	1	p2	(TC)6	12	61	72	AGCTACACTCACCGTCTGAGAA
scaffold111671_15.9	1	p2	(CT)6	12	895	906	CGATTGCTCTCCGATCTCTC
scaffold111690_14.2	1	p2	(CT)8	16	327	342	GCAAGACATGCAAGGCAGT
scaffold111946_19.4	1	p2	(AG)7	14	360	373	TTGGGTTGTCCCTTGATCTC
scaffold111984_16.3	1	p2	(TA)8	16	366	381	CAGCAAAGTGCTAAATGGTTCA
scaffold112119_15.4	1	p2	(TA)9	18	200	217	TTGGTGGTTTGTATGCTATCG
scaffold112224_14.1	1	p2	(AT)10	20	4280	4299	GCCCCTCCTAGCAATTTGA
scaffold112265_10.6	1	p2	(AT)9	18	110	127	ACTCCGCATGTGTGTTGAAA
scaffold112267_10.4	1	p2	(AT)8	16	63	78	TTGGGATTAAGGCTTTGGTG
scaffold112270_13.2	1	p2	(AT)6	12	116	127	GAAACAACGAATCCATTAAGTGAAG
scaffold112290_15.2	1	p2	(AT)7	14	481	494	TTTCGGGACACGTTCTCTCT
scaffold112382_16.8	1	p2	(CT)6	12	309	320	CCCCTCATTTTCATTCCAAA
scaffold112447_13.6	1	p2	(CA)6	12	2553	2564	TGTCATTGGTTGTGGCTGTT
scaffold112464_15.4	1	p2	(TA)7	14	1726	1739	AATGCCCCTATTTTTGGAGG

scaffold112500_11.	1	p2	(AT)7	14	204	217	ATGGACGTCGTGACCACATA
scaffold112660_13.	1	p2	(GA)6	12	116	127	CACAATGGGGGTATTTGCTT
scaffold112791_17.	1	p2	(CT)8	16	953	968	CCCTAACTCGACCCAGATCA
scaffold112990_15.	1	p2	(TA)9	18	1315	1332	TCGAGTTTGTTTGCGAGATG
scaffold113105_11.	1	p2	(TC)6	12	175	186	TCCCAATCAAGACAAGTCCC
scaffold113114_15.	1	p2	(AG)6	12	644	655	TAATTTGGTTGGCCCATTGT
scaffold113121_15.	1	p2	(TA)7	14	111	124	CCATTTGCAATACTAAGGCTTTT
scaffold113201_16.	1	p2	(CT)6	12	861	872	TTTCAAGAAAAGGGTGCCAT
scaffold113205_12.	1	p2	(TA)7	14	186	199	ACGTCGGTTTGGTTTAAAGG
scaffold113231_10.	1	p2	(TA)7	14	99	112	GACCCATTTAGAACCCACGTT
scaffold113488_17.	1	p2	(TA)8	16	210	225	TGGAACAATTTTTGCCACAT
scaffold113630_13.	1	p2	(GA)6	12	126	137	GAAAAACGACGTGAGGGAGA
scaffold113781_17.	1	p2	(AT)9	18	163	180	TTTTGGAGTATTCCGTGCCT
scaffold113924_12.	1	p2	(AT)9	18	730	747	CACTTGACGAGGTCACTGGA
scaffold114052_13.	1	p2	(AG)7	14	386	399	AATATTTCATTCATGCCACGC
scaffold114239_12.	1	p2	(TC)6	12	1733	1744	GTCGAGGAGTATACGGAGCG
scaffold114339_10.	1	p2	(TA)7	14	162	175	ACGTAAAAACCCTTCCACCC
scaffold114404_16.	1	p2	(TA)6	12	195	206	ATGCATGCACGTGAATATGG
scaffold114476_10.	1	p2	(TA)7	14	218	231	ACGGATATGCCCTTGTATGC
scaffold114555_13.	1	p2	(GA)8	16	50	65	GATGCTTACCTGAACAGCACA
scaffold114904_11.	1	p2	(TC)6	12	115	126	ACAAGGATTGCGAACTCAGC
scaffold114905_10.	1	p2	(TC)7	14	113	126	CCCCTCTCAACAACCACAAT
scaffold115033_17.	1	p2	(CT)12	24	4753	4776	AGAAATTGCCTGCTTCCAAA
scaffold115143_15.	1	p2	(GA)7	14	258	271	CCGGGTTTAAAGCAATCAAA
scaffold115376_15.	1	p2	(CT)9	18	3613	3630	CCACTTCCTAGGCAAACACC
scaffold115419_14.	1	p2	(CT)8	16	296	311	GGGACTGGACCAAGAATTGA
scaffold115517_18.	1	p2	(TA)8	16	706	721	GGTGCAGTGGTAGAGCATCA
scaffold115672_15.	1	p2	(GA)6	12	388	399	TTGACCACAATCAAACACCAA
scaffold115696_14.	1	p2	(CT)6	12	583	594	TTGATTTCCCACCACCATTT
scaffold116113_10.	1	p2	(AG)6	12	52	63	GGTGGTGTGGAGGAGAGAAG
scaffold116128_11.	1	p2	(AT)7	14	762	775	TGATTTTCCATTATTTTCGTTGG
scaffold116210_14.	1	p2	(GT)7	14	2457	2470	TTAATGCTTTGAAGGGGTGC
scaffold116266_12.	1	p2	(AT)6	12	659	670	ACAAATCCCACCTGCGTAAG
scaffold116286_18.	1	p2	(CT)6	12	115	126	TAATTCGTATTTCGGTCCGC
scaffold116335_13.	1	p2	(TA)6	12	226	237	CCCAAAAAATTTAACGACCCA
scaffold116391_14.	1	p2	(AT)7	14	327	340	TGTTACATGGTTGTCGGTTCA
scaffold116554_10.	1	p2	(AG)7	14	54	67	CCATGTTGTTTGTAATTATTGTAGGG
scaffold116716_16.	1	p2	(AT)7	14	736	749	ATTTGGAAACCTCCCACTCC
scaffold117227_10.	1	p2	(TC)6	12	335	346	CTCTCGCTAGGCGACTTTGT
scaffold117620_17.	1	p2	(TC)8	16	190	205	GCAGCTAGGCTCCCTCCTAT
scaffold117645_10.	1	p2	(GA)6	12	75	86	GGGGTCGGTGGAAAAATAGA
scaffold117924_15.	1	p2	(AT)7	14	2134	2147	CAAAGAACCAACATCCACACA
scaffold118160_16.	1	p2	(CT)14	28	396	423	ATGTCACGTCAAGCATCAGC
scaffold118164_10.	1	p2	(GC)6	12	359	370	CGCTATGAGTCACGGGTACA
scaffold118256_12.	1	p2	(AT)8	16	274	289	TGAAACAATGCCTGGAAACA
scaffold118351_14.	1	p2	(TA)7	14	160	173	GCAACTGTACACGTGTGGCT
scaffold118603_16.	1	p2	(AG)7	14	316	329	CGAAGAATTTTGTGCCATGA
scaffold118763_12.	1	p2	(AT)9	18	566	583	TTGTTGAACGCATAATTCGATA
scaffold118777_15.	1	p2	(AT)6	12	148	159	CGTTCCTCAGAGTTTCCAGC
scaffold118901_12.	1	p2	(AG)6	12	66	77	CACAAACTTTCTGGATTGACTTTG
scaffold118931_18.	1	p2	(AC)7	14	62	75	TCAACACTCTGTTTTTCTCTCACA
scaffold119077_11.	1	p2	(GA)6	12	537	548	CGTGTCCTCCTCAAACTGGT
scaffold119101_14.	1	p2	(AT)9	18	45	62	TCTATTATATGTCATGTTTTGCATTTT
scaffold119124_17.	1	p2	(TC)6	12	103	114	CCCATCCCTTAATCAACCCT
scaffold119131_10.	1	p2	(GA)6	12	68	79	GACGCGAGATTTACGTGGTT
scaffold119299_16.	1	p2	(GA)6	12	381	392	TTTCATGTTTAGCATTTGCG
scaffold119359_14.	1	p2	(TC)7	14	226	239	CAATCCGGTGATGTGTCAAG
scaffold119453_13.	1	p2	(GA)7	14	543	556	CTTTGCGACGTAATTCCCAT

scaffold119511_16.2	1	p2	(CA)8	16	1252	1267	GCAGGAAGTCATGGTTGCTT
scaffold119593_14.2	1	p2	(TA)11	22	1250	1271	ATTTAATCACGTGCAACGCA
scaffold120058_15.3	1	p2	(CA)10	20	1031	1050	CATCCAATAGCCGAACAAAAA
scaffold120216_16.8	1	p2	(TC)6	12	1531	1542	AACTGCGATGCTCCAAAAGT
scaffold120263_12.8	1	p2	(AG)10	20	613	632	AGAAAGATCCCTGCGGTTTT
scaffold120352_15.1	1	p2	(TA)10	20	39	58	AGCACAATACAAACATGTCCAC
scaffold120409_11.9	1	p2	(GT)6	12	105	116	TTGTGTGTTATACGTGTGGGTG
scaffold120583_11.1	1	p2	(AT)7	14	194	207	TCAAGGTCTTCGCTGGTTCT
scaffold120643_14.5	1	p2	(TA)9	18	356	373	TATATGATGTAGGCCGCGTG
scaffold120882_14.8	1	p2	(TG)7	14	1075	1088	TGGACATGGCAATTATTCTTGA
scaffold120953_15.0	1	p2	(AG)7	14	564	577	ATGGGTTCCTTACCCCTTTG
scaffold121065_18.7	1	p2	(GA)6	12	290	301	GACAGAGGTCCCCTGGTTTT
scaffold121079_20.0	1	p2	(AT)9	18	330	347	CCAAGTCTCACCTACAAATCCA
scaffold121135_12.0	1	p2	(AG)6	12	56	67	GCAAGGGAAACTGATGGTGT
scaffold121210_15.3	1	p2	(TA)9	18	45	62	CGGATTTAGCGGTTATTACCTGA
scaffold121646_16.7	1	p2	(AT)7	14	1132	1145	GTTTAGATTCCGCATCAGGC
scaffold121793_12.6	1	p2	(GT)7	14	138	151	CAGTTGTGTTGTGGCAGCTT
scaffold121822_11.9	1	p2	(TC)6	12	82	93	TTTGAGATCGGAGTGGCTCT
scaffold121845_16.0	1	p2	(TA)7	14	616	629	ATCCGACGGTTGTAGTGGAG
scaffold121887_16.9	1	p2	(AG)6	12	3958	3969	TTCAACCGTGCGTGTATGTT
scaffold122450_16.6	1	p2	(GA)6	12	165	176	AAGATGATGGTGAAAGGGGA
scaffold122524_10.6	1	p2	(AT)6	12	91	102	ACTCACTTAGGGATATATTTAGGGAA
scaffold122594_10.8	1	p2	(TA)7	14	286	299	GACATGCATCGTTTGTACTCTTC
scaffold122648_10.4	1	p2	(AT)11	22	852	873	GGCTCAATTTTAATGGGCCT
scaffold122699_12.7	1	p2	(AC)6	12	324	335	GATCAACGCCCCATATTGTT
scaffold122819_16.1	1	p2	(TC)7	14	2446	2459	GATATTTCAGGGTCCCCGTT
scaffold122877_13.1	1	p2	(AC)6	12	389	400	TCTCCTTCTCAGGATCTCCG
scaffold123109_10.7	1	p2	(TC)7	14	63	76	GAACGGGCAGTACTCCAAAA
scaffold123324_13.3	1	p2	(CT)6	12	216	227	AAATGAAGGGTTGAGCATCG
scaffold123673_11.1	1	p2	(GA)7	14	232	245	AAGAACGTTGGGAGGGAAGT
scaffold123681_15.6	1	p2	(TA)7	14	807	820	CTGAACCTGAACCACCAACC
scaffold123762_14.3	1	p2	(AT)9	18	379	396	GTTGATAAATTACAAAAATTTAAGCG
scaffold123928_14.5	1	p2	(AG)6	12	556	567	ACACCAACCCATTTGCTCTC
scaffold123946_16.3	1	p2	(GA)6	12	70	81	TGTGTATATCTGATAGCCGTAGCA
scaffold124340_10.0	1	p2	(TA)8	16	47	62	AGGGGAGTTATCACTGGATCA
scaffold124770_14.3	1	p2	(AG)6	12	1431	1442	TAGAGATGCGAAGATGGCCT
scaffold124784_10.9	1	p2	(GA)8	16	756	771	GTCCCCAGCCTCAGATACAA
scaffold124800_15.2	1	p2	(TA)7	14	1157	1170	CAGATGATCACACGCTGCTT
scaffold124869_16.5	1	p2	(AT)8	16	6182	6197	TCCTCTGCCTTATTGATGGG
scaffold124892_10.0	1	p2	(AT)13	26	215	240	CGTGTTACCCTCTCAATTTATCA
scaffold124952_14.7	1	p2	(GT)6	12	705	716	TTTAGGCATTCCCACCTTTG
scaffold125082_19.0	1	p2	(CT)6	12	171	182	CCCAACTCTTCGGCTCAATA
scaffold125401_11.6	1	p2	(AT)9	18	49	66	GTCTGCAAGAAAATGGGTGG
scaffold125498_15.4	1	p2	(TC)6	12	206	217	AGAGATTGTGGGGCTTGATG
scaffold125582_10.7	1	p2	(TC)6	12	383	394	ACCAACCCAAACCCACTTTC
scaffold125628_17.8	1	p2	(CT)6	12	101	112	AGCATCTCTCTCTTGCTGTCA
scaffold125686_10.8	1	p2	(TA)9	18	297	314	CATTTTGACATGATCGACGG
scaffold125739_20.2	1	p2	(AT)8	16	802	817	CGTGTCTACAAAACTTGCTGC
scaffold125758_11.3	1	p2	(AG)8	16	424	439	TTCAAGGCATGGGAGGATAG
scaffold125767_14.8	1	p2	(AT)6	12	957	968	CACACGATAGAGGCAGACGA
scaffold125781_15.7	1	p2	(TA)11	22	293	314	TCAACTTTCGGAAGCGTACA
scaffold125784_10.8	1	p2	(AT)6	12	581	592	CGTCCTATTGGCCCATTTAT
scaffold125793_13.6	1	p2	(AT)8	16	1538	1553	TGCGCTTGGTTTGTAGACTTT
scaffold125849_13.7	1	p2	(TA)6	12	560	571	CTGTCTCCGGTCCATGAAAT
scaffold125852_15.0	1	p2	(TC)9	18	750	767	GCGAAAACAACAGACAGCAA
scaffold126248_15.2	1	p2	(AG)7	14	5697	5710	GGCTTGTGTGCATCTTCTTTC
scaffold126303_13.4	1	p2	(AT)6	12	267	278	TGTCGTGGTTCGGATATTCA
scaffold126342_15.7	1	p2	(AT)6	12	2128	2139	ACATATTTTTCCCCTTTCCACA

scaffold126470_15.	1	p2	(AG)6	12	2681	2692	CAAAATTGCGTTTTATGGGG
scaffold126743_11.	1	p2	(CT)8	16	423	438	TCGCCATTTCCCTGTCTTAC
scaffold126855_12.	1	p2	(TA)7	14	40	53	TCGTGATATTGGGAAACAATG
scaffold126879_14.	1	p2	(TA)10	20	419	438	GCATTAAAATTGTTGGTCCCT
scaffold126943_10.	1	p2	(GT)6	12	89	100	TAGGATACCCTCCCAAACCC
scaffold127066_15.	1	p2	(AT)8	16	685	700	GCGGATTTTATTCTCGTTCA
scaffold127079_10.	1	p2	(AT)6	12	390	401	TGGAAAAGGTAGGGACAAAA
scaffold127175_16.	1	p2	(AT)6	12	427	438	CAAGCAACAAGCCAATAGCA
scaffold127388_15.	1	p2	(GT)7	14	263	276	AGTTATCAAGATGGCCACGG
scaffold127434_12.	1	p2	(TA)8	16	130	145	TTTACCCAAAACACCCCTGA
scaffold127499_18.	1	p2	(TG)8	16	282	297	TTTTTGGGAAATCCTTGCAC
scaffold127512_11.	1	p2	(AT)6	12	602	613	TATCGATTCACCACACGAGG
scaffold127733_15.	1	p2	(TC)6	12	388	399	ACGAAAGTGAACTCAACCCG
scaffold127784_15.	1	p2	(TA)8	16	48	63	TGCTCCTAGTTAGCACACAACTT
scaffold127801_12.	1	p2	(TA)8	16	45	60	TGAAGTTAGGAAATAAGGAGGTGTT
scaffold128053_15.	1	p2	(TA)7	14	2149	2162	GCCCCATTTTCTTAGGGTTT
scaffold128141_16.	1	p2	(AG)6	12	2128	2139	CTTGGAGGCTCAGAGGTTTG
scaffold128227_15.	1	p2	(TC)7	14	2564	2577	GCATCACCTCTTCTACGGGT
scaffold128276_13.	1	p2	(TG)6	12	317	328	GTGCTTTTAGCTTGGGCAAA
scaffold128364_10.	1	p2	(AT)7	14	219	232	CACGAACGGCTGGAATATCT
scaffold128431_14.	1	p2	(CT)6	12	163	174	TAATAGGTGCGGGTTTGAGG
scaffold128731_12.	1	p2	(GA)7	14	52	65	TGGAGGAATGAAGGTGAAGG
scaffold128748_16.	1	p2	(GA)9	18	589	606	ATGGAGAGAGGGAGGGAGAA
scaffold128752_13.	1	p2	(TA)7	14	106	119	CCCTTGGTATTCTCCCTGTG
scaffold128901_13.	1	p2	(AT)6	12	547	558	TGCTGTGGCAATATGATGCT
scaffold128937_14.	1	p2	(AT)10	20	5618	5637	TGACATACATGGTTTGGGGA
scaffold129128_14.	1	p2	(CT)7	14	610	623	GCTAATGCTTCAGCACCACA
scaffold129149_14.	1	p2	(AG)6	12	459	470	ACACACCCACACCATTGAAA
scaffold129229_14.	1	p2	(TA)7	14	415	428	TAAGGAGATGTGTGCATGGG
scaffold129814_13.	1	p2	(AT)10	20	684	703	CACCTCACTTTCAATGCTCG
scaffold129952_14.	1	p2	(TA)6	12	116	127	CCAAAACTCCACCTTCAACTG
scaffold130133_11.	1	p2	(CT)7	14	246	259	GTTGGCAAACAGGTCCCTTA
scaffold130197_10.	1	p2	(TA)8	16	491	506	TCATGGGGAAAAGAGTTATCA
scaffold130364_10.	1	p2	(CT)11	22	54	75	TTGATTCATACAAGTCATCTTTATGTT
scaffold130409_13.	1	p2	(TA)12	24	37	60	GGAAATAAGGAGGTGTTATGATATG
scaffold130514_15.	1	p2	(AG)6	12	1189	1200	TGTTGTGACTGGATTGGCAT
scaffold130608_15.	1	p2	(TA)8	16	270	285	AAAAATGAACCGTAACCGGC
scaffold130800_14.	1	p2	(TA)6	12	1214	1225	GTGAGAGGAAGACAGGCGAC
scaffold130880_13.	1	p2	(TA)7	14	219	232	ATGCAACTCAAAGGGAGGAA
scaffold130998_12.	1	p2	(TA)10	20	108	127	ATCAATGGCCACAAATGGTT
scaffold131001_11.	1	p2	(TA)7	14	114	127	TGATTTTGGTGTGTTGGCAT
scaffold131003_14.	1	p2	(AT)6	12	513	524	CATAAAACATACCTCGGCATCA
scaffold131096_14.	1	p2	(AT)10	20	485	504	AATCACGTCAATTCCGAACC
scaffold131183_12.	1	p2	(TA)6	12	670	681	TGCCACTATAATTGTATGGTCTCG
scaffold131323_10.	1	p2	(CT)6	12	235	246	CACCTTACCCACCCAACCTA
scaffold131332_14.	1	p2	(TC)6	12	98	109	CACAAACACACTTGGGAGGA
scaffold131342_15.	1	p2	(AT)7	14	849	862	AGCTCTTGAGCATATTGCGA
scaffold131424_17.	1	p2	(TC)6	12	495	506	CTGTGTGCTGGTGCTGATTT
scaffold131576_14.	1	p2	(AT)7	14	165	178	ACGTTTTTGTAAACGTTGTCCT
scaffold131710_12.	1	p2	(AT)9	18	396	413	GTGGACGCTCCAGATTGTTT
scaffold131968_17.	1	p2	(GA)6	12	105	116	ATGGTGCATGCAGTCAAATC
scaffold132012_12.	1	p2	(CT)7	14	447	460	TGGCACCTAAACCATAAGGC
scaffold132029_11.	1	p2	(TA)6	12	50	61	CATTTAGGATATTTTCTATTCTTGCAT
scaffold132146_13.	1	p2	(AG)6	12	467	478	AGGATACCGGAGTGTTCACG
scaffold132174_12.	1	p2	(TA)7	14	739	752	CTCCGCCCAGTTGGATACTA
scaffold132394_14.	1	p2	(AT)10	20	275	294	CACCACCTGTCCACTCAAAT
scaffold132412_16.	1	p2	(AT)11	22	33	54	TTACTCACACGCACACCCAC
scaffold132432_14.	1	p2	(AG)7	14	802	815	CTAGGGCCAAGGAGTTAGGG

scaffold132695_11.	1	p2	(AT)10	20	417	436	AATCACGTCCTTATTAACCAAGTT
scaffold132735_14.	1	p2	(AT)9	18	580	597	GTGATGCATGATGGGTATCG
scaffold132854_10.	1	p2	(TA)9	18	236	253	GGTCTCCGGTCCATGAAATA
scaffold132924_13.	1	p2	(TA)6	12	209	220	GTGAATAGCCGTTGAGGCAT
scaffold132936_13.	1	p2	(CT)8	16	998	1013	AAGCAAAAATCAGACCTAACCG
scaffold133005_13.	1	p2	(AT)9	18	331	348	ACAGAAACATTGACTCCGGG
scaffold133012_14.	1	p2	(AT)11	22	249	270	TTGTGCGAACCATGAAAAAC
scaffold133044_15.	1	p2	(AT)7	14	250	263	GCAAAGGTCGCGAAAGATAC
scaffold133325_13.	1	p2	(TA)6	12	113	124	TATTGGTTATCACCGGATCG
scaffold133413_10.	1	p2	(CT)8	16	234	249	CGACAGAAAGTAACCCCCAA
scaffold133602_11.	1	p2	(AT)7	14	928	941	TGTTACCCCCACTTCATTCA
scaffold133928_18.	1	p2	(AG)6	12	164	175	CGTTTCCATTGTTTAGCCGT
scaffold134022_15.	1	p2	(AT)6	12	205	216	ATTGGTCGAGAGAAAGGGCT
scaffold134090_14.	1	p2	(GT)6	12	37	48	AAGTGATCTACGTCCACGGG
scaffold134151_16.	1	p2	(GT)7	14	721	734	GTATGTCCGGTGCAAGGAGT
scaffold134369_15.	1	p2	(AT)6	12	6372	6383	ATTGCACAAGTTTGGCCTTC
scaffold134409_14.	1	p2	(CT)8	16	239	254	GTTGGCAAACAGGTCCCTTA
scaffold134698_15.	1	p2	(AT)6	12	1643	1654	ATTCAACACACGACATGGGA
scaffold134717_14.	1	p2	(AT)6	12	1177	1188	TAAATAATGATTGGGGGCCA
scaffold134784_11.	1	p2	(CT)7	14	62	75	AGCATCTATTTTCGACCACTGA
scaffold134872_10.	1	p2	(TA)7	14	291	304	CTGCTTAAAGCCCAGTCCAG
scaffold135133_12.	1	p2	(AC)6	12	571	582	CCGCGGTTGAGGATAGATAG
scaffold135138_10.	1	p2	(TA)8	16	172	187	TTTGCTGAGAAATCTAATGCG
scaffold135165_10.	1	p2	(TC)6	12	248	259	CCAACCCATTATCAAAACCC
scaffold135207_10.	1	p2	(TA)6	12	72	83	CCACCTTGAGTTACATGCTCC
scaffold135210_11.	1	p2	(AC)8	16	519	534	TGACGAATTCTCAAGTTTGTCAC
scaffold135252_17.	1	p2	(AG)6	12	662	673	CACTCCCGACCATCTCACTT
scaffold135415_14.	1	p2	(TG)7	14	2382	2395	GAGAGAGAGTCGGCAATTCG
scaffold135523_12.	1	p2	(GA)6	12	241	252	TTCATTCCTCTCCAGCTCGT
scaffold135589_15.	1	p2	(AT)9	18	252	269	TACGATGGGCTTTAAGCAGG
scaffold135600_14.	1	p2	(AT)8	16	112	127	TTTCTGCATTGTTGCATAGC
scaffold135755_10.	1	p2	(TC)6	12	320	331	CCTCAAATCGTTGACACGAA
scaffold135790_14.	1	p2	(TG)6	12	2369	2380	GTGCGCATTGATGTTCCTAA
scaffold135819_14.	1	p2	(TA)7	14	1507	1520	AATGGTCCGGGGTGATTT
scaffold135911_14.	1	p2	(GC)6	12	58	69	TCACAGGCATTGTCAGTGTGT
scaffold136059_11.	1	p2	(CT)6	12	212	223	TGTGCCAAGAACAACTCCTCT
scaffold136111_16.	1	p2	(AT)11	22	274	295	TAGGGATTGAGGGTGATTGG
scaffold136205_15.	1	p2	(AG)6	12	161	172	TGGATAGACTCATAGCCCGTG
scaffold136448_13.	1	p2	(AT)10	20	152	171	TGACATTGCCTAGAAAGTGGG
scaffold136763_15.	1	p2	(AT)9	18	58	75	AGGGCTGAGTACACGAATGC
scaffold137230_16.	1	p2	(TA)9	18	455	472	AAGAACACACAATTCATGTGGAA
scaffold137346_10.	1	p2	(AT)6	12	410	421	TGGATGTCTTTGATTTGCGA
scaffold137390_11.	1	p2	(AG)7	14	251	264	CTATAGCCCCCGATTCACAA
scaffold137438_12.	1	p2	(AG)6	12	607	618	ATTGGGAGAAAAGAGGGGAA
scaffold137780_11.	1	p2	(AT)7	14	219	232	AAGAGGGTTGATGGGTGATT
scaffold137789_10.	1	p2	(CA)10	20	130	149	TCCATTCCGAAAATCAAAGG
scaffold137813_16.	1	p2	(AC)6	12	706	717	AAATGAAACATCAACAATCCAAA
scaffold137897_14.	1	p2	(AG)9	18	566	583	TTAATTTCAGTCCGGGAACG
scaffold137920_18.	1	p2	(TA)6	12	72	83	AAAATCAAAGGCCCACAATG
scaffold138057_13.	1	p2	(GA)8	16	488	503	TGTGTATGTGTGAGTGTTCGTGA
scaffold138194_18.	1	p2	(TC)6	12	948	959	AATCCATGATCCGAAAATGC
scaffold138213_13.	1	p2	(AG)6	12	157	168	CCAATGGAACAGTAGCCGAT
scaffold138330_14.	1	p2	(GA)8	16	346	361	AACACAGAGACAAGCACCCC
scaffold138477_14.	1	p2	(GT)7	14	32	45	TTGTGAGTGACTGCGTGTGA
scaffold138478_16.	1	p2	(AT)7	14	401	414	ACGGTCGAGAAAGAGTCGTG
scaffold138523_14.	1	p2	(AG)7	14	313	326	GGTCCTTGAACAGGACAGGA
scaffold138569_11.	1	p2	(AT)6	12	1608	1619	CCCATCCTCATTTTTCTTTCA
scaffold138639_10.	1	p2	(TA)6	12	194	205	CACGTGTCAGCCGAAAGATA

scaffold138708_10.	1	p2	(AG)6	12	212	223	GAATTTTTCGGGTTTTGGGT
scaffold138744_14.	1	p2	(AG)6	12	51	62	CCCATGTTGTAATTAATGTAGGGA
scaffold139049_13.	1	p2	(TA)7	14	115	128	CCTTAAATCAATCCCAGCCA
scaffold139129_15.	1	p2	(TA)8	16	872	887	CTCCCACGCACACATACATC
scaffold139144_10.	1	p2	(AG)6	12	222	233	TGGTTACTGTTCCTCAGCCC
scaffold139226_15.	1	p2	(CT)8	16	515	530	TTCTCAGTTCTCCCCTCAAA
scaffold139487_12.	1	p2	(TC)6	12	172	183	TTCACGTGGACTGCTTTCAG
scaffold139578_12.	1	p2	(TA)7	14	234	247	ACTCCGTTGAATCTTGCCAT
scaffold139640_10.	1	p2	(TA)6	12	317	328	TCAGGGGCATATGTGTCAAA
scaffold139797_11.	1	p2	(GA)8	16	72	87	GTCCACGGTGGTTTGAGAGT
scaffold140267_12.	1	p2	(CT)8	16	590	605	CCAAGTTTGGGACTTAAGCG
scaffold140311_14.	1	p2	(AG)7	14	281	294	TATATTGTGGGGTGGATGGG
scaffold140332_13.	1	p2	(AT)6	12	754	765	CCAGCATTGTTTCCCATTTC
scaffold140346_15.	1	p2	(CA)6	12	124	135	AATATCCGATCCCTTGGAGC
scaffold140372_11.	1	p2	(AT)9	18	429	446	CCACATTTGAAGGTGATCTTTC
scaffold140654_10.	1	p2	(AT)6	12	116	127	CCAATCTAGGGTTCATCACCA
scaffold140657_12.	1	p2	(AT)6	12	395	406	CGAACGAATATGTTGCATCC
scaffold140788_19.	1	p2	(AT)6	12	112	123	AACTACGAGCATCATCATGTGTTT
scaffold140801_14.	1	p2	(AG)7	14	100	113	TCCACTGCCAATGAAATGAA
scaffold140806_10.	1	p2	(AT)11	22	757	778	GATTGGATGAGAAGAACCGC
scaffold140823_20.	1	p2	(TC)6	12	245	256	TTTGTCGGGTCATTACTATTACGA
scaffold140863_16.	1	p2	(CT)10	20	186	205	AGATCATCTCGGGTCCAAGG
scaffold140891_16.	1	p2	(AT)8	16	2916	2931	ACGGTCCGAGTTCATAGGTG
scaffold140953_14.	1	p2	(TA)10	20	109	128	ACCATGTTTCCATCGGTTGT
scaffold141180_14.	1	p2	(GA)6	12	117	128	TCTCTCTCAAACGCATGTGG
scaffold141436_14.	1	p2	(AG)8	16	93	108	TCTCTCTCTGACGCCATTCA
scaffold141497_14.	1	p2	(GA)6	12	32	43	TGAGTAAAACGTGTTTGTCAGAA
scaffold141554_18.	1	p2	(CT)7	14	138	151	GGATCGAAAAGAGAGGGAGG
scaffold141808_16.	1	p2	(CT)6	12	113	124	TCTGCTACACCCAAAATCCC
scaffold141860_12.	1	p2	(TC)6	12	190	201	AATGGATGAAAAGCTGCCAC
scaffold141889_12.	1	p2	(AT)7	14	610	623	AGCCTTCAGATCCCCTGTTT
scaffold142090_15.	1	p2	(TG)6	12	498	509	TGCAAAATACCTTTTGTCGG
scaffold142252_15.	1	p2	(AT)6	12	3169	3180	TGGAGTCCTAAACTAAACCTCTAAAA
scaffold142265_10.	1	p2	(AC)6	12	173	184	GCTGCAATTCCTATTCAGCA
scaffold142291_17.	1	p2	(CT)10	20	6690	6709	ACCCTATTTTGGCGTAGCCT
scaffold142434_16.	1	p2	(AT)9	18	46	63	TCTTGATAGTACTTTTCATGGAACTTT
scaffold142840_16.	1	p2	(AT)7	14	4138	4151	ATTGTTGCTTGAATGAGGGC
scaffold142854_11.	1	p2	(AT)7	14	64	77	TTTTATTTTTGTGTGGTTTTGATTT
scaffold142899_16.	1	p2	(GA)6	12	316	327	AGAGATCGACGCCTTGACAT
scaffold142945_12.	1	p2	(TA)7	14	1263	1276	CATATCAGCCAAAGGGAGGA
scaffold142970_11.	1	p2	(GA)7	14	50	63	AAATGCAGGGAAGATTGTGG
scaffold143391_14.	1	p2	(GA)6	12	848	859	GGAACATGTGTGTGCTCCAG
scaffold143536_11.	1	p2	(GA)6	12	107	118	CCGAGATGGCTGCATTAAA
scaffold143599_16.	1	p2	(TA)6	12	1213	1224	GATTCGTGTCGGATTAGCGT
scaffold143600_13.	1	p2	(AT)7	14	49	62	TTGCACAGTACATGCGTTCA
scaffold143614_14.	1	p2	(AT)10	20	1100	1119	ATTCTGAGCTGGCGTGAAAG
scaffold143806_15.	1	p2	(AG)8	16	172	187	GGTGGAGTTGGTTCGAAGTT
scaffold143875_12.	1	p2	(AG)7	14	170	183	TGAAAAACAGAAACCGAGATCA
scaffold143997_13.	1	p2	(TC)6	12	26	37	GGGATGCCATTCGTAAGTCC
scaffold144094_17.	1	p2	(CT)8	16	112	127	CGCTAAATTTGATCGTCTTCC
scaffold144329_10.	1	p2	(CT)12	24	46	69	CACGTTGGACTTTGGATTGA
scaffold144450_12.	1	p2	(AT)6	12	204	215	GAAGGCAGATGGACGGTAGA
scaffold144549_12.	1	p2	(TA)8	16	488	503	CCTTCTTTGAATAGCGTGCC
scaffold144565_10.	1	p2	(AT)10	20	328	347	CCCCCTCTTCGAACTTCTCT
scaffold144585_15.	1	p2	(AT)6	12	1568	1579	CCCGAAAGGTTTGTTTCTGA
scaffold144594_14.	1	p2	(TC)7	14	1108	1121	AACTCCACTGCCATCTCACC
scaffold144598_18.	1	p2	(AG)6	12	1117	1128	GCATCAGCATGCTCAACAAA
scaffold144600_16.	1	p2	(AG)9	18	852	869	ACGGTTGTGATCATTCGTCA

scaffold144618_12.5	1	p2	(CA)9	18	67	84	GCACTCGCCACAATGTCA
scaffold144634_13.4	1	p2	(AT)10	20	849	868	CCCTTCTTCAAAAAGTCCGA
scaffold144635_14.1	1	p2	(GT)7	14	122	135	TTTTTGAGATTAGGCTATAAGGAATTA
scaffold144817_14.1	1	p2	(AG)6	12	303	314	AGTTTTCTCCCCTTCGTTGC
scaffold144838_16.8	1	p2	(TA)6	12	635	646	ACATGATGGACAAGTCGCAA
scaffold144868_15.9	1	p2	(CT)6	12	277	288	AGGGACCTAATATGCCCACC
scaffold144915_13.5	1	p2	(GA)6	12	345	356	GGATTCGAAAAGACATCCCA
scaffold144924_13.8	1	p2	(AG)9	18	375	392	GGCCTATCGATGTCGGTAAA
scaffold145058_16.0	1	p2	(CT)7	14	821	834	TCTGTACGTGTGTGAATGGCT
scaffold145073_13.4	1	p2	(TA)8	16	281	296	GGTGGGGTTACATTGGAGAA
scaffold145227_13.6	1	p2	(AG)6	12	955	966	TATTACAGAATGCACCGCCA
scaffold145254_13.8	1	p2	(CT)6	12	1778	1789	GATTGAAGGGGTGCTTGAAA
scaffold145382_16.8	1	p2	(GA)7	14	110	123	AAACACGCAACACAAAGCAG
scaffold145391_11.1	1	p2	(TA)9	18	47	64	ACCATCCCACCAGCATTTAG
scaffold145398_14.5	1	p2	(TA)7	14	409	422	GAGCCTCTGCTATTGGCATC
scaffold145462_17.8	1	p2	(AT)6	12	2672	2683	CCCAGCCAATGGAGATTACA
scaffold145663_14.7	1	p2	(CT)7	14	366	379	GCAGCTGAGGTGCATAACAA
scaffold145674_15.3	1	p2	(TA)7	14	115	128	TGAACATGCTCCTATTTTAATACACC
scaffold145867_14.4	1	p2	(AT)7	14	609	622	AAAATGCCCTTGTATGCTGC
scaffold145894_16.7	1	p2	(AG)6	12	391	402	ACAGCAAAATTTGGCAGAGG
scaffold146060_13.7	1	p2	(TA)6	12	398	409	CCAACGCTACTTGGCCTTAC
scaffold146115_16.0	1	p2	(AT)7	14	218	231	TGCATTCTTGAAAGCTGGTG
scaffold146234_17.3	1	p2	(CA)7	14	1019	1032	GTAAGAACGAAAGCAGGCCA
scaffold146402_14.1	1	p2	(CT)7	14	376	389	AGTCACTCACCAGTCCCCAC
scaffold146485_16.1	1	p2	(TC)6	12	346	357	TGACATCTTTTGATTTGTTTTGC
scaffold146534_10.4	1	p2	(CG)6	12	236	247	ATAGTGGTATGGTGTGGGGG
scaffold146662_14.0	1	p2	(CT)6	12	3679	3690	AGGGCAATACGTTTTTCGTG
scaffold146665_14.5	1	p2	(TC)9	18	286	303	GCATGCTTCTGACCAATTCA
scaffold146887_15.8	1	p2	(CT)7	14	76	89	ATTACAAATGGCCAAGAGGG
scaffold146904_10.2	1	p2	(CT)11	22	599	620	AATAATCCACGCCAAACTGC
scaffold146937_12.2	1	p2	(TA)6	12	557	568	GAGAAAGCATGTTCTGCACG
scaffold146994_13.5	1	p2	(TC)6	12	173	184	TAGTTGGGCTTAGTGGGGGT
scaffold147222_17.4	1	p2	(TA)6	12	175	186	ATGCCATCTGCAATCATCAA
scaffold147274_14.8	1	p2	(GA)8	16	1269	1284	AGGGCTGAGAGCCTGAAACT
scaffold147313_14.5	1	p2	(TC)6	12	53	64	ATGAGAATGGCCGAGAGTTT
scaffold147451_15.9	1	p2	(TC)7	14	386	399	CCTCTCAACGCTTGGCTAAC
scaffold147458_13.8	1	p2	(TA)9	18	171	188	TCTTTGTCCGTTTTTCGTGA
scaffold147622_14.2	1	p2	(TC)6	12	117	128	TGAGGGGTGCCAAGACTTTA
scaffold147638_13.9	1	p2	(AT)8	16	67	82	GTGCCGTAATAAATTGGATCA
scaffold147689_10.7	1	p2	(AT)6	12	65	76	CGTTAATGCACACAGCTTCAA
scaffold148474_12.5	1	p2	(GA)7	14	335	348	TATTGATGGTGCAGCAATGG
scaffold148539_11.0	1	p2	(AT)8	16	78	93	CACCAAAAACACACATTGGA
scaffold148550_13.8	1	p2	(TC)6	12	114	125	GTCAACTTTGGCAACGGAAT
scaffold148606_18.3	1	p2	(CT)7	14	171	184	TCCCATAGCATCTTTTGCTCT
scaffold148639_11.0	1	p2	(TA)7	14	566	579	TTTTGGGCAAAAATACCCCT
scaffold148722_16.4	1	p2	(TA)8	16	1658	1673	ACCGCCATATTTGGTTGACT
scaffold148784_15.7	1	p2	(AG)6	12	1567	1578	GGTGTGACTGAAGTGATTTGCT
scaffold148963_18.1	1	p2	(CT)6	12	71	82	TGGTACAAAATTTAGGGTTATTACAGA
scaffold149080_10.5	1	p2	(AT)10	20	543	562	GAGATTGACGGCTGGAAAGT
scaffold149123_11.9	1	p2	(CT)6	12	1026	1037	CGCATACCACATATCATCGC
scaffold149304_15.1	1	p2	(AT)6	12	429	440	TGGCTCCAACTTGTGTTTTG
scaffold149368_10.7	1	p2	(TC)6	12	67	78	TACCAACCCAACCCACTCAT
scaffold149466_14.5	1	p2	(AG)6	12	1110	1121	CGATTCGAAGAAATGCATCA
scaffold149488_13.1	1	p2	(CT)6	12	114	125	CAAATTCCGAAATTCTCCCA
scaffold150017_14.1	1	p2	(GA)6	12	410	421	CATTCTCAAGCCACTCCCTC
scaffold150168_11.7	1	p2	(AT)9	18	46	63	TGGGTGAGAAAGAGAGATAGAGA
scaffold150331_14.3	1	p2	(AT)6	12	241	252	GCAAAAGTAATAAAGAGCGACACA
scaffold150397_17.3	1	p2	(CT)7	14	49	62	GGAAATTTTCTTTCTTCCTCACG

scaffold150477_18.	1	p2	(AG)7	14	1599	1612	CCATTACTCACCCCCACAAA
scaffold150496_15.	1	p2	(AT)9	18	909	926	GCTCAGGACCGATGAATGAT
scaffold150509_10.	1	p2	(AT)7	14	116	129	TGTAGCCGGAATATGAGCCT
scaffold150651_15.	1	p2	(AC)7	14	2638	2651	TGGACTGTGGGAATACTGGA
scaffold150785_12.	1	p2	(TA)8	16	67	82	TTCGATGATAACTATGGGTTTTG
scaffold150787_11.	1	p2	(TA)9	18	79	96	TCGAAATTTGGCAAACAATCT
scaffold150796_12.	1	p2	(AT)9	18	673	690	GCCTATCCGTTACCCTCCAC
scaffold150813_15.	1	p2	(TA)8	16	5265	5280	CGGTTCGGATTACGGTTTTA
scaffold150856_15.	1	p2	(GA)8	16	1127	1142	CATTGTTTGTGTGTCGGAGG
scaffold151144_17.	1	p2	(TA)8	16	43	58	ATCGGTTATTACCGGATCGC
scaffold151270_13.	1	p2	(TG)6	12	59	70	TTGAATTAATGATGTCAGATATTGTT
scaffold151488_14.	1	p2	(AT)6	12	199	210	AATTTTCTACAAAACAAGACCAATC
scaffold151535_14.	1	p2	(AC)6	12	333	344	TTGCTCTAAGCTTCATCCGC
scaffold151586_16.	1	p2	(GA)6	12	357	368	CCTCCGATTTCGTCTTCAAA
scaffold151648_15.	1	p2	(AT)6	12	72	83	TCCGAAAATCGGTCAAAAAC
scaffold151895_11.	1	p2	(TA)7	14	335	348	TGCTCTTATGCTTTGTTAAATTAGG
scaffold151909_15.	1	p2	(TA)6	12	1180	1191	CAAGCTATTTCGAGGCAACA
scaffold151962_15.	1	p2	(CT)7	14	41	54	TGAAAGTAGCCGAGAGTTTACAA
scaffold152054_11.	1	p2	(TA)6	12	374	385	CCCCATCCAAGAAAAGATCA
scaffold152099_15.	1	p2	(GA)7	14	214	227	TCGAGAAATGCCACATGCTA
scaffold152389_17.	1	p2	(GA)9	18	804	821	AAAATCACCGCGAAAAATTG
scaffold152474_14.	1	p2	(TA)12	24	41	64	ACCATATTTAAGGGTTATCACCTG
scaffold152541_12.	1	p2	(AT)8	16	384	399	GGATTAATAGGCTGCCCCTC
scaffold152609_16.	1	p2	(TA)6	12	207	218	TGCCAAGTCTAAAGCCACTG
scaffold152773_11.	1	p2	(CT)8	16	370	385	TCCAACTTGTTCCCTCATTTG
scaffold152781_15.	1	p2	(TA)6	12	82	93	ACAATATTTAACGCAGCTAAACG
scaffold152796_15.	1	p2	(TA)10	20	2427	2446	AGGCCTACCGATCCAAACTT
scaffold153004_19.	1	p2	(AT)7	14	560	573	TCCCACTCGCCTGATACCTA
scaffold153193_18.	1	p2	(TC)6	12	168	179	TCATTCTCTCCCTCATTTTTGAA
scaffold153246_16.	1	p2	(AT)8	16	241	256	CCCTAAATTTTGTATCCGAATG
scaffold153417_13.	1	p2	(TA)9	18	1455	1472	TTTTAGAAGTAAGTGGTGTTCGG
scaffold153569_16.	1	p2	(CA)6	12	1386	1397	CATGCAGGAATTTTCACCAA
scaffold153614_17.	1	p2	(CT)6	12	68	79	AGCATCTCTTGCTCTCTCATTG
scaffold153636_11.	1	p2	(AG)9	18	324	341	ATTTCCTTTCAATGGGGGAC
scaffold153643_15.	1	p2	(TA)6	12	523	534	GGCGGGGGAGATATAGAGAG
scaffold153665_12.	1	p2	(AT)6	12	185	196	GCATGCTCTATCTGTTACAGGG
scaffold153666_12.	1	p2	(TA)8	16	79	94	GATTGCCCAAGATCTACGGTT
scaffold153685_13.	1	p2	(CA)6	12	832	843	TGCAGATGTCCTCCTTTCCT
scaffold153692_13.	1	p2	(AG)10	20	405	424	TGCCATCTCGAAAAACAATG
scaffold154134_15.	1	p2	(AG)7	14	99	112	TGGAATCCGAGAAATTCAGG
scaffold154251_12.	1	p2	(GA)6	12	37	48	GACTTAAATTGCTGCAGACGC
scaffold154489_14.	1	p2	(TA)8	16	232	247	TGCACTAACCACCCTTGATTT
scaffold154687_12.	1	p2	(TA)8	16	1103	1118	ATTAGGGTTGAGGTTGACCG
scaffold154694_14.	1	p2	(GA)6	12	153	164	CACTAGGCCTACGTCGCATT
scaffold154719_15.	1	p2	(AG)10	20	360	379	GAATGCTGGGCTGATAAGGA
scaffold154724_12.	1	p2	(TA)9	18	257	274	TTCTCTCTGGTTGGCTGCTT
scaffold154962_15.	1	p2	(AG)6	12	1627	1638	TGGCAATGGAAAGAAACACA
scaffold155233_15.	1	p2	(TC)6	12	39	50	GGCAACGGAATACCATTTGT
scaffold155274_14.	1	p2	(AT)8	16	3561	3576	CAACCATCCAACCACAACAA
scaffold155476_14.	1	p2	(GA)9	18	517	534	TTGCTCTTGTCGACATGGTT
scaffold155617_12.	1	p2	(AT)8	16	151	166	TGCAACCTCAATGCTTCTCA
scaffold155618_12.	1	p2	(TA)8	16	846	861	TGAATCCGTATCCTTATTGTTGC
scaffold155625_11.	1	p2	(TA)7	14	140	153	TGTCAACATTTTGTGCATTGG
scaffold155659_11.	1	p2	(TA)7	14	52	65	TGATTGGTCAGTTTGTCCGA
scaffold155763_13.	1	p2	(CT)6	12	180	191	CCCAGCTCTCTCACTCTGCT
scaffold155795_11.	1	p2	(AT)7	14	1960	1973	TATGGAGTGGAGCAAAACGG
scaffold156140_10.	1	p2	(TA)12	24	311	334	TTTAAACCCTAAAACGCGCA
scaffold156367_15.	1	p2	(AT)6	12	2418	2429	TCACCTAATTGCATCCCCAT

scaffold156398_14.5	1	p2	(AG)6	12	1417	1428	AGAGAGAGGCGATGCAAAAA
scaffold156563_14.9	1	p2	(AT)9	18	727	744	CAAAACTAATTGGGGAGCAAA
scaffold156607_14.7	1	p2	(GA)6	12	3519	3530	CGGATAATATAGCTCCGGCA
scaffold156718_14.0	1	p2	(TA)6	12	1098	1109	CATTCATCATCATCAATATCACAGTC
scaffold156806_15.9	1	p2	(AT)8	16	85	100	AATCTGACGGCCGATATTTG
scaffold156819_12.0	1	p2	(TA)7	14	1141	1154	TCAGATCTGCGCTGAAAATG
scaffold157076_15.9	1	p2	(CT)7	14	151	164	GTGTGCATGCATGGTTTAGG
scaffold157090_11.7	1	p2	(AT)9	18	132	149	TTAGCCCTTAATGGCCTGCT
scaffold157091_16.0	1	p2	(AG)6	12	841	852	TGGTGACTTTGAGGAGGGAG
scaffold157159_12.9	1	p2	(AT)11	22	894	915	AGTGAGGCCCCTTTTACGTT
scaffold157268_13.6	1	p2	(TA)6	12	111	122	AATTGAAATAAAGGCGCCAG
scaffold157292_14.8	1	p2	(AT)6	12	1028	1039	AATCGTGGTTCAAAAATCGG
scaffold157305_13.1	1	p2	(AT)9	18	308	325	TTCGGTTGCAATTTTAGTTGTTT
scaffold157428_13.4	1	p2	(TA)8	16	1065	1080	CAGGGGCATATGTGTCAAAA
scaffold157502_11.4	1	p2	(AG)8	16	284	299	AAGTTGGAGTGGAGGTGTCG
scaffold157515_10.5	1	p2	(AT)8	16	319	334	ATTTGAAACCGGACCGAACT
scaffold157516_13.0	1	p2	(AT)8	16	146	161	GGTCCATTGGTCTTTTGTATTGA
scaffold157555_12.7	1	p2	(CA)6	12	824	835	GATACGACCTGTAATGCCCC
scaffold157729_16.2	1	p2	(AT)6	12	129	140	TCATGGGGCAATGGGATA
scaffold157754_13.8	1	p2	(AT)8	16	2216	2231	GTGGTGGAAGAGGCAATGTT
scaffold157829_12.0	1	p2	(AT)7	14	555	568	AATAGGTCCATCCCTGCCTT
scaffold157849_14.7	1	p2	(AT)7	14	376	389	AAAAGGAGTTTTGACGGGATT
scaffold157932_13.6	1	p2	(TA)9	18	289	306	GTAAATAAGGCGGTGGGTGA
scaffold157942_10.0	1	p2	(CT)6	12	63	74	AAAAGTAATGCATATGTTTTCCTAAG
scaffold157980_16.9	1	p2	(TA)9	18	47	64	CATGCACCTGAACATGCC
scaffold157989_11.5	1	p2	(AT)6	12	486	497	TGGTTGAATTTCGTACCCGT
scaffold158113_11.5	1	p2	(TC)6	12	54	65	CCTACCCAAACCCACTACCA
scaffold158303_14.8	1	p2	(CT)6	12	275	286	AAGCACTCAACCAAACACCC
scaffold158405_10.3	1	p2	(AG)6	12	605	616	TGATGGTTTGATGGGGTTTT
scaffold158455_19.1	1	p2	(TA)9	18	301	318	ATAAATGTTCAAACCGGCCA
scaffold158511_16.6	1	p2	(TC)6	12	479	490	GCACCGAGGGAATCAAATAA
scaffold158537_12.7	1	p2	(GA)6	12	220	231	CAAAGAAGAGTGGGCTTTGG
scaffold158730_13.6	1	p2	(AT)10	20	2214	2233	GTCAATCCAACGTCCCAAAT
scaffold159213_16.3	1	p2	(AG)7	14	272	285	CCTCTCGCATTTCTCTTGCT
scaffold159314_13.3	1	p2	(TA)6	12	246	257	AATCACATCAACACCTCAGCC
scaffold159372_12.6	1	p2	(AG)9	18	311	328	TCCCCTACTACACTCGCCAC
scaffold159433_12.7	1	p2	(TC)6	12	628	639	AGCAAATCCTCCCCAAATCT
scaffold159750_14.9	1	p2	(AG)10	20	2049	2068	CATCGCCCTTGATCTCTCTC
scaffold159899_13.6	1	p2	(AT)7	14	2248	2261	ACTAGAGGGGTCAGCCCATT
scaffold160005_12.4	1	p2	(AC)7	14	425	438	AACCACATTAGGCCATGCAC
scaffold160181_16.2	1	p2	(AG)10	20	490	509	CAACGTCGCTTTTAGGGTTG
scaffold160267_12.2	1	p2	(AT)7	14	115	128	TATGCATTTGCACCTGAGGA
scaffold160303_13.7	1	p2	(AG)6	12	664	675	AGGGGTGTAGGCAAAAGACC
scaffold160488_13.9	1	p2	(AT)7	14	2704	2717	TAGGGCAATTGGTAGGTTCG
scaffold160560_15.9	1	p2	(CA)6	12	581	592	CTTCCAGAGTCAATCCAGGC
scaffold160605_15.0	1	p2	(AG)6	12	139	150	GCTTCCAAAAGAAAGAGCCC
scaffold160831_16.1	1	p2	(TA)10	20	430	449	TGTTTCCCGTTTTATCAGCA
scaffold160961_10.7	1	p2	(TA)6	12	75	86	TCATTTATGAAGCAAGGGGG
scaffold161261_14.1	1	p2	(AG)7	14	290	303	TGCAAATTGATGAGGCCATA
scaffold161421_14.9	1	p2	(CT)8	16	67	82	CAACCCTACCTCCTTCTCCC
scaffold161559_13.7	1	p2	(TC)6	12	2167	2178	GGTGGCAAAAAGTGAGGAAA
scaffold161750_14.2	1	p2	(AG)7	14	2721	2734	TATAGGGCGGTGGTAGTTGC
scaffold161818_15.6	1	p2	(GA)6	12	797	808	TGGTGAAGATGTGGGTTGAG
scaffold161932_14.0	1	p2	(TC)7	14	1459	1472	GCACGTAACATACATTGCCC
scaffold161946_15.0	1	p2	(GA)10	20	748	767	GGCTCACTGCTTCTTTCTCG
scaffold161969_19.0	1	p2	(TA)7	14	117	130	CAATTGGTAGCAAACCATGAA
scaffold161992_15.1	1	p2	(CT)6	12	56	67	TTTGAAAACCCCATTTCGTC
scaffold162156_13.8	1	p2	(TA)10	20	43	62	CCCAAAAATGGGTTATTATTTGA

scaffold162356_10.	1	p2	(TA)15	30	447	476	CACCGTTGTCTTTAAGCCGT
scaffold162372_16.	1	p2	(TC)6	12	852	863	GCTGATCTCCATCTCCAAGC
scaffold162517_16.	1	p2	(AT)6	12	286	297	TTGGGAAAAATAAAGAGGAAACC
scaffold162570_12.	1	p2	(TC)6	12	219	230	AAATCCCACCTACCCAAACC
scaffold162670_12.	1	p2	(TA)6	12	828	839	GCAATCCCCACTGCATCTTA
scaffold162709_12.	1	p2	(TA)7	14	497	510	CCCTCCCTCTCTCTTTTCGT
scaffold162802_15.	1	p2	(TA)7	14	1752	1765	TCCTAATTTGGAAAGTACTGGGTT
scaffold163064_12.	1	p2	(TC)6	12	132	143	GCTCGAAATCGGAAAATCTG
scaffold163117_13.	1	p2	(CT)6	12	46	57	GTTGGCTGGATCTCCTGAAA
scaffold163260_13.	1	p2	(AT)11	22	213	234	TCATTCCGAAAATCAAAGGC
scaffold163280_13.	1	p2	(TG)6	12	226	237	GCATTTAAGTTTACGGGGGA
scaffold163287_15.	1	p2	(TA)10	20	456	475	TGCACGTTTCAAAGCATAGG
scaffold163360_10.	1	p2	(TA)7	14	566	579	TCTCAGAATCCCATTAGAAGGGT
scaffold163625_11.	1	p2	(AT)8	16	310	325	GAAATTGAAGGGATAAGAATTTCAA
scaffold163693_10.	1	p2	(TA)6	12	371	382	ACCTGATTCCAGTTGGATGG
scaffold163908_15.	1	p2	(TA)7	14	3076	3089	ACCGATCTTTTGGCATTCAA
scaffold163927_15.	1	p2	(TC)7	14	581	594	AAATCCTATCCGGTCAACCC
scaffold163959_13.	1	p2	(AG)6	12	227	238	GGGTGAAAGGAGAGGGAGAG
scaffold164119_16.	1	p2	(AT)8	16	3020	3035	TTGTCGGGCTCGAATTTATC
scaffold164141_13.	1	p2	(AT)9	18	873	890	CCCATACACAATTTGGGGTC
scaffold164177_13.	1	p2	(TG)8	16	181	196	ATCTCGGCTACGAAGTGCAT
scaffold164195_13.	1	p2	(AT)6	12	342	353	GCTTGGTGAAGGAAGTGAGG
scaffold164259_16.	1	p2	(AT)6	12	53	64	GTCCTCCGAACTCATGGTGT
scaffold164403_16.	1	p2	(AT)6	12	508	519	TTACCCGGACAATAAATCCG
scaffold164476_14.	1	p2	(AT)12	24	1265	1288	GCTTCTTCTTCTCCGCATTG
scaffold164500_13.	1	p2	(AG)9	18	997	1014	TCCCATTCAACCATTTTCAA
scaffold164622_15.	1	p2	(AT)6	12	196	207	CAACGCACGGGTAAAAGACT
scaffold164636_15.	1	p2	(AT)7	14	763	776	GAGCATTTTCATGCCATTTTT
scaffold164668_12.	1	p2	(TA)7	14	51	64	GCACACAAGTTATTGGTTTCTATTTG
scaffold164671_10.	1	p2	(AT)10	20	198	217	TTTTACTGCCTTGTGTTGCG
scaffold164825_12.	1	p2	(TA)9	18	292	309	AATTGTGGAGTTGCCGTTTT
scaffold165037_11.	1	p2	(TA)10	20	95	114	ACCAATTTGATGAGGGTCCA
scaffold165231_15.	1	p2	(AT)9	18	167	184	TTCTGGATTATCCTGCGGTC
scaffold165239_11.	1	p2	(AG)6	12	271	282	GTGTCGGGGGTACAAAAGTG
scaffold165276_15.	1	p2	(GC)7	14	75	88	AAAATTATATTCTCGCTTCTTCGC
scaffold165283_17.	1	p2	(TA)8	16	181	196	AAAGCCTACCTTGCTTCCGT
scaffold165428_13.	1	p2	(TA)7	14	285	298	TGTCGGAAGCTCAACACTTG
scaffold165437_13.	1	p2	(GA)7	14	145	158	CGCGTTTTTGGGGTTAAATA
scaffold165564_13.	1	p2	(TA)8	16	286	301	AAGGTGGGAAAGAATTTGGC
scaffold165753_12.	1	p2	(TA)7	14	376	389	CGAAATTGAATGGCAAGGAT
scaffold165755_13.	1	p2	(TA)10	20	385	404	ATCGAGGCGTGACATCTACC
scaffold165819_10.	1	p2	(AT)10	20	196	215	CGGAAGAATAAGAAACGGCA
scaffold165857_11.	1	p2	(TA)6	12	262	273	TCAAAAGTGCAACAAATCTGC
scaffold165998_15.	1	p2	(AT)7	14	682	695	GGAATGTAGTGTGCGCAAGA
scaffold166171_14.	1	p2	(TC)6	12	184	195	TGAGCTCGGACCTCCAGTAT
scaffold166249_15.	1	p2	(AT)7	14	167	180	TGCAACGAACAAATCTCATTG
scaffold166484_14.	1	p2	(AT)8	16	726	741	CGTCAATCAATGATGCGATTA
scaffold166540_16.	1	p2	(TC)12	24	2259	2282	AGTTTTGGACGAATTCCACG
scaffold166703_15.	1	p2	(AT)6	12	925	936	ATCCAACACCCACCACATTT
scaffold166787_10.	1	p2	(AG)6	12	66	77	ACTCGGAACAACGAAAATCG
scaffold166871_11.	1	p2	(TA)6	12	213	224	GGCCATGATTCATTTTCTGC
scaffold166895_12.	1	p2	(AT)6	12	324	335	TTCCATTTCAGACCCAAAAGA
scaffold166935_15.	1	p2	(GA)6	12	2212	2223	CGAAAATTGAAAATTTATTCCCC
scaffold166938_15.	1	p2	(AT)13	26	1314	1339	TCATGGACCTCATATGTCATAACC
scaffold167156_13.	1	p2	(AT)6	12	212	223	CGTATACTTGCGGGGTTGTT
scaffold167161_18.	1	p2	(AC)8	16	115	130	AAGTCTCTCACCCTTCGCAA
scaffold167215_16.	1	p2	(CT)6	12	157	168	TCGATGTTGTAATTCATCCGAG
scaffold167506_10.	1	p2	(CG)8	16	1164	1179	TATGCCCATGGAGGTATGGT

scaffold167528_16.	1	p2	(TC)7	14	1237	1250	GCATCCATTCTGAATCACTCAA
scaffold167619_17.	1	p2	(GA)6	12	229	240	GAGTCAGCTGCTCTTGGCTT
scaffold167624_15.	1	p2	(CT)6	12	302	313	CATGGATTCGGGTAAACACC
scaffold167675_10.	1	p2	(TA)10	20	45	64	AATTTACTAATTTATCCACCTCGATTT
scaffold167759_10.	1	p2	(CT)6	12	151	162	ATGAGGTGGCATGTAGACCC
scaffold168086_10.	1	p2	(TC)6	12	317	328	TCTCCTTCTCTCCCCCATTT
scaffold168186_16.	1	p2	(TA)6	12	1098	1109	TTGCCGACCTTATCTCCATC
scaffold168314_11.	1	p2	(AG)6	12	217	228	CGACATTGAGTAGCCGTCTG
scaffold168373_17.	1	p2	(TC)10	20	67	86	GCTCTTCGAATTCTCCTCCC
scaffold168587_14.	1	p2	(TA)8	16	51	66	AAAACCGTTCTCACCCCTTC
scaffold168626_17.	1	p2	(TA)11	22	196	217	ACGGTTAAGATTCAGCACGC
scaffold168975_11.	1	p2	(CT)7	14	170	183	ACTTCAATTTTCGAGCCCAA
scaffold169133_10.	1	p2	(TA)10	20	66	85	CATGTTAAATAATCGTCAAGTTGAGT
scaffold169243_10.	1	p2	(TA)8	16	411	426	TGTCGAATGCTAATGGGAGA
scaffold169520_15.	1	p2	(AG)12	24	216	239	TTTTCTTTTTCCCGGTGATG
scaffold169548_11.	1	p2	(GA)6	12	209	220	TTCGTGTCTATCCTCACCCC
scaffold169595_17.	1	p2	(TC)6	12	733	744	TGATCGTTCTTCACTCTCTTGC
scaffold169652_12.	1	p2	(AT)8	16	717	732	CCAGATCGCGACCCTATAGAT
scaffold169687_10.	1	p2	(AT)8	16	198	213	AAAATCAAAGGCCCACAATG
scaffold169790_13.	1	p2	(TA)7	14	277	290	TCATTAGCAGCTGGGGATTT
scaffold169889_11.	1	p2	(CT)6	12	176	187	CATAGTTGACGCCCTTCCTC
scaffold170158_10.	1	p2	(TG)6	12	224	235	ATTTGGGTCAAACCCCTTTT
scaffold170328_14.	1	p2	(TA)8	16	414	429	TTTTTACCAATTTGCCCTCG
scaffold170418_16.	1	p2	(TA)7	14	320	333	GAGCTGTTACCTCCGTGGAC
scaffold170502_16.	1	p2	(AG)7	14	286	299	AGACATGGCGATACGACGTT
scaffold170506_11.	1	p2	(CT)6	12	118	129	GTGTCCAACATCCCATTTCC
scaffold170509_16.	1	p2	(CT)6	12	84	95	AGCATCTCTTGCTCTCTCATTG
scaffold170605_13.	1	p2	(AT)8	16	189	204	TATTTTGGACGATTTTGCCC
scaffold170672_13.	1	p2	(AG)9	18	85	102	TTTTGTTGTTTCCCAAGTTGC
scaffold170974_10.	1	p2	(TA)10	20	64	83	TTTGCTTGATCCAATGGTGT
scaffold170977_18.	1	p2	(AT)7	14	117	130	TGCGTGATGCAGACATATTG
scaffold170979_17.	1	p2	(AT)6	12	1684	1695	TGTCCCCATCTCGTGTTGTA
scaffold171007_15.	1	p2	(TA)6	12	484	495	CATGCAGTCATGCACAATCA
scaffold171067_13.	1	p2	(AT)7	14	702	715	TTTGACCTTGCATTGCTGTC
scaffold171092_13.	1	p2	(TA)7	14	181	194	AAGGAGGTGTTATGAAGGGATT
scaffold171093_17.	1	p2	(GA)6	12	224	235	AATTGATGGAAGAAGGCACG
scaffold171246_13.	1	p2	(AC)6	12	180	191	CTCCATCGTCGAAGTCATCA
scaffold171255_16.	1	p2	(TA)9	18	211	228	GTGCGTGTGTATGCTGAGGT
scaffold171486_16.	1	p2	(TA)9	18	407	424	TGGCGCATTTTACTGATATTTG
scaffold171628_16.	1	p2	(AC)6	12	208	219	CGCAACGTTCTGAAACTGAA
scaffold172005_12.	1	p2	(CT)6	12	52	63	TCTTGCACTCGTCTCTGTCG
scaffold172073_15.	1	p2	(AT)6	12	657	668	GGAAGGAATATTTCATCACACCTT
scaffold172121_12.	1	p2	(AT)8	16	104	119	TCGATAATGCACTTTATCAGAGTT
scaffold172144_13.	1	p2	(TA)8	16	281	296	TGGATGTGGTTGGTGAGTTG
scaffold172398_16.	1	p2	(AT)6	12	638	649	GATGATCACGATGAAGCCAA
scaffold172559_11.	1	p2	(AT)7	14	750	763	CATGCACGGAAAACTTGAAA
scaffold172844_12.	1	p2	(AG)6	12	918	929	TTGGTTCAAGCCATTGTGAA
scaffold172854_13.	1	p2	(GT)6	12	1914	1925	TGCGTTTTACAGCCAAAAGA
scaffold172948_15.	1	p2	(TA)6	12	510	521	CGAATAGTAGAAGCTGCGGG
scaffold172974_20.	1	p2	(AT)7	14	76	89	TTGGTGTATACTTTTGTAGTGATCAA
scaffold173074_11.	1	p2	(CT)6	12	161	172	ACCCGAATTTTTCGGATACC
scaffold173396_16.	1	p2	(GA)7	14	32	45	GAGAATAGATAGTTAGAGAGAGACC
scaffold173428_12.	1	p2	(AG)6	12	282	293	CTTCTCACCGTCGACCAAAT
scaffold173472_12.	1	p2	(TA)9	18	247	264	TTCTCAGCATATGGGAAGGG
scaffold173508_18.	1	p2	(CA)6	12	1523	1534	TGACTGGACTGCCTTTTTCC
scaffold173509_14.	1	p2	(TA)8	16	126	141	TGAGCCTATCTTGGAGCACA
scaffold173530_13.	1	p2	(AC)7	14	140	153	TTCTTTGAATCATCTTCCACCTT
scaffold173658_11.	1	p2	(AT)6	12	267	278	ACTCGTGCTGGCAATCTTCT

scaffold173740_18.	1	p2	(CT)6	12	106	117	AACAAAAATGGCCAAAATCG
scaffold173862_10.	1	p2	(TA)6	12	479	490	CAACTCCACATGTTGCCATC
scaffold173933_14.	1	p2	(AG)7	14	49	62	TTTTTAGCATGCGAGAGGAA
scaffold173949_11.	1	p2	(GA)7	14	171	184	TCAACAACATGCAAGCATCA
scaffold173981_18.	1	p2	(GA)9	18	471	488	GGATGAGAGACTCGGGTTCA
scaffold174269_13.	1	p2	(GA)7	14	1289	1302	CCATTTCTTTGGCAAGTTGA
scaffold174392_10.	1	p2	(GC)6	12	576	587	TCAGCCCAGCCCAATATTAC
scaffold174455_14.	1	p2	(CT)11	22	771	792	GACATTTGGTTCAGCGCTTT
scaffold174523_17.	1	p2	(AG)8	16	2585	2600	TGATCATCGAGGCAGAGAAA
scaffold174754_10.	1	p2	(TC)7	14	169	182	GGGCAAAACTTGAACAGCTC
scaffold174974_14.	1	p2	(CT)6	12	916	927	CCCTGTCTTAGGTACTGGCG
scaffold175116_11.	1	p2	(TC)7	14	40	53	GCACAACCACTCCACAAAGA
scaffold175173_12.	1	p2	(TC)6	12	741	752	TTCCTACTCCCCTAGGCCAT
scaffold175292_14.	1	p2	(AT)6	12	334	345	ACCGTTCATTTTCGGTTCAG
scaffold175294_15.	1	p2	(GA)6	12	309	320	TCGAAGGTGAACTCGGTCTT
scaffold175297_16.	1	p2	(CT)10	20	578	597	CCCTAACTCGACCCAGATCA
scaffold175387_13.	1	p2	(AT)8	16	49	64	AGAGTTCACCAAGGTACTTTAATATG
scaffold175434_14.	1	p2	(TA)8	16	1479	1494	TGGGCACATTTGAATCTTGA
scaffold175442_13.	1	p2	(GA)7	14	925	938	CCAAACGAAGTGACTTGCAG
scaffold175544_11.	1	p2	(TC)7	14	354	367	TAGCCGATAAAAATGGCACC
scaffold175572_14.	1	p2	(AT)10	20	554	573	ACACACACTCACTCACTCCCA
scaffold175836_13.	1	p2	(GA)6	12	188	199	GTTCCGGGAATCACACCATA
scaffold176052_12.	1	p2	(TA)12	24	40	63	AAGGGTTATCACCTGATTTTCTC
scaffold176180_14.	1	p2	(GA)10	20	663	682	AAGGATCTTGTTACGGGCCT
scaffold176280_14.	1	p2	(GA)7	14	1884	1897	TTGACTGATTGGAGCAGTGG
scaffold176320_10.	1	p2	(GA)7	14	177	190	TCAAATCTTCAACATGCAAGC
scaffold176511_10.	1	p2	(TA)10	20	457	476	TTTTCTTGGACCAGATTGCC
scaffold176747_14.	1	p2	(GC)6	12	425	436	CACGTGCGTCAACTCCTTTA
scaffold176848_11.	1	p2	(GA)7	14	116	129	AAACACGCAACACAAAGCAG
scaffold177379_14.	1	p2	(CA)7	14	806	819	AGCCCTGTAGAGGAGCATCA
scaffold177501_18.	1	p2	(AT)8	16	337	352	TGGGGTTATCACTGGATCGT
scaffold177572_13.	1	p2	(TA)6	12	590	601	TAAACCGTTGTTTTGGCTCC
scaffold177580_10.	1	p2	(AT)8	16	212	227	CACCAAATCTGTTAGTTTACCAAA
scaffold178175_10.	1	p2	(AG)6	12	368	379	AGATGCCCATTTTGATCAGG
scaffold178465_15.	1	p2	(TC)6	12	586	597	CCCGATTATCGCAAGAACAT
scaffold178502_11.	1	p2	(AT)6	12	311	322	TTTTTCACGCACAAGCTGAG
scaffold178523_13.	1	p2	(AT)10	20	204	223	TTTGTGCTTTGCTGCTGTTT
scaffold178540_14.	1	p2	(TC)6	12	119	130	CGATCTCCTCTCTCTCGTCG
scaffold178544_15.	1	p2	(GA)6	12	52	63	CACGAGTGAAGAAAGGGAGAG
scaffold178585_14.	1	p2	(TA)8	16	162	177	AATACTTTCCGTCACCGTCG
scaffold178813_14.	1	p2	(CT)8	16	1249	1264	CCCATTCACAAGACCTCCTC
scaffold179106_11.	1	p2	(AT)8	16	491	506	GAGGAAGATAAATGTGGGACG
scaffold179397_16.	1	p2	(TA)8	16	258	273	TTTGGCCGAATTGTCTTTTC
scaffold179684_12.	1	p2	(AT)6	12	856	867	AAGGGGAAGTTCTGCATGTG
scaffold179886_14.	1	p2	(AT)7	14	67	80	CGTCAGAAACCTCTCGCATT
scaffold179887_17.	1	p2	(AT)6	12	385	396	AAACATCCCAATCCCATCAA
scaffold179890_14.	1	p2	(CT)8	16	147	162	GAACACGAGGGATATTGGGA
scaffold179959_12.	1	p2	(TA)8	16	67	82	TGTGTTGTCTTTTAGATCAATGTTTG
scaffold180081_16.	1	p2	(AT)6	12	4881	4892	TCAAGGGTAATTTTTCAGGCA
scaffold180421_12.	1	p2	(AT)7	14	300	313	TAGTTAGCATGGGGGAATGC
scaffold180599_12.	1	p2	(TA)6	12	115	126	TAATTTGGCCGGATTGTCTC
scaffold180618_14.	1	p2	(TA)8	16	1888	1903	TGCGCGTTGATTAATCTCAA
scaffold180702_19.	1	p2	(AT)8	16	1094	1109	CCTCCAAGCACAGGTACAGG
scaffold180784_12.	1	p2	(TA)6	12	305	316	CCACTTAGGAATTTCATCAAATGATA
scaffold180893_14.	1	p2	(AC)6	12	432	443	TGGACACAAGTATGGCTCTCA
scaffold180916_14.	1	p2	(GA)9	18	1009	1026	TCAATCAAAACTGCACCCAA
scaffold180957_15.	1	p2	(GA)7	14	1155	1168	ACAGATGAGCGAAAATTGGG
scaffold181000_15.	1	p2	(AG)6	12	704	715	AGTGAACAACAATCCCCACC

scaffold181082_16.	1	p2	(GA)9	18	187	204	CTGAAATTGGGATTTGTGGC
scaffold181160_12.	1	p2	(AT)6	12	116	127	TGTAATGCTACAGTTCTTAATTTGGT
scaffold181185_13.	1	p2	(TA)8	16	2272	2287	TAGTGGAAAACCCAACGACC
scaffold181192_15.	1	p2	(GA)6	12	326	337	TCCCTAATCGACCTGACACC
scaffold181228_19.	1	p2	(AC)10	20	641	660	GCAAACTGATTGACCCGAAT
scaffold181299_11.	1	p2	(TA)9	18	69	86	GCTTAAACAAAATGGCATTAAAAA
scaffold181301_10.	1	p2	(TA)6	12	36	47	ACGGTTAAGATTCAGCACGC
scaffold181377_11.	1	p2	(AC)6	12	53	64	TCACGAAAACACACGCACTC
scaffold181378_16.	1	p2	(TC)6	12	774	785	ATTGGGCATTTTGACGGATA
scaffold181525_14.	1	p2	(TA)7	14	93	106	CAGTTATCACCGGATCACGA
scaffold181809_17.	1	p2	(AT)9	18	152	169	CTCAACGGTATGCTCGGATT
scaffold181864_14.	1	p2	(TA)6	12	344	355	GCACCCCGTATTTTAGGACC
scaffold182113_12.	1	p2	(TA)7	14	1314	1327	AATCACAACTTCACCCGGAA
scaffold182478_14.	1	p2	(AG)6	12	182	193	GCCCTTGCAGAGAAAAGAGT
scaffold182751_16.	1	p2	(AT)6	12	176	187	CAACCTATAAATAAGATCTCAACCTG
scaffold182813_14.	1	p2	(TA)6	12	810	821	CCTGCTGGTTCTTGCTTCTC
scaffold182903_13.	1	p2	(TA)6	12	413	424	CATTTCGCACACAGAGATGC
scaffold182924_10.	1	p2	(TA)10	20	571	590	CAAATTACCCCCGTATGCAG
scaffold182933_10.	1	p2	(AG)8	16	303	318	TCAATGGTGACATTTGGGTG
scaffold182986_14.	1	p2	(TA)7	14	691	704	CGGTTAGAAACCAGACCGAA
scaffold183028_15.	1	p2	(TC)7	14	1284	1297	CATGCATTCAACCCTCTTGA
scaffold183053_13.	1	p2	(AT)9	18	304	321	GGGCATAAATGCCAATTTTTA
scaffold183085_13.	1	p2	(AT)7	14	207	220	TTAAACCTTTGTGCGGTTGC
scaffold183253_15.	1	p2	(TA)9	18	520	537	TGTTCTGGTCCAAACCCAAT
scaffold183308_13.	1	p2	(TA)7	14	782	795	CTTCGACCGGATGAATCCTA
scaffold183318_12.	1	p2	(CT)11	22	812	833	TATGATGGAAAAAGGCCGAG
scaffold183512_14.	1	p2	(AC)6	12	1002	1013	CCAGTGTAAAAAGATCGAGCAA
scaffold183586_14.	1	p2	(TA)10	20	1084	1103	CGAAGATGGTTTCGTGTAAGC
scaffold183606_13.	1	p2	(AT)8	16	749	764	CATGTAGTACGCCTCGCTGA
scaffold183608_16.	1	p2	(CT)6	12	2152	2163	CTGTATCCCTGGATGCCTGT
scaffold183616_14.	1	p2	(TA)9	18	325	342	AGCACGTGTTCTTGCTCGTA
scaffold183807_14.	1	p2	(TC)6	12	187	198	CAACATCACCAAAAACCCCT
scaffold183817_16.	1	p2	(TA)8	16	145	160	GCACACTCAGATCACACAGGA
scaffold183868_13.	1	p2	(TA)7	14	131	144	ACCAAGATTTGATCATGGGC
scaffold184487_13.	1	p2	(TC)6	12	278	289	ATGGAGGCAAGCTACTCGAT
scaffold184538_12.	1	p2	(AT)8	16	2855	2870	CGGGAAACATGATCCGAATA
scaffold184721_11.	1	p2	(CT)6	12	107	118	ATATTGCAAATGGCCGAGAG
scaffold184867_17.	1	p2	(GA)7	14	285	298	GCCGAGTGATCCTCTCTCAT
scaffold184874_16.	1	p2	(AG)8	16	3399	3414	AGGATCATGGCCACGTAGAG
scaffold185187_10.	1	p2	(TA)12	24	475	498	GAGAAGGAGGTTGGGAGGAA
scaffold185243_14.	1	p2	(AT)6	12	1205	1216	TCCACCTCACTTTTCCCTTG
scaffold185247_12.	1	p2	(AT)6	12	399	410	CAGCTCTTCAAACTGGACACA
scaffold185293_15.	1	p2	(TA)7	14	1179	1192	AACCGGTTAAAAATCGGACC
scaffold185421_16.	1	p2	(TC)6	12	114	125	CAAACACCTGGGACCTCAAT
scaffold185738_16.	1	p2	(CT)7	14	75	88	CAACCCTACCTCCTTCTCCC
scaffold185757_10.	1	p2	(GA)7	14	411	424	CAACTGTTCTGAATGCGAGC
scaffold185915_15.	1	p2	(TC)6	12	1907	1918	CTGGCAAAGATTCTTGGGAT
scaffold186032_16.	1	p2	(TA)7	14	172	185	TGACATTGCCTAGAAAGTGGG
scaffold186114_11.	1	p2	(AT)8	16	241	256	TGTTGCCAATTAAGATTGCG
scaffold186192_13.	1	p2	(TC)6	12	82	93	TCATTCACATCGTCTCTGCAA
scaffold186385_14.	1	p2	(AT)7	14	774	787	CCCTCGAATGCACTCAAACT
scaffold186705_14.	1	p2	(TC)6	12	1246	1257	GCCGCATTGTATGAAAATTG
scaffold186741_10.	1	p2	(TA)7	14	553	566	GGAGAACCGTCGACATGATT
scaffold187029_15.	1	p2	(AT)7	14	293	306	TCGAATCTATGCATCCACCA
scaffold187070_12.	1	p2	(AT)10	20	69	88	TCCATAGAAAATGTTGTTAGCAGG
scaffold187138_13.	1	p2	(AT)6	12	158	169	CAGATTTTGAAACCTGTAAGTGAAA
scaffold187175_11.	1	p2	(AT)7	14	349	362	TCAATTCATAAATATGTCGAAGAACA
scaffold187195_14.	1	p2	(CT)9	18	802	819	CCCTCATCTTTTGCGAATTG

scaffold187238_16.	1	p2	(AT)6	12	1679	1690	TGCTGCAAGCATGTATTTGTC
scaffold187445_14.	1	p2	(TA)8	16	1129	1144	AACTCAAGTTCCGATCGTGC
scaffold187508_10.	1	p2	(TA)8	16	380	395	CGTCGATGTTTGTCCATTTG
scaffold187813_20.	1	p2	(AT)9	18	226	243	TTCTGACGAAATTGCCCTTC
scaffold187863_12.	1	p2	(TC)6	12	493	504	CCTCTCCTTGCCCTCCTTAC
scaffold187951_18.	1	p2	(AT)7	14	3323	3336	CGCCATATCGGACAAACTCT
scaffold187966_16.	1	p2	(TA)7	14	1005	1018	CGTCCAACGAATCAAGACAA
scaffold188087_14.	1	p2	(TA)7	14	39	52	GGAGCCTCCGAACTTTGAA
scaffold188126_15.	1	p2	(AC)6	12	1740	1751	TTGTGTACCAAGACATTTGTGTG
scaffold188252_16.	1	p2	(AT)6	12	197	208	CGACTATCTGCAGGAGGCAT
scaffold188270_14.	1	p2	(AC)9	18	430	447	ATTTCATCTCCCCACAGACG
scaffold188698_15.	1	p2	(AT)10	20	47	66	TGGATAAGTCTATCAAGATTTAATTG
scaffold188824_14.	1	p2	(AC)6	12	103	114	CACCGTTTATTCCCCATGTC
scaffold188826_14.	1	p2	(AG)6	12	613	624	ACTTTTGTGGAAAAGTGGCG
scaffold188877_17.	1	p2	(TG)6	12	56	67	TGATCATAACTCTCTCTCGCGT
scaffold188966_11.	1	p2	(AG)6	12	173	184	TTGTGAGTCGTTTGTTCTTGG
scaffold189204_11.	1	p2	(AT)7	14	578	591	TGACCACCCAACCACACTAA
scaffold189325_10.	1	p2	(AT)6	12	179	190	TTAATCTCCCCGGAATAATTG
scaffold189349_14.	1	p2	(AT)8	16	379	394	GAGGAATGAGGGGAGGGTAG
scaffold189580_15.	1	p2	(TA)6	12	185	196	TGTTCATTGAGGAAATTATAAAGCA
scaffold189611_14.	1	p2	(TA)6	12	505	516	TGTTGAGGGTTGTTTATTATGGG
scaffold189697_11.	1	p2	(AT)9	18	1258	1275	TTAATGGTGGGGACATGCTT
scaffold189862_16.	1	p2	(TC)6	12	532	543	AAACCCACTAACCCAAACCC
scaffold190021_10.	1	p2	(AT)7	14	652	665	AAAAACCCTTCCACCCATTT
scaffold190744_10.	1	p2	(TA)6	12	971	982	TGTGATGTGTGTGTGTCGTGT
scaffold190970_13.	1	p2	(TA)10	20	224	243	TTTTCCGAAGGTAATTTTAGTGTT
scaffold191180_13.	1	p2	(CT)12	24	2887	2910	TCACCCACCAAAATCAAACA
scaffold191238_13.	1	p2	(TA)7	14	271	284	CGGACGGTCGAATCAATTA
scaffold191276_14.	1	p2	(AG)7	14	273	286	TTCTCGTGTTTATCCTCGCC
scaffold191618_15.	1	p2	(TC)6	12	49	60	GGGAAACAATGGATACTCCTTC
scaffold191636_13.	1	p2	(AT)8	16	106	121	CATAAATGCGGTGGAGATGT
scaffold191774_13.	1	p2	(AG)7	14	135	148	TTGCGTACCAAGTTTTTGGC
scaffold191936_10.	1	p2	(CT)6	12	769	780	TTGGTAGCCTGGATAGCACC
scaffold192015_10.	1	p2	(TG)6	12	297	308	GAGACTTGCAAACTCTCGGC
scaffold192053_11.	1	p2	(GA)6	12	333	344	CAAACCCTAGCCCAAGAACA
scaffold192135_12.	1	p2	(TA)7	14	195	208	ATCTTTCCCATTTTGCCCTT
scaffold192188_14.	1	p2	(TA)9	18	360	377	CGCCCAAAAATCTAACATTCC
scaffold192220_15.	1	p2	(AT)9	18	2423	2440	CTCTTCTTCGTCCCAAGCAC
scaffold192262_17.	1	p2	(TA)7	14	445	458	AAAGGGCGGTATCATTTGAA
scaffold192834_15.	1	p2	(TC)8	16	135	150	CCTTCGGCTTGAAAAACAAG
scaffold193013_15.	1	p2	(AC)6	12	269	280	CTAGCTTCGGTACAAACCGC
scaffold193231_10.	1	p2	(AG)6	12	356	367	ATGGGATATGATTCCGGTCA
scaffold193337_10.	1	p2	(GA)6	12	438	449	TGCAGCAGCAGAAGAGAGAG
scaffold193450_10.	1	p2	(TA)6	12	444	455	TAGCAGGCTGACCGTAGTGC
scaffold193729_11.	1	p2	(AT)7	14	434	447	TGTGTGGTCTGAAAACTCGC
scaffold193864_10.	1	p2	(GC)6	12	223	234	ATATTCTCGCTTCTTCGCCA
scaffold194094_11.	1	p2	(AT)7	14	476	489	ACCCTCCTTCAGCCAAAAAT
scaffold194259_13.	1	p2	(GC)8	16	317	332	CGTTGCCGGATAATTCAAAC
scaffold194383_17.	1	p2	(TC)6	12	235	246	ATGTTTTGGCGTTGGCTATC
scaffold194565_16.	1	p2	(AG)10	20	298	317	ACCAAGAACATTGAGGCTGC
scaffold194603_10.	1	p2	(TA)8	16	170	185	TGGTAGCTTTGAGACACGATT
scaffold194669_15.	1	p2	(TA)6	12	151	162	TGGTTCGGACCATGATTTATT
scaffold194676_15.	1	p2	(GA)6	12	207	218	TTTTTCGATTGTGCTTGCTG
scaffold194855_12.	1	p2	(TA)7	14	425	438	TTGATGGTGAACAAACGGAA
scaffold195046_13.	1	p2	(AG)6	12	185	196	GCGTGGAAGAAAAGATCCCT
scaffold195180_11.	1	p2	(TC)6	12	193	204	CCCATTTCTAACTACCCAAATCC
scaffold195208_11.	1	p2	(AT)8	16	1121	1136	TGAAACATGGATTGCCACAT
scaffold195262_11.	1	p2	(AT)7	14	819	832	CGAGTATGCTGACGGGAAAT

scaffold195448_15.3	1	p2	(AT)9	18	387	404	TGTTAACCAAAAAGAAGAATCGT
scaffold195575_14.7	1	p2	(AT)7	14	264	277	ATGCCCTTCTATGCTGAGGA
scaffold195687_15.7	1	p2	(TA)6	12	2344	2355	CGGGCTGTATTTTAACGGTC
scaffold195723_16.5	1	p2	(TA)6	12	117	128	CCATTTGCAATACTATGGCTTTC
scaffold195724_17.5	1	p2	(CT)6	12	47	58	TGAAAATGGGCGAGAGTTTT
scaffold195884_13.9	1	p2	(TA)7	14	53	66	GGTGTCCGAACTTTATATGGC
scaffold195954_12.8	1	p2	(TC)6	12	159	170	AGATGACAACCTTCGGCTTG
scaffold195995_13.7	1	p2	(AT)7	14	307	320	TGGTATAGGATCCGTCTGGC
scaffold196067_11.3	1	p2	(CT)9	18	261	278	AGAAGGAAAAACCACGGGAC
scaffold196121_17.0	1	p2	(AT)6	12	1457	1468	GCAAATAAAAATTATGGTTTTGGG
scaffold196268_14.1	1	p2	(AT)7	14	69	82	AAACTCGTAAAGTGTCGCGG
scaffold196353_13.8	1	p2	(GT)6	12	55	66	GGAAAATATCAAGTCAACACAAAA
scaffold196496_13.6	1	p2	(TA)7	14	738	751	TTTTTACCATTTTGCCCTGG
scaffold196632_17.1	1	p2	(TA)6	12	482	493	GGGACAATGGAGTTCACGTT
scaffold196753_14.6	1	p2	(TA)8	16	1687	1702	ATGAATTTGGTGTGTTGGCA
scaffold196787_11.4	1	p2	(AT)6	12	183	194	TGCCAACAGTCAAAGTGACC
scaffold196893_13.4	1	p2	(TA)8	16	896	911	TGTCGCCATATACGATCACTTC
scaffold196924_14.4	1	p2	(AG)6	12	93	104	TCTGCTTCAGCTCAGTGTGG
scaffold197312_13.3	1	p2	(TA)11	22	235	256	TAGGGGTTATCACCGGATCA
scaffold197542_13.2	1	p2	(AT)6	12	105	116	CCGAAAATTCAATCCTCGAT
scaffold197602_12.5	1	p2	(AT)7	14	40	53	TCCCAACTAAAATATGCTGCAA
scaffold197665_10.2	1	p2	(AG)7	14	274	287	TGACAGTTTGGCATCAGAGC
scaffold197686_12.0	1	p2	(GA)7	14	105	118	TGCAGAAAATGGAGAGGAGAA
scaffold197886_13.3	1	p2	(TA)7	14	1369	1382	CGAACGGTATAGGATCGGAA
scaffold197903_11.4	1	p2	(CT)7	14	357	370	TAATAGGCTGCCCTCCTCCT
scaffold198177_15.0	1	p2	(TA)8	16	887	902	AGGGCTGAGCAAAAATCAAA
scaffold198463_15.5	1	p2	(TA)8	16	92	107	CAACACAACAATACCACACAGG
scaffold198470_11.4	1	p2	(AT)6	12	829	840	TGTAGATGGCCTAAGACGGTG
scaffold198516_10.3	1	p2	(AG)6	12	363	374	GCTCCAAATCAAAATCCCCT
scaffold198531_10.5	1	p2	(AT)7	14	51	64	TTTGTTCCTACTCACTCACATTAAAA
scaffold198630_14.9	1	p2	(TA)7	14	152	165	TGAATTAACTTCCCAAAACGTG
scaffold198695_10.4	1	p2	(TA)7	14	255	268	CAGACATTGAGGTTTGGATGG
scaffold198826_14.6	1	p2	(AG)7	14	255	268	GTGGGTCGAATTTCGTGAAC
scaffold198946_10.6	1	p2	(TA)6	12	189	200	GGAACCTATGTGACATCCAGC
scaffold198950_13.7	1	p2	(TA)9	18	77	94	ATACCCTACCCGTTTACCCG
scaffold198951_16.1	1	p2	(AT)11	22	1156	1177	ATGCACATGTTTATCGCACG
scaffold199179_10.4	1	p2	(TA)11	22	320	341	TCGCTCATCCAAGTAAGTCG
scaffold199218_16.6	1	p2	(AC)7	14	389	402	GAAGACGCATGCCAGCTAAT
scaffold199316_10.3	1	p2	(TA)11	22	849	870	CTCTTTCCTTGCTCCCCTCT
scaffold199527_10.8	1	p2	(TA)12	24	191	214	TTATCAGCATTTGGGAAGGG
scaffold199716_13.5	1	p2	(AT)9	18	121	138	ATGTGCGCCTTTTAACCTTG
scaffold199793_10.4	1	p2	(GT)6	12	95	106	AATACGGTCCGTGCATGTTT
scaffold200082_11.5	1	p2	(TC)6	12	119	130	AGAACAAGCTAAGGCACCCA
scaffold200146_13.7	1	p2	(TA)7	14	571	584	CCTCCAAGTCTAAGCAGCCT
scaffold200343_10.1	1	p2	(TA)6	12	188	199	CCTCAGGTTCCGATCTCAAG
scaffold200431_12.4	1	p2	(CA)6	12	219	230	TCGTTGATTGCATAGTGGGA
scaffold200667_16.0	1	p2	(AC)7	14	1168	1181	TGTTCTTTGGGATCTGCCTC
scaffold200983_13.9	1	p2	(AG)6	12	286	297	TCCTCCCCAATTTTGTGTGT
scaffold201012_13.1	1	p2	(TC)6	12	605	616	ATGTAGCAGGTTTTGTCGCC
scaffold201538_15.3	1	p2	(TA)7	14	708	721	TTGGTGAGTGTATGGAGCCC
scaffold201747_15.0	1	p2	(TA)8	16	458	473	AAAATCAAAGGCCCACAATG
scaffold202245_13.2	1	p2	(TA)6	12	183	194	GAGTCACACAGTTTGGCACTT
scaffold202365_10.9	1	p2	(AT)6	12	183	194	GCCTTAAAAGGTGGTGTGGA
scaffold202459_16.0	1	p2	(TA)6	12	996	1007	AATGCAACACAACCAAAGCA
scaffold202841_12.1	1	p2	(GA)6	12	50	61	TTGCTGTGTTGGATGGAAAA
scaffold202996_15.0	1	p2	(TC)6	12	371	382	ATGAGCCACAGTTCCAATCC
scaffold203037_12.7	1	p2	(TC)6	12	305	316	CCTGTCTCTTCGGCGTAGTC
scaffold203116_16.8	1	p2	(GA)7	14	326	339	TCGTAAGTCTTCCGCTGGTT

scaffold203349_14.	1	p2	(TA)7	14	290	303	AATGAATGCACCGGATTAGC
scaffold203460_12.	1	p2	(AT)6	12	471	482	GCAATGTGGGCTGAAATCTT
scaffold203469_14.	1	p2	(TC)6	12	1195	1206	ATTCGTCATCAAATTAAAGCCT
scaffold203483_10.	1	p2	(TA)6	12	546	557	GGCGAGAATGGAGGAGAAA
scaffold203486_18.	1	p2	(AG)8	16	816	831	AGCCAGTCTCCACCTCAAGA
scaffold203983_10.	1	p2	(TA)8	16	235	250	TCGAATTCGGGATACCAGAG
scaffold204082_17.	1	p2	(AT)6	12	251	262	GCCTAATAGGGTTGTGTGCC
scaffold204378_12.	1	p2	(GA)7	14	162	175	GAGACGAGAGAAAAGAGTGCGT
scaffold204428_12.	1	p2	(AT)7	14	773	786	GGCAAAAAGCTAATATTTTCAGG
scaffold204647_13.	1	p2	(AT)8	16	193	208	CACCGTTGTCTTTAAGCCGT
scaffold204685_11.	1	p2	(TC)6	12	159	170	GTCGCAGTGATGTCCTTCCT
scaffold204743_10.	1	p2	(AT)6	12	179	190	TCCTCGTATCCGTTCTCCAC
scaffold204769_14.	1	p2	(AT)7	14	2054	2067	CTAACCAGTGGCATGGGAGT
scaffold205077_13.	1	p2	(AT)8	16	1531	1546	ATACATGTCATGCCCGTTTG
scaffold205310_15.	1	p2	(GA)7	14	581	594	AAGCTATGGTGGTTTTGTAAACG
scaffold205493_14.	1	p2	(TG)7	14	108	121	AACACCTGTGAAAGGGATCG
scaffold205539_12.	1	p2	(CT)6	12	419	430	GTTGGCAAACAGGTCCCTAA
scaffold205559_15.	1	p2	(TA)8	16	83	98	TTCGGAGTTATGAAGTTAGCACC
scaffold205565_10.	1	p2	(CT)6	12	257	268	GATTAGCAAATTTCGGGACG
scaffold205620_13.	1	p2	(CT)6	12	1527	1538	CGACCATAACAAAGAAAACACG
scaffold205673_11.	1	p2	(TA)7	14	425	438	CGCAGATCTGATGGTCCAG
scaffold205706_12.	1	p2	(TA)8	16	124	139	GGAGGAGAGGAAATTGAGGG
scaffold205947_10.	1	p2	(AG)7	14	508	521	GGTGCTCAAAAATCCGAAAA
scaffold206176_11.	1	p2	(TA)8	16	253	268	TGAGATAAGGGGGTGTTTGC
scaffold206359_11.	1	p2	(TA)7	14	175	188	ACCCTCCTTCAGCCAAAAAT
scaffold206493_10.	1	p2	(AT)9	18	333	350	TCCCTATTTTTCGTCTCCCA
scaffold206497_17.	1	p2	(AT)6	12	385	396	CGAAGAGTGTGGAATCAAACC
scaffold206978_13.	1	p2	(AT)7	14	623	636	CATCGAAAGAATGTAAGATGCG
scaffold207222_15.	1	p2	(TA)6	12	548	559	TGATTTAAGGGGGTGTTTGC
scaffold207600_14.	1	p2	(AT)8	16	185	200	TGATTAGTACCGATGAATCAACCA
scaffold207843_14.	1	p2	(GA)6	12	91	102	ACCTATGGAAGCCCCAAACT
scaffold208012_15.	1	p2	(GA)7	14	3830	3843	TTGGGAGATTTCAAGAACGG
scaffold208063_15.	1	p2	(GA)6	12	384	395	TCAACATGCAACCAACAAAAA
scaffold208075_22.	1	p2	(CT)6	12	282	293	CAGGAACCCTTTCTCTCATCC
scaffold208112_13.	1	p2	(TA)6	12	1032	1043	ATTTTTGGATGCCAATGCTT
scaffold208204_13.	1	p2	(TA)7	14	359	372	ATTGACATGGCATCGTCTCA
scaffold208354_15.	1	p2	(CT)8	16	2025	2040	TGGCTCTTGTCTTCCTGCTT
scaffold208400_12.	1	p2	(AG)6	12	193	204	CGTGTTCTTCATCCTTTCCC
scaffold208469_14.	1	p2	(AG)10	20	69	88	GCATGGTTTGTTCAATGCAG
scaffold208631_11.	1	p2	(AC)6	12	88	99	CCTCGGCTCTGATACCAAAC
scaffold208674_17.	1	p2	(TC)7	14	344	357	CCTTCCCATTTCCTCTCTCC
scaffold208726_15.	1	p2	(TA)6	12	154	165	CATTGGCATTGTAAGCTTCG
scaffold208882_16.	1	p2	(AT)12	24	46	69	TATCCTCCTCCCAATCGAAA
scaffold209343_18.	1	p2	(TA)8	16	119	134	TGATGGAGGACGACAATGAA
scaffold209354_21.	1	p2	(TA)6	12	241	252	TCACTAACGGCCGGAATATC
scaffold209357_16.	1	p2	(TC)6	12	667	678	AAGGGGTGTTGTGTTGTGCT
scaffold209468_15.	1	p2	(TA)7	14	73	86	GCGAATGTAGGCTGGATCAT
scaffold209533_15.	1	p2	(GA)6	12	951	962	GCATGCATATCGCAGAGAGA
scaffold209593_11.	1	p2	(GA)6	12	168	179	GTTGGAGCTGCTAGGATTCG
scaffold209717_14.	1	p2	(TA)7	14	353	366	TCAACATCGTTTATCAGTTTTGTT
scaffold209718_14.	1	p2	(TA)13	26	1584	1609	TTAATACCCAAAATGCCCCA
scaffold209748_11.	1	p2	(TA)14	28	42	69	TTTTGACAATATTTAGGTGTTTTGA
scaffold209817_13.	1	p2	(AG)7	14	344	357	CGACTCCCAATCAGCAAAAC
scaffold209969_14.	1	p2	(AT)10	20	385	404	TCTCTCTCGACGGTGAAGGT
scaffold210204_17.	1	p2	(AT)6	12	70	81	GTAAGGCTTTTCTAACTTATTGGAAC
scaffold210915_18.	1	p2	(TA)6	12	154	165	CGGCCGGAATATCTAAAGTG
scaffold211083_15.	1	p2	(AT)7	14	962	975	GGTTCAATTTTGCCAACCAC
scaffold211301_10.	1	p2	(TA)8	16	166	181	TGGTGGCCATATATACGCAAT

scaffold211408_10.	1	p2	(TC)6	12	38	49	CTTTGGCAACGGAATACCAC
scaffold211562_14.	1	p2	(CT)6	12	964	975	TCCAAATACCCAGTCCCAAA
scaffold211597_14.	1	p2	(GA)6	12	97	108	CTCTATCTTCGGCCCCTTTC
scaffold212436_12.	1	p2	(AG)9	18	580	597	GCGAAGCTTTTCCAACTCAC
scaffold212590_18.	1	p2	(CT)6	12	716	727	TACACGAATAGCGGTTGCTG
scaffold212657_14.	1	p2	(CT)8	16	428	443	CCTTGGAGAAAAGGACGACA
scaffold212700_13.	1	p2	(GA)6	12	871	882	CCCACAAAACCTAAAGCCAA
scaffold212778_12.	1	p2	(TA)7	14	237	250	ATGGGTTATTACCGGATCGC
scaffold213144_15.	1	p2	(AT)8	16	2022	2037	AAAACTTCAAACCACGGGAT
scaffold213406_16.	1	p2	(TC)7	14	1293	1306	TCACAAGCATGCAAGATAAGG
scaffold213409_10.	1	p2	(AT)6	12	106	117	GGATGGACCGGATGTTAGAA
scaffold213424_18.	1	p2	(TA)6	12	310	321	GGAAAATTTGACGTCGGAAA
scaffold213511_14.	1	p2	(TA)6	12	23	34	ACAAGCACGAACACACACAC
scaffold213638_15.	1	p2	(CT)10	20	3974	3993	AAGCTAAGGATTGAAGCGCA
scaffold213684_15.	1	p2	(CT)8	16	993	1008	ACCATCGATTTTCTGCAACC
scaffold213772_12.	1	p2	(TA)6	12	162	173	CCCATGCATGTAACAAACCA
scaffold213806_14.	1	p2	(CT)9	18	851	868	GCAGTTGGGAAGGCACTAAA
scaffold214000_16.	1	p2	(AC)6	12	141	152	AAAATGCCCTTGTATGCTGC
scaffold214055_10.	1	p2	(AG)6	12	202	213	TTGGATTCAGATCGTGGAAA
scaffold214073_18.	1	p2	(CT)7	14	42	55	TTAAATTTTCGAACGCCTGC
scaffold214079_16.	1	p2	(TG)8	16	138	153	TATCACCATAACGCACCCCT
scaffold214314_11.	1	p2	(CA)8	16	979	994	GTTCGGGGTTGCACTGTATT
scaffold214464_13.	1	p2	(TA)6	12	756	767	TCTAGTTTCGCCCCTGCTTA
scaffold214612_13.	1	p2	(TA)6	12	895	906	TGAAGGGGATAGCATTTTGG
scaffold214689_10.	1	p2	(TA)8	16	536	551	CCTTGGATCACATCAGAACG
scaffold214727_17.	1	p2	(AT)6	12	238	249	AAGAAAGCCCACCTGATTTG
scaffold215004_16.	1	p2	(TC)6	12	1340	1351	TAAATTGCTTGCCTCTGCCT
scaffold215094_13.	1	p2	(CT)6	12	159	170	AGCAAGGAGAATCGAACCTG
scaffold215230_10.	1	p2	(TC)8	16	166	181	GGGGACCACAAAATATTCCC
scaffold215238_15.	1	p2	(CA)6	12	163	174	CGTCCACGGAGAGGTTAGAG
scaffold215266_12.	1	p2	(TC)6	12	658	669	ATGCCATACGGACGTTGAAT
scaffold215457_18.	1	p2	(TA)7	14	52	65	TCGAGTTATGAAGTTAAGAAATAAGG
scaffold215555_10.	1	p2	(GA)7	14	78	91	CGGTACCATCGTCTCTCGTT
scaffold215666_15.	1	p2	(GA)13	26	1384	1409	CAAGTTCCACCCAGGTGTCT
scaffold215887_10.	1	p2	(TA)7	14	328	341	TGCATAGGCTGTCTCTTGGA
scaffold215951_11.	1	p2	(TA)9	18	382	399	CCCTTGTATGCAGCCATTTT
scaffold215970_15.	1	p2	(TA)9	18	560	577	TTCGAGTCATACGGAGGAGG
scaffold216094_11.	1	p2	(AT)7	14	175	188	TGGGCATCACAAATAGACGA
scaffold216128_19.	1	p2	(TA)8	16	754	769	TAAAAAGTTGAGCCCACCCA
scaffold216133_17.	1	p2	(AT)8	16	171	186	TCCTTTCGTTTAACTCCTCCA
scaffold216170_13.	1	p2	(TC)6	12	143	154	TACCGTTGGTTAATCCTGCC
scaffold216222_15.	1	p2	(CT)6	12	1057	1068	TATGCGGTGTTTTGGTTTGA
scaffold216402_11.	1	p2	(AT)10	20	681	700	ATCTTGACCGCTGATTTTGG
scaffold216411_14.	1	p2	(AT)6	12	491	502	GGATCCCACTGAATTGTGCT
scaffold216421_16.	1	p2	(TA)6	12	459	470	AAGAGGAATTGAACCCAGGA
scaffold216795_12.	1	p2	(TA)9	18	162	179	AGGCAATTAAGATTCGCCCT
scaffold216990_12.	1	p2	(TC)6	12	46	57	AGGGGGTGAATAGCCTCACT
scaffold217146_12.	1	p2	(AG)6	12	455	466	GCCCATTTGAGCCAATCTAA
scaffold217414_12.	1	p2	(TA)8	16	138	153	ATTGCCCCTCATATGCAGTC
scaffold217620_13.	1	p2	(TA)8	16	809	824	GGCTAATTTGATGCACGGAT
scaffold217795_11.	1	p2	(AT)10	20	196	215	AAAAATCACGCCACCATTAG
scaffold217964_18.	1	p2	(TA)7	14	178	191	TGGATCAAATGTTTGGTTGC
scaffold218120_13.	1	p2	(AG)6	12	139	150	AAGCAGCCATTAAGAGTCGG
scaffold218440_13.	1	p2	(GA)6	12	149	160	GACGCCTGAATATCGGTCAT
scaffold218514_17.	1	p2	(TC)6	12	226	237	AACCCATGCCAGGAATACAA
scaffold218545_11.	1	p2	(TA)6	12	352	363	TGCCCTCAATCTCGAAAAAT
scaffold218840_15.	1	p2	(TC)6	12	1787	1798	GCGGTTAGGCTTCCACCTAT
scaffold218862_10.	1	p2	(AG)7	14	65	78	AAAACTCCTCCAAACTTCCTCC

scaffold218920_11.	1	p2	(TA)6	12	117	128	TCTCCTTACATAATTTGCCCTCA
scaffold219033_11.	1	p2	(CT)6	12	110	121	TCCTCACTCTCACTAGCCGC
scaffold219072_13.	1	p2	(AT)11	22	1453	1474	TACCTGCCACAACACCAGAG
scaffold219080_14.	1	p2	(CT)6	12	73	84	CAGCCCTCTACCCTTCTTCC
scaffold219363_11.	1	p2	(GA)6	12	289	300	TTGATGTCCCTTCTCCTTGC
scaffold219370_15.	1	p2	(CT)6	12	595	606	CTGTTCACGGGAGCTTTGAT
scaffold219783_16.	1	p2	(TA)7	14	507	520	CGAGTGCATGAGCTTGAGAG
scaffold219866_16.	1	p2	(AT)8	16	5050	5065	TGGTGATGGTGATGAATGTTTT
scaffold220072_17.	1	p2	(CT)6	12	170	181	CCATGCATGCAAAATTGAAC
scaffold220088_17.	1	p2	(TA)6	12	924	935	AACTCTCAATGCCCAAATCC
scaffold220119_14.	1	p2	(TC)12	24	203	226	AAGGGGTCAACACAGTGGAA
scaffold220264_18.	1	p2	(AT)10	20	1341	1360	GAACTGATCAAACCGTCCGT
scaffold220473_14.	1	p2	(TA)6	12	274	285	TGATGCAGTATATAATCCTTAATCAA
scaffold220553_12.	1	p2	(AT)10	20	1101	1120	ATCCAAAGGGACAAAATCCC
scaffold220638_12.	1	p2	(AC)6	12	215	226	TTCAAGCTGAGATCGACGAA
scaffold220806_13.	1	p2	(TA)7	14	207	220	TGCATGCACCTGATTACAAA
scaffold220855_11.	1	p2	(AT)6	12	97	108	TCCATATCATTATCAAATGTTGACTT
scaffold220938_10.	1	p2	(TG)8	16	280	295	CAGAATCACCATCAACACCG
scaffold220955_10.	1	p2	(GA)7	14	384	397	GTAGGAGATGGAGTTGGGCA
scaffold220974_13.	1	p2	(TA)9	18	255	272	TCATGCAATGAAATCCGAAA
scaffold220995_10.	1	p2	(TC)6	12	169	180	ATATCTGGAGGCGGGAACTT
scaffold221261_13.	1	p2	(TC)7	14	114	127	TACCCAAACCCACCAACCTA
scaffold221589_16.	1	p2	(CT)6	12	232	243	GCACCATCAGAGCAACAGTC
scaffold221668_17.	1	p2	(TC)6	12	223	234	AGGTGGGGTGTTAGGAGGAT
scaffold221848_11.	1	p2	(AT)10	20	441	460	CGACTCATGTTGTTCCATGC
scaffold221883_16.	1	p2	(TA)8	16	3520	3535	TCCTCTAATGGCCGAAAATG
scaffold222102_10.	1	p2	(CT)7	14	158	171	TAGATGGGCTAAGTGGGGTG
scaffold222236_13.	1	p2	(TG)6	12	232	243	GGAAAGTCTCACTCGCAAGG
scaffold222290_12.	1	p2	(AT)10	20	1258	1277	ATCATGCGGTATCATGGTGA
scaffold222358_10.	1	p2	(AT)7	14	772	785	TGATCCAGTCACGTTTCACAA
scaffold222455_13.	1	p2	(AG)6	12	55	66	GATCTCGCCTCAACGAGAAG
scaffold222496_16.	1	p2	(TA)6	12	264	275	CATTCAAGGGGCATTTTTGT
scaffold222589_15.	1	p2	(TA)7	14	369	382	CTCATTGAGTTGACCCAGCA
scaffold222790_16.	1	p2	(CT)6	12	835	846	TCACACCCTCTCCCACTCTC
scaffold222824_12.	1	p2	(TA)7	14	227	240	ATGCTGTCAATTAGTGGGGG
scaffold222857_10.	1	p2	(GT)8	16	52	67	AATTTTCTGGCAGCCTTTGA
scaffold222863_10.	1	p2	(AT)6	12	180	191	ATGCAAGCACAATTCGATCA
scaffold223163_11.	1	p2	(TG)7	14	610	623	CAACCATTTTAAGCCCTTCG
scaffold223175_16.	1	p2	(TA)7	14	157	170	AACGGTATGCTCGGATTTTG
scaffold223291_10.	1	p2	(AT)11	22	416	437	TAACCGTTGTCTATGCACGC
scaffold223441_10.	1	p2	(TC)6	12	233	244	ATTGCTTTTGGCTTGTTGCT
scaffold223497_12.	1	p2	(AT)8	16	271	286	AAATATACCCCCGCATGCTA
scaffold223658_12.	1	p2	(GA)7	14	226	239	AGGGAAGAACGAATTGAGGC
scaffold223795_11.	1	p2	(TC)7	14	145	158	ATTCGCACAAATGATCGTGA
scaffold223923_23.	1	p2	(TA)6	12	54	65	GGCTTTCTTAACTTGTTGGAACC
scaffold224010_10.	1	p2	(AT)9	18	378	395	TTGAGCACAGGTTGATCACG
scaffold224042_11.	1	p2	(CT)6	12	509	520	ATCTTGCTAGATGTGCGCCT
scaffold224085_11.	1	p2	(AT)6	12	181	192	ACAAGGGGCAGAAGGATTTT
scaffold224507_16.	1	p2	(TC)7	14	454	467	TAAGAGATCCGAAGCCAAGG
scaffold224830_11.	1	p2	(AT)11	22	183	204	GCTACTTCCGACTCTCTCGC
scaffold225025_13.	1	p2	(AT)7	14	391	404	GGAAGCAAGGTAGGCTTTCG
scaffold225086_17.	1	p2	(TC)9	18	1286	1303	CTGGAATCGAAATGATGAAGC
scaffold225152_12.	1	p2	(AT)9	18	237	254	GGGGAGGGTGGTTAGGTTAG
scaffold225279_11.	1	p2	(AT)6	12	377	388	GTGTGCGGTCAAGGGTACTT
scaffold225452_16.	1	p2	(TC)6	12	587	598	TTTTTGGTGGGTTTCGTCAT
scaffold225489_12.	1	p2	(AT)7	14	242	255	AAGGTGGGAAAGAATTTGGC
scaffold225752_15.	1	p2	(CT)9	18	1613	1630	GATGCCCAAACTTCCTACCA
scaffold225753_12.	1	p2	(AG)7	14	87	100	TTTTGTTGTTTCCCAAGTTGC

scaffold225882_14.5	1	p2	(TA)8	16	887	902	TCATCCCAAAAATACCCTCG
scaffold226074_16.1	1	p2	(TC)6	12	651	662	TCAAGGACTTACCGCTGGAC
scaffold226076_15.4	1	p2	(TA)6	12	1474	1485	CAAACTCCCCCTTCCTCAAT
scaffold226167_14.9	1	p2	(AT)8	16	1146	1161	CTCGAGCTGGATGAGAATGG
scaffold226282_13.1	1	p2	(CG)6	12	239	250	GTTGCCGGATAATTCAAACG
scaffold226317_11.6	1	p2	(TA)11	22	109	130	GTCGCTTGAATTGCGACATA
scaffold226548_14.4	1	p2	(TA)11	22	180	201	TATGGGTTAGCGTGTGATCG
scaffold226561_15.9	1	p2	(AG)9	18	4215	4232	AAGAACCCCAGCATGAATTG
scaffold226568_15.5	1	p2	(TC)6	12	711	722	GGAAAATGTCTTGTGGTCCC
scaffold226587_12.2	1	p2	(AT)11	22	266	287	TTCGGACTTATGAAGTTAGCACC
scaffold226796_16.5	1	p2	(GT)6	12	57	68	GGCTGTGAGATCTAGCGTGA
scaffold227468_11.8	1	p2	(GA)6	12	109	120	TGATCTATGGAAGCCCCAAA
scaffold227758_16.8	1	p2	(AG)6	12	77	88	CCCATGTTGTAATTAATGTAGGGA
scaffold228015_11.5	1	p2	(AT)9	18	637	654	CGAATTTGCAAAACCGAAAT
scaffold228042_10.7	1	p2	(AG)6	12	147	158	TCCATGAAAGCTCACCCTCT
scaffold228253_10.5	1	p2	(GA)6	12	717	728	ATGGAATTGGGTGTTGGATG
scaffold228272_15.6	1	p2	(GA)6	12	583	594	AAGTTCACCGCCTGCTCTTA
scaffold228654_10.0	1	p2	(TC)8	16	181	196	CGCTCAAATCACAAACCCTT
scaffold228698_15.6	1	p2	(AT)8	16	3097	3112	TTGCCTTGTTTAACTTCGGG
scaffold228785_14.9	1	p2	(AT)6	12	443	454	TCAGTTAATATCCCCCGCAG
scaffold228983_12.7	1	p2	(AG)8	16	488	503	TTGTTTGTACCGAATGCGAG
scaffold228985_16.3	1	p2	(AT)6	12	760	771	GAGCTGAATTGGTTCGCTTC
scaffold229230_16.0	1	p2	(TC)6	12	143	154	TGGAGGATTTTCTTTTCCCA
scaffold229298_14.9	1	p2	(TG)7	14	1331	1344	GCAAGTTTCCGTAGCTGGAG
scaffold229592_10.8	1	p2	(CT)7	14	319	332	ACACAGATCATCTCGGGTCC
scaffold229625_15.7	1	p2	(AG)6	12	394	405	ATCGATCGGCTTATGAAACG
scaffold229749_12.4	1	p2	(AG)6	12	1193	1204	AAGAGATGGTTCCGCTCTGA
scaffold230403_11.8	1	p2	(TA)8	16	211	226	GGAGGTTCGACGTGGTTTC
scaffold230637_16.8	1	p2	(TA)6	12	106	117	TCACACCACATCTCAAATGACTC
scaffold230656_16.5	1	p2	(TA)6	12	355	366	GGCTTCAACCTTGACGAAAC
scaffold230670_14.1	1	p2	(TA)6	12	239	250	GGCCTCACTCCCTTTTTCTC
scaffold230710_12.0	1	p2	(AT)6	12	220	231	TTTTCAAGCCTTGTTGAGCA
scaffold230888_10.4	1	p2	(TC)6	12	87	98	AGATGATCCACCGACTCCAC
scaffold230967_17.9	1	p2	(AG)6	12	44	55	GCGATGAGAGAAGGAAATGG
scaffold231010_17.6	1	p2	(TA)8	16	867	882	GCACTGCTTTTTGGTGATGA
scaffold231468_10.4	1	p2	(AT)6	12	208	219	ACCCTAGAAACCCGATCGTT
scaffold232828_10.0	1	p2	(TA)6	12	169	180	AAACATGCAGGTTAGGTGCC
scaffold233077_10.7	1	p2	(TA)9	18	48	65	ATTACCATATTTAAGGGTTATCATCTG
scaffold233385_12.7	1	p2	(TC)10	20	483	502	ATTTTTCCTCTTTCCCCACG
scaffold233696_14.6	1	p2	(AG)7	14	2881	2894	AAGGCGTCTCGAGTGAAAAA
scaffold234041_10.0	1	p2	(TA)6	12	240	251	CAAATACGACACCGAAAGGG
scaffold234359_11.6	1	p2	(AG)7	14	1025	1038	AGAGTCGGTGGAAATGGATG
scaffold234371_11.5	1	p2	(TA)8	16	762	777	TGGCCGGCAGTTTATATAGG
scaffold234988_17.3	1	p2	(TC)6	12	237	248	TGACACCTAGCCCAAACCTC
scaffold235022_11.2	1	p2	(TC)6	12	71	82	TCTGAGACGACGGTGATACAA
scaffold235045_15.3	1	p2	(TC)6	12	1128	1139	CCTCGCACATTCAATTTCCT
scaffold235562_15.3	1	p2	(AT)10	20	36	55	GAAAAAGTCAGCCGAGAGAAAA
scaffold235653_12.6	1	p2	(TA)7	14	419	432	TGATGTTGATTTGGGTTCAAG
scaffold235891_15.3	1	p2	(CT)8	16	49	64	CACTCACTCTCACTAGCCGC
scaffold236163_21.5	1	p2	(GA)7	14	76	89	TGATTTTCTGAAATCGCACG
scaffold236226_15.2	1	p2	(AC)6	12	1292	1303	GGCTCAAATCCGATGATTCT
scaffold236548_17.8	1	p2	(TA)9	18	821	838	ACCACGGAAATTACGGAAAA
scaffold236592_15.0	1	p2	(CT)6	12	566	577	TCTGCTAGGGTTGGGAGAGA
scaffold236645_13.1	1	p2	(AT)9	18	144	161	TTTGGACGATTTTTCCCTTTT
scaffold236858_13.9	1	p2	(AT)6	12	534	545	GCAAACATCCAACTACGAGC
scaffold236993_11.9	1	p2	(AG)6	12	306	317	CTTCGGAACTCTATCCACCG
scaffold237031_16.5	1	p2	(AT)8	16	393	408	CCCCAATTTTGTACCCGAA
scaffold237067_12.7	1	p2	(AC)7	14	632	645	AATTGTGGAGGTTTGAAGCG

scaffold237148_16.	1	p2	(TA)9	18	397	414	CGGCCTCAACCTATATTTGG
scaffold237226_12.	1	p2	(TA)8	16	438	453	TGAAAACTGAAACTAGGAACGAAA
scaffold237280_13.	1	p2	(TA)9	18	2950	2967	ACCATGCTCGAATATCTGGC
scaffold237837_12.	1	p2	(AT)7	14	322	335	CGTCCGTATGAAATTCCAGG
scaffold238266_16.	1	p2	(TC)7	14	171	184	GTCAACTTTGGCAATGGGAT
scaffold238425_12.	1	p2	(TA)10	20	367	386	CGCCTTTAAATCAGGTGCAT
scaffold238583_16.	1	p2	(AT)11	22	1228	1249	CGCTACAGTTCACACGTTCG
scaffold238737_10.	1	p2	(TG)6	12	72	83	TCAAAATTTCCAAAAATCAAAGC
scaffold238853_11.	1	p2	(TA)6	12	150	161	CTCAGGTTCCGACCTCAAAC
scaffold238983_12.	1	p2	(TC)6	12	139	150	TTCAAGGCATTTATCTGGGC
scaffold239219_11.	1	p2	(TC)7	14	273	286	GCCCCTTGAAGTTTCGTAGA
scaffold239249_17.	1	p2	(TA)8	16	2303	2318	TTCCTTGGGACACAATCCAT
scaffold239432_17.	1	p2	(AG)7	14	1157	1170	GGGCTAGTCCTGCAACACAT
scaffold239459_11.	1	p2	(AT)8	16	537	552	CCCGATTTGTAAGGTTCCATT
scaffold239647_10.	1	p2	(CT)6	12	44	55	GCTCTACAATATTACAATGGGCAA
scaffold239769_10.	1	p2	(TC)6	12	182	193	TGTGATAGGATAGGGCCAGC
scaffold239846_14.	1	p2	(TC)6	12	91	102	AGGACACGTTGGACCTGAAG
scaffold239960_16.	1	p2	(TA)6	12	1006	1017	GCTTGAAAAGCCATGCAAAT
scaffold239998_18.	1	p2	(AT)9	18	555	572	AACGTGAATCTCATCCGTCC
scaffold240085_14.	1	p2	(TA)9	18	1599	1616	TGATTTCCAAGTGAAGGCTG
scaffold240099_11.	1	p2	(TA)11	22	523	544	TTGTCATTGTTAATCCCAAAACA
scaffold240190_12.	1	p2	(AG)6	12	334	345	TTATTGAAGCAGCAGCAACG
scaffold240355_16.	1	p2	(AT)6	12	177	188	AGCACGGCTTGTGCTATCTT
scaffold240369_13.	1	p2	(CT)8	16	2539	2554	CCCCAGAAACACCAACTTGT
scaffold240425_11.	1	p2	(TA)7	14	323	336	TATAACGACACGGCCATTGA
scaffold240746_14.	1	p2	(TA)6	12	83	94	CAAGTGGTAGCAAACCATGAA
scaffold240836_14.	1	p2	(TA)7	14	846	859	AGAATTCGTGCCCCTCATTA
scaffold241004_14.	1	p2	(AT)8	16	313	328	GAACGTTAGTGAGGACGGGA
scaffold241339_14.	1	p2	(TA)6	12	813	824	CCCGGTATGCTGACGATAAC
scaffold241379_13.	1	p2	(AG)6	12	248	259	ACATGTTCACCAAGCCACTG
scaffold241664_12.	1	p2	(GA)6	12	28	39	GGAGGGAGGGAGAGATAGGA
scaffold241735_16.	1	p2	(GA)8	16	37	52	GGAAGAATGATGGAATTGGG
scaffold241806_12.	1	p2	(TC)7	14	1053	1066	TGAACAATTGAACACCGGAA
scaffold241938_16.	1	p2	(TA)8	16	263	278	ATGACACGCATAAAGGGACC
scaffold241944_15.	1	p2	(GA)7	14	349	362	TCACAATAGGGCATGGGACT
scaffold242054_13.	1	p2	(CA)7	14	69	82	CACTCACACTTTGCACACTGAA
scaffold242072_13.	1	p2	(CT)6	12	389	400	GGCAGATGCCTTTGAAGAAC
scaffold242170_16.	1	p2	(CT)6	12	427	438	TTAAAACAAGAAAGCCCACCA
scaffold242351_16.	1	p2	(CA)6	12	469	480	TCAAATCTCTAATTGCACCCTTC
scaffold242363_16.	1	p2	(TA)6	12	220	231	AGTTGAAAGAGCCATCAGCC
scaffold242477_15.	1	p2	(AT)7	14	1046	1059	AAATGGGGAGATGATGAACG
scaffold242486_11.	1	p2	(AT)6	12	292	303	CCATTCAAGTCGTGGTCCTT
scaffold242623_10.	1	p2	(AT)8	16	267	282	TGGACGTAAATACCCTTTTACCA
scaffold242685_15.	1	p2	(AT)6	12	116	127	ACACAACAATACCACGCAGG
scaffold242959_13.	1	p2	(GT)6	12	208	219	TTGTTGCCGTTAAAGTGTGG
scaffold242962_12.	1	p2	(AG)7	14	205	218	GGGAGAGAAGGGAGGAGAGA
scaffold243021_11.	1	p2	(GA)6	12	98	109	GGATTTGTCAACCGGAAAAC
scaffold243145_14.	1	p2	(TC)7	14	901	914	AAAGCAACACCATCAGACCC
scaffold243199_10.	1	p2	(GA)6	12	171	182	TCAACAACATGCAAACACCA
scaffold243221_17.	1	p2	(CT)6	12	212	223	CACCCCTCCACTCTCTCATT
scaffold243316_12.	1	p2	(AT)9	18	166	183	ACCACGCATGGTTGAGTACA
scaffold243762_14.	1	p2	(TC)6	12	412	423	CACCAACATCATCGAACAGG
scaffold243931_16.	1	p2	(AG)11	22	1698	1719	TTGTCACATACACGTTGGGAA
scaffold244306_15.	1	p2	(AT)6	12	81	92	CACCACAATGAAGTGGATGC
scaffold244372_15.	1	p2	(TA)10	20	219	238	ACAACAATGTCGCGAAACAA
scaffold244393_16.	1	p2	(CA)6	12	139	150	TCAATCTCTCGTGCTCACTGAT
scaffold244762_11.	1	p2	(CA)8	16	569	584	TCAAAAGCAATCAAATATCCCA
scaffold244828_10.	1	p2	(TA)10	20	479	498	CAAAAGATCGGCTATTTGGTG

scaffold244940_16.	1	p2	(GA)6	12	410	421 TGGATGCCTTTCATTTAGGTG
scaffold245015_12.	1	p2	(GT)10	20	661	680 CGGAAGCGCACATTAAGATT
scaffold245367_12.	1	p2	(AC)7	14	157	170 CACTTGGCAAAAAGCACAAA
scaffold245653_13.	1	p2	(GA)7	14	600	613 CATTCTCACCGGAACCCTAA
scaffold246200_12.	1	p2	(TG)6	12	399	410 TCAATAGAAAATGAGTTTGAGTTTCG
scaffold246523_14.	1	p2	(AT)7	14	291	304 ATGCATCCTGGCCTTGTTTA
scaffold246897_13.	1	p2	(AG)7	14	2093	2106 AGAATGATGAACCCCTTCCC
scaffold246965_12.	1	p2	(CT)8	16	611	626 GTTCTTGCTTGCTGTCCCTC
scaffold247028_13.	1	p2	(GT)6	12	402	413 CAAGCTGTCAACCCAAAACA
scaffold247219_13.	1	p2	(CT)10	20	398	417 GTCGGCAAACCAGAGCTAAC
scaffold247256_15.	1	p2	(TA)7	14	176	189 TTTTACCCTCCCATGCTTTG
scaffold247353_16.	1	p2	(TA)6	12	314	325 CCAGGTTCAACTCTCTTCCG
scaffold247459_20.	1	p2	(TA)8	16	78	93 CCATTTGCAATACTAAGGCTTTC
scaffold247565_14.	1	p2	(TA)10	20	1126	1145 AGGAATAGGGCCGAGAAAAA
scaffold247692_14.	1	p2	(TA)8	16	2165	2180 ATCAACTAAATTTGGCGCGT
scaffold247711_16.	1	p2	(TG)7	14	2528	2541 GACATTGGCATTTTCTGCAA
scaffold248051_11.	1	p2	(GA)6	12	73	84 TCTTGGATGATGAGGCTTGA
scaffold248103_13.	1	p2	(GA)6	12	1558	1569 TTTTCTCCTTGTAGCGTGGG
scaffold248110_14.	1	p2	(AT)8	16	240	255 TCGTCAAAAACTAATTAAGGCCA
scaffold248264_14.	1	p2	(GA)6	12	55	66 TGAATTACTTGAAGAATGATGAGAG
scaffold248329_10.	1	p2	(CT)7	14	100	113 TAACCAAACCCCCAATTTCA
scaffold248478_15.	1	p2	(AT)7	14	924	937 CAGGAAGCTTCAACTCCAGG
scaffold248621_12.	1	p2	(AG)6	12	54	65 GTGAAATTGCTTTTTGGGGA
scaffold248634_16.	1	p2	(CT)13	26	2274	2299 GCCAGCTAACACATCAAGCA
scaffold248651_15.	1	p2	(AC)7	14	525	538 TCAATGCAACTCAAATCCCA
scaffold248670_13.	1	p2	(TG)6	12	495	506 TGTGTGCAATGTGTGTGTGTT
scaffold248820_17.	1	p2	(CT)6	12	221	232 ACACATGCTCGGCATACAAA
scaffold248988_15.	1	p2	(AG)8	16	3697	3712 AACAACCACTGGCAGAATCC
scaffold249102_16.	1	p2	(AT)7	14	2543	2556 CACTTCTGCGGCTGAAAAAT
scaffold249107_14.	1	p2	(TG)6	12	1211	1222 TTTGTTTCCTCCCTTTGTGC
scaffold249134_10.	1	p2	(AC)6	12	158	169 CAGATACGCGGGTTCATTCT
scaffold249452_10.	1	p2	(TG)6	12	67	78 TCTGTGCTCTCTTTCTCAGTCG
scaffold249548_17.	1	p2	(TA)7	14	50	63 ATGAAGTTAGAAAATAAGGAGGTGT
scaffold249652_11.	1	p2	(TG)10	20	289	308 AAACTGCCCTCCAATGCTAA
scaffold249770_12.	1	p2	(TA)9	18	255	272 CACAGAAATCACGTTGCAAAA
scaffold249883_11.	1	p2	(TA)7	14	167	180 TGTGGCATCCTATCAACCCT
scaffold249933_12.	1	p2	(AG)6	12	137	148 ACCTCCCCTGCTCCATACTT
scaffold250351_12.	1	p2	(AT)9	18	874	891 GGCCATTCACTTCAATGCTT
scaffold250610_11.	1	p2	(GA)6	12	31	42 TTGCCGATTAGGATTTCGTT
scaffold250906_11.	1	p2	(TA)6	12	41	52 CAAGCACTATGAAAGCTAAATACTA
scaffold251053_11.	1	p2	(GT)6	12	207	218 ACGCTTGTCCCCTTAATCCT
scaffold251127_15.	1	p2	(TA)10	20	381	400 TCAATTCCGAAAATCAAGGC
scaffold251245_12.	1	p2	(GA)6	12	805	816 TCGTGTGTGTGAGTGAACCA
scaffold251435_13.	1	p2	(TA)10	20	329	348 AGGGAGGAATAGAGCCGAAA
scaffold251609_15.	1	p2	(TA)6	12	158	169 AACCGTAGGCTTGCTTCTGA
scaffold251710_15.	1	p2	(TA)6	12	1319	1330 TCCAGTGACAAAAACCGACA
scaffold251777_15.	1	p2	(GA)6	12	1904	1915 CAGACAGAGAGATGCCACCA
scaffold252123_12.	1	p2	(AT)7	14	300	313 CCAATTGATCGGGAATTGAT
scaffold252167_13.	1	p2	(AT)6	12	627	638 TTGGAGCTTGCTGCAATTTT
scaffold252283_11.	1	p2	(TA)8	16	267	282 AGAGTTTTGCGTGCATGTTG
scaffold252301_13.	1	p2	(AT)6	12	108	119 ATCCATCCTGTTTCTCCCCT
scaffold252337_13.	1	p2	(AT)11	22	919	940 CAAAATCCGTTACATATCTTGGG
scaffold252587_14.	1	p2	(AT)9	18	633	650 AACCCAACCCACAATAAACG
scaffold252630_13.	1	p2	(TA)6	12	109	120 CCACCGAGCACCAAGTAAAT
scaffold252825_11.	1	p2	(TC)6	12	162	173 AGTTGGGCTTAATGGTGTGG
scaffold253319_13.	1	p2	(AG)6	12	103	114 GGAGATGGAGAGAAAGTGTCG
scaffold253770_11.	1	p2	(GT)6	12	218	229 GAATCAACTCCAATCCGGTG
scaffold253906_16.	1	p2	(TA)6	12	517	528 AAGGGGTTTTCTCTGGATCG

scaffold254087_16.	1	p2	(CA)6	12	635	646	AATGGGACCTCCTTTACGCT
scaffold254272_14.	1	p2	(AG)6	12	62	73	GTGGATGATGAGGAGGAGGA
scaffold254351_14.	1	p2	(CT)10	20	604	623	TACTGCTCTTGAACTCGCCA
scaffold254451_12.	1	p2	(CT)6	12	38	49	TTACAATGGCCAAGAGGATT
scaffold254628_13.	1	p2	(AG)8	16	195	210	AGTTGGTCATTTGAAGCGAGA
scaffold255067_13.	1	p2	(AG)6	12	105	116	TTTTGTTTGTTCCCAGGTTG
scaffold255334_11.	1	p2	(AG)6	12	234	245	CTTCCTCTCCCTTCCGTTTC
scaffold255358_14.	1	p2	(GA)7	14	409	422	AGATTTGAACTTGGAGGGCA
scaffold255458_13.	1	p2	(CT)6	12	106	117	TGCATGGTTAATGTTGTAAGGG
scaffold255463_13.	1	p2	(TC)6	12	201	212	TGCGTCGTGTTCTGATTTTC
scaffold255507_13.	1	p2	(AT)7	14	52	65	AGGGCTGAGTACACGAATGC
scaffold255617_18.	1	p2	(TA)6	12	171	182	GCTTTCAAGGAGTGAGGCAC
scaffold255638_14.	1	p2	(TA)9	18	262	279	TTGGGATCTAGGCAATCCAG
scaffold255727_14.	1	p2	(TA)6	12	3411	3422	TCCAGTTTTCAATGGTGCAA
scaffold256399_11.	1	p2	(AC)6	12	181	192	TTCTCACATCCTTCTCGCCT
scaffold256411_11.	1	p2	(AT)7	14	601	614	TTGCATGCCACCTTTATTTT
scaffold256973_16.	1	p2	(AG)8	16	5940	5955	ACTGGCCGGCTAAGTTGATA
scaffold257036_13.	1	p2	(TC)6	12	37	48	GAATACCGCTCGTAAGTCCG
scaffold257089_10.	1	p2	(TA)8	16	331	346	TGATTTTGGTGTGTTGGCAT
scaffold257472_14.	1	p2	(CT)6	12	1522	1533	TGATCATACCAAGGCGATCA
scaffold257487_14.	1	p2	(CT)7	14	485	498	CATATGGCGCTCCACCTACT
scaffold257844_15.	1	p2	(AT)6	12	100	111	TGAAATCTCCCGTACTTCCG
scaffold257958_11.	1	p2	(TA)6	12	177	188	TGCCCATACGGTTGTATGAA
scaffold258004_11.	1	p2	(TA)8	16	52	67	TTTTATCTGAATGCTAGATGTTTGG
scaffold258131_16.	1	p2	(TC)7	14	281	294	GAAAAATAGCATGCCTTCGC
scaffold258209_14.	1	p2	(AT)7	14	358	371	ACGGAAATACGAATGCGAAA
scaffold258229_12.	1	p2	(AC)6	12	53	64	TGTGTACTTCCCTACTCATAAGCAA
scaffold258504_11.	1	p2	(CT)6	12	272	283	GTACAGCCATTCGTCCACCT
scaffold258753_15.	1	p2	(AT)9	18	1033	1050	TTAGCATGTGGGAAGGGTTC
scaffold259181_16.	1	p2	(AC)6	12	3523	3534	ACCGGCGTATAAAGACATGC
scaffold259281_14.	1	p2	(TA)9	18	184	201	TATGATGGGAAGGGTGGGTA
scaffold259290_15.	1	p2	(TA)8	16	205	220	TCACGAAAACACGACACACA
scaffold259505_15.	1	p2	(AG)7	14	425	438	GGTGGGAGCAGACAGAAAAG
scaffold259609_13.	1	p2	(TC)7	14	461	474	GAAGCGCAGTCATTTAAGGC
scaffold260213_12.	1	p2	(CT)6	12	51	62	CTCATTGTAATCTCTCTCCAAAGTT
scaffold260377_12.	1	p2	(GA)6	12	55	66	CACCTTCATCTTCACCACCA
scaffold260493_16.	1	p2	(CT)7	14	362	375	ACACTAAACCCGCGTATTGC
scaffold260799_15.	1	p2	(GT)6	12	268	279	TAGGATACCCTCCCAAACCC
scaffold260844_12.	1	p2	(GC)6	12	223	234	ACGAGCCTCGAGGTAGCTG
scaffold260952_17.	1	p2	(AG)6	12	74	85	GTCCACGGTGGTTTGAGAGT
scaffold261186_13.	1	p2	(AG)6	12	615	626	CGAATGGGAGAGAGTGGATG
scaffold261262_12.	1	p2	(AG)7	14	49	62	CAATTACAATGTTTATGAAAATCCA
scaffold261323_13.	1	p2	(TA)8	16	387	402	CTCAAACTTCAGCCCGTACC
scaffold262190_17.	1	p2	(CT)7	14	52	65	TCCTCACTCTCACTAGCCGC
scaffold262347_14.	1	p2	(AG)6	12	236	247	ATATAGCCGTTGGGCTTGTG
scaffold262529_14.	1	p2	(TC)6	12	36	47	CATCAACTCACCCTCACATTTC
scaffold262560_12.	1	p2	(AT)6	12	694	705	TCCAAGAAACTACGCCAACA
scaffold262870_11.	1	p2	(AT)10	20	144	163	TGGAGTTTAAATGTAGAGGCGA
scaffold262937_14.	1	p2	(TA)7	14	48	61	TTTAGTGTTTTGACATGATTACTCG
scaffold262944_19.	1	p2	(CT)9	18	327	344	TTCGAACGAAAACGTGTCAG
scaffold263142_14.	1	p2	(AC)6	12	1693	1704	GCATTAGCAAATCCCGAAAA
scaffold263490_13.	1	p2	(TC)6	12	168	179	ATGTTCGAAGCAGCCAAACT
scaffold263539_11.	1	p2	(AG)7	14	208	221	TGTTCCGGTCCGAGTTTATT
scaffold263559_17.	1	p2	(CT)6	12	90	101	TCCTTCTTAAAGGTCTTAATCGGA
scaffold263571_16.	1	p2	(GA)7	14	464	477	TTGGGGGTTTAGGGTTCTCT
scaffold263572_15.	1	p2	(AT)6	12	2900	2911	CCGTCGAACTACCGGTTCTA
scaffold263702_11.	1	p2	(TC)7	14	262	275	ATTGAAACTACGTCCACGGG
scaffold263874_14.	1	p2	(TC)6	12	232	243	AGACCCAACTACCAAACCCA

scaffold263950_16.8	1	p2	(AT)7	14	2151	2164	ACGATCCTACACAATGGCG
scaffold263964_17.0	1	p2	(TG)7	14	150	163	CATGATTGGGGACTGACCTT
scaffold264109_16.9	1	p2	(AC)6	12	240	251	TGGCAACAAACAAAGCTGAG
scaffold264305_16.9	1	p2	(AT)8	16	242	257	GGTGATGATGGAAAACCTGG
scaffold264356_11.2	1	p2	(GA)8	16	284	299	CCAAGGATCACAAGTGGATG
scaffold264494_12.5	1	p2	(TA)8	16	337	352	TTTTGTCGGCCATTTTCTTT
scaffold264729_11.8	1	p2	(AT)7	14	159	172	TGATTGATCTTAACTGCAAAAGAGA
scaffold265133_18.5	1	p2	(AT)6	12	69	80	TTCACGAATAAACATGTTCCAGA
scaffold265371_13.4	1	p2	(AT)6	12	199	210	CGCCCACAATCCTGATATTT
scaffold265627_13.3	1	p2	(CT)9	18	416	433	CGCACCTATTAGGGTCGGAT
scaffold266076_17.3	1	p2	(CT)7	14	631	644	TAACGAGAAAATTCGGCCAC
scaffold266140_11.5	1	p2	(TC)6	12	142	153	CCGAGGTGGAGTAGTATCCG
scaffold266357_14.2	1	p2	(AG)9	18	2040	2057	CTAGAACCCCCTCATCCGA
scaffold266693_12.8	1	p2	(AT)10	20	448	467	GGATCGTAGGAGCAGATGGA
scaffold266745_10.8	1	p2	(AT)7	14	257	270	TTTTCGCAAGCCACTAAAAA
scaffold266766_15.4	1	p2	(TA)9	18	2350	2367	CAGGAAAGAAATGGGCTTCA
scaffold266830_13.4	1	p2	(TA)8	16	115	130	AAGCGAAACTGTTGTATGCTG
scaffold266838_11.7	1	p2	(TA)6	12	119	130	TCGAGCTGTTATGCGTTTTG
scaffold266841_15.7	1	p2	(AT)6	12	120	131	CCCGAGTTGAGGTCCTGATA
scaffold266875_13.5	1	p2	(AT)8	16	249	264	ACTCAACCGATTGACGATCC
scaffold266923_15.7	1	p2	(CT)6	12	204	215	TTGGAAGATGGAGAAATAAGGC
scaffold266956_16.8	1	p2	(GA)7	14	2016	2029	TGGTTTGGTTGTCACTTTCTTG
scaffold267035_12.1	1	p2	(TA)6	12	169	180	TTAGTTAGCAAGGGGGAGGG
scaffold267046_17.2	1	p2	(CT)7	14	469	482	AACCCATACTTAATTCATAACCCAA
scaffold267279_10.0	1	p2	(GA)6	12	198	209	CTGCAGACATTTCTCGGTGA
scaffold267310_14.0	1	p2	(TA)6	12	70	81	TTCGATGATAACTATGGGTTTTG
scaffold267411_18.0	1	p2	(TA)7	14	354	367	CTCTCAATGGACCAGCACCT
scaffold267639_13.8	1	p2	(TA)11	22	504	525	GATGGAGAAGTTACGATGGCA
scaffold267677_15.4	1	p2	(AT)7	14	51	64	GGTTTTGACATAACTTAGGTGTTTTG
scaffold267732_13.1	1	p2	(AG)7	14	503	516	CTGACACAACCCTCCATGTG
scaffold267791_15.3	1	p2	(GA)6	12	632	643	AGGGAAAAAGACATCAGCCA
scaffold267839_15.1	1	p2	(TA)8	16	1839	1854	TGCTCCGAGACCTTAGACTCA
scaffold267868_11.8	1	p2	(AT)8	16	254	269	AGAATCCCGAGATTTCATGC
scaffold267874_10.9	1	p2	(TA)6	12	167	178	GCTGGAAGATAAGATGTGAACG
scaffold267986_13.7	1	p2	(AC)7	14	429	442	GACAAAGCTAACGGAACCCA
scaffold268090_11.2	1	p2	(TA)7	14	1187	1200	GTCCAAAATTGTGTTACGGG
scaffold268098_13.3	1	p2	(CT)6	12	928	939	GAAGAGAAAGCGCGATCATT
scaffold268137_14.6	1	p2	(AT)6	12	68	79	GTGGGTTAGCACGTGATCG
scaffold268230_18.3	1	p2	(GA)8	16	3843	3858	GGGATTTAGGCCAAACGATTA
scaffold268422_16.8	1	p2	(GA)8	16	1713	1728	AATTAGTCGTGGCCGTGAAC
scaffold268616_12.3	1	p2	(TA)9	18	487	504	GCCATGATCTCATGATTCAAAA
scaffold268741_11.6	1	p2	(TA)8	16	260	275	TTCGGTTAATCCAAAGGTCAA
scaffold268915_12.1	1	p2	(TA)10	20	85	104	AATTGAATGGCAAGGATTGG
scaffold268949_10.8	1	p2	(TA)11	22	716	737	TGTAATAGTACATACAATGCAGGGA
scaffold269277_14.0	1	p2	(GA)6	12	76	87	AGCCCCAAACTTTGCTGAAT
scaffold269502_18.6	1	p2	(TG)6	12	105	116	GATGTGGAGATGGGCTGACT
scaffold269522_15.8	1	p2	(TC)6	12	117	128	CGCGCACAAAGAACTTTACA
scaffold269583_17.1	1	p2	(CT)7	14	72	85	CACTTGGACCTGAAAAGGGA
scaffold269682_13.6	1	p2	(CA)8	16	3628	3643	GCCTTTTGGCATGCAGTATT
scaffold269694_15.4	1	p2	(TC)7	14	404	417	CGTGCAAGCATGAATCACTC
scaffold269737_19.7	1	p2	(GT)6	12	565	576	GGAATGCGAGATGGAAGAAA
scaffold270090_16.1	1	p2	(TA)7	14	493	506	TGTCTCGGTGTTCATGGATT
scaffold270168_13.6	1	p2	(TA)8	16	508	523	GAAAATTGGTTGTTATCCACAAG
scaffold270307_11.6	1	p2	(CT)6	12	141	152	CAATACCGTGACATGCCTTG
scaffold270452_15.7	1	p2	(AG)8	16	4383	4398	CAAGAAAATCCCACCTCCAA
scaffold270525_11.6	1	p2	(TA)6	12	178	189	TCATGAGAAGCGTGGATTTG
scaffold270569_12.5	1	p2	(AG)7	14	53	66	GGCCACCACACGAGTATATCA
scaffold270585_14.9	1	p2	(AC)8	16	2844	2859	TCCTCTTTCTTTTTGCGAGC

scaffold271008_12.	1	p2	(TA)9	18	330	347	TGTAGGCGCCTCTGATCTTT
scaffold271098_10.	1	p2	(AT)6	12	117	128	TCGCGTTCGACTCCTTAACT
scaffold271239_15.	1	p2	(CT)6	12	113	124	TGCTCTCTTTGTAATCTCTCCCA
scaffold271381_14.	1	p2	(TG)6	12	674	685	GTCAGCAGAGGAGGAGTTGC
scaffold271462_12.	1	p2	(CT)7	14	223	236	GCGAAATCAAAGAATCCGAA
scaffold272471_14.	1	p2	(AT)8	16	683	698	GGAAATCAATCACAGCCGTT
scaffold272573_13.	1	p2	(TA)9	18	586	603	TAAAAAGATGAGCCCACCCA
scaffold272606_16.	1	p2	(TA)8	16	390	405	TATGATGGGAAGGGTGGGTA
scaffold272617_14.	1	p2	(CT)6	12	293	304	GAAATGAAATCCTGGCTTCG
scaffold272685_18.	1	p2	(TC)8	16	76	91	TCAGAAACTTGGAGCAGAAGAA
scaffold272917_12.	1	p2	(TC)6	12	117	128	CAAGCCCAAAAGCACAAAGT
scaffold273254_11.	1	p2	(CA)9	18	881	898	TCTTTTCAATATTTATACCAACCGA
scaffold273522_15.	1	p2	(TC)7	14	1869	1882	CCCCAAACATCACACACAAG
scaffold274081_14.	1	p2	(TC)6	12	195	206	AAATGGTTGTTTGTCCCCAA
scaffold274090_18.	1	p2	(TA)11	22	523	544	TACTTGCTCCCGAGCTCAAT
scaffold274243_12.	1	p2	(TC)7	14	603	616	GATTCCCCATCACCATCATC
scaffold274368_13.	1	p2	(GT)7	14	412	425	TTGACATGATTTGTTAACGGG
scaffold274576_12.	1	p2	(TA)6	12	133	144	TTTTTCATCCCGTTTCATCG
scaffold274662_10.	1	p2	(TC)7	14	104	117	GAGGACACGTTGGACCTGAT
scaffold275039_13.	1	p2	(CT)6	12	48	59	CTCACTCTCACTAGCCGCAG
scaffold275042_18.	1	p2	(CT)6	12	105	116	CAATCATCTAGCCCTCTAACATCTC
scaffold275207_15.	1	p2	(GA)7	14	805	818	TTCTCTGTCGCCAGATCCTT
scaffold275653_18.	1	p2	(GA)6	12	119	130	AGAGCCACGTTAGGCTCAAG
scaffold275672_13.	1	p2	(AG)8	16	350	365	TGCAAACCCATTTAAAACCC
scaffold275848_11.	1	p2	(TA)7	14	905	918	GATATGGAAGAGTGGCACCG
scaffold275876_14.	1	p2	(CT)6	12	384	395	CCGGCTACTTGTGAATTCCT
scaffold276066_11.	1	p2	(AT)8	16	744	759	ATGTCGATGAACACGGATGA
scaffold276335_17.	1	p2	(AT)6	12	1367	1378	ATTTTAGAACGGGGGTGGAC
scaffold276343_16.	1	p2	(TG)7	14	263	276	TGGTTGGAGGAAAATCTTGTG
scaffold276448_12.	1	p2	(CA)6	12	104	115	CGTGTAATCACCATCATCGG
scaffold276908_19.	1	p2	(CT)8	16	65	80	GGAGTCTCTCTCGCTGATGC
scaffold277841_10.	1	p2	(TA)8	16	588	603	GGGACAAAGCAAAACGAAAA
scaffold278081_13.	1	p2	(GA)6	12	225	236	CGGCTCCTTTGTGTAGTTCC
scaffold278301_13.	1	p2	(AT)7	14	374	387	GCCACGTGTGTTCATTGAGA
scaffold278354_13.	1	p2	(AT)6	12	1212	1223	CGAAAACCTTGAGAGCTCGTT
scaffold278390_13.	1	p2	(AT)6	12	660	671	CGGAGTTTCGTATCTTGGGA
scaffold278514_14.	1	p2	(AT)9	18	2291	2308	AGGGGAAAAGAAGAGTGGGA
scaffold278538_12.	1	p2	(AT)7	14	787	800	TCCATTTGCATATTATTTTTGCAC
scaffold278679_13.	1	p2	(TA)6	12	1295	1306	TCAAGAGCCTCCGACTTTTC
scaffold278700_12.	1	p2	(AG)14	28	326	353	CGAGCGAGAGGAGAGAGAAA
scaffold278911_10.	1	p2	(CT)7	14	30	43	CAAATGGCCAAGAGAGTTTACA
scaffold279147_13.	1	p2	(AT)6	12	532	543	GCCTGAATCGACGACAAACT
scaffold279349_10.	1	p2	(TA)10	20	215	234	CGATTTGGATTCGAATTCTGT
scaffold279401_17.	1	p2	(TC)6	12	772	783	CAAAGAACGTGCACACACAA
scaffold279605_16.	1	p2	(AG)10	20	515	534	ATGTGAGATGGTGGTGGTCA
scaffold279810_16.	1	p2	(GA)7	14	2147	2160	AAGGTAAGGGGGTGGGTATG
scaffold279907_12.	1	p2	(TA)8	16	272	287	TTTGAAATGGATGGTGGTGA
scaffold280012_10.	1	p2	(GA)7	14	293	306	AGGGGCTTAAGATCCCAGAA
scaffold280044_10.	1	p2	(TA)8	16	168	183	AAAAACCCTTCCGCCCTT
scaffold280052_18.	1	p2	(TA)6	12	408	419	CTACTCTCAATTCCCGTCGC
scaffold280205_13.	1	p2	(CT)6	12	575	586	CTGCGCACCGATATGATAGA
scaffold280254_14.	1	p2	(CT)6	12	145	156	CCCTAAGATAATGCCACCCA
scaffold280275_13.	1	p2	(TC)6	12	322	333	GGCCCTAACTTGACCCAGAT
scaffold280276_14.	1	p2	(AC)6	12	42	53	GAACAAAGCTTGTCACACGG
scaffold280280_15.	1	p2	(GC)6	12	732	743	CCCAGACTCGATAACTGGCT
scaffold280296_14.	1	p2	(GT)7	14	433	446	AGGATTTGAGTTGGCTGTGG
scaffold280734_17.	1	p2	(GA)6	12	166	177	CCAAAAGACGATCTGGGATG
scaffold280804_11.	1	p2	(TA)8	16	307	322	ACGCTGCCTTGTCTTGATTT

scaffold281078_16.	1	p2	(TA)8	16	294	309	TGCGAGCCATCAACATGTAA
scaffold281148_16.	1	p2	(AT)9	18	3364	3381	TCATGCACGAAACTCTTGGA
scaffold281530_17.	1	p2	(TA)8	16	343	358	TGTATTCCTTGAATATGAGAACTTGT
scaffold282023_13.	1	p2	(TC)6	12	440	451	CCAAACATGGGGATATGAAA
scaffold282127_12.	1	p2	(TC)6	12	411	422	TATTTTCCACCAACCCAACC
scaffold282163_14.	1	p2	(GA)6	12	183	194	CTTACGATCAGGGTTGTCCG
scaffold282572_17.	1	p2	(CT)8	16	4521	4536	TTTTCTTGGCCATAGGCATC
scaffold282679_14.	1	p2	(TG)6	12	1231	1242	GCATGCATCCACCACTCTAC
scaffold282734_11.	1	p2	(TA)8	16	169	184	AAATCTGAATTTCGATGCCG
scaffold282744_15.	1	p2	(TC)9	18	1097	1114	CCCAAATTCACATGCTTTCC
scaffold282970_14.	1	p2	(TA)9	18	3304	3321	CCATTAGCACAACACATCGC
scaffold283163_10.	1	p2	(AT)11	22	77	98	TTTAAATGCACACCCCTTTCT
scaffold283293_12.	1	p2	(TA)7	14	176	189	TAAAATTCACCCAAGACGGC
scaffold283313_16.	1	p2	(TC)7	14	233	246	GAGAGAGTTGATTGTGGGGG
scaffold283358_10.	1	p2	(GA)6	12	162	173	GTTGGAATCAGTAATGGCGG
scaffold283626_12.	1	p2	(GA)6	12	89	100	ATACAGTGCAGATGCGCGTT
scaffold283810_15.	1	p2	(TC)9	18	189	206	ATTTCGCTGCACTCCAACAC
scaffold283878_16.	1	p2	(TA)6	12	241	252	AAATGTTTCAGCCCATAGAATTT
scaffold283992_12.	1	p2	(AG)6	12	99	110	AGCTCACGGTGGAAGAAGAA
scaffold284077_13.	1	p2	(TA)7	14	197	210	CTTCTTCCCAAATTGCCCTT
scaffold284078_18.	1	p2	(TC)6	12	1450	1461	CATAATGAGAGGCGGTTGGT
scaffold284128_11.	1	p2	(AT)8	16	192	207	TGTATGCACCTGAACATGCC
scaffold284468_13.	1	p2	(TC)6	12	319	330	GAGTCCCCTTGGTCTGATGA
scaffold284492_12.	1	p2	(TA)11	22	845	866	TTACCCCCATATGCAGTGGA
scaffold284545_14.	1	p2	(TA)7	14	142	155	TTTGGCTTGTTTTTGCACCT
scaffold284750_11.	1	p2	(TA)8	16	449	464	CCCAGCTATATTGCATTCACAA
scaffold284883_10.	1	p2	(CT)6	12	446	457	AGGGGGCTTTTAGACACGTT
scaffold284909_13.	1	p2	(AT)9	18	224	241	GAGGAACCTCTTTAAATGCAGTG
scaffold284953_17.	1	p2	(TG)8	16	370	385	CCGACGGTTGTAGTGGAGTT
scaffold285210_12.	1	p2	(TA)12	24	482	505	TGTAATGCGCACGTTGAAAT
scaffold285289_12.	1	p2	(GA)7	14	49	62	TCGGCTGTCAAAGACAAAAA
scaffold285332_15.	1	p2	(CT)9	18	791	808	GATGAAGGGGCCTATGTGAA
scaffold285381_17.	1	p2	(TC)6	12	708	719	GCCCCACCCTTCTATCTCTC
scaffold285628_10.	1	p2	(AT)6	12	67	78	GGCTTTCTTAACTTGTTGGAACC
scaffold285629_14.	1	p2	(GA)6	12	546	557	ATGATGGAATTTGGGTGCTG
scaffold285644_16.	1	p2	(AC)6	12	1851	1862	AGGGGTTGATTGCTACGATG
scaffold285829_14.	1	p2	(GT)6	12	453	464	CTGGGGGAGATTTGTTGAGA
scaffold285921_12.	1	p2	(TA)7	14	103	116	TCTCACGCACCTTCACTCAC
scaffold286109_21.	1	p2	(GA)6	12	39	50	CAGATTTAAACAGTGGCTGCG
scaffold286375_10.	1	p2	(AT)7	14	246	259	GTTCGAAAGCCTACCTCGCT
scaffold286603_11.	1	p2	(GA)6	12	236	247	GGTGTCTGGAACAAGGGAAA
scaffold286753_12.	1	p2	(TA)6	12	1348	1359	TGGTTAGTATTGGAACGCGA
scaffold286759_12.	1	p2	(AG)8	16	342	357	GTTATGCGATCTGCTCGTGA
scaffold286835_11.	1	p2	(AT)8	16	1204	1219	TCTGATTCGGGAAAACATGA
scaffold287109_14.	1	p2	(TC)11	22	1469	1490	ATTGGTTTGCAGGTACGAGG
scaffold287184_14.	1	p2	(AC)6	12	2263	2274	TAAAACTGGCCCCAAAATGA
scaffold287248_17.	1	p2	(AT)7	14	202	215	AGGAAGCGAGGTAGGCTTTC
scaffold287508_15.	1	p2	(TC)6	12	4524	4535	CGAGAGAGGTTCGGACGTAG
scaffold287640_11.	1	p2	(AT)6	12	197	208	CAATTTATTTACCGAGGGTTCG
scaffold287841_11.	1	p2	(TA)7	14	436	449	AATTATCGTCCGTCCCCAAG
scaffold287872_11.	1	p2	(AT)11	22	352	373	GAAATATCCACCGAACGGAA
scaffold287896_15.	1	p2	(AG)7	14	681	694	GGGAAGAGGGGACTGAAAGT
scaffold288123_10.	1	p2	(AT)7	14	70	83	TCATTTAGAATTGGTGGAATGAT
scaffold288599_11.	1	p2	(AT)10	20	294	313	TTCGAGTTATGAAGTTTGCACC
scaffold288721_10.	1	p2	(AT)8	16	222	237	CCTCCGTGGACGTAGATCAT
scaffold289165_10.	1	p2	(AT)8	16	220	235	TAACGTCCCAGATTTGCTCC
scaffold289410_15.	1	p2	(AT)10	20	5550	5569	TCTCGTAAACTCCCCCTCAA
scaffold289501_12.	1	p2	(TA)7	14	355	368	CAATAGTGACGTTCGCCTCA

scaffold289506_16.4	1	p2	(AT)8	16	5484	5499	TGCAGGTTTGTTGAATTTCG
scaffold289566_17.0	1	p2	(GA)6	12	41	52	CACGAGAGTTGAAAGGGAGC
scaffold289905_15.1	1	p2	(TA)7	14	239	252	CAAATGGAGGTGAGAGGTTTG
scaffold290213_14.3	1	p2	(CA)8	16	190	205	TTCCTCTCTTTTTCCAGCCA
scaffold290369_11.4	1	p2	(TC)7	14	753	766	GGCCAGTAACATTACCCACCT
scaffold290517_10.9	1	p2	(GA)6	12	112	123	AATAGAGCAGCAGACGCGAT
scaffold290802_17.9	1	p2	(CT)7	14	89	102	GAGGCGGTTAAAGAAACGTG
scaffold290803_12.4	1	p2	(CT)10	20	159	178	AGATGAAGCTGAACCGGCTA
scaffold291072_10.9	1	p2	(AT)6	12	276	287	GTCGTATACTGCCGCCACTT
scaffold291225_11.7	1	p2	(CT)6	12	107	118	GGAGAGGAATCAAGTCGACAA
scaffold291416_16.2	1	p2	(AT)6	12	166	177	TGATGAAGAAATGGAAGGGG
scaffold291781_14.9	1	p2	(GA)6	12	1592	1603	CGTGTTTATCCTCACCCGTT
scaffold291813_14.4	1	p2	(AT)6	12	941	952	AAGGCTAGCACAAGAATGGC
scaffold291860_10.2	1	p2	(CT)6	12	67	78	CAAATGGCCAAGAGAGTTTACA
scaffold291947_16.6	1	p2	(AT)7	14	183	196	CAAACATAGAAACATGGACGC
scaffold291962_14.6	1	p2	(TA)6	12	407	418	ATTCATACCTTTCTGCCCCC
scaffold292006_17.5	1	p2	(AT)10	20	939	958	TGTCATGTATAGGCGCATCTG
scaffold292035_12.0	1	p2	(TA)11	22	286	307	TCTCAAGCTTGTCAACCCCT
scaffold292338_14.2	1	p2	(AG)6	12	1922	1933	AGCGAGTTCCGAAATGAAGA
scaffold292617_10.7	1	p2	(GA)6	12	88	99	TTCTGTCTTGGATGATGAGGC
scaffold292629_17.6	1	p2	(TG)7	14	205	218	GGCAATTATGTTGGAGGTGG
scaffold292631_10.9	1	p2	(CT)6	12	72	83	CACATACCTCACCTTCTCTCCA
scaffold293334_15.3	1	p2	(AC)7	14	178	191	AAGTCCACCACGATGTCCTC
scaffold293353_13.7	1	p2	(AG)7	14	363	376	TTTGTCCCATAAAACTCGCC
scaffold293385_18.3	1	p2	(GA)6	12	282	293	TAGGGGAGACAGGGGGTAAC
scaffold293435_20.6	1	p2	(TC)7	14	208	221	GGGGTTGAAGTAAATGAGGTG
scaffold293581_10.2	1	p2	(GA)7	14	256	269	TGTCAAGATTGGTCTCGTTTT
scaffold293743_14.3	1	p2	(TC)6	12	763	774	TACCCTGGTTTTGGAAGGTG
scaffold293793_12.0	1	p2	(TC)6	12	167	178	CCTAAGTGCCTACGTGTTGGA
scaffold294082_13.3	1	p2	(AC)10	20	273	292	CCAGATGCCTTCATTTTTCA
scaffold294170_16.3	1	p2	(AT)9	18	1194	1211	CGACGAGGCTTGGATTTCTA
scaffold294223_16.3	1	p2	(TA)6	12	915	926	TCTGGCTCTTTTCCAGAGCA
scaffold294327_14.3	1	p2	(TG)8	16	211	226	GAAGTTTTGATCAATTTTCACTCG
scaffold294351_11.8	1	p2	(TA)6	12	176	187	CAACTCCACATGTTGCCATC
scaffold294353_15.5	1	p2	(TA)8	16	4448	4463	CCATGAGTCCATGACCCTTC
scaffold294394_18.6	1	p2	(CT)8	16	534	549	GGAGTCTCTCTCGCTGATGC
scaffold294559_15.3	1	p2	(TA)6	12	750	761	TCTTCTATAAGGGCGGCTGA
scaffold294566_17.2	1	p2	(GA)6	12	47	58	GGAGAAAAAGAGATTGAGAGGGA
scaffold294622_11.7	1	p2	(TA)6	12	166	177	TTCAAACGTGAGGTGATGGT
scaffold294677_15.6	1	p2	(GA)6	12	529	540	TAGTTTTCAGTTCGGGCGAT
scaffold294795_14.8	1	p2	(TC)6	12	87	98	TACGTTGGACCTGAAAAGGG
scaffold294813_17.3	1	p2	(TC)6	12	353	364	GGCAAAGGAATACCTCCGAT
scaffold295048_15.0	1	p2	(CT)6	12	112	123	CCTTGAACCGAGAAAATGGA
scaffold295139_16.9	1	p2	(TC)7	14	302	315	CCTTGGCGGATCATATCACT
scaffold295140_11.3	1	p2	(AT)6	12	1100	1111	ATGGACGTCGTGACTGCATA
scaffold295210_13.4	1	p2	(TA)8	16	105	120	ATGAGTTATCACCGGATCGC
scaffold295275_10.8	1	p2	(TA)8	16	1018	1033	TATGTGATAGGCTACGGCCC
scaffold295510_14.5	1	p2	(AG)6	12	52	63	AGCTGTTAGGGTTGTATAGTGAGTAG
scaffold295532_18.7	1	p2	(AT)6	12	209	220	CCCCAGTAGTTCCCATCAAA
scaffold295539_17.5	1	p2	(CT)7	14	85	98	TACCCAACCCACTAACCCAA
scaffold295704_19.0	1	p2	(AT)6	12	1225	1236	GAAGCAAAGAGGATCCCACA
scaffold295897_10.6	1	p2	(TC)6	12	47	58	CAATGTTACAAAATGGGCGA
scaffold296494_13.0	1	p2	(AT)6	12	902	913	CATTTGATAGTTGTTTTTGTGGTGA
scaffold296635_14.6	1	p2	(GA)6	12	93	104	TGACTTATGGGGGCTCAAAC
scaffold296661_10.6	1	p2	(AT)12	24	267	290	GGGGCGTGACATTATGAAAT
scaffold296714_16.5	1	p2	(TA)10	20	1249	1268	TTGGATTGATTATGCTTTGCC
scaffold296880_13.2	1	p2	(AT)6	12	573	584	CCCAGACACCGTAAGGAAAA
scaffold297488_11.4	1	p2	(TC)6	12	79	90	ATTCCGTTTTTAAGTCCGGC

scaffold297588_16.	1	p2	(AT)7	14	196	209	ACCCTTTTGTAACATAAAAATTCTAA
scaffold298109_13.	1	p2	(AT)7	14	155	168	AAGTCCCAACCACTTTCACTG
scaffold298158_13.	1	p2	(TA)6	12	502	513	TTTTCTGCAAATTTGAGGGC
scaffold298289_11.	1	p2	(TA)8	16	93	108	ATTGCCCACGAGAGAGATTG
scaffold298920_13.	1	p2	(GA)6	12	38	49	TCAACAGAGAATGCAAGCAAA
scaffold298997_13.	1	p2	(AG)9	18	151	168	TATGCGGGCTGGAAGACTAC
scaffold299095_17.	1	p2	(AC)8	16	2119	2134	GAAAAGCACCACACTGCAAA
scaffold299249_14.	1	p2	(CT)7	14	177	190	CCTAGCAAGGCTTCCATCTG
scaffold299354_10.	1	p2	(TA)7	14	216	229	ACGCACACACTCTCACGAAC
scaffold299435_17.	1	p2	(CT)6	12	4254	4265	CCATTTCAGTTGCAGAAGCA
scaffold299742_13.	1	p2	(GA)7	14	192	205	CCTTGAAGACAATGAAATTTTGG
scaffold299756_12.	1	p2	(GA)6	12	162	173	AAACACGCAACACAAAGCAG
scaffold299799_18.	1	p2	(AG)7	14	243	256	TCGGGAGTCTGTATTGAGCC
scaffold299860_16.	1	p2	(GA)6	12	1470	1481	GGAGAAATCAAGAGGAGGGG
scaffold299876_11.	1	p2	(GA)8	16	122	137	TTGTGGTTCGATCGTAATTGA
scaffold300019_16.	1	p2	(CT)6	12	115	126	GGTTCTCACAGGAGGGTTCA
scaffold300023_13.	1	p2	(TG)6	12	473	484	GCAATTGAGAGTGAGTGCGA
scaffold300209_13.	1	p2	(AC)6	12	441	452	ACCCTCTCTGGTTCACGAAA
scaffold301074_15.	1	p2	(TG)7	14	278	291	TTTTTACGATTTTGCCCTCG
scaffold301347_16.	1	p2	(CA)6	12	1387	1398	GGACACGGTTTCTAATGTTTTGA
scaffold301432_11.	1	p2	(TA)8	16	250	265	CCTTTCATGTTATTCTTTTCTCACC
scaffold301487_10.	1	p2	(TA)7	14	165	178	AAGTTATCACCGGATCGCTA
scaffold301501_22.	1	p2	(CT)7	14	580	593	GAACCAAAGTGAGCCCGATA
scaffold301583_19.	1	p2	(TA)10	20	349	368	GCTGACGAGGTGATGAGTGA
scaffold301959_22.	1	p2	(TC)6	12	103	114	ATGGATCGTATCACAAGCCC
scaffold301988_10.	1	p2	(CT)7	14	142	155	TAGCCGATAAAAATGGCACC
scaffold302108_10.	1	p2	(TC)6	12	239	250	CGATTCCCATACCATTCGAC
scaffold302449_10.	1	p2	(TA)7	14	360	373	ATCCTTGACGACTGTTTGGC
scaffold303182_17.	1	p2	(CA)6	12	893	904	TGCCAATTTGATAGAAGCCC
scaffold303184_16.	1	p2	(TA)9	18	465	482	TCGTGGAAATTCCTTTAATGTG
scaffold303431_11.	1	p2	(AT)7	14	457	470	TTAGCACCCGAACCAATTTC
scaffold303827_10.	1	p2	(TC)7	14	155	168	CGGAGTGTATTGCGAACTCA
scaffold303941_20.	1	p2	(CT)6	12	108	119	TTCTCTCTCTCGCTGCACAC
scaffold304124_20.	1	p2	(CA)8	16	316	331	GTTTCCATGTTTCACCCACC
scaffold304672_16.	1	p2	(TA)6	12	1403	1414	TTTGACCTCGAAGGATTTGG
scaffold304939_13.	1	p2	(AT)12	24	467	490	GCAGGTGAGGGACAAGAATG
scaffold305168_16.	1	p2	(TC)6	12	2194	2205	ACACCGTCAATCACAACACA
scaffold305277_12.	1	p2	(TC)6	12	296	307	ACTGCGGATGCCCTAATATG
scaffold305452_13.	1	p2	(TA)9	18	183	200	TGAATCCTTTTTAAACGCGG
scaffold305630_11.	1	p2	(TA)7	14	75	88	ACCCACACCAGACCAACATA
scaffold305688_14.	1	p2	(AG)12	24	1929	1952	CCATCTCCTCGAGCTCAATC
scaffold305885_14.	1	p2	(TG)9	18	185	202	TCCTTTAGGCCGACAACATT
scaffold306069_12.	1	p2	(CG)8	16	215	230	GCATCGCGTTTCAATACAGA
scaffold306095_11.	1	p2	(AT)8	16	244	259	CCGCCATAACCTGTTCAACT
scaffold306100_19.	1	p2	(AT)9	18	215	232	ATTGGTCGAGAGAAAGGGCT
scaffold306172_14.	1	p2	(AT)11	22	780	801	CCATGGGAAATGGTTAGTTGA
scaffold306363_10.	1	p2	(TA)6	12	114	125	TTGAATGGAAATACCCTCTTAGG
scaffold306451_11.	1	p2	(TC)9	18	356	373	GTGGTATGGAAAATGGGCAC
scaffold306597_13.	1	p2	(TC)6	12	1771	1782	TGTTTTGTAGGCCTGCCTTT
scaffold306633_15.	1	p2	(TA)6	12	92	103	ATGCTTTTCCCCTTTTTCGT
scaffold306843_11.	1	p2	(AT)6	12	587	598	TGACCAAAATTTAGCGAGGG
scaffold307006_15.	1	p2	(TA)7	14	252	265	TACCGGCTTCAACAGCTTCT
scaffold307273_12.	1	p2	(TA)6	12	31	42	GAATCTTGTCACATTTACCAATGTAT
scaffold307296_15.	1	p2	(TA)8	16	3336	3351	GGTTTTGGGAATTCCATCCT
scaffold307602_12.	1	p2	(AT)7	14	101	114	TTTGCACAAGTGCCAAAGAG
scaffold307896_14.	1	p2	(AG)9	18	1772	1789	AGGTCAAGGGTACCATCCTG
scaffold308095_15.	1	p2	(GA)7	14	1706	1719	TCTCAAGCTCCTCCAACGAT
scaffold308408_13.	1	p2	(AT)6	12	367	378	TGGCTCATTCCCTAACTTGC

scaffold308593_15.	1	p2	(TG)8	16	289	304	TGTAAGGGGAGCAATCGAAG
scaffold308613_16.	1	p2	(AT)9	18	1329	1346	TCACATTCTGCGATTGCTAA
scaffold308852_12.	1	p2	(AT)6	12	184	195	ACTCATGACCCTACCAACGG
scaffold308922_10.	1	p2	(AT)6	12	53	64	GACCGGTTAGACCGGATTTT
scaffold308965_17.	1	p2	(CT)6	12	230	241	AAGTCCGGCCATCTCTTTCT
scaffold309030_11.	1	p2	(AC)8	16	309	324	TGACGAATTCTCAAGTTCCTCAC
scaffold309241_12.	1	p2	(GA)6	12	98	109	AAGCTGCTCCTTTCCACAGA
scaffold309624_15.	1	p2	(AT)11	22	2110	2131	ACAAGTTGAAGGATGGCCTG
scaffold309717_15.	1	p2	(TC)6	12	313	324	AGCCAAGGTATGGTAGCCCT
scaffold309783_17.	1	p2	(GA)8	16	143	158	GAGAGAAAAGGTGGCAGGTG
scaffold309788_11.	1	p2	(TC)6	12	173	184	CATAGGCCAAAGCCCAAATA
scaffold309906_13.	1	p2	(AG)6	12	708	719	TGGCCTGGCTTAGTTGTATTG
scaffold310416_10.	1	p2	(AG)6	12	43	54	GTCTTCTCCGCCTTTGTGTG
scaffold312002_10.	1	p2	(AT)8	16	442	457	ACGTCAGCATCTACCCCAAC
scaffold312074_10.	1	p2	(TC)6	12	53	64	CAACACATTCAATACATTCTCCAA
scaffold312178_12.	1	p2	(AG)8	16	517	532	AATGTTTGATGCATTTCGCA
scaffold312298_14.	1	p2	(TC)7	14	1914	1927	CTCTCTCGCCTCGCTTTCTA
scaffold312378_13.	1	p2	(AC)6	12	336	347	GACGAGATTGTCGAGTGCAA
scaffold312843_15.	1	p2	(GA)6	12	1232	1243	CGACGAGAAAGTCGTGTCAA
scaffold312914_10.	1	p2	(GT)6	12	136	147	TCATGTAAATTCTTGGTCATTCTCA
scaffold313011_13.	1	p2	(TG)7	14	77	90	CCCAAGCTATCACTCATCACC
scaffold313094_14.	1	p2	(TC)7	14	445	458	TGTTTTCGCGTTTCCTCTCT
scaffold313419_16.	1	p2	(TC)6	12	101	112	GCAACGGAATACCACTCGTT
scaffold313480_13.	1	p2	(TA)6	12	144	155	AATACGCGAGTTCATGGAGG
scaffold313665_13.	1	p2	(AT)6	12	320	331	TGCACGTAGGCATGTTCAAT
scaffold313673_12.	1	p2	(TA)6	12	244	255	CATTCAAGGGGCATTTTTGT
scaffold313763_11.	1	p2	(CT)14	28	512	539	GGGCTCGAATTCAAAACTGA
scaffold313781_14.	1	p2	(TC)8	16	51	66	GAGGGTTTTAGCGTGATAGGG
scaffold313828_16.	1	p2	(TC)6	12	104	115	CACCCAAACCCATTATCACC
scaffold314026_10.	1	p2	(GA)10	20	209	228	GCATTTGGAGCAAGGCTAAG
scaffold314032_15.	1	p2	(AG)7	14	99	112	CCCATGTTGTCATTAATGTAGGG
scaffold314073_10.	1	p2	(TA)8	16	233	248	TTCTCAGCATATGGGAAGGG
scaffold314135_14.	1	p2	(TA)9	18	490	507	TCTGGACCATCAGATTTGGA
scaffold314230_12.	1	p2	(GA)6	12	107	118	AGAAAATGCATGCGAAGAGC
scaffold314251_15.	1	p2	(TA)7	14	176	189	AAAGGGAAAACAGTTGGAAGC
scaffold314688_13.	1	p2	(CT)6	12	45	56	CAATATTACAATGGCCAAGAGAG
scaffold314815_10.	1	p2	(GA)7	14	202	215	CATTCGGAGCAAGGAGAAGT
scaffold314816_14.	1	p2	(AT)8	16	159	174	TTGCCATATTTAAGCCGAGG
scaffold314983_18.	1	p2	(AG)6	12	76	87	TGTCTTTTCGTGTTGAGTCGTT
scaffold315188_14.	1	p2	(TA)6	12	875	886	CATGATTTTGCAACTTACCATTTC
scaffold315253_13.	1	p2	(AG)6	12	160	171	CCCTCAACAATGCAAAAAGC
scaffold315266_17.	1	p2	(AG)6	12	603	614	TTCGGCCAAAAGAAAAGAAA
scaffold315297_15.	1	p2	(AT)10	20	1283	1302	AGTCGTCACCCCGAACATAG
scaffold315303_15.	1	p2	(TA)7	14	409	422	GAAATGAGAAGCCCAATGGA
scaffold315351_15.	1	p2	(CT)6	12	441	452	CCGTTGCCTCTTTTGAACTC
scaffold315354_10.	1	p2	(GA)6	12	83	94	GCCGGAGGTTTGATATGGTT
scaffold315615_14.	1	p2	(AG)12	24	1613	1636	CCCTGTCTTCCAAAAACCAA
scaffold315657_12.	1	p2	(TG)6	12	161	172	GTGGCATGGGGAAGCTACTA
scaffold315702_17.	1	p2	(GA)8	16	73	88	CACTGTGTAGAAACATAAACTGCG
scaffold315755_15.	1	p2	(CA)7	14	1106	1119	AGCCGTGGGACATAAGAGTG
scaffold315912_11.	1	p2	(TA)6	12	270	281	GGGTTTTGCAGGATTGTGAT
scaffold316021_14.	1	p2	(AT)6	12	843	854	TTGTGTTACAATGATGGGGG
scaffold316027_16.	1	p2	(CT)8	16	442	457	GTTGGAGGTGCCAAAACTGT
scaffold316120_16.	1	p2	(AT)8	16	113	128	GGGTGTTTTGACCTAATCGC
scaffold316285_15.	1	p2	(CA)10	20	3770	3789	CGAAATAGGGTTGGTGAAGC
scaffold316422_10.	1	p2	(GA)6	12	523	534	CGGAACCCTCTCTCTTACCC
scaffold316630_15.	1	p2	(TA)6	12	412	423	GAAAACGACGAAGAAATGGC
scaffold316689_15.	1	p2	(GA)6	12	515	526	TCAAGTGAAAATGGCAACCA

scaffold316940_11.	1	p2	(AG)6	12	195	206	AGCTGGAATAGTCCGACACG
scaffold317113_17.	1	p2	(TC)11	22	2104	2125	ACCGAAGTTCCTGCTCACAG
scaffold317119_14.	1	p2	(AG)6	12	154	165	CCAAACGCATCAAATTCTCA
scaffold317153_18.	1	p2	(AT)6	12	1544	1555	TCCATTTCACATCCGATGAA
scaffold317265_10.	1	p2	(TA)7	14	150	163	AAACAGTCTTCGGGACACCA
scaffold317410_10.	1	p2	(CA)7	14	896	909	TCTACGTCCACGGAGAGGTT
scaffold317520_10.	1	p2	(AT)9	18	705	722	CCGAACTTTTGGCCTTCATA
scaffold317598_13.	1	p2	(TC)6	12	2974	2985	AACTTCTCCTCCCAATCGCT
scaffold317609_11.	1	p2	(GT)7	14	89	102	TACGATACCCTCCCAAACCC
scaffold317645_14.	1	p2	(AT)6	12	2246	2257	TCTGCATGCAAGATAGTACGG
scaffold317699_16.	1	p2	(AG)6	12	535	546	ATTGCCATCACCTTCTCCAC
scaffold317857_14.	1	p2	(TA)10	20	772	791	TCAAAATCTTTGAAACGGGTG
scaffold317870_10.	1	p2	(CT)9	18	422	439	ACTAGAATTCCCTCTGCCCC
scaffold317926_19.	1	p2	(TA)9	18	447	464	GTCTGTGAGGTGGGCTGAGT
scaffold318201_11.	1	p2	(AT)6	12	667	678	GGGGTCCCAGAAAACTGATT
scaffold318303_14.	1	p2	(GC)6	12	148	159	ATATTCTCGCTTCTTCGCCA
scaffold318340_15.	1	p2	(AT)6	12	554	565	TTTTGCCTCTCGCAAAAAGT
scaffold318363_14.	1	p2	(AT)6	12	356	367	TCACCACGAAGTCTACAAAAACA
scaffold318533_14.	1	p2	(TC)8	16	49	64	CGCGCCTACAATTCAAAGTA
scaffold318607_18.	1	p2	(AG)6	12	449	460	ATCCCCACTTTTTCGCTTTT
scaffold318858_12.	1	p2	(TA)9	18	587	604	CATAATGCCCTCGAATGCTAA
scaffold319053_15.	1	p2	(AG)12	24	262	285	GGTATATGGAGGAATGCCCA
scaffold319991_15.	1	p2	(AT)8	16	2774	2789	GAGAATCTGGTTCTGGTGGC
scaffold320117_15.	1	p2	(AT)6	12	90	101	CACATCAACACACCCACACA
scaffold320125_14.	1	p2	(AT)6	12	1553	1564	GACCGATCGAAACACACTGA
scaffold320396_15.	1	p2	(AT)8	16	1511	1526	CGGTTTCCACAACAATAGCC
scaffold320407_12.	1	p2	(TC)6	12	92	103	ATGAGTCGTAGTTGACGCCC
scaffold320614_12.	1	p2	(AG)7	14	230	243	GGAAATTGATGGATTTGGGA
scaffold320646_14.	1	p2	(GT)7	14	262	275	GGAATGCGTCGAGTACCACT
scaffold320698_14.	1	p2	(AG)6	12	71	82	CCCATGTTGTAATTAATGTAGGGA
scaffold320978_15.	1	p2	(AG)6	12	983	994	TAGTTGGAGCAGGGGAAGAA
scaffold321005_15.	1	p2	(AC)6	12	125	136	CCCCTCCTAACTTTGCTGC
scaffold321194_11.	1	p2	(CA)7	14	183	196	TGACCCACCATTGTCAAGAA
scaffold321259_15.	1	p2	(GA)6	12	697	708	GTCCCACAAAAGCTCAGAGG
scaffold321417_13.	1	p2	(TA)10	20	158	177	CTCAGCATTTGGGAAGGGTA
scaffold321803_12.	1	p2	(TA)10	20	744	763	AACAATACGGAAGCAATTTTATCA
scaffold321960_10.	1	p2	(GA)8	16	153	168	TTGATGTCCCTTCTCCTTGC
scaffold321999_15.	1	p2	(GA)7	14	1051	1064	TGCCTTCCATGTTTGTTTCA
scaffold322026_17.	1	p2	(CA)6	12	242	253	TCTGTGCCGCATTTATGATT
scaffold322075_10.	1	p2	(TA)8	16	82	97	TTTTCGAGTTATGAAGTTAGCACC
scaffold322082_13.	1	p2	(GA)6	12	151	162	ACCCAAGGTCAGTGGAACAA
scaffold322106_15.	1	p2	(TA)8	16	517	532	ACATAGCAATTTTCGGGGTG
scaffold322170_17.	1	p2	(TA)8	16	1366	1381	TGGTTTTCTCCTTCTCAACGA
scaffold322395_14.	1	p2	(AT)6	12	610	621	GCTACCCTTTTTGACCTACGG
scaffold322408_15.	1	p2	(TA)10	20	1470	1489	CTTCAATGGACCAGCACCTT
scaffold322936_17.	1	p2	(AT)8	16	71	86	CCTGCACGAAGAAAGGATTC
scaffold323072_15.	1	p2	(TC)6	12	48	59	TTGGTTCACACAACCACTCC
scaffold323272_16.	1	p2	(AT)9	18	151	168	TGAATGATTTAATAACCTATGGTGC
scaffold323277_14.	1	p2	(AT)6	12	437	448	CGTCGTGCTCAAACTTCAAA
scaffold323464_14.	1	p2	(CT)6	12	80	91	CAATGTGAAATGGGCAAGAG
scaffold323820_15.	1	p2	(CT)6	12	83	94	GTTCGCACAACCTCTCCACT
scaffold323925_15.	1	p2	(GA)7	14	803	816	TGCAAGAAAATCCAGCTTCA
scaffold324006_11.	1	p2	(CT)7	14	355	368	CAATTCCAAGCTACAACGCA
scaffold324010_16.	1	p2	(AC)8	16	1231	1246	AACAAAACCACGAATCCAGC
scaffold324194_16.	1	p2	(TA)6	12	468	479	TAGCGTGATTTGTGGACGAG
scaffold324215_17.	1	p2	(CT)6	12	53	64	CACTCACTCTCACTAGCCGC
scaffold324218_16.	1	p2	(CT)6	12	285	296	TGAGCAAAGCATTTTGGATG
scaffold324418_16.	1	p2	(TA)7	14	86	99	CCATTTGCAATACTAAGGCTTTC

scaffold324446_16.	1	p2	(GT)9	18	855	872	GAGCAATAGCAGGTTCGGAG
scaffold324788_14.	1	p2	(TA)8	16	232	247	CAAGCATATTGGCAAGAAACA
scaffold324951_10.	1	p2	(GA)6	12	116	127	AGTTTGGGGCTTGATTGATG
scaffold325007_17.	1	p2	(TC)6	12	291	302	CAAGCAAACCACTCACTCTCC
scaffold325142_12.	1	p2	(TA)11	22	163	184	CTGAGATTTCACATGGCAACA
scaffold325269_11.	1	p2	(CT)6	12	194	205	GAAGCAAACACGTCACTCCA
scaffold325313_16.	1	p2	(CT)6	12	1948	1959	AATTCATTTCCCCTCGACCT
scaffold325338_11.	1	p2	(AT)9	18	377	394	GGTCCATTGGTCTTTTGTATTGA
scaffold325517_14.	1	p2	(AT)6	12	133	144	TGCATCACGTCTCCTCAATC
scaffold325695_13.	1	p2	(CA)6	12	432	443	CTCACGCTCTCTCACTCACG
scaffold325869_12.	1	p2	(AT)7	14	372	385	GACCACCCAACCATCAAATC
scaffold326122_14.	1	p2	(TA)10	20	1059	1078	CAATCCCAGCCATTCATTTT
scaffold326194_10.	1	p2	(TC)6	12	33	44	TCTCATTCTCTTCTCTATCTCTCTCG
scaffold326712_11.	1	p2	(GA)6	12	944	955	TAACTGCCATTTCCCGATTC
scaffold326718_12.	1	p2	(TA)10	20	349	368	TACCTTTTTGCCCTCGAATG
scaffold326912_13.	1	p2	(TG)7	14	340	353	AATTAATGTGGCATGGGGAA
scaffold326949_14.	1	p2	(TA)6	12	76	87	ACAGTAGGGTGGAAAACAAAAA
scaffold327064_11.	1	p2	(AT)6	12	77	88	TGCATTTTCTTCTTTCTTTTTCA
scaffold327099_10.	1	p2	(GA)8	16	68	83	TGGAGAAGAAAGAATGAGGAATG
scaffold327145_12.	1	p2	(AT)6	12	62	73	CAGATGGAGGGTGTGTGAAA
scaffold327246_14.	1	p2	(AT)6	12	643	654	CGTTTAGCCGCAAGTTTCTC
scaffold327419_17.	1	p2	(TA)7	14	263	276	CGAATTTTGTGTGGACCGTA
scaffold327547_12.	1	p2	(AG)7	14	158	171	AAGGCCAAGCAAGGAAAAAT
scaffold328349_13.	1	p2	(CT)6	12	119	130	TGGCTTCTCTTGCTCTCTCA
scaffold328452_12.	1	p2	(CT)6	12	687	698	GCCGAGTCTTGTTGATGATG
scaffold328697_15.	1	p2	(TA)6	12	776	787	GAGTCAAGGGCGGATACAAG
scaffold328755_11.	1	p2	(TA)6	12	289	300	TTGTAATGTGGCATGCGTTT
scaffold328967_18.	1	p2	(TA)9	18	358	375	AGGTGGCACGCATCTGTAAC
scaffold329265_11.	1	p2	(TA)6	12	344	355	TTGATGTTTAAAGTCGTCGGC
scaffold329603_16.	1	p2	(AG)6	12	867	878	TGTTCATGCTGGCTGATAGG
scaffold329862_16.	1	p2	(GA)6	12	901	912	TGCAAGCCTATGGTGGGTAT
scaffold330369_12.	1	p2	(AT)9	18	136	153	GCCGAGAGAGATGAGGAGTG
scaffold330708_16.	1	p2	(GA)7	14	3123	3136	GGCCCTGATCAGAATCAAAA
scaffold330732_10.	1	p2	(AT)6	12	162	173	GGAAAAGGGAAGAACAAGGC
scaffold330861_17.	1	p2	(GA)7	14	2640	2653	CAGAGGGGACCTTCCTTTTC
scaffold331413_16.	1	p2	(GA)7	14	2199	2212	TGCAAAAGCTTAGGTGGACA
scaffold331432_14.	1	p2	(GA)8	16	1168	1183	TGATTGCTTTGGCCCTACTC
scaffold331777_12.	1	p2	(TA)6	12	73	84	CTGACGTCTTGTGGGAGTGA
scaffold332162_11.	1	p2	(AT)8	16	470	485	TTTCGTCGCTCTCAACTTCA
scaffold332332_11.	1	p2	(GA)6	12	404	415	ACCCCAATCTCCGTTCTTCT
scaffold332545_16.	1	p2	(CT)7	14	9125	9138	TCACCTTTGCCTTGGGTATC
scaffold333233_11.	1	p2	(TA)9	18	207	224	TCGGAATTCACTTCTTTGCTG
scaffold333356_16.	1	p2	(GA)6	12	499	510	TGTTGGACTGTGTTGGGCTA
scaffold333858_10.	1	p2	(AG)7	14	69	82	TTGTGGGACTTTGAAAGAGGA
scaffold333865_16.	1	p2	(TA)9	18	1027	1044	CAACGGTATGCTCGGATTTT
scaffold333989_16.	1	p2	(GA)6	12	79	90	GGCTCAAGCTTGCTGTTTTC
scaffold334347_15.	1	p2	(AT)6	12	216	227	GGTTGTAATGAGGCTTTCGG
scaffold334580_16.	1	p2	(GA)6	12	615	626	ATCATCCAATTCCAATCCCA
scaffold334757_15.	1	p2	(CA)7	14	279	292	GGTGTGGCTCTGTGGATTCT
scaffold334891_14.	1	p2	(TC)6	12	969	980	TGTGAGATTGTGTGTGGCAA
scaffold334969_13.	1	p2	(TA)7	14	469	482	ATCGGCCGAGATTTGTTATG
scaffold335149_11.	1	p2	(GA)7	14	525	538	TGAACATCCATGGTCCAAAA
scaffold335722_16.	1	p2	(TC)7	14	1205	1218	CCCACACCTCTTTGCTTTGT
scaffold335902_13.	1	p2	(AT)7	14	505	518	AACCCGTTTGCTGCATAGTT
scaffold336129_13.	1	p2	(AT)9	18	300	317	TCGAAGAGGAAAATAAAATAATCCC
scaffold336159_15.	1	p2	(TG)9	18	2694	2711	TTTTGGAGAGGTTGGAGGTG
scaffold336169_10.	1	p2	(TA)8	16	206	221	CGTCTAATCCACCGCCTAAA
scaffold336306_11.	1	p2	(AT)6	12	329	340	TCTTCGATGTTGCTGGATTG

scaffold336327_17.3	1	p2	(AT)6	12	477	488	AATGGCTGCAATTATCCCTG
scaffold336438_11.2	1	p2	(AT)7	14	223	236	CATGATCAAATCTTGGTGCG
scaffold336460_12.4	1	p2	(CT)7	14	68	81	CAAATGCCCAAGAGGGTTTA
scaffold336476_16.6	1	p2	(AG)6	12	300	311	GGCTGTACCATAAAAGCCCA
scaffold336568_13.4	1	p2	(TC)6	12	253	264	CCGAATTTTCCACTCCAGAA
scaffold336742_16.0	1	p2	(AT)7	14	2427	2440	TTGCCCAAACAAATGAAAAA
scaffold336786_19.9	1	p2	(AT)6	12	159	170	CGATCAATAAAGCTGCACACA
scaffold336870_13.0	1	p2	(CT)6	12	296	307	CGCACTACTAGGGTTTGGGA
scaffold337112_19.2	1	p2	(GA)6	12	150	161	CATTCTCAAGCCACTCCCTC
scaffold337344_17.7	1	p2	(TC)8	16	104	119	TGAAAAAGGACTCTTGGGCA
scaffold337506_16.5	1	p2	(TC)7	14	673	686	AGAGGTAGCCATTTACGCGA
scaffold337681_11.8	1	p2	(TC)6	12	89	100	TAGGCAATGGAATACCTCCG
scaffold337783_11.3	1	p2	(TA)8	16	320	335	CACCACCACCTCACTGTCAC
scaffold337813_10.9	1	p2	(TA)10	20	563	582	CAAATTCTTGATTCGCCACC
scaffold338083_14.2	1	p2	(CA)6	12	1134	1145	GGTTGCTCTCCTTTGAGCAC
scaffold338132_16.6	1	p2	(AG)8	16	2073	2088	CCTGGCTCGTTAGCTGATCT
scaffold338234_15.0	1	p2	(AC)6	12	1390	1401	TTCCAAAGCAACGTAACATGA
scaffold338395_11.5	1	p2	(AG)6	12	615	626	AGGTCGTGGTGAAAAAGGGT
scaffold338474_11.3	1	p2	(TA)6	12	109	120	TCTGCATGCTCTATGCAAGAAT
scaffold338497_14.3	1	p2	(CT)6	12	47	58	CAATGATTGTCAAAATTAGAGTTCAA
scaffold338688_16.7	1	p2	(GT)7	14	100	113	TAGGATACCCTCCCAAACCC
scaffold338716_14.2	1	p2	(CT)6	12	418	429	AAAAGGGGCATTTTGCACTA
scaffold338858_13.7	1	p2	(TA)8	16	255	270	TGCACAGCATATGCCTTCAT
scaffold338959_16.7	1	p2	(CT)11	22	436	457	GCTCCTCCTTGGTACTCACAA
scaffold339016_18.1	1	p2	(TC)6	12	218	229	CGAGATGTCTTCAGGGCATT
scaffold339153_13.8	1	p2	(CA)6	12	208	219	CTCCTTCTATCTCCCCTGCC
scaffold339183_15.3	1	p2	(TA)6	12	397	408	ACGCTCTTGAAATATGCGCT
scaffold339911_18.9	1	p2	(CT)7	14	83	96	CTCTCTCACCTCCCCAAACC
scaffold339963_15.9	1	p2	(TC)6	12	202	213	AAAGGTTAGTGGGCTGAGGAA
scaffold340103_13.5	1	p2	(TA)7	14	319	332	TGAGCTAGCTTTTGTGGTGG
scaffold340139_10.6	1	p2	(TC)6	12	448	459	CACGCACAAGTACATCTCGG
scaffold340231_19.1	1	p2	(TA)7	14	689	702	GCCTTGGTCATGCCATTTAT
scaffold340387_11.0	1	p2	(TA)6	12	211	222	CGACGGTTGAGGAAGAAACA
scaffold340409_12.7	1	p2	(TA)7	14	145	158	CACCGTCCAATAAACCGAAG
scaffold340809_10.4	1	p2	(TA)7	14	254	267	GAAAATCAAAGGCCCACAAA
scaffold340813_14.2	1	p2	(CT)6	12	345	356	AGAAGGCAATCTATCCCGTG
scaffold340821_17.1	1	p2	(TC)9	18	507	524	TCGTCGTTGTTACTGGCCTA
scaffold340852_12.5	1	p2	(TA)9	18	861	878	TCTGATAAGGTTCGAATTCACG
scaffold340956_16.9	1	p2	(TA)14	28	1108	1135	ATGGGCTTCGAGTTTGGATA
scaffold341328_13.9	1	p2	(AG)6	12	424	435	GTAGCGGTGGTTGACTGGTT
scaffold341543_13.2	1	p2	(AG)8	16	649	664	TGGTAGTGTTGAGTTGGCGA
scaffold341822_16.2	1	p2	(AT)10	20	584	603	TGCAGATTCAGGATGAGACG
scaffold342015_13.6	1	p2	(TA)7	14	193	206	CAAGATTCGAAATCACATTCAAA
scaffold342495_16.0	1	p2	(AG)8	16	110	125	GTCCACGGTGGTGCTAGAGT
scaffold343175_14.6	1	p2	(TC)7	14	1140	1153	ATTCTTCTTCAACCTCCGCC
scaffold343896_16.3	1	p2	(CT)8	16	379	394	TGCCCTTAAGTTAGGACACTAAA
scaffold344024_11.5	1	p2	(TA)6	12	298	309	TTTTAGGGGTGCGAAAGTTG
scaffold344062_14.5	1	p2	(CT)6	12	46	57	TCATCTTGGCATGGTCAAAG
scaffold344160_15.0	1	p2	(CT)6	12	73	84	CCTAGTTCCTACCGCGTGTC
scaffold344442_13.9	1	p2	(GA)7	14	120	133	ACTTGAGCGTAACCACGTCC
scaffold344486_12.2	1	p2	(TA)6	12	139	150	CTGCTTAAAGCCCAGTCCAG
scaffold345111_16.4	1	p2	(TA)6	12	265	276	AGGGCATTATTTTAACCCCG
scaffold345129_10.6	1	p2	(TC)6	12	409	420	ATTGAATCTACGTCCACGGG
scaffold345147_18.3	1	p2	(GA)6	12	38	49	GAGTTTAGAGAGAGGAAATGGTATTC
scaffold345172_16.0	1	p2	(TC)6	12	2068	2079	TCGAAATCCCATCTACCCAC
scaffold345277_15.4	1	p2	(CT)6	12	2308	2319	TGACAACCATCACCTCGAAA
scaffold345489_12.7	1	p2	(TC)6	12	53	64	TCCTGCCATCTCTCAATGTG
scaffold345774_15.4	1	p2	(GT)6	12	653	664	GACACCAAAACGGAGGAAAA

scaffold345781_15.	1	p2	(GA)7	14	351	364	GCCAACACTCCAAAGAAATGA
scaffold345835_17.	1	p2	(CT)7	14	76	89	TTCCTCCTCAATATTTTCAACACA
scaffold345880_14.	1	p2	(GA)6	12	224	235	CAAGCCATGAAACAACACGA
scaffold346132_10.	1	p2	(CT)8	16	308	323	GCGTGTGGAAGAGGACAAA
scaffold346164_16.	1	p2	(GA)6	12	2946	2957	AGCTTCAGTGTGTGTGCGAG
scaffold346510_10.	1	p2	(TA)7	14	326	339	TGCAATGCATGGAGGAAATA
scaffold346752_16.	1	p2	(TA)6	12	98	109	TCCATTCCGAAAATCAAAGG
scaffold346987_10.	1	p2	(AG)6	12	312	323	TCTGGAAATGGGGAAAACAG
scaffold347086_12.	1	p2	(TA)6	12	227	238	ATCTTGACCGCTGATTTTGG
scaffold347321_15.	1	p2	(AT)6	12	108	119	TCTGAAACCCTTCCCATCTG
scaffold347380_18.	1	p2	(CT)7	14	443	456	TCGGAAGACACCTATTTGCC
scaffold347437_14.	1	p2	(AC)6	12	663	674	CCACCATCTCTCATCCCTCT
scaffold347530_13.	1	p2	(AT)11	22	1631	1652	GAACGCAAATGCGATATGAA
scaffold347858_15.	1	p2	(AT)6	12	1407	1418	AAACCTTACTGTCACGCGCT
scaffold348045_17.	1	p2	(CT)6	12	635	646	TATCCCCGCCAACTTAACTG
scaffold348283_11.	1	p2	(AT)9	18	29	46	TCTATATACAACTCGCATACCCAAA
scaffold348289_16.	1	p2	(TA)6	12	349	360	CATGATTTCAGAATCGTGCG
scaffold348322_12.	1	p2	(CT)9	18	528	545	CTGAGCAGACCAGTCCAACA
scaffold348369_10.	1	p2	(AG)7	14	272	285	CTCGTCCCTTTGTGCTTGTT
scaffold348410_13.	1	p2	(AT)7	14	195	208	AAAGGTATGGGGAAAATGCC
scaffold348498_12.	1	p2	(AG)6	12	238	249	GCCCCACGTATGATTGTCTT
scaffold348513_12.	1	p2	(AG)7	14	51	64	TTTCTCATGTTGTAATTAATGTAGGGA
scaffold348556_17.	1	p2	(GA)6	12	119	130	GCCACTTTCCTTAAACCAAAA
scaffold348569_16.	1	p2	(CT)6	12	57	68	TGTCCTCACTCGTTTCCTCT
scaffold348571_13.	1	p2	(CT)6	12	743	754	AGATGTGAACCAAGAACCCG
scaffold348599_10.	1	p2	(CA)7	14	51	64	CTAACCTTGGGCTCTGATGC
scaffold348650_14.	1	p2	(GA)6	12	147	158	GCATCAGAGCCCAAGGTTAG
scaffold348911_14.	1	p2	(TA)8	16	407	422	TGAGGAATCGAACAAGGACA
scaffold349088_16.	1	p2	(CA)6	12	4609	4620	GGAATTTGATCCCCACACAC
scaffold349526_18.	1	p2	(TC)6	12	252	263	CATCACCTCCATTTTCCCAC
scaffold349549_14.	1	p2	(TG)7	14	448	461	ATGCCAAAGGGGAAACAAAT
scaffold349946_10.	1	p2	(AT)11	22	173	194	ATAAACTGTTACTCCTGGGTGC
scaffold350008_15.	1	p2	(GA)6	12	1507	1518	TCGAACCATTCACATCCTGA
scaffold350079_11.	1	p2	(AT)6	12	279	290	TGTGCCATAAAAATGGTTCAT
scaffold350124_10.	1	p2	(TC)6	12	274	285	GGGGTGGTAACCGATGTATG
scaffold350195_12.	1	p2	(TA)11	22	376	397	AGAGTTTTGCGTGCATGTTG
scaffold350315_10.	1	p2	(TA)10	20	87	106	TGTTGCGCGTGCTTTAAATA
scaffold350387_14.	1	p2	(AT)6	12	1540	1551	TATTATGATTCCGGGTTCCG
scaffold350624_16.	1	p2	(GA)7	14	283	296	TGTGCTTCCACCAAATCAGA
scaffold351156_12.	1	p2	(TC)6	12	72	83	GCTCTTTTGATCGATCTGCC
scaffold351651_13.	1	p2	(TA)13	26	471	496	CACGCATGAATTCTGTTGGA
scaffold351933_13.	1	p2	(CT)6	12	1097	1108	CCCACCCCAGATCATAGAAA
scaffold351935_15.	1	p2	(TC)7	14	591	604	TTGAGCATTGAGGTTGCTTG
scaffold352010_16.	1	p2	(TA)7	14	133	146	GAAGGAGGAGAAGTTTGGGG
scaffold352266_11.	1	p2	(AG)7	14	27	40	AGAATGAGGGAGGGAGGAGA
scaffold352290_13.	1	p2	(AT)6	12	598	609	GCCCCTGATCATAACTCGAA
scaffold352456_14.	1	p2	(AG)6	12	401	412	GGCATGTGTTGTGTGGACTC
scaffold352567_10.	1	p2	(TA)8	16	240	255	TCACAAATCGATGGTCTGGA
scaffold352700_10.	1	p2	(AG)6	12	199	210	CGAGTGCCATTCTGACAGTG
scaffold352946_10.	1	p2	(GA)6	12	41	52	GAACCAACTCTGTGAGAACCAA
scaffold353094_11.	1	p2	(AG)6	12	104	115	TCATCGTGTTCTTCGCTCAC
scaffold353137_18.	1	p2	(CT)6	12	406	417	CTTCCAACTTCGACAGCTCC
scaffold353197_15.	1	p2	(AG)6	12	462	473	CGGAACGCTTAATGCAAAAC
scaffold353403_12.	1	p2	(CT)6	12	278	289	GCACACCTCGTCTCTCACAA
scaffold353862_14.	1	p2	(CT)6	12	231	242	TCCACGGAGAGGTAAAAAGC
scaffold354188_15.	1	p2	(CT)9	18	218	235	GGGCTTGTCGCATTCATATT
scaffold354245_17.	1	p2	(AC)9	18	967	984	GCATTTGCCTTTAGGAGCTG
scaffold354354_15.	1	p2	(TA)6	12	161	172	AAATGCGCAATTTTAAACCC

scaffold354359_14.	1	p2	(AT)9	18	61	78	CCGAAATCTGTAAATCCTAGCC
scaffold354581_13.	1	p2	(AG)7	14	93	106	CATTAAATGCGCCTACACTTT
scaffold354707_15.	1	p2	(CA)6	12	2912	2923	GATAACCGTGTGGCATTTGA
scaffold355276_12.	1	p2	(AT)8	16	1433	1448	TGCCAATGATCACCAAACC
scaffold355557_12.	1	p2	(TA)6	12	73	84	TTCAAATGCACGTGTTGGAT
scaffold355899_11.	1	p2	(TC)6	12	67	78	GCTGATGCACCGAGCTAGTA
scaffold356064_15.	1	p2	(AC)6	12	431	442	GTGCTGAAAGCCCCAATTTA
scaffold356309_17.	1	p2	(CA)6	12	4376	4387	GAGTTCTAGCCTCAAGCAACG
scaffold356606_14.	1	p2	(CA)7	14	332	345	ATTCATTCTGCCACCTCTGG
scaffold356760_15.	1	p2	(AT)9	18	277	294	CATTCAAGGGGCATTTTTGT
scaffold356797_18.	1	p2	(CA)6	12	297	308	CTGTCACCATCACCAACCAC
scaffold356813_11.	1	p2	(AC)6	12	126	137	TCTGTTGGCAAATAGGCACA
scaffold356981_10.	1	p2	(TC)6	12	305	316	TTTCTCTCGATGCACTCTCG
scaffold357004_14.	1	p2	(TA)8	16	48	63	TTCGATGATAACTATGGGTTTGT
scaffold357095_14.	1	p2	(GA)7	14	442	455	TAGGCAAAAACTTCCGTCCA
scaffold357116_11.	1	p2	(AT)8	16	272	287	CAATGAAAATGCCACGTCTG
scaffold357152_13.	1	p2	(AG)6	12	164	175	TAGTTGACGGTGGTGGTTCA
scaffold357274_13.	1	p2	(AT)8	16	423	438	CCACATTTTTCCCGACTGTT
scaffold357307_13.	1	p2	(CT)7	14	110	123	CCCACCAACTCTCGTCACTT
scaffold357980_10.	1	p2	(TC)7	14	245	258	TTTTAGGGCATTCAACTGGG
scaffold358049_11.	1	p2	(TC)6	12	155	166	AGGGCTGAGGAAAACCTGAT
scaffold358318_12.	1	p2	(TG)6	12	193	204	CGAGTGAGAGAGTGAGTGCG
scaffold358450_10.	1	p2	(AT)6	12	264	275	TCACACAGCACCTGATCACA
scaffold358681_12.	1	p2	(AT)11	22	865	886	TACGATCCGAGTGCCTCTTT
scaffold358892_13.	1	p2	(AT)8	16	659	674	TCGAATACCCTAATAACCCGAA
scaffold358974_13.	1	p2	(AT)8	16	1740	1755	AGTTTGATGAGGGCATCCAC
scaffold359031_12.	1	p2	(CT)6	12	67	78	CTCCACAAAGATCTCGCACA
scaffold359042_15.	1	p2	(TA)8	16	422	437	TTGTTTTGTCCACACTTGGC
scaffold359242_16.	1	p2	(AT)6	12	165	176	CATGCAGACATGGGAGTTTC
scaffold359290_14.	1	p2	(TA)13	26	621	646	GTGGACGTCCCAGATTGTTT
scaffold359358_10.	1	p2	(GA)8	16	180	195	CGCGAACTTAGATGGGCTAC
scaffold359487_13.	1	p2	(TA)6	12	1727	1738	CGAAAACTCAATTTAAAAGGCTTG
scaffold359575_13.	1	p2	(TA)10	20	553	572	CACTTGTCAAAATCTCCTTAATTTG
scaffold359726_13.	1	p2	(CT)6	12	536	547	GCTCATCGTCATTCTCCACC
scaffold359728_16.	1	p2	(CT)8	16	1060	1075	GAGGAGAGGGGGATCGATAG
scaffold359752_15.	1	p2	(AT)7	14	685	698	CCTGCACCAAATTTAGCCAT
scaffold359771_12.	1	p2	(TC)6	12	56	67	CACGCTATCTCGTTGCTCTCT
scaffold359834_14.	1	p2	(TC)8	16	3864	3879	CCTTTTGCTTCAACCACCAT
scaffold360089_13.	1	p2	(AT)9	18	1929	1946	TTTTTGCGGTGTGCATTTAG
scaffold360400_13.	1	p2	(CT)11	22	1047	1068	TAGTTGCAGGCCCTCTTGAT
scaffold360547_12.	1	p2	(TA)8	16	786	801	TCATGCACAAAATAAAAAGGGA
scaffold360592_12.	1	p2	(TA)9	18	42	59	TCTCACACACGTTTACACCCA
scaffold360611_14.	1	p2	(TA)7	14	1392	1405	GCCATCTTCTTTCCCCATTT
scaffold360654_16.	1	p2	(TC)6	12	489	500	CCCTCTGTTCTCTCTCACCG
scaffold360688_14.	1	p2	(AG)6	12	1589	1600	ATGTAGGTGCCTGTGCCTCT
scaffold360789_10.	1	p2	(TC)6	12	385	396	TAGCCGTCCTCTCCATCACT
scaffold360894_16.	1	p2	(TA)8	16	479	494	GCGATTGACACGAAATGAAA
scaffold361048_14.	1	p2	(CA)8	16	447	462	TCGGATCGGATACCCAAATA
scaffold361190_11.	1	p2	(AT)10	20	350	369	CCACGGAAGGAACTGACAAT
scaffold361588_12.	1	p2	(AT)7	14	218	231	GGTCTGACAGGTTCAGAGGC
scaffold361716_11.	1	p2	(GT)7	14	98	111	TCTTTCAGGTCCAGGTGTCC
scaffold361740_14.	1	p2	(AT)6	12	202	213	CCTTCTCCATCACCACCTTG
scaffold361995_15.	1	p2	(AC)6	12	944	955	CTCTTGTCCACCCACCACTT
scaffold362057_17.	1	p2	(TA)8	16	59	74	CCGGTCTAAACCCGGAATA
scaffold362379_16.	1	p2	(TC)9	18	791	808	AACACAAACGCTAAACCCGT
scaffold362560_14.	1	p2	(TG)6	12	1280	1291	TGTAGTCATCCATGGGGGTT
scaffold362651_17.	1	p2	(CT)6	12	313	324	TTGAGATCCATTCCCTCAAA
scaffold363042_12.	1	p2	(TG)6	12	126	137	GGTTATCACCTGATTTTCTCCC

scaffold363404_15.	1	p2	(TA)11	22	969	990	GCCGAAGATTTACTCCTAATTAACAC
scaffold363441_11.	1	p2	(TA)9	18	177	194	GGCTAGATGCAAGCCTTTGA
scaffold363486_13.	1	p2	(AT)6	12	65	76	TCAAATCTTCGAGTACAGAAATGG
scaffold363619_12.	1	p2	(TG)7	14	854	867	GCAGCTGATGCACATATTCC
scaffold363720_13.	1	p2	(TA)7	14	212	225	CTTCACTTGAATTGAGGGGG
scaffold363724_10.	1	p2	(CT)7	14	238	251	TTATTTTCTTGGGTCGCTGG
scaffold363943_15.	1	p2	(TA)7	14	234	247	ATGCGCGTTTTTAGGGTTTA
scaffold364125_17.	1	p2	(TA)6	12	148	159	TCCATTCCGAAAATCAAAGG
scaffold364236_13.	1	p2	(AT)6	12	56	67	TTTTGTGAAACAATAATGACTTTGA
scaffold364374_17.	1	p2	(TA)6	12	774	785	TGGGCGTTTATTATTCCAGC
scaffold364596_15.	1	p2	(GA)7	14	452	465	CCACTCTCTCACACGCAGAA
scaffold364664_12.	1	p2	(TA)10	20	555	574	GCAAAAGGCAGCCTAAAGAG
scaffold364797_14.	1	p2	(TG)6	12	2113	2124	TTATGGGAAGAGGGGGAGAC
scaffold364819_12.	1	p2	(TA)8	16	897	912	CAATGCACCAGATTTGTTCCT
scaffold364875_19.	1	p2	(TC)7	14	993	1006	AAAGGTCACGCCCTACAAAA
scaffold365151_15.	1	p2	(TC)6	12	270	281	TTGGTGCATGCCTTTTGTTA
scaffold365250_13.	1	p2	(TA)6	12	2312	2323	TGAAAAACAAGCGAGCAACA
scaffold365268_12.	1	p2	(TA)8	16	502	517	GGCGAATGCTATGCATTTTT
scaffold365275_17.	1	p2	(TG)6	12	238	249	CACAACACACATCCTTCATGC
scaffold365457_14.	1	p2	(TA)10	20	1896	1915	AGTTGATGGTGTTCCCCTTG
scaffold365480_16.	1	p2	(CT)6	12	2090	2101	TGTGCATTCCACATTTCCAC
scaffold365654_13.	1	p2	(TA)7	14	44	57	TCCCAGGTGTGAATAGCATTT
scaffold365696_13.	1	p2	(TA)11	22	497	518	GGAAATGATCACAGGCCATC
scaffold365997_14.	1	p2	(TA)6	12	26	37	AGCGGTTATTACCGGATCG
scaffold366151_13.	1	p2	(AT)10	20	859	878	AGTGGTTAGCACATGATCGC
scaffold366341_10.	1	p2	(AG)6	12	102	113	GTCGGCAGTGAGCTTCTAGC
scaffold366548_13.	1	p2	(AG)6	12	678	689	TGGGCAAACCAAGATACACA
scaffold366746_13.	1	p2	(AT)6	12	740	751	TCCTTAAACATAACGAGATCAAAAA
scaffold367089_10.	1	p2	(TA)7	14	300	313	TTTTTACCAATTTGCCCTCG
scaffold367132_16.	1	p2	(CT)6	12	80	91	CTCTTTCTCTCTCCGCCCTT
scaffold367201_15.	1	p2	(TA)9	18	502	519	CAAATCCACCAGAAACCCAC
scaffold367394_14.	1	p2	(CT)8	16	222	237	ATCTCTTTTCCCCCACGAGT
scaffold367424_11.	1	p2	(AT)9	18	422	439	ATTACGGCCACGCTAAGTTG
scaffold367446_13.	1	p2	(TC)7	14	453	466	ATCCCCTCTCATTCAACACC
scaffold367502_14.	1	p2	(TA)6	12	137	148	ACCTACTGCCGTGTTCGATT
scaffold367612_12.	1	p2	(TA)9	18	73	90	TTCATGAATGGATGTGTTTTGTT
scaffold367760_13.	1	p2	(TA)11	22	38	59	TTTAGTGTTTTGACATGATTACTCG
scaffold367767_17.	1	p2	(TA)7	14	118	131	ATTTGCTTGATCCAACGGTC
scaffold367849_10.	1	p2	(TA)7	14	706	719	TCTACCCTTCATTGTCATTCTCA
scaffold367932_16.	1	p2	(CT)6	12	1914	1925	GTGAGATTCGATGCCCATTC
scaffold367983_11.	1	p2	(TA)10	20	84	103	TGGCCGTGAATGTATGAGAG
scaffold368078_13.	1	p2	(TC)6	12	145	156	TGAAGAAAATAGGACTAATGAGGTG
scaffold368148_13.	1	p2	(TA)11	22	299	320	ATCGTGAGAAGCGTCGATCT
scaffold368239_13.	1	p2	(CA)11	22	599	620	GCTTCTCGTTTTCTTGTCGG
scaffold368277_10.	1	p2	(AT)9	18	207	224	TTTTCGGATCGGTAGAAGGA
scaffold368315_11.	1	p2	(AG)9	18	619	636	CCAAATGCATGCAGCTTCTA
scaffold368360_14.	1	p2	(AG)7	14	258	271	CCTGTAGACGGCCAAATGTT
scaffold368405_10.	1	p2	(TC)6	12	462	473	TGGAAGCCATGCAAAATAAA
scaffold368503_17.	1	p2	(CT)7	14	1436	1449	CTCCATCGAACATCTCACGA
scaffold368639_13.	1	p2	(TG)7	14	2276	2289	TTTCTTTTGTGACGCAATCG
scaffold368710_17.	1	p2	(TA)11	22	4860	4881	TGGCGAAGCAGAAAGAAACT
scaffold368855_16.	1	p2	(CT)6	12	31	42	CAAATGGCCAAGAGAGTTTACA
scaffold368911_10.	1	p2	(TA)9	18	515	532	TCAAAGATGGAGGTTGGAGG
scaffold368992_16.	1	p2	(TA)6	12	6490	6501	GTCTCACGCGGGTAAGTGAT
scaffold369003_13.	1	p2	(AT)6	12	62	73	CGTTCGATTTGCCGTTTTAT
scaffold369209_16.	1	p2	(TC)8	16	1173	1188	GCAAGAAAAATAAAGGGCAGC
scaffold369467_14.	1	p2	(GA)7	14	271	284	AGAAATCAGACGGGCAGTTG
scaffold369547_13.	1	p2	(TA)7	14	1280	1293	TTAGGGTTTAAAATCGCGCA

scaffold369554_12.5	1	p2	(TC)7	14	74	87	GAGGACACTTGGACCTGAAAA
scaffold369608_10.9	1	p2	(GA)8	16	618	633	AAGTCACCGCCGTTCATATC
scaffold369711_17.7	1	p2	(AT)8	16	511	526	CCGTGATTTAAGGAGTCGGT
scaffold370064_14.9	1	p2	(AG)6	12	48	59	AGCTGTTAGGGTTGTATAGTGAGTAG
scaffold370280_12.2	1	p2	(TC)6	12	193	204	AGTGATGTGGTGTTGGAACATT
scaffold370431_14.4	1	p2	(TA)8	16	2578	2593	CACCAAGTCCAGCCTTCTTC
scaffold370466_18.7	1	p2	(CT)6	12	483	494	CACGTGGAGGATCGTTTTCT
scaffold370601_15.9	1	p2	(TA)10	20	164	183	GGAGTGTCGGTCTGAAGGTC
scaffold370749_17.2	1	p2	(AG)6	12	1436	1447	AGACGGGAGTGCGAGAAGTA
scaffold370930_16.5	1	p2	(AG)11	22	261	282	GCAAGCTTCTCTAACACGGC
scaffold370934_17.1	1	p2	(AT)6	12	401	412	TGCATGTTGCGATTTCATTT
scaffold370940_19.4	1	p2	(TA)8	16	4025	4040	TCTACCTGTTGCTGTGTGCC
scaffold371293_12.3	1	p2	(TA)6	12	117	128	TCAAATGAACATAATCCTGTAATGC
scaffold371622_13.2	1	p2	(TA)11	22	706	727	CCAAATCATTGTATTTCATGTTTCA
scaffold371784_12.1	1	p2	(AT)10	20	640	659	CACCAAATTTCATCATTTTCAA
scaffold371909_17.7	1	p2	(CA)10	20	1795	1814	AGCTTTATGCGTTTGCAGGT
scaffold372201_10.1	1	p2	(GA)6	12	372	383	TCATCAACATGCAACCAACA
scaffold372353_14.5	1	p2	(TA)9	18	1176	1193	ATTATCAACGGCTGCAAAAG
scaffold372390_15.7	1	p2	(GA)7	14	3003	3016	TGCCAGTTGCCATATTTTCA
scaffold372437_15.5	1	p2	(GA)10	20	50	69	TTGAGAGGAAGAAAGAAGATGGA
scaffold372474_14.3	1	p2	(AT)8	16	738	753	TCTAAAGAAAACAAAAGAAGTTCAA
scaffold372585_14.9	1	p2	(AT)6	12	362	373	TGGAGCAACAAAGATGGAAA
scaffold372698_14.4	1	p2	(TA)7	14	468	481	TCCTAACAAAGAAAGGCGGA
scaffold372885_16.9	1	p2	(TA)6	12	559	570	ATCCCTTTTGCTTTTGCTGA
scaffold372897_16.1	1	p2	(GA)6	12	1642	1653	TGATCCTTGCTCTCTTGCCT
scaffold373129_13.6	1	p2	(CA)6	12	1115	1126	AACGCAAGATGGGAAAAATG
scaffold373236_15.0	1	p2	(AT)7	14	277	290	CAAGCAGGTAAATATCAGTTTTCG
scaffold373293_14.0	1	p2	(TC)6	12	557	568	AGGATCCCAAATCACCAACA
scaffold373316_14.3	1	p2	(AG)8	16	848	863	CCACCAACTCCGGTAAAGAA
scaffold373380_10.0	1	p2	(TA)8	16	293	308	ATAACCGACCACGACACCAT
scaffold373479_10.1	1	p2	(TA)8	16	50	65	GGTTATCACCGGATCACGAC
scaffold373565_10.4	1	p2	(AG)6	12	151	162	GCGGTAGGAGTTGATGATGG
scaffold373581_15.0	1	p2	(AT)6	12	848	859	CGGAATGTGATCGAATAGCA
scaffold373636_13.2	1	p2	(TA)8	16	2765	2780	GCTGCTGTGCGTTGATTTT
scaffold373789_16.9	1	p2	(CT)10	20	1103	1122	TGTCGAATGCAGGGTTGATA
scaffold373818_10.1	1	p2	(AT)8	16	303	318	CAAGAAACGCGCCATGTAT
scaffold373830_13.8	1	p2	(AG)6	12	2335	2346	TCAGGAAGATCATCTGCGG
scaffold373870_15.4	1	p2	(TC)6	12	752	763	AGCAGCAATTTCCGAAAAGA
scaffold373874_11.4	1	p2	(CA)6	12	153	164	AACACTGCACGCATTTTGAG
scaffold374115_11.2	1	p2	(GA)6	12	234	245	GACGGAGAAATCAGACGAGC
scaffold374390_14.9	1	p2	(GA)6	12	369	380	TCCAGTGTCTCCATCTCGTG
scaffold374392_16.8	1	p2	(AT)9	18	1724	1741	CACATTCTTGCTTCTGCTGC
scaffold374575_11.2	1	p2	(TA)9	18	67	84	TTCAACAAAGCAACAAAACATTG
scaffold374684_11.8	1	p2	(AG)6	12	229	240	CTTGAGCATGTGGAGAGCAA
scaffold374704_13.7	1	p2	(AT)9	18	66	83	TTTTGAATGGCACAGATTGG
scaffold374974_16.9	1	p2	(AT)6	12	483	494	AGAGATGCTGGTAGAGGCGA
scaffold375227_12.1	1	p2	(AG)6	12	236	247	CCATAAACACCGTGTCCAAA
scaffold375266_12.0	1	p2	(TG)7	14	570	583	TTTGGCATCAATGCATCCTA
scaffold375467_16.3	1	p2	(CT)6	12	373	384	AAAATGGTGCACAAACCCAT
scaffold375768_17.0	1	p2	(TG)6	12	3495	3506	ACACATCGGCACAGGTACAA
scaffold375824_15.4	1	p2	(AC)6	12	1262	1273	TTTTATTGCAGCTGTCACGC
scaffold376233_17.0	1	p2	(TA)9	18	242	259	GCAGACGAACCAGTAGAGGC
scaffold376275_16.1	1	p2	(AT)7	14	3186	3199	TCCGTTTTGCTAAGCCTTGT
scaffold376691_10.1	1	p2	(AT)6	12	194	205	GTCCTCCGAACTCATGGTGT
scaffold377186_13.6	1	p2	(TA)6	12	65	76	CCTCTCGCATTTCTCTTGCT
scaffold377467_18.8	1	p2	(TA)6	12	318	329	CCAAAGTGCCCTTTTATGCT
scaffold377571_15.5	1	p2	(TC)10	20	151	170	GGTGACCACATGTCGAAAAA
scaffold377819_14.8	1	p2	(TA)8	16	1080	1095	GGATCTACGAGATTTGCTCCC

scaffold377922_15.	1	p2	(AT)9	18	539	556	TGAAGCGTGAAAGTCAATCG
scaffold377960_12.	1	p2	(CT)6	12	1206	1217	TGAAATTATACGAAGCCGGAA
scaffold378185_12.	1	p2	(TC)6	12	154	165	GATGCAGTGGGGTTTTGTTC
scaffold378623_13.	1	p2	(TA)6	12	1138	1149	CAAAATGGGCGGCATAAATA
scaffold378659_12.	1	p2	(TA)8	16	310	325	CACCGAGTACCGAAGGGATA
scaffold378687_14.	1	p2	(AC)6	12	357	368	TTCCCTTCTCATTTCCATGC
scaffold378818_11.	1	p2	(CT)6	12	183	194	AAGGCAACATCTATCGAGGG
scaffold378868_10.	1	p2	(GA)6	12	370	381	AGTACTGCAATTCTGCCCGT
scaffold379478_16.	1	p2	(CT)7	14	315	328	TGGTTGGAGATCTTTGGAGG
scaffold379905_16.	1	p2	(AT)9	18	389	406	TGGGTTTTAGGTGTCATTGCT
scaffold380203_10.	1	p2	(GA)6	12	254	265	CGGTTGGATTGCTGAAAACT
scaffold380377_16.	1	p2	(TC)6	12	121	132	AGCAGCGAAGGAAAAACTTG
scaffold380904_13.	1	p2	(CT)8	16	448	463	TTTCTCTCCGACCACATTCC
scaffold380999_18.	1	p2	(AG)7	14	642	655	GACAGGGAGATGGGGAATTT
scaffold381047_13.	1	p2	(AG)7	14	295	308	TGGAACCATGTTCAATCCCT
scaffold381070_11.	1	p2	(AT)6	12	751	762	GGATAGTGGGCAGAGATGGA
scaffold381136_12.	1	p2	(AT)7	14	634	647	GCCCACCTGATTTTCTTCAA
scaffold381164_11.	1	p2	(TC)9	18	243	260	TATGACTCGCCACCTCTTCC
scaffold381240_11.	1	p2	(TA)6	12	337	348	AAGGGTTGGTATCATTTGAACA
scaffold381274_14.	1	p2	(TC)6	12	160	171	CCGGGTATCGGAAATTAGGT
scaffold381365_16.	1	p2	(TA)10	20	181	200	GTGAAACCCCCAATTGTGTC
scaffold381517_17.	1	p2	(AT)6	12	197	208	TCTGCGTTTAAACAACCCAA
scaffold381663_13.	1	p2	(TA)6	12	167	178	TTTATTTTTCTCAAATGCTATGCAA
scaffold381873_10.	1	p2	(TC)6	12	185	196	AGCACCAATTCTTCCAAACG
scaffold381903_15.	1	p2	(GA)8	16	163	178	TTGGGAGAATTTGTGGGAGA
scaffold381921_12.	1	p2	(TA)9	18	770	787	TAACCCCCGGAGTGAAGAAT
scaffold382176_16.	1	p2	(CT)6	12	215	226	AGCATAACAGCTGGCAAACA
scaffold382189_15.	1	p2	(AT)8	16	329	344	TTAGCTCTGGTTTGGTTCCG
scaffold382261_13.	1	p2	(TA)7	14	486	499	CAGATTACTGTGTGCGGCTG
scaffold382322_18.	1	p2	(AT)6	12	1781	1792	AACTTCCGAATTCCAATTACCA
scaffold382684_11.	1	p2	(AG)6	12	251	262	TGAGCTCATTCCGCATTAAA
scaffold382792_17.	1	p2	(CT)6	12	55	66	TTGCCCCTTCACTCTCATCT
scaffold383021_15.	1	p2	(AT)7	14	542	555	TGGTTGGAGTTGTCAGTTCCT
scaffold383144_12.	1	p2	(GA)6	12	168	179	TTGACCAAGGTGAGAATTTGAA
scaffold383190_12.	1	p2	(TA)8	16	135	150	CTTTTTCCTATGTGTGACAAAGC
scaffold383281_15.	1	p2	(CT)6	12	395	406	AGCATTTACCTGGGCATTTG
scaffold383354_13.	1	p2	(TG)7	14	239	252	CATGCTCCGAAACATGAAAA
scaffold383463_15.	1	p2	(GT)6	12	343	354	TCATGCTGGAAGCACGTAAC
scaffold384039_13.	1	p2	(TA)7	14	1456	1469	CGCACTGATCCAACTTTTCA
scaffold384261_13.	1	p2	(TC)7	14	79	92	CCCTAAGTTTGCATCTCCCA
scaffold384332_10.	1	p2	(CT)8	16	239	254	CCACCCTCTCACTTCCACTC
scaffold384389_14.	1	p2	(TA)8	16	251	266	CTTGGCCGATGAAGAAAGAG
scaffold384639_16.	1	p2	(CT)6	12	3513	3524	TAGTTCCTTTGCCAACGGTC
scaffold384660_10.	1	p2	(TA)7	14	145	158	TGTCCCGTTTTCTTCGTTTC
scaffold384887_18.	1	p2	(AT)6	12	717	728	ATGTGGAGAAAGCTCTGCGT
scaffold385095_12.	1	p2	(TA)8	16	248	263	CGATGGCCAAGATTGCTCTA
scaffold385414_13.	1	p2	(AT)7	14	101	114	TCCTTTTCTTTTTCTGAGCACC
scaffold385530_18.	1	p2	(TC)8	16	368	383	CATGCTGTGCAGCAGTAGGT
scaffold385563_20.	1	p2	(TA)8	16	229	244	TACCGGACCTTGGTCTGAAC
scaffold385653_14.	1	p2	(TA)12	24	571	594	TTTCCTACCAAATCTCCCCA
scaffold385747_14.	1	p2	(GT)9	18	3487	3504	TGGATCTCGGAATATCCAGC
scaffold385874_17.	1	p2	(GA)7	14	728	741	CATCCCTACCTGTTGCCACT
scaffold385922_15.	1	p2	(CT)6	12	602	613	CCAAGAAAACTATCGGCAGC
scaffold386012_10.	1	p2	(AT)6	12	340	351	TCACTCACGCAGACAACACA
scaffold386094_13.	1	p2	(TA)7	14	344	357	GCGTGGAAAAGAAGATGCTC
scaffold386210_10.	1	p2	(GT)6	12	191	202	CCGTGAATGAAGGGATTTCA
scaffold386375_13.	1	p2	(GA)6	12	51	62	GCGAAGCACCGAGACTACTG
scaffold386471_15.	1	p2	(TA)6	12	401	412	CCGTAAGGCTCGTATGCTGT

scaffold386689_13.	1	p2	(AT)11	22	342	363	AATGCACTGACTTGGCATGA
scaffold386807_12.	1	p2	(TA)7	14	257	270	TGATCGATTTTCAGCCATGA
scaffold386919_10.	1	p2	(TG)10	20	163	182	CTTGGCCTAAAATCCCAACA
scaffold387006_12.	1	p2	(AG)7	14	53	66	CGAACTCAATTTGATCCGAAA
scaffold387041_13.	1	p2	(AT)6	12	204	215	CCACTTTGGTGACTAACGCA
scaffold387052_17.	1	p2	(CT)8	16	390	405	TATTTCCGGTTCAAACTCCG
scaffold387091_11.	1	p2	(TC)6	12	92	103	TACCCAACCCACTAACCCAA
scaffold387146_13.	1	p2	(TC)7	14	287	300	TTTTCGTCAAATCGACAACG
scaffold387158_12.	1	p2	(AG)9	18	507	524	GGTGAAGACGGATCGTCAAT
scaffold387251_20.	1	p2	(TC)6	12	474	485	CGAATCCGTTTTCCAACAGT
scaffold387422_11.	1	p2	(TA)7	14	71	84	TTGATTCAAAGGCTGATAATGG
scaffold387594_12.	1	p2	(TA)9	18	203	220	TGTGATCGACGATTGGAAAG
scaffold387840_13.	1	p2	(AT)9	18	210	227	GGAAATTATTGGGAGGGAATG
scaffold387854_12.	1	p2	(CT)6	12	83	94	CACGCACAAAGAAGATCTCTACA
scaffold387911_14.	1	p2	(TA)8	16	172	187	CAATTTGCCCTTTCATGCTT
scaffold387941_15.	1	p2	(GA)10	20	1506	1525	CCTGTATGTTGGGGTGTGTG
scaffold388098_13.	1	p2	(TA)10	20	148	167	TTTCCTCCCAGCTTCTACCA
scaffold388245_10.	1	p2	(CT)6	12	452	463	TCCCACTTTGTCTCCCAATC
scaffold388298_16.	1	p2	(GA)6	12	283	294	CAGGAGAACTCGGCTGAATC
scaffold389022_18.	1	p2	(CT)6	12	3086	3097	CATTCAGTGAAAACATGGCG
scaffold389075_10.	1	p2	(GA)6	12	192	203	TCTCACTAATGGGCCAAAGG
scaffold389132_14.	1	p2	(TC)7	14	774	787	AAGTTCGAATTCTCCCCACC
scaffold389181_10.	1	p2	(TA)7	14	669	682	TTGTTGTTTCACAAAATTTAAGCTG
scaffold389191_13.	1	p2	(TA)7	14	252	265	TGGACGAAATTGGTGTGTTG
scaffold389243_15.	1	p2	(GC)7	14	170	183	CACGTGCGTCAACTCCTTTA
scaffold389600_15.	1	p2	(AG)6	12	67	78	CAATTACAATGTTTATCCAATCTCA
scaffold389897_20.	1	p2	(TA)8	16	592	607	TTCACGTACCCCTCATGTCA
scaffold389990_14.	1	p2	(TA)6	12	381	392	GATCCAGTTCAAGTGCCCAT
scaffold390145_11.	1	p2	(TA)8	16	65	80	AAATGCATGCACCTGATTACA
scaffold390368_12.	1	p2	(TA)13	26	581	606	ACGCAACAGCTCATGACAAG
scaffold390395_14.	1	p2	(TC)6	12	517	528	ACGAACCACTGGCTGAAATC
scaffold390458_15.	1	p2	(TA)9	18	67	84	TGAAGTGTTATGCGTTTTGACA
scaffold390624_13.	1	p2	(TC)6	12	439	450	TTCAACTGCATTGTTTCCCA
scaffold390643_17.	1	p2	(TA)10	20	132	151	TGATCTTACGCGCACATCTT
scaffold390808_11.	1	p2	(CT)6	12	403	414	GAAGAGACCAGAAGTCCCCC
scaffold391188_10.	1	p2	(TA)8	16	265	280	GGTGGGCTTTTCTGACTCAA
scaffold391745_14.	1	p2	(AT)8	16	231	246	CCCCAAATGAGGAACTTTGA
scaffold391772_16.	1	p2	(CT)6	12	201	212	CACACATGCGTTCATTCACA
scaffold391820_15.	1	p2	(AT)6	12	179	190	TAAAACCATGCACGTAGGCA
scaffold392025_13.	1	p2	(AG)8	16	640	655	TTCGAGTTTGATTCCATCCA
scaffold392142_11.	1	p2	(TA)8	16	567	582	GATTTTCCTGTCTCCTTTCTCAA
scaffold392160_11.	1	p2	(TA)7	14	156	169	TACCTTTTTGCCCTCGAATG
scaffold392489_16.	1	p2	(TG)7	14	103	116	AACACCTGTGAAAGGGATCG
scaffold392571_15.	1	p2	(TC)6	12	375	386	TCGGAATTTTACGTGGTTTGA
scaffold393129_13.	1	p2	(TA)6	12	164	175	AAACGAAGGAGACGATCGAA
scaffold393488_19.	1	p2	(GT)6	12	85	96	AGTGGGCTTTGGCACAAGTA
scaffold393678_14.	1	p2	(GA)6	12	423	434	GCTGGTTTGAGGGAGATGAG
scaffold393822_10.	1	p2	(GA)6	12	433	444	TCAAAAATCCAAGGGTGGAG
scaffold393882_14.	1	p2	(TC)8	16	216	231	CAAACCGTTGTGGATCTGAA
scaffold394585_13.	1	p2	(CG)8	16	303	318	ATGGTGGTATGGTGTGGAGG
scaffold394634_18.	1	p2	(TA)8	16	177	192	CGGAAATGACCCCATAATGA
scaffold394761_11.	1	p2	(TC)7	14	80	93	CAGAAATGGCATTGGTTGTTC
scaffold394922_14.	1	p2	(AT)7	14	611	624	CGCATGATGTAACGTGAAGG
scaffold394982_16.	1	p2	(TG)7	14	401	414	TTGATTATTCCGCTTACGTTTTT
scaffold395246_13.	1	p2	(AC)6	12	73	84	TCACATCCTCAGCACAAACC
scaffold395910_15.	1	p2	(CT)6	12	613	624	TGTTCACGGGTGCTTTGATA
scaffold396150_14.	1	p2	(AT)8	16	79	94	CAGAATTAGCCTTACCAAGATGG
scaffold396192_15.	1	p2	(CT)6	12	175	186	AGATCAACGCTCCTCGTGAT

scaffold396458_11.	1	p2	(TA)6	12	374	385	AAGAGTTATCACCGGATCGC
scaffold396597_14.	1	p2	(GA)6	12	163	174	GGATGCAAGGTGAACTTGGT
scaffold396652_11.	1	p2	(GA)7	14	814	827	AGAAGAAGCAGAGACCGACG
scaffold396874_10.	1	p2	(TG)9	18	449	466	TGGGGTTGGAGGTTTTTGTA
scaffold397028_12.	1	p2	(TA)11	22	841	862	ACACTAACGCTCGACCTCGT
scaffold397140_15.	1	p2	(AT)6	12	2264	2275	TGCGGATTATCACATTGAGG
scaffold397338_10.	1	p2	(TA)8	16	199	214	AATACCCTTCGCATCCACTG
scaffold397502_15.	1	p2	(GT)7	14	268	281	CGCCGGACTATTCTCTGAAG
scaffold397641_18.	1	p2	(AG)7	14	755	768	CGGGCTTGCATGAGTTTAAT
scaffold398006_14.	1	p2	(TG)6	12	659	670	TCAATCAAATTTTATCAAACAAGAA
scaffold398020_15.	1	p2	(AT)12	24	493	516	ACAACCCCGGACTATCGAAT
scaffold398025_12.	1	p2	(AT)6	12	298	309	AAAAGATTACTCATGTGATATTGCG
scaffold398093_12.	1	p2	(GC)8	16	170	185	TCCGGTCCAATTCCAATAAG
scaffold398360_15.	1	p2	(AT)8	16	1856	1871	GCTGACGTAGTAGTTCCGGC
scaffold398756_16.	1	p2	(AT)11	22	3005	3026	TGGTTTTCGTACACAATTCGAG
scaffold399077_15.	1	p2	(AC)7	14	5432	5445	TGGAACCAAGACATATGGGAA
scaffold399165_15.	1	p2	(CT)8	16	126	141	TACGTGATCGGACACGAGAA
scaffold399410_14.	1	p2	(TG)10	20	4683	4702	ATCCTCCTTGCTTCCTCCAT
scaffold399472_10.	1	p2	(AG)6	12	1001	1012	CGAAGGTTCTGCGATTTGTT
scaffold399622_13.	1	p2	(TA)6	12	250	261	CGTCAAAATGCAAGACGTGA
scaffold399990_11.	1	p2	(AT)8	16	230	245	AAAAATCAAACCTCAACCCG
scaffold400138_14.	1	p2	(GA)6	12	4229	4240	GGTAGAGGAGCTGATGTGGC
scaffold400146_10.	1	p2	(AT)8	16	479	494	CCCCTTACTGCTAACACCGA
scaffold400149_15.	1	p2	(GC)7	14	1056	1069	TCAGTTTTGCAAGGATTGAGAG
scaffold400153_10.	1	p2	(GA)6	12	382	393	GTGGTGGGAAACAAGAACCT
scaffold400154_15.	1	p2	(CT)7	14	677	690	CGCTAAGGAGAGGCAAAATG
scaffold400157_15.	1	p2	(TA)9	18	695	712	CCCTACAGATGGCAGGTTGT
scaffold400164_14.	1	p2	(AG)6	12	2764	2775	AAATGCTCCTGCACTTCTCG
scaffold400185_13.	1	p2	(TA)9	18	483	500	ATGTGTCAATTCCTGGGCTT
scaffold400186_15.	1	p2	(GA)9	18	1932	1949	CACCAATTCCATCAGCCTCT
scaffold400208_13.	1	p2	(TA)8	16	1435	1450	CGGTTGCAAGTTTGGAAAA
scaffold400220_13.	1	p2	(TC)6	12	205	216	TACTAAAATACCCCCGCGAA
scaffold400238_11.	1	p2	(CT)6	12	340	351	GGCTTAATGGGGTGGAAAAT
scaffold400281_10.	1	p2	(TA)8	16	198	213	ACGAAAAACGAAGGAGACGA
scaffold400647_15.	1	p2	(AT)6	12	604	615	TTGATTTTAAGAGGTGATATGATACG
scaffold400735_14.	1	p2	(AT)10	20	235	254	GCAGAAATTCTTTCTTCTGTTTTAGG
scaffold400851_10.	1	p2	(AT)6	12	387	398	GTTTTTGTACATCGGCGGAG
scaffold400989_10.	1	p2	(CT)7	14	69	82	ACAAATGGCCAAGAGAGAGTT
scaffold401005_16.	1	p2	(GA)6	12	601	612	GGAGGTGCGGTGTTAGAGAG
scaffold401012_14.	1	p2	(AT)7	14	1707	1720	TTATCAAGCCCACCGTAAGTG
scaffold401018_11.	1	p2	(AT)6	12	416	427	CAACGAAAAGAGAAAGAGGGC
scaffold401057_13.	1	p2	(AT)11	22	45	66	TGAATTCATGTACACATTTGGAA
scaffold401142_10.	1	p2	(TA)7	14	260	273	GAGATATACGCAGGGGACGA
scaffold401234_14.	1	p2	(TA)8	16	290	305	TGCGTTTTGACAAGATTTGC
scaffold401311_19.	1	p2	(TA)8	16	68	83	CGGAAGAAACAAACTAGAAAGAACA
scaffold401380_11.	1	p2	(TC)7	14	151	164	AGCGATGAAATGTACGTTAGAGA
scaffold401429_12.	1	p2	(GA)7	14	314	327	GCTACTAACTTGATGCGGGG
scaffold401436_10.	1	p2	(GA)6	12	46	57	GGAGGGATGATGAAGATGGA
scaffold401490_12.	1	p2	(TC)6	12	313	324	GCACCAGATGTCGTGGATTT
scaffold401514_15.	1	p2	(GT)6	12	1214	1225	TGAATGGATTTTTGGCATGT
scaffold401696_15.	1	p2	(CT)6	12	176	187	TGTTTTATTAACCTCAATTGTGAAA
scaffold401812_13.	1	p2	(AC)6	12	1354	1365	GAAGATGGGAAACCCCTTGT
scaffold401915_13.	1	p2	(TC)7	14	1094	1107	CCGAAATTTTACGTGGTTCG
scaffold402069_12.	1	p2	(AT)9	18	195	212	GATGCATGCACGTGAATAAGA
scaffold402088_16.	1	p2	(CT)6	12	279	290	TAGGGTTTCAAAACATCGCC
scaffold402250_16.	1	p2	(AC)6	12	121	132	TCTTTCGGGTTCTCAACCAC
scaffold402276_16.	1	p2	(TA)6	12	442	453	AGCGATTCTTCCGTATGCTG
scaffold402344_16.	1	p2	(AG)6	12	110	121	ATGGTGGTTTGGTGGAAGAA

scaffold402366_15.2	1	p2	(CG)6	12	185	196	TTTGCATACTGCATGGGCTA
scaffold402473_10.6	1	p2	(TC)6	12	37	48	GGCAACGGAATACCATTTGT
scaffold402522_16.1	1	p2	(CA)9	18	362	379	TACCAAAGCCGCTCCTAATG
scaffold402653_19.4	1	p2	(AT)8	16	77	92	GCTTAAAACAATTATTGAACCCG
scaffold402863_16.5	1	p2	(TC)6	12	285	296	CCAGTTCGGCGATATATGGTA
scaffold402887_17.2	1	p2	(GA)6	12	1664	1675	GATGGGAAAAGAAGGGAAGG
scaffold403408_11.1	1	p2	(TC)7	14	96	109	TAATGGCTGCCTATCAACCC
scaffold403506_14.9	1	p2	(AT)7	14	1526	1539	CATGTGAGAAACGTCCCCTT
scaffold403665_18.9	1	p2	(TA)10	20	68	87	CAAAATTTAAGGGTTATTATTGGATCA
scaffold403865_16.4	1	p2	(CT)6	12	2656	2667	CCCCTCATTTTTCGTTTTCA
scaffold403875_19.8	1	p2	(GT)6	12	333	344	TCAGTTTCCACACGCCAATA
scaffold403911_10.0	1	p2	(CT)7	14	80	93	TCATCATGAAACACCCTAGAAAA
scaffold404001_14.7	1	p2	(TA)6	12	264	275	TTGACCCACCTTTGACCAAT
scaffold404029_10.0	1	p2	(TG)6	12	340	351	ATCGTAGTGAAGTAGCCGCC
scaffold404095_13.1	1	p2	(TA)7	14	145	158	TGTGAGTTGGTGAGGCAAAG
scaffold404858_14.7	1	p2	(CT)6	12	71	82	TGTTGCTGATGCAGACAGGT
scaffold404867_16.0	1	p2	(AG)6	12	167	178	TGGAGTAGGGAGCCTCGTAA
scaffold404901_13.6	1	p2	(AT)10	20	46	65	TGGTTATTACCTGATCACCATCC
scaffold404903_12.7	1	p2	(AT)8	16	181	196	GTGGACCGGTGGAAAGAATA
scaffold404905_15.3	1	p2	(TC)6	12	374	385	TTTAATGGACACCTCTGCGG
scaffold405055_12.6	1	p2	(TA)6	12	228	239	GTTTTGTTTCCTGGGTTTGG
scaffold405121_10.3	1	p2	(AT)6	12	387	398	AATACATCCAGTCATCCCGC
scaffold405149_13.2	1	p2	(GT)6	12	1046	1057	ACCACTCGTGCATCACTCAA
scaffold405486_15.3	1	p2	(CT)8	16	986	1001	AGTCAAATTGGCATTACGGG
scaffold405603_16.7	1	p2	(TA)6	12	3021	3032	CCCTTCCATTTTGTTATATGGG
scaffold405673_17.1	1	p2	(CA)6	12	2666	2677	GGGGCTTTGAATCTACCAAA
scaffold405790_10.5	1	p2	(AT)6	12	198	209	ATCCATCTCATGTTGGGCAC
scaffold405888_15.5	1	p2	(GA)6	12	2307	2318	TAGAGGGAGGGGAGGGTTTA
scaffold405920_21.2	1	p2	(TA)7	14	77	90	TGAACTAAGGAGGTGTTATGACAGA
scaffold406006_11.9	1	p2	(AT)10	20	207	226	AAACAAACCGTGTTAACATCCC
scaffold406051_15.9	1	p2	(CT)9	18	89	106	TCTCATCTCTCGCTCTCCCT
scaffold406089_20.1	1	p2	(GA)7	14	118	131	CCCGTTCCATCACACTTCTT
scaffold406177_16.3	1	p2	(AT)8	16	946	961	TGCTTGGAAAGACAATTGAATG
scaffold406516_10.7	1	p2	(AG)11	22	546	567	CGAGCCAAGCCAGAAGTATT
scaffold406583_17.8	1	p2	(GA)6	12	1118	1129	CGAAGGTTGGGTGGTAGAGA
scaffold406618_12.1	1	p2	(AG)6	12	51	62	CAATACAACTGCCGAGCTGA
scaffold406732_12.3	1	p2	(TA)6	12	121	132	TGCTTGATCCAACGGGTTAT
scaffold406850_22.9	1	p2	(AT)14	28	1180	1207	CCCAAATCCGTGGATAAAAA
scaffold406994_11.9	1	p2	(CT)6	12	256	267	CTTTCTCAACCGAGCTCACC
scaffold407041_13.7	1	p2	(AG)8	16	793	808	TAATGGCCACCAAGCTTTTC
scaffold407116_15.4	1	p2	(AG)6	12	1514	1525	GAACGACGGAAATATGGAGC
scaffold407164_21.5	1	p2	(CT)6	12	474	485	ACACTTGCCAAGGGCATAAC
scaffold407591_16.3	1	p2	(TA)10	20	64	83	TGATGGTTGTGATTTGTTAGAGG
scaffold407660_12.4	1	p2	(TA)10	20	784	803	CGGCTGAGGACGAGAATTAG
scaffold407672_16.0	1	p2	(TG)6	12	516	527	CGGGTTTGAACCCTCAATAA
scaffold407690_15.3	1	p2	(AG)8	16	571	586	ACTGCCCAACAATGGCTTAC
scaffold407708_13.8	1	p2	(AT)9	18	68	85	TAAGGGCGGTATCACCTGAA
scaffold407715_16.7	1	p2	(CT)7	14	984	997	CCAACACTCTGCTCTCTCCC
scaffold407854_13.7	1	p2	(AT)8	16	964	979	ACGTAAACCCCTGGTCAAAA
scaffold407950_10.5	1	p2	(CT)9	18	328	345	TCCCAAATTATATCCTCTCCCA
scaffold407995_14.4	1	p2	(AT)6	12	156	167	AAAAATCAAGTTTAGGTGCGTCA
scaffold408020_15.3	1	p2	(TA)7	14	77	90	TCCATTCCGAAAATCGAAAG
scaffold408070_16.2	1	p2	(AG)6	12	214	225	ATGTCCGTCGTTGGTTCTTC
scaffold408124_14.4	1	p2	(AT)6	12	575	586	CCACTGATGTGAGCCAACTG
scaffold408141_17.5	1	p2	(AT)8	16	493	508	CTTGCCGATGTTTACCGTTT
scaffold408275_13.8	1	p2	(AT)9	18	211	228	GACTCTCAATGCCTTCTACCC
scaffold408388_14.0	1	p2	(CT)13	26	1926	1951	TCAAAGAATCCACCATGCAA
scaffold408495_15.4	1	p2	(AG)6	12	52	63	AGCTGTTAGGGTTGTATAGTGAGTAG

scaffold408515_16.4	1	p2	(GA)6	12	282	293	GCATTAGGTTGAGGGGGAAT
scaffold408630_16.4	1	p2	(GA)7	14	51	64	GCGGTGGTAGGAAGAAACTG
scaffold408683_10.1	1	p2	(TA)8	16	203	218	TGCATGTGGGCATGTTTAAT
scaffold408704_14.7	1	p2	(TG)6	12	245	256	ATTTTATGGGACGGAGGGAG
scaffold408751_13.8	1	p2	(TA)7	14	1372	1385	GGAATTGAATGTGGGAGTGC
scaffold408798_15.5	1	p2	(AG)6	12	2838	2849	CAATGTGGCCTGCCTATCTT
scaffold408805_16.8	1	p2	(TA)10	20	186	205	CCCAGTACCCCTCTTTGGAC
scaffold408850_15.9	1	p2	(TA)7	14	120	133	AAAAATGCAGATTATGCTCCAC
scaffold408928_14.6	1	p2	(CA)8	16	679	694	TCAATATCATCGCCATTTTGAA
scaffold408939_12.4	1	p2	(AT)11	22	853	874	GGCCGGTTTAAGATTCATCA
scaffold408949_13.6	1	p2	(TA)9	18	461	478	GGCGACAAAATGGATGACTT
scaffold409011_14.8	1	p2	(GA)6	12	772	783	AGGTGCATATTGAACCCGAG
scaffold409174_17.0	1	p2	(CA)6	12	189	200	TGCACAATATGTTGGGAGGA
scaffold409209_14.2	1	p2	(TA)7	14	256	269	GTGTCAAACTGTTCGCCTCA
scaffold409317_13.6	1	p2	(AT)6	12	260	271	GCATCGTTAGAAGCGTCGAT
scaffold409322_15.5	1	p2	(GA)6	12	121	132	CAAACGAGGAGCAAAAATCA
scaffold409342_11.3	1	p2	(TA)7	14	514	527	TTTGTCCAAACAAATGAAAACA
scaffold409368_10.0	1	p2	(GA)7	14	53	66	GTGAGGGATGGACGAGAGAG
scaffold409407_16.2	1	p2	(AT)9	18	2608	2625	CCTCACTGAAGTTCGAAAACG
scaffold409485_15.0	1	p2	(TA)8	16	269	284	AGCCACGATTCCTGATTTTG
scaffold409598_14.9	1	p2	(GA)6	12	89	100	AAACACGCAACACAAAGCAG
scaffold409613_20.3	1	p2	(GT)7	14	748	761	GTTCCTCATGCACCTTGGAT
scaffold409660_12.5	1	p2	(TA)6	12	162	173	ATCATCGGGGTGTAACGAGA
scaffold409697_14.6	1	p2	(TC)7	14	925	938	CACTGCCAGCAGTCGATAAA
scaffold409751_13.7	1	p2	(AT)8	16	66	81	AATGGATGGTTGTGATTGAGTT
scaffold409755_15.5	1	p2	(CT)7	14	526	539	GTCCACGTGCTTTCCTCTGT
scaffold409765_11.3	1	p2	(TA)11	22	220	241	AGTCGAAGGTCGCGTGTAAT
scaffold409969_15.9	1	p2	(AG)6	12	844	855	GCTGGCAATCCTTTCTTCCT
scaffold410086_11.5	1	p2	(AT)7	14	154	167	TTTTGCCCTCGAATGCTATC
scaffold410087_14.1	1	p2	(GA)7	14	75	88	TCCCACATTGCATGAGAGAG
scaffold410118_18.3	1	p2	(TG)7	14	42	55	CATTGTGTTTTCTCCATATTTTCA
scaffold410162_14.4	1	p2	(AG)7	14	822	835	ACACAATGGTGATGGCAGAA
scaffold410219_12.1	1	p2	(AG)7	14	53	66	TGTTTGAGTGGTTTTTCCTTGA
scaffold410233_13.7	1	p2	(CT)7	14	29	42	CCTCTCACTCCCACTCCATC
scaffold410279_15.9	1	p2	(GT)7	14	56	69	CCTGAAACTCCAAATATTCTTCTTG
scaffold410312_12.4	1	p2	(GA)9	18	742	759	CTTGCCTTACATCAGCCCTC
scaffold410595_14.0	1	p2	(CA)6	12	470	481	CCGGTGAACTTCTCCAACTC
scaffold410606_15.7	1	p2	(AG)6	12	136	147	AGAAAAAGTTGGGACGGAGG
scaffold410696_14.0	1	p2	(TA)6	12	268	279	TTGTTCGAAACCTAATGCCA
scaffold410788_10.4	1	p2	(TA)8	16	371	386	AAAAAGGAAGGAGGGAGCTAA
scaffold411136_20.8	1	p2	(AT)6	12	121	132	TGTAAAACATGTATGGGATTGAAGA
scaffold411195_17.6	1	p2	(AT)7	14	3901	3914	TGTGGTTGCGTCCTTATGAA
scaffold411312_16.1	1	p2	(TA)8	16	1885	1900	CATGGAGGGGTCAAACATTC
scaffold411410_14.5	1	p2	(AT)7	14	637	650	GGGGTGAAATTGGGAGAGTT
scaffold411492_12.1	1	p2	(GT)7	14	35	48	GGATACCCTCCCAAACCCTA
scaffold411532_21.2	1	p2	(CT)6	12	97	108	TCTCATTCACGCTTTTCAGC
scaffold411615_15.0	1	p2	(TA)9	18	1060	1077	TTTTGAGCTTCCGCGAGTAT
scaffold411763_16.4	1	p2	(TA)10	20	173	192	TGGACTTAAGTACCCTTTTACCAA
scaffold411790_15.0	1	p2	(GA)7	14	1563	1576	GGGGTGGTTAAGTTGTGGTG
scaffold411810_13.4	1	p2	(AT)8	16	336	351	TTTGCTAGGGACCGAAACC
scaffold412001_14.7	1	p2	(TA)12	24	471	494	AGTATGCTGACGCTGGGTTT
scaffold412042_14.4	1	p2	(CT)8	16	117	132	CTTGGGCTAAAATCCCAACA
scaffold412086_16.6	1	p2	(GA)6	12	1819	1830	GGTTGATTGGTTTTCATGGC
scaffold412159_10.5	1	p2	(AG)7	14	69	82	CAAATATTTTGTAGTTTCCCATGTTG
scaffold412247_17.0	1	p2	(GA)12	24	4389	4412	TTCGAGCTCTCCTTTTTGGA
scaffold412258_10.4	1	p2	(AG)6	12	360	371	CCCCACCAGAAGTCCAACTA
scaffold412459_11.1	1	p2	(AG)6	12	86	97	GGATTTTCGAAATTTTCTCGC
scaffold412476_14.9	1	p2	(AT)6	12	1414	1425	CTGCATCGAGTATCGCTCAA

scaffold412534_10.	1	p2	(GA)6	12	55	66	CGTGGTTCGATCGTAATTGA
scaffold412841_15.	1	p2	(AT)6	12	1033	1044	TTTCTTTAATCACCGCACCA
scaffold412863_13.	1	p2	(GA)6	12	463	474	TCTGGTCGAGCTGGAAGATT
scaffold412869_12.	1	p2	(CA)9	18	55	72	TGTGATTTGTTCCCACAAGAA
scaffold413066_20.	1	p2	(CG)6	12	60	71	GCACTGTGTTACGCCGATTA
scaffold413130_16.	1	p2	(CT)7	14	295	308	AAAAGAAAAAGTGAAGGGCTCA
scaffold413146_13.	1	p2	(CA)6	12	743	754	TTCCTAAAAACGTTCCGCTG
scaffold413147_11.	1	p2	(AG)7	14	35	48	GAAGAACAATTACAATGTTTATCCAA
scaffold413223_17.	1	p2	(TC)13	26	2490	2515	CTGCAGAGCTCCATGACAGA
scaffold413315_18.	1	p2	(GA)6	12	53	64	TCAACAGAGAATGCAAGCAAA
scaffold413360_13.	1	p2	(TA)8	16	181	196	AACATGATTTGATGGTGCCTC
scaffold413363_11.	1	p2	(TA)9	18	45	62	TGCGTTTTGACAATATATAGGTGTTT
scaffold413392_16.	1	p2	(TC)6	12	122	133	CTTCCCAGGATCGATTTGAA
scaffold413411_16.	1	p2	(AT)9	18	609	626	AATGCAAAAATATGAGGCCG
scaffold413460_16.	1	p2	(GA)6	12	72	83	TTGGTGGAAAAAGGTTAACGA
scaffold413678_11.	1	p2	(TA)7	14	51	64	GGTTTCTGGTGAAGATGACGA
scaffold413693_15.	1	p2	(TA)9	18	45	62	AAGGGGGTTATTAGTGGATCA
scaffold413719_12.	1	p2	(AT)7	14	169	182	TGTGCGTGTATGCAATGTGT
scaffold413983_23.	1	p2	(AT)9	18	1048	1065	ATGGAACGTTGATTGCCATT
scaffold414075_11.	1	p2	(GA)6	12	217	228	TCCTGCATCCTATCACATGG
scaffold414101_14.	1	p2	(CA)6	12	65	76	TCTCGACTAATTATTATGCCTACCA
scaffold414271_10.	1	p2	(AT)11	22	67	88	AATTAAAATTTGGGGAGGGG
scaffold414329_13.	1	p2	(GA)12	24	1026	1049	CAGACCGTCGAATTTAGACCA
scaffold414359_12.	1	p2	(CT)6	12	81	92	TTTGGGACGATTTTCTCTCTATG
scaffold414787_12.	1	p2	(AG)6	12	952	963	TGCTGCAGAGAAGGTAGGGT
scaffold414830_10.	1	p2	(TG)6	12	108	119	CTCGTTTGTGTGTTCTTCGTG
scaffold414890_15.	1	p2	(GA)6	12	306	317	TGGTTGTTTTAATTTGCTCCC
scaffold414923_15.	1	p2	(CT)6	12	577	588	CCTTTCCTTTACACCACAAGGA
scaffold414974_17.	1	p2	(TA)8	16	70	85	TCAATGGCTCAAAAAGTTTCA
scaffold414982_14.	1	p2	(TA)8	16	235	250	AAATGAAATAGAATTCGCGAGG
scaffold415123_11.	1	p2	(AT)6	12	122	133	CACACACATTACATTAAACCGATG
scaffold415129_14.	1	p2	(AT)6	12	532	543	GATCGCATGTTCGATCTTCA
scaffold415154_16.	1	p2	(TC)7	14	62	75	CACATCCCACCCAACTCTCT
scaffold415294_14.	1	p2	(AT)6	12	592	603	TGGACGTAAATACCCTTTTACCA
scaffold415324_15.	1	p2	(CT)7	14	270	283	GAGCCCAAACCTCAATCAAC
scaffold415374_14.	1	p2	(AT)9	18	660	677	GGGCATGAATTCCAAAACTC
scaffold415578_17.	1	p2	(TA)6	12	2523	2534	CTCGGAAAAGTCTACCGGC
scaffold415641_15.	1	p2	(AG)6	12	881	892	AGTGAGCCTACACCACCACC
scaffold415744_13.	1	p2	(AT)6	12	190	201	CCCCAATGCTATGGACAAAC
scaffold415894_10.	1	p2	(GT)7	14	199	212	CGTCTGAGCTCGGTAGAAGC
scaffold416075_16.	1	p2	(AT)7	14	325	338	AGATCCGATGTCCCAAACAC
scaffold416092_16.	1	p2	(CT)6	12	3138	3149	ATGTGCTCTTCATGGGGAAG
scaffold416164_15.	1	p2	(TG)9	18	116	133	CATCCCAACCACTCATTTCG
scaffold416549_13.	1	p2	(AT)6	12	1990	2001	AACTGGTATGTGCGTGTGGA
scaffold416621_16.	1	p2	(CA)7	14	48	61	GGTTAATCTCTCTATCTCTCTCACACA
scaffold416719_10.	1	p2	(TA)7	14	120	133	GCAGTGTAGTTAGGCGGTTTG
scaffold416903_13.	1	p2	(TA)7	14	867	880	TTGTCGGTCATTGAATTGTGA
scaffold417101_11.	1	p2	(TG)7	14	79	92	TTTTCATTTGATCACCTCCC
scaffold417120_13.	1	p2	(TA)9	18	264	281	GATCTGCGAAATGCTTAGCC
scaffold417421_16.	1	p2	(CT)6	12	626	637	ACATCATCTTCCTTACGCGG
scaffold417455_11.	1	p2	(AT)8	16	223	238	CTGGAACAACAGCTACGCTC
scaffold417477_11.	1	p2	(TA)10	20	514	533	GCTCACAGATCCCACCTGAT
scaffold417608_11.	1	p2	(TA)9	18	44	61	AAGGAGGTGTTATGAAGGGATT
scaffold417668_10.	1	p2	(TA)10	20	77	96	CCCCTGTATGCACCTCATTT
scaffold417669_11.	1	p2	(CT)6	12	623	634	TTCTGTCCTCAACCACCCTC
scaffold417751_16.	1	p2	(TA)6	12	406	417	TTGGCACTGAGTACCCATTTT
scaffold417866_10.	1	p2	(CT)6	12	38	49	CCCAGGTCTCAATCTTTTTGG
scaffold418001_16.	1	p2	(GT)7	14	120	133	TGCTGCTATTGAAGCCATTG

scaffold418271_19.	1	p2	(AT)6	12	1501	1512	GAAGGTGAACGTCGGTAGGA
scaffold418293_16.	1	p2	(TA)7	14	486	499	TGATAGAAACACTTCGCGAGC
scaffold418387_14.	1	p2	(CT)6	12	324	335	CACGCATCTCTCTCTTCCCT
scaffold418652_17.	1	p2	(TA)7	14	823	836	TGAGGCTCCAGATTTGCTCT
scaffold418660_11.	1	p2	(TA)6	12	158	169	GAGGCCTACTTCCTGGATCA
scaffold418727_12.	1	p2	(CT)6	12	180	191	GGAGTTTCTATCCGCCCTTC
scaffold418728_17.	1	p2	(AG)6	12	123	134	CGATGGTCTGAGTTATCCTCTG
scaffold418969_17.	1	p2	(AT)7	14	120	133	TCGTGTGTAGGAAAAACATCG
scaffold418971_15.	1	p2	(TA)7	14	46	59	CGATCACGTTTTCCAGTTCC
scaffold419114_17.	1	p2	(TG)9	18	307	324	CGTTTTGATGATGAGCTGGA
scaffold419138_12.	1	p2	(AT)8	16	165	180	GCGGTTTGAGCCTAATTTTG
scaffold419196_16.	1	p2	(TA)6	12	159	170	TTCGTTTACAGCATACACCGA
scaffold419210_16.	1	p2	(AG)7	14	385	398	GAGTGCTGCAGCGTATGTGT
scaffold419272_14.	1	p2	(TA)12	24	534	557	CAATTGCTATAAATGAAACCGGA
scaffold419294_12.	1	p2	(TA)7	14	197	210	AAACTTGCTTCCGTTGGATG
scaffold419457_12.	1	p2	(AG)6	12	76	87	TCCTCAATTTCAGTGTGGAAAA
scaffold419514_16.	1	p2	(TC)7	14	262	275	CACGGGGTTTCCAGACTTTA
scaffold419515_12.	1	p2	(TA)6	12	97	108	AAATTAAGTGGGGGTGGAGG
scaffold419849_19.	1	p2	(TC)6	12	236	247	CCCAAATCTAGAAGCCACGA
scaffold419894_15.	1	p2	(AT)6	12	1423	1434	TTCGATACGAATTTTCATACCAT
scaffold420131_15.	1	p2	(CT)6	12	84	95	GATTTTGGGACGATTTTCTCTC
scaffold420137_20.	1	p2	(CT)6	12	86	97	GCGAGTGTCGCCTAGTGTAG
scaffold420231_16.	1	p2	(AT)7	14	542	555	TGAGCACGTATGGACACGAT
scaffold420236_16.	1	p2	(AG)7	14	2638	2651	GAGCCACGGCCTATTACAGA
scaffold420243_12.	1	p2	(TA)6	12	563	574	TTGAATCCAGGATCTTGAGC
scaffold420246_12.	1	p2	(AT)7	14	215	228	CCCAAGCCAGAGTGAGAGAG
scaffold420279_12.	1	p2	(AT)7	14	54	67	TTTGCTAGAGGTTTTGACGAGA
scaffold420446_18.	1	p2	(AG)6	12	2478	2489	TGGATTGAAGAATGGAAGCA
scaffold420448_14.	1	p2	(GA)8	16	2338	2353	CATTCACTTGAGGAATGGGG
scaffold420479_15.	1	p2	(GA)7	14	1799	1812	ATCCCGTCTGCGTTTATCAC
scaffold420492_15.	1	p2	(AT)6	12	2491	2502	TTCAAACGTGGCACCAATTA
scaffold420502_14.	1	p2	(TA)9	18	50	67	CACAAGATTTATGGGTTATCATTTG
scaffold420506_11.	1	p2	(AT)10	20	369	388	AAAAGGTTAAGGGTGGGGTG
scaffold420516_15.	1	p2	(TA)6	12	215	226	TTCCCATCAGTCAAGATCTACC
scaffold420555_16.	1	p2	(TA)8	16	584	599	TCCTCGACTGTTTTTCCCAC
scaffold420617_13.	1	p2	(AT)8	16	1637	1652	GCAATGGTGTTGCATATGTGT
scaffold420686_14.	1	p2	(TC)6	12	2224	2235	TGCTACGAAGACATCCACCA
scaffold420693_15.	1	p2	(AT)6	12	267	278	GCCTCCTTTTCTTTTTCTCG
scaffold420864_10.	1	p2	(CA)6	12	61	72	TGGGAGAATTTTCTGCTCTTG
scaffold420921_10.	1	p2	(AG)6	12	114	125	CCTCCCAACCCCAAATTTAT
scaffold420938_15.	1	p2	(AT)10	20	43	62	ATCGGTTATTACCGGATCGC
scaffold420988_14.	1	p2	(GA)6	12	895	906	CTTAAATCCACCGCCATTGT
scaffold421052_14.	1	p2	(TG)6	12	1275	1286	TGAGGGACTTGGGTAGTTGC
scaffold421219_15.	1	p2	(AG)6	12	1193	1204	ACAGAAGAACGGGCTTTGAA
scaffold421249_10.	1	p2	(AC)6	12	691	702	TTTTTAATTCATCTTAACTGATGCAA
scaffold421276_17.	1	p2	(TC)6	12	364	375	GCGCAAAAATACTCGCTTTC
scaffold421297_11.	1	p2	(CT)6	12	209	220	ATCTACCCCTCATTCCCGAC
scaffold421350_12.	1	p2	(CT)6	12	43	54	GATCTTTCCACAAACCGAGC
scaffold421401_10.	1	p2	(AT)6	12	221	232	ACATTTTCGGCCATGACAAT
scaffold421501_17.	1	p2	(TC)6	12	330	341	TCCACATTGGTTTGGCCTAT
scaffold421528_11.	1	p2	(TA)9	18	1212	1229	CCAATTCGAAAACCGGTAAA
scaffold421589_16.	1	p2	(TA)8	16	69	84	GGGCTAAGTGTTGAGATTGGA
scaffold421735_14.	1	p2	(GA)6	12	731	742	TGCGTTTGATCGTTAGCTGT
scaffold421831_13.	1	p2	(AT)7	14	189	202	TGCACGTAGGCATGTTCAAT
scaffold421857_14.	1	p2	(GA)9	18	1035	1052	CCATCCATGCCTTGGTACTT
scaffold421859_11.	1	p2	(TA)7	14	67	80	CGAGTGATCGTGAGACAGTGA
scaffold421881_18.	1	p2	(GA)8	16	306	321	GCGAAGAAACATTCAGGGAA
scaffold421989_16.	1	p2	(TC)7	14	692	705	ATCGAGTAAACTAGGCGCGA

scaffold422116_16.	1	p2	(TA)8	16	119	134	ATGCATGTGTGCCAAGTGTC
scaffold422117_14.	1	p2	(AT)8	16	1849	1864	CAAAATGTCGAAAAATTCGC
scaffold422118_15.	1	p2	(TA)6	12	123	134	TATCCATGGAATGCCCAAAT
scaffold422119_17.	1	p2	(AG)6	12	898	909	TTACATGGATGGATGGGTTG
scaffold422224_13.	1	p2	(AT)6	12	63	74	GCAAACCAAACATGTATCAAAA
scaffold422267_10.	1	p2	(TA)8	16	306	321	GAATCCATTTTGTGTTGGGC
scaffold422280_15.	1	p2	(TA)6	12	4265	4276	TCTGGACCTTTCGGTTCTTG
scaffold422353_15.	1	p2	(AT)9	18	241	258	AAGCAGGAGGTCCACAGTTG
scaffold422364_12.	1	p2	(AT)7	14	920	933	GTGCTCTCAAGGTTCTTGCC
scaffold422520_16.	1	p2	(TA)6	12	481	492	GCTGGTGCATCCTCTTCCTA
scaffold422748_15.	1	p2	(TA)9	18	491	508	TGCGTTGGATCAATTTGTGT
scaffold422789_17.	1	p2	(TG)8	16	663	678	ATCGCACGTGCTAGATCCTT
scaffold422798_14.	1	p2	(AT)7	14	1356	1369	TTGCAATCCGGATCAAAAGT
scaffold422812_16.	1	p2	(TG)6	12	1406	1417	TGCAACATGATTTTGTCGGT
scaffold423108_15.	1	p2	(AT)6	12	71	82	TGAGCAAAAGTAATAAGAGCGACA
scaffold423140_15.	1	p2	(AG)7	14	42	55	TTGTAATTATTGTAGGGAATAAAAGG
scaffold423167_10.	1	p2	(TG)6	12	177	188	ATCTCAGTGCGTGTGAGTGC
scaffold423191_17.	1	p2	(TA)6	12	503	514	TAGACGCCCCAGACTGTTTC
scaffold423248_13.	1	p2	(TA)9	18	44	61	AAGGGTTATCACCTGATTTTCTC
scaffold423264_12.	1	p2	(AC)7	14	447	460	CTCAACGGTATGCTCGGATT
scaffold423388_16.	1	p2	(CT)9	18	105	122	CACTCACTCTCACTAGCCGC
scaffold423463_14.	1	p2	(CT)8	16	341	356	ACGGCTATAGCAAGGGTCAA
scaffold423534_14.	1	p2	(GA)6	12	152	163	CACGATGGACGATTGAACAC
scaffold423746_15.	1	p2	(AT)6	12	764	775	TGGCTGTGAATCATTGTTCG
scaffold423864_15.	1	p2	(TA)7	14	224	237	AAATGCGCAATTTTAAACCC
scaffold424034_10.	1	p2	(TC)8	16	355	370	CGGCACCAATTTATTGTGAA
scaffold424097_15.	1	p2	(AG)8	16	120	135	GGTTGGTCCACAAGATTTACAG
scaffold424539_13.	1	p2	(CT)7	14	299	312	CATACCTCCCCTTACCATCG
scaffold424560_17.	1	p2	(AT)7	14	612	625	TCCGAAATTTAAGGAGTCGG
scaffold424609_11.	1	p2	(AC)6	12	234	245	AAGGAGATCATGGGATCGTG
scaffold424652_18.	1	p2	(TC)7	14	122	135	TCTCAGGTGACAATAGGGGG
scaffold424791_15.	1	p2	(CT)6	12	1294	1305	CTCATTTTGCACGTCTTCCA
scaffold424806_14.	1	p2	(TA)6	12	199	210	AGAAACGTTTTCCCTGAGCA
scaffold424825_17.	1	p2	(CT)6	12	846	857	AATGGTGGTGCACTTTTGGT
scaffold425061_10.	1	p2	(AT)9	18	146	163	CCGGGGTATGCTATAAACGA
scaffold425067_13.	1	p2	(TA)8	16	212	227	CCCTTCGCATCTTACTGCAT
scaffold425087_11.	1	p2	(TA)8	16	267	282	TTCTCACAAGCAAAGACCCA
scaffold425112_15.	1	p2	(TA)7	14	2022	2035	GAGCGTAATATCAAATTTTTGGG
scaffold425153_15.	1	p2	(TA)6	12	123	134	TCGAAAATCAAAGAGCCTCAA
scaffold425160_14.	1	p2	(AT)6	12	69	80	TTCTTAATTTGCATGTTCGTTATACA
scaffold425173_11.	1	p2	(TA)8	16	48	63	GGTGCAAGTGTCAATAGAAGAGTT
scaffold425283_13.	1	p2	(AG)7	14	48	61	AGAAACTTGACGTGTGCGTG
scaffold425316_13.	1	p2	(CT)11	22	667	688	TCTGAAGTCCAGCAACAGGA
scaffold425420_11.	1	p2	(GC)6	12	361	372	GTGGAGAGGCAAGAAACTGC
scaffold425461_15.	1	p2	(GA)7	14	111	124	CATTCTCAAGCCACTCCCTC
scaffold425615_17.	1	p2	(AC)6	12	307	318	TCCAGGTTTGCTGCTAGGTT
scaffold425741_13.	1	p2	(GA)6	12	68	79	TGGATACGAGATTCGGGAAG
scaffold425790_15.	1	p2	(CT)6	12	2595	2606	TTTTGGTAAAGTTTTGAGATTCCA
scaffold425805_15.	1	p2	(GA)9	18	892	909	GATCCACGGGTCTCTTGAAA
scaffold425813_10.	1	p2	(TC)7	14	412	425	TTCAACCTTTTCCTTGTCTCC
scaffold425837_19.	1	p2	(TA)8	16	72	87	ACCAATTTGATGAGGGACCA
scaffold425850_11.	1	p2	(GA)7	14	145	158	TGGTTGAAAATCATTGTGGG
scaffold425858_14.	1	p2	(AT)7	14	560	573	AAAGGGAATTTTGTCAACTGGA
scaffold425875_16.	1	p2	(CA)6	12	1829	1840	TGGAGCCTACCATGACCATT
scaffold425897_14.	1	p2	(CA)7	14	1181	1194	AACGCGAAGAACACAAGAGG
scaffold426067_16.	1	p2	(TA)6	12	382	393	ACACGTGCCTCGTTTGAAAT
scaffold426141_15.	1	p2	(AC)7	14	5809	5822	GAAAAAGGCAGAAATGCAGC
scaffold426235_18.	1	p2	(TG)6	12	824	835	GGCCAACATATGGGATTTTG

scaffold426255_20.	1	p2	(AT)8	16	510	525	CAGAAGCCTCCAACACCAAT
scaffold426258_11.	1	p2	(AT)6	12	56	67	CGACGTTGTCTTAACCTTGGA
scaffold426344_13.	1	p2	(AT)7	14	2172	2185	TAGTTAAACTCACGCACGGC
scaffold426406_15.	1	p2	(AT)6	12	407	418	TTTCCCTTCTTTTGGGAGGT
scaffold426448_15.	1	p2	(GA)6	12	189	200	GTTGGAGGAGAGCTGTAGCG
scaffold426483_11.	1	p2	(TA)10	20	46	65	CACCCAAAATGGGTTATTATTTG
scaffold426514_13.	1	p2	(TA)6	12	164	175	GCACGTTTTTGGCCTGATA
scaffold426515_18.	1	p2	(TA)9	18	112	129	GCGGGGTTGTTGAAGAATTA
scaffold426557_13.	1	p2	(CA)11	22	291	312	TTACTGTTGCATGGACTGGG
scaffold426572_14.	1	p2	(AT)11	22	72	93	GGTATTCGTGATCGTGATTCCT
scaffold426666_19.	1	p2	(AT)6	12	34	45	GGGTTCGTAACCTAGGAGCTG
scaffold426740_15.	1	p2	(CT)7	14	123	136	CAAGCGGAACAAACAAACAA
scaffold426812_14.	1	p2	(AT)6	12	206	217	TGCTCAGCATACATGAAGGG
scaffold426859_13.	1	p2	(TA)11	22	940	961	ATCAAGCCTGATATGTTTGACTC
scaffold426865_14.	1	p2	(TC)6	12	3005	3016	GGCTGTTCAGCAATATGCAA
scaffold426905_12.	1	p2	(TA)6	12	53	64	CGGATTTAAGGGTTATTACATGA
scaffold426947_13.	1	p2	(CT)6	12	293	304	CATTTTTCCACCTTGTGCCT
scaffold426952_15.	1	p2	(AT)8	16	255	270	GGAGGGCTGTGTGATTGATT
scaffold426959_15.	1	p2	(CA)6	12	59	70	ATCGTCGCCTCTAGCCACTA
scaffold427000_11.	1	p2	(AT)7	14	67	80	GGTTTTACGAACCACAATCCA
scaffold427267_14.	1	p2	(TA)8	16	121	136	TTTGCACCTGAGGAGGTGTT
scaffold427325_16.	1	p2	(TG)6	12	1077	1088	TCTTTGCAGCTTGCACATTC
scaffold427377_12.	1	p2	(TC)6	12	607	618	TTCTCCTATCTTCCCCAGCC
scaffold427419_15.	1	p2	(AT)7	14	389	402	AACTGGCATCCATACGAAGC
scaffold427532_13.	1	p2	(CT)9	18	895	912	AATCTCTCAATCGGCACACC
scaffold427668_14.	1	p2	(TA)8	16	151	166	AGGGTTTAAAATCGCGCATA
scaffold427679_16.	1	p2	(CT)6	12	517	528	TCCCATTGGTTATGGGAAGA
scaffold427836_14.	1	p2	(TA)8	16	627	642	ACACAGGAGTTTGCGGATTC
scaffold427838_10.	1	p2	(TA)9	18	143	160	ACACCCACAAATCAACCACA
scaffold427860_15.	1	p2	(AT)9	18	449	466	CAAACCAAGGTCGAGAGTTGA
scaffold427929_13.	1	p2	(AG)7	14	89	102	CTTCACGTGACTTGCTTCCA
scaffold427936_13.	1	p2	(CT)6	12	446	457	AGGTGATTTGGCATTAAGGG
scaffold427997_13.	1	p2	(TA)10	20	365	384	AAAGCAATTTCAACATAGGTCGT
scaffold428103_17.	1	p2	(CT)6	12	125	136	ACTCGCCCCTCAAGTTTCTT
scaffold428155_16.	1	p2	(AG)7	14	431	444	CTGTAGTCGTGGTGGGCTTT
scaffold428381_15.	1	p2	(TA)8	16	574	589	TTCACAAACCCAGATATCATAATCA
scaffold428453_13.	1	p2	(AT)9	18	1317	1334	CTTCTAAAGAACCCTCCCCG
scaffold428478_11.	1	p2	(AG)9	18	221	238	AAGCACCGGTACTCGACATC
scaffold428564_16.	1	p2	(AT)6	12	53	64	TGTGATGTTGTATTTTGGTACATGA
scaffold428615_16.	1	p2	(CT)6	12	200	211	ACAAACGGTAATTCCCCTCC
scaffold428663_17.	1	p2	(TC)6	12	72	83	GCAACGGAATACCACTCGTT
scaffold428783_10.	1	p2	(AT)11	22	291	312	TGCTATTGCATGCTAAGAAGTGA
scaffold428850_12.	1	p2	(TA)9	18	526	543	TGTGGAATGGGAGATAACAGAA
scaffold428853_11.	1	p2	(AG)6	12	73	84	GTGTTGGACGCATCAGGTAT
scaffold428904_12.	1	p2	(CT)6	12	486	497	ACAACAATCCGGAGGTGAAG
scaffold429019_12.	1	p2	(TA)6	12	205	216	ATCAAATCTTGGTGCGGAAC
scaffold429064_16.	1	p2	(GA)9	18	115	132	TTACCTTTCTCGATCGGGTG
scaffold429075_15.	1	p2	(TA)6	12	293	304	TCGCTTAATTGGTGATTGTGA
scaffold429223_15.	1	p2	(AT)8	16	299	314	ATTTTTCGGCGAGATTGCTA
scaffold429241_11.	1	p2	(TA)7	14	55	68	TCAATCAATTAGATTTTCGGCTC
scaffold429341_11.	1	p2	(AG)7	14	123	136	AACAGCAGGTGAGTTGGAGG
scaffold429349_17.	1	p2	(TA)6	12	1849	1860	TTTCACTGTTTCCACACATGC
scaffold429418_13.	1	p2	(CT)7	14	410	423	AGAGCCATGTCTCCTTCACG
scaffold429574_18.	1	p2	(CT)6	12	1150	1161	CTTTGAGTTGGATGGCTGGT
scaffold429637_10.	1	p2	(AC)6	12	169	180	TCTTTTCTCTCCCTCCCCTG
scaffold429645_14.	1	p2	(CT)6	12	877	888	GCTTCTATCGCGCTCTCTCT
scaffold429765_11.	1	p2	(TG)6	12	39	50	TGTTCTTCGTGTTCTATATTTCTCG
scaffold429849_15.	1	p2	(CT)8	16	10638	10653	TGAAATGTGTTGGCTGGGTA

scaffold429899_18.	1	p2	(TA)7	14	936	949	CATGTTCAGTTTTTGGGGCT
scaffold429909_14.	1	p2	(AT)7	14	72	85	TATCAAAACAACCCCCGGAC
scaffold429923_20.	1	p2	(TC)7	14	225	238	GAGGAGAATTCATGGGGTGA
scaffold430155_10.	1	p2	(CT)8	16	331	346	CAAGTCAAGCAAGGTGGACA
scaffold430183_11.	1	p2	(GA)6	12	53	64	GCGACAAGTCTGCGTGTTAT
scaffold430184_11.	1	p2	(TC)7	14	288	301	CACATTCTCCGGTTTTTCGT
scaffold430292_14.	1	p2	(TA)7	14	254	267	TAACATGGAGGACAGGGGTC
scaffold430432_16.	1	p2	(TC)7	14	556	569	TCTCAAGATGAGAACTCGGAGA
scaffold430448_16.	1	p2	(AC)6	12	587	598	CAATAAAGTGGGGCCAAAAC
scaffold430506_15.	1	p2	(GA)10	20	5349	5368	CCTCTGGTTGTTGGAATGGT
scaffold430547_16.	1	p2	(CT)6	12	536	547	CAAAGAAGGCAATCTATCCCA
scaffold430793_15.	1	p2	(TC)10	20	253	272	AATCCCAATTTCCCAACCTC
scaffold430851_13.	1	p2	(TA)6	12	2322	2333	ATGGACCCCACCTGTCATAA
scaffold430971_13.	1	p2	(CT)6	12	181	192	CTCACCCTTGTCATCACCCT
scaffold430995_10.	1	p2	(TA)6	12	349	360	CGCACTCACACACTCTGACA
scaffold431008_16.	1	p2	(AT)11	22	491	512	TGCACCGTTAACAAAAATGA
scaffold431020_14.	1	p2	(TA)7	14	741	754	ATTGCTAGGGTAGCCTCCTT
scaffold431075_14.	1	p2	(AC)6	12	1527	1538	AAACGCCATGCAAAAATACG
scaffold431142_14.	1	p2	(CT)6	12	120	131	AAGCTGCACGTGTTACACCTAA
scaffold431283_14.	1	p2	(TC)6	12	126	137	AAATAAAAGAGGAAGGCTGAGCTA
scaffold431315_14.	1	p2	(CA)6	12	2916	2927	TCTTTCCCACTTCCCACATC
scaffold431376_16.	1	p2	(CT)6	12	92	103	CAGTCACTCTCACTAGCCGC
scaffold431464_16.	1	p2	(TC)10	20	283	302	CTGAATGCTCGTTGTCTCCA
scaffold431640_14.	1	p2	(AT)6	12	628	639	CGCGCACACACTTACAAACT
scaffold431694_17.	1	p2	(CT)7	14	750	763	TCTTCTCCCTCTCTCCCTCC
scaffold431723_13.	1	p2	(CT)6	12	583	594	TGCCCACAAAGATTTCATCA
scaffold431801_15.	1	p2	(CT)6	12	52	63	GCATCTCTTGCTCTCTCGTTG
scaffold431913_16.	1	p2	(AT)6	12	126	137	AGGCATCCATCCTTTACTGC
scaffold432000_15.	1	p2	(AT)6	12	1369	1380	AAGGTAAACAAACAATCAAGGGA
scaffold432031_13.	1	p2	(TA)6	12	65	76	TCCACCGTTGTCTTTAAGTCG
scaffold432050_12.	1	p2	(GA)8	16	346	361	GAAAAACGACGTGAGGGAGA
scaffold432181_13.	1	p2	(CA)6	12	1152	1163	ATCGTTGGAAATATGCTGCC
scaffold432269_14.	1	p2	(CT)6	12	125	136	AGCATCTCTTGCTCTCTCATTG
scaffold432282_16.	1	p2	(AG)6	12	256	267	CCCTTTCTTCCCAAACAACA
scaffold432431_15.	1	p2	(TG)6	12	674	685	GCACCAAGACAATGCCCTAT
scaffold432486_13.	1	p2	(TC)6	12	114	125	CGTGTTTTACCGAAATGCGT
scaffold432512_15.	1	p2	(TA)6	12	73	84	CAATCCTTTGAGTATGGATTGATG
scaffold432518_16.	1	p2	(AT)8	16	1069	1084	CGATCCGTCGACTAAACCAT
scaffold432525_15.	1	p2	(AT)9	18	1201	1218	ATGCGAGAACGGAAAGAAAA
scaffold432570_11.	1	p2	(TA)12	24	399	422	CCTATGCCGCTTACCTTTTT
scaffold432878_15.	1	p2	(TA)8	16	606	621	CCAACTACTGATGGTCCAAGC
scaffold432885_11.	1	p2	(TC)6	12	347	358	CCCACTCCACCTTCTCCTAA
scaffold433106_15.	1	p2	(AG)7	14	1286	1299	TCTAACACGCGAATCTGACG
scaffold433413_12.	1	p2	(AT)6	12	98	109	TCGTGAATGGCATGACTGAT
scaffold433759_18.	1	p2	(TA)7	14	110	123	GAGGTACGGTGATATCATGCTTAGT
scaffold433773_16.	1	p2	(GA)8	16	1965	1980	ATGGGGAGTTCAATGTCGTC
scaffold433954_13.	1	p2	(TA)10	20	333	352	CCACGAAACATCAGCATACG
scaffold433958_17.	1	p2	(TA)8	16	250	265	CATATCTGACGGCCCAGATT
scaffold433975_11.	1	p2	(TA)8	16	533	548	TGGACGCCCAATATTGTTTC
scaffold434190_14.	1	p2	(AG)7	14	212	225	TGTAGAGGAAGTTGGGGGTG
scaffold434340_12.	1	p2	(AC)7	14	164	177	CGGTTAGTCCGTCCATCACT
scaffold434418_15.	1	p2	(AG)7	14	445	458	GGATCGCGTCGAATTAGTGT
scaffold434439_16.	1	p2	(GA)6	12	603	614	ATCAGCATCTTTACCGCCAC
scaffold434554_15.	1	p2	(GA)6	12	1177	1188	CTATGGCACTATGCCGGATT
scaffold434622_11.	1	p2	(TG)7	14	231	244	ACGCACACTTACGCATTCAG
scaffold434730_15.	1	p2	(GA)14	28	198	225	TGCAGCTGAATGAAAAATGTG
scaffold434785_10.	1	p2	(TA)9	18	284	301	AATCATCTCCTCACTAATTCCATC
scaffold434864_12.	1	p2	(TG)7	14	1316	1329	TACGTGTGTGCAGTTGCTGA

scaffold434867_13.	1	p2	(TA)9	18	120	137	GACCGCAGGATAATCCAGAA
scaffold434869_14.	1	p2	(TA)6	12	799	810	TTGGACTTTTCGAAGAGCAT
scaffold434870_12.	1	p2	(TA)6	12	260	271	CCCGATTTCCATGCTTAAAA
scaffold434873_13.	1	p2	(AT)6	12	561	572	GTCAAGGAAGGCATCCACAT
scaffold434908_14.	1	p2	(AT)6	12	2259	2270	TTAGCTCCAAGGGCCCTAAT
scaffold435013_10.	1	p2	(AT)7	14	226	239	CTTCTGTTGGGGCGAAATTA
scaffold435172_13.	1	p2	(TA)7	14	139	152	CCAATTGACTTCGTGGAGGT
scaffold435260_16.	1	p2	(TA)9	18	209	226	AGACCATGGTTCGGAGAGTG
scaffold435404_19.	1	p2	(AC)7	14	2069	2082	TCGCTGATCCCCAATATAGC
scaffold435427_11.	1	p2	(AT)12	24	410	433	TCACGTTATGGGGAGAATCC
scaffold435448_11.	1	p2	(AC)7	14	1226	1239	CAACGATGGTTGTTGAAACG
scaffold435474_13.	1	p2	(AT)9	18	48	65	TGCGTTTTGACAATATATAGGTGTTT
scaffold435490_13.	1	p2	(AT)8	16	301	316	TTCAGTGGAACATGGTTTGC
scaffold435531_12.	1	p2	(AT)7	14	346	359	GGTTGCCGCCTTCATTATTA
scaffold435561_14.	1	p2	(GA)9	18	487	504	GCATGCATCAACTGCAAATC
scaffold435569_10.	1	p2	(TA)7	14	104	117	CTTTAGGGCCCTTGATTTCC
scaffold435630_11.	1	p2	(TA)7	14	402	415	GTTGCTTCCATCGTCACCTT
scaffold435741_15.	1	p2	(TA)9	18	257	274	GCAGAATTTTGGCCTTTGAT
scaffold435941_15.	1	p2	(TC)6	12	449	460	TCTCGTCTCCCTTGTTTGCT
scaffold435951_12.	1	p2	(AT)8	16	73	88	GGGTGCTTGAAGATAAACATGA
scaffold436007_12.	1	p2	(CT)6	12	540	551	CTAAATTCGCATGGGAAGGA
scaffold436135_18.	1	p2	(TC)7	14	247	260	CGCGAAGAACACAAGAGGAT
scaffold436190_12.	1	p2	(CT)6	12	343	354	CGCGAACTCAAATACCCTTC
scaffold436372_10.	1	p2	(AG)6	12	307	318	GTAGCCGTCTATTCCGAACG
scaffold436384_18.	1	p2	(GA)6	12	832	843	TCCAAACAAGGCTCTATGGC
scaffold436389_14.	1	p2	(AG)7	14	582	595	ATTGTGTCACCGTCGTCTCA
scaffold436456_16.	1	p2	(CA)6	12	1746	1757	TTCATGCCCGTTTTATTTGA
scaffold436479_14.	1	p2	(AT)8	16	205	220	GGATATCCGATCCGGTTTTT
scaffold436550_15.	1	p2	(CT)7	14	49	62	TTGCTCTCATTGTAATCTCTCTCAA
scaffold436577_14.	1	p2	(CT)6	12	543	554	ATGCTTAGGTGGATTTCCCA
scaffold436602_14.	1	p2	(TA)6	12	163	174	CACCATAATTTGACACACACACA
scaffold436607_15.	1	p2	(TA)6	12	97	108	GCATATGATGTGCATATACGAAA
scaffold436609_11.	1	p2	(CT)8	16	363	378	GCTTATCCCTTCACCGTTCA
scaffold436611_14.	1	p2	(CT)6	12	377	388	CGAAATGTGAAGCGTTTGAA
scaffold436645_15.	1	p2	(TC)7	14	335	348	TTGAACTCACCACGTGAAGG
scaffold436675_15.	1	p2	(AT)8	16	2927	2942	GGACAAAGGGTTTGCGATAA
scaffold436740_13.	1	p2	(GA)7	14	328	341	CAGGGGTAAAGTAGTCATTGTCG
scaffold436750_13.	1	p2	(GA)9	18	391	408	AGCGTACATGGAATCCCAAC
scaffold436786_10.	1	p2	(AT)10	20	227	246	TCTGTCACGTCATTGTGTCG
scaffold436888_10.	1	p2	(GA)9	18	71	88	GGTGGTGCGAGAGTGATTGT
scaffold436936_12.	1	p2	(TC)6	12	99	110	CACTAGCCGCAGCTCTCTCT
scaffold437346_13.	1	p2	(GA)6	12	174	185	GAGAAATTGGCAATCGGAAA
scaffold437365_11.	1	p2	(TA)12	24	48	71	CACGTTATATTTATAGTTTTGTGGGG
scaffold437427_17.	1	p2	(TA)6	12	105	116	CGGTTGTATGAAACCGTTAGTTG
scaffold437595_13.	1	p2	(AT)6	12	55	66	TCGGAGCTAAAACGGAGAAA
scaffold437597_16.	1	p2	(AG)6	12	223	234	CTGCTCGAGAGATGCAAGAG
scaffold437761_14.	1	p2	(AG)6	12	127	138	CCTTCCAACAGAACAAACTCG
scaffold438096_10.	1	p2	(AT)8	16	332	347	ATGCGCGTTTTTAGGGTTTA
scaffold438109_15.	1	p2	(GT)7	14	1951	1964	TGCTCTTTGACCAGCTGTTTT
scaffold438126_14.	1	p2	(TC)7	14	124	137	TCTTACTTGCCTTGACCCTGA
scaffold438230_11.	1	p2	(AT)6	12	216	227	AAGGGGGTTATCATGAGATCAA
scaffold438314_12.	1	p2	(AT)8	16	54	69	AACGGTAGCCATCACAATTTTT
scaffold438372_10.	1	p2	(AT)13	26	137	162	ACGACTGTCGATCCACACAA
scaffold438470_18.	1	p2	(TG)6	12	2418	2429	TCGAAACAGATCAAAACTGCC
scaffold438640_13.	1	p2	(TA)7	14	160	173	AGTCCCAACTTGCTCATTTCA
scaffold438733_15.	1	p2	(CT)12	24	1832	1855	TTCGATCTTCATCGCCTCTT
scaffold438849_12.	1	p2	(TG)8	16	49	64	AAACTCTGAAAGTTGTCGAGCAG
scaffold438850_14.	1	p2	(AG)6	12	155	166	AGCGAGTTTCGAAATGGAGA

scaffold438895_12.	1	p2	(TA)8	16	210	225	TGATAGCGTCATTGTTTGGC
scaffold439017_15.	1	p2	(TC)6	12	1913	1924	GTTTCTTCTGCCAGCACCTC
scaffold439280_17.	1	p2	(TG)6	12	2461	2472	TGTTTACGGCTGCAAATTCA
scaffold439316_10.	1	p2	(GA)6	12	36	47	CGTGGTTCGATCGTAATTGA
scaffold439522_17.	1	p2	(TA)9	18	441	458	TAAAACCATGCACGTAGGCA
scaffold439577_14.	1	p2	(TA)10	20	453	472	TGCATCTTTGTACTCAGCCCT
scaffold439758_11.	1	p2	(AT)8	16	276	291	GCCGAGTGTCACCCATATCT
scaffold439771_15.	1	p2	(AT)9	18	120	137	TTAAAGCTCGGTTCAATTTCA
scaffold439773_17.	1	p2	(AT)7	14	124	137	ATTGTTTGTGTGGCCCAGAT
scaffold439903_16.	1	p2	(TA)8	16	74	89	TTGATCCAAGGGTGTATAATGG
scaffold440161_10.	1	p2	(TA)9	18	596	613	TCATGACTCCATCCTTCACTTC
scaffold440214_13.	1	p2	(TA)7	14	74	87	GTTGACAACTTGACATCAAATACAT
scaffold440217_13.	1	p2	(TC)6	12	112	123	TGACACGTTGGACCTGAAAG
scaffold440247_10.	1	p2	(AT)9	18	572	589	TGTAGTCAATGCTTTTGAGATTATG
scaffold440356_16.	1	p2	(TA)6	12	543	554	CGGATTTAATCGTGGCTGTT
scaffold440453_14.	1	p2	(AT)6	12	719	730	TTCAACCCGAACAACAATGA
scaffold440521_17.	1	p2	(TC)6	12	127	138	TCTTTCAATTTTCAGCCCTCA
scaffold440572_15.	1	p2	(CT)8	16	3210	3225	TGCTTGCATTTGAAGTAGCG
scaffold440690_11.	1	p2	(GA)6	12	262	273	TGGTGTTCTTGGTGTTTTGG
scaffold440894_15.	1	p2	(TA)7	14	260	273	TCACCTTATCAACGATCCGA
scaffold440943_15.	1	p2	(AT)6	12	156	167	TGGAAATTTTCGGGGAATAA
scaffold440980_15.	1	p2	(GA)8	16	480	495	GTGCCTATTGCCGACGTAGT
scaffold441052_18.	1	p2	(GA)6	12	195	206	CGCTGTAGATCCAACAAGCA
scaffold441171_13.	1	p2	(TA)8	16	340	355	TTCGATTCGACGCTTTTTG
scaffold441178_10.	1	p2	(AG)7	14	77	90	CGCCCCATGGAGAAGTTTAT
scaffold441226_15.	1	p2	(TC)6	12	740	751	CGTGTCATAGGAAAACGAGC
scaffold441269_15.	1	p2	(AG)7	14	1965	1978	CAGCATGGCCATTACAACAG
scaffold441278_16.	1	p2	(TA)10	20	531	550	ATAATCGTGGTGATAGGCGG
scaffold441329_20.	1	p2	(CT)6	12	1044	1055	AAACGAGAAGAAAGCAGCCA
scaffold441540_14.	1	p2	(TA)8	16	484	499	ATACAAAGTCCCACGACCGA
scaffold441568_14.	1	p2	(CT)6	12	342	353	ACTTGCTTGACTTGCAACGA
scaffold441570_16.	1	p2	(CA)8	16	429	444	ATCAACGCTTTGGATGTGCT
scaffold441612_10.	1	p2	(CT)6	12	362	373	CGCCGAGTTGGTTCTCTCTA
scaffold441635_15.	1	p2	(TC)7	14	3918	3931	CCAAGCTTGCCTCTTCATCT
scaffold441796_11.	1	p2	(AT)9	18	737	754	TTCAGGATAAATATCAGTTTCATGG
scaffold441928_14.	1	p2	(AT)6	12	127	138	TGCAATCACACAATAACAAGCA
scaffold441941_10.	1	p2	(AT)9	18	345	362	CAACGCTAATATCAACCGCA
scaffold441967_15.	1	p2	(AT)6	12	71	82	ATCCGGAGTAAGTTCGAGGA
scaffold441970_14.	1	p2	(GA)6	12	341	352	TTCCAAACCTTTGTTCCGAG
scaffold441990_12.	1	p2	(GA)6	12	605	616	CGATCCTTGAGTAAAAGCCG
scaffold441993_17.	1	p2	(AT)7	14	2201	2214	CCGAAACCGTGTTCTTCAGT
scaffold442403_13.	1	p2	(GC)6	12	432	443	CAACGGCTCTTTTCTCCAAC
scaffold442518_15.	1	p2	(GA)7	14	411	424	GCATTGTTTTTGTCGGCTTT
scaffold442531_14.	1	p2	(AT)6	12	503	514	CTGGGGGTTAGGTTGGTTTT
scaffold442532_10.	1	p2	(TC)6	12	128	139	AGAGTTGGGCTAGGTGGGAT
scaffold442534_16.	1	p2	(TC)6	12	1316	1327	CCTTTCTTGAGTTTCAACCCC
scaffold442614_18.	1	p2	(CT)6	12	1502	1513	ATTCACAAGCGGCACTTCTT
scaffold442704_17.	1	p2	(AG)9	18	2441	2458	CTGAGGCAGTTTTCAGAGCC
scaffold442736_14.	1	p2	(CT)8	16	351	366	TGGCATAGTTTGGTTGTGGA
scaffold442746_16.	1	p2	(TC)6	12	1371	1382	TGGCCGAAGTAATTGAAAAA
scaffold442753_14.	1	p2	(GT)9	18	565	582	ACATACCACCGATTTTTCCG
scaffold442792_12.	1	p2	(AC)6	12	1279	1290	TGCAAGGAAGAAAAACAAACAA
scaffold442903_13.	1	p2	(CT)7	14	449	462	ATGGGACGGAGGGAGTATTT
scaffold443037_15.	1	p2	(AG)8	16	73	88	TCCCATGTTGTAATTAATGTAAGGAA
scaffold443178_16.	1	p2	(TC)7	14	71	84	TGAGAATGGCCGAGAGTTTT
scaffold443386_16.	1	p2	(CA)6	12	4710	4721	TGCAAACATCAGCCATTTTC
scaffold443489_16.	1	p2	(GA)7	14	4672	4685	TGGGAAGAGGAAATGGACAG
scaffold443506_14.	1	p2	(AG)7	14	73	86	GAATCAGGGGAGGGAGAGAG

scaffold443552_15.	1	p2	(AT)9	18	2185	2202	TTCATACACACCCTTGCAGC
scaffold443560_12.	1	p2	(TA)7	14	415	428	TCTCCAGGAGTCGTGCTTGT
scaffold443562_16.	1	p2	(AT)6	12	45	56	TTTGGTCCCTCAACAAATAATAAA
scaffold443611_12.	1	p2	(AT)9	18	379	396	TTCCTGTGCTTTCAATTTGG
scaffold443731_12.	1	p2	(TA)12	24	1033	1056	AGTCCCTGATTCTTCCCTCG
scaffold443754_12.	1	p2	(AG)12	24	52	75	GCTTCAGCCATCGAGTTTTC
scaffold443838_13.	1	p2	(AG)6	12	53	64	AGCTTCCGAACTTATGGGCT
scaffold443929_16.	1	p2	(CT)6	12	1591	1602	CGAAAAATGGTGGGAAAGAA
scaffold443950_11.	1	p2	(CA)6	12	226	237	AGTTTCATTTCCGGCTTCCT
scaffold444027_11.	1	p2	(TA)10	20	158	177	TGTAGTCCGCTTTGCTGATG
scaffold444098_16.	1	p2	(CT)11	22	442	463	AGCATAATAACCACGCAGCC
scaffold444228_12.	1	p2	(TA)6	12	868	879	ACGAACACTCACGCACTCAC
scaffold444229_14.	1	p2	(AC)6	12	9157	9168	TGGTGACCAGATCAGGGAAT
scaffold444285_19.	1	p2	(CT)6	12	85	96	CGAGGAACTTGGGACGATT
scaffold444499_15.	1	p2	(TA)6	12	5587	5598	CTCCTGCCTCGTAGCAGTTC
scaffold444506_13.	1	p2	(AT)8	16	226	241	GACAACAGAAAAACCACGCA
scaffold444525_16.	1	p2	(CT)7	14	777	790	TGGCAGGTTGGAGACACATA
scaffold444563_15.	1	p2	(TA)7	14	1269	1282	TGCCTGCCCCTACTAGAAAA
scaffold444568_15.	1	p2	(AG)6	12	54	65	TGTGCACTGTTTCTCTCTCTCA
scaffold444683_15.	1	p2	(AT)10	20	4189	4208	GTCGGTGGCTGAAAGAAAAC
scaffold444818_16.	1	p2	(GA)6	12	128	139	TGATTCAGATGTCAGCGAGC
scaffold444820_16.	1	p2	(CA)6	12	57	68	TTTGATGTCCAAAGTGGCTG
scaffold444989_10.	1	p2	(AT)7	14	84	97	AGTCGATTGTGTAGTTGTGGG
scaffold445019_13.	1	p2	(TA)6	12	713	724	TGGTTCTAAATTCATGTTTCTTGG
scaffold445118_14.	1	p2	(CT)8	16	1344	1359	TGTGAGAGGTGTGAAGCAGG
scaffold445135_16.	1	p2	(CT)6	12	260	271	CTCTCTTGCCTTCCTCCTCC
scaffold445177_12.	1	p2	(TC)6	12	590	601	ACCCTCATCCCTCAATTTCC
scaffold445375_16.	1	p2	(TG)7	14	2343	2356	AAGAAACGGAGGGTGTTGTG
scaffold445519_14.	1	p2	(CT)6	12	873	884	TCTCTTTGCAAAACCCTCGT
scaffold445535_13.	1	p2	(TA)10	20	45	64	TCACGTTAAAGGAGGGTATCA
scaffold445544_14.	1	p2	(TG)6	12	1289	1300	AATTTCACTCTAGCGGGGCT
scaffold445546_11.	1	p2	(TA)10	20	407	426	GGCGCAGCATATATACACGA
scaffold445673_16.	1	p2	(CT)6	12	220	231	AATTGCCATCCCTCACACTC
scaffold445695_12.	1	p2	(TA)9	18	1985	2002	TCGATCGGCCTATTTTTCTG
scaffold445706_16.	1	p2	(AT)6	12	439	450	TCGACTCCATAGTAGCCGAGT
scaffold445707_16.	1	p2	(CT)7	14	479	492	TTCCATCCTTTCTTCCATGC
scaffold445864_13.	1	p2	(AT)6	12	384	395	ATTTTGGTCGAAACCGAATG
scaffold445930_15.	1	p2	(AG)9	18	521	538	CCCCTGTCCTCGACAGAAT
scaffold446002_16.	1	p2	(TA)7	14	1054	1067	TTGGCAGGTTGATCATAAATTG
scaffold446039_16.	1	p2	(AT)8	16	7721	7736	TGATTCTAGGATATCGCGGC
scaffold446141_14.	1	p2	(AT)7	14	323	336	GCTGATCTTGGTCAGGCTCT
scaffold446386_15.	1	p2	(AT)9	18	54	71	CCCTTTTATGCTCACATCTCTTTT
scaffold446522_14.	1	p2	(TG)7	14	770	783	TTACGTGCCTGGCTTAGGTT
scaffold446803_18.	1	p2	(AG)9	18	1155	1172	TTATTGCGTCACCTCATCCA
scaffold446921_14.	1	p2	(AT)6	12	129	140	ATTTTAACATTGTTGGCGGC
scaffold446922_14.	1	p2	(TA)9	18	1509	1526	AAACCGTGTTTTTACTGGCG
scaffold446976_17.	1	p2	(CT)6	12	1075	1086	GGAAATGGCGTGAACTGTTT
scaffold447069_15.	1	p2	(GA)6	12	122	133	CGATTTGCAAGTCTATGGCA
scaffold447084_13.	1	p2	(TA)7	14	51	64	CATTGGTTAGCACTTGAATGAGA
scaffold447203_11.	1	p2	(AT)6	12	143	154	TGCACCATAACAATATTCGACA
scaffold447313_15.	1	p2	(CT)9	18	1421	1438	CGAAACGAGTTGCTGCTGTA
scaffold447412_14.	1	p2	(AG)7	14	1253	1266	AACACACAGCCGCTACTCCT
scaffold447449_12.	1	p2	(CG)7	14	48	61	ATAGTGGTATGGTGTGGGGG
scaffold447606_14.	1	p2	(TC)8	16	790	805	GCCCTCCTTGATACCACAAA
scaffold447776_13.	1	p2	(GA)8	16	444	459	AAAGGACCCGACCTTTTCAT
scaffold447938_15.	1	p2	(CT)6	12	789	800	TCCTTGATGAACTGTGGGTG
scaffold448015_12.	1	p2	(TA)9	18	587	604	ACGACGTGCATCATTTCTCA
scaffold448164_17.	1	p2	(CA)7	14	1073	1086	CATTTCAGGCCAAATCCTGT

scaffold448181_12.	1	p2	(CT)6	12	558	569	CCTTCTTCTTGGCGTCAACT
scaffold448215_16.	1	p2	(AT)6	12	136	147	TCTACGGAGGACGAGCTGTT
scaffold448332_16.	1	p2	(GA)6	12	353	364	CTCGACTCAGGGACCTTCAC
scaffold448399_14.	1	p2	(AT)9	18	1370	1387	GCGCCACATCTTGTTGAATA
scaffold448405_10.	1	p2	(AT)6	12	148	159	TGTGATCAGGTGCTGTGTGA
scaffold448413_13.	1	p2	(TA)6	12	657	668	TTCTCAGCATATGGGAAGGG
scaffold448444_10.	1	p2	(GT)7	14	409	422	ATGCATGTGTGCAGGTGTTT
scaffold448513_17.	1	p2	(CT)9	18	545	562	TCGTTGACCGTATGGGATTT
scaffold448672_13.	1	p2	(CT)10	20	220	239	CAAACAAAGTCTGCAACCCC
scaffold448718_11.	1	p2	(AT)10	20	732	751	TGTTTTGCGAGCTTTTATTGG
scaffold448783_10.	1	p2	(TA)8	16	48	63	CGGATTTAAGGGTTATTACCTGAT
scaffold448805_17.	1	p2	(AT)6	12	1114	1125	CCTGCCCTCCAAGATCATAA
scaffold448840_10.	1	p2	(TA)7	14	51	64	ATTTCTCACGCTGAAATGCC
scaffold449111_14.	1	p2	(CT)6	12	54	65	CAATGGCCAAGAACGTAACT
scaffold449133_13.	1	p2	(AG)7	14	1268	1281	TTTCCTTTTGCAGCTGGAGT
scaffold449178_14.	1	p2	(TA)13	26	39	64	CCAATTTGAATGGTTATCACCTG
scaffold449266_18.	1	p2	(AG)8	16	348	363	GCACAATCAAACCTTGCCTT
scaffold449471_10.	1	p2	(TA)6	12	76	87	AACAATTGCACCTTTAATAGCAA
scaffold449525_10.	1	p2	(CT)6	12	60	71	AATGTCTCTTCCTCCTCGCA
scaffold449528_15.	1	p2	(CT)6	12	284	295	GCACCGGAGTATAACCCAGA
scaffold449560_13.	1	p2	(AG)6	12	2777	2788	GCTTTTATCAATGCCCTCCA
scaffold449704_11.	1	p2	(TG)9	18	47	64	GTTATCACCGGATCGCAAC
scaffold449710_15.	1	p2	(TA)7	14	942	955	TGTTTATTTGAAGGGGCAGG
scaffold449770_14.	1	p2	(AT)7	14	6969	6982	TGGCGGCATTCTATATGACA
scaffold449968_14.	1	p2	(TA)7	14	3281	3294	TTGATGTTTTCCCCATTTTTG
scaffold450103_19.	1	p2	(AG)9	18	414	431	CCCATCTTCTGCAAAAATCC
scaffold450162_14.	1	p2	(CA)6	12	1085	1096	TATTTTTGGGTTTGGGGTCA
scaffold450194_16.	1	p2	(GA)6	12	1190	1201	GCACCCTTTTGGTGGTAGAA
scaffold450199_14.	1	p2	(TA)8	16	178	193	TGTGTCATTCCTTCCACTGC
scaffold450227_14.	1	p2	(AT)13	26	555	580	TCATTTAATATGGTCTGTGCGAA
scaffold450238_10.	1	p2	(TA)8	16	209	224	TTAGGGTTTAAAATCGCGCA
scaffold450239_15.	1	p2	(AG)7	14	1417	1430	TGGGTTAGCCCAAAAATGAG
scaffold450311_15.	1	p2	(TA)6	12	153	164	TTGTATTAGATTGTGGCTCCG
scaffold450336_10.	1	p2	(CT)7	14	55	68	CACTCACTCTCACTAGCCGC
scaffold450354_14.	1	p2	(TG)6	12	1014	1025	AAGCAATGGTGGTCTTCTCG
scaffold450522_14.	1	p2	(CT)7	14	154	167	CACCATCGTTCCTCACACAC
scaffold450655_14.	1	p2	(AT)9	18	521	538	TCTGCCTGTCGATCTCACAC
scaffold450701_14.	1	p2	(AT)8	16	528	543	GCATTGGTAAAACCGGGATA
scaffold450732_16.	1	p2	(TG)7	14	65	78	TGGTTATTACCTGAATACTCCCA
scaffold450777_10.	1	p2	(AG)6	12	130	141	TGGTCGTCCAAATCTCCTTC
scaffold450909_12.	1	p2	(AT)8	16	257	272	GGATATAACCACCTCACCCAAA
scaffold450970_10.	1	p2	(TC)6	12	295	306	ATCGTAGTTGATGCCCTTCG
scaffold451112_15.	1	p2	(TG)7	14	127	140	TGTTGTCGATCTGGCACTCT
scaffold451162_11.	1	p2	(AT)8	16	50	65	ACCCAGATCGCACTCGAATA
scaffold451184_11.	1	p2	(AT)8	16	161	176	AGTCATTCGGGCCACATAAT
scaffold451291_10.	1	p2	(CT)6	12	331	342	TGAGCACGTACAGATAAAAGGG
scaffold451480_13.	1	p2	(CT)6	12	994	1005	CGACACCACTCCACCTTTTT
scaffold451526_12.	1	p2	(TA)9	18	123	140	GTGGCAGCATATCAACCCTT
scaffold451527_11.	1	p2	(AT)8	16	126	141	CGTGGCAGGCTAATATCCAT
scaffold451531_12.	1	p2	(TA)10	20	48	67	ATTGTTCGATGTCAGCTTCG
scaffold451545_11.	1	p2	(CT)7	14	1271	1284	ATCGACATTCTTCTGCAGGC
scaffold451554_16.	1	p2	(AG)8	16	126	141	CTCATTATTTCTCACTCACCAAGA
scaffold451758_11.	1	p2	(GT)6	12	116	127	TTCTGCTCTCTCTCGGTGGT
scaffold451814_14.	1	p2	(TA)9	18	1035	1052	ACTTAGGACCAAAGCCCGAT
scaffold451830_14.	1	p2	(AG)6	12	859	870	TGGATTTTAGGGCTCATGCT
scaffold451861_14.	1	p2	(TC)13	26	3204	3229	CCAGTAAAGGACCATTCGGA
scaffold451894_13.	1	p2	(TA)9	18	1493	1510	CAGTTTCACCAAGTCACCCA
scaffold451914_11.	1	p2	(TA)8	16	79	94	AAAATCAAAGGCCCACAATG

scaffold451938_13.8	1	p2	(CT)7	14	279	292	CCGTGTCCAGTCTGTGTTTG
scaffold451963_17.0	1	p2	(TG)6	12	476	487	AATTACACAATCCTCGTGGGA
scaffold451998_15.0	1	p2	(AT)11	22	1265	1286	GCCTAATGTCATTGCCTGCT
scaffold452414_11.9	1	p2	(TC)6	12	556	567	GGACCCACATGGAAGAGAGA
scaffold452548_17.2	1	p2	(GA)7	14	153	166	CTCCCTCCGTCCCATAAAAT
scaffold452601_11.5	1	p2	(AT)6	12	179	190	ATTGTTGGGTATTGTTGGCG
scaffold452701_12.2	1	p2	(TA)6	12	998	1009	GGGGAAGAGAAGAGTGAGGC
scaffold452897_19.5	1	p2	(AT)6	12	57	68	CGGATTTATTGGTTATTACATGATT
scaffold452900_14.9	1	p2	(AG)6	12	82	93	CTTCGGAACTCTATCCGCC
scaffold452909_15.2	1	p2	(TC)7	14	128	141	GCAGATCCAGATGCTCCAAT
scaffold452911_12.4	1	p2	(AG)7	14	267	280	GCAACGTGCCAAACTTCATA
scaffold452914_15.4	1	p2	(CT)6	12	1350	1361	TCTTGCCTTCGTTCCAAGTT
scaffold452934_10.7	1	p2	(TA)6	12	51	62	ATCCTAAGTTCGCCCCTGAT
scaffold452953_14.9	1	p2	(TA)9	18	108	125	CGAAATTGAATGGCAAGGAT
scaffold453079_14.3	1	p2	(AT)6	12	600	611	GCAGGTTAACTCTAATTAATCCGTACA
scaffold453153_14.5	1	p2	(TA)6	12	999	1010	CTTCCCCCACATTCAAAAGA
scaffold453157_16.6	1	p2	(GA)6	12	1128	1139	TGAAGAGAAATGGCAATGGA
scaffold453247_11.2	1	p2	(TA)6	12	461	472	CCCCGGTTTCATTTATAGCA
scaffold453268_15.3	1	p2	(CA)6	12	122	133	CCGGTGAACTTCTCCAACTC
scaffold453311_14.3	1	p2	(TA)6	12	524	535	ATGAGTTATCACCGGATCGC
scaffold453467_11.4	1	p2	(AG)8	16	75	90	CCCATGTTGTAATTAATGTAGGGA
scaffold453518_13.7	1	p2	(TA)7	14	173	186	CCGTGCATCCTATCCTGTTT
scaffold453528_13.0	1	p2	(AT)9	18	261	278	TCAATCGCAACCATCAATTT
scaffold453594_16.0	1	p2	(TA)7	14	304	317	GGCCGATATTTGCTCGTAGT
scaffold453666_12.7	1	p2	(AG)6	12	261	272	AATGGTGAGAGTGGAATGGG
scaffold453672_12.7	1	p2	(TA)8	16	220	235	AAGATCTACCTTTGGGTAACCG
scaffold453704_14.5	1	p2	(AT)7	14	276	289	TTTTCCCGCAATAACCACTC
scaffold453751_14.0	1	p2	(TC)6	12	273	284	ACAGAACAAGCATACGCACG
scaffold453822_15.6	1	p2	(TC)9	18	2818	2835	TCGTGCACTGGTGTTCTCTC
scaffold453921_15.4	1	p2	(TA)8	16	288	303	GTGACCCTTTGTGGGAAGAA
scaffold453926_15.3	1	p2	(TA)6	12	281	292	GGACTGGTTTGACACCTTTGA
scaffold453957_10.5	1	p2	(AT)6	12	275	286	CCCATTACTCCAAACCCAAA
scaffold454024_13.8	1	p2	(GA)6	12	2383	2394	ACGATCCATGAAAGCAAACA
scaffold454039_15.4	1	p2	(AT)6	12	77	88	TGCTCAAACTTGAACTTGAATAAA
scaffold454052_12.0	1	p2	(GT)8	16	256	271	ATGCCTTGGTCTTCCTCATC
scaffold454063_15.0	1	p2	(TC)6	12	170	181	TGATGAATGAAAGATGAAATGGA
scaffold454095_12.0	1	p2	(AT)7	14	383	396	TCTTTCACCCGCTTTAGGTG
scaffold454144_10.7	1	p2	(AT)9	18	257	274	GGAGAAGAGGGAGGATCGAG
scaffold454300_11.2	1	p2	(AT)8	16	169	184	ACCGATTGCTGAGCATTTCT
scaffold454347_15.2	1	p2	(TC)8	16	492	507	TGGAAAACCAAAGCAAAACA
scaffold454399_14.4	1	p2	(CT)8	16	354	369	CCAATGAAGCTCGTCAGGTT
scaffold454403_11.2	1	p2	(TA)7	14	491	504	CGAGCTGGCTTGAGCTACTT
scaffold454421_18.0	1	p2	(CT)6	12	502	513	AATACACCCCTGTCGCACTC
scaffold454491_12.9	1	p2	(AT)6	12	353	364	TAATGGGTGTTTGTGCGAAG
scaffold454620_15.8	1	p2	(GA)6	12	369	380	ACCGTTGCAGTAAACCTTGG
scaffold454627_14.7	1	p2	(AT)7	14	4420	4433	TGGGGTAAATATTTTGGGAGG
scaffold454637_16.8	1	p2	(TA)8	16	2708	2723	GCGGGACAACTACCAACAGT
scaffold454692_17.0	1	p2	(GA)8	16	2446	2461	GCTTCCCCCTAGTGAACACA
scaffold454816_18.6	1	p2	(TA)6	12	130	141	GGGCAATGTCTTATGGCCT
scaffold454869_10.8	1	p2	(TA)9	18	577	594	TTAGGGTTTAAAATCGCGCA
scaffold454955_14.5	1	p2	(TA)6	12	815	826	CCTCAATGGTATGCTCGGAT
scaffold455058_16.4	1	p2	(TC)6	12	33	44	GCAACGGAATACCCCTCTTT
scaffold455230_19.8	1	p2	(GA)8	16	1554	1569	GGTGCTCCATGTTTGTGAGA
scaffold455253_17.8	1	p2	(AT)6	12	418	429	GCTCAAAAGGTGATGGGTGT
scaffold455261_18.1	1	p2	(AT)8	16	332	347	CCAAAATTCAGTAAGGGTAACAAAA
scaffold455299_12.8	1	p2	(TA)8	16	68	83	TTATCACTTGATCATCCCCC
scaffold455343_10.9	1	p2	(AG)8	16	86	101	GAAGTTCGGCCATTCTTACG
scaffold455446_13.7	1	p2	(AT)6	12	775	786	TTGGTGGATTTTTGGAATGTC

scaffold455593_15.3	1	p2	(AT)7	14	427	440	CTGCAACCATAGCTCGATCA
scaffold455606_16.2	1	p2	(GA)6	12	165	176	TTGGGCTTTGATTCTTGCTT
scaffold455616_14.9	1	p2	(TC)6	12	52	63	CAGAAATTGCCTTGGTTGTTC
scaffold455678_15.0	1	p2	(AG)6	12	247	258	GCCGAGGTCACACCATACTT
scaffold455917_16.4	1	p2	(AG)7	14	129	142	CCTCGGATAAATTATGGGAAAA
scaffold455958_13.4	1	p2	(AG)7	14	78	91	TGTGCAAGGTTGAACCAAGA
scaffold455975_18.4	1	p2	(TA)6	12	130	141	TCTTGCCATTGATTTTGGTG
scaffold455976_15.4	1	p2	(AT)9	18	125	142	CGTTTTTGTGAATGTTGCCA
scaffold455977_14.3	1	p2	(GA)9	18	687	704	AAGGTGTAGATCTGGCGGTG
scaffold456219_13.9	1	p2	(GA)6	12	130	141	TTTGAGAATGGGGAGGTGAG
scaffold456238_14.9	1	p2	(TA)10	20	703	722	AACAGTTTCAATTCGCCACC
scaffold456257_10.1	1	p2	(TA)8	16	421	436	CACTCAAGGGGCATTTTTGT
scaffold456278_16.2	1	p2	(TC)8	16	347	362	GAGTTCGTCAAACCTCCCAA
scaffold456322_11.1	1	p2	(TA)8	16	52	67	TTTGTTCCTACTCACTCACATTAAGA
scaffold456326_10.1	1	p2	(GA)6	12	53	64	GAGGAGAGTTGATGGTGAGGA
scaffold456540_11.1	1	p2	(TA)11	22	225	246	GCAGGGGTTGCACAATATG
scaffold456619_11.4	1	p2	(TA)6	12	212	223	TTAGGTTGGACCAAAAAGCC
scaffold456821_18.0	1	p2	(CT)6	12	535	546	TACTCCGTGGTGTTCCCAGT
scaffold456822_19.7	1	p2	(AT)6	12	529	540	ACAATGGAGGCTGGAGGAG
scaffold456897_12.0	1	p2	(AG)6	12	130	141	TGAGAAATGCTCCAAAGCCT
scaffold456906_14.5	1	p2	(AT)8	16	370	385	CTTATTTGCATTTGGGCCAC
scaffold456934_10.3	1	p2	(TA)6	12	158	169	ACCGGATACCGAAGGGATAG
scaffold457006_16.5	1	p2	(TC)6	12	389	400	GTTGTCACGGCGTGTGATAG
scaffold457007_17.7	1	p2	(TA)6	12	490	501	TTGACCAAATTAGCCCCAAC
scaffold457127_13.2	1	p2	(AG)11	22	234	255	TTGAGTGGTTTGGTTGGAGA
scaffold457186_12.8	1	p2	(TA)9	18	76	93	TTCCTCAATTTTCGAATTCTCC
scaffold457194_17.1	1	p2	(TA)6	12	578	589	TGTGCCATTGATTTCTGAGG
scaffold457267_15.6	1	p2	(GA)6	12	2005	2016	AGGGAGAATCTATGGCAGCA
scaffold457577_20.2	1	p2	(AG)6	12	131	142	GAATGCTTAATGGGAAGCCA
scaffold457579_15.6	1	p2	(CT)8	16	256	271	TCAAGTTGAGCCTCCAAATCT
scaffold457838_19.3	1	p2	(TA)7	14	209	222	TATGGGAAGGACATTTTCGG
scaffold458004_10.4	1	p2	(AT)6	12	264	275	TCCCTTTATGATCATTCGGC
scaffold458129_11.8	1	p2	(TA)6	12	366	377	AATGTGATGTGGGTTGGGTT
scaffold458162_18.3	1	p2	(CT)8	16	323	338	GGAGGTGCAATGCGATATTT
scaffold458203_17.5	1	p2	(TC)6	12	2693	2704	CAAGCAAGCATTTCCTCCTC
scaffold458350_18.3	1	p2	(AG)6	12	524	535	TCACCTTTCTTCATGGCTCC
scaffold458514_12.4	1	p2	(TC)7	14	332	345	CGTTGTGCTTCTTTTCTCCC
scaffold458561_13.9	1	p2	(TC)7	14	460	473	TGGTTTAAACAAATCGTGTTCG
scaffold458611_17.8	1	p2	(GA)6	12	2835	2846	AAGAGGCTACGGTGAGGTGA
scaffold458616_13.8	1	p2	(AT)7	14	283	296	AGGTTGCTCTAAGGTGCCAA
scaffold458646_13.9	1	p2	(TA)8	16	48	63	TGGTTATTACTGGAACGCGA
scaffold458647_12.1	1	p2	(AT)11	22	47	68	GGGGTTATCACTGGATCACG
scaffold458667_15.4	1	p2	(CT)6	12	2297	2308	AAACAATCCTCCAATTCCCC
scaffold458714_12.7	1	p2	(AT)12	24	207	230	TGGGAAGAGTGGGTATGAGG
scaffold458731_11.3	1	p2	(AT)7	14	235	248	CGAACGACAATGGTTTGAGA
scaffold458741_16.4	1	p2	(AG)6	12	437	448	ACGAACATCACCATTCCCTC
scaffold458743_14.5	1	p2	(AT)7	14	499	512	GCAGATTCCCAAATCCAAAA
scaffold458771_17.9	1	p2	(CT)6	12	205	216	TCACGCATTCTCTCTTCGAC
scaffold458798_19.9	1	p2	(CT)9	18	804	821	AAGTTATTGCGAAACCCACG
scaffold458839_16.5	1	p2	(TG)7	14	246	259	TGATGCACGATGTATGTCGAT
scaffold458934_16.0	1	p2	(AG)6	12	3090	3101	GGAGAGAAAAGGGAAATCGG
scaffold458952_10.2	1	p2	(AT)6	12	239	250	AACACCCTGTGTATCCCAGC
scaffold459041_14.2	1	p2	(TA)12	24	493	516	TGGTTGGGCATTCCATTATT
scaffold459115_15.1	1	p2	(TA)6	12	1143	1154	AAACTCATATTCCATCCAAAGGTT
scaffold459175_17.2	1	p2	(CT)6	12	56	67	CAATATTACAAATGGCCAAGAGA
scaffold459181_12.8	1	p2	(AC)6	12	431	442	AGTGCTTTGGAAAACTCATGC
scaffold459406_16.3	1	p2	(CT)6	12	239	250	ATGGGAAGAAAACGCAACAC
scaffold459449_15.6	1	p2	(AG)6	12	2389	2400	CATTTGAGACGGACACATGC

scaffold459494_16.	1	p2	(GA)10	20	192	211	CGTGGTTCGATCGTAATTGA
scaffold459505_14.	1	p2	(AT)6	12	264	275	TCACATGAATGGACCCCTATC
scaffold459518_15.	1	p2	(CT)7	14	107	120	GGGATTTGGGACGATTTTCT
scaffold459519_14.	1	p2	(GA)6	12	2362	2373	GTGTGAAAGCCGAGAGAAGG
scaffold459565_12.	1	p2	(AT)6	12	415	426	GCCTCAATAACATGAGGCGT
scaffold459568_13.	1	p2	(TC)7	14	1468	1481	TTCGAGATGATGGTTGGTGA
scaffold459607_10.	1	p2	(TA)11	22	498	519	TAACAATCGCAATGCCAAGA
scaffold459624_12.	1	p2	(AT)7	14	196	209	CATCGATCAGTTATCATGGGA
scaffold459641_16.	1	p2	(AT)6	12	79	90	CAACCGAGTACCTAACCACAA
scaffold459669_15.	1	p2	(CT)6	12	744	755	AGGATAGGGAATAGCGTCCC
scaffold459741_11.	1	p2	(TA)12	24	437	460	ATGAAACAGAGAGCCCCCTT
scaffold459753_10.	1	p2	(GC)7	14	225	238	TATGGCAGGTGTCGGTATCA
scaffold459779_14.	1	p2	(TA)6	12	667	678	TTGAACTTGAAAGCCCAACA
scaffold459885_16.	1	p2	(TC)12	24	3463	3486	CCTTCTCCATCAACTGTGGG
scaffold460109_17.	1	p2	(TC)6	12	123	134	TCCATTTTCAGGTCCTCACC
scaffold460190_14.	1	p2	(TA)9	18	418	435	TAGCCGATAAAAATGGCACC
scaffold460257_13.	1	p2	(CT)6	12	229	240	CTCACCCTTGTCATCACCCT
scaffold460381_13.	1	p2	(GA)8	16	371	386	AGTATGCAACATGCCACCAA
scaffold460386_15.	1	p2	(TA)10	20	123	142	TATGCAGTGGGTTTTTGGTG
scaffold460387_11.	1	p2	(AT)8	16	128	143	TAGGACCACATTTTGTCGCC
scaffold460389_15.	1	p2	(CT)13	26	1113	1138	CAGATGGTGGTGTACGGTTG
scaffold460542_15.	1	p2	(CT)6	12	573	584	GCAGTGAGACCGAGTTGACA
scaffold460583_15.	1	p2	(CT)9	18	947	964	ACAATGACCGTTGCAAATGA
scaffold460635_14.	1	p2	(CT)6	12	562	573	TGCAAATCGTTACCAACCAA
scaffold460662_17.	1	p2	(TA)9	18	408	425	GCCAACCTTCAATCAACACA
scaffold460663_14.	1	p2	(TA)8	16	399	414	TCAGAACCGTTGTCTTTCAGC
scaffold460731_17.	1	p2	(TA)7	14	173	186	TGATCCCTAAATTGCCCTTC
scaffold460752_10.	1	p2	(CT)6	12	131	142	GCCTATCTCTCTTGCTGAAATTG
scaffold460764_12.	1	p2	(TA)10	20	44	63	GGCTGATATCACCATAACGCA
scaffold460802_15.	1	p2	(TA)6	12	54	65	TCACACACGTTTATTCGAGACA
scaffold460841_11.	1	p2	(GC)7	14	113	126	ATATTCTCGCTTCTTCGCCA
scaffold460850_16.	1	p2	(AG)7	14	3737	3750	ATCGGAAGGAGCCTTGTTCT
scaffold460927_13.	1	p2	(TC)8	16	1248	1263	GCCATTATGCACTTCCCAAT
scaffold460934_19.	1	p2	(AG)7	14	726	739	ATGTGGAATGAGGGTGAAGG
scaffold460950_13.	1	p2	(TA)7	14	779	792	CATCGTATGTTGCTTGGGAA
scaffold460959_15.	1	p2	(AG)7	14	897	910	TTCTGTGATCGCAAAAGGTG
scaffold460968_10.	1	p2	(AT)11	22	47	68	TGACAAATAAATGAAATACAAGACA
scaffold461007_15.	1	p2	(CT)6	12	132	143	CTTTCATGGGTGATGGAAGC
scaffold461013_16.	1	p2	(AG)6	12	2904	2915	GACGCTTCCAGAAGTATCGC
scaffold461019_13.	1	p2	(TC)8	16	49	64	TCGGTTGACTCTTTTACTTTAGCC
scaffold461125_14.	1	p2	(TA)6	12	363	374	CAATTGGGCCTTTCGTAAAT
scaffold461194_13.	1	p2	(AT)7	14	51	64	GATCTAGGAGAAAAGTGACATTCTT
scaffold461260_16.	1	p2	(TG)7	14	945	958	CTGCACGTTACAACACCGAC
scaffold461366_14.	1	p2	(TC)6	12	744	755	CTTGCCGAATGTTTGTCTCC
scaffold461445_14.	1	p2	(AT)8	16	957	972	CATGGGGAATATGCATCCAC
scaffold461458_17.	1	p2	(AT)6	12	370	381	GCTTGGTCCGAAAATTTCAA
scaffold461508_16.	1	p2	(AT)6	12	252	263	CGTTTCGCGTGCTAATTTCT
scaffold461571_13.	1	p2	(AT)7	14	136	149	CGTCGCGTTGGATTAATTTT
scaffold461601_16.	1	p2	(AG)8	16	609	624	TGCTTGTGGGTTTTGTTTTG
scaffold461692_14.	1	p2	(GA)6	12	248	259	TGCACTGATGAATGATGCTG
scaffold461694_14.	1	p2	(GA)8	16	124	139	CAGAGGAGATGGGAATGGAA
scaffold461882_13.	1	p2	(AT)8	16	504	519	GGACAAGCTGTCGGATAAGC
scaffold461924_15.	1	p2	(AG)9	18	4523	4540	TACATGCCACATGTTGGGTC
scaffold461947_16.	1	p2	(AG)7	14	851	864	TCCGATGATCAAGTCAGTGC
scaffold461953_11.	1	p2	(CT)7	14	129	142	CCATCAAAAATTCCTCCCCT
scaffold461976_15.	1	p2	(TA)7	14	130	143	CAACGGACGCTATCGGTTAT
scaffold462053_14.	1	p2	(GA)6	12	94	105	CATCTCAATCCCGTCACCTT
scaffold462111_10.	1	p2	(CT)7	14	277	290	GGGGGATGCCACTGTAGATA

scaffold462145_13.5	1	p2	(AT)8	16	438	453	GGAGAATTCGAGAGATTGCG
scaffold462246_18.1	1	p2	(AG)7	14	371	384	TTCGTACAGCCGTTTGATGA
scaffold462254_16.3	1	p2	(TG)7	14	187	200	TAGATGCACCGGTTAGGAGG
scaffold462301_17.9	1	p2	(AG)6	12	671	682	AGTTCTCCAACATCATCGCC
scaffold462328_16.0	1	p2	(CT)6	12	649	660	GCCATGCCATTTTCTTCACT
scaffold462532_14.4	1	p2	(TC)6	12	755	766	CTTTCTCACAGTCGCTGCAC
scaffold462626_16.1	1	p2	(AG)10	20	123	142	TTCAACCTGATTTTCCCCAC
scaffold462642_12.6	1	p2	(CA)11	22	75	96	TGTGCGTAAATTAGCGTTCG
scaffold462732_12.8	1	p2	(TA)10	20	219	238	AACGGCCGAGATTTGTTATG
scaffold462766_11.3	1	p2	(TA)6	12	391	402	GCATGTGCTCCTGCTCATAG
scaffold462954_15.0	1	p2	(AT)7	14	1165	1178	TATTGGTTGGGTACGGGTTG
scaffold462955_15.9	1	p2	(AG)6	12	53	64	TTTCTCATGTTGTAATTAATGTAGGGA
scaffold463052_12.6	1	p2	(CT)6	12	536	547	AAATCAACGAAATCGAACCG
scaffold463338_13.1	1	p2	(TA)7	14	837	850	GGAACAAATGAGACTGTTTCTGC
scaffold463342_18.0	1	p2	(TC)7	14	352	365	AACATTCCCTTTCTTCCACG
scaffold463353_14.3	1	p2	(AT)7	14	476	489	TTTTTCTTCTATCTTTTGATTACCG
scaffold463367_15.7	1	p2	(AG)7	14	320	333	ATTCCACATGGGGTGTCAGT
scaffold463370_15.9	1	p2	(GA)7	14	753	766	TGCAACAAATGATCCCAGAA
scaffold463424_15.0	1	p2	(AT)6	12	734	745	AAAGTTTGGTGAAGTCCGCA
scaffold463437_19.9	1	p2	(TA)6	12	330	341	GTGTTGTGCCTTAGCCCATT
scaffold463617_16.5	1	p2	(TC)10	20	610	629	TTGTGGAGGTGATGTGGAAA
scaffold463694_15.6	1	p2	(AG)7	14	3230	3243	TGCAAGAAATTGACATGTTGG
scaffold463773_13.2	1	p2	(TA)8	16	64	79	GGGAAATTCTTGTACCTCCTCC
scaffold463826_13.6	1	p2	(GA)6	12	171	182	AGCGTAAACACGTCCCCATA
scaffold463842_10.8	1	p2	(TA)10	20	155	174	CCGGAATCGCATCAATACTT
scaffold463892_12.6	1	p2	(GA)6	12	361	372	TCTTCTGAAGTTGCGACCCT
scaffold463919_20.9	1	p2	(AC)6	12	51	62	CTCCTATCTCCAATCCATGC
scaffold464095_15.8	1	p2	(TA)6	12	1300	1311	TTTGGGCCTCTTTGAATGAC
scaffold464137_14.1	1	p2	(TA)6	12	527	538	CACCGACGATCACTCCCTAT
scaffold464150_14.9	1	p2	(AT)9	18	963	980	AATGGGAAAGGGGCTGTAAT
scaffold464161_15.1	1	p2	(CT)7	14	3114	3127	TATTTGGTGGTGGGAGTGGT
scaffold464176_14.7	1	p2	(AT)7	14	221	234	GGGTCGTATCATTCAGCCAT
scaffold464200_12.4	1	p2	(AG)7	14	1097	1110	GAGTGGGGAGAAAGGAAAGG
scaffold464262_14.3	1	p2	(CT)9	18	538	555	CCTTGACTTCACGCCTTCTC
scaffold464366_14.6	1	p2	(GA)6	12	437	448	CGGACAAAATGTACCCCAAC
scaffold464381_13.2	1	p2	(TC)8	16	187	202	TATGGTGGACCGATACATGC
scaffold464389_12.8	1	p2	(TA)6	12	1961	1972	GTCGAAATTGCCCCCTGTAT
scaffold464524_14.0	1	p2	(TA)6	12	132	143	CGTGTTAAGCCTTGGGAAAA
scaffold464593_14.0	1	p2	(CT)8	16	208	223	AACCATTGCACATGAGACGA
scaffold464626_16.7	1	p2	(TA)6	12	133	144	AAAGGATTCGAACCCAGGAT
scaffold464628_12.7	1	p2	(TA)7	14	130	143	GCCATCCATTCTGAAGATCAA
scaffold464686_18.1	1	p2	(AG)7	14	272	285	TGGGACTGTTAAGTTTCCGC
scaffold464695_15.4	1	p2	(AT)7	14	81	94	AATATGAAACCCAACGTCGC
scaffold464715_13.0	1	p2	(GA)7	14	447	460	ATGGAACCACTTGTTGACCG
scaffold464730_10.3	1	p2	(AT)8	16	167	182	GAACTGCAGACGCGTGAAT
scaffold464764_12.4	1	p2	(AT)7	14	1507	1520	ACGTAAGTTCGCAACAACCA
scaffold464864_11.9	1	p2	(TA)6	12	68	79	AACCGAACTCGAGCTTCTCA
scaffold464917_11.7	1	p2	(TA)8	16	684	699	TTTTGAACCCTAAAAACTCGC
scaffold464940_13.3	1	p2	(AC)6	12	154	165	TTGTGTCTTAAAGTATAAAGGCATGA
scaffold465068_12.0	1	p2	(AT)9	18	995	1012	TCAAGGGTTTTCGCAGAGAC
scaffold465112_11.2	1	p2	(CT)6	12	106	117	AACCCCTACACCACCCCTAC
scaffold465175_17.6	1	p2	(TA)6	12	802	813	TACATGCTTTGTTGGGGACA
scaffold465255_14.1	1	p2	(AT)8	16	546	561	TCACCTTTCCTCCCAAATGA
scaffold465413_15.7	1	p2	(GA)6	12	132	143	CATAGGATTTGTGAAGGCCG
scaffold465504_14.1	1	p2	(AC)7	14	1188	1201	TCCATTCAACCAAATAGCCC
scaffold465569_10.0	1	p2	(CT)7	14	53	66	GCATCTCTCTCTTGCTCTTATTG
scaffold465579_14.8	1	p2	(AG)7	14	2076	2089	GCGTACGAATCCAAACCCTA
scaffold465809_13.9	1	p2	(AG)6	12	868	879	AGAGATCGGGTTTGCTGAAA

scaffold465823_17.	1	p2	(CT)6	12	123	134	CTTTCCCCACCATTTTTCCT
scaffold465937_16.	1	p2	(TA)7	14	67	80	TCAGTTTCGAGTTATGAAGTTAGGAA
scaffold466310_18.	1	p2	(TA)7	14	858	871	GGTTATAGCTACGTGGGCGA
scaffold466337_13.	1	p2	(AG)14	28	1138	1165	GAAACCGAGTGTGCATCTCA
scaffold466365_12.	1	p2	(AC)8	16	73	88	CACCCACGCATATACACACA
scaffold466389_10.	1	p2	(CT)8	16	374	389	TCATGCTGAAATCGTTCGAG
scaffold466441_19.	1	p2	(TA)6	12	319	330	TAGGTCACGGGTTCGAATTT
scaffold466463_10.	1	p2	(AG)8	16	76	91	TCTACGTCCACGGAGAAAGG
scaffold466570_14.	1	p2	(AG)6	12	1962	1973	AAAACGTCATTTTTGGCCTG
scaffold466606_12.	1	p2	(TA)6	12	350	361	AATTGAGGGAGTGGGTGTTG
scaffold466630_14.	1	p2	(TA)8	16	128	143	GGAAGCTAGGCGGTTTTGAT
scaffold466647_10.	1	p2	(TC)12	24	235	258	CTTCAGCCCCTCTAGGTTTG
scaffold466653_14.	1	p2	(AT)9	18	2212	2229	TGTTGTATTGTAAAGCCGCAA
scaffold466656_13.	1	p2	(AT)6	12	1568	1579	AATCCGTAAGAATAATCCATGC
scaffold466667_10.	1	p2	(AT)8	16	164	179	ACGCGCGTTTTTGGATTTA
scaffold466686_17.	1	p2	(AG)8	16	4973	4988	GGCGGATGAATAAACCTCTG
scaffold466706_15.	1	p2	(CT)7	14	1474	1487	GTCAAAACCCTGCCTTCAAA
scaffold466737_14.	1	p2	(TA)8	16	320	335	TACTTGGTTGAGCTTGGCG
scaffold466773_13.	1	p2	(TG)7	14	415	428	CGATATGGACGCCTCAGATT
scaffold466826_16.	1	p2	(AT)6	12	2855	2866	ACATTTAACTTCGCCCCTGA
scaffold466935_14.	1	p2	(TA)7	14	145	158	ATTTGCTCCAACAAACCTCC
scaffold467017_11.	1	p2	(TA)7	14	369	382	GCTTGCTGATTGTGGTTCAA
scaffold467115_17.	1	p2	(AG)7	14	296	309	GCCAATTCATATTTATTTGTGATCTTT
scaffold467144_13.	1	p2	(AG)9	18	225	242	AAAAATCTTGCTGCACCCAC
scaffold467178_15.	1	p2	(AT)14	28	52	79	TTGACATTCGCATTTTAAGAGTAG
scaffold467184_15.	1	p2	(TA)10	20	2210	2229	ACTTGTGGCTATGCCTTTGG
scaffold467263_13.	1	p2	(TA)9	18	179	196	TGGCTATCATGGATGCAAAA
scaffold467355_21.	1	p2	(TA)12	24	2221	2244	GCAACCAAAACACACACACA
scaffold467417_17.	1	p2	(TC)6	12	1483	1494	TCTGTCTCGAATTTGCGATG
scaffold467443_14.	1	p2	(TA)7	14	1820	1833	ACCGGGCACTAAGGGATTAT
scaffold467669_14.	1	p2	(TA)7	14	267	280	ACCTTGACCTTCAGGCTTCA
scaffold467676_13.	1	p2	(AT)10	20	577	596	TATGTGCGCGTTTCAATGAT
scaffold467753_15.	1	p2	(CT)7	14	2133	2146	TGAAAATCTGACGAGCATGG
scaffold467817_17.	1	p2	(GA)6	12	4116	4127	TGTGAGAGTGAGAGAGGGGG
scaffold467875_13.	1	p2	(TC)8	16	121	136	CTGATTCGCACAAATGATCG
scaffold467887_11.	1	p2	(TA)10	20	41	60	CGGATTTAAGGGTTATTACCTGATT
scaffold467902_13.	1	p2	(TC)6	12	711	722	TTCCCCTCATCTTCAAGTGG
scaffold467922_14.	1	p2	(AT)9	18	177	194	TTGCGTGTCAGTGTTTTTCC
scaffold467952_15.	1	p2	(AT)8	16	327	342	CTTCATCCCTCAATCCCTCA
scaffold468007_10.	1	p2	(GA)6	12	348	359	CGCGAAATGAGGAGCTTAAC
scaffold468115_11.	1	p2	(TC)6	12	188	199	GGAAACCCACAATCATCACC
scaffold468146_15.	1	p2	(AG)9	18	1724	1741	TTACAACCCGAAAGAAACCG
scaffold468164_12.	1	p2	(AT)10	20	730	749	CCCCCTTATTTTATCCCAACA
scaffold468420_11.	1	p2	(AT)6	12	401	412	CCGTTGCTTTCTCTCTCGTT
scaffold468591_11.	1	p2	(CT)10	20	511	530	CTCAGAAATCAAGCCGAACC
scaffold468609_20.	1	p2	(TC)6	12	307	318	CAGCGAGGAGGTTGAGGTAG
scaffold468615_14.	1	p2	(AT)9	18	202	219	CAGTATTACAGCCGTGGCAA
scaffold468639_17.	1	p2	(AT)6	12	1565	1576	TTCCCTTCCAGTTACACCGT
scaffold468658_16.	1	p2	(AT)7	14	1998	2011	TCAAGTCCTCACACACTGATGA
scaffold468668_12.	1	p2	(GT)7	14	747	760	CACGAGCTCTTATTTGGCCT
scaffold468669_12.	1	p2	(AT)8	16	365	380	GGATGGAACGCACAAAACTT
scaffold468740_15.	1	p2	(TA)6	12	1678	1689	TGGACAATTCAATAGAAAACCG
scaffold468785_14.	1	p2	(TA)9	18	664	681	GGTTTGGTGAAAATGATGGC
scaffold468805_10.	1	p2	(CT)6	12	299	310	GCTTCTTTCGCTTTCTCATTG
scaffold468828_11.	1	p2	(TA)9	18	150	167	GTATTCCCGGGTTTCTCCAG
scaffold468909_13.	1	p2	(AC)6	12	1271	1282	GGACGTTTCCTCGTTTTTCA
scaffold468921_18.	1	p2	(AG)9	18	4646	4663	GGCTTTTTGCTAATTGGCTG
scaffold468936_13.	1	p2	(CT)6	12	319	330	AACCAGCTCGGTGATATATGG

scaffold469003_19.	1	p2	(TA)8	16	39	54	TGACGGGATTTAGGTGTTTTG
scaffold469083_15.	1	p2	(CG)6	12	202	213	CACTCATTTGGGGGATTGTT
scaffold469108_17.	1	p2	(CT)9	18	1112	1129	CACTGACATTTCCTCGCTCA
scaffold469290_12.	1	p2	(GA)6	12	1248	1259	TGGCCACCTCCATTTCTAAC
scaffold469291_16.	1	p2	(AT)8	16	338	353	TCCCCTTAGGAAAACCGTTC
scaffold469304_18.	1	p2	(AG)8	16	130	145	ACACACGCCACCTTTTTAGG
scaffold469357_15.	1	p2	(CA)7	14	3774	3787	AGTCACCAAAGCTCCCACTC
scaffold469366_11.	1	p2	(CT)8	16	409	424	AAAGTATGCAAGGCCCACAC
scaffold469468_12.	1	p2	(CT)6	12	122	133	GGATCGAAAAGAGAGGGAGG
scaffold469580_13.	1	p2	(GA)7	14	572	585	AGTCACCTTGTTCAAACGGG
scaffold469620_20.	1	p2	(GA)6	12	227	238	GCGGTGTTGTCTGAGTGTGT
scaffold469651_14.	1	p2	(GA)6	12	426	437	GGTTGCTTCTTACAGGCTGG
scaffold469720_11.	1	p2	(TA)7	14	609	622	GCATATCGGTTCGGTCTCAC
scaffold469818_14.	1	p2	(GT)6	12	917	928	CATCAGTCCAGCCTTCTTGG
scaffold469847_11.	1	p2	(TA)7	14	406	419	TGATGTTTGCATTTGAAGAGG
scaffold469952_10.	1	p2	(TA)11	22	51	72	CGTTTTGACAATATATAGGTGTTTTGA
scaffold469953_13.	1	p2	(TA)6	12	329	340	ATCAACGCCCATGATCAAAT
scaffold469956_14.	1	p2	(CT)6	12	48	59	TTTCTCAGCCAAGCTCACCT
scaffold470011_15.	1	p2	(AT)6	12	659	670	TTCCCCTTTATCTCCTCATTCA
scaffold470052_18.	1	p2	(CT)7	14	311	324	TCTAAAACCCTCGCCTCTCA
scaffold470085_16.	1	p2	(AT)6	12	1852	1863	TGATTCCATTCCATGCTTCA
scaffold470181_17.	1	p2	(TA)6	12	719	730	GATTTTCGTAATCCCCTTTTCA
scaffold470248_11.	1	p2	(AT)8	16	431	446	GTTTCCTGTTCGGCTGTTGT
scaffold470271_10.	1	p2	(TA)11	22	305	326	AGACCACCGAAAAATGTTGG
scaffold470304_15.	1	p2	(CT)6	12	2820	2831	AGGCTTGCAAGAAGCTGAAG
scaffold470381_14.	1	p2	(AT)10	20	685	704	TCAGCGCCACGTATCCTAGT
scaffold470409_13.	1	p2	(AG)6	12	415	426	TCATTTCGGGTTATTTTCGG
scaffold470459_13.	1	p2	(CT)6	12	212	223	ACAGGTCCCTGAAACAAACG
scaffold470540_15.	1	p2	(CT)7	14	109	122	TCCTTTCAGAGGCAGAAACC
scaffold470544_10.	1	p2	(AT)9	18	154	171	GCATGCAAAATCAAGCTCAA
scaffold470585_14.	1	p2	(TC)6	12	53	64	CCTGCCATTTCTCTCGTGTT
scaffold470587_14.	1	p2	(CT)6	12	33	44	ACAAAATGGCCAAGAGAGTTT
scaffold470597_13.	1	p2	(GA)6	12	429	440	TTGAACAACAAGGCCAGTGA
scaffold470660_16.	1	p2	(TA)8	16	624	639	CAGAACCCGAAGTGAAGAGG
scaffold470702_14.	1	p2	(TC)8	16	130	145	TCCACAGCAGAGTCTCCTCA
scaffold470708_16.	1	p2	(AC)7	14	2283	2296	ACAGAAAACTTTCATGCCGC
scaffold470795_15.	1	p2	(TA)6	12	2063	2074	CGAGCTCACCTTGTGTTGAA
scaffold470874_15.	1	p2	(TG)6	12	2687	2698	CCAGCAAGTGCAGAGTGGTA
scaffold470877_14.	1	p2	(TA)6	12	437	448	TTTCTCTCCCGTGGACGTAG
scaffold470992_10.	1	p2	(CT)6	12	815	826	AGCAAGGTGATGCGAGACTT
scaffold471041_15.	1	p2	(CA)6	12	1291	1302	CGGGTATACTTGGAGAAACACA
scaffold471121_17.	1	p2	(TG)6	12	812	823	TGCACATGTAAAACGATCCA
scaffold471175_13.	1	p2	(AT)8	16	86	101	GGACGGTTAAATTTTGTCCC
scaffold471176_14.	1	p2	(GA)6	12	714	725	GGTGCAGAAGAGAAATTCCG
scaffold471351_11.	1	p2	(AG)6	12	205	216	TCGAATCCACATCAGATCCA
scaffold471425_15.	1	p2	(TC)6	12	393	404	CATGGGCCTTGCATGTATAA
scaffold471453_15.	1	p2	(CT)6	12	133	144	TCTCGTTGCTATTCTTGCCA
scaffold471519_12.	1	p2	(TC)7	14	77	90	GAAAGGATGAAAATCATTGGC
scaffold471536_14.	1	p2	(AT)6	12	223	234	CCAATGGTTATCATCCCACC
scaffold471557_15.	1	p2	(CT)11	22	470	491	ACTCTCTCTCACCGCCACAT
scaffold471578_16.	1	p2	(TA)6	12	206	217	AATTAGCGTGTATGCTGGGG
scaffold471586_16.	1	p2	(CA)6	12	272	283	TAAAGGCAGAAAACGGAGGA
scaffold471610_16.	1	p2	(AC)6	12	584	595	CACTGGAAAAATGGCACCTT
scaffold471622_12.	1	p2	(GA)6	12	687	698	GAACGAGGGCCTTCTTCATT
scaffold471656_15.	1	p2	(TA)6	12	1664	1675	GGTAAATCAATGTGAAATGATGGA
scaffold471667_17.	1	p2	(TA)6	12	2158	2169	CTATGGACCCTTGCAGGAAC
scaffold471777_10.	1	p2	(CT)7	14	424	437	GAAGAATCACCGGACTGAGC
scaffold471800_17.	1	p2	(TC)6	12	638	649	CTTGTGACCCTCACCACCTT

scaffold471822_10.	1	p2	(AG)10	20	288	307	TCTTTGCGCCTAGATTTCTCA
scaffold471955_13.	1	p2	(TA)6	12	134	145	CCCAAAGATTTATAGGTTTTATTTCAA
scaffold472039_14.	1	p2	(TA)8	16	148	163	AACCACAGCCCTACATCTCG
scaffold472141_13.	1	p2	(TA)6	12	52	63	CCAATTTGAATGGTTATCACCTG
scaffold472148_18.	1	p2	(TC)6	12	68	79	GATAATATGGCCGAGAGTTTGC
scaffold472149_12.	1	p2	(TA)9	18	294	311	AGCCACACATGTCACAAATGA
scaffold472183_11.	1	p2	(TA)10	20	42	61	CGGATTTAAGGGTTATTACCTGAT
scaffold472273_16.	1	p2	(CT)6	12	409	420	TGGAGAGCTCGAGAGAGAGG
scaffold472312_13.	1	p2	(AT)6	12	217	228	GCAAAAGCTTTCTCGACCAC
scaffold472600_10.	1	p2	(CT)6	12	351	362	CTTCAAGCGGTCTTGATTCC
scaffold472606_13.	1	p2	(AG)6	12	307	318	TAGGGGGTGGTTGGTGTTTA
scaffold472691_16.	1	p2	(GA)6	12	2033	2044	ATCGTCGTCGTCTTCTTCGT
scaffold472806_11.	1	p2	(AT)8	16	605	620	TTCAATTAATGTTGTCATTATTCCAAG
scaffold472807_17.	1	p2	(TA)7	14	545	558	GACTTGCCAACGGTCAATCT
scaffold472925_14.	1	p2	(TC)6	12	208	219	GACTCATGCTCGGCATACAA
scaffold472941_12.	1	p2	(AT)9	18	48	65	TCAAGGCCGATAAGATGGAT
scaffold473012_15.	1	p2	(AT)9	18	323	340	TAACGATGGACTAGGGGCTG
scaffold473018_12.	1	p2	(GA)6	12	87	98	TAAATATGCAGCAGACGCGA
scaffold473142_10.	1	p2	(AT)8	16	257	272	TCGGAAAGGAAAACCGTAAA
scaffold473266_15.	1	p2	(TC)6	12	134	145	ATCGGCTGAATAGCCGTATG
scaffold473401_17.	1	p2	(AT)7	14	294	307	ACCTCGTCGTCCAACTCACT
scaffold473465_16.	1	p2	(TC)9	18	180	197	CAGCTCCACTACTTCCTCCA
scaffold473475_11.	1	p2	(AT)6	12	324	335	GAAAGGGCTGAGGTATGGTG
scaffold473491_12.	1	p2	(TA)10	20	69	88	AAAAATGGTTATTATTGGATCGC
scaffold473547_14.	1	p2	(TC)6	12	154	165	CGTAGAGAATGTTGCCACGA
scaffold473586_15.	1	p2	(TA)6	12	525	536	GTTTTTGAACCCCCTCCTTC
scaffold473603_13.	1	p2	(AT)7	14	1357	1370	ATGCGCGGGTGTAAAGTTAG
scaffold473664_10.	1	p2	(AC)7	14	80	93	AGCCTCGGATTTCCTGTTCT
scaffold473793_12.	1	p2	(TC)6	12	577	588	GCCTTCGGATCTGGGTATTT
scaffold473955_11.	1	p2	(AG)8	16	1004	1019	GCTTCAGTCATGTCGTTCCA
scaffold474132_13.	1	p2	(AG)6	12	795	806	GCAACGAAGATGGGAAATTG
scaffold474140_15.	1	p2	(TA)6	12	62	73	CATCACACCACAAATGACTCTCT
scaffold474259_15.	1	p2	(AT)6	12	3913	3924	CGGCGTAACTACCATTCACC
scaffold474486_16.	1	p2	(TA)8	16	152	167	TGTGGTTTGCTAGACATCGC
scaffold474566_18.	1	p2	(CT)8	16	82	97	GGACCTGAAAAAGGACTTTGG
scaffold474623_15.	1	p2	(AT)6	12	2506	2517	ATGGCTGCTCCAATATCACC
scaffold474648_15.	1	p2	(GA)10	20	74	93	ATTCAGAAATGGCGATGACA
scaffold474851_16.	1	p2	(AT)7	14	583	596	AAAAGCCGATCGAGTTCGTA
scaffold474929_13.	1	p2	(CT)6	12	44	55	TCCACCCTCTCACTTCCACT
scaffold475149_10.	1	p2	(TG)6	12	177	188	ACCACGAGATGGGGACATAA
scaffold475165_14.	1	p2	(TC)7	14	282	295	ATTTGCGGAAACAATCCAGA
scaffold475200_23.	1	p2	(AT)6	12	350	361	TCGATTCGACTGGATTCGTT
scaffold475308_12.	1	p2	(CT)6	12	134	145	TATAGTCCACCCAACCCGAG
scaffold475369_19.	1	p2	(CT)6	12	1230	1241	TTGGAGTTGGAGATGAAGGC
scaffold475474_14.	1	p2	(TG)7	14	71	84	CTAGCGGATTTCTCTGGCTC
scaffold475525_11.	1	p2	(TA)8	16	46	61	ATCGGTTATTACCGGATCGC
scaffold475712_12.	1	p2	(AC)7	14	898	911	TCAATACCCGAGAATTGCAT
scaffold475714_17.	1	p2	(AT)6	12	185	196	TCCAATTTCAGTTAAACACACCA
scaffold475720_12.	1	p2	(CT)9	18	50	67	CACTCACTCTCTCTAGCCGC
scaffold475833_10.	1	p2	(GA)6	12	127	138	AGATATGTCGGCAAGCGAAT
scaffold475932_12.	1	p2	(TA)8	16	83	98	GCATCCAATACCAATATCTCAGC
scaffold475937_14.	1	p2	(TA)9	18	478	495	TTCCACATTGATTCCTGGGT
scaffold476008_17.	1	p2	(GA)6	12	721	732	AGTGCTTCTTGAAGCTGGGA
scaffold476039_11.	1	p2	(TA)7	14	496	509	GTAATAGAACGTGCCCCCAA
scaffold476154_17.	1	p2	(TC)6	12	594	605	GGAGGATTTTCCTTTCCCAA
scaffold476203_12.	1	p2	(TA)6	12	129	140	GAATGCGGAGTTGGAATCAT
scaffold476209_16.	1	p2	(TA)8	16	361	376	TTTTTCCTAACCGGACCACA
scaffold476319_11.	1	p2	(CT)6	12	251	262	TCCCCATTGTTCTACCCAAA

scaffold476333_10.	1	p2	(GA)6	12	42	53	TTTGTGTGAGGAATTGTTGAAGA
scaffold476452_16.	1	p2	(TA)8	16	308	323	TTTTTGGGTTGAAAATAGCG
scaffold476505_16.	1	p2	(TC)9	18	716	733	CCAACCATTGCAGAATCCTT
scaffold476601_14.	1	p2	(TA)6	12	135	146	GCACACATTTTTCTCCCCAT
scaffold476603_15.	1	p2	(AT)8	16	132	147	TTACTTTTCCGGCAACATCC
scaffold476649_15.	1	p2	(TC)9	18	354	371	CCTAGCCAAGTTTCACGAGC
scaffold476674_14.	1	p2	(TA)8	16	112	127	ATACCGGGATCGAATCTTCC
scaffold476922_17.	1	p2	(AG)7	14	180	193	GAAAAGAAAAAGAAGGCACTCG
scaffold476982_12.	1	p2	(AT)6	12	331	342	CCATCATGGGGTTTTCTTACA
scaffold477044_13.	1	p2	(TC)6	12	136	147	CAAATCAACGCGAATTCAAC
scaffold477161_10.	1	p2	(TC)12	24	483	506	CTTCTTCAAACACCCCCAGA
scaffold477283_10.	1	p2	(GA)7	14	279	292	ATTTGGATGGTGATTGTGGC
scaffold477406_13.	1	p2	(TC)6	12	552	563	GAGGAGCCCAAGATGTCAAG
scaffold477464_15.	1	p2	(TA)10	20	803	822	ACAAGAATGCCCCTGTATGC
scaffold477485_14.	1	p2	(TA)7	14	318	331	ATCCACTGCCAACCTCATTC
scaffold477491_13.	1	p2	(TC)9	18	46	63	CAAGCCCAAAAGCACAAAGT
scaffold477517_18.	1	p2	(GA)6	12	936	947	GAGGATTTGTCAACCGGAAA
scaffold477630_13.	1	p2	(TA)6	12	542	553	GATGCTTTTCCCCTTCTTCC
scaffold477650_17.	1	p2	(CT)6	12	1200	1211	CTCCCTTTACCTCCCCAAAG
scaffold477723_16.	1	p2	(GA)6	12	399	410	ATATGGTTTGACGCCTTTGC
scaffold477735_15.	1	p2	(TC)6	12	322	333	GAAGGAGGAGAAGTTTGGGG
scaffold477748_11.	1	p2	(CT)6	12	55	66	CCCAATACTCTTTCCCAACC
scaffold477768_19.	1	p2	(AG)7	14	90	103	TGAGGACGGTGAGGATTAGG
scaffold477770_16.	1	p2	(AG)7	14	133	146	ATCCCGACTGATTTCGATTG
scaffold477802_15.	1	p2	(GA)6	12	865	876	GCACAACTGCAGACCAAGAA
scaffold477993_12.	1	p2	(CT)7	14	109	122	CACTTTCTCTCTTCCGACCG
scaffold478000_11.	1	p2	(AG)6	12	149	160	GAATATTGTGCGTCCCCATC
scaffold478024_15.	1	p2	(TA)10	20	1302	1321	GCGTGCGAATTTAATGATGA
scaffold478034_17.	1	p2	(AT)8	16	672	687	AAGCCGCATTTTAATCGAGA
scaffold478044_10.	1	p2	(TA)7	14	72	85	GATCGGATACGGATCGAAAAT
scaffold478075_14.	1	p2	(AT)7	14	44	57	TGCTTTTCTAAATGGAGAGTTGG
scaffold478111_14.	1	p2	(AT)7	14	83	96	TGCTGTAAATGAAACTGTTGTATGC
scaffold478135_12.	1	p2	(AT)6	12	179	190	CCAACTTGAAACCGGAAAAA
scaffold478152_13.	1	p2	(TC)6	12	1559	1570	GGCGGGATATACTAATGTCCAA
scaffold478305_12.	1	p2	(TA)6	12	34	45	ACTTTTAAGGATCAAGGATATTCG
scaffold478362_15.	1	p2	(GA)6	12	250	261	CTCGAGTGTAAACACGTCCCT
scaffold478378_11.	1	p2	(TA)8	16	332	347	TCCGGATACCTACTACTGCGA
scaffold478448_14.	1	p2	(CT)6	12	297	308	TTGGTATACAACTTTGATTCCCC
scaffold478586_18.	1	p2	(TG)7	14	880	893	ATGCACACCGAGATGTGGTA
scaffold478666_14.	1	p2	(AG)7	14	550	563	TTCAACGGAGTGGAAGATCC
scaffold478755_12.	1	p2	(AT)10	20	442	461	CAGGTTCGAGCTTCCATAGG
scaffold478879_11.	1	p2	(TA)9	18	361	378	AGCCTTTAATCAGCAATATAAGTCA
scaffold478890_16.	1	p2	(AT)6	12	265	276	AGGGCTACAAATTGCAAGAA
scaffold478967_14.	1	p2	(AT)7	14	355	368	TATCGGTTATCATCGGATCG
scaffold479173_10.	1	p2	(TC)7	14	130	143	GCACAACCACTCCACAAAGA
scaffold479248_15.	1	p2	(TA)9	18	1389	1406	CGATGTTTGTTGGCTGTCTG
scaffold479312_15.	1	p2	(GA)7	14	1169	1182	TTGGAACCAACTAATTGCCA
scaffold479338_17.	1	p2	(AT)6	12	109	120	ACGTTCATACCTTTGTGGCA
scaffold479341_16.	1	p2	(CT)6	12	234	245	TCATTTCATCGATTTTTCCTCTC
scaffold479345_15.	1	p2	(TA)6	12	214	225	TTCAATTTCTTGGCTCAGGG
scaffold479655_15.	1	p2	(GA)6	12	6101	6112	AAAGCAAAATACCACCACGC
scaffold479701_17.	1	p2	(GA)6	12	2931	2942	GAGCTAACTGCATTCCAGACG
scaffold479715_10.	1	p2	(AG)12	24	667	690	GGGATCGGTTTATGTGTTGG
scaffold479734_17.	1	p2	(AT)6	12	86	97	AGAATCACGGCCATTTTCAG
scaffold479803_15.	1	p2	(TA)6	12	1047	1058	TCTTGTTGGCATGAGCTTGT
scaffold479806_12.	1	p2	(GA)7	14	442	455	AAGGACGGAGAGAGAGAGCA
scaffold479996_16.	1	p2	(AT)6	12	428	439	CGCATTCATTAGCTACACCC
scaffold480058_11.	1	p2	(AT)6	12	331	342	AAATGAATGTTGTGTTTGTTTGTAA

scaffold480164_16.	1	p2	(AG)8	16	528	543	AAACCCACCTGCTGCATAAT
scaffold480179_10.	1	p2	(GA)6	12	108	119	ATATCGTCGTCTCCCGATGA
scaffold480225_14.	1	p2	(TG)7	14	1041	1054	TCTCAAATCGTTTCTATCGTGC
scaffold480380_11.	1	p2	(AG)10	20	78	97	TGTGCAAGGTTGAACCAAGA
scaffold480407_17.	1	p2	(TA)6	12	786	797	GAAGAGGAGGAAAGAAAACGC
scaffold480425_14.	1	p2	(AT)7	14	1389	1402	AATTGCGTTAGGGATTTGATT
scaffold480443_14.	1	p2	(TA)7	14	564	577	GACTTGCCAACGGTCAATCT
scaffold480473_12.	1	p2	(GA)9	18	80	97	ATGGAACCACTTGTTGACCG
scaffold480525_18.	1	p2	(AG)9	18	52	69	CGAAGAACAATTACAATGTTTATCCA
scaffold480654_14.	1	p2	(TA)6	12	55	66	TGCACCTGATCATGAACCTA
scaffold480660_13.	1	p2	(CT)7	14	1434	1447	TGACTCTCCCCTTCCATCAC
scaffold480678_12.	1	p2	(TA)10	20	1090	1109	TTTTTAGAAGGATACTCACTACTCCA
scaffold480754_15.	1	p2	(AT)8	16	389	404	ATATTCCCCGGTATGCCAAC
scaffold480777_14.	1	p2	(AG)7	14	487	500	ATCAAAGAAAACGGTGGTGG
scaffold480831_14.	1	p2	(AT)6	12	1302	1313	ATCTCCCACCAATGCACTTC
scaffold480839_16.	1	p2	(TA)6	12	1279	1290	AGCACATTTAATTCCAGGTCG
scaffold480889_12.	1	p2	(CT)6	12	157	168	CGAGCTCTGAAAATTCTCCC
scaffold480928_16.	1	p2	(CT)6	12	137	148	GGCGGATAGCAAATCAAAAA
scaffold480930_18.	1	p2	(CT)6	12	165	176	CAGCCTCCATTTTGTTACCG
scaffold480954_16.	1	p2	(GA)11	22	3796	3817	AAAGAGAAAACGAGGGGTGC
scaffold480979_16.	1	p2	(GA)7	14	737	750	GGACAACCCATAACCCACAC
scaffold481059_17.	1	p2	(AT)6	12	736	747	AGTTTGGAGCACACGAGCTT
scaffold481083_16.	1	p2	(AC)7	14	237	250	TATTCAACTCCATCTCCCCG
scaffold481239_13.	1	p2	(AT)11	22	2240	2261	TTCAACGGTCCCACAAATTA
scaffold481407_14.	1	p2	(AT)9	18	175	192	CATCAGATCTGCGCTGAAAA
scaffold481541_10.	1	p2	(AT)10	20	300	319	TCACTGGCAGCGAATATGAA
scaffold481564_12.	1	p2	(TC)6	12	182	193	GTCCAATGTTTAGGCCCGTA
scaffold481807_16.	1	p2	(GA)12	24	5944	5967	GCAATAAAGAGGCTGGTGCT
scaffold481870_15.	1	p2	(CT)9	18	623	640	AGCCCTCATTCCTCCCTTTA
scaffold481939_13.	1	p2	(TA)8	16	133	148	GGCAATATGCTGACAGACGA
scaffold482126_14.	1	p2	(CA)7	14	54	67	GGAGTCTGGAAAAGAGAGAGTTG
scaffold482141_14.	1	p2	(CT)8	16	515	530	CATTCTTTCTCCTCCCCACA
scaffold482147_16.	1	p2	(AT)6	12	121	132	AAACGACATCATGACGCAAC
scaffold482179_12.	1	p2	(TA)10	20	42	61	AAGGGTTATCACCTGATTTTCTC
scaffold482219_13.	1	p2	(AT)7	14	60	73	TCTAAATTGCGAGAATATGAGAGTTT
scaffold482271_11.	1	p2	(AT)9	18	610	627	TGCTTCAAGGTAGGTTTATTAGGC
scaffold482306_15.	1	p2	(TG)9	18	236	253	TCGTATTGACGGGAGAAACC
scaffold482356_11.	1	p2	(TA)10	20	734	753	TGGCTGCTCCTCATCCTTAT
scaffold482531_14.	1	p2	(GA)6	12	4017	4028	ACTCGCGAAGTTCCTTCAGA
scaffold482608_12.	1	p2	(GA)7	14	227	240	AGAACTCCACTTGCACAGCA
scaffold482617_16.	1	p2	(GC)6	12	3215	3226	CACCACATAATGGACGTTGG
scaffold482656_14.	1	p2	(GA)8	16	1414	1429	CGAGCTTTTATCGAACGGAG
scaffold482744_14.	1	p2	(TC)8	16	3120	3135	GCTATGGTGGCCAATGTCTT
scaffold482749_15.	1	p2	(AG)6	12	1196	1207	AACTCCCCTTTCCTTTGCAT
scaffold482821_12.	1	p2	(TA)6	12	682	693	GGCAAATGATTGATTGCCTT
scaffold482961_11.	1	p2	(AT)6	12	1054	1065	TGACTTTCATGTAGCGTGGC
scaffold483020_17.	1	p2	(AG)6	12	8248	8259	TTTGCTGTGCGTCGTATTTC
scaffold483083_11.	1	p2	(GA)6	12	112	123	TGCCACTTATTTCAGGAGGT
scaffold483092_17.	1	p2	(GA)9	18	3339	3356	TTAGCACCTGATTACTCCCGA
scaffold483164_16.	1	p2	(TG)6	12	91	102	CCGTGGACGTAGATCCTTGT
scaffold483239_15.	1	p2	(TC)8	16	1021	1036	TCTGGTGTGCTTTCTGCAAC
scaffold483247_10.	1	p2	(GA)6	12	30	41	GGGGGAGAATTGAATTGCAG
scaffold483367_12.	1	p2	(TA)9	18	2452	2469	TGCAAATACGAATATCATTATTCAA
scaffold483414_13.	1	p2	(CA)6	12	234	245	TTCAATCCAAAAAGACACATGC
scaffold483446_16.	1	p2	(AT)6	12	307	318	ACATTGTATCTTGTCTTGCCCT
scaffold483487_13.	1	p2	(AT)7	14	712	725	ATTACCTTGATCGACGACGC
scaffold483599_14.	1	p2	(CT)6	12	1969	1980	CCTCTCAGCCCTAGCTTCCT
scaffold483707_11.	1	p2	(CT)6	12	267	278	TTTAAATGGGCGGGAAAATA

scaffold483770_15.	1	p2	(CT)6	12	1193	1204	CATCCTCAATTTCAGCACCC
scaffold483772_16.	1	p2	(TA)8	16	359	374	TGCTGACCCTCTGCTGTATG
scaffold483878_13.	1	p2	(TA)8	16	4861	4876	CCTCTCCTCGTCTTGTGCTT
scaffold483924_11.	1	p2	(TA)7	14	464	477	ATTTGTTTGCATACGGCCTC
scaffold484129_11.	1	p2	(TA)7	14	136	149	GGCTTGTTTGAACCATTTTGA
scaffold484163_14.	1	p2	(AT)8	16	251	266	CATGTCAATATCATCACGAGTTTGT
scaffold484191_13.	1	p2	(TA)8	16	526	541	TTTTGGAGGGAAAACCACTG
scaffold484194_14.	1	p2	(TA)8	16	133	148	AAAATCAAGGGCTGTGATGG
scaffold484195_15.	1	p2	(AT)8	16	1784	1799	TAGGATCCCGGATAATCCAT
scaffold484295_13.	1	p2	(AC)8	16	1006	1021	GCTGAGCATATTTTTCACCCA
scaffold484331_13.	1	p2	(CT)6	12	106	117	TGCATTGTTCGACGATGTAAC
scaffold484469_15.	1	p2	(AT)8	16	71	86	TTAACACCAAACCATCTAATTAGTAC
scaffold484521_12.	1	p2	(GA)6	12	235	246	GGTTACCGTCGTGGTTATGG
scaffold484528_11.	1	p2	(AT)10	20	43	62	TGGCAGAAAGATTTTAGATATAGAC
scaffold484720_17.	1	p2	(AG)7	14	1162	1175	GCAGTCTGTAAGGCCTGGTC
scaffold484887_17.	1	p2	(TA)8	16	147	162	ACCCAACCACCCTTTATTCC
scaffold484888_14.	1	p2	(TA)10	20	1860	1879	TTTTACAATTTTGCCCCTCG
scaffold484957_15.	1	p2	(TA)9	18	881	898	GGCAAGTTGAAGGAACAAGG
scaffold484995_11.	1	p2	(AG)6	12	116	127	TTCCTCTCGTGTTTCATCCC
scaffold485004_10.	1	p2	(AT)7	14	81	94	GGACAAAAGAAAAACCACGC
scaffold485103_13.	1	p2	(AT)9	18	286	303	CCGAAAATCAAAGGCCTACA
scaffold485222_12.	1	p2	(TA)7	14	222	235	TGGCACAGAGAGTACATAGTTTCC
scaffold485296_15.	1	p2	(AT)6	12	1036	1047	TCATGCACAAGGTGGAATGT
scaffold485325_18.	1	p2	(GA)9	18	259	276	AAAGGTGAGGGAGAGTGGGT
scaffold485502_15.	1	p2	(TA)6	12	661	672	TTTGTTGCAAATATCAGGTCTTTT
scaffold485528_11.	1	p2	(AT)6	12	725	736	TGCTGACCCTCTGCTGTATG
scaffold485542_12.	1	p2	(TA)7	14	828	841	ATAACAGTGGTGGCCGAAAA
scaffold485569_14.	1	p2	(GA)6	12	165	176	GGGTGCTTGAGGGAGTTGTA
scaffold485715_17.	1	p2	(TG)6	12	638	649	TTGCTTGGGATTTTATTTTGAA
scaffold485769_10.	1	p2	(AT)6	12	30	41	TTTGTATGGGTCATTGGACG
scaffold485863_14.	1	p2	(GA)7	14	95	108	GGATTTGGGGGTGAGAAGAT
scaffold485868_10.	1	p2	(AT)6	12	334	345	AGGAGCAAATTGAGGCTGTC
scaffold486007_10.	1	p2	(AT)7	14	192	205	TTCGGGACCTCTTTGTATCG
scaffold486057_19.	1	p2	(AC)7	14	319	332	GCGCATTTTCTGCTGTTAGA
scaffold486154_16.	1	p2	(CT)6	12	106	117	TTCGATGTTGTAAGGGAGGA
scaffold486203_16.	1	p2	(CT)7	14	270	283	TCCACCGCTAATGAATGACA
scaffold486204_11.	1	p2	(GA)6	12	138	149	GGTGCAAGGGTTTCAAAGAG
scaffold486205_12.	1	p2	(AT)9	18	226	243	CATATTTCAAATGCATGCCG
scaffold486206_21.	1	p2	(GA)7	14	136	149	TAACACCAGCCTCTCTGCCT
scaffold486222_11.	1	p2	(AT)7	14	400	413	TCGGCTATATTAGCGATCCG
scaffold486247_16.	1	p2	(AT)11	22	51	72	ATGAAGTTAGGAAATAAAGAGGTGT
scaffold486299_15.	1	p2	(TA)8	16	333	348	TCTGATTCCAAACCCCAGTC
scaffold486692_16.	1	p2	(TA)8	16	865	880	CTATTCCAACTTCGGGACCA
scaffold486706_10.	1	p2	(TC)6	12	70	81	TTTCAGAAATTGCCTTGGTTG
scaffold486719_16.	1	p2	(TA)6	12	2886	2897	GGGAACCATCATGGAAATTG
scaffold486816_17.	1	p2	(AT)9	18	136	153	TTCGGAGCATGATTTAAGTGG
scaffold486903_14.	1	p2	(CT)7	14	136	149	CCAATGCCAATCATCCTCTT
scaffold486948_16.	1	p2	(GA)6	12	138	149	AAGGAAAAACATGAGTTTAGGGG
scaffold486991_12.	1	p2	(AG)6	12	245	256	GCTGTTGCATTTCGATGTTG
scaffold487025_15.	1	p2	(TC)7	14	1003	1016	ATCCAGATCCTTGTGGTTGG
scaffold487054_15.	1	p2	(TC)6	12	168	179	TCCTATCTTCTGCGACGCTT
scaffold487173_18.	1	p2	(AC)6	12	479	490	TTCCCTTCTCATTTCCATGC
scaffold487404_12.	1	p2	(TA)7	14	234	247	TCAACGATTTTGGTTTGTTCC
scaffold487557_16.	1	p2	(CT)8	16	5335	5350	ATTCTCCACCACCCCACATA
scaffold487593_16.	1	p2	(AT)9	18	368	385	TGGAGAAGCTCTTACGGCAT
scaffold487797_11.	1	p2	(GA)10	20	636	655	AATGGTTGTGGATCGCCTAA
scaffold487885_11.	1	p2	(GC)7	14	261	274	TCCGGTCCAATTCCAATAAG
scaffold487974_14.	1	p2	(AT)9	18	133	150	TTGCAGTAAATATCGGTTTTCG

scaffold487992_16.	1	p2	(TA)6	12	352	363	AAAAATGAAACCGGCCAAA
scaffold488063_16.	1	p2	(AT)8	16	2775	2790	GCCCTTCGAACAACAAAAAG
scaffold488176_15.	1	p2	(TC)7	14	95	108	CCTCCACTGTTTTGTGCCAT
scaffold488196_16.	1	p2	(GA)6	12	925	936	CTCGTGAAGCGACGTGAATA
scaffold488227_13.	1	p2	(GA)6	12	736	747	ATGATGGAATTGGGTGTTGG
scaffold488246_18.	1	p2	(AT)9	18	464	481	TGCTTTGATGTGTTGGCATT
scaffold488248_14.	1	p2	(TC)6	12	242	253	ACAAGATCGAACGGAACGAG
scaffold488249_10.	1	p2	(TC)7	14	46	59	GAAAATTCGAAAATTCCCCA
scaffold488306_11.	1	p2	(GT)10	20	236	255	AGATAACGGCCTAGGCGAAG
scaffold488321_16.	1	p2	(TC)6	12	295	306	TCACTCAATCTGATGCACACTC
scaffold488369_12.	1	p2	(AT)6	12	307	318	TAATCTTGGCCGCTGATTTT
scaffold488429_14.	1	p2	(GT)6	12	138	149	TAATTTTCGTCGGGATGGTT
scaffold488447_10.	1	p2	(TC)8	16	84	99	TCTTTCTCGACGTTTCCTGC
scaffold488488_11.	1	p2	(AT)6	12	1116	1127	TCAAATTTTGCGTAGCATCTC
scaffold488511_16.	1	p2	(CT)6	12	60	71	TGAATCTGACTTCGATTATTTGTGA
scaffold488512_14.	1	p2	(AG)6	12	917	928	CAATTGGTGCAAGAAGACGA
scaffold488592_16.	1	p2	(CT)8	16	288	303	CTTGGGCTAAAATCCCAACA
scaffold488891_16.	1	p2	(AT)10	20	486	505	CCAGGCAAAAATGCGCTA
scaffold488918_12.	1	p2	(TA)6	12	1896	1907	CAAAAACCGGTGAAAAATCG
scaffold488989_16.	1	p2	(CT)9	18	382	399	CACGCATTCTTCCAAACAAA
scaffold488994_19.	1	p2	(CT)7	14	914	927	TTGGTAAATGTTTGGGCAGA
scaffold489067_16.	1	p2	(TA)6	12	1332	1343	GGCGTGGTTTGCAGACTATT
scaffold489079_13.	1	p2	(CT)11	22	155	176	TATGGTTTTTGGCCACTTCC
scaffold489104_14.	1	p2	(CT)8	16	81	96	CATTCACATGGTCCCCTCTT
scaffold489143_16.	1	p2	(CT)6	12	1362	1373	ATAGAGCCCCACGTTCACAG
scaffold489194_10.	1	p2	(AG)6	12	245	256	AGGGTGCCAAGATTAACACG
scaffold489276_17.	1	p2	(TA)6	12	132	143	ATATTCGAACGGCCTTGTTG
scaffold489281_15.	1	p2	(AT)8	16	353	368	CACACTCAAGCACACACACG
scaffold489583_12.	1	p2	(TG)7	14	1481	1494	AGCATTTGATTAATCCCCCA
scaffold489584_12.	1	p2	(AC)6	12	422	433	AACAGCACGGACAGCTTCTT
scaffold489639_13.	1	p2	(TC)6	12	482	493	CGTAGCGAAGAAGCGAGAAT
scaffold489656_14.	1	p2	(GA)9	18	1137	1154	TGAGAGAGGAGACGCCATTT
scaffold489675_14.	1	p2	(TA)9	18	772	789	TGATTGTAAATGAATTGAGTCGAA
scaffold489686_12.	1	p2	(TA)8	16	535	550	AACAGGAACCGCTGATTTTG
scaffold489687_14.	1	p2	(AT)6	12	138	149	GGTGCTTTGACTTATGTAAAGTTG
scaffold489894_12.	1	p2	(GA)6	12	283	294	TGGAGATATGGTAGCGGTCC
scaffold489924_10.	1	p2	(TC)6	12	65	76	TTGTTTTCTGTTCTGGCGTC
scaffold489950_15.	1	p2	(CT)6	12	54	65	CGCGAGTTCATAACTCTCTCTC
scaffold490102_10.	1	p2	(TG)8	16	176	191	AACTCAGCATACAGCAGTTTCA
scaffold490116_13.	1	p2	(GA)8	16	1060	1075	GAATAATGGGGGTGATGTGC
scaffold490162_14.	1	p2	(AG)10	20	460	479	TGGTTTCAATTTGGGTGGAT
scaffold490276_10.	1	p2	(GA)10	20	184	203	ATTCGGAGCGAGGCTAAGTT
scaffold490293_10.	1	p2	(GT)6	12	228	239	TCCCAACTCGTCAATCCTTC
scaffold490471_13.	1	p2	(GA)6	12	93	104	GCTTCCATTTCACTTGAATGTTT
scaffold490493_15.	1	p2	(TA)9	18	6282	6299	ATTGGGCCTATCAATGCAAG
scaffold490501_11.	1	p2	(AT)6	12	832	843	AAGTGGTATAAACGGGCGTG
scaffold490513_12.	1	p2	(GA)6	12	242	253	CGTTTGAGAGGAATCATGGC
scaffold490523_17.	1	p2	(AG)10	20	48	67	GAATTAGCATACTGGCTCATTTATT
scaffold490557_15.	1	p2	(AT)7	14	274	287	CGTTGAAGAGATTACGCAACA
scaffold490585_18.	1	p2	(GA)6	12	87	98	AAAACGAATTTGGTGTTGGAA
scaffold490590_10.	1	p2	(TA)10	20	685	704	CGGCCATCAGATATGGAGAT
scaffold490612_17.	1	p2	(AT)7	14	3470	3483	TAACCACTCAAGGCCGGTAG
scaffold490622_10.	1	p2	(TA)8	16	34	49	ACAAACTAATCAAGTTCCGCA
scaffold490635_15.	1	p2	(AT)6	12	235	246	CTTTTCACACGAGGTCACGA
scaffold490652_17.	1	p2	(AG)6	12	544	555	CACAGGATGATGCAGAGGAA
scaffold490705_15.	1	p2	(TA)7	14	1036	1049	CGCGATTTTAAACCCTAAAGAA
scaffold490719_17.	1	p2	(AT)6	12	87	98	GAAATTTCATTATTTCGTCGTTATT
scaffold490725_17.	1	p2	(AT)7	14	138	151	CCAAAGAAAAGTGCATTACAAAA

scaffold490744_16.	1	p2	(TA)7	14	964	977	TGGGAAAATTGAAGAACATTTG
scaffold490752_11.	1	p2	(AT)7	14	1140	1153	CAAGCTGATTTCCCACCCTA
scaffold490840_12.	1	p2	(GA)6	12	246	257	GATTTCTTGGTTCCGGATGA
scaffold490859_16.	1	p2	(TC)6	12	1007	1018	ATTTGATCAACAGGCGATCC
scaffold491074_12.	1	p2	(AG)6	12	752	763	CCAATGTGCACGCAAAATAC
scaffold491383_14.	1	p2	(AT)6	12	361	372	AGCTGGGAGGCTTGGTAAGT
scaffold491520_13.	1	p2	(TG)6	12	734	745	GTTCCCGCGTCATAAAAAGA
scaffold491538_15.	1	p2	(CA)6	12	1702	1713	TGGAGAGGGCTAAACAGTCG
scaffold491562_12.	1	p2	(GA)6	12	120	131	GAAGCGAGAAGGGAGGAACT
scaffold491578_14.	1	p2	(TA)7	14	137	150	TATGCTCCTTTTGGTTTGGG
scaffold491579_17.	1	p2	(AT)6	12	1773	1784	GGGCGCTTGTAGACTTTTCA
scaffold491600_13.	1	p2	(TA)9	18	2131	2148	ACAACACATTGCCACACCAA
scaffold491613_11.	1	p2	(TA)6	12	258	269	GCGTTGACGTACACAGCTTC
scaffold491696_15.	1	p2	(TA)6	12	446	457	TGAAATATGTCTCCTCCGGC
scaffold491700_15.	1	p2	(TC)10	20	1925	1944	ATCTCCACCTTCAATGTGCC
scaffold491790_20.	1	p2	(CT)7	14	289	302	CAGCTGTCGAATCTGCTCTG
scaffold491806_10.	1	p2	(CA)7	14	1066	1079	TGAGTGGTGTTGAGAAACGC
scaffold491910_15.	1	p2	(AT)7	14	295	308	TTGAATTTTGTTGAAATTGGGA
scaffold492031_15.	1	p2	(AT)8	16	3307	3322	AACGCGATATGGATGAAACC
scaffold492129_10.	1	p2	(TA)7	14	121	134	GATATGAAGTGTCACAATATAAGCAT
scaffold492255_17.	1	p2	(GA)6	12	153	164	CTCAGAGAGGTTCACGGTCC
scaffold492310_13.	1	p2	(TA)6	12	140	151	ATTACATGAATGCCGAGCTG
scaffold492379_13.	1	p2	(TC)7	14	174	187	AAGACCTTGTTGCCACGAAC
scaffold492455_16.	1	p2	(AT)6	12	2148	2159	CGACGACTCAGTCAAACCAA
scaffold492474_13.	1	p2	(CT)9	18	414	431	GGAACAAACCATCCTCAACC
scaffold492658_10.	1	p2	(GA)7	14	54	67	GCGAAGCACCGAGACTACTG
scaffold492865_10.	1	p2	(TC)6	12	309	320	TGGACTTGGCTAAGAATGGC
scaffold493039_17.	1	p2	(TG)8	16	2472	2487	TCATTTCGGATGGAAGGAAC
scaffold493090_17.	1	p2	(AT)6	12	54	65	CAGCACGAATCACACAGTAACA
scaffold493143_16.	1	p2	(TC)7	14	4550	4563	AACTGACGGGTGATCAAAGG
scaffold493238_15.	1	p2	(AT)9	18	133	150	TTATGAGTTTGCTCCTGGGG
scaffold493240_15.	1	p2	(AT)8	16	135	150	TATATCACGGGGGACTCGAC
scaffold493258_13.	1	p2	(AT)9	18	802	819	TGCCTCAATCTCCATAAATCAA
scaffold493345_10.	1	p2	(GT)7	14	330	343	GCGTAGACGGAATAAAATTCG
scaffold493384_13.	1	p2	(AT)6	12	222	233	CCAGGGAATCTTTTGAGCAC
scaffold493642_17.	1	p2	(AT)7	14	585	598	CCAAATCGGGGACACATTAC
scaffold493686_13.	1	p2	(TA)6	12	1557	1568	TGCATAATTGTAGATAATGGACCG
scaffold493704_14.	1	p2	(CT)9	18	345	362	GGGAGTGAAGATTGGCAGAG
scaffold493801_19.	1	p2	(TA)8	16	891	906	ACGGTGGGCACTACAAGAAC
scaffold493810_15.	1	p2	(AG)6	12	538	549	GAAGCGGGATGAAGAATTGA
scaffold493822_11.	1	p2	(TA)6	12	154	165	AAATATCGGCCGTCAGATTG
scaffold493907_10.	1	p2	(TC)6	12	157	168	GCTTGGTTGGCTTGAGTTTC
scaffold493967_12.	1	p2	(CT)7	14	431	444	CGGTCAACATGTCAGTGTCC
scaffold493993_14.	1	p2	(CT)6	12	47	58	TCTCTCTTGGTTGGTGAAGAAA
scaffold494079_17.	1	p2	(TC)9	18	497	514	CCTCTTGATTTTCTCGCTCC
scaffold494116_16.	1	p2	(GA)8	16	301	316	TATGGTGATCGGGTTTGACA
scaffold494172_14.	1	p2	(AT)6	12	72	83	CAAAACTTCACGAAGAAAACACA
scaffold494225_12.	1	p2	(AG)11	22	31	52	AGAAACTTGACGTGTGCGTG
scaffold494246_10.	1	p2	(TA)10	20	332	351	ATGCTTAAAAGAAAGCGGCA
scaffold494302_14.	1	p2	(CT)8	16	2800	2815	CGGTGGATGTCTTGGTCTTT
scaffold494310_13.	1	p2	(GA)6	12	114	125	AGATTTTCGGACATCGCATT
scaffold494403_10.	1	p2	(GC)7	14	238	251	CGTTGCCGGATAATTCAAAC
scaffold494446_15.	1	p2	(GA)6	12	69	80	TCCAGTATACAATTCCAACAGGAG
scaffold494453_10.	1	p2	(CA)6	12	685	696	TAGTTTGTTTCCCGCCAAAA
scaffold494489_14.	1	p2	(AG)6	12	93	104	TTTCCTTCTTGGATTATGCGA
scaffold494559_14.	1	p2	(TC)6	12	70	81	CACCACACCCTCACTCTCCT
scaffold494580_11.	1	p2	(AT)8	16	136	151	GGGGAATGTAACAGGGGATT
scaffold494593_10.	1	p2	(AG)8	16	65	80	TGTTTTGTAATTTCCCATGTTTG

scaffold494604_10.	1	p2	(TA)9	18	260	277	TGGTATCACATCACAACTTTTCA
scaffold494683_15.	1	p2	(GT)7	14	1207	1220	CCGCTTTCTCATTTCTTCCA
scaffold494748_13.	1	p2	(CT)6	12	557	568	CCCTTAGATGTCTTCATCCCA
scaffold494793_12.	1	p2	(AT)8	16	534	549	AAAATGGTCCACATGTTGTAAAAA
scaffold494826_14.	1	p2	(AG)7	14	197	210	TCAAAGTGGAGAAGGCATGA
scaffold494921_15.	1	p2	(TA)9	18	172	189	TCGTATGCTGCCCCTAAAAC
scaffold495194_15.	1	p2	(AT)9	18	649	666	TGTGCTATCCTAACCAAAAGC
scaffold495255_10.	1	p2	(TA)10	20	91	110	GAAAAATCAAAGGCCCACAA
scaffold495354_18.	1	p2	(TG)8	16	118	133	ATGAATTTTCTGCGAATGGG
scaffold495798_12.	1	p2	(CT)7	14	237	250	GGGTGAATTTTTGGGGTCTT
scaffold495834_15.	1	p2	(AC)6	12	67	78	ATTGCCCATGAATGTCACCT
scaffold496019_12.	1	p2	(GA)6	12	471	482	AGAAATCAACCAATCGGCAC
scaffold496036_10.	1	p2	(GA)6	12	70	81	CACAGAAGGAAAAGAGCGAGA
scaffold496548_15.	1	p2	(TA)6	12	154	165	CTAGGCATGGAATCCGAGAA
scaffold496587_14.	1	p2	(GA)7	14	79	92	CCACAAAGTTCCAATCTTTTAGC
scaffold496753_12.	1	p2	(AT)10	20	86	105	TTACGGCATTAGAGATAATGATTAAA
scaffold496760_17.	1	p2	(TA)6	12	164	175	TTCTAACAGAATAGAGCTTGGGG
scaffold496839_17.	1	p2	(GA)6	12	583	594	ATATACGCCCACATGCGATT
scaffold496843_14.	1	p2	(TA)8	16	137	152	TATGGCCAATTCCGAACTTT
scaffold496880_18.	1	p2	(AT)6	12	91	102	TTTGAGCAGTTCCAATCTCTTG
scaffold496922_14.	1	p2	(TA)8	16	694	709	TCTCGTACACGTGTCCAGTTTT
scaffold496962_14.	1	p2	(AT)6	12	895	906	GAGGGTGGTATTTCGTGTCG
scaffold496983_14.	1	p2	(TA)7	14	65	78	GGGTCATCATGGGATCAAGT
scaffold496994_15.	1	p2	(GA)6	12	196	207	CTTAAGCCGAAAATTCCACG
scaffold497065_15.	1	p2	(AT)6	12	787	798	TGGTGATTGAAATGATTAGCAAC
scaffold497090_14.	1	p2	(AT)6	12	999	1010	ACATCCGGGAGAAGGGTTAG
scaffold497190_15.	1	p2	(TC)7	14	1148	1161	GAAGCAACTTTCTTGGCTGC
scaffold497235_21.	1	p2	(AG)8	16	193	208	GGCAAGCTTTCTCCTTCCTT
scaffold497267_12.	1	p2	(TA)6	12	503	514	CAATTCCTCCCTTGGAGACA
scaffold497528_17.	1	p2	(CT)6	12	1217	1228	ATCATCAGCCGCTTTATTGG
scaffold497539_11.	1	p2	(AT)8	16	349	364	CATAAACCGTCGCACCTGTA
scaffold497540_16.	1	p2	(GA)6	12	5527	5538	TGTTGCTTGTTTCTTGCACC
scaffold497601_13.	1	p2	(TA)14	28	39	66	ATTAAAACCTCGCTCGGATG
scaffold497615_15.	1	p2	(AC)6	12	2135	2146	CATAATAGTGCAGGTGGGGG
scaffold497649_15.	1	p2	(AT)6	12	2529	2540	TAGGGGCCTGCTAAAATTCA
scaffold497663_10.	1	p2	(TA)12	24	249	272	TTCGCTACATTTACGGATTGTG
scaffold497668_14.	1	p2	(CT)6	12	342	353	GCGAGAACCACAAAGCTCTC
scaffold497695_16.	1	p2	(AT)6	12	538	549	CAATTGTTGCAAACAACCAAA
scaffold497741_11.	1	p2	(AT)6	12	411	422	TCGGTTGTTCCATCTCTAATCC
scaffold497742_12.	1	p2	(AT)9	18	197	214	TGTTGGCGTTTTAATCTCCC
scaffold497882_16.	1	p2	(AT)9	18	699	716	TCCCCATCTTCTTCAGTTGG
scaffold497895_11.	1	p2	(TA)10	20	46	65	CCACATTTAAGGGTTATCACCTG
scaffold498040_20.	1	p2	(TC)6	12	122	133	GGGATTCAATCTAGTCGACAATC
scaffold498167_14.	1	p2	(GT)8	16	234	249	AGGGTGGTGAATGCTGAGAG
scaffold498519_12.	1	p2	(AT)10	20	2042	2061	GAAATTAAGAATGTGGAGTGCAA
scaffold498665_11.	1	p2	(TA)6	12	142	153	CCAAAGGTGAAAATCGCACT
scaffold498672_10.	1	p2	(TA)6	12	141	152	TGAATTCAATTTATTTATTGTCGATGA
scaffold498673_15.	1	p2	(AT)9	18	136	153	ATGTGTGATGTATCCCCGCT
scaffold498769_12.	1	p2	(AT)6	12	126	137	GTTTTGCAGGATGGAACTCA
scaffold498841_13.	1	p2	(TG)9	18	888	905	ATAACCCGGTCAACAAGCTG
scaffold498890_15.	1	p2	(AT)6	12	1937	1948	CCACGTGGAAGGACTGAAAG
scaffold498933_16.	1	p2	(AT)6	12	1153	1164	TTTGAGGGGTGGATTTGTTC
scaffold498995_17.	1	p2	(AT)6	12	85	96	TCCGGAGTAAGTTCGAGGAT
scaffold499012_10.	1	p2	(AT)6	12	89	100	TTGAGGCGGTACAAAGGAAC
scaffold499044_11.	1	p2	(TA)8	16	281	296	CAAAGGATGAAAACGAGGGA
scaffold499085_10.	1	p2	(AT)6	12	188	199	ATTGGCTGAGGCATTTGAAC
scaffold499133_13.	1	p2	(TA)11	22	1641	1662	AGCCGTAGAGCCCTGTATGA
scaffold499136_15.	1	p2	(AG)6	12	432	443	TCCTTTAGAGTCGTTGCACAAA

scaffold499167_14.2	1	p2	(TC)6	12	3263	3274 GAAAGATCTGGTCACGACAGC
scaffold499341_10.3	1	p2	(AT)9	18	324	341 AGAGGGGGTATGATGGGAAC
scaffold499418_12.4	1	p2	(CA)6	12	287	298 TGATTTGGCAGTTTGAGAGG
scaffold499517_10.1	1	p2	(AT)6	12	731	742 AACGTAAATGAGAAACATGCAA
scaffold499644_13.8	1	p2	(TC)6	12	2245	2256 ATTTCGAGCCAGACACTGCT
scaffold499710_13.7	1	p2	(TA)6	12	584	595 TTCCCTACAAAACGAGACCAA
scaffold499800_11.5	1	p2	(TA)10	20	169	188 TACGTAAAAACCCTTTCGCC
scaffold499852_15.0	1	p2	(AG)6	12	142	153 TTCCATGATCAGAACGGATTC
scaffold499993_16.3	1	p2	(TA)6	12	269	280 ATCACATCGGAAATTCGTCC
scaffold500074_17.1	1	p2	(AT)9	18	1224	1241 GGTGGGCAAATCAAATGTTC
scaffold500116_14.4	1	p2	(TG)9	18	3262	3279 GCAGAAGCGGGAACTAACTG
scaffold500121_13.4	1	p2	(TA)10	20	47	66 GGTGACAGGCAGCTGAATCTA
scaffold500173_16.8	1	p2	(AG)6	12	1296	1307 TTTGAACGAGGCGGATTTAG
scaffold500254_16.6	1	p2	(TG)8	16	476	491 TTTGACGGGGTAAAATAAAACAA
scaffold500268_11.4	1	p2	(TC)10	20	89	108 AAAAACATCGCTCTCTCCCC
scaffold500393_21.0	1	p2	(TA)6	12	113	124 TGGAACAGTTTGACACAACCA
scaffold500534_16.1	1	p2	(TC)6	12	290	301 TCGTAGTCCCCTTCAGATCG
scaffold500546_15.4	1	p2	(TC)11	22	587	608 ATGCTTGAAGCTATGGGTGC
scaffold500550_12.9	1	p2	(AT)11	22	573	594 TTCCCATCGCCCTACTTATG
scaffold500626_16.6	1	p2	(AT)7	14	3286	3299 ATCCCTCTACCGCCTTAGGA
scaffold500637_14.7	1	p2	(AG)9	18	4280	4297 CAAATTTCACCAAGAACGCA
scaffold500648_16.7	1	p2	(TA)8	16	3490	3505 AATCGAAAATAACGTTGGCG
scaffold500684_13.5	1	p2	(AT)9	18	807	824 CTTTTTGCTATGCAGCCTCC
scaffold500698_11.4	1	p2	(AT)9	18	608	625 AATCATAGCCACGCATGTCA
scaffold500701_14.9	1	p2	(AG)6	12	562	573 CCAATCGTCCTTGCTTCATT
scaffold500706_15.1	1	p2	(AT)6	12	2545	2556 TTTCGCTGTGCAATTCATTC
scaffold501002_10.8	1	p2	(TA)6	12	190	201 CTCACACACCCATATGTCCC
scaffold501014_15.0	1	p2	(CT)6	12	524	535 AAATTGATTTCCCTCCACCC
scaffold501038_11.4	1	p2	(AT)6	12	927	938 AACACATATGGGGACACGCT
scaffold501049_15.9	1	p2	(TC)7	14	3899	3912 TGCGACGTATTGAGAAGCAG
scaffold501077_18.4	1	p2	(AG)6	12	1563	1574 ATGTTCTCTCAGGCCACCAC
scaffold501119_15.7	1	p2	(AG)7	14	219	232 TGGGTGAAAAGAAAAGGCAC
scaffold501146_13.3	1	p2	(TC)7	14	1206	1219 AATATCGCCAAACACCTTGC
scaffold501159_11.4	1	p2	(AG)10	20	137	156 CAAGTCAACAAGCAAGCCAA
scaffold501161_16.1	1	p2	(AG)8	16	2477	2492 CCATCTCGAAAAGATGGGAA
scaffold501214_13.0	1	p2	(TA)7	14	453	466 TGGCTAAAGATCGATGTGACTT
scaffold501282_13.6	1	p2	(TA)9	18	662	679 CGTGAATATGCTGATGCTGG
scaffold501288_11.8	1	p2	(AT)6	12	56	67 TACAAGTGCAGCGGAAATGA
scaffold501475_16.0	1	p2	(CT)14	28	197	224 GGTTATGGTTCTTGATGGGG
scaffold501482_16.3	1	p2	(CT)9	18	202	219 GCGGTGGTGGAGAGAAAATA
scaffold501598_12.8	1	p2	(TA)8	16	772	787 ATGCATCGGGGCAATATTTA
scaffold501608_15.9	1	p2	(TC)8	16	659	674 CCTCCCTCAGATGCAAACTC
scaffold501615_14.7	1	p2	(CT)8	16	221	236 ATAAGGTGGCGATGAGTTGG
scaffold501624_11.7	1	p2	(TC)6	12	106	117 AGGACACGTTGGACCTGAAA
scaffold501678_16.0	1	p2	(TC)6	12	123	134 GTACCGCTGGATAATCCCCT
scaffold501687_14.7	1	p2	(TA)7	14	693	706 TTACGGGAGAATTCACGACC
scaffold501754_16.4	1	p2	(TG)7	14	140	153 TGGTTGTCACATCTTCATGC
scaffold501867_16.5	1	p2	(CT)8	16	1872	1887 GTCAATGTGGGTGCTGTGTC
scaffold501958_18.1	1	p2	(TA)9	18	1395	1412 TGCATGGTCTTCGAAGTAGG
scaffold502044_15.4	1	p2	(CT)7	14	271	284 TCGCATGCAACGATAGTAGG
scaffold502048_12.6	1	p2	(GA)8	16	232	247 TCAACGTCTTCAACGCAAAG
scaffold502063_18.6	1	p2	(AC)6	12	574	585 ACTTCACCGCCAAAACTCTG
scaffold502098_14.6	1	p2	(TA)9	18	326	343 TGATACATAGTGTTATTCTTTGGCG
scaffold502136_10.6	1	p2	(AT)8	16	86	101 GGATCTATTACTAACCGCCCC
scaffold502171_18.3	1	p2	(AT)6	12	809	820 TATCAGGCTGCCTACTCGGT
scaffold502221_14.0	1	p2	(AG)6	12	749	760 GCAGGACAACTACCATACGGA
scaffold502222_13.9	1	p2	(TC)8	16	1577	1592 TGAGGAAGAAGGGATGATGG
scaffold502297_14.1	1	p2	(AT)8	16	1679	1694 ATTGAGGCGTGTTTAGGCAT

scaffold502410_15.	1	p2	(TA)8	16	2420	2435	TTTGAGGTGGGCCAAAATAG
scaffold502515_13.	1	p2	(AT)9	18	533	550	AAAGCAAACCCATGTTCTTCA
scaffold502589_14.	1	p2	(TC)8	16	4487	4502	GTGCTGTTAAGCATCCCCAT
scaffold502636_16.	1	p2	(AT)7	14	141	154	GTCCTCCGAACTCATGGTGT
scaffold502669_15.	1	p2	(GA)7	14	424	437	CGCAATCGATTTTCAAACCT
scaffold502792_12.	1	p2	(AG)7	14	98	111	AAATGCGCCTATCACTTTAATTC
scaffold502861_18.	1	p2	(TC)6	12	625	636	CCCAAACTTGGTTGCTCTTC
scaffold503032_17.	1	p2	(TG)6	12	2089	2100	GCTATGAATGGCATCGAAGA
scaffold503122_17.	1	p2	(TA)7	14	401	414	TGCAACTTTTGTACTCAGCCC
scaffold503129_17.	1	p2	(TA)6	12	2315	2326	TTCCCAAAATAACCGTCAGC
scaffold503262_14.	1	p2	(GT)8	16	32	47	ACTGACATTCACAGGCATTGT
scaffold503293_10.	1	p2	(AT)6	12	265	276	TTGTAGCCCCTTTGAGCCTA
scaffold503315_10.	1	p2	(TG)6	12	138	149	TCCTCAGAAACTTCAACGCTT
scaffold503338_19.	1	p2	(TC)6	12	333	344	ACTATCGACGTCCGGAGCTA
scaffold503385_11.	1	p2	(CT)6	12	88	99	GTCGTTTACTCTTTCCGGCT
scaffold503389_11.	1	p2	(CT)7	14	581	594	TGAAATGGATCACATGCAAAA
scaffold503415_16.	1	p2	(TA)8	16	204	219	TGACGAAAATTGCTTTGATCC
scaffold503417_14.	1	p2	(GA)10	20	981	1000	ACCCAAAACCTCCCATATCC
scaffold503544_12.	1	p2	(AT)7	14	53	66	AGATTGGGCTATTCGAGCCT
scaffold503698_16.	1	p2	(TA)8	16	139	154	GGAAACAAGTGGATGACGGT
scaffold503721_15.	1	p2	(TC)8	16	1647	1662	CAGTTTTGTGTGTCCATGTGC
scaffold503724_13.	1	p2	(CT)6	12	247	258	GTTGGATAATACATGGCGGG
scaffold503840_14.	1	p2	(CT)12	24	38	61	TTTCGAATTTTTCCTCTTTTGTG
scaffold503850_14.	1	p2	(TA)8	16	1483	1498	TTGATCCTTCCTAGGATAACCG
scaffold503862_10.	1	p2	(GT)6	12	25	36	GCGTGTGTGTAACCGTGTGT
scaffold503887_13.	1	p2	(TA)10	20	875	894	AAATCGAGGAGCTGTCATCC
scaffold503971_10.	1	p2	(AT)7	14	857	870	ACTACGTCGATCCAACGGTC
scaffold504093_15.	1	p2	(CT)6	12	254	265	GGCTCGGTATAAAAATGGCA
scaffold504119_15.	1	p2	(TA)7	14	1505	1518	CACAATCCATCTTCAACCCA
scaffold504136_17.	1	p2	(GA)6	12	4755	4766	GACCCAAATGATTGTACGGG
scaffold504224_22.	1	p2	(AT)6	12	358	369	GCTTAAAGTGCGGCCAAA
scaffold504275_17.	1	p2	(TG)7	14	689	702	GTATGGCGTGGTTCCAGTTT
scaffold504299_17.	1	p2	(AG)6	12	768	779	TAAGTTGGGCCTCTCGATCA
scaffold504329_10.	1	p2	(AT)8	16	104	119	ACGAAACACGGAAAAAGCAT
scaffold504357_11.	1	p2	(TA)12	24	477	500	CAATGATGATGCCAATCCAG
scaffold504370_11.	1	p2	(TC)6	12	106	117	CAAATGGCCGAGAGGATTTA
scaffold504413_13.	1	p2	(AG)7	14	210	223	CGCAGCAAAGTAGCATACGA
scaffold504424_10.	1	p2	(TA)8	16	47	62	TTTAGTGTTTTGACATGATTACTCG
scaffold504517_10.	1	p2	(AT)7	14	449	462	GCGTGTGGGAGTTGGTAAAT
scaffold504529_21.	1	p2	(TA)7	14	64	77	ATGAACTAATCAAGTTCCGCA
scaffold504533_15.	1	p2	(AT)8	16	3402	3417	TAGTAGGGTGCAGGGGATTG
scaffold504565_12.	1	p2	(TA)7	14	206	219	CCCGATAGGCTTGAAGGATT
scaffold504687_11.	1	p2	(AT)8	16	91	106	TTACCTACATGGCCCTGCTC
scaffold504752_15.	1	p2	(TC)8	16	871	886	CGTGAAGTCCATCTCCCACT
scaffold504790_16.	1	p2	(TC)6	12	308	319	ATTAATAAAATTTGGAATGATAGAGG
scaffold504791_12.	1	p2	(TA)7	14	227	240	AAACTACCCTTGATCGCACG
scaffold504801_16.	1	p2	(AT)7	14	405	418	CGACTCAGTCATGCACCATT
scaffold504806_18.	1	p2	(AT)10	20	46	65	TGAAGTTAGGAATTAAGGAGGTGTT
scaffold504837_15.	1	p2	(TA)6	12	5356	5367	TTCCTCACGAATAAACCAAGC
scaffold504907_16.	1	p2	(TG)8	16	832	847	GAACGATTTGTTATCGAGGGA
scaffold504910_16.	1	p2	(TA)6	12	143	154	TTTGACTATGTCTGCGTGCC
scaffold505032_13.	1	p2	(AT)6	12	1345	1356	CCTACAAAGCCACTCTAAGCG
scaffold505057_15.	1	p2	(CA)11	22	2040	2061	TCGAGTTGTACCGACACTGC
scaffold505394_15.	1	p2	(AG)6	12	817	828	CTGAAAACTGCAGCACGAGA
scaffold505496_11.	1	p2	(TA)10	20	547	566	TCACAAGTGCAAGCACAATTC
scaffold505505_10.	1	p2	(TA)6	12	221	232	CTCGTCTCAAGAAGGTGCTTT
scaffold505643_16.	1	p2	(TA)7	14	743	756	AGCGCTGAATGTCATTGGAT
scaffold505737_12.	1	p2	(TA)10	20	382	401	TGGGAAGGGTTGTTACTGGA

scaffold505831_15.	1	p2	(TA)6	12	1282	1293	TGATGGCTGTGAATTGGAGA
scaffold505873_23.	1	p2	(TC)7	14	78	91	CCCTAGCTTTGCCCTCTTTC
scaffold505889_11.	1	p2	(AT)8	16	1400	1415	TCAAGTAAGCGAGATTTTCTACATTG
scaffold506111_17.	1	p2	(AG)8	16	50	65	TGATATCTTTGAAGAACAATTACAAT
scaffold506223_17.	1	p2	(AC)7	14	5021	5034	TTTGGCCGAGTTCGGTATAG
scaffold506265_13.	1	p2	(AT)12	24	1247	1270	AAAAAGGGAACAAAAACGGC
scaffold506456_16.	1	p2	(AT)6	12	51	62	TGATGATGAGATTTTAGTCCAAGG
scaffold506478_16.	1	p2	(TG)6	12	2987	2998	CCTTCTCCGTCTGCAAACTC
scaffold506694_14.	1	p2	(GA)6	12	143	154	CACAGCCCTAATGCTACGTG
scaffold506824_16.	1	p2	(TA)8	16	658	673	AGATCTGGGCAATGTGTGGT
scaffold506871_17.	1	p2	(GA)8	16	55	70	GAGCTGGTTTGAGGGAGATG
scaffold506980_12.	1	p2	(AT)6	12	55	66	CCAATTTACTAATTCTTGATGAATCC
scaffold507005_14.	1	p2	(AT)6	12	1533	1544	GTGGTCTAGGATGGGAGCTG
scaffold507055_10.	1	p2	(TA)6	12	186	197	GGGGTGGGAATTAAACACCT
scaffold507056_14.	1	p2	(AT)10	20	81	100	CGCATCCGACTCCTCAATTA
scaffold507062_15.	1	p2	(AT)12	24	1396	1419	TGAATGGGGATCAATTCCTT
scaffold507138_18.	1	p2	(TC)6	12	195	206	CGCCCTCCACTGTTAATGTT
scaffold507150_15.	1	p2	(CT)8	16	139	154	AGGGATCCCAAGGCACTACT
scaffold507161_13.	1	p2	(TA)7	14	192	205	GGCATTTTGGGAAAGACAAA
scaffold507240_12.	1	p2	(TC)6	12	237	248	ATGATCGCCACAAACATCAA
scaffold507312_19.	1	p2	(AC)7	14	656	669	CACCATCAACCTCACCACCT
scaffold507569_10.	1	p2	(TA)8	16	50	65	TGAAAGAAGTGGTGGTGGAG
scaffold507847_12.	1	p2	(TA)9	18	170	187	GACATGCAGAGTTCAACAGCA
scaffold507850_14.	1	p2	(AC)7	14	307	320	GGGGTAAGACCCACCTCATT
scaffold507862_18.	1	p2	(CT)6	12	109	120	TAGCAGCCCACAATTCAACA
scaffold508070_14.	1	p2	(GA)6	12	835	846	CCGGAGAAGTTTGTGGAGAG
scaffold508180_16.	1	p2	(AT)7	14	1091	1104	GGACGCTGACCATCACTGTA
scaffold508197_17.	1	p2	(TC)6	12	144	155	TCAACATTTTTCCCAGAATCG
scaffold508364_14.	1	p2	(TA)7	14	660	673	ATCATCAGTAGCGCCACCTT
scaffold508417_10.	1	p2	(AT)9	18	503	520	TCAAATTCGAAATTCGGACC
scaffold508434_12.	1	p2	(TA)7	14	135	148	TCTGAAAATCAAAGGCCCAC
scaffold508517_14.	1	p2	(CT)7	14	414	427	TACGTTCTTCCCCGTTTTTG
scaffold508523_10.	1	p2	(TA)6	12	211	222	TGGTTGGAGTTGTCAGTTCCT
scaffold508668_17.	1	p2	(GA)6	12	532	543	CGAAACCCCTTTCTCTCTCC
scaffold508676_20.	1	p2	(CA)6	12	211	222	TCTCCCTCGGTAATTCCCTT
scaffold508826_16.	1	p2	(AT)9	18	194	211	GGGGTGTATTAAAATAGGAGCA
scaffold508912_16.	1	p2	(GA)8	16	2696	2711	CCTCCATCATGAAAACCGAG
scaffold508935_15.	1	p2	(CT)6	12	457	468	CTCCTCTGCACCAACCTCTC
scaffold508982_16.	1	p2	(AT)7	14	644	657	CACAAAACTCATACCCGTGC
scaffold509015_13.	1	p2	(AG)6	12	100	111	CCAAAATAGATGGCATTCAAGA
scaffold509043_14.	1	p2	(CT)6	12	72	83	TGGAAGTTCTCTCCTCTCGC
scaffold509125_16.	1	p2	(AT)9	18	398	415	ATCGTGGGCGTAAATCATGT
scaffold509145_13.	1	p2	(AT)7	14	71	84	GGTTATGACTTGATCATGACCCT
scaffold509161_10.	1	p2	(TA)8	16	209	224	GCATATCAAATGGTGTTTGGG
scaffold509190_13.	1	p2	(TA)10	20	218	237	GGTGGCGTATGCTGAGAGAT
scaffold509321_17.	1	p2	(TC)6	12	365	376	TCTCTTTCGTCCTTTTTCCC
scaffold509346_15.	1	p2	(TA)8	16	141	156	TTCCCGAGTAAGATGGATGG
scaffold509350_14.	1	p2	(TC)6	12	269	280	TTCCCTCACTCCTCTTCTGC
scaffold509352_18.	1	p2	(CA)6	12	73	84	GAACACACGAAGATTGGGAGA
scaffold509453_10.	1	p2	(CT)7	14	661	674	CAAATACGACGGAAAATCGG
scaffold509514_16.	1	p2	(AT)8	16	70	85	AATGAAATCTTACTACTCCAAAAATC
scaffold509822_12.	1	p2	(TA)8	16	301	316	TCTTTCGGCTGACTTTTTCTTT
scaffold509990_13.	1	p2	(TA)6	12	309	320	AAGATCTACGTCCACGGGAG
scaffold510106_11.	1	p2	(TA)8	16	482	497	TGACTGCCCAAGAAATCACA
scaffold510120_20.	1	p2	(AG)6	12	993	1004	TGATTACTTCCGCACCATTG
scaffold510258_19.	1	p2	(GA)7	14	1703	1716	AACAGAAAGCCACACATGTCA
scaffold510339_12.	1	p2	(TA)9	18	44	61	CGGATTTAAGGGTTATTACCTGAT
scaffold510348_16.	1	p2	(CT)6	12	88	99	CCTTCTTTTCACGCATTTCC

scaffold510359_17.3	1	p2	(TA)8	16	576	591	TTTGCCGACCTTATCTCCAC
scaffold510432_13.3	1	p2	(AC)9	18	559	576	TGGCTTCAGCAGACAATGAG
scaffold510436_10.4	1	p2	(TA)7	14	143	156	ACGAGATCGAAGGGAGACAA
scaffold510443_15.5	1	p2	(GC)6	12	516	527	TCACGATGCGTCACAAGTTT
scaffold510476_17.8	1	p2	(AG)6	12	3397	3408	TGTTTGGTAGCCCACACAAT
scaffold510607_11.8	1	p2	(TC)7	14	257	270	TAAGGCAAAGCACGTGAGTG
scaffold510664_13.0	1	p2	(AG)7	14	1425	1438	TCAGATGAGTTGAATGGAACAGA
scaffold510665_12.3	1	p2	(TA)8	16	711	726	CACTCGCATAAGTATGCATGAAA
scaffold510688_15.5	1	p2	(AT)8	16	501	516	CACTCACACACACGCACTTG
scaffold510755_14.2	1	p2	(TA)6	12	92	103	CAAGAGCTTGAGCTCGGAGT
scaffold510875_12.4	1	p2	(AT)9	18	399	416	TTTCAAATTGCATCCTAGCAAA
scaffold511000_16.2	1	p2	(CA)6	12	145	156	GAGAGTGGAGGCCATTTCTG
scaffold511062_19.8	1	p2	(CT)9	18	519	536	TCAACAACCAGTCCACTCCA
scaffold511146_10.0	1	p2	(TA)9	18	327	344	TGCGTCAAAAGCTCTTCAAA
scaffold511185_10.4	1	p2	(TA)8	16	145	160	TCCAGATTTGTTCCTACGCA
scaffold511230_15.5	1	p2	(GT)6	12	238	249	CCACAAATCCCTTCATTTGG
scaffold511392_14.8	1	p2	(AT)9	18	699	716	CTCAAATTGGAATTGGGCTG
scaffold511413_16.9	1	p2	(GA)9	18	47	64	GGGAGAAGAGAGAGTTAGGGTGA
scaffold511442_16.6	1	p2	(GA)6	12	233	244	TGGAGCTTTGATCCTTGCTT
scaffold511512_13.8	1	p2	(AG)6	12	55	66	AACCACCTTTACAAATGAGCTAGT
scaffold511567_17.4	1	p2	(CT)7	14	56	69	TCACTTCATTACGAAAAACACCA
scaffold511640_14.0	1	p2	(AC)7	14	2437	2450	TGTGTCATCTAGTCCGGTGG
scaffold511663_15.0	1	p2	(TC)7	14	2401	2414	TCCATTTCCTCCACCGTTAG
scaffold511734_13.0	1	p2	(AT)11	22	1312	1333	CACCGACCAAACATATGCAC
scaffold511842_15.2	1	p2	(TA)9	18	241	258	AAAGTCATCCGCTATCTCGAA
scaffold511891_13.8	1	p2	(TA)9	18	104	121	TTTTCATTCTTGACCCCTTCTC
scaffold511919_10.2	1	p2	(TG)9	18	50	67	AAGCTGCATGCATTTCAGAG
scaffold512007_14.9	1	p2	(AG)6	12	129	140	GCGCCGCCTATCACTTTAAT
scaffold512067_16.7	1	p2	(AT)8	16	782	797	AGCGACGAACGGAAAAAGTA
scaffold512207_18.3	1	p2	(AT)7	14	144	157	CCACATTTTTCCCGATTGTT
scaffold512216_15.3	1	p2	(GA)9	18	1327	1344	AATGAGCAAAACGGTCCTTG
scaffold512392_13.2	1	p2	(CT)7	14	62	75	ACAAAAAGGGATGAGCGACA
scaffold512399_21.1	1	p2	(AG)9	18	140	157	TGTTTCCCATTTTCACCACA
scaffold512434_14.7	1	p2	(TC)8	16	96	111	CATGAGGCCCCAAGATAATG
scaffold512565_18.2	1	p2	(TA)6	12	252	263	TCTGCAAATGTCACACGTCA
scaffold512604_13.0	1	p2	(AC)8	16	1184	1199	CCAAGAGGAGTTGAAGTCGC
scaffold512679_10.6	1	p2	(TA)7	14	487	500	CACCGCCAAATATCACCTCT
scaffold512742_17.6	1	p2	(CA)6	12	253	264	ACGTGGTCTCTCCCCTTTTT
scaffold512772_17.3	1	p2	(CT)6	12	1280	1291	AAGAGGAGAGACGGAGAGGC
scaffold513022_10.1	1	p2	(TA)10	20	172	191	TGCTGTGAATTGTCCAGCTC
scaffold513095_13.9	1	p2	(CT)6	12	436	447	GAAGTAAACGGCCAAAGTGC
scaffold513106_11.4	1	p2	(AT)7	14	66	79	CGAAATCTTACTTTGCGGCT
scaffold513134_13.8	1	p2	(GA)6	12	1557	1568	CATCAAGTTTCCCAAGGCAT
scaffold513238_14.6	1	p2	(TC)7	14	30	43	TGGTTGGTGGAAGAAATCAA
scaffold513266_15.1	1	p2	(TA)6	12	704	715	TTAAATACGACCGGGCTCAC
scaffold513300_14.7	1	p2	(CT)13	26	2032	2057	TGCCCAAAAACATTTCAACA
scaffold513337_12.2	1	p2	(TA)12	24	87	110	AGGGGTTATCACCTGAATGC
scaffold513383_13.2	1	p2	(AG)6	12	168	179	TGTTATCCTTTGTGAGCCCC
scaffold513562_12.0	1	p2	(GA)6	12	830	841	ACCATCGCTGTTACCACCTC
scaffold513704_13.0	1	p2	(TA)10	20	138	157	CTGACATTTGACCTGAGCGA
scaffold513706_18.4	1	p2	(AG)6	12	94	105	TTGGAAAATAACATGCATAGAAAA
scaffold513797_13.1	1	p2	(TA)9	18	278	295	CCGAAACCAGAATGAGAACC
scaffold513800_10.7	1	p2	(TC)6	12	542	553	GCCGTAGTAACTCCAGCCAC
scaffold513804_12.5	1	p2	(TA)6	12	547	558	CACTAGCAGGTCGACACGAA
scaffold513852_16.7	1	p2	(AT)6	12	468	479	TTCATCTCAAATTTCATTGTGGA
scaffold513959_16.0	1	p2	(GA)10	20	2736	2755	TAGCTTTCCCCCACATACCA
scaffold513983_14.4	1	p2	(TA)7	14	348	361	CGAATGAAATTATTTGTTTTCCC
scaffold514008_11.0	1	p2	(TA)8	16	198	213	CCCACATTAACACCCAATCC

scaffold514093_13.	1	p2	(TA)7	14	572	585	GGCCAAGTTGGTGAAGTAGG
scaffold514102_15.	1	p2	(TC)6	12	585	596	TAAAAACACAGCCTCCCTGC
scaffold514257_18.	1	p2	(AT)6	12	237	248	CGTCGTTTCGTGTTCTTTCA
scaffold514268_13.	1	p2	(TA)6	12	236	247	TCATGGTTGGGTGTTTTTATCA
scaffold514361_13.	1	p2	(AT)9	18	93	110	TTGATCCAAGGGTGTATAATGG
scaffold514373_13.	1	p2	(TA)9	18	406	423	CGCTCAGGTTTGAATCTGTTT
scaffold514392_15.	1	p2	(CT)6	12	1253	1264	CATGGTTGCAAAGGTGATTG
scaffold514411_12.	1	p2	(CT)6	12	2164	2175	GGAACAACTGCACCGAATTT
scaffold514424_16.	1	p2	(TA)7	14	5081	5094	CTGGTGCAATGCTTGAGAAA
scaffold514512_17.	1	p2	(AT)6	12	501	512	GAATGTCATGAGTTGAGGCG
scaffold514571_12.	1	p2	(TA)7	14	569	582	AAACTCCCGCTCAAATAGCA
scaffold514639_15.	1	p2	(AT)7	14	1623	1636	TCTGTTTGCGAAATTTGTTGA
scaffold514667_13.	1	p2	(TA)6	12	168	179	TGTTTCGGACTAAACTGGCG
scaffold514668_16.	1	p2	(AT)6	12	881	892	AGATTGGGCTATTCGAGCCT
scaffold514758_18.	1	p2	(TC)6	12	302	313	ACTTTTGCGTCCTTTGTCGT
scaffold514788_13.	1	p2	(TA)8	16	50	65	ATGAGTTATCACCGGATCGC
scaffold514794_15.	1	p2	(AG)6	12	92	103	TGCTACGGTTTCTTCTTCCG
scaffold514822_15.	1	p2	(GA)8	16	2999	3014	ACGATCGCCCACTTATTGAG
scaffold515106_12.	1	p2	(AT)8	16	143	158	AGCTTGTAGAACGAGCCGAG
scaffold515216_16.	1	p2	(GT)7	14	2903	2916	CAAAGCATGAACAAATGCGT
scaffold515220_17.	1	p2	(TA)10	20	250	269	AATTGCTGGCAAATCGTAGC
scaffold515228_13.	1	p2	(AG)6	12	418	429	TGAAGCAATCAAAAACGGTG
scaffold515241_18.	1	p2	(AT)7	14	691	704	GGTCCAACTCCGATTCAAAA
scaffold515309_17.	1	p2	(CT)8	16	52	67	TTGATTGTAATTCTCTGCACCA
scaffold515425_10.	1	p2	(GA)6	12	55	66	AAAAACTGTAGTGGGTTAAAATTCA
scaffold515431_13.	1	p2	(AT)7	14	145	158	TGTGACGAGCTTATGAAACTATACG
scaffold515448_11.	1	p2	(AT)8	16	143	158	TATTAACCCTTCATTGTTTTTAAATG
scaffold515502_10.	1	p2	(AG)8	16	52	67	CAAATGAGCATGAGGGAGGT
scaffold515512_16.	1	p2	(TA)8	16	88	103	AACGGCCGAGATTTGTTATG
scaffold515658_21.	1	p2	(CT)6	12	40	51	TTGATTCCTCCCCACAATTC
scaffold515689_15.	1	p2	(TG)6	12	481	492	GTATGCTGACGTCCTCACGA
scaffold515852_18.	1	p2	(TC)7	14	4205	4218	CAGAAGCAAGATTCGACCAA
scaffold515866_11.	1	p2	(TA)7	14	266	279	TTTCTCCCCATCGATAACCA
scaffold515898_16.	1	p2	(CT)8	16	1073	1088	CTTGGGATGGGGGAGTATTT
scaffold516004_13.	1	p2	(AG)6	12	440	451	CCCAGTATCCCAAACTCGAA
scaffold516047_15.	1	p2	(GA)8	16	1030	1045	TGCTTTTCCATGGTGACTGA
scaffold516215_17.	1	p2	(AT)6	12	2072	2083	TGAGAACCAAACACAAATGTCA
scaffold516234_18.	1	p2	(GA)8	16	898	913	CCGAGAATCAGGACTCGAAA
scaffold516363_11.	1	p2	(AG)11	22	295	316	GGTATTGGCAAATGCAGGTT
scaffold516543_16.	1	p2	(TC)7	14	246	259	AAACGCACCAATTTCCTTCA
scaffold516577_15.	1	p2	(GT)6	12	318	329	TTTGACATGATCACACCCCT
scaffold516598_15.	1	p2	(AG)6	12	147	158	CGACTGGGCCTATCCTATCA
scaffold516654_13.	1	p2	(CT)6	12	102	113	GCCTTCTAGCTTCTCTTGCTTTC
scaffold516814_12.	1	p2	(AG)8	16	690	705	TAGATGCGTGCATAATTGCC
scaffold516967_13.	1	p2	(AT)9	18	221	238	TGTTTAAATGCACACCCCTTT
scaffold517060_15.	1	p2	(AG)6	12	1873	1884	ATCGAACCGTTTTTCTGTCG
scaffold517061_14.	1	p2	(CT)6	12	55	66	GCCTTCTAGCATCTCTTGCTC
scaffold517082_14.	1	p2	(CT)7	14	50	63	CACTCAATTCATTTCACCTCCA
scaffold517277_10.	1	p2	(AT)10	20	180	199	TCTCTCCACCAAATGTCCAA
scaffold517291_13.	1	p2	(AG)6	12	109	120	GCGGCACACGAGGTATAAAA
scaffold517306_17.	1	p2	(TA)6	12	436	447	TTTGTGGTATCAGAGCCACG
scaffold517487_12.	1	p2	(CT)6	12	69	80	TCTTTTGCTATGTCCTCACTCG
scaffold517510_15.	1	p2	(GA)6	12	98	109	CAGGGAGGCAAAAAGAGGTT
scaffold517547_16.	1	p2	(AT)6	12	169	180	TGGGATATAGCGAGTTTGGTG
scaffold517585_10.	1	p2	(TA)6	12	165	176	TGGGGTTTTACAAGAATGCC
scaffold517610_10.	1	p2	(GT)7	14	1677	1690	GTGCGTGTGAGTGTGTGTCA
scaffold517667_14.	1	p2	(CT)9	18	1349	1366	CCGTCTTCTTCTCCATTCCA
scaffold517741_14.	1	p2	(TA)8	16	1571	1586	TGGGATGAAAATAGGGGAAA

scaffold517769_20.	1	p2	(TA)6	12	51	62	TGACGGGATTTAGGTGTTTTG
scaffold517790_11.	1	p2	(CT)6	12	76	87	AAGGGGGATCAAATCTAGTCTTTT
scaffold517856_12.	1	p2	(TA)8	16	395	410	CATTCAAGGGGCATTTTTGT
scaffold517861_16.	1	p2	(CA)9	18	2609	2626	GCATAGTGCTCCAAAAAGGC
scaffold517907_12.	1	p2	(CT)6	12	93	104	GCCATCTCTCCCTAACCTCC
scaffold518056_15.	1	p2	(TC)6	12	95	106	AGCATCTCTTGCTCTCTCGTT
scaffold518062_13.	1	p2	(AG)6	12	503	514	TCGTCTTCGTTCTCCGTCTT
scaffold518123_14.	1	p2	(TA)6	12	53	64	TTTCTCACTATAAGGTGGTGTTCC
scaffold518166_15.	1	p2	(TG)8	16	1352	1367	GAATACTTGCCTCAGCTCCG
scaffold518253_11.	1	p2	(TC)6	12	368	379	ATTGAATCTACGTCCACGGG
scaffold518271_14.	1	p2	(AG)7	14	494	507	GCCAGCTTTTTCTTCTCCAA
scaffold518297_17.	1	p2	(TA)6	12	147	158	CCCTTTACCTCACTGGTGGA
scaffold518305_13.	1	p2	(CT)6	12	365	376	TCACCCCCATCTTCTCTCAC
scaffold518461_15.	1	p2	(GA)6	12	1040	1051	CAGGTTCTCATCGCTCTGTG
scaffold518562_16.	1	p2	(AG)6	12	889	900	CATGGTGATAGAGCCGGATT
scaffold518631_16.	1	p2	(AT)6	12	48	59	CTTCTCGTGTCCGACTCCTC
scaffold518633_16.	1	p2	(AT)7	14	146	159	AATCGAGGGCGAAGAGAAAT
scaffold518685_15.	1	p2	(AT)6	12	682	693	AAAATATGGGGTTTTCCCAAA
scaffold518832_17.	1	p2	(AT)6	12	4862	4873	CTTGGGCTTTCATGACGAAT
scaffold518849_13.	1	p2	(TA)8	16	244	259	AACCCAAGACCTCAAGCTCA
scaffold518856_16.	1	p2	(TG)7	14	1387	1400	TGTTGAAATCTTGAACGGGTC
scaffold518881_10.	1	p2	(TA)8	16	181	196	AAAAACGCGAATTTTTAGGG
scaffold518886_14.	1	p2	(AT)10	20	39	58	TATTTGTGCGTGCACCTGAT
scaffold519004_15.	1	p2	(AT)7	14	1051	1064	AGCACTGAGCAGAAAAGGGA
scaffold519034_10.	1	p2	(TA)7	14	49	62	ATCGGTTATTACCGGATCGC
scaffold519053_16.	1	p2	(CT)7	14	146	159	GCGTTGAGAAGAAGGGAGAA
scaffold519056_13.	1	p2	(CT)9	18	261	278	TCCCCTAATTCCCTCATTCA
scaffold519132_13.	1	p2	(AG)6	12	756	767	GGTGAAACTTGAACAACCCC
scaffold519194_14.	1	p2	(GA)6	12	1013	1024	TGGAACAAGGTGGTGGAAAT
scaffold519237_14.	1	p2	(GA)7	14	358	371	GGAGATCAGCTACGGTCTGC
scaffold519306_15.	1	p2	(CT)6	12	1524	1535	GCTCCCCTTGTGACACTGTT
scaffold519325_13.	1	p2	(AG)12	24	460	483	TCCATCAGACAGTTTCTTGCAT
scaffold519551_17.	1	p2	(CT)7	14	312	325	TCCCTCCTCAAATTTACCCC
scaffold519559_16.	1	p2	(TA)8	16	517	532	CGGGATCTTCATCCAATTCA
scaffold519655_11.	1	p2	(AT)9	18	423	440	TTGGAATAGGGTTTTCAGGG
scaffold519867_11.	1	p2	(TA)9	18	347	364	GAAAGGCACAAAGCGATAGG
scaffold519926_14.	1	p2	(AT)11	22	1367	1388	CGGCGTTTATTTTGTTTGCT
scaffold519946_15.	1	p2	(AG)8	16	93	108	GCTCGTACGAAACCCTTGAG
scaffold520102_15.	1	p2	(TC)6	12	606	617	AATTTCCCGGTGGACTCATT
scaffold520310_11.	1	p2	(GT)6	12	319	330	GCATGAGAAACCTCAAAGGC
scaffold520362_14.	1	p2	(TC)7	14	901	914	ATGCAACCCTCCCTTTCTCT
scaffold520396_10.	1	p2	(AT)6	12	63	74	GACCTACAGACCGATCATGAAA
scaffold520468_20.	1	p2	(AT)6	12	56	67	TGCTCACATCTCTTTTTCTCTTTTT
scaffold520495_13.	1	p2	(AT)6	12	72	83	TGCCTTATAAGCTCGAGAAAAA
scaffold520516_17.	1	p2	(TA)6	12	564	575	TGAGCCCAATTTAGTCAGCC
scaffold520533_12.	1	p2	(AT)6	12	1344	1355	CATCGCATTGACACATAATCG
scaffold520538_15.	1	p2	(AT)10	20	1323	1342	TAGCCGTTTATGACCGTTGA
scaffold520641_14.	1	p2	(TC)8	16	1612	1627	TTTTGGGATGGACCAAGTTT
scaffold520747_17.	1	p2	(TC)9	18	2108	2125	TCAAAGCCTTTTTGCCTCAT
scaffold520886_18.	1	p2	(TG)7	14	2414	2427	CGATGCTTTAAAAGATGTCAACC
scaffold520938_11.	1	p2	(AT)6	12	123	134	AAGAAAGAAATAGAGCTGCTGGAA
scaffold520954_10.	1	p2	(AT)7	14	353	366	TCGTCCTGGTTGTTCCAAAT
scaffold520955_16.	1	p2	(AT)7	14	1034	1047	CGACTTGGCTCCATGTTGTT
scaffold521129_17.	1	p2	(AT)7	14	2201	2214	TGCATCCAGTGGCGTATCTA
scaffold521220_11.	1	p2	(AT)9	18	117	134	GAATTCGGATTCGAGTCATATAAT
scaffold521286_12.	1	p2	(AT)9	18	679	696	CAGGATGAAGACGATGCTGA
scaffold521408_12.	1	p2	(GA)6	12	55	66	GAAGCTTCAATGGAGGTGATTC
scaffold521482_18.	1	p2	(GA)6	12	889	900	TTCGGAATTGGATTATGTTGC

scaffold521593_18.	1	p2	(TA)7	14	147	160	ACCCTCGAATGCTATGACCA
scaffold521658_13.	1	p2	(CT)7	14	359	372	TCCCCTTATTTGTCCACACC
scaffold521670_16.	1	p2	(TA)6	12	522	533	ACACATCTTGCAACCCACAG
scaffold521699_14.	1	p2	(TA)6	12	53	64	CCAATTTGAATGGTTATCACCTG
scaffold521706_16.	1	p2	(AT)6	12	809	820	GAGGCTTAAAGCTGTGCTGG
scaffold521806_11.	1	p2	(AT)7	14	147	160	GGATAAATGTGGCGAATGCT
scaffold521816_15.	1	p2	(CT)10	20	59	78	TCCATCATCATAGGCGTCAC
scaffold521843_10.	1	p2	(CA)7	14	290	303	CCATCATCCTCTCTCCCAAA
scaffold521862_14.	1	p2	(AT)9	18	1753	1770	AGGTGGCACTCTGAAATCAA
scaffold521863_14.	1	p2	(AG)8	16	245	260	TTTGGTTCAAGGATTTGATGC
scaffold522013_17.	1	p2	(AT)6	12	215	226	GCGTATGGGTAGAGCGAGAG
scaffold522123_13.	1	p2	(AT)9	18	1207	1224	GAAGAAGCCGACAATTTGCT
scaffold522237_15.	1	p2	(CA)8	16	673	688	TTCTACCGCAACACAAGGTG
scaffold522319_15.	1	p2	(TA)6	12	1335	1346	GCTACGTGGGAGCTCAAGTC
scaffold522440_11.	1	p2	(TA)6	12	921	932	CGACTCCATTTGGGTTTTGT
scaffold522484_13.	1	p2	(CT)11	22	444	465	CAGATCTTGGCAACTCCCTC
scaffold522508_16.	1	p2	(AT)9	18	2851	2868	ATGTCGAAGAATCCGAATGG
scaffold522528_18.	1	p2	(AT)6	12	573	584	TGGACCGGTTAGATCGGATA
scaffold522531_14.	1	p2	(CT)6	12	916	927	CATCCCCACCGTGGTATTTA
scaffold522566_16.	1	p2	(AC)7	14	1664	1677	ACCGTTTGTGAAAAGAACGC
scaffold522588_13.	1	p2	(TA)6	12	317	328	TCATTTTTCTTGTAGCGTATTACTCA
scaffold522605_16.	1	p2	(AG)7	14	323	336	CGTTCATCCCCTTTGTGTCT
scaffold522698_14.	1	p2	(TA)7	14	92	105	GTTGTTTTGTTAGCCACTGTGA
scaffold522715_18.	1	p2	(AT)8	16	92	107	GACTGTAATGCATGGCTGGA
scaffold522847_12.	1	p2	(TA)6	12	2470	2481	CCATCGATGCCGATAGATTT
scaffold522869_15.	1	p2	(GA)9	18	147	164	AAATTGGATCGTTGCCAGAG
scaffold522989_14.	1	p2	(AT)6	12	683	694	ATCTCGTTGAGGATGCTTGC
scaffold523075_14.	1	p2	(CT)10	20	2281	2300	AAACACCACCTCCCTCACTG
scaffold523079_11.	1	p2	(GA)6	12	144	155	CACGGTTAGGCTCGAGAGAG
scaffold523160_14.	1	p2	(AG)6	12	352	363	TTTACGAAAATGCCACCACC
scaffold523224_19.	1	p2	(CT)6	12	133	144	AGCATCTCTCCATCACTCTCA
scaffold523268_10.	1	p2	(TA)7	14	215	228	TTCGAACCTGGTTTTCGTTC
scaffold523277_15.	1	p2	(TA)6	12	99	110	TACCTTGATGTGGTGGTGCT
scaffold523306_15.	1	p2	(TA)6	12	1410	1421	AAAACTCCCAATTTCCACCA
scaffold523356_15.	1	p2	(GA)8	16	791	806	TCCCCTAGTCTAAGCCGAAA
scaffold523390_16.	1	p2	(AT)6	12	313	324	GTGGGAGATGGTGGAGAGAG
scaffold523630_16.	1	p2	(GA)7	14	4354	4367	GCTTTTGCTTTTGCTTTTGG
scaffold523684_16.	1	p2	(GA)9	18	113	130	TTTGAAGGGTACTGCCATCA
scaffold523898_11.	1	p2	(AG)6	12	961	972	TCACCTTTTCCCTCTTCCCT
scaffold523962_14.	1	p2	(GA)7	14	740	753	ACTCCCATCCGAGGTCCTAA
scaffold524079_16.	1	p2	(CA)7	14	2361	2374	TAGTCCGTGGGTTTACCGAG
scaffold524086_16.	1	p2	(GA)6	12	1970	1981	TGGTGCAGATGGAAGTGAAG
scaffold524131_18.	1	p2	(AT)6	12	56	67	AGCAAAGAAGGAATGCAACC
scaffold524160_13.	1	p2	(TG)6	12	302	313	GCGCGATTATCGAAGAGAGA
scaffold524199_11.	1	p2	(TA)10	20	249	268	GCATGAGAGCCAAGCAAAAT
scaffold524201_16.	1	p2	(TA)12	24	1388	1411	CAGATCTGATGGCCCAGATT
scaffold524290_15.	1	p2	(AG)6	12	1903	1914	CGTGTTCCTAATCCCCATGT
scaffold524333_12.	1	p2	(AT)6	12	573	584	TTTTACGGGCAACGTACTCC
scaffold524368_13.	1	p2	(TA)6	12	146	157	AGCTATAAGATTGACTAGATCAACGA
scaffold524582_11.	1	p2	(AT)6	12	293	304	TCGCGTCAGACTCCTCACTA
scaffold524704_11.	1	p2	(TA)9	18	530	547	CTCAATGATGGCCGAAAACT
scaffold524729_16.	1	p2	(TC)6	12	1067	1078	GCCGTTGATCATTACCTCGT
scaffold524753_14.	1	p2	(GT)7	14	294	307	TGCCCTTTCTTTTAGGAGCA
scaffold524816_15.	1	p2	(CA)6	12	94	105	AACGAACACGAGAGGTTTGG
scaffold524854_13.	1	p2	(AT)9	18	1393	1410	ACGGTGAAAATGGATCTTGG
scaffold524905_12.	1	p2	(AT)7	14	270	283	AAATGACCAAAAAGGGACGA
scaffold524947_20.	1	p2	(AT)6	12	356	367	AACGGCGCGACAGTTATAGA
scaffold524998_12.	1	p2	(AG)7	14	546	559	TGCATGAGCACTAATGAGCC

scaffold525042_13.	1	p2	(TA)10	20	837	856	GAATGGCCCGAGATTTGTTA
scaffold525077_13.	1	p2	(TA)6	12	1353	1364	AGTGCCGTAGCCACAAAAAT
scaffold525332_14.	1	p2	(TA)8	16	428	443	TTTTGCCCTCGAATGCTATC
scaffold525619_17.	1	p2	(CT)7	14	269	282	AACCGTGATGGTTGGGATTA
scaffold525657_17.	1	p2	(TA)9	18	761	778	TCCTCAACTCTGAGCCGAAT
scaffold525662_14.	1	p2	(TA)7	14	354	367	TTTAATGATGCGTTTTGGCA
scaffold525811_11.	1	p2	(TA)8	16	1351	1366	ATGGGATAGTACCGGAACGC
scaffold525881_14.	1	p2	(CA)7	14	415	428	TTCACTCACACACACTCGCA
scaffold525897_13.	1	p2	(TC)6	12	94	105	AATGAGGCTTTTGGATCGAC
scaffold525934_15.	1	p2	(AT)7	14	649	662	AATGGCACACAGGTGAATGA
scaffold525956_12.	1	p2	(AG)8	16	717	732	AATCATCCAATTTGCTTGCC
scaffold525990_14.	1	p2	(AG)6	12	150	161	GCAACAACAACAACTGACGC
scaffold526002_16.	1	p2	(AC)13	26	6219	6244	TGGAGATCATTTCAGGCACA
scaffold526101_14.	1	p2	(TC)6	12	537	548	CACCATTTTGGTATTTGCCC
scaffold526115_16.	1	p2	(TA)10	20	648	667	AGGGGGTCAAACTCCTTGAA
scaffold526144_15.	1	p2	(TA)10	20	330	349	TTTTCCATCAACTAACCCGC
scaffold526272_12.	1	p2	(TA)6	12	112	123	TCATTTCACCCATGAGCTTT
scaffold526273_13.	1	p2	(CT)8	16	1073	1088	TCCAACTCTTCACACTCCCC
scaffold526306_15.	1	p2	(CT)6	12	138	149	TCATACACGATGGGATCGAA
scaffold526347_16.	1	p2	(TC)6	12	2828	2839	AACGTCAAGTATTCCGCCAC
scaffold526358_17.	1	p2	(TC)6	12	376	387	TCCGCGAGAGAATTAAGGAA
scaffold526371_14.	1	p2	(AC)6	12	1582	1593	TGACATGGAAGGAAAAAGGG
scaffold526395_12.	1	p2	(TA)8	16	71	86	TCTCCAAATTTGAGGGTTATCA
scaffold526456_13.	1	p2	(CT)6	12	41	52	CAAATGGCCAAGAGAGTTACAA
scaffold526473_20.	1	p2	(GA)9	18	213	230	TCGTGTTTATCATCACCCCA
scaffold526572_12.	1	p2	(TA)9	18	43	60	CGGTTATTACCGGATCGCT
scaffold526602_16.	1	p2	(CT)6	12	69	80	TACAAATGGCCAAGGGAGTT
scaffold526623_16.	1	p2	(GA)6	12	1261	1272	GGGTTTGAGTGAGTGGAGGA
scaffold526674_14.	1	p2	(TA)10	20	377	396	AGAAATGACATCACCACGCA
scaffold526719_11.	1	p2	(AT)7	14	54	67	TCAAACAACTAGATTAGTCCATATCC
scaffold526732_17.	1	p2	(TC)6	12	3500	3511	AAACAGCAGGTTTTTGGTGG
scaffold526842_15.	1	p2	(AG)8	16	3266	3281	AGAGAAGTGAAAGGGGCTCG
scaffold526844_14.	1	p2	(CT)6	12	72	83	ACAATGGCAAGAGAGTTGCT
scaffold526854_14.	1	p2	(GA)13	26	424	449	CGAATACCTACCCCGTGAGA
scaffold526855_13.	1	p2	(CT)7	14	1425	1438	CACTCCGCTCTCATTCCTTC
scaffold526990_14.	1	p2	(TC)6	12	150	161	TCTCTTCAATAAGGTAACAACCAAA
scaffold526998_17.	1	p2	(TA)7	14	658	671	GGGTGTGGAAGCAAAGAAAA
scaffold526999_14.	1	p2	(AT)6	12	866	877	TTCAACATGATGGTGCCAAT
scaffold527086_10.	1	p2	(CT)7	14	96	109	CAAAATTAAAAGTGTTCCATCCC
scaffold527201_16.	1	p2	(CT)13	26	4467	4492	GACCAGTTCAAGGGAGGTGA
scaffold527218_15.	1	p2	(TA)8	16	888	903	ATGGCCACAAATGGTTCCTA
scaffold527220_18.	1	p2	(TA)8	16	248	263	CATTCAAGGGGCATTTTTGT
scaffold527235_15.	1	p2	(TC)6	12	445	456	CCACGGGAGAAAGGTGTTTA
scaffold527498_14.	1	p2	(TA)8	16	1308	1323	TTGACACGCAAGATTTGCTC
scaffold527557_15.	1	p2	(GA)6	12	834	845	CTACGCGACCCATTCTTGAT
scaffold527689_13.	1	p2	(AT)7	14	2126	2139	CCAGTATTTGAGAGATGGGCA
scaffold527736_10.	1	p2	(GA)6	12	96	107	TGTCTTTAGCTCTGGTGTGGC
scaffold527849_10.	1	p2	(AC)6	12	295	306	ACTCCAGCCACCATCTTCAC
scaffold527888_14.	1	p2	(TC)6	12	319	330	GGGACGGAGGGAGTAGTTTC
scaffold527929_14.	1	p2	(TA)7	14	295	308	CGATGTTTTAACGCCGAGAT
scaffold528044_17.	1	p2	(TC)8	16	147	162	GACCAAGCATGTGGTTCCTT
scaffold528063_16.	1	p2	(TA)6	12	321	332	CCGTTAAATTACATGATTTTCCCT
scaffold528107_15.	1	p2	(TA)7	14	1904	1917	AACCACGTTTTGGCTAGTTCA
scaffold528184_18.	1	p2	(GA)6	12	1028	1039	CAAGAAACAACAGGGGGAAA
scaffold528219_12.	1	p2	(TG)6	12	53	64	TGTTCCTCGTGTTCCTCCTC
scaffold528321_11.	1	p2	(TA)8	16	194	209	GTGCGTGTGTATGCTGAGGT
scaffold528405_13.	1	p2	(AT)6	12	284	295	GACAAGATCGTGCCAACAAA
scaffold528419_12.	1	p2	(TA)8	16	1395	1410	TCGATTCGAATTATGAGGGC

scaffold528502_11.	1	p2	(AC)9	18	465	482	ATGGCAAAAGGCATCAAAAG
scaffold528634_13.	1	p2	(TC)7	14	1300	1313	CTTCACGCGCTCAATAAACA
scaffold528669_13.	1	p2	(AT)6	12	54	65	CATGGTAAGCAGATTGGTTTTAAT
scaffold528677_10.	1	p2	(TA)6	12	54	65	TCAGATTTGTTATGTGTTTTGACA
scaffold528684_15.	1	p2	(AG)8	16	863	878	GACCAGGAGTTGAAGATGCC
scaffold528879_16.	1	p2	(AT)6	12	94	105	CAACTTGGAACCCGATTCTC
scaffold528925_15.	1	p2	(CT)8	16	1390	1405	TGGTCTCCATCTTCCGTCTC
scaffold528950_16.	1	p2	(AT)6	12	426	437	TGAAAAATGCAACCAATGGA
scaffold529057_18.	1	p2	(AG)7	14	360	373	AGGCCGTGTTCGTATTGTGT
scaffold529086_13.	1	p2	(CT)6	12	486	497	ACTCATGTCACGGCACACAT
scaffold529088_15.	1	p2	(AT)7	14	235	248	AAAAGCTCCTCCACAATTTGA
scaffold529093_12.	1	p2	(TC)7	14	116	129	GATTCGCACAAATGAACACG
scaffold529096_17.	1	p2	(TA)6	12	79	90	TTGTCGATCAGCGGTTACAG
scaffold529132_13.	1	p2	(TA)11	22	600	621	TCAACCGCCAGGATTATTTC
scaffold529221_15.	1	p2	(AC)7	14	184	197	CACGTGGCATGATAATAGCG
scaffold529264_12.	1	p2	(TA)6	12	96	107	TACTCAAGCCCACGATCTCC
scaffold529327_14.	1	p2	(TA)6	12	256	267	TTGTTCGTATTTGGAAGTCGTG
scaffold529373_21.	1	p2	(TC)6	12	44	55	TGCCCTCTTTCTCTATCTCTCTTG
scaffold529422_10.	1	p2	(AT)9	18	56	73	TCCACCGCTTTAAATTGCTT
scaffold529497_15.	1	p2	(AT)6	12	759	770	CGACCAAACTCATAGCGTCA
scaffold529506_16.	1	p2	(TA)10	20	2858	2877	AAAATGCAGTTCGGTTGGAG
scaffold529512_16.	1	p2	(TA)7	14	266	279	CTTTTTCCATCAACCAACCC
scaffold529531_12.	1	p2	(AC)7	14	365	378	TCACGGAATTACTAAGCCCC
scaffold529560_13.	1	p2	(GA)10	20	54	73	TCTTCCGATCTCAGTTTTTCAA
scaffold529580_17.	1	p2	(GT)7	14	653	666	AACAAGCTGGGTTTCTGCAC
scaffold529615_15.	1	p2	(GA)8	16	475	490	GCCTGCAAGAAAGCAATCTC
scaffold529655_12.	1	p2	(CT)8	16	41	56	CATACTCACTCTCACTAGCCGC
scaffold529681_12.	1	p2	(AT)7	14	164	177	GTTGGAGGAATGGAGGGAAT
scaffold529705_17.	1	p2	(CA)6	12	279	290	GATCTTTTCACTCGAGCCCA
scaffold529936_13.	1	p2	(CT)11	22	106	127	TTGCATTGCAGCAGTAGAGG
scaffold529942_16.	1	p2	(AT)6	12	749	760	CTTGTTTTGGAACCAGCCAT
scaffold529962_14.	1	p2	(AG)9	18	1149	1166	GACTCCTGCAACTTGCCTTC
scaffold530007_12.	1	p2	(CT)11	22	1743	1764	ATGTTCCCATTTCACCTTGC
scaffold530214_13.	1	p2	(TG)7	14	184	197	GCTGCCTACAACAGCAACAA
scaffold530217_10.	1	p2	(GT)6	12	479	490	TTACTATGTGGTTGCGGTGC
scaffold530231_15.	1	p2	(AT)9	18	3411	3428	ATCAGGCCCATATTTCGATG
scaffold530431_13.	1	p2	(TA)8	16	409	424	TTTTCGCCTCCCACTAAAAA
scaffold530576_13.	1	p2	(AT)7	14	95	108	GCAATGCTCCATTTTCCAAC
scaffold530636_16.	1	p2	(TC)6	12	2563	2574	TGGCTGTAGTGGAAATGTGG
scaffold530746_15.	1	p2	(TG)7	14	1002	1015	GGTTAGCGTGTCGTGTCAGA
scaffold530850_12.	1	p2	(AT)6	12	1265	1276	TCCCTTGCTAGATGGCAGTT
scaffold530856_14.	1	p2	(AT)7	14	150	163	CGGCCATCAATATACACCAA
scaffold530894_11.	1	p2	(TA)6	12	79	90	TCGGTTACCCTATAGCATTCG
scaffold530932_15.	1	p2	(TC)9	18	4429	4446	TAACCACGGATGCCACTGTA
scaffold530963_11.	1	p2	(GC)7	14	78	91	CTACGAGCCACGGCTACAC
scaffold531126_14.	1	p2	(CT)6	12	334	345	TATCGCCGTTAAGCTGCTCT
scaffold531227_16.	1	p2	(AG)7	14	1040	1053	AAAGATGGGAAAATGGGACC
scaffold531228_12.	1	p2	(AG)9	18	32	49	AGAAACTTGACGTGTGCGTG
scaffold531273_15.	1	p2	(AT)6	12	2102	2113	AATGAGGTAAATTTGAGAATGATGA
scaffold531296_10.	1	p2	(TA)9	18	67	84	CAAAGGCCCACAATGGTTAT
scaffold531314_10.	1	p2	(AG)9	18	146	163	GTGTTTGGTCTCCCCTCCTT
scaffold531380_15.	1	p2	(GA)6	12	77	88	GTGGTTCGATCAAGGTGAGC
scaffold531386_12.	1	p2	(TC)6	12	245	256	TGGGCATTTGTATACCCGTT
scaffold531528_11.	1	p2	(AG)7	14	209	222	AATTTGCCCTCTCCCTCTTC
scaffold531532_14.	1	p2	(TA)8	16	838	853	CAAAACAGTATACAACGGGCA
scaffold531535_11.	1	p2	(AT)6	12	457	468	TGCTATCGGCTAACGGTTTT
scaffold531609_13.	1	p2	(GA)6	12	331	342	CACAATCGATCAATAAAGCTGC
scaffold531706_13.	1	p2	(TA)10	20	99	118	TGAGGCTTAGAGGGTGTTTTG

scaffold531730_15.	1	p2	(GA)8	16	1202	1217	AGCCTTACCAAAGGGGAAAA
scaffold531751_10.	1	p2	(CT)6	12	199	210	GGAAGAATTGGAAACTCGTGA
scaffold531765_18.	1	p2	(TA)6	12	196	207	ATGATCTACGTCCACGGGAG
scaffold531768_18.	1	p2	(AT)7	14	149	162	CCTTCCAATGGACTTCCTCA
scaffold531854_11.	1	p2	(AT)7	14	209	222	GCAAAAGCTTTCTCGACCAC
scaffold531873_15.	1	p2	(CT)6	12	140	151	GCATGATCGACATTGTAAAGGA
scaffold531924_13.	1	p2	(AG)6	12	152	163	ATTGCTTCCCCTCTTCCATT
scaffold531925_17.	1	p2	(CT)9	18	1740	1757	CATGCCATGGAGTCGTTCTA
scaffold531939_10.	1	p2	(TC)6	12	85	96	GTTGATGCCCTTCGTCAACT
scaffold531952_16.	1	p2	(GA)9	18	146	163	AACGCTTTCTGCTTCTGCAT
scaffold532051_18.	1	p2	(GA)7	14	937	950	CTCGTTGGAGGCCAATAAAA
scaffold532075_15.	1	p2	(TA)10	20	69	88	GGAAATAAGAAGGTGTTATGAAGGG
scaffold532213_14.	1	p2	(AT)6	12	227	238	TCGCAGAAAATCAACTTCTCAA
scaffold532235_12.	1	p2	(AT)8	16	3036	3051	CTTACACAGTGCCTGCTCCA
scaffold532243_12.	1	p2	(AT)8	16	170	185	GGAGAAAATCAGGTGATAACCCTT
scaffold532336_14.	1	p2	(AC)6	12	152	163	TGCGAATCAATTAGTGTGAGAA
scaffold532425_10.	1	p2	(AG)7	14	184	197	TGGTGTTCTTGGGGTTTTGT
scaffold532428_10.	1	p2	(TC)6	12	414	425	TTTGAGATCGGAGTGGCTCT
scaffold532453_14.	1	p2	(GT)7	14	52	65	TCTTGGGAGTGAACATACATACA
scaffold532728_16.	1	p2	(TA)6	12	2863	2874	ACAGCAAGCATCCAGAAAGC
scaffold532772_11.	1	p2	(AC)8	16	225	240	AGAATATGCGTGATCGCCTT
scaffold532773_13.	1	p2	(AC)6	12	225	236	AGAATATGCGTGATCGCCTT
scaffold532833_16.	1	p2	(AG)13	26	80	105	ACCACGGCTGAATAAATTGC
scaffold532867_12.	1	p2	(GC)6	12	275	286	GTTGACGGATAACCCAAACG
scaffold532896_13.	1	p2	(CT)6	12	1921	1932	GGGTTTAGGGGACAGGTGAT
scaffold532957_20.	1	p2	(AT)6	12	299	310	TGCGCCCTTTAAAACTAAGG
scaffold532958_13.	1	p2	(AT)9	18	348	365	TTGTCCAAACAAATGAAACATTC
scaffold532975_14.	1	p2	(AT)9	18	673	690	TGGATTTGGGATTCCTTCAA
scaffold532979_13.	1	p2	(AT)10	20	734	753	ACAATTTTGCCCTTGAATGC
scaffold533009_21.	1	p2	(GA)7	14	624	637	TGCGTTTACATTCAAGCAGTG
scaffold533036_17.	1	p2	(TC)6	12	638	649	CCTCCCACTCCTCACTTCAA
scaffold533091_12.	1	p2	(AG)6	12	145	156	GTGTGTGTGCATGAGTGTCG
scaffold533209_12.	1	p2	(TG)8	16	98	113	TGATTTTTAATGCCTTTCAGCTT
scaffold533237_15.	1	p2	(TA)10	20	199	218	TTCAAAAGGTTTGGGCTTTTT
scaffold533258_13.	1	p2	(TA)7	14	749	762	TGCACCTCCTCCTAATTAATCC
scaffold533371_15.	1	p2	(TC)6	12	40	51	TCTCTCTTTTGGTTGGTGAAGA
scaffold533416_21.	1	p2	(AG)6	12	334	345	TGCAGCTGAAATCAATGAAAA
scaffold533428_14.	1	p2	(GA)9	18	831	848	TCTACGCATGGAATCAGTCG
scaffold533512_15.	1	p2	(GA)6	12	750	761	CTTGATTCATCGAACGCAAA
scaffold533568_17.	1	p2	(AT)7	14	1762	1775	ATGCGATGTTTTGCATTTTT
scaffold533584_13.	1	p2	(AT)7	14	28	41	CCAAAGTTTATTTAACACGGAAGAA
scaffold533624_10.	1	p2	(AT)6	12	710	721	TTCTTTCAATCGACGCTCCT
scaffold533631_14.	1	p2	(CT)6	12	136	147	TTGCTAAGCTCCAGCAACG
scaffold533796_15.	1	p2	(TC)7	14	100	113	CAATCTGGACGATACTCAATCG
scaffold533971_16.	1	p2	(CT)9	18	2810	2827	ATCTGTTTCTTCTGCGGCTC
scaffold533976_12.	1	p2	(AG)6	12	440	451	AAATTGATGGCAAGAGCAGG
scaffold533977_16.	1	p2	(AG)12	24	4211	4234	GGTTGGTTTGAGTTCCTCCA
scaffold534145_11.	1	p2	(AG)8	16	50	65	TCCATACACACCAAATAAAAAGACA
scaffold534511_19.	1	p2	(GA)9	18	156	173	TTGGGGAAATAATGTCGATCT
scaffold534587_14.	1	p2	(CT)8	16	4379	4394	GCATAAAGCTCATCTTGCACA
scaffold534592_12.	1	p2	(AG)6	12	241	252	GATCGGTGAAGATTGGAGGA
scaffold534624_12.	1	p2	(GA)6	12	399	410	CCGCATTCTGTTTGTTGTTG
scaffold534675_16.	1	p2	(GA)6	12	1520	1531	GTACAACGAGGATGTGGGCT
scaffold534749_20.	1	p2	(GA)6	12	53	64	CCTTTGGTCTCGGTTGAAAT
scaffold534819_11.	1	p2	(TA)6	12	112	123	CATGAAAGACTCTATAGACAAGAAA
scaffold534878_18.	1	p2	(GA)8	16	148	163	AGGGTGTGTGAGAGACCGAG
scaffold534921_19.	1	p2	(TG)8	16	306	321	TGGCTTGTATGTTCTGATCACC
scaffold534955_12.	1	p2	(AT)6	12	169	180	GTTCGAAAGCCACAAATGGT

scaffold534973_13.	1	p2	(GA)10	20	58	77	GCTAGGGCGATTGTATTGATG
scaffold534988_14.	1	p2	(TA)11	22	370	391	TGATGTTGAAGAATCAGCGG
scaffold535061_11.	1	p2	(TC)7	14	65	78	TACCGTTGGTTAATCCTGCC
scaffold535282_14.	1	p2	(TA)13	26	167	192	TTTCGAAAACATGCAATGGA
scaffold535311_16.	1	p2	(AG)6	12	697	708	ATCACCCCTCACAAGAACCA
scaffold535348_18.	1	p2	(GA)6	12	148	159	AGAAGGGCAATGAATTGGTG
scaffold535466_15.	1	p2	(AT)7	14	225	238	AAATATCGGCCGTCAGATTG
scaffold535493_15.	1	p2	(AG)7	14	796	809	AGCAAATGCCAATAAGGTGG
scaffold535580_13.	1	p2	(AG)7	14	159	172	ATTGAGTCCCAATCTCGTGG
scaffold535615_14.	1	p2	(CT)6	12	102	113	CACTCTGCTAGGGTTGGGAG
scaffold535662_11.	1	p2	(TC)6	12	149	160	AACTGTGGCAAGATCCATCC
scaffold535695_12.	1	p2	(CA)7	14	197	210	TTCGAATTTTATTATTGATTGAGCA
scaffold535748_16.	1	p2	(TC)7	14	372	385	GCAATTTTAAGATCGAATCCCA
scaffold535940_14.	1	p2	(TC)6	12	190	201	TTGCATGAACAACGTGGAAT
scaffold535998_10.	1	p2	(TA)10	20	325	344	TGTCACCTTGAAAGAATTACAAACA
scaffold535999_15.	1	p2	(TA)7	14	57	70	GAGTGACATCTTCGAGTGTTCG
scaffold536032_14.	1	p2	(TA)7	14	564	577	TTAGCAGCTTATACGTGTGAAAA
scaffold536055_16.	1	p2	(TA)11	22	2079	2100	TCCTTCTAATCGATTCTTCCACA
scaffold536076_17.	1	p2	(TA)6	12	9802	9813	TGAAGAAGACGTGGTCGAGA
scaffold536227_15.	1	p2	(TC)10	20	2582	2601	ATCCCTTCTGGTTCTCCCAC
scaffold536347_11.	1	p2	(TA)7	14	103	116	GAAGCGACACGGGTTATTTT
scaffold536501_17.	1	p2	(AG)9	18	148	165	GGGACTCGGATAAAAAGGGA
scaffold536690_15.	1	p2	(TA)6	12	2905	2916	GCTGAGGCTTCTTCCATGTC
scaffold536760_16.	1	p2	(TA)8	16	40	55	CACACTCACTCACAAACACACAA
scaffold536837_12.	1	p2	(TA)9	18	1195	1212	CGTTGAACGTACCCTCGATT
scaffold536838_17.	1	p2	(AT)7	14	152	165	TCCCTAGACTCCGTAATTGGAA
scaffold536849_19.	1	p2	(CG)7	14	395	408	TGTCCCACATTGGAAAATGA
scaffold536949_12.	1	p2	(AG)8	16	228	243	AAAACAAAACCTGGTGCTCG
scaffold536955_15.	1	p2	(TA)9	18	1240	1257	ATCATGTAGTCGCGTGCTGT
scaffold537069_10.	1	p2	(TC)6	12	222	233	TGAACAATTGAACACCGGAA
scaffold537092_13.	1	p2	(CT)9	18	1010	1027	TGCTGTCCCTCTAGCAGGTT
scaffold537140_15.	1	p2	(TA)9	18	45	62	TGCGTTTTGACAATATATAGGTGTTT
scaffold537198_18.	1	p2	(GA)6	12	252	263	TATGCAAGAGCGAGCAGAGA
scaffold537238_12.	1	p2	(GT)6	12	297	308	TGTCCAAGCCGATCCTTATC
scaffold537291_12.	1	p2	(TG)6	12	1102	1113	AATTATGTGCAAGCTCATCCG
scaffold537352_15.	1	p2	(TC)6	12	233	244	ACACCCCACAAAATCGAGAG
scaffold537491_16.	1	p2	(TA)7	14	328	341	TCACGTGTCATTGTAACCGC
scaffold537565_15.	1	p2	(AG)10	20	2369	2388	AATTGATTGCTGCTGCTGTG
scaffold537615_14.	1	p2	(TG)6	12	561	572	TCTCCCCCTTCTGTGGTATG
scaffold537707_16.	1	p2	(CT)6	12	4125	4136	CGGAGAATTGATGTTCCCAT
scaffold537803_12.	1	p2	(AG)10	20	352	371	TGCAGCTAATTTTCTGCTGG
scaffold537808_15.	1	p2	(CT)9	18	46	63	CGCCTTTCTCTTTCTAACCTCC
scaffold538092_13.	1	p2	(TG)6	12	294	305	TCTCAACCAATGATGAGCCA
scaffold538481_12.	1	p2	(AT)10	20	388	407	CGGATCGAAAATTCTCCTTATG
scaffold538790_12.	1	p2	(GA)8	16	258	273	CCACGAGATGGGGACATTTA
scaffold538824_13.	1	p2	(AG)11	22	383	404	TACCCTCTCCTCCTCCGATT
scaffold538862_15.	1	p2	(TG)6	12	1393	1404	GAAATGCATCTCATTCGGGT
scaffold538950_12.	1	p2	(AT)11	22	1303	1324	TACGGTTCGGTTCCAGTTTC
scaffold539112_12.	1	p2	(GA)6	12	428	439	CAATGGAAAACACGCAACAC
scaffold539188_14.	1	p2	(AC)6	12	770	781	CGCTGAGGGATCTGGTATGT
scaffold539258_13.	1	p2	(TA)8	16	1777	1792	GCTGGATTTTTGGCATTCAT
scaffold539313_18.	1	p2	(TC)9	18	1240	1257	TTTTTCGGTTCGGTTCAAAG
scaffold539453_12.	1	p2	(TA)6	12	256	267	GTTTCACTTTGGTACCCGGA
scaffold539480_12.	1	p2	(AG)6	12	432	443	AAGTCGGCCAAGAAGAGAAA
scaffold539543_11.	1	p2	(AG)6	12	123	134	CTAAGCGATGCCTAAGGCTG
scaffold539547_17.	1	p2	(CT)6	12	89	100	CTCACTAGCCGCAGCTCTCT
scaffold539558_12.	1	p2	(TG)6	12	66	77	GGAAAATATCAAGTCAACACAAAA
scaffold539586_14.	1	p2	(TA)7	14	716	729	TGATTAGCATCACAGCCCAA

scaffold539681_15.	1	p2	(TA)6	12	144	155	CAACGCTAAAACATCTGAGAACA
scaffold539845_14.	1	p2	(TA)7	14	338	351	GATATGGATGCCCCAGATTG
scaffold539847_15.	1	p2	(AG)7	14	145	158	TGATTTTGGACGTTCTGCAC
scaffold539861_13.	1	p2	(AG)8	16	159	174	GACGATGGAAGGAGGTGAGA
scaffold539911_11.	1	p2	(TA)8	16	136	151	TTTTCCGAAGTACGAGCTGC
scaffold539915_11.	1	p2	(AT)7	14	281	294	GGATTAGAATTCGGAACACTCG
scaffold539974_11.	1	p2	(CA)6	12	131	142	TCAAATGCACAAATTCAATGG
scaffold539996_15.	1	p2	(GT)7	14	472	485	AAGTAGGGGGCTTCAATCCA
scaffold540025_12.	1	p2	(TA)8	16	680	695	ACATTTCGATTAGGTGTGACAA
scaffold540038_19.	1	p2	(AC)6	12	750	761	TACAAATCGTGAGCAGCAGG
scaffold540104_15.	1	p2	(AT)7	14	926	939	TTTTCTTTGTCTTCAATGCCA
scaffold540209_10.	1	p2	(AT)8	16	68	83	CACAATAAGGGTTGGTATCATTTG
scaffold540216_15.	1	p2	(AT)6	12	911	922	GGATAAAGTACGATGATTGACCA
scaffold540268_17.	1	p2	(TC)6	12	1275	1286	TGAAGGAGGCAGGCTTTAGA
scaffold540326_14.	1	p2	(GT)11	22	610	631	TCATTTTGCTTGCAGTGTCC
scaffold540344_14.	1	p2	(TA)7	14	126	139	ATAGGTGTGGCCCAGTTTGA
scaffold540391_13.	1	p2	(TC)6	12	100	111	ACGTTGGACCTGAAAGAGGA
scaffold540409_18.	1	p2	(TA)9	18	48	65	CATGGGTTATCACTTGAATGAGAC
scaffold540461_15.	1	p2	(AC)6	12	208	219	TTAGATGTGCAGCCGACAAG
scaffold540534_14.	1	p2	(GA)6	12	544	555	TCCCGTAATATAGGTCCCAAAA
scaffold540681_12.	1	p2	(AC)6	12	115	126	GGTTCTGAAACCGGGATAGG
scaffold540711_16.	1	p2	(AT)8	16	464	479	CCTAAAAGGAACTGTGGAGGC
scaffold540728_12.	1	p2	(TA)6	12	1138	1149	TTGACCTTTTACCTTGCCCA
scaffold540984_17.	1	p2	(GA)6	12	285	296	GTCCGCGAAGAAACACTCAC
scaffold541174_10.	1	p2	(AT)6	12	155	166	AGGAGCAATACTGCTTGTGGA
scaffold541255_16.	1	p2	(TA)6	12	234	245	GAGAGGGCTTCTTCTGGGAT
scaffold541271_16.	1	p2	(GA)7	14	184	197	TTGGGTAGAAGGCATTGAGAG
scaffold541320_13.	1	p2	(AT)8	16	798	813	AACATCAATCATAGTTCAACTTTAGG
scaffold541387_16.	1	p2	(CA)6	12	417	428	AGACTCCAAGCCCTGTTGTG
scaffold541395_14.	1	p2	(TA)9	18	202	219	ATTATGTGGCCCGAATGACT
scaffold541485_11.	1	p2	(TA)6	12	752	763	ATATTCGATCCGGAAGGGTC
scaffold541594_13.	1	p2	(TA)11	22	869	890	GATCCAGTAATTTGGGAAGGC
scaffold541711_11.	1	p2	(TC)6	12	73	84	CCTTTGGATATGGTGATTTGG
scaffold541780_14.	1	p2	(TA)8	16	425	440	CCCGAGCTTCCATAAATCAA
scaffold541845_15.	1	p2	(AT)6	12	1666	1677	ACCGCACAAATCATTTCCTC
scaffold541858_14.	1	p2	(TA)13	26	515	540	AACCTCTATCCCGTGCAATG
scaffold541881_13.	1	p2	(TC)7	14	54	67	CATGGCCCTTTCTTCACATT
scaffold541913_15.	1	p2	(AG)7	14	102	115	TTCCATAAAAAGTTAGGCAAGTCT
scaffold541955_16.	1	p2	(AT)7	14	331	344	ACAACATTCATCGTTCCCCT
scaffold542003_10.	1	p2	(TA)6	12	889	900	TTGTTTCCACACCCATGTTG
scaffold542038_11.	1	p2	(GA)8	16	723	738	GGCTGGCTCCAGTAGTTGTT
scaffold542086_16.	1	p2	(GA)6	12	249	260	TCTGTGTGTTGAGAGATCAGTGAG
scaffold542128_16.	1	p2	(AG)6	12	93	104	CAAAAACAGAGTGAGGGGGA
scaffold542231_15.	1	p2	(TA)6	12	263	274	TGTCCTTTTGGATCCAGTCC
scaffold542295_14.	1	p2	(TC)9	18	76	93	TTGCTGCCCTATTTTCTTTGA
scaffold542375_15.	1	p2	(TC)6	12	455	466	ATTGGCAGCAGAAGGAATTG
scaffold542381_15.	1	p2	(GA)12	24	830	853	CGCTCATTTTCTCACACCAA
scaffold542432_16.	1	p2	(AT)9	18	1635	1652	TATGCAAGAAACATGGCTGC
scaffold542816_14.	1	p2	(CT)6	12	333	344	TAAACACTTCGCGCAGACAA
scaffold542999_15.	1	p2	(TG)8	16	151	166	AACTCACATCAGATTCCCCAA
scaffold543162_13.	1	p2	(GA)9	18	227	244	GCTTGGTTCGAGACTTGAGG
scaffold543204_17.	1	p2	(TA)6	12	875	886	TCAGCGGCTTAACATGTTTCT
scaffold543227_12.	1	p2	(GA)9	18	865	882	TCCAAATGACCAACCAAACA
scaffold543234_15.	1	p2	(TA)6	12	61	72	CGGCTGGATTTCATCCCTAT
scaffold543418_15.	1	p2	(GT)7	14	970	983	GCCCTGTTCGTTCATGTCTT
scaffold543507_17.	1	p2	(TA)10	20	68	87	TCCAATGGATGAGGATGGTT
scaffold543524_17.	1	p2	(TA)6	12	194	205	TATTTTGGACGATTTTGCCC
scaffold543708_18.	1	p2	(AG)6	12	399	410	GGCTTTTGAGGGATGGAGAT

scaffold543803_11.3	1	p2	(GA)6	12	364	375	GGCGAGTCTCGTCCTTGTAG
scaffold543910_19.2	1	p2	(TC)6	12	1278	1289	GTTCCTTGCTGCTGTCCATT
scaffold544054_16.2	1	p2	(AG)7	14	45	58	CCATGTTTGTAATTATTGTAGGGAA
scaffold544061_13.1	1	p2	(TA)6	12	169	180	GTGATCGACGGTTGGAAAGT
scaffold544076_22.1	1	p2	(CT)6	12	556	567	GCATGTGAGACCCATTCTCC
scaffold544082_11.3	1	p2	(TC)9	18	238	255	GATTCTGATCGACCAGTGGG
scaffold544117_17.7	1	p2	(TC)6	12	366	377	TCGATTGACCCCTCATCTTC
scaffold544424_11.8	1	p2	(TC)6	12	56	67	GGCTGGGAATTGCTGATATT
scaffold544487_13.2	1	p2	(GA)7	14	154	167	CCTCCCTTAGGGTTCCTCAC
scaffold544646_14.5	1	p2	(TC)9	18	413	430	AGCCGGTCAAGTAGAGGGAT
scaffold544675_14.1	1	p2	(GA)7	14	150	163	CGAGCAAGGAATAGACCGAG
scaffold544766_15.6	1	p2	(TA)6	12	136	147	AATTTAATTCCGTGCAACGC
scaffold544884_14.8	1	p2	(AT)7	14	99	112	ATGTTTCCTCTTGGGTGGGT
scaffold545085_15.1	1	p2	(AT)11	22	423	444	CGACCCTGAGAGATTCCTTG
scaffold545256_10.6	1	p2	(TC)8	16	735	750	TCTCAACATGCTGTCTTCGG
scaffold545380_12.6	1	p2	(TA)8	16	49	64	TCACCATGAAGAAACCCACA
scaffold545478_16.2	1	p2	(AG)6	12	1505	1516	GAGGGTCCGCAAATGTTAGA
scaffold545524_16.5	1	p2	(CT)9	18	2587	2604	TAGAGAAGCCGGATGCAGAT
scaffold545642_17.8	1	p2	(GA)6	12	875	886	ACCTGGGAGCATGTTTCTTG
scaffold545650_11.7	1	p2	(AT)6	12	641	652	TTCGGTTTTTACTCCCACTATG
scaffold545653_17.9	1	p2	(AG)7	14	185	198	ACCACAGCTACCCCGTCTTA
scaffold545663_14.5	1	p2	(CT)9	18	1903	1920	CCAGAATTTGCTGGGTTAGG
scaffold545676_18.3	1	p2	(CT)6	12	41	52	TCAAGCTTAATTAGAAGAAAAGAATG
scaffold545786_11.3	1	p2	(GA)6	12	440	451	TTGGAAAAAGTGGGTTGGAG
scaffold545832_10.1	1	p2	(TA)6	12	262	273	TTCGTCCGAAATACTCCCAC
scaffold545965_11.9	1	p2	(CA)6	12	1961	1972	CTCAAATCTCTGCCCTCTGC
scaffold546043_12.7	1	p2	(AT)6	12	221	232	TGCTGTGGTATGCTTTGATTG
scaffold546051_11.8	1	p2	(AT)8	16	50	65	TTCCCGTATACAAATTCCAACA
scaffold546338_10.5	1	p2	(AT)9	18	340	357	GGATAATCAGAATCCCCGGT
scaffold546431_12.5	1	p2	(TG)6	12	488	499	GTCGTTGTTGAATGTCGGTG
scaffold546483_10.8	1	p2	(TC)6	12	886	897	CCTCTCCTCTCATTCCACCA
scaffold546487_10.4	1	p2	(GA)8	16	214	229	ATTTTCTGTCGAATGGTCCG
scaffold546553_13.3	1	p2	(TC)7	14	67	80	GCTGCATGAACACCAAGAAA
scaffold546579_12.5	1	p2	(TA)7	14	802	815	AATAATAATTCCCTCCTCTCGATT
scaffold546668_10.7	1	p2	(AT)9	18	151	168	CAAATCCCCGTTCCATCATA
scaffold546887_12.3	1	p2	(TA)9	18	98	115	TTTGATATACATGGTATTTAATTTTCG
scaffold546894_16.1	1	p2	(TC)6	12	55	66	CCCTAGCTTTGCCCTCTTTC
scaffold546930_14.0	1	p2	(AT)9	18	51	68	TCGATTTGGATTCGAATTTGT
scaffold547078_16.6	1	p2	(GA)6	12	917	928	TTTGGTAGTTCTGCAAGGGG
scaffold547102_13.8	1	p2	(TA)6	12	592	603	TGGTGACGATTATAAAATCAAAAA
scaffold547135_13.7	1	p2	(GA)6	12	317	328	ACTGGACTTCGACCTGGATG
scaffold547231_16.1	1	p2	(CT)7	14	569	582	GCGGTCCTCTCTCTCAAATG
scaffold547309_12.1	1	p2	(TA)6	12	53	64	CGGACTGAGCTGAGCTAAAA
scaffold547466_18.6	1	p2	(CT)6	12	222	233	CCAGCTCCATCATCTCTTCC
scaffold547470_10.3	1	p2	(TA)6	12	223	234	TCCACCATTGATTTCCAAGA
scaffold547654_15.1	1	p2	(AT)7	14	91	104	GACCCACGTGCACTTCTTTT
scaffold547670_13.4	1	p2	(CA)6	12	300	311	TCGAAAGCATTTCCGAGTTC
scaffold547682_13.0	1	p2	(CT)7	14	425	438	CAGCCTGTGAATTGTTGCAT
scaffold547695_10.2	1	p2	(AT)6	12	94	105	GATGAACACCCGAACCACTT
scaffold547850_14.1	1	p2	(TC)6	12	89	100	GGCAACGGTATACCACTCGT
scaffold547944_10.1	1	p2	(TA)6	12	123	134	GACATCTTCGAGTGCTCGTT
scaffold547969_16.2	1	p2	(CT)7	14	2120	2133	CCCTCTTTCCCTCTCCAAAA
scaffold548030_10.5	1	p2	(CT)9	18	589	606	GCAGCAGAAATGAAGGGAAG
scaffold548080_11.8	1	p2	(TA)6	12	53	64	GATCTCCACCATTTACGGGA
scaffold548088_10.9	1	p2	(AT)7	14	182	195	TGCTAATCTACGAATTTGGGA
scaffold548101_12.4	1	p2	(TA)7	14	110	123	TAAGGGCGGTATCACCTGAA
scaffold548211_17.5	1	p2	(CA)6	12	31	42	TCCACACAGAGACACTGGAACT
scaffold548231_10.9	1	p2	(CT)9	18	280	297	GGAAGATAGGGATAAAAGGCAA

scaffold548317_10.	1	p2	(AC)6	12	35	46	TTCTTTATTCACAATGAACTCAGATT
scaffold548389_15.	1	p2	(AT)10	20	889	908	TCAATGATCACCGGATGAGA
scaffold548394_12.	1	p2	(TA)6	12	1197	1208	AGCTAGGGGTCTGCAAATCA
scaffold548420_15.	1	p2	(TA)11	22	3532	3553	GAAAGGCTCAGCCACTTCAG
scaffold548439_15.	1	p2	(TA)6	12	1277	1288	TCGAGCATTTGCAGACAATC
scaffold548492_15.	1	p2	(TA)7	14	2009	2022	TCAAGGGCTTTTGTTAATTGTG
scaffold548523_14.	1	p2	(CT)6	12	884	895	ATCACGTTGAGGATTCGGAG
scaffold548642_20.	1	p2	(CA)6	12	107	118	GCACTCACACACACGAAAGAA
scaffold548688_16.	1	p2	(TA)7	14	824	837	AGCTCTCTATCATCCACGCA
scaffold548721_14.	1	p2	(GA)7	14	608	621	TCTTTACCCTTGGTTGGTGG
scaffold548756_15.	1	p2	(TA)7	14	5093	5106	AACAAAAATGATGGTGAAGTGG
scaffold548781_11.	1	p2	(TC)6	12	224	235	TTGAACCTTGGGCTAAAGTATT
scaffold548869_16.	1	p2	(TC)6	12	576	587	TGACCACCACCTTGTTGAAA
scaffold548871_15.	1	p2	(AT)10	20	749	768	TGACAAACTCACATGGGTCAA
scaffold548934_14.	1	p2	(CA)8	16	1073	1088	CAAACATTTGAGGAAGGCGT
scaffold549006_11.	1	p2	(AT)6	12	218	229	CAAGCTTGGCGTTATGAATG
scaffold549065_16.	1	p2	(CT)8	16	357	372	ACCCCTTGTTTGCCTTTCTT
scaffold549189_15.	1	p2	(AT)9	18	568	585	GCATCGTCTCAACCCTTGAT
scaffold549201_15.	1	p2	(GA)6	12	1121	1132	AGGCATTTTTGAATTGGGTG
scaffold549206_15.	1	p2	(AG)6	12	4751	4762	GGGTACAGCTGCCACAAAAT
scaffold549313_14.	1	p2	(AT)7	14	245	258	ATTTTGCCCACGAATTAGCA
scaffold549324_15.	1	p2	(CT)6	12	381	392	ACCCATCTCCTAACACGCAT
scaffold549403_11.	1	p2	(TA)6	12	77	88	GGTCTGTTTTCCATGGCCTA
scaffold549483_10.	1	p2	(TA)6	12	182	193	ACGTGTCGCAATCAGAATGT
scaffold549522_20.	1	p2	(CA)6	12	136	147	CACAACACACACGGACATCA
scaffold549525_10.	1	p2	(GA)8	16	42	57	CACGAGTGAAGAAAGGGAGAG
scaffold549577_15.	1	p2	(TG)7	14	371	384	GAACACGACACGATACGCAC
scaffold549595_16.	1	p2	(CT)6	12	136	147	GCATCTCTCCCTTGCTCTCTT
scaffold549705_15.	1	p2	(AT)10	20	483	502	TGAAGACATGGTTGGACAAAA
scaffold549767_10.	1	p2	(GA)8	16	73	88	TGAAACGGAGGGAGTACACA
scaffold549803_13.	1	p2	(TA)7	14	155	168	GATGCTGACCTAACCCCAAA
scaffold549820_18.	1	p2	(CT)7	14	58	71	TGGTTATGCCTTCTTCTTCCA
scaffold549902_12.	1	p2	(TA)6	12	359	370	ATGCGTTCCCAATAGCATTC
scaffold549908_16.	1	p2	(CT)7	14	156	169	CTGCAAAAGCATCACCAGAA
scaffold549950_17.	1	p2	(AT)7	14	722	735	ATCAATTTTTGAGTTATGATGTTTGT
scaffold549977_13.	1	p2	(TA)10	20	103	122	GTGGACGCTCCAGATTGTTT
scaffold550135_10.	1	p2	(CT)7	14	116	129	GAGGGATTTTGGGACGATTT
scaffold550146_15.	1	p2	(AT)11	22	76	97	TTGTGTGGTTGTGATTTAGTTATTTG
scaffold550178_19.	1	p2	(CT)6	12	235	246	AGACTAAAGGCCAAGAGGGC
scaffold550185_17.	1	p2	(AG)10	20	690	709	ATGACAGTTGGGTTTCTGGG
scaffold550186_14.	1	p2	(CT)7	14	155	168	ACGTCTCTTCATGCACCAAT
scaffold550261_12.	1	p2	(TA)8	16	200	215	TTCAACATACAGGCACGAAAA
scaffold550296_12.	1	p2	(TA)8	16	198	213	GGAACCCATCCACCCTATTT
scaffold550523_15.	1	p2	(GA)7	14	4540	4553	ATTTTGGCGCGAAACATAAG
scaffold550548_18.	1	p2	(CT)6	12	59	70	GTCACACACACTCACGGCTT
scaffold550708_13.	1	p2	(TG)6	12	309	320	CCGAAATCTCAAAATCCGAG
scaffold550971_11.	1	p2	(AG)6	12	419	430	ATGGTCCCCTCAACACAAGA
scaffold551117_11.	1	p2	(TC)7	14	76	89	CCTAGCCTTTGCCCTCTTTT
scaffold551260_17.	1	p2	(AT)6	12	157	168	CAAACATTCATCAATATACACACGA
scaffold551306_10.	1	p2	(GT)8	16	76	91	CTGGAAGCACGTGACAGCTA
scaffold551489_12.	1	p2	(AG)6	12	393	404	CAGAGAAAAGTGAGCTCGGG
scaffold551538_15.	1	p2	(TA)11	22	2161	2182	CAGGTGGAGTTTCATCCACA
scaffold551597_18.	1	p2	(CT)6	12	1020	1031	GCTCCTCCCTTACTTGCCTT
scaffold551614_15.	1	p2	(AG)9	18	880	897	TGGTTCACGTAAAACAGCCA
scaffold551618_11.	1	p2	(CT)8	16	313	328	ATAATTCAACCCACACCCCA
scaffold551741_10.	1	p2	(TA)9	18	295	312	AAACCCATCACCCACGTTTA
scaffold551754_12.	1	p2	(TA)9	18	755	772	TTTGCGAGCAAATGAATAAGA
scaffold551800_10.	1	p2	(TA)8	16	219	234	CCTTACGAGGCCAAGAATGA

scaffold551848_13.	1	p2	(TA)6	12	243	254	TTTGGGCTATTTCCCAACAG
scaffold551941_17.	1	p2	(GA)7	14	941	954	TCATCCCATGCGTGTATGTT
scaffold551952_11.	1	p2	(AT)7	14	54	67	GGCTTTATGATCCATTCTCAAA
scaffold551965_14.	1	p2	(TC)6	12	462	473	GTTCCTCAAGCCGAAATCTG
scaffold552111_16.	1	p2	(GA)10	20	922	941	CCAAACCAATTCAAAAGGGA
scaffold552132_11.	1	p2	(TA)6	12	272	283	TCCCAGATGTTGAAATGGTG
scaffold552153_14.	1	p2	(TA)9	18	294	311	ATTCCAAAAATCAAAGGCCC
scaffold552264_10.	1	p2	(CT)8	16	654	669	TCCCTAATTCCAATTCCCCT
scaffold552288_11.	1	p2	(TA)11	22	43	64	TGCGTTTTGACAATATTTAGTGTTT
scaffold552360_10.	1	p2	(TA)8	16	48	63	ATCGGTTATTACCGGATCGC
scaffold552395_13.	1	p2	(AT)11	22	236	257	CACATAAAGGATTCCCGTGG
scaffold552604_11.	1	p2	(TA)6	12	139	150	TCAAAAACAGAGGAGAAGGGA
scaffold552690_16.	1	p2	(CT)6	12	1449	1460	GCTTGATCGGCCTTGTAAGA
scaffold552898_13.	1	p2	(AT)6	12	133	144	GGCCAAGTCTGGCCTATTTA
scaffold552919_12.	1	p2	(AG)7	14	190	203	CACGGTTAGGCTCGAGAGAG
scaffold553085_28.	1	p2	(TC)6	12	292	303	TTTGTGGCAACAAGTTTTCG
scaffold553295_16.	1	p2	(TC)9	18	106	123	TCGATTTCAGCATCATTGGT
scaffold553331_14.	1	p2	(CG)6	12	46	57	ACCAATGGTGGTATGGTGTG
scaffold553473_18.	1	p2	(CT)6	12	210	221	TCGTATGATCCAACTTCGCA
scaffold553529_11.	1	p2	(AG)9	18	255	272	GCTAATGGTGTTGCTGGGTT
scaffold553545_17.	1	p2	(GA)8	16	381	396	TGGCAGAACAAAACTCATGC
scaffold553570_16.	1	p2	(AG)7	14	157	170	TATGAGGCCAAACTGGGAAG
scaffold553589_17.	1	p2	(AT)6	12	7942	7953	CCATGCCACCTTCTATTGGT
scaffold553785_16.	1	p2	(GC)6	12	2420	2431	GGTGGTATGGTGTGGAGGAC
scaffold553822_16.	1	p2	(AT)6	12	697	708	GCGAAAATTCCACCATAGTCA
scaffold553845_14.	1	p2	(TC)13	26	994	1019	CAACAAATTAGCTGAATGGCA
scaffold554002_14.	1	p2	(AT)6	12	440	451	AGGGAGATCGACGTGAGAGA
scaffold554140_10.	1	p2	(GA)7	14	52	65	TGGGGCCTACGAGAAATATG
scaffold554161_20.	1	p2	(CT)6	12	296	307	GTCACCTCACACACCACTCG
scaffold554228_11.	1	p2	(AT)7	14	228	241	AAACAATGCCCGAAGATTGA
scaffold554469_18.	1	p2	(GA)7	14	516	529	AGAAACGAAAGCACGACGAT
scaffold554497_15.	1	p2	(TA)7	14	91	104	TCTTATAGCATCAACCGCCA
scaffold554694_11.	1	p2	(TA)7	14	163	176	TGCAATCCAGTCGCATTTAG
scaffold554868_17.	1	p2	(TA)7	14	52	65	GGGGTTATCATGGGATCAAG
scaffold555019_13.	1	p2	(CT)13	26	1305	1330	AACTGCCCCTCTATTCCGAT
scaffold555038_15.	1	p2	(AG)8	16	573	588	TCAGGATCAGAACACCATCAA
scaffold555065_12.	1	p2	(TA)6	12	2168	2179	GAATCGTAACATGTAACACACAAAA
scaffold555076_13.	1	p2	(TA)7	14	676	689	ACCGTGCAATCCAATTTAGC
scaffold555353_14.	1	p2	(TA)6	12	295	306	GGCGGCATTCTATGAGGTAA
scaffold555599_16.	1	p2	(AC)8	16	47	62	GAAAAGCTTGGCCATTCAAC
scaffold555678_10.	1	p2	(AT)6	12	52	63	TGATTGTAAAACATGTATGGGATTG
scaffold555837_13.	1	p2	(AT)6	12	135	146	ACCTCGTGATCATTCTTGCC
scaffold555844_14.	1	p2	(CA)6	12	81	92	TTAGATCCGAGATGGTTGGG
scaffold555903_11.	1	p2	(TA)7	14	114	127	AATAAGTTCACTTTATGCGAAAGAA
scaffold555974_15.	1	p2	(CT)6	12	265	276	AACCCCCAACCAACTCCTAC
scaffold555981_10.	1	p2	(TC)6	12	82	93	CCGCCATTGACCTCATACTT
scaffold556006_17.	1	p2	(CA)7	14	471	484	CGTGTCTGGTGTTTCAATGG
scaffold556037_15.	1	p2	(GA)8	16	1058	1073	GAAGCCCACAAAGTTGCATT
scaffold556055_13.	1	p2	(TA)10	20	46	65	TGACGGGATTTAGGTGTTTTG
scaffold556067_17.	1	p2	(CT)7	14	410	423	CTCTCACCAACTCGCTTTCC
scaffold556089_12.	1	p2	(TC)7	14	105	118	TGCTTCATTGGTGGTAACGA
scaffold556121_10.	1	p2	(CT)6	12	420	431	AACCATGTCGAGGGTTTCAG
scaffold556174_16.	1	p2	(AT)6	12	1325	1336	ACGGTTGAAACGTGGGTATG
scaffold556192_15.	1	p2	(TA)8	16	197	212	TGAAATGAAATCATGCCCCT
scaffold556269_14.	1	p2	(AT)6	12	603	614	CTGCTATTGAAACAACCCCG
scaffold556283_10.	1	p2	(CT)6	12	215	226	ATTCACAATGGCAAGGAACC
scaffold556286_11.	1	p2	(GA)6	12	542	553	CTCGAGTTTTCTTCGCAACC
scaffold556602_11.	1	p2	(TA)7	14	478	491	TGGATGCACCAGATTGTTTC

scaffold556686_12.	1	p2	(TC)10	20	51	70	CTGCTCCTTCTCACTCTTCCA
scaffold556812_19.	1	p2	(TG)7	14	65	78	CGGTTATCACCGGATCGC
scaffold556875_15.	1	p2	(AT)7	14	1219	1232	AGTTGGGAATTGGGATAGGG
scaffold556934_16.	1	p2	(TA)11	22	60	81	CCTAAAACTTCAAACTGTGGGG
scaffold556952_14.	1	p2	(CT)7	14	86	99	CTCTTCACTCTCACTAGCCGC
scaffold556985_15.	1	p2	(CT)8	16	1738	1753	CTCATTTTCTCCGCATCACA
scaffold557004_14.	1	p2	(GA)6	12	159	170	GCACTTAGGAGAGAGATTGTTGG
scaffold557047_10.	1	p2	(TG)6	12	291	302	GCTCGAGGCATGTAAGAAGC
scaffold557147_16.	1	p2	(TA)7	14	1118	1131	CAACATGTGCAGGTTGAGGT
scaffold557180_10.	1	p2	(GC)7	14	268	281	TTCCGAACATTGCACCATTA
scaffold557232_20.	1	p2	(GA)7	14	532	545	CTACCCTTTCCGAACATCCC
scaffold557276_13.	1	p2	(AT)8	16	935	950	AGGACCGAAAGTAGCGAACA
scaffold557296_12.	1	p2	(CT)7	14	392	405	TGCTTATCGAGTTTGGGACA
scaffold557306_11.	1	p2	(CT)7	14	261	274	ATTCATTCTCCAACCATCGG
scaffold557313_14.	1	p2	(TA)6	12	206	217	GTGGTATAGCGGTTGGCATC
scaffold557332_16.	1	p2	(TC)6	12	211	222	CCATCATTTCCCTCACCTCA
scaffold557435_18.	1	p2	(TC)7	14	409	422	TTCCATCAATCCACTCCACC
scaffold557470_17.	1	p2	(AG)9	18	2321	2338	CGTACACCCATTTTGAAGGG
scaffold557475_12.	1	p2	(AG)6	12	159	170	GGGTGAGTAACGGTGCAAGT
scaffold557476_13.	1	p2	(AG)6	12	159	170	TTTGGGACTCAACGAAGACA
scaffold557488_11.	1	p2	(CG)6	12	164	175	GTGTGGAAAAGGGAGTGCAT
scaffold557500_14.	1	p2	(AG)7	14	1341	1354	AGAGGCTCGCCATTGATAGA
scaffold557574_10.	1	p2	(GT)6	12	481	492	ATGCGACAGAGTGTGTGAGG
scaffold557614_11.	1	p2	(AT)7	14	372	385	TGTTTTGGGCCTAAATGGAC
scaffold557697_14.	1	p2	(AT)11	22	220	241	GGAGAGGAAAAATGGGGAAA
scaffold557765_16.	1	p2	(TA)6	12	100	111	GCGTTGACGCTATTGAAATG
scaffold557828_11.	1	p2	(TC)7	14	158	171	AATCGGAGTGGATTTGATGC
scaffold557920_11.	1	p2	(TA)6	12	183	194	AGAAACGTCGGTGACCAATC
scaffold557982_13.	1	p2	(TA)10	20	47	66	GGATTTAGCGGTTATTACCTGAA
scaffold557989_15.	1	p2	(AC)6	12	63	74	CTCTCGAGCCTAACTGTGGC
scaffold558019_14.	1	p2	(AT)6	12	93	104	TTTCCAATTTTGGGAAATACTATGA
scaffold558075_15.	1	p2	(GT)6	12	89	100	GGAGAGTTGTAGAGTCAAGTTGTAA
scaffold558294_15.	1	p2	(TA)6	12	4394	4405	AAAGAGCATCAAACATCATTTCC
scaffold558310_11.	1	p2	(AT)9	18	50	67	TTCCCGTATACAAATTCCAACA
scaffold558330_10.	1	p2	(CT)6	12	543	554	AGAACCACCAAAGCAATACCA
scaffold558377_11.	1	p2	(TA)10	20	395	414	CGGTACAGATTGCACACGAC
scaffold558501_12.	1	p2	(TA)6	12	85	96	TCACTTAGCTCTTGATTTTCATCAC
scaffold558671_17.	1	p2	(GA)6	12	272	283	TTGGAGTCTCTCTGAACTCGG
scaffold558710_12.	1	p2	(TA)8	16	488	503	CGACCGAATACTCACCCCTA
scaffold558807_14.	1	p2	(TA)6	12	160	171	CAAGGAAGGAACCTCCATTTT
scaffold558808_15.	1	p2	(TA)7	14	158	171	TTTCGATATGGCTCGGTAGG
scaffold558810_15.	1	p2	(AT)8	16	160	175	ACGGCTGGCATTTGTTAGAG
scaffold558855_14.	1	p2	(AT)8	16	267	282	AAACTGCTGTAGCGAACCGT
scaffold558875_13.	1	p2	(TC)6	12	571	582	CAATTCTCCATGCACACCAG
scaffold558941_10.	1	p2	(CT)6	12	83	94	GCCCTAGAATCTGCCCTCTT
scaffold559054_10.	1	p2	(AG)8	16	699	714	GCCAGTCCAATGGTCGTACT
scaffold559395_17.	1	p2	(GT)6	12	1579	1590	ATCATCAGCTCGTGTGCTTG
scaffold559424_15.	1	p2	(GT)6	12	193	204	CTCGTGAGAGTGCGTGAGAG
scaffold559628_16.	1	p2	(TC)7	14	106	119	ATTCCCAACTGATTGGCTTG
scaffold559895_15.	1	p2	(AG)10	20	153	172	TGAGCAAGGGACAAATGTGA
scaffold559935_15.	1	p2	(AT)6	12	612	623	ATTGAAACCATGCCCATTTC
scaffold559963_15.	1	p2	(TA)12	24	41	64	CCAAATTTAAGGGTTATCACCTG
scaffold559978_11.	1	p2	(TC)6	12	319	330	TATCCCATGATCGAGTTCGG
scaffold559987_18.	1	p2	(AG)9	18	154	171	TATGAAGCATAACCATGCCG
scaffold560056_10.	1	p2	(GA)8	16	390	405	CTGAGTGCCTGTCACGAAAA
scaffold560209_13.	1	p2	(TA)7	14	67	80	TTGAGCTGTTATGCGTTTTGA
scaffold560222_10.	1	p2	(TA)9	18	498	515	GTTTTAGAGTTGGCATCGGG
scaffold560259_14.	1	p2	(AC)7	14	2118	2131	GGCCAAGGGAAAGCTTTTAT

scaffold560291_18.	1	p2	(TC)6	12	232	243	CGGCTTGAAAACGAGAAATC
scaffold560350_14.	1	p2	(GA)7	14	90	103	GCAGGAAAATGAAAAGTGGG
scaffold560464_16.	1	p2	(CT)6	12	743	754	CTTCTCCTTGTCGTGCCTTC
scaffold560569_11.	1	p2	(AT)7	14	452	465	AGTAAGCAACTCCGGTGGGT
scaffold560607_16.	1	p2	(AG)6	12	1332	1343	CTCTGGAAGAAGAGCCATCG
scaffold560639_13.	1	p2	(TC)9	18	219	236	AATTTTGACGGCTCCAAGTG
scaffold560740_11.	1	p2	(CT)6	12	146	157	GCATCTACTCTGGCTCTCATTG
scaffold560834_16.	1	p2	(TC)6	12	2839	2850	AATGGACCGGACGTGAACTA
scaffold560851_13.	1	p2	(TA)9	18	139	156	AACATGTTGATCTAAATAACGCAG
scaffold560857_11.	1	p2	(TA)10	20	985	1004	CGTATTGCAGTGAAATTTTAGCA
scaffold560899_15.	1	p2	(TC)10	20	1794	1813	CAGACATGTGTACCACCCCA
scaffold560969_13.	1	p2	(AC)6	12	806	817	ACCGACCACCCTCTTTTTCT
scaffold561070_10.	1	p2	(AT)7	14	98	111	CACCTGATCGCGACCCTAT
scaffold561218_17.	1	p2	(TA)6	12	1787	1798	TCTACACGCGCATGTCATTT
scaffold561260_13.	1	p2	(TA)7	14	160	173	TTACCACAATTTCCCTTGTTTT
scaffold561304_12.	1	p2	(TG)6	12	439	450	GTTTCAGTTGGCAGTGCAGA
scaffold561453_12.	1	p2	(TA)6	12	94	105	TTTGCCCTTATTTAGCACGG
scaffold561464_12.	1	p2	(TA)6	12	535	546	GACAATTGAAAGAGCACTCGC
scaffold561612_15.	1	p2	(GA)6	12	347	358	ACCTGCCCAGATCTCTCTGA
scaffold561613_15.	1	p2	(AG)7	14	348	361	CGGTTTCGAGAGAGAAGTGG
scaffold561727_13.	1	p2	(AT)7	14	67	80	CGTATATTTGCGGGGTTGTT
scaffold561754_19.	1	p2	(AC)6	12	1016	1027	GTAAGGCCAGGCACATTCAT
scaffold561839_12.	1	p2	(TA)6	12	161	172	TCGAATTTCTAGCGTGATGG
scaffold561840_15.	1	p2	(TA)6	12	161	172	GCTTAATGCGTAGCTGGGAT
scaffold561841_10.	1	p2	(AT)10	20	53	72	CAAACGTGAGTGGGAGATGT
scaffold561868_12.	1	p2	(AT)10	20	654	673	ATGGCGTTAGAATGCGAAAC
scaffold561885_17.	1	p2	(TG)8	16	2299	2314	AGTTTTCGTGGCCTCACATT
scaffold562217_14.	1	p2	(CA)6	12	317	328	TGATAGCCAAAATTTACAACGTG
scaffold562222_12.	1	p2	(TA)10	20	601	620	TGTGCTTATCCACCGACAAA
scaffold562231_14.	1	p2	(AG)7	14	94	107	AAAACTACGATCTGCCACCG
scaffold562239_16.	1	p2	(CT)8	16	158	173	TCAATTGCGGCTTAAACTCC
scaffold562316_15.	1	p2	(GA)7	14	704	717	GAAATTCGCCGCAGTATAGC
scaffold562358_12.	1	p2	(AT)9	18	579	596	AATTTTTGTTTGCTGCCGAT
scaffold562426_18.	1	p2	(TA)6	12	258	269	ATTACGTCGATCCAACGGTC
scaffold562454_10.	1	p2	(AG)6	12	380	391	GGATGGATGAAAAGGCTCAC
scaffold562505_14.	1	p2	(TA)7	14	624	637	CACCAAATTTTATCATTTTTAATTCTC
scaffold562583_10.	1	p2	(AT)7	14	49	62	TTGGAGCTTCAAAACTTAGGC
scaffold562623_12.	1	p2	(CT)6	12	1092	1103	CACTTCACCATTCCACCATTT
scaffold562626_13.	1	p2	(AG)6	12	572	583	ACTTCGTGGATTGGATTTCG
scaffold562635_17.	1	p2	(GA)8	16	58	73	GCGACAATTCTGCGTGTTAT
scaffold562686_16.	1	p2	(TC)12	24	2686	2709	TGAGCATAATCTTGGGGCTC
scaffold562688_12.	1	p2	(TG)7	14	67	80	CGGTTATCACCGGATCGC
scaffold562697_11.	1	p2	(AT)8	16	78	93	TTCGGAGCATGATTTAAGTGG
scaffold562808_11.	1	p2	(CT)7	14	83	96	TTCCCCTTTGCCCTCTATTT
scaffold562856_11.	1	p2	(TC)6	12	407	418	ATCAGCGACGAGTCCAAGAC
scaffold562890_14.	1	p2	(TA)10	20	526	545	CCAACAAAAGGTGTGTGCAT
scaffold562958_12.	1	p2	(AG)6	12	154	165	GCGACAGAAAAAGAACGAGG
scaffold562967_15.	1	p2	(CT)9	18	829	846	GGGTTGAAAATGGTGTCAGC
scaffold562985_16.	1	p2	(GT)6	12	3496	3507	TGCTGCTGCTGATCAAATTC
scaffold563044_17.	1	p2	(TA)8	16	1544	1559	CGAGGCTTAATGGGGACATA
scaffold563053_15.	1	p2	(TA)7	14	719	732	GCCACCTCACTCTTGCTACC
scaffold563133_16.	1	p2	(GA)6	12	4354	4365	CGATTGAGTTTCAGCGCATA
scaffold563196_17.	1	p2	(AT)7	14	159	172	AAACCGCTCGAATCCGTACT
scaffold563197_11.	1	p2	(TA)7	14	160	173	CTTTAGGGCCCTTGATTTCC
scaffold563215_11.	1	p2	(CT)6	12	95	106	TCTTGGTTGGTGGAAGAACA
scaffold563220_16.	1	p2	(CA)6	12	286	297	AGGATTGTGGAGGATGGTGT
scaffold563255_13.	1	p2	(TA)6	12	1151	1162	CAATTTTCAATCACAAGTTATAGTGG
scaffold563510_12.	1	p2	(AT)9	18	139	156	AATTATTTCGGGCTAACGGG

scaffold563554_13.5	1	p2	(AT)7	14	168	181	AGTGATGGAACCAACCTTGC
scaffold563620_16.5	1	p2	(AT)6	12	97	108	TCCCTTGCTTTCTAACCCCT
scaffold563709_11.5	1	p2	(GA)6	12	242	253	TTCCTTTGTCATTCCAACCA
scaffold563752_15.4	1	p2	(TC)6	12	162	173	ATAAGTTTGTGCCTCCCGTG
scaffold563879_14.3	1	p2	(AG)10	20	832	851	TGGGAAAGTGTTGGGATTTC
scaffold563932_13.8	1	p2	(GA)6	12	2574	2585	TCCTAAGCTTTTCCTGCTGC
scaffold563953_17.2	1	p2	(CT)6	12	525	536	TGTTTGATGGCTCTTTGCAG
scaffold564036_11.5	1	p2	(AC)6	12	79	90	CGAAGTGTTGATTGAATTGCC
scaffold564148_16.2	1	p2	(AT)6	12	2412	2423	GTACAATCTTCCTGCCACCC
scaffold564242_20.4	1	p2	(TA)6	12	134	145	CTATTGAAACAACCCCGGAC
scaffold564251_12.5	1	p2	(AC)6	12	469	480	TGGCAGTTACCTATCCCCAC
scaffold564312_12.1	1	p2	(AG)6	12	231	242	GGAGGTGAATGGAGAGTGGA
scaffold564395_13.3	1	p2	(TA)7	14	221	234	ACACATTTTTCTTTTGGGCG
scaffold564462_18.1	1	p2	(AT)9	18	155	172	TCTTCGGTCCGACCTTGTAT
scaffold564465_17.6	1	p2	(GA)6	12	433	444	GGAACCCATGAATTTGTGCT
scaffold564515_13.0	1	p2	(TC)6	12	54	65	TCTCTCACCTCACCTCTCCA
scaffold564538_16.7	1	p2	(AG)8	16	37	52	TGAAGAACGATTACAAAGTTTATCCA
scaffold564579_11.7	1	p2	(TA)7	14	160	173	CACAGAACATAATTCCGCAAAA
scaffold564630_18.5	1	p2	(TA)8	16	158	173	GAGGGGTGGACTATTTCTTGC
scaffold564646_19.3	1	p2	(TA)8	16	357	372	CCAGGGCATATACCCATTTG
scaffold564706_12.3	1	p2	(TA)8	16	322	337	GTACCTGGCTGTAGGATGCC
scaffold564717_14.3	1	p2	(CT)6	12	1596	1607	ACCTACCGTCACAATCTCGG
scaffold564724_15.0	1	p2	(AT)6	12	1193	1204	ATTGGATGGAAATGCTCTGC
scaffold564772_10.8	1	p2	(TA)8	16	69	84	ACAAACTAATCAAGTTCCGCA
scaffold564776_13.4	1	p2	(AG)6	12	80	91	ACGGTGGGCCGAGTATATTA
scaffold564797_10.9	1	p2	(AG)9	18	484	501	AGTGAAGGTGACGAAATGGG
scaffold565051_13.3	1	p2	(TG)6	12	262	273	TGCTCTAGGTAAACCCACGG
scaffold565097_14.3	1	p2	(TC)7	14	1385	1398	CCATTCCTGCAAACCATCTT
scaffold565098_15.0	1	p2	(AG)9	18	157	174	TTCTTGGCGTGGTGTTGTAG
scaffold565111_14.5	1	p2	(GA)8	16	1156	1171	GAGTCGTTCGGGTACGTGTT
scaffold565137_21.4	1	p2	(TA)9	18	388	405	TTTCAAATGGAATTCATATAGCCA
scaffold565267_10.6	1	p2	(CT)7	14	182	195	GCCACTCAGCCTACATCCAC
scaffold565292_11.0	1	p2	(AT)11	22	245	266	ACGAGACTGTCGGTCAACAA
scaffold565336_10.4	1	p2	(AT)8	16	200	215	ATTGCAATGACTTGGCATGA
scaffold565357_17.1	1	p2	(CT)6	12	140	151	GGATCGAAAAGAGAGGGAGG
scaffold565407_11.9	1	p2	(AT)12	24	906	929	CGGTCGTTTTCCAATTTGTT
scaffold565538_15.3	1	p2	(TA)6	12	1133	1144	CATCAATTTTCAGGCCAACA
scaffold565619_15.7	1	p2	(AC)7	14	1696	1709	CCTGCGATATCCTCACCAAT
scaffold565636_18.2	1	p2	(AT)7	14	1849	1862	TGGTGAGAGAAAATGGAGGG
scaffold565677_16.9	1	p2	(TA)6	12	1347	1358	CCGCCGAAAAGACAAATAAC
scaffold565809_20.4	1	p2	(TC)6	12	420	431	CTCCAACTCCATCACCATCA
scaffold565819_16.4	1	p2	(GA)7	14	333	346	TTGCAAAGTCAGACGTCATTG
scaffold565878_10.9	1	p2	(AT)8	16	386	401	CCTCAGTTAGGATTCACTGATCATATT
scaffold565964_16.7	1	p2	(TC)6	12	192	203	TGACACCTAGCCCATAACCC
scaffold565978_14.3	1	p2	(AT)8	16	179	194	TCATTTGATCACAAACCCCC
scaffold565995_13.8	1	p2	(AT)6	12	266	277	TGTGCAGAAAACAGAGCTGG
scaffold566013_14.1	1	p2	(TC)6	12	708	719	CAGCTGACTGACAGAATGGG
scaffold566026_11.4	1	p2	(GA)7	14	329	342	TACCCCAATAATCAGCCCAA
scaffold566083_18.1	1	p2	(AT)9	18	464	481	CGGATTCAAGCTGTGAGAAA
scaffold566115_15.9	1	p2	(TC)8	16	522	537	GGATGTTGAGATCAGAACCACA
scaffold566295_17.9	1	p2	(CT)6	12	1854	1865	TTGGGAACTGGATACAAGGC
scaffold566366_13.7	1	p2	(AT)11	22	108	129	TGAGAAGGAAATTAATGTGTTTTAAG
scaffold566395_11.2	1	p2	(AT)6	12	89	100	TGTCATGTAATAGCCGTGCAA
scaffold566425_15.5	1	p2	(GA)6	12	2011	2022	CAGCACTCTGCATTTCCCTT
scaffold566539_13.0	1	p2	(TA)7	14	287	300	GCTTGAAGGATGAAGGTTGG
scaffold566575_12.2	1	p2	(TA)7	14	207	220	GCGAGTTGTTTCATGCCATA
scaffold566696_13.6	1	p2	(CA)8	16	314	329	GCTCAAAAGCACATCTGCAA
scaffold566713_18.2	1	p2	(AG)6	12	164	175	TGGCATTTTCCCACGTTAAT

scaffold566720_14.	1	p2	(TG)7	14	135	148	CATTTGGTGAGGAGGGAGAA
scaffold566756_14.	1	p2	(AC)7	14	722	735	CATGTTTTTGCGCAATTTCT
scaffold566772_12.	1	p2	(AT)6	12	267	278	TTCTCAGCATATGGGAAGGG
scaffold566830_11.	1	p2	(GA)6	12	323	334	GAGAGTGGAGAGAGAGAGGGAA
scaffold566861_14.	1	p2	(TA)11	22	88	109	CCCTTTATTTGGTTGATCTAATGG
scaffold566885_20.	1	p2	(TC)6	12	423	434	TGTGCGAGTCGGTAATTCTG
scaffold566929_17.	1	p2	(TA)6	12	100	111	TAGCATGCAAAAGGAACACG
scaffold566974_13.	1	p2	(TG)6	12	1684	1695	GAATTGGTATGCAAACGTGG
scaffold567063_16.	1	p2	(TC)7	14	644	657	TTTGACGGCACAATTCTGTT
scaffold567128_10.	1	p2	(TA)9	18	475	492	CACGTGGCATGATAATAGCG
scaffold567273_17.	1	p2	(CA)6	12	76	87	CCTCACCCATTCACACACAC
scaffold567281_16.	1	p2	(AT)7	14	262	275	CACATTTGCAGATGACAGCA
scaffold567287_12.	1	p2	(TA)10	20	65	84	TCCAATGGATGAGGATGGTT
scaffold567478_14.	1	p2	(AT)7	14	990	1003	GCCACTTGAGGGAGTTGAAA
scaffold567594_12.	1	p2	(TA)13	26	39	64	TAAGAAATGCATGCACCTGA
scaffold567631_10.	1	p2	(TA)8	16	304	319	CTGCTCGTTAATGCGAGTGA
scaffold567690_14.	1	p2	(TA)12	24	86	109	CAAAAATCTAACGGCCCAGA
scaffold567693_10.	1	p2	(TA)6	12	337	348	ATTGTGTGACGGGAAAAACC
scaffold567744_21.	1	p2	(AG)6	12	42	53	CGCTCTATCTTCTTTCTCTTCAGG
scaffold567770_16.	1	p2	(AT)6	12	180	191	AAATAGCAAATGTTTAGCATGCAC
scaffold567804_15.	1	p2	(TA)6	12	2523	2534	TTTTTGGGAACTTGTCCTGG
scaffold567861_17.	1	p2	(AT)8	16	111	126	CATTTTCAATGACCCGAACA
scaffold567942_15.	1	p2	(TC)7	14	161	174	CGTGACCTTTTGGTCTCAGG
scaffold567943_16.	1	p2	(TC)8	16	159	174	CCTGATCCTCCTCCATTTCA
scaffold567951_13.	1	p2	(CT)6	12	70	81	GAGGACATTTGGACCTGAAAA
scaffold568052_14.	1	p2	(GA)7	14	4573	4586	AAAATTGCAGTGCCATCACC
scaffold568086_12.	1	p2	(AT)9	18	211	228	GTCGCAATTCAAGCGACATA
scaffold568170_16.	1	p2	(CT)6	12	488	499	TGAGAAATGCAAAAAGCATGA
scaffold568177_12.	1	p2	(GT)6	12	163	174	GATATACCGGAAGGGGGAGA
scaffold568178_13.	1	p2	(CT)8	16	111	126	CACTACTAGGGTTTGGGAGGG
scaffold568252_12.	1	p2	(AT)6	12	243	254	TGTCACCCAAGTCTCATGCT
scaffold568265_12.	1	p2	(TA)8	16	365	380	AGGATTTGGGTTGTGAGGTG
scaffold568346_10.	1	p2	(AT)9	18	263	280	CCGATTGTGAGCATGAAAAC
scaffold568371_15.	1	p2	(CT)6	12	128	139	AAGAGGGGCGACGAAATTAG
scaffold568405_16.	1	p2	(TC)6	12	1216	1227	GCCCCATCTCCATCTATTCA
scaffold568640_14.	1	p2	(AT)6	12	408	419	TCGCTGAGAACACAAGCATT
scaffold568703_11.	1	p2	(CT)6	12	348	359	GTCAACAGCTCGGTACAGCA
scaffold568707_13.	1	p2	(TA)8	16	97	112	TCAATCTAACGAAATCTGCGG
scaffold568719_13.	1	p2	(AT)10	20	411	430	GTTTTTGGTTGTCGTGGGTT
scaffold568758_10.	1	p2	(GC)7	14	287	300	CACTATTATGGCCGACCGTT
scaffold568823_13.	1	p2	(AT)6	12	89	100	GGATATCCGAAACATCCGATT
scaffold568828_14.	1	p2	(TA)7	14	162	175	TGCACCCATACCTACACGAA
scaffold568897_10.	1	p2	(TA)7	14	201	214	AAACCCTTCTGCCCCTTCTA
scaffold568922_10.	1	p2	(AT)6	12	257	268	AGATGGAACGACCCTGTGAG
scaffold568930_11.	1	p2	(AG)6	12	69	80	AACCACCACCATTGAAAGGA
scaffold569112_18.	1	p2	(TC)6	12	400	411	TCCAACACATCCCTACAACTTTT
scaffold569140_15.	1	p2	(GA)6	12	3243	3254	GGCTGATGTTGTTGTTGGTG
scaffold569145_16.	1	p2	(AT)10	20	1070	1089	CCAAAAATATGGCCGTGAAC
scaffold569250_12.	1	p2	(AC)6	12	65	76	GTTAGGAAACGAAAGGGGGA
scaffold569413_13.	1	p2	(GA)6	12	252	263	TGGCTGAGGATGAATGAACA
scaffold569448_14.	1	p2	(CT)8	16	2168	2183	TGCATGCATTTATTTGACAGC
scaffold569456_14.	1	p2	(TA)8	16	1285	1300	TTTTGGAGATTCTGGGTTCG
scaffold569605_13.	1	p2	(TA)9	18	1076	1093	TTAAGGTGGTGTTTGCATGG
scaffold569609_16.	1	p2	(TA)7	14	1626	1639	AAGGTGATCTACGTCCACGG
scaffold569684_11.	1	p2	(TA)8	16	50	65	TAAAAACAGGGGCAAAGGTG
scaffold569781_17.	1	p2	(AT)7	14	162	175	AACTCGAATTGCAACGAAAA
scaffold569872_17.	1	p2	(TG)6	12	1972	1983	TGGGAGGATCTTCAGATTGG
scaffold569911_16.	1	p2	(AG)6	12	122	133	CCCAAAACATGCAAACACAG

scaffold569943_18.	1	p2	(TA)8	16	46	61	TGCGTTTTGACGATATATAGTGTTT
scaffold570049_17.	1	p2	(GA)6	12	2288	2299	AAACCTTCTGGCTGAACCAA
scaffold570085_14.	1	p2	(GA)6	12	419	430	GAAGCACATTGCAGCAAAAA
scaffold570105_18.	1	p2	(TA)12	24	306	329	TTGTGCTGAAAATCTCCTCAGA
scaffold570235_14.	1	p2	(GA)6	12	3089	3100	AGCAAGTCAATTGGGGAATG
scaffold570245_19.	1	p2	(AT)8	16	161	176	GAAGAAAGAGGGAAGTGGGG
scaffold570287_18.	1	p2	(TA)8	16	67	82	CGGTTATCACCGGATCGC
scaffold570313_15.	1	p2	(GA)11	22	471	492	TTGCACTCTGTGGAGCAATC
scaffold570441_16.	1	p2	(AG)7	14	58	71	GATTTGATTCCTTTTGTCCCC
scaffold570591_13.	1	p2	(TA)6	12	1015	1026	TGCATTACAGCTTGTTGCAG
scaffold570592_12.	1	p2	(AT)9	18	601	618	GCAATTGATTGAAATGCCCT
scaffold570616_11.	1	p2	(TC)6	12	211	222	AGAGGCGGCCTTTTTATTCT
scaffold570680_17.	1	p2	(GT)7	14	88	101	TCCTCTTTCAGGTCCAAGTG
scaffold570721_12.	1	p2	(GT)6	12	501	512	GATCAAGCTTCAGACCGGAG
scaffold570867_14.	1	p2	(TC)6	12	264	275	GTGGGCTATGGCTCAAGTGT
scaffold571049_10.	1	p2	(AT)10	20	83	102	CGTCCACGACCTCCACTATT
scaffold571050_15.	1	p2	(GA)6	12	4839	4850	CAAGAAACCATGGAGAATGGA
scaffold571122_15.	1	p2	(TA)7	14	452	465	CCATGAATCTTTCACATTTTTCA
scaffold571314_15.	1	p2	(TC)6	12	55	66	TCTCTCTCTTTTTGGTTGGTGA
scaffold571363_16.	1	p2	(CA)6	12	2140	2151	TTTCCCAAATTATGCTCACTCA
scaffold571404_13.	1	p2	(GA)6	12	1331	1342	GTGATCTCGCCGCTTTAGAC
scaffold571712_13.	1	p2	(AC)6	12	110	121	CTCTCTCGAGCCTAACCGTG
scaffold571731_12.	1	p2	(TA)9	18	330	347	GGTGCATAGAAATTGCTGCC
scaffold571780_13.	1	p2	(CT)8	16	270	285	TTTAAAGGGTGGTCCCATCA
scaffold571856_10.	1	p2	(AT)6	12	280	291	ATTCACTTCGGCAAAATTGG
scaffold571857_15.	1	p2	(CT)8	16	1060	1075	GACGTGTAAACCATCACCCC
scaffold571925_12.	1	p2	(CT)7	14	53	66	AATCCCTTTCTCCTCTCCCA
scaffold571966_15.	1	p2	(TA)6	12	489	500	TTTCAAAATTTGGCACTTAGCA
scaffold571992_14.	1	p2	(AT)10	20	1311	1330	TCTTCCTCGCAATCACTTTCT
scaffold572265_15.	1	p2	(CT)6	12	1426	1437	TTGCTGGCGACATTATCAAG
scaffold572289_14.	1	p2	(TA)13	26	41	66	GAGGGTTATCATGGGATCAAG
scaffold572297_16.	1	p2	(TA)12	24	430	453	TCATATGCGTTCGTCATTCC
scaffold572415_14.	1	p2	(CT)6	12	395	406	TCTTCCCTCCCTCATTTCCT
scaffold572621_10.	1	p2	(AT)9	18	243	260	ATGGCGTTAGAATGCGAAAC
scaffold572622_14.	1	p2	(AG)7	14	2440	2453	TCATGCAAACAAACATGGTG
scaffold572672_18.	1	p2	(CT)6	12	1235	1246	TGATCGGCCTTGTATCACAC
scaffold572762_12.	1	p2	(AT)9	18	284	301	AATACCACCCGATCATTTGAA
scaffold572917_11.	1	p2	(CT)6	12	332	343	TGGGATGAAAGGCTTCAAAC
scaffold572993_12.	1	p2	(TA)9	18	955	972	TCCTCCGTTAAAGACTGTTCATC
scaffold573045_12.	1	p2	(AT)8	16	162	177	TCCCAACTTTTTCTTCAAAATCA
scaffold573074_16.	1	p2	(TA)9	18	41	58	GGAAATAAGGAGGTGTTATGATATG
scaffold573221_16.	1	p2	(CT)6	12	1441	1452	GCTGGACTTGTGCAACAGAA
scaffold573223_11.	1	p2	(TG)6	12	342	353	CCGAGCTGAAAATCCACAAT
scaffold573226_14.	1	p2	(TA)8	16	113	128	GCACGCAAATAATGGTTTCTT
scaffold573229_10.	1	p2	(CA)6	12	373	384	GGATAAATGTGGCGAATGCT
scaffold573319_11.	1	p2	(TC)6	12	928	939	CAGTGCTGTATTGCAACGGT
scaffold573338_17.	1	p2	(CT)6	12	54	65	CACGTTAGACCTTGAAGGGG
scaffold573439_15.	1	p2	(AT)8	16	1210	1225	AATCCTGCAGATGGGATGAC
scaffold573497_11.	1	p2	(TA)7	14	571	584	TGCGGATCTGTGAAAAATGT
scaffold573586_17.	1	p2	(TA)7	14	51	64	TGAAGTTAGGAAATAAGGAGGTGC
scaffold573637_15.	1	p2	(TG)8	16	1526	1541	TTTGGGAGGTTCTTCAGGTG
scaffold573693_14.	1	p2	(AG)6	12	47	58	CTCTGGATATTGCTCGTCGG
scaffold573732_23.	1	p2	(TA)7	14	605	618	CAGGCTGGATGAACTGAGTG
scaffold573736_12.	1	p2	(AT)7	14	389	402	GAATAAAACGGCGCCTACAA
scaffold573831_16.	1	p2	(TA)11	22	94	115	TTTATTTTGGCGTTTCGTGC
scaffold573991_16.	1	p2	(TA)6	12	1026	1037	CCACCGAGGAACATACAAGG
scaffold574001_16.	1	p2	(GA)8	16	631	646	TATAAGCCAACCATCTCCCG
scaffold574175_13.	1	p2	(AT)6	12	514	525	GGTCATTTCTGTTTATTTCGATTG

scaffold574192_17.	1	p2	(AG)13	26	386	411	CTGGGGATGGCGTTATTAGA
scaffold574207_16.	1	p2	(CT)8	16	906	921	ACCAGACCCACACGTTTCTC
scaffold574218_16.	1	p2	(CT)6	12	1071	1082	ACTTTGCCACCTCATATGCC
scaffold574278_17.	1	p2	(TA)7	14	164	177	GTGACCCGGTCTGATGAGTT
scaffold574293_14.	1	p2	(TA)7	14	111	124	TCATCTACAGGTCAATGGTGACA
scaffold574294_11.	1	p2	(TA)9	18	47	64	ATGGGTTATCACCGGATCG
scaffold574311_15.	1	p2	(AT)9	18	145	162	GAAAAATCAAAGGCCCACAA
scaffold574553_14.	1	p2	(GA)6	12	970	981	ATGGCATTCCCCATACACAC
scaffold574601_10.	1	p2	(TA)8	16	209	224	AAATGCACACCCCTTTCAAT
scaffold574625_14.	1	p2	(AG)6	12	135	146	ATGAACACCCCTAGTGACCG
scaffold574639_16.	1	p2	(GA)6	12	181	192	TTATTCTTGATGGAACGGGG
scaffold574869_10.	1	p2	(TC)9	18	85	102	TGGCCATGTTGGTAGATTCA
scaffold574923_11.	1	p2	(TC)6	12	1128	1139	TTGCCTACATCATCCCACAA
scaffold574942_11.	1	p2	(TA)10	20	852	871	TGGTTGCACCATAACACACC
scaffold574976_16.	1	p2	(GC)6	12	95	106	GGTGGTATGGTGTGGAGGAC
scaffold575005_16.	1	p2	(TC)7	14	781	794	CACCCCCAGATGAGCTAAAG
scaffold575075_11.	1	p2	(TC)7	14	74	87	TCGCTCACCGAGATAGGTTC
scaffold575114_12.	1	p2	(TG)6	12	658	669	CTCACCGCCTTAATATGCGT
scaffold575124_15.	1	p2	(TA)6	12	65	76	TTCTAATCAAATCAAGCGACCA
scaffold575158_16.	1	p2	(GA)6	12	145	156	ACCACCACATTACTGCCACA
scaffold575222_15.	1	p2	(AG)6	12	1409	1420	CGTGCGACGACTTAACTGAG
scaffold575250_13.	1	p2	(AT)6	12	916	927	ATTCGAATGTCTTGCCCTTG
scaffold575273_17.	1	p2	(TC)6	12	341	352	CGTAGAGAATGTTGCCACGA
scaffold575296_19.	1	p2	(CT)6	12	247	258	TTCCTGCTGTTCACAACTCG
scaffold575304_10.	1	p2	(AT)6	12	192	203	TTTCATCTGGTTCCCTTTGG
scaffold575361_14.	1	p2	(AT)8	16	1200	1215	CATCTGGGCCTCTCTGGATA
scaffold575414_17.	1	p2	(TC)6	12	211	222	CAGGCAAATCAGGCAATTTT
scaffold575493_15.	1	p2	(GA)6	12	510	521	ATTTGATGGAACGGGGATTT
scaffold575519_10.	1	p2	(TA)6	12	88	99	TGTGTGATGTTGGAGTTGGG
scaffold575528_15.	1	p2	(GT)6	12	1796	1807	TGATGGTTTATGCTCGTAAGGTT
scaffold575602_16.	1	p2	(AT)6	12	634	645	TCCTTGTTGCACTGTGGTGT
scaffold575619_16.	1	p2	(AG)7	14	129	142	TTCCACTTGAAACTATCAGTCCA
scaffold575674_13.	1	p2	(AG)7	14	51	64	CGGCACGAATCCAGTTTTT
scaffold575683_17.	1	p2	(CT)7	14	176	189	TCATCTTGCAAGCTCCATCA
scaffold575745_12.	1	p2	(AT)7	14	209	222	TCTTATAGCATCAACCGCCA
scaffold575761_13.	1	p2	(AT)6	12	271	282	CCCATCATCTCAATCCAACT
scaffold575764_13.	1	p2	(AT)6	12	538	549	AAATGAGTGGCTGGATTTCG
scaffold575774_11.	1	p2	(AG)7	14	644	657	GAGAGAGGAAGGGAGATGGG
scaffold575780_15.	1	p2	(TC)6	12	736	747	CCGTGAATTCATGCCTGTC
scaffold575827_14.	1	p2	(AT)11	22	228	249	TCATCCCCAAAATACCCTCA
scaffold575952_11.	1	p2	(AT)8	16	243	258	AATTTCTCTGGCCGACACTG
scaffold576028_15.	1	p2	(TA)6	12	195	206	TCAATAAACCCTCCGAATGC
scaffold576165_12.	1	p2	(TA)6	12	321	332	AATCGATTCAACTCATGGGG
scaffold576196_13.	1	p2	(TA)9	18	493	510	GAAGAAGGTGATGTCATGGGA
scaffold576378_11.	1	p2	(AT)12	24	530	553	TGCGTGCATGTATATGCTGA
scaffold576439_17.	1	p2	(TA)10	20	463	482	CCATAACCGTCGCATAACTC
scaffold576527_14.	1	p2	(GA)6	12	67	78	GGGGAGGGTTTAGGTAGAGG
scaffold576538_11.	1	p2	(CT)8	16	691	706	AAAAAGAAAAAGGGGTGGGA
scaffold576566_12.	1	p2	(AG)6	12	251	262	CCGATGATGACGAACCTTCT
scaffold576606_13.	1	p2	(AT)8	16	49	64	GGGGTGACAACTATCAACCAA
scaffold576687_10.	1	p2	(AG)6	12	112	123	CGGCCATTCTCTTTTCCTTT
scaffold576693_15.	1	p2	(GA)7	14	164	177	AAAGGTGAACTTGGGGCTTT
scaffold576740_14.	1	p2	(CT)7	14	117	130	AAGCTCCACCATCTCTTCCA
scaffold576804_15.	1	p2	(AT)6	12	2546	2557	TTTTTACAAACCTGCCACCC
scaffold576826_12.	1	p2	(TA)8	16	366	381	ATTATATTGTACGTAAAAGCGAAAAA
scaffold576903_13.	1	p2	(AC)6	12	114	125	CTTACCCAATCTTGGTGAACA
scaffold576978_14.	1	p2	(AG)8	16	683	698	ATTTCTCTCAGTCGGTGCGT
scaffold577031_13.	1	p2	(TA)6	12	94	105	CGGAGGGAATACAATGCTTTT

scaffold577068_15.	1	p2	(AG)6	12	166	177	TTGGTTTGGTAGCCCTTTTG
scaffold577136_15.	1	p2	(AT)6	12	552	563	GGAATATTAGCGGTGGCTATG
scaffold577194_11.	1	p2	(AT)7	14	357	370	GGCACTTTGGCTACTTTTGC
scaffold577238_14.	1	p2	(TA)6	12	100	111	GCGCAGATCTAATGGTCCAG
scaffold577306_12.	1	p2	(AT)8	16	808	823	GACCTTTTTACTCCCAGCCC
scaffold577370_13.	1	p2	(GA)7	14	867	880	TAGCAATTTGATTCCGTGCT
scaffold577424_13.	1	p2	(TA)6	12	398	409	CGAGTCCATGGAAACAGATG
scaffold577511_16.	1	p2	(TC)8	16	1130	1145	CCACAAGTTCTCCACAGCAA
scaffold577513_16.	1	p2	(AG)8	16	45	60	GAAGAACAATTACAATGTTTATCCAA
scaffold577613_15.	1	p2	(TC)6	12	1880	1891	ATTCGTTCAAAAACGGCAAG
scaffold577637_16.	1	p2	(TA)6	12	228	239	ACGCAAATACGACTGGCTTT
scaffold577639_18.	1	p2	(AG)6	12	2031	2042	GAAGATGAAGGCAAGTGGGA
scaffold577642_16.	1	p2	(AG)10	20	1305	1324	GCATCCTTCCAACAAGTAGCA
scaffold577806_14.	1	p2	(TC)6	12	186	197	TGCTTCGATTCTCAATGTTCC
scaffold577807_13.	1	p2	(TC)7	14	190	203	GCTTCGATTCTCAGTGTTCCA
scaffold577811_13.	1	p2	(GA)6	12	478	489	CGAGAAACTTTCAAGGACGC
scaffold578132_17.	1	p2	(AT)8	16	455	470	CGATGAACTAGGGGCTGAAG
scaffold578155_16.	1	p2	(TC)6	12	1159	1170	TGCTTACTTTCCGTTTTGGG
scaffold578337_11.	1	p2	(TA)6	12	548	559	TATTCTGAAACATGCTGGCG
scaffold578340_17.	1	p2	(TA)8	16	46	61	AAGGGTTATCACCTGATTTTCTC
scaffold578433_14.	1	p2	(AT)9	18	331	348	TTCAATACTTCCAGCCACCA
scaffold578483_10.	1	p2	(AT)8	16	113	128	TGTGTTCTTGAGTCGTTTGGA
scaffold578491_21.	1	p2	(AT)6	12	467	478	ACTTCAATTTTGGGTTCCCC
scaffold578596_10.	1	p2	(CT)6	12	476	487	AGTGAGGGGATGTTGGAGTG
scaffold578642_12.	1	p2	(AG)6	12	254	265	GCCCATTTGAGCCAATCTAA
scaffold578667_15.	1	p2	(TA)9	18	745	762	GAATACAGGCCGGCTAACAA
scaffold578727_15.	1	p2	(AG)9	18	3622	3639	TGCGGTCATGTGATGATTTT
scaffold578810_13.	1	p2	(AT)7	14	59	72	ACATGCAGGGCTGAGTACAA
scaffold579003_17.	1	p2	(CT)7	14	36	49	AAAATTTTCCTCACTGCACG
scaffold579028_13.	1	p2	(TC)8	16	164	179	TGGTTTTGTGCTTCTTGCTG
scaffold579038_17.	1	p2	(TA)7	14	24	37	CAGTTATCACCGGATCGC
scaffold579075_14.	1	p2	(CT)7	14	378	391	CCCCTTCCCATCTCTACTCC
scaffold579118_11.	1	p2	(TA)7	14	52	65	TGGCCCATGTACACTGCTTA
scaffold579194_16.	1	p2	(TA)6	12	816	827	ACCTCGACGACAGGAAAAGA
scaffold579231_13.	1	p2	(TA)6	12	1158	1169	ACTTCATGGGGGAAAACAGA
scaffold579279_16.	1	p2	(TG)8	16	463	478	CCCATGATTCCATGATCTCC
scaffold579315_11.	1	p2	(GA)6	12	167	178	CCAAGAGACGTTTTTGTTGAAA
scaffold579406_15.	1	p2	(AC)7	14	450	463	TTGCAGCACTTTCAACATCA
scaffold579468_16.	1	p2	(AT)6	12	512	523	GAAGCACATGCAAGGATTGA
scaffold579555_18.	1	p2	(CT)6	12	33	44	TCTCTCTCGTTCTTCCTCTCTCT
scaffold579586_14.	1	p2	(AT)8	16	163	178	GGATCGTACCTTTTGCTTGC
scaffold579587_13.	1	p2	(AT)8	16	163	178	GAAAAGCCTGTTGGCAGGTA
scaffold579588_16.	1	p2	(TA)8	16	176	191	CCCAAAAAATCTAACGGCCTA
scaffold579632_20.	1	p2	(CA)6	12	726	737	TTATTCGGTTCCGCCATTAC
scaffold579794_10.	1	p2	(TA)9	18	308	325	CATCATTCAAGGGGCATTTT
scaffold579841_15.	1	p2	(AT)6	12	734	745	GCATATCGCTCGATCAAAAA
scaffold579980_12.	1	p2	(TC)6	12	54	65	GGTTTCTGAATTTGATCCGC
scaffold580125_16.	1	p2	(AG)7	14	1699	1712	AAAGGACCGAAGAGGTGGAT
scaffold580128_16.	1	p2	(TA)6	12	73	84	GTTATCACCGGATCGCAAC
scaffold580132_17.	1	p2	(TC)10	20	978	997	GTTGGTCTGGCAACCATCTT
scaffold580141_11.	1	p2	(TG)6	12	157	168	CCGTTGCACAAGTCACAGAG
scaffold580243_16.	1	p2	(AC)6	12	1088	1099	TATGATAGGCCACCGGTTTG
scaffold580313_20.	1	p2	(TA)6	12	378	389	CCCATCGAAAAATTAATGCAA
scaffold580327_10.	1	p2	(AT)9	18	233	250	ATGTGAGAGACCCAGGTTCG
scaffold580547_17.	1	p2	(TA)9	18	862	879	TTTCAAATACGGTAGACTTCCCA
scaffold580560_16.	1	p2	(GA)8	16	240	255	TGATTCACACGAGAGTGCAG
scaffold580709_11.	1	p2	(TA)8	16	165	180	GGGGTTATCACTGGATCACG
scaffold580754_12.	1	p2	(AT)8	16	603	618	TTCCCTTCATTTTCGTTTTATTTT

scaffold580788_12.	1	p2	(TA)7	14	480	493	GGGTTATCCCCGCTATCATT
scaffold580828_13.	1	p2	(AT)6	12	137	148	CATTACCCACACACACACTTCA
scaffold581004_16.	1	p2	(TA)7	14	166	179	AGAAGTTAGCACGTCAAGGGA
scaffold581058_13.	1	p2	(AT)8	16	99	114	GTTCCATGTTACCCGTGGAC
scaffold581122_13.	1	p2	(CT)9	18	367	384	GGGCCCATTATTTCATCTCA
scaffold581188_12.	1	p2	(TA)7	14	411	424	CATGTATTTTTCCTATGGACCGA
scaffold581193_12.	1	p2	(AT)6	12	264	275	ATCCGATGACTGGATGCTCT
scaffold581236_13.	1	p2	(AT)7	14	147	160	TTTTCTTGATAAGCTCGAAGCA
scaffold581369_17.	1	p2	(CT)8	16	165	180	TCATCATCACACGCTGCTTT
scaffold581473_10.	1	p2	(GA)6	12	219	230	TTCAGTATCGGGCCATTTTC
scaffold581479_19.	1	p2	(TG)8	16	102	117	AATGCACTCATGGAAAAGGC
scaffold581722_16.	1	p2	(AT)6	12	1385	1396	GCTCAAGGTCACACAAGCAA
scaffold581779_10.	1	p2	(TC)6	12	40	51	TTTCTCTTGGTGGAAAACTCTT
scaffold581840_15.	1	p2	(GA)6	12	361	372	AGATTGTTGTGAGGCGGAAG
scaffold581858_12.	1	p2	(TG)6	12	77	88	TGGAGTTGAGATAATTTGCTGG
scaffold581910_11.	1	p2	(TA)9	18	48	65	TGCGTTTTGACAATATATAGGTGTTT
scaffold581929_15.	1	p2	(AG)8	16	39	54	GTGCACAAGCAGGGGAAA
scaffold581963_14.	1	p2	(CT)6	12	994	1005	TCTACGTTCCTCAGGCTGCT
scaffold582130_11.	1	p2	(GA)7	14	645	658	GCTTTCCTTCCTCCTTGCTT
scaffold582218_20.	1	p2	(AT)7	14	116	129	TCTCTCGTTAACGTCCCATTT
scaffold582223_11.	1	p2	(AT)7	14	54	67	CATAAACTAAGGTGGAGATTGTTATG
scaffold582253_10.	1	p2	(TC)6	12	49	60	TTGTTATGTTTCCATGAGCAGA
scaffold582341_12.	1	p2	(AT)8	16	199	214	GGATCTTATAGCATCAACCGC
scaffold582389_18.	1	p2	(AC)6	12	509	520	CCGTTTTTACACCCCCTACA
scaffold582535_11.	1	p2	(CT)6	12	282	293	AATTGCGAGTCGCTGATTTC
scaffold582548_19.	1	p2	(TA)9	18	683	700	GGAATAAAACCGTTTCACCG
scaffold582646_15.	1	p2	(CA)6	12	38	49	CTCTCACACTTTGCACACTGAA
scaffold582727_18.	1	p2	(AT)7	14	605	618	TGTATGGCCACTTAGGCAAA
scaffold582883_10.	1	p2	(TA)6	12	456	467	GTTCATCGTGAACTCGCGTA
scaffold582920_11.	1	p2	(AT)6	12	658	669	AGCGTGCCATGTGTTATCAG
scaffold582934_17.	1	p2	(TA)11	22	67	88	AAATCTTGTGGATGTTAGTGGTTAG
scaffold582977_18.	1	p2	(TG)6	12	6939	6950	AAATCTGAAGAGCTCCACGC
scaffold583012_13.	1	p2	(GA)6	12	97	108	TCGTTCGTCCTCTTCCTGTT
scaffold583100_16.	1	p2	(TC)6	12	315	326	TGATCCACGGTCTTTACGAA
scaffold583106_15.	1	p2	(AG)7	14	638	651	ACACACAACCACCACCAGAA
scaffold583165_13.	1	p2	(AT)9	18	549	566	AGTTATGATGGGAAGATGGGG
scaffold583337_19.	1	p2	(GA)6	12	87	98	GACGATTTGCAAGCCTATGG
scaffold583392_16.	1	p2	(CA)6	12	531	542	GGGGATACACACCTACCGTC
scaffold583560_16.	1	p2	(TC)8	16	4605	4620	TCCAAAATGGAAATGGGAAA
scaffold583566_22.	1	p2	(TA)7	14	167	180	ACTCCCCAAAAATCCAAACC
scaffold583646_16.	1	p2	(GA)8	16	706	721	CATGAGCAGGCTGTTTTTGA
scaffold583778_10.	1	p2	(AT)8	16	69	84	AGTTATGATGGCAGGATGGG
scaffold583935_16.	1	p2	(TA)8	16	853	868	GACCAGACCTGGACCTACCA
scaffold583988_11.	1	p2	(CT)6	12	113	124	CGACAATCATCTAGTCCTCTAGCA
scaffold584103_14.	1	p2	(TG)6	12	785	796	CACCAAAAGGAAGCCATCAT
scaffold584156_10.	1	p2	(AT)6	12	53	64	ACGACTGTCGATCCACACAA
scaffold584194_15.	1	p2	(CT)6	12	688	699	CCCTCCATCCAAAGTTGCT
scaffold584230_13.	1	p2	(TC)7	14	117	130	AGCTTCTCTTGCTCTCTCATTG
scaffold584319_17.	1	p2	(TC)6	12	383	394	AATTTCTGCATGTTTTCGGC
scaffold584324_12.	1	p2	(TA)7	14	313	326	TGAGAAATAAGAAACAATCTGGGG
scaffold584328_14.	1	p2	(GA)6	12	80	91	TGGTTGTGTGAACCAACTCTG
scaffold584341_10.	1	p2	(AT)7	14	375	388	TCCATGACTCTCAATGCCTTC
scaffold584538_13.	1	p2	(AC)6	12	289	300	CATCTTTCTTCTTCGACGCC
scaffold584646_15.	1	p2	(TA)6	12	4341	4352	TGGATCAAACGTCGTCTCAC
scaffold584671_11.	1	p2	(AT)8	16	437	452	TCTCCGAATTTCAAGAGGGA
scaffold584683_12.	1	p2	(TG)6	12	191	202	TTTCGTCCATTGTAAGCAGTTC
scaffold584706_10.	1	p2	(TA)11	22	251	272	TTCTCAGCATATGGGAAGGG
scaffold584993_12.	1	p2	(TA)7	14	51	64	GCATATGTGCGTTTTATTCTTTC

scaffold585030_13.	1	p2	(TA)8	16	358	373	CCCATCGGGAACAAGTCTAA
scaffold585161_15.	1	p2	(AG)7	14	755	768	GCTCTTATGATGGCCGAAGT
scaffold585165_10.	1	p2	(TA)7	14	324	337	AAAAGCAATTAATGCGTTCACA
scaffold585280_15.	1	p2	(AT)6	12	193	204	CATTGCTACTGAATATTGTTCTTGTTC
scaffold585352_17.	1	p2	(TA)6	12	348	359	CTTCAGTCCGTGAAAGGAGC
scaffold585398_14.	1	p2	(TA)6	12	1381	1392	GTGGACCGCATAGGAATCAT
scaffold585400_13.	1	p2	(TG)6	12	99	110	CCCATTTGTGTTTTCTTCGTG
scaffold585420_10.	1	p2	(AG)6	12	292	303	CCTGCTTTGTGCAATCTTCA
scaffold585507_15.	1	p2	(TA)6	12	566	577	TCTCACATCGCCATTTTCAA
scaffold585578_16.	1	p2	(AT)10	20	77	96	AAGAGGAAAATCCATCGGCT
scaffold585592_10.	1	p2	(AG)14	28	594	621	GGCATCACTGTCAGCAGGTA
scaffold585687_16.	1	p2	(GA)6	12	172	183	TTGTTGAATTGGTCCTGCAA
scaffold585737_11.	1	p2	(AT)7	14	168	181	TTCAAATCTTTTTCACCGCC
scaffold585774_19.	1	p2	(AT)7	14	549	562	GAAAGGGCATGGTAGTCAGC
scaffold585816_17.	1	p2	(TA)6	12	170	181	TGCATCACTACCTCCTTGTTG
scaffold585858_11.	1	p2	(TA)6	12	221	232	TTGGTTGGATTGGATTTTGG
scaffold585961_16.	1	p2	(AT)6	12	727	738	CCAAATCGGACTAATGCTGAA
scaffold585979_11.	1	p2	(AT)6	12	225	236	AACTCGATAACGGATGCTCG
scaffold586020_15.	1	p2	(TA)8	16	863	878	ATCCCAGCCACACATTTCTT
scaffold586021_16.	1	p2	(AT)6	12	171	182	CGAGTCCAGGCTACATCACA
scaffold586022_12.	1	p2	(AT)6	12	1295	1306	AAACCACCACCTTTCTCCCT
scaffold586034_10.	1	p2	(AT)9	18	188	205	GGTGTTGGTGAGGCTGTTCT
scaffold586126_17.	1	p2	(CT)6	12	118	129	GCGTGACAACAACAATTTCG
scaffold586152_17.	1	p2	(GA)8	16	506	521	TCAGTGAGTTTCAAGCCGTG
scaffold586154_20.	1	p2	(TC)6	12	1378	1389	ACTATCCAACCACACGCACA
scaffold586214_11.	1	p2	(CT)6	12	158	169	GAGGATTCGACATTGGGAGA
scaffold586341_14.	1	p2	(GA)6	12	256	267	TACACAGCCCGTGTTCATTC
scaffold586379_18.	1	p2	(GA)6	12	698	709	TTCCTCAGATTTCTGCACACT
scaffold586400_12.	1	p2	(AG)7	14	184	197	CTGCTTTGTGTTGCGTGTTT
scaffold586455_16.	1	p2	(CT)6	12	704	715	TAGGATCTTTTCACGCGGTT
scaffold586466_11.	1	p2	(GA)6	12	55	66	TTGAAAGATGGGTGTGTTCTTG
scaffold586522_13.	1	p2	(TA)6	12	120	131	CCCTACCCATTTACCCGTTT
scaffold586645_17.	1	p2	(AG)8	16	509	524	GGTTCCAACTCCAAGGTGAA
scaffold586750_10.	1	p2	(AT)6	12	136	147	GTAGTTGGCTGCATTTGTGG
scaffold586752_15.	1	p2	(TA)7	14	2246	2259	TGCCTTGAAAATGGGAAAAG
scaffold586821_13.	1	p2	(AT)9	18	957	974	GGATGCGAAATTGGACACTA
scaffold586830_14.	1	p2	(AT)9	18	249	266	AGGAGAGAGCGAGAGGAGAGA
scaffold586925_14.	1	p2	(TC)12	24	3580	3603	TAACTGGCCCCAACTTATGC
scaffold586936_12.	1	p2	(AT)8	16	334	349	GTGAAGCGCTGATCTTGTGA
scaffold587033_12.	1	p2	(AT)7	14	423	436	TGAGGCAGAATGAATTGTCG
scaffold587102_15.	1	p2	(AT)6	12	648	659	CGGGTAATGTCGAGAGTGGT
scaffold587105_13.	1	p2	(TC)10	20	118	137	AAACCAAAGACGATGTTGCC
scaffold587202_15.	1	p2	(AT)6	12	170	181	TCCCAATCGTTTCAAAATTCA
scaffold587246_14.	1	p2	(TA)6	12	90	101	CGTAGACCTGGCATCTTGTG
scaffold587270_15.	1	p2	(AT)6	12	316	327	TTGAAATGTAACACAAAAGGAGAA
scaffold587307_17.	1	p2	(TC)7	14	60	73	TGATTTGTCATTGTTGGGGTT
scaffold587326_14.	1	p2	(AT)7	14	230	243	AACGAGAGAACTTTCGACGC
scaffold587377_14.	1	p2	(TC)6	12	171	182	AAGAGCTTCTGCGTCTTTCG
scaffold587406_14.	1	p2	(GA)7	14	102	115	CATGCAAGGGTTTCGCTAGT
scaffold587423_12.	1	p2	(GA)12	24	989	1012	TGCTGGATTAACGATTTCCC
scaffold587430_14.	1	p2	(TA)6	12	705	716	CATGCTCCTATTTTAATACACCCC
scaffold587455_13.	1	p2	(GT)7	14	720	733	AATCGAGCTTACACCCCAAA
scaffold587505_10.	1	p2	(AG)6	12	66	77	GAAGACGACGAGAGGGTGAG
scaffold587521_13.	1	p2	(TA)6	12	2093	2104	GCAAAAATGTCCCCTGCTAA
scaffold587526_14.	1	p2	(AT)9	18	295	312	CACCAAATTTCATCATTTTTAATTC
scaffold587648_13.	1	p2	(GA)6	12	375	386	TCGGTTTTTCTTGGGAGAGA
scaffold587662_10.	1	p2	(AT)6	12	496	507	CATAACATGATTTTGCCCCC
scaffold587708_12.	1	p2	(CA)6	12	388	399	CTTGCAAAATGATCCCCAAC

scaffold587721_17.	1	p2	(TC)6	12	155	166	GGCAAACACAGGATCGATTT
scaffold587778_14.	1	p2	(TG)6	12	937	948	CTCAAACTTAAGCACCCCCA
scaffold587788_15.	1	p2	(AG)6	12	425	436	CCCCTCGGAAAATCCTAGTC
scaffold587811_16.	1	p2	(GA)6	12	920	931	TTTCCCTTCCAATTTTGTCG
scaffold587905_15.	1	p2	(TG)6	12	3619	3630	TAACGGCCCAGATCTTGTTT
scaffold588053_14.	1	p2	(AT)6	12	66	77	GGGCCGAGATTTGTTAGAGG
scaffold588081_15.	1	p2	(AC)6	12	1914	1925	CGTCACTGTTGCTCCGACTA
scaffold588142_15.	1	p2	(AT)11	22	1072	1093	TTTTGATTTTCAAGTCCGGC
scaffold588186_13.	1	p2	(TA)7	14	852	865	CGAAATTGAAATCGGACCAT
scaffold588235_14.	1	p2	(AG)8	16	41	56	AGAAGGATGGCGGAGAGTTT
scaffold588239_11.	1	p2	(AG)6	12	262	273	TGTGAAAAACAGTGGCAGGA
scaffold588247_14.	1	p2	(TC)8	16	546	561	CAGCAATTGGTTTTGAGGGT
scaffold588272_16.	1	p2	(TA)8	16	318	333	TGAGTTTGGTGTGTTGGCAT
scaffold588306_18.	1	p2	(AC)7	14	1243	1256	CGCGGAGGAAATTATTTTTG
scaffold588492_17.	1	p2	(TA)6	12	327	338	AGTTCGGGAGTGAGCTCGTA
scaffold588539_14.	1	p2	(AT)13	26	65	90	GGATATGCTCAGTCCGGGTA
scaffold588543_14.	1	p2	(CT)6	12	112	123	AGAAACACGTTTTGCTTTTGA
scaffold588780_10.	1	p2	(GA)9	18	104	121	CACAATGCGTGTATTGACAGTG
scaffold588793_16.	1	p2	(TC)6	12	505	516	GGCATGAATTCTTGGATTGC
scaffold588826_14.	1	p2	(TC)6	12	546	557	GACCCGGCCTAACATATTCC
scaffold588894_17.	1	p2	(CT)6	12	172	183	TGAATTAACAGCGAGCATGG
scaffold588902_15.	1	p2	(AG)10	20	1930	1949	TTCCCGTAGTCCTGAGATGG
scaffold588980_13.	1	p2	(TA)8	16	119	134	GCGTCCGACACCTCAATTAT
scaffold589079_14.	1	p2	(GA)7	14	72	85	GACGCGAGATTTACGTGGTT
scaffold589104_17.	1	p2	(TG)6	12	2574	2585	ATCAAAGCACTTGAGCCCAC
scaffold589147_13.	1	p2	(TA)6	12	559	570	CCCCATCCATGTTGTTTTTC
scaffold589162_14.	1	p2	(AG)6	12	56	67	TAACACCTTCATCGAGCGAG
scaffold589210_15.	1	p2	(GA)7	14	402	415	GCTCTCTTTTTGGCTGGATG
scaffold589390_10.	1	p2	(AT)8	16	284	299	GTCCCTTTTTACCCCTCAAA
scaffold589497_10.	1	p2	(TA)7	14	47	60	GGAAATAAGGAGGTGTTATGATATG
scaffold589681_15.	1	p2	(TA)8	16	168	183	GCAGTAACCCTCTCATCGGA
scaffold589682_12.	1	p2	(TA)8	16	315	330	GGAACCAGCTCCGATTAACA
scaffold589683_12.	1	p2	(TA)7	14	170	183	TGGACGAAAATGTCCTTCTTG
scaffold589879_13.	1	p2	(TA)8	16	305	320	GACCGAATGTAATGAACCCG
scaffold589909_11.	1	p2	(GA)12	24	349	372	AGAGCGGGAACAAAAGTGAA
scaffold589962_10.	1	p2	(TA)11	22	307	328	TGCATGCACCTGATTACACA
scaffold590006_14.	1	p2	(TA)6	12	1414	1425	GGCAGCTAGGGTTGAAAGAA
scaffold590039_11.	1	p2	(TC)6	12	166	177	TACACGCACATCAACCCACT
scaffold590117_13.	1	p2	(TG)6	12	786	797	TTCATTTGCCTGACCTACCC
scaffold590126_14.	1	p2	(AT)9	18	2195	2212	GAATTGCCATGTCCATGTGT
scaffold590233_14.	1	p2	(GT)7	14	2003	2016	TGGGGCCAATTTACTCTCTG
scaffold590366_19.	1	p2	(TA)7	14	386	399	TCCGTAGGGAGCAAAGTGAT
scaffold590422_16.	1	p2	(AT)9	18	454	471	GATTTTGAGTTCATGGGCGT
scaffold590531_11.	1	p2	(AT)8	16	225	240	GAACTATCTACAGGCCAGGGG
scaffold590537_16.	1	p2	(CT)7	14	126	139	TTGTATGGACGACACGCACT
scaffold590553_15.	1	p2	(TA)8	16	500	515	GGGGTACGTGCCATAAAAAC
scaffold590606_17.	1	p2	(CT)6	12	972	983	GCATTCTCCAGCGTCTTTTC
scaffold590709_12.	1	p2	(CT)6	12	158	169	GCATCTCTCTCGCTCTCATTG
scaffold590746_11.	1	p2	(TC)6	12	491	502	TCCCATTCAAAATCTTTCCA
scaffold590833_16.	1	p2	(TG)7	14	358	371	CAATCCAGTTAGTCGGAGCC
scaffold590922_13.	1	p2	(TA)7	14	483	496	CCGATCCCCATATAACCGAT
scaffold590940_16.	1	p2	(GA)9	18	3699	3716	CTGAATGACCTGCCTCCATT
scaffold590965_10.	1	p2	(CT)6	12	140	151	GCTCTCTTTGTAATCTCCCCC
scaffold590989_17.	1	p2	(AT)6	12	351	362	TCCCTCTTCATCCTCCCTCT
scaffold591004_13.	1	p2	(TC)6	12	346	357	CTGGGTTTCCTTCCTCTTCC
scaffold591038_16.	1	p2	(CT)7	14	5638	5651	CACAAAACCCTCACACCCTT
scaffold591112_17.	1	p2	(AG)6	12	803	814	GACCCAGCACTGCTTCTAGG
scaffold591131_13.	1	p2	(TC)6	12	231	242	CAAGGGCTTGAGTAGCTTGG

scaffold591201_18.	1	p2	(AT)6	12	241	252	AACGCGTCACACGTAATTCA
scaffold591300_16.	1	p2	(AG)7	14	1675	1688	GTGCCATAGCCACCTGATCT
scaffold591418_13.	1	p2	(CA)6	12	258	269	CTCTGTCTAGTGGCGAAGCC
scaffold591595_11.	1	p2	(AG)8	16	114	129	GGGTGAGACAAGATGAGGGT
scaffold591630_13.	1	p2	(TG)8	16	65	80	CCTTGACCAATCGATTTCTTG
scaffold591659_11.	1	p2	(GC)6	12	370	381	CACTCGCTACGAGCCACAG
scaffold591722_10.	1	p2	(GC)6	12	104	115	CCATCACCGCATTTTCTTCT
scaffold591745_10.	1	p2	(CT)7	14	67	80	TCACCCACAAACTTTTCAACTTC
scaffold591839_11.	1	p2	(AT)6	12	392	403	CGAGAAGCTTGCTTCAAACC
scaffold591864_15.	1	p2	(TC)11	22	5223	5244	TGCAAACGGATGGTCTGATA
scaffold591925_15.	1	p2	(TA)6	12	53	64	AAAATAATCCCAAAACCAATGA
scaffold592066_14.	1	p2	(AT)8	16	50	65	AACGCACAACAAAATACAAAAGA
scaffold592112_12.	1	p2	(TA)11	22	120	141	GCATCATTTTGGCCTTTGAT
scaffold592241_18.	1	p2	(TC)6	12	370	381	ACCCTGCCCAAAACTCTCTT
scaffold592259_15.	1	p2	(TC)7	14	744	757	CCCATTTCCATGCTTCAACT
scaffold592270_19.	1	p2	(TA)7	14	120	133	GCGGGTAAATATCAATTTCGAG
scaffold592287_13.	1	p2	(AT)11	22	1305	1326	AATTGTGGCCTCACCTTCAG
scaffold592305_13.	1	p2	(TA)8	16	72	87	TGGGTTAGCACTTGATCGTG
scaffold592442_15.	1	p2	(AT)12	24	1215	1238	TCAAACTACATTTGGGGGAG
scaffold592531_17.	1	p2	(AT)6	12	342	353	TCGATTCGAATTTTCATACACA
scaffold592579_15.	1	p2	(TA)8	16	286	301	TGGTATGACAATTGCAAGCAT
scaffold592611_16.	1	p2	(AT)7	14	227	240	CAGCCAACTCGATCTCATCA
scaffold592631_17.	1	p2	(TA)8	16	565	580	GCTTTGTGCATTCTTCCCTT
scaffold592632_15.	1	p2	(TC)9	18	49	66	TGCTTCTCCAAATCCATCTTC
scaffold592652_12.	1	p2	(AT)8	16	574	589	AAGTGTGCCCAACACCTTTC
scaffold592676_14.	1	p2	(TC)6	12	430	441	TTGTTCGAAAAGGAGTTGCC
scaffold592854_12.	1	p2	(CT)8	16	40	55	CACTCACTCTCACTAGCCGC
scaffold593027_15.	1	p2	(TC)6	12	154	165	CAATACCGTGACATGCCTTG
scaffold593076_14.	1	p2	(TA)13	26	1689	1714	ATGGCTGTTGATGTGGACAA
scaffold593214_15.	1	p2	(TC)8	16	3492	3507	GCCAGAGCTTCTATGGTTGC
scaffold593224_10.	1	p2	(GA)7	14	228	241	TTCGAACTCCAATAGCAGCA
scaffold593254_17.	1	p2	(AG)9	18	439	456	ATTTGTGCAAAAGTTTGGGG
scaffold593363_13.	1	p2	(AT)10	20	397	416	TTGGTGAACCTCTCCCAAAT
scaffold593364_13.	1	p2	(AT)9	18	168	185	TGGACAAGACAAGGCTAGGG
scaffold593375_16.	1	p2	(TA)7	14	5302	5315	ATGGCACACCATACCAGGAT
scaffold593389_17.	1	p2	(AG)8	16	1010	1025	GCCCTTTTCATTGCTGTCAT
scaffold593479_10.	1	p2	(TC)6	12	107	118	AACGGTGACGAATGGTTCTC
scaffold593504_15.	1	p2	(AC)6	12	550	561	AATTGGAAACATGGCGAGAC
scaffold593542_13.	1	p2	(TA)6	12	538	549	GGTCCAAACAACGAACCAAC
scaffold593579_10.	1	p2	(TC)6	12	357	368	AAAACCCCACACTCTCCTCA
scaffold593613_11.	1	p2	(TA)9	18	252	269	GAATGGTGGTGTTTGTTCCC
scaffold593649_19.	1	p2	(AT)8	16	1537	1552	TTAAATGGGGTGACAGGCTC
scaffold593655_10.	1	p2	(AT)7	14	308	321	CGTGGACAAGTCTCGCCTAT
scaffold593676_10.	1	p2	(TC)10	20	358	377	TAGTGGTGACAAGTGTGGGG
scaffold593801_10.	1	p2	(AT)10	20	165	184	CACCCACATTACATTAAACCGA
scaffold593943_13.	1	p2	(TC)6	12	425	436	TGCCACATCAGCTTCTTCAC
scaffold593970_10.	1	p2	(CT)6	12	159	170	TCGCTGCCATATTCTTGACA
scaffold593986_18.	1	p2	(GA)6	12	710	721	AACAGCCATTAAAAGTCGGC
scaffold593987_15.	1	p2	(AG)6	12	173	184	CCTATTCCCTCGATTCAGCA
scaffold593988_11.	1	p2	(TG)8	16	66	81	CCTTGACCAATCGATTTCTTG
scaffold594002_10.	1	p2	(AG)6	12	499	510	ATCCACGAGGATGATGAAGC
scaffold594094_15.	1	p2	(CT)8	16	1068	1083	TTTTCATTTGATTAGAAGTTCTGGA
scaffold594177_15.	1	p2	(CA)6	12	500	511	TCAGCAAACTGAAGAACAAGGA
scaffold594189_10.	1	p2	(TC)7	14	725	738	TAGCCAACTCGCTTAGCCTC
scaffold594233_13.	1	p2	(AG)7	14	146	159	GTCTGGTAATGGCCGGACTA
scaffold594246_12.	1	p2	(TC)6	12	126	137	TTGGCAATGAGATACCGATG
scaffold594267_14.	1	p2	(TC)8	16	893	908	TGAAATTTGAAGTCCATGCG
scaffold594277_11.	1	p2	(AT)6	12	388	399	CACACGAACTCATTTGACGG

scaffold594438_16.5	1	p2	(TC)6	12	728	739	GAACAAGTTTGAGGGTGCGT
scaffold594451_14.5	1	p2	(CT)6	12	1162	1173	GCGTAACATTATGAAGGCGA
scaffold594463_14.7	1	p2	(TA)10	20	166	185	AAAAAGCGCTCGTACATTTTATG
scaffold594573_11.8	1	p2	(CT)6	12	290	301	AATAAATTCAGCGCAAACCG
scaffold594714_15.2	1	p2	(AT)6	12	721	732	TATGAATTCCGTGTTGGGGT
scaffold594764_15.0	1	p2	(AT)6	12	587	598	TCTTTTTGACATTTGGGTTCA
scaffold594769_15.1	1	p2	(AG)7	14	507	520	TGGGTTGTTCTGATCTGGGT
scaffold594816_15.6	1	p2	(TG)6	12	678	689	CGCATGGTGACATCAGTACA
scaffold594868_18.0	1	p2	(TA)6	12	405	416	TGCGTTAATGTACACAACTTCCA
scaffold594993_14.0	1	p2	(CT)6	12	414	425	GTTGGGAACGAATTGGAGAA
scaffold595018_14.1	1	p2	(TG)8	16	240	255	GCCATGATCTCCTGATTCAAA
scaffold595036_13.7	1	p2	(TA)6	12	1376	1387	ATCACGTTTGCAGCATGTTT
scaffold595161_14.8	1	p2	(TA)7	14	70	83	AGTGTTACGATAGAATCACGCC
scaffold595242_11.4	1	p2	(TC)6	12	198	209	TCTTGCCTCCACCATCTTCT
scaffold595285_10.7	1	p2	(TA)11	22	69	90	TGACGCTTAGAGGGTGTTTTG
scaffold595297_13.4	1	p2	(TA)9	18	40	57	TTTTGACAATATATAGGTGTTTTGACC
scaffold595344_14.8	1	p2	(CT)7	14	275	288	AAATGGCATTGCTCCTCAAC
scaffold595345_15.3	1	p2	(AT)7	14	235	248	CGCGGTGTTTTAACTTGCTT
scaffold595366_15.6	1	p2	(TA)7	14	552	565	CTCGATTAAATGGGACCGAA
scaffold595370_14.5	1	p2	(CT)7	14	548	561	CCTCACGACGACTCCAAAAC
scaffold595393_10.9	1	p2	(AG)8	16	373	388	CTCGTTTCGATCCATTTCGT
scaffold595399_11.8	1	p2	(TC)7	14	435	448	TTGTGTGGGTCGATCTGAAA
scaffold595618_12.1	1	p2	(TA)11	22	1010	1031	TGCGCGTTTTTAGGGTTAAT
scaffold595708_16.6	1	p2	(TA)8	16	170	185	TTTGAGTTGGGAGAGGGATG
scaffold595743_17.0	1	p2	(AG)9	18	566	583	TTCAGTGGCTACAAATCCCC
scaffold595784_16.1	1	p2	(CT)6	12	917	928	TTGTTCCCTGTGGGATTAGG
scaffold595787_12.8	1	p2	(TA)8	16	524	539	TGACGGTTGGATTTTGTCCT
scaffold595807_11.5	1	p2	(TA)6	12	171	182	AGGCTTGAGTTTCCTCACGA
scaffold595880_11.0	1	p2	(TA)9	18	169	186	ATTGGTGACGTGGCATCATA
scaffold595882_18.1	1	p2	(AC)6	12	309	320	TAAAGACATATCGCGACCCC
scaffold595883_14.2	1	p2	(CT)6	12	3462	3473	TCACATCTCGATCTTCGCAC
scaffold595886_16.7	1	p2	(TC)6	12	1417	1428	ACAGTCTGCAGGCCAAAACT
scaffold595926_10.6	1	p2	(CT)6	12	561	572	GCCCAATAGCCCGTATATCA
scaffold595941_14.1	1	p2	(TA)6	12	205	216	AAACGCGTCATGGATAAACC
scaffold595970_21.1	1	p2	(TA)8	16	50	65	ATGGGAAGAGGGGTATGAGG
scaffold596181_14.9	1	p2	(GA)7	14	574	587	GGGACGATTCTGAAAGGTGA
scaffold596222_14.5	1	p2	(AT)8	16	170	185	TGCAATGCATGGAGGAAATA
scaffold596228_10.4	1	p2	(TC)6	12	122	133	CAATTTGCAGCCCTCATTTT
scaffold596307_15.0	1	p2	(CT)8	16	835	850	ATACCCACCCACCCTCTCTC
scaffold596377_21.3	1	p2	(AG)8	16	456	471	CTCGAATTCGGTTCCAGAAA
scaffold596379_10.2	1	p2	(TC)6	12	38	49	ATCTCCTCCTCCACCGTGA
scaffold596380_12.3	1	p2	(TC)6	12	38	49	ATCTCCTCCTCCACCGTGA
scaffold596389_15.6	1	p2	(AC)9	18	3109	3126	CGAGTTGCCAATCATTTCCT
scaffold596409_18.1	1	p2	(CT)6	12	496	507	GTCCACCTTAGGCACGACAT
scaffold596443_22.9	1	p2	(TG)6	12	1242	1253	GACACGGGAAGCGTGATAAT
scaffold596452_13.9	1	p2	(AT)10	20	633	652	CGATCTTGCTCTACGTCTGG
scaffold596523_10.7	1	p2	(TC)8	16	61	76	TCTCGCTCTACACTTTCGGTC
scaffold596573_10.8	1	p2	(TA)10	20	485	504	CGAATCCAGGTAAGGCTTGA
scaffold596627_16.7	1	p2	(AG)8	16	1092	1107	TCTCGACTAGTTGGCGCATA
scaffold596723_13.7	1	p2	(TC)9	18	657	674	CGGCGGCTCTATAAAATTGA
scaffold596762_16.2	1	p2	(AG)8	16	1356	1371	TAGGTCATGGATCGACACGA
scaffold596793_16.1	1	p2	(AT)7	14	6368	6381	TCCAGGGCTACTGGAGGTAA
scaffold596900_16.6	1	p2	(TC)6	12	358	369	TGACTTGGGGTCCATCTCTC
scaffold596976_16.9	1	p2	(CA)7	14	2438	2451	CATGCATCAAGGAAAAACGA
scaffold596991_11.4	1	p2	(AT)7	14	521	534	CATTGCATTTTATGCAGAGCA
scaffold597012_17.1	1	p2	(AT)6	12	754	765	ACTCAGGTGGTTCAAATCGG
scaffold597124_16.0	1	p2	(AT)8	16	1620	1635	GTTGTGTTGCCTGCAGTTTG
scaffold597168_15.4	1	p2	(GA)7	14	407	420	ATCACCCAAAGCCATTTCAC

scaffold597246_13.	1	p2	(AG)6	12	279	290	AGTTTGAAGAAGACCGCACG
scaffold597256_18.	1	p2	(AG)6	12	249	260	GATGTGTGCCCAAAAGGAGT
scaffold597363_14.	1	p2	(CT)10	20	52	71	AGTGCTCGAATATCTCCCCC
scaffold597440_17.	1	p2	(AG)6	12	1685	1696	ATTGATGTCCGAATGCAACA
scaffold597663_14.	1	p2	(AT)6	12	391	402	CACACCTTCAGAAATGCAATG
scaffold597844_13.	1	p2	(TC)7	14	141	154	CCTAGCTTTGCCCTCCTTCT
scaffold597929_10.	1	p2	(TC)6	12	287	298	GTCTTGCTCCTCCATTGCAT
scaffold597976_12.	1	p2	(TG)7	14	606	619	ATTCAAACCACATCCTTCGC
scaffold598058_12.	1	p2	(TC)6	12	34	45	TGTAATCTCTCTCGAAGTTATAGTGA
scaffold598091_11.	1	p2	(GA)6	12	417	428	CGAGATTTACGTGGTTCGGT
scaffold598230_11.	1	p2	(AT)9	18	354	371	ATTAGAGCCACAGCGGCATA
scaffold598286_13.	1	p2	(AT)7	14	604	617	AACTCATTAAATGTGCCGCC
scaffold598289_17.	1	p2	(AC)7	14	2446	2459	ATTTCGAAGATCAAAGGCCC
scaffold598327_13.	1	p2	(TC)8	16	796	811	CATGCCCACAAACACTCAAG
scaffold598350_14.	1	p2	(AT)6	12	505	516	TGACATTTACGCAGTTTGTCG
scaffold598357_15.	1	p2	(GA)7	14	4641	4654	ATTGTTTGAGCTTGGTTGGG
scaffold598366_14.	1	p2	(TG)7	14	909	922	GGCTCCCACAATGAACAACT
scaffold598378_15.	1	p2	(GA)8	16	117	132	CGAAGACACGATGTTGAACG
scaffold598476_17.	1	p2	(TA)7	14	392	405	CCCAGAATTGTAAAGCGCAC
scaffold598568_17.	1	p2	(AC)6	12	103	114	GCACCGAAACAGAGCTGATA
scaffold598605_14.	1	p2	(AG)10	20	51	70	AGAATGAGGGAGGGAGGAGA
scaffold598702_19.	1	p2	(AG)9	18	170	187	CTCGGAGACCCATTTCTCTG
scaffold598785_12.	1	p2	(GA)7	14	389	402	TCTGCAGCTGAGGAAGTTCA
scaffold598802_16.	1	p2	(TG)7	14	1593	1606	GTTGGGAAGGGAAGAAGGAG
scaffold598939_17.	1	p2	(CT)6	12	722	733	GCTCTTGAATTTGTCCGAGC
scaffold599037_15.	1	p2	(GT)6	12	1611	1622	GAGGCTTTTCGCTTTCCTTT
scaffold599049_17.	1	p2	(TA)6	12	100	111	TTTTATCCCATGTTTGTGCAT
scaffold599175_17.	1	p2	(AG)6	12	3324	3335	CAGCGAATGTAACCGGATCT
scaffold599322_15.	1	p2	(CA)7	14	1790	1803	GTTAGGTGACCCACCTTCCA
scaffold599337_12.	1	p2	(AT)7	14	491	504	TCTTTCGAGTCAGGGCATCT
scaffold599361_14.	1	p2	(CT)6	12	807	818	CTTCAACACATCCATCACCG
scaffold599405_11.	1	p2	(TA)8	16	49	64	TGCGTTTTGATGATATATAGGTGTTT
scaffold599512_17.	1	p2	(AG)7	14	592	605	GTGGACCACGGTGATCTTTT
scaffold599525_11.	1	p2	(TA)13	26	278	303	AAGGGGCACGTAAGCCTAAT
scaffold599559_17.	1	p2	(TG)8	16	1073	1088	CTTGTTACGGGGAAAGTGGA
scaffold599563_13.	1	p2	(TC)9	18	1004	1021	AACTCCGCGAGAGAAATTGA
scaffold599567_14.	1	p2	(CT)7	14	282	295	TTTTTGCACCATTGGTATTG
scaffold599578_12.	1	p2	(AT)9	18	527	544	TGACGAATGATACCATTTAAGCA
scaffold599600_11.	1	p2	(TA)7	14	313	326	GAACTAAAAACGATGAAATTTGGTG
scaffold599602_13.	1	p2	(TA)9	18	243	260	AGTCACAACATTCAAGGGGC
scaffold599635_16.	1	p2	(AT)6	12	1036	1047	TGTGGTTTACCCGTCTGACA
scaffold599677_14.	1	p2	(AT)8	16	1929	1944	TTTTCACGAATATACATGTTCCAAA
scaffold599755_14.	1	p2	(TA)6	12	905	916	TGCCCTAACGCCTTATCTTG
scaffold599771_15.	1	p2	(TG)7	14	2349	2362	TGGAAAATCTGTTGCAGGTG
scaffold599916_12.	1	p2	(AT)8	16	51	66	GAGAGGAGTGAGATTGAGCGA
scaffold599919_14.	1	p2	(TA)8	16	2546	2561	CCCTACCCATTTACCCGTTT
scaffold600080_10.	1	p2	(CT)6	12	1011	1022	TTCTTCCCCACTGCTCATCT
scaffold600115_11.	1	p2	(AG)7	14	52	65	CTGCTCCATTTTCACAACTGA
scaffold600146_12.	1	p2	(AG)8	16	297	312	TTGGCCGTGAGTTCATTGTA
scaffold600193_11.	1	p2	(AG)6	12	110	121	TGAGCCGTCAGTGCATTAAA
scaffold600276_11.	1	p2	(TA)11	22	208	229	TGATGTAGCCCGCATGACTA
scaffold600294_14.	1	p2	(GA)6	12	300	311	ATGCATACATGACTCGAGCG
scaffold600295_10.	1	p2	(TC)6	12	617	628	CGGGCCGTGTACTTTACAAT
scaffold600308_18.	1	p2	(AG)6	12	107	118	CGCGTTACGAATCCAAGTTT
scaffold600309_15.	1	p2	(TA)9	18	205	222	TTTTTAGGGTTTAAAATCGCGT
scaffold600368_12.	1	p2	(TA)6	12	542	553	AGATGATGGACAAGGCATCC
scaffold600426_13.	1	p2	(TA)11	22	66	87	AAGGCCCACAATGGTTATTAG
scaffold600532_10.	1	p2	(GA)6	12	69	80	GAGAGGGGCGAGAGGTAGAG

scaffold600567_12.	1	p2	(CT)8	16	102	117	TTGTGACGGTGACTAGAGCC
scaffold600707_10.	1	p2	(TA)6	12	51	62	ACCATATTTAAGGGTTATCACCTG
scaffold600784_17.	1	p2	(GA)7	14	336	349	AAGGGCTACTGTTCCCGACT
scaffold600812_14.	1	p2	(AG)6	12	115	126	CGTTTCCCATGTTGCTTGTA
scaffold600826_14.	1	p2	(TA)7	14	1000	1013	GATTCTCCCAATCTGACGGA
scaffold600901_11.	1	p2	(AT)6	12	530	541	TTTGGTTGTTTGAGATTGTGG
scaffold601142_14.	1	p2	(TA)7	14	300	313	TGCCTTTCTTTCCCCTCTTT
scaffold601244_15.	1	p2	(AT)7	14	460	473	ACTGTGAACGGCGCTAATCT
scaffold601248_11.	1	p2	(TA)10	20	51	70	TTTCTCACATAACTTAGCTGTTCTCA
scaffold601249_16.	1	p2	(TA)7	14	175	188	TTATGATGGGAATGGTGGGT
scaffold601315_13.	1	p2	(TC)6	12	86	97	TGGCTAATTTGGCAGCTTCT
scaffold601343_16.	1	p2	(AT)6	12	1289	1300	AACCGGTTAAAACCCAGACC
scaffold601417_16.	1	p2	(TA)8	16	457	472	GTTATCACCGGATCACGACC
scaffold601452_15.	1	p2	(AG)7	14	2063	2076	ATTTCAGAATTCGCTGGTGG
scaffold601464_14.	1	p2	(CT)6	12	194	205	GTGTGTGCATGCATTTGTTG
scaffold601503_16.	1	p2	(CT)14	28	1099	1126	GGTGGGAAGAAGTGTCTGGA
scaffold601628_15.	1	p2	(TC)6	12	339	350	CCATCCGAGCAAGAAAGGTA
scaffold601691_13.	1	p2	(TC)7	14	330	343	GCATGATCAATGTTGTAGAGGG
scaffold601750_13.	1	p2	(AT)9	18	814	831	GTCAACCAATGCAGATGCTC
scaffold601808_12.	1	p2	(AC)6	12	782	793	CTCACCAGCACCTTCTCTCC
scaffold601837_16.	1	p2	(GA)6	12	1709	1720	GAACACTCCCTTCTTCACGG
scaffold601969_12.	1	p2	(TA)9	18	266	283	TTAGAAACGGCATACCCAGG
scaffold601970_15.	1	p2	(GA)6	12	465	476	ATTTTCAAGGTTGTGCTGCC
scaffold602214_16.	1	p2	(AT)11	22	1028	1049	GGTTCCCTCTTCTCTAACGCT
scaffold602417_12.	1	p2	(AT)6	12	93	104	AACTCGAGATCGGTCCACCT
scaffold602422_15.	1	p2	(TA)7	14	175	188	CCCAAAGGTCTCATTTCCAC
scaffold602537_15.	1	p2	(GA)10	20	5660	5679	GTTGTCAAAAGCACCAGCAA
scaffold602562_20.	1	p2	(AG)7	14	1090	1103	CGGTCGCAGAAAAAGCTAAC
scaffold602610_15.	1	p2	(TC)9	18	442	459	TCCACAGACAACCTCACCAA
scaffold602630_15.	1	p2	(CT)7	14	146	159	CACGAGGAACTTTGGACGAT
scaffold602745_17.	1	p2	(GA)6	12	137	148	TGGGCGATTGAACACTTACA
scaffold602852_20.	1	p2	(TC)6	12	155	166	GGACTGCTGGATAATCCCCT
scaffold602878_14.	1	p2	(AT)6	12	379	390	ATCACTCCCTGTTACGGCAC
scaffold602884_12.	1	p2	(TA)7	14	80	93	GCTCGGTAAGTCGTTAATGGA
scaffold602948_10.	1	p2	(AT)6	12	167	178	CGATGCTGCTGTGAACAAAC
scaffold602989_15.	1	p2	(TG)6	12	2828	2839	ACGGGAATGGTGTGTTGATT
scaffold603047_13.	1	p2	(GA)6	12	1830	1841	TGTGGCAACACCAATCACTT
scaffold603104_16.	1	p2	(AG)6	12	1310	1321	AAACTCCAGCTACCGAAGCA
scaffold603136_15.	1	p2	(TC)8	16	845	860	TAGCGATGAAGACGACGATG
scaffold603193_15.	1	p2	(AG)6	12	1504	1515	CCATCGTTTGGTGGTTCTCT
scaffold603282_10.	1	p2	(GT)6	12	56	67	TTCGATTTGGGGTGTAACAA
scaffold603289_14.	1	p2	(GA)7	14	2607	2620	TTCCGGCGAGGATATATGAG
scaffold603386_16.	1	p2	(CT)7	14	53	66	ACAAAAAGGGAAGAGCGACA
scaffold603423_14.	1	p2	(TA)7	14	176	189	GGATCCGACGTCCAATATACA
scaffold603449_13.	1	p2	(TG)7	14	469	482	AGTTTCGCGATCTCAACCAG
scaffold603455_11.	1	p2	(TA)6	12	483	494	AAAAATGATGCCAATCCAGC
scaffold603469_14.	1	p2	(GA)6	12	55	66	TGATTCTTTTGTTTGGTTTGC
scaffold603471_16.	1	p2	(AT)6	12	1331	1342	GGTGTTTTTGGATTGGTTGG
scaffold603568_16.	1	p2	(TA)6	12	1118	1129	CCGCAATAATCCATACCTCAA
scaffold603841_16.	1	p2	(GA)7	14	495	508	GGTGATTCGAGATGATCCGT
scaffold603899_14.	1	p2	(CT)6	12	1081	1092	AAACTCACCATTTGCCAACC
scaffold603912_14.	1	p2	(CT)8	16	728	743	TGACGTGGTGTTGTGGTTTT
scaffold603920_13.	1	p2	(AG)6	12	112	123	GTGAATCACACTCCCCCATC
scaffold603931_15.	1	p2	(CA)6	12	1680	1691	CTGCCCAAGAAGGATTTGTC
scaffold603938_14.	1	p2	(TC)12	24	412	435	CGAACTGGGAAAGGAGAAAA
scaffold603947_15.	1	p2	(AT)14	28	420	447	GACACTCTTCTTCACCCCCA
scaffold604026_16.	1	p2	(CT)6	12	266	277	CCGTGGACGTAGGTTCATCT
scaffold604182_12.	1	p2	(TA)12	24	751	774	CTGCTGCCCAAAAACTTAGC

scaffold604267_15.	1	p2	(CT)6	12	66	77	CGGGATGCCATTTGTAAGTC
scaffold604337_21.	1	p2	(GA)6	12	307	318	GGATTGTTGACTGCCAGGTT
scaffold604360_15.	1	p2	(GA)6	12	1872	1883	TCTGGATGTCAAGGCATACG
scaffold604442_16.	1	p2	(GA)12	24	4925	4948	AGGTCACCTCCTGCAAGAAA
scaffold604450_12.	1	p2	(TA)7	14	302	315	CTGAATGCTTACCGATGCGT
scaffold604503_13.	1	p2	(CT)8	16	383	398	TCACCCTTTCTTTGATGGGT
scaffold604560_15.	1	p2	(TA)8	16	425	440	GTCATGAATCGGTGCATTTG
scaffold604568_14.	1	p2	(TA)11	22	812	833	TTTCGAGAACTCGGGATGAG
scaffold604572_11.	1	p2	(TA)6	12	558	569	TCCTTTTCCATTATCCATGTTTTT
scaffold604576_16.	1	p2	(TA)10	20	1128	1147	GGTGCATAGGTTAAAGGGCA
scaffold604580_10.	1	p2	(AG)9	18	512	529	TGGATTGCATACCAACCAGA
scaffold604583_13.	1	p2	(TC)6	12	613	624	TCTCCTTGGATCTTGATGGC
scaffold604677_13.	1	p2	(AC)6	12	2373	2384	TGAAGGCTTTGATTCATCTCTC
scaffold604775_16.	1	p2	(AT)7	14	749	762	CTTCCGCCCATTCTACAAAA
scaffold604778_14.	1	p2	(AC)6	12	364	375	TGGAATTCGCAATATCCAAA
scaffold604910_15.	1	p2	(AG)6	12	659	670	CAATGCTGGGATCGATTTTT
scaffold604993_11.	1	p2	(TA)10	20	1356	1375	TGGCTTCATTTTGCAGTCAC
scaffold605049_13.	1	p2	(TG)6	12	791	802	GGCGGACATCAAAGGAATTA
scaffold605309_17.	1	p2	(TG)6	12	398	409	ATCACGGACCCCACATACAT
scaffold605417_15.	1	p2	(CT)7	14	127	140	ATTTGCAATGGACTGCCTCT
scaffold605521_15.	1	p2	(AT)6	12	178	189	GGAATGTTATTGTTCGTGCG
scaffold605566_10.	1	p2	(AT)9	18	335	352	GGATTGTCCCGTCAAGAGAA
scaffold605578_10.	1	p2	(AT)6	12	394	405	TGAGCAAGCGCATTGTTTAT
scaffold605583_18.	1	p2	(TC)8	16	410	425	CTTCCCAACACCACCCTAAA
scaffold605696_12.	1	p2	(TC)7	14	1451	1464	TCCTTTCTGCATTTGGGTTC
scaffold605702_11.	1	p2	(CT)9	18	644	661	GGCTGGTGTGTGTTTTTGAA
scaffold605779_14.	1	p2	(GA)7	14	172	185	AACGGGATGCTTTCAAAATG
scaffold605887_11.	1	p2	(CA)7	14	1418	1431	TCCATAAACAGGGAAGATGTGA
scaffold605940_13.	1	p2	(GA)8	16	898	913	AAAATTCTGAAACCCCCAGG
scaffold605955_17.	1	p2	(TC)7	14	129	142	GGCAACGGAATACGATTTGT
scaffold606086_12.	1	p2	(GA)6	12	605	616	ATTTGGGGTGATGGGTTTTT
scaffold606093_13.	1	p2	(CA)6	12	571	582	GACCGAAATGCAACGATAAA
scaffold606111_12.	1	p2	(TA)14	28	128	155	TGCTATGGATGTGGTTGGTG
scaffold606139_12.	1	p2	(GA)7	14	410	423	CGAAGTAGCTCGAGCCGTAG
scaffold606208_14.	1	p2	(CT)6	12	95	106	CCAAAATTGAACAGCCGATT
scaffold606262_19.	1	p2	(TA)8	16	198	213	CAATCTCGAAAATGGATGGC
scaffold606291_11.	1	p2	(TA)8	16	372	387	GGGGAAAAGGGTGATGTTTT
scaffold606433_14.	1	p2	(GA)6	12	153	164	GCGGGGTTGTTGAAGAATTA
scaffold606469_10.	1	p2	(GA)6	12	372	383	GGGGACAACGCCATTTATAG
scaffold606654_15.	1	p2	(AT)8	16	2470	2485	TGAGGATATTCCAGTGTGTGAAA
scaffold606655_17.	1	p2	(AT)6	12	673	684	TTCAACGTCGGACAAGACAA
scaffold606729_13.	1	p2	(TA)7	14	1323	1336	TGAAAGCAGACAGGGGAATC
scaffold606741_10.	1	p2	(CT)8	16	151	166	TCCTCTAGCATCTCTTGCTCTC
scaffold606877_12.	1	p2	(TA)6	12	180	191	CCGATAGAAGCCCACATGTAA
scaffold607125_18.	1	p2	(TA)8	16	684	699	TGCAGTGAGTTGCCCAAATA
scaffold607170_16.	1	p2	(TA)8	16	1020	1035	TCCCCGCGTATAGAAATCAC
scaffold607201_16.	1	p2	(TA)6	12	2960	2971	CAAGATGATGAAGGTCAAACGA
scaffold607266_13.	1	p2	(TA)8	16	47	62	GAGAAGGGTTATCACTTGAATAGGA
scaffold607304_15.	1	p2	(TG)7	14	286	299	ATAGGCACCCCTGGAAAAAG
scaffold607366_16.	1	p2	(AG)7	14	178	191	GGTGAACCGCGTAAATCTGT
scaffold607414_14.	1	p2	(AC)6	12	313	324	TGCGAATCAGTGCTCCATAG
scaffold607568_10.	1	p2	(GA)9	18	343	360	GGCACCATACTGCCGATATT
scaffold607580_15.	1	p2	(TA)9	18	174	191	CAACGGATAAACCGATTGCT
scaffold607598_15.	1	p2	(TG)7	14	822	835	GCGATGGATTGATTCACGTA
scaffold607634_19.	1	p2	(TC)7	14	178	191	TTCACCCATTGTTTGCGATA
scaffold607735_15.	1	p2	(GT)7	14	229	242	TTTTCCGATTGACAAATCCC
scaffold607765_13.	1	p2	(TA)9	18	1464	1481	ACGTCAGCATCCACGTGTTA
scaffold607774_10.	1	p2	(AG)6	12	181	192	TTGTGCACGAGAATACATCCA

scaffold607777_14.	1	p2	(AG)10	20	471	490	GAGAAGGTGAGAGGCAGACG
scaffold607854_10.	1	p2	(AT)11	22	295	316	CATGCCTGATTACATCACCG
scaffold607952_17.	1	p2	(GA)9	18	1968	1985	GACAATTGCTCGCAAAGGAT
scaffold608060_12.	1	p2	(TA)7	14	1388	1401	TTCTCATTTGCAACCGATGT
scaffold608110_15.	1	p2	(CT)7	14	1338	1351	GCTGTTTCTCAGATCCTCGG
scaffold608130_17.	1	p2	(TC)7	14	514	527	CATGACCCACCAAACATGAC
scaffold608205_12.	1	p2	(TC)7	14	29	42	TCTCTCTTGGTTGGTGAAGAAA
scaffold608255_12.	1	p2	(AG)12	24	422	445	TTGTTGGCTATTTGTTGCTCA
scaffold608302_15.	1	p2	(AG)13	26	1197	1222	TGGTACTTGCAATGTTGGGA
scaffold608523_18.	1	p2	(GA)6	12	316	327	CAAAATTTGGCATCAAATTCAA
scaffold608615_15.	1	p2	(GA)6	12	297	308	GGATGGGAGTCAATCCAGAA
scaffold608646_11.	1	p2	(GA)6	12	320	331	CAACGAGATACGCTGCAAGA
scaffold608671_13.	1	p2	(AT)8	16	51	66	TGTACATCTAGCTCTGTTGAATCTTG
scaffold608672_11.	1	p2	(AT)10	20	173	192	TGGAGATGTGAAACATGCCT
scaffold608790_10.	1	p2	(TG)8	16	126	141	TCGGTTTGGCCAATATTTCT
scaffold608952_11.	1	p2	(AG)7	14	413	426	GATATTTGATTTTGCGGGGA
scaffold608958_13.	1	p2	(TC)6	12	1359	1370	TGCTTTGGTGACTGAATGATG
scaffold609042_16.	1	p2	(CG)6	12	100	111	ATGGTGGTATGGTATGGGGA
scaffold609074_12.	1	p2	(TA)8	16	438	453	CAAATTCGGACTTAAGGGCA
scaffold609126_11.	1	p2	(AT)9	18	338	355	AGGGGGTACCATTGTTCAAA
scaffold609371_15.	1	p2	(TA)6	12	2056	2067	AGCAAGGACACTGGAACAGG
scaffold609482_12.	1	p2	(TC)7	14	1120	1133	TTCGATCTACTGGGCCACAT
scaffold609516_10.	1	p2	(AG)7	14	721	734	ATGGACTCGCTGGTCTCTGT
scaffold609568_17.	1	p2	(TC)6	12	410	421	GGCAAAATTAAAAATGCCAC
scaffold609571_17.	1	p2	(AC)6	12	988	999	TATCTGCTCCAAAAGCCTGC
scaffold609823_13.	1	p2	(AT)7	14	240	253	TGCCTACCAAACACTAGGGG
scaffold609837_14.	1	p2	(AT)6	12	908	919	CCGTACCGGAATTTAACGAA
scaffold609855_17.	1	p2	(AG)7	14	2442	2455	GCCATGTCTAGCATTGGGAT
scaffold609896_14.	1	p2	(AT)8	16	1202	1217	CTGCCATAACCCGAAAAAGA
scaffold609899_12.	1	p2	(AT)6	12	263	274	TGCCGTGTTATTGTGAGTCC
scaffold609975_14.	1	p2	(TC)6	12	2162	2173	TTTGCCCATCTTCAAACTCC
scaffold609985_16.	1	p2	(TC)9	18	2733	2750	CATCATTGCCTGTCATTTCG
scaffold609992_16.	1	p2	(AG)7	14	2600	2613	TGGAATCGCGATGAGATTTA
scaffold610007_12.	1	p2	(TA)9	18	378	395	ACTTGCGAGCCACCAATTAC
scaffold610039_14.	1	p2	(CT)6	12	229	240	AGTGTCGGCACAAACAAACA
scaffold610092_15.	1	p2	(AG)6	12	463	474	GGTCCTTTCGAAACACGAGA
scaffold610125_16.	1	p2	(AC)6	12	586	597	GTGCATTGGGTCAAAGAGGT
scaffold610175_15.	1	p2	(AC)6	12	160	171	CCATGTCCTGGCTTACCTGT
scaffold610209_14.	1	p2	(GA)6	12	2831	2842	TTTTGATCGAAAGGGAATCG
scaffold610267_17.	1	p2	(CT)6	12	759	770	GCACACCATCTTCAAGCAAA
scaffold610390_15.	1	p2	(CT)6	12	684	695	GAACGGTTTATTCGGGTTCA
scaffold610506_19.	1	p2	(AT)6	12	182	193	CACGTGACATAAAATGCATCG
scaffold610560_10.	1	p2	(TA)6	12	76	87	TGAAACCAGGGGAAAAAGG
scaffold610563_16.	1	p2	(TC)7	14	210	223	CGGCACAAAATTTTCCACTT
scaffold610664_11.	1	p2	(TA)6	12	890	901	TTGCTGCGGTACTTTCATTTT
scaffold610696_12.	1	p2	(TA)9	18	387	404	ACCGAAATACCCCCAAACTC
scaffold610729_14.	1	p2	(TA)9	18	106	123	TTCACAGTTTTCATTTGATCACC
scaffold610812_13.	1	p2	(TG)6	12	129	140	GGCTATAGAGCCGTTGAATG
scaffold610851_19.	1	p2	(TC)8	16	177	192	ACGGGACCCTCATCTTCTCT
scaffold610882_17.	1	p2	(CT)6	12	523	534	TACAAACCACCTTAACTTCCGC
scaffold610938_16.	1	p2	(TG)6	12	1052	1063	CATATATGGTTGCACAGGCG
scaffold610971_16.	1	p2	(GT)6	12	130	141	CGAGCCACAATACTTCGGAC
scaffold611003_11.	1	p2	(TA)7	14	52	65	CGGATTTAGCGGTTATTACCTGA
scaffold611010_17.	1	p2	(GA)7	14	507	520	AACAAGAAGATGCCGAAGGA
scaffold611054_15.	1	p2	(TA)11	22	43	64	AGGGAGTGCTCTCACCTGAA
scaffold611113_16.	1	p2	(GT)6	12	2216	2227	TTCTGACATACCGTCCTCCC
scaffold611171_10.	1	p2	(AT)8	16	326	341	GGGTTCTCGTGATAAGCTCG
scaffold611182_12.	1	p2	(TA)9	18	47	64	GAGGGTTATCATGGGATCAAG

scaffold611282_17.	1	p2	(CT)8	16	274	289	GTGGATCTCGGGTAGGGATT
scaffold611283_13.	1	p2	(AG)7	14	180	193	GGTTGTGGCTCTGGTTCTGT
scaffold611386_10.	1	p2	(TA)7	14	53	66	TGTGTGATGTTGGAGTTGGG
scaffold611417_16.	1	p2	(GA)8	16	2446	2461	ATCGCGAGAAATTGAGAAGG
scaffold611462_18.	1	p2	(TG)7	14	186	199	TTGATGTGGATGACGAGGTC
scaffold611494_21.	1	p2	(TC)7	14	121	134	CGTTGATTTGAGGCAGGTTC
scaffold611506_14.	1	p2	(CT)11	22	1194	1215	GGTGTCCGAGTTGTAGGCAT
scaffold611526_15.	1	p2	(AC)6	12	444	455	TGCCAGTTTACTCCGAAAGG
scaffold611572_17.	1	p2	(TC)6	12	68	79	GCTTCAAGTTTCCTCCTTTTG
scaffold611576_14.	1	p2	(TC)13	26	2358	2383	GTTGGAGAGTTGACGGTGGT
scaffold611588_12.	1	p2	(AT)8	16	466	481	TTTTCTCGATCTCACGCCTC
scaffold611598_13.	1	p2	(AG)6	12	181	192	CATGGACCAATGGGACCTAC
scaffold611724_11.	1	p2	(TA)9	18	422	439	TTTGTTTCTGGTCCAGTCCC
scaffold611943_14.	1	p2	(CT)6	12	333	344	AACTCCATGCAAATCACACG
scaffold611952_16.	1	p2	(TA)8	16	281	296	GCGGGTAGGGTAGGGACTAT
scaffold611973_14.	1	p2	(TG)6	12	182	193	CGCTTCGAGTTGTTTTCACA
scaffold611995_14.	1	p2	(GA)6	12	254	265	GGAAATGGGAATGGGTTCTT
scaffold612013_15.	1	p2	(TA)7	14	2458	2471	TGCAAATCTTACAGAATCAGCAAC
scaffold612027_17.	1	p2	(GA)6	12	1462	1473	CCACTCCCTGAGTATCCCG
scaffold612149_12.	1	p2	(TA)6	12	603	614	CCATCCCAATTATACGGTCC
scaffold612161_12.	1	p2	(TA)8	16	338	353	CATGATGTCAATCCAGTGGC
scaffold612194_15.	1	p2	(TA)9	18	520	537	AGGAGGGGAAATGGATCAAC
scaffold612243_13.	1	p2	(CT)10	20	1025	1044	CATTTATTCCCCGCAACAAC
scaffold612303_13.	1	p2	(CT)6	12	106	117	AATCCCTTTCTCCTCTCCCA
scaffold612451_16.	1	p2	(GA)10	20	2054	2073	CACAGCATGGACTTTGTTGG
scaffold612507_15.	1	p2	(AG)10	20	2136	2155	CAAAGCAACCCTTAAGAGCG
scaffold612548_17.	1	p2	(TG)9	18	177	194	GTTTTGAGATGGGTGGTTGG
scaffold612565_11.	1	p2	(AT)6	12	128	139	CCCCAGGAATCTTGTTTTCA
scaffold612803_18.	1	p2	(AC)6	12	470	481	TAGCCGGGTCGTGACATAAT
scaffold613039_14.	1	p2	(CT)7	14	228	241	ACACATGCCTGGAACACAAA
scaffold613074_12.	1	p2	(TA)11	22	431	452	CCACATGCTATGCCTCAAAC
scaffold613115_12.	1	p2	(AT)10	20	592	611	TTATCTACAAAACGAGACCAATCTT
scaffold613129_13.	1	p2	(AT)10	20	1420	1439	TCTATCCGCCAGTGCTCTTT
scaffold613180_20.	1	p2	(TA)6	12	861	872	TGGCATTACAAACTTCAAACCA
scaffold613299_16.	1	p2	(AC)6	12	2764	2775	CAACACTGCATCAGTCCCAT
scaffold613513_13.	1	p2	(CA)7	14	116	129	CTTGAGCTCTGATGCCACAA
scaffold613543_13.	1	p2	(GT)7	14	277	290	AAGACTTCGCATCTCGGAAA
scaffold613592_15.	1	p2	(TC)6	12	75	86	GAGTTGGTCATTCTCAAGATGG
scaffold613604_10.	1	p2	(AT)10	20	280	299	GCGGAACTTTCACTTCGCT
scaffold613675_15.	1	p2	(AC)6	12	295	306	CTCTCCCTTCCTGAATGCTG
scaffold613857_10.	1	p2	(CT)6	12	54	65	TTTGGACTAGGCCATTCACC
scaffold613976_12.	1	p2	(AG)7	14	1896	1909	GGCCCATGTGTTAAATCAAGA
scaffold613984_12.	1	p2	(TA)9	18	358	375	TTAAATGACCTTGGGATGCG
scaffold614031_12.	1	p2	(TA)12	24	293	316	AGCGCCTAGCGATTTCTACA
scaffold614054_16.	1	p2	(TA)10	20	3861	3880	CGCTCACCCATCGAAAGTAT
scaffold614067_15.	1	p2	(CT)6	12	741	752	TCTCTCGCTCACCCTCTCTC
scaffold614099_13.	1	p2	(AG)8	16	785	800	TAAGATACGGGCAGCGAAAC
scaffold614225_16.	1	p2	(TA)8	16	258	273	CTTCCCCTGTTCTTGCATGT
scaffold614277_13.	1	p2	(TA)8	16	620	635	CGCGGAGCATTGTTCATAC
scaffold614372_16.	1	p2	(TC)6	12	184	195	ATTTCACCCCCAAGTCTCCT
scaffold614384_10.	1	p2	(TA)6	12	53	64	TTTTTGTCTATATCGCTCAGTCAAT
scaffold614467_13.	1	p2	(TA)6	12	170	181	TGGCGAAAAATGTTGACAGA
scaffold614511_10.	1	p2	(TC)6	12	264	275	GAACCTCTGCACTCTCCAGG
scaffold614541_16.	1	p2	(TG)6	12	1068	1079	GGAGTCCCTTCTTCCCAGTC
scaffold614549_16.	1	p2	(TA)6	12	1079	1090	TCTGCAATGAACGAAAATGC
scaffold614562_12.	1	p2	(AT)9	18	456	473	CATGTGTCCATGAATGAGGG
scaffold614678_10.	1	p2	(AC)9	18	63	80	CTAAACGGGTCGGGCTAAC
scaffold614820_17.	1	p2	(AG)6	12	2397	2408	TGAATCCACCATGGAAGAGA

scaffold614829_11.	1	p2	(TA)6	12	324	335	TCCAAAGGTGGCCAAAATAC
scaffold614962_10.	1	p2	(TA)8	16	279	294	TAAGGGCGGTATCACCTGAA
scaffold614988_18.	1	p2	(AT)7	14	911	924	TGGGCATAAAAACGTGCATA
scaffold615030_17.	1	p2	(CT)9	18	50	67	TCATCAACAGCGAAGCAAGT
scaffold615142_10.	1	p2	(TA)12	24	290	313	GGCAGCACCAGAATTACTCC
scaffold615163_16.	1	p2	(GA)7	14	1141	1154	GGCAAATTGTTGAAGTCGGT
scaffold615235_17.	1	p2	(AG)7	14	182	195	GTAAAACAGCGCCCGTACAT
scaffold615294_10.	1	p2	(CT)6	12	523	534	GATCGGAGCTCTGTTAAGCG
scaffold615323_12.	1	p2	(AT)7	14	357	370	AGCGGAAGACTTGTAACGGA
scaffold615334_12.	1	p2	(TA)6	12	39	50	GGGACCACTAGACATTCGCT
scaffold615340_15.	1	p2	(AT)6	12	766	777	TCGCTTAAACTTCGAGGGTG
scaffold615374_14.	1	p2	(CT)7	14	1282	1295	CATTGCGAGAAAAGCAGTCA
scaffold615379_15.	1	p2	(AG)6	12	896	907	GGATGAGAGATTTGGGTTCG
scaffold615445_15.	1	p2	(TA)9	18	48	65	TTAGTTAGCATGGGGGAAGG
scaffold615475_11.	1	p2	(TC)6	12	350	361	CCGCTCAAATCACTCACTCA
scaffold615477_12.	1	p2	(TA)8	16	48	63	ACCCCACATTTGTGGCATA
scaffold615562_10.	1	p2	(TA)9	18	329	346	ATCTCAACGCATCAACCGTC
scaffold615703_15.	1	p2	(CT)6	12	244	255	CTGCCCGAGGTCTGTTTCTA
scaffold615794_13.	1	p2	(AC)9	18	178	195	CCAACGAAACCACTGACAAA
scaffold615841_15.	1	p2	(TA)6	12	612	623	TTCGATTCGCAACAATTGAG
scaffold615895_15.	1	p2	(AG)6	12	1678	1689	AGCACCCTTATTGTGGCTTG
scaffold615926_13.	1	p2	(TA)8	16	58	73	GATGGGTTATTATTGGAACGAGA
scaffold615929_14.	1	p2	(AT)7	14	1919	1932	TTGTACGTCCAATATGTAAATTATGTT
scaffold615938_15.	1	p2	(AT)6	12	2961	2972	TTGCATGTGCATAACGGTTT
scaffold616050_10.	1	p2	(GA)6	12	248	259	CTTCAATGGAGGTCGGAGAG
scaffold616097_17.	1	p2	(TA)7	14	183	196	CAGGACGGTATTTTCCCCTT
scaffold616181_17.	1	p2	(AC)8	16	1107	1122	CCAGAATGTACGAGTTGGGG
scaffold616202_16.	1	p2	(TA)10	20	177	196	ACCTAAGGGGGTGTTTGCAT
scaffold616209_11.	1	p2	(TA)6	12	67	78	AGGGTCAACAATGACGGAAC
scaffold616210_14.	1	p2	(TA)7	14	65	78	AGGGTCAACAATGACGGAAC
scaffold616217_14.	1	p2	(GA)6	12	1850	1861	TTCTGGTGGAAGGCCTAATG
scaffold616222_12.	1	p2	(TA)6	12	381	392	GGTGATAGAAGGCTACGGCA
scaffold616223_15.	1	p2	(CT)6	12	577	588	CTCAAATCCTTCCATTCCCA
scaffold616325_17.	1	p2	(TG)6	12	1274	1285	TTTTTGCGATGGAACATGAA
scaffold616397_14.	1	p2	(AT)8	16	213	228	AAAATAATCGGGTTGGGTCC
scaffold616440_10.	1	p2	(CT)9	18	114	131	TCGACGACTTGTTGGAAATG
scaffold616467_16.	1	p2	(TC)6	12	658	669	TATTCTTTTACGCATGCCCC
scaffold616479_16.	1	p2	(TA)9	18	48	65	TCATCTATAGGGAAGTTATCACTGGA
scaffold616483_13.	1	p2	(TA)9	18	96	113	CAACGGATTTGGTTTGTTCC
scaffold616484_15.	1	p2	(AT)6	12	185	196	TTCAGAAACGAGGGCATTTT
scaffold616514_16.	1	p2	(CT)6	12	184	195	TTGGTCATCCCTTTCTGACC
scaffold616516_15.	1	p2	(GT)6	12	889	900	TTGAATTGATATTCAGTGAACGTG
scaffold616654_20.	1	p2	(GA)6	12	1463	1474	CCCACAATTCCAGCATCTCT
scaffold616679_10.	1	p2	(TA)9	18	203	220	TGGGGTGTCATGATAAGTGG
scaffold616817_13.	1	p2	(AT)11	22	40	61	CGGATTTAAGGGTTATTACCTGATT
scaffold616830_16.	1	p2	(TC)6	12	185	196	CCCAATCCCGTAGGAATTTT
scaffold616965_15.	1	p2	(TA)8	16	293	308	AAATTACACCTTTGTCATTTTTCAG
scaffold616966_13.	1	p2	(TA)9	18	805	822	TCGTTAAAGGGAATGCACAA
scaffold616993_18.	1	p2	(AG)6	12	547	558	GGAGTGGGGGTTTTGAGTTT
scaffold617016_15.	1	p2	(AT)6	12	643	654	TTGCAATCCGATATCAACCA
scaffold617133_14.	1	p2	(CT)6	12	4366	4377	AACTTGGTTCCACGCAAAAC
scaffold617134_14.	1	p2	(TA)6	12	375	386	TTGAAGCATGACCTGCAAAT
scaffold617135_16.	1	p2	(TA)8	16	1053	1068	ATGCCGTTCACCTTCAACTC
scaffold617185_13.	1	p2	(TA)6	12	130	141	GGGATAAGATTGGTGGTGATG
scaffold617208_11.	1	p2	(TG)6	12	392	403	AATGCCTGCTTGCCTTAAAA
scaffold617275_16.	1	p2	(AT)7	14	299	312	TTTTTCTCCCAAAATTGCC
scaffold617345_16.	1	p2	(GA)9	18	473	490	CTGGATGAAGTTATGCGCTG
scaffold617346_15.	1	p2	(CT)7	14	392	405	CACATCACCCCTTCGTTTTT

scaffold617463_10.	1	p2	(AC)6	12	118	129	AGCTGGGCACTTGAAACCTA
scaffold617473_16.	1	p2	(AG)8	16	180	195	CTCTTTCCAGTTGTGTCCTGG
scaffold617543_12.	1	p2	(AG)7	14	165	178	GGCATACCGCAAATCAACTT
scaffold617739_10.	1	p2	(TC)9	18	610	627	CTTCCTCCCACCTTCGTCTT
scaffold617830_14.	1	p2	(GA)7	14	649	662	GCTGCAGCAGTATCAATCCA
scaffold617837_17.	1	p2	(TA)6	12	985	996	CCGCTACACCTTTTGGATGT
scaffold617861_12.	1	p2	(CT)8	16	82	97	ATCTTCCCGCCATTCTTTCT
scaffold618062_11.	1	p2	(AT)12	24	298	321	CCATTTCCCTATCTATACCAATCAA
scaffold618076_13.	1	p2	(GA)7	14	403	416	AAGGAGAGGAAGGTTGGCAT
scaffold618099_15.	1	p2	(TC)7	14	602	615	AGAGCGAGTTGGAACTTGGA
scaffold618134_17.	1	p2	(GT)7	14	1186	1199	CGTTCGCTATCCAAGTCAAT
scaffold618300_15.	1	p2	(AT)11	22	580	601	TATAACATCAACCGCCAGCA
scaffold618374_16.	1	p2	(AT)7	14	754	767	AATTCCCAAGATAATCTCAATCG
scaffold618449_14.	1	p2	(AG)8	16	1647	1662	GCTCCCGTAGAACTTTCCCT
scaffold618490_12.	1	p2	(TA)6	12	285	296	TGAGGAGCGTTGATCTTGTG
scaffold618502_10.	1	p2	(TC)6	12	342	353	TGCAACAAGATGGTGCTCTC
scaffold618541_10.	1	p2	(TA)9	18	67	84	AAGGCCGAGATTTGTTAGAGG
scaffold618562_10.	1	p2	(TA)6	12	92	103	TGAAGTTCGGAAATAAGGAGG
scaffold618568_16.	1	p2	(TA)6	12	285	296	TCTTATCCATTTCGCCATCC
scaffold618714_15.	1	p2	(TC)10	20	177	196	TGGAGGGCTGTTTCTTCATC
scaffold618726_13.	1	p2	(AT)7	14	289	302	GGTGGGAAATCATCCCTTCT
scaffold618865_18.	1	p2	(TC)6	12	235	246	GACCAAGTTGCTCTTCTCGG
scaffold618867_12.	1	p2	(CA)6	12	349	360	CACTCCCCTCCCTTTTCTTC
scaffold618917_15.	1	p2	(AG)6	12	115	126	TGAGCCGTCAGTGCATTAAA
scaffold618933_13.	1	p2	(TA)6	12	2053	2064	ACATAAATTTGGCAAAGAGAAAA
scaffold618956_10.	1	p2	(TA)10	20	118	137	CCGGGAATTTTGAATGAACA
scaffold619031_15.	1	p2	(GA)6	12	756	767	ACCCGTCTAGCAGAGACGAA
scaffold619067_14.	1	p2	(CT)6	12	82	93	TTGCCCCTTCACTCTCATCT
scaffold619130_12.	1	p2	(TG)7	14	206	219	TGACGTGGGTGTTGGAATAA
scaffold619131_12.	1	p2	(TG)7	14	566	579	CGAGATTTGCTCATGTTGGA
scaffold619154_14.	1	p2	(AG)6	12	186	197	AAACAGCGCCCATAATCTTG
scaffold619162_17.	1	p2	(TG)8	16	498	513	CAAGCCATCTGTGGTTGAGA
scaffold619428_16.	1	p2	(GA)13	26	296	321	TGGTTGAAGGAGGCTTAGGA
scaffold619479_14.	1	p2	(AG)9	18	1661	1678	TGATTTCATCCGAATGTCCA
scaffold619490_11.	1	p2	(TA)11	22	869	890	TGTGGGTTCACTGGATACGA
scaffold619515_10.	1	p2	(AT)7	14	446	459	GGACAAATTTGGAATTTTAGGG
scaffold619537_11.	1	p2	(AG)6	12	260	271	ATCGATCCACGTTCGAAAAC
scaffold619688_15.	1	p2	(CT)7	14	668	681	TAATGTCTTCCCATCCAGCC
scaffold619793_12.	1	p2	(AT)9	18	185	202	TGGCCGGTTTTGAATCTATC
scaffold619874_16.	1	p2	(TA)7	14	1703	1716	GGGTTTCATTTTGATTCCCA
scaffold619876_16.	1	p2	(CT)14	28	370	397	CTTTCTTGCGAGAACCCTTG
scaffold619925_14.	1	p2	(AT)7	14	297	310	TTTTTGACCAAATCAATCCCA
scaffold620078_14.	1	p2	(GA)6	12	1831	1842	CTCGTCCTATGCAAGCAACA
scaffold620096_15.	1	p2	(CT)6	12	164	175	GGATTCAGCATTGTAAGGGG
scaffold620098_16.	1	p2	(AT)6	12	399	410	TGAGAAAGCAGCTGGTGAGA
scaffold620187_11.	1	p2	(TA)6	12	115	126	AAAAGAGTTGGGAAAAGTTATGAGT
scaffold620244_14.	1	p2	(GC)6	12	140	151	CGCTATGAGTCACGGCTACA
scaffold620289_10.	1	p2	(AT)7	14	214	227	CCATAACCGTCGCATAACTC
scaffold620540_13.	1	p2	(CT)9	18	1528	1545	TTCAATTACAAGCCGCAGTG
scaffold620561_15.	1	p2	(AT)7	14	67	80	TTTTTGCTAGAGGATTTTGTTAATATG
scaffold620656_14.	1	p2	(GA)6	12	754	765	CGAAAGTTTTGGAATTTGAAGG
scaffold620665_10.	1	p2	(AC)7	14	119	132	GCACCATCTTCTCAACACCA
scaffold620809_15.	1	p2	(AG)6	12	131	142	GAAAAGGCACTCGAATTTCC
scaffold620813_15.	1	p2	(TA)8	16	3485	3500	TTTTACGCTAACGAAACGGG
scaffold620885_16.	1	p2	(TC)7	14	1278	1291	GGCTTAGGTGAGGTGGAGTG
scaffold620904_14.	1	p2	(AT)8	16	960	975	CAATAGAGCAGGAAGAGCCG
scaffold620983_16.	1	p2	(TA)7	14	68	81	CCACACTTTTAAATATTTTAGCTGGC
scaffold620992_13.	1	p2	(AG)6	12	134	145	GCTAGAGCTCACTTCACGAGC

scaffold621049_16.	1	p2	(TA)6	12	1665	1676	TTATTCCCCAAGCAGGAATG
scaffold621101_12.	1	p2	(AG)7	14	279	292	TTTAGAATGCCAATGACGCA
scaffold621114_12.	1	p2	(AT)8	16	1189	1204	TATCCGATCCGAAGTATCCG
scaffold621155_11.	1	p2	(TA)6	12	200	211	AGATGCCAATCTTCCATTGT
scaffold621173_10.	1	p2	(TC)8	16	995	1010	AACCCCAGCAACATCAACTC
scaffold621178_15.	1	p2	(TA)10	20	591	610	ACTTGAAAATGCGATGAGCA
scaffold621342_13.	1	p2	(GA)7	14	437	450	TGAGGGGTGAAGACTTTTGG
scaffold621443_15.	1	p2	(TG)8	16	2489	2504	CCCTTGGTCCTTGAGCATTA
scaffold621451_10.	1	p2	(AT)7	14	88	101	TTCTACTGGAACTGACGCCC
scaffold621454_12.	1	p2	(TA)9	18	48	65	CACCCAAAAAGGAGTTATTATTTGA
scaffold621473_15.	1	p2	(TA)7	14	1639	1652	GAGGAGAGAAGAGCGGACCT
scaffold621481_14.	1	p2	(CT)6	12	1950	1961	TTTTGCTTTGTTTTTGCTGG
scaffold621542_17.	1	p2	(AT)8	16	184	199	AAAATCAGCGAGGCAGAAAA
scaffold621594_16.	1	p2	(AT)6	12	784	795	GGTTGTTTAAATGCCCCCTT
scaffold621684_15.	1	p2	(TG)7	14	1543	1556	GCAAATTCTGTGTGGGTGTG
scaffold621819_17.	1	p2	(TA)6	12	3239	3250	GAATGACACTCGACGAAGCA
scaffold621872_13.	1	p2	(AG)8	16	1495	1510	AGAGAGGGGAGGAGATTGGA
scaffold621898_17.	1	p2	(TC)6	12	36	47	TCTCTCCCTTTCCACACTCG
scaffold621903_12.	1	p2	(GA)7	14	454	467	TGGACCATTCGACGGATAAT
scaffold621904_10.	1	p2	(GA)6	12	464	475	GAAAGCCGTCGATGTAGCTT
scaffold621941_10.	1	p2	(AT)6	12	135	146	GGATGAAATGGCACCCAATA
scaffold621958_10.	1	p2	(AT)8	16	90	105	CTCTCAATGCCTTCTACCCAA
scaffold621969_10.	1	p2	(AT)6	12	146	157	TGGCCCACCCATTTTTACTA
scaffold622355_13.	1	p2	(TA)8	16	79	94	TGATTGCACCATAATGCACC
scaffold622418_11.	1	p2	(AG)6	12	135	146	CCAGTTATCCATCCATTCCA
scaffold622445_13.	1	p2	(TA)8	16	830	845	TTCAGATCCACTAGACATTTGAGC
scaffold622473_11.	1	p2	(TA)6	12	187	198	CTGCGCAGATCTAATGGTCA
scaffold622576_12.	1	p2	(CT)6	12	65	76	TCCCTCCAATCAATTTTCCA
scaffold622593_18.	1	p2	(AG)8	16	363	378	TTGGGAGGAGGAGATTGTTG
scaffold622612_10.	1	p2	(TA)8	16	1093	1108	CGAAACAAGTGGCTGCATAA
scaffold622627_14.	1	p2	(AT)8	16	746	761	TTATGGGCCAATTATGCTCC
scaffold622748_13.	1	p2	(AC)6	12	43	54	GGAGAGTTCGCGAAATAACAT
scaffold622754_15.	1	p2	(TC)7	14	1093	1106	TGGACTGCCTTCATCTTCCT
scaffold622771_15.	1	p2	(AT)8	16	183	198	CGTGCAGCAAGTAAACGAAA
scaffold622782_14.	1	p2	(TA)6	12	4780	4791	ATTAATGCATCGATGGAGGG
scaffold622906_13.	1	p2	(AT)8	16	279	294	CTTGCTGGCAACAAAAACAA
scaffold622952_18.	1	p2	(AG)9	18	1176	1193	AGCTGTTGCAGAAGCCATTT
scaffold623107_17.	1	p2	(TC)6	12	188	199	AACAAAGCTCTCTTCTGGCG
scaffold623118_15.	1	p2	(GA)6	12	1420	1431	AGGGGATTGTAACATGTGGG
scaffold623147_16.	1	p2	(TC)8	16	184	199	CTGCAACACCATTGCAGAGT
scaffold623210_12.	1	p2	(TA)7	14	981	994	GGGTGTTGAGGATGCACATA
scaffold623236_15.	1	p2	(GA)6	12	189	200	ACCCTTCACCCCCATAACTC
scaffold623271_15.	1	p2	(GA)9	18	2559	2576	GGCTGGCTTTCACTTCTCAT
scaffold623324_16.	1	p2	(AT)6	12	252	263	GAGAATTTTAATTCGTTCATCTTGC
scaffold623354_18.	1	p2	(CG)6	12	1405	1416	TGGTGGTATGGTGTGGAGAA
scaffold623376_11.	1	p2	(TA)6	12	245	256	GTAGGGGTGTACATGGTCCG
scaffold623431_11.	1	p2	(GA)6	12	291	302	TGCCGTGGTTCGATATACCT
scaffold623438_18.	1	p2	(AC)7	14	1149	1162	ACAAATGCGTGGGCTTATTC
scaffold623484_17.	1	p2	(TA)6	12	628	639	CATCCAAAACTCGAACCCAT
scaffold623582_14.	1	p2	(AG)6	12	920	931	CCCGTGCTTCAATATCCTGT
scaffold623651_15.	1	p2	(AT)6	12	139	150	AATGAGTTTCCAGCGCAAAG
scaffold623689_10.	1	p2	(AT)8	16	101	116	ATGATTGTGCTCAATGGCAG
scaffold623692_13.	1	p2	(AC)6	12	788	799	CACTCCACGAATGGTCAACA
scaffold623798_15.	1	p2	(TG)7	14	4567	4580	TGTTCAACTAAATAATGCAGCG
scaffold623813_12.	1	p2	(TA)9	18	259	276	TTCGTCCGAAATACTCCCAC
scaffold623895_12.	1	p2	(CT)6	12	135	146	TGCATGATCAATGTTGTAAGGA
scaffold623992_13.	1	p2	(TA)11	22	44	65	GGGGTTATTAGTGGAGTAAGCC
scaffold624028_15.	1	p2	(GA)9	18	990	1007	AGGTGGTTTCTTGCCTGAAG

scaffold624046_11.	1	p2	(AT)7	14	105	118	TCGGGAGGAAGAAGAAGAAA
scaffold624130_18.	1	p2	(CT)7	14	309	322	GGCCACTTTGTTGTGCTGTA
scaffold624179_10.	1	p2	(AT)8	16	1433	1448	TGACTTGAGGATTGTGTGCC
scaffold624231_20.	1	p2	(AT)6	12	398	409	GCAGGATCGCCATAAGGATA
scaffold624521_11.	1	p2	(TA)6	12	51	62	TTTAGTGTTTTGACATGATTACTCG
scaffold624546_14.	1	p2	(AC)10	20	205	224	CTCGGAGGCTCCAACATCTA
scaffold624576_16.	1	p2	(CT)6	12	391	402	GCACCAGTTCGGTGACATA
scaffold624593_13.	1	p2	(TC)9	18	499	516	TTGCTCCTTGCAACTTGATG
scaffold624763_11.	1	p2	(CG)6	12	67	78	TATGGTGGTATGGTGTGGGG
scaffold624769_15.	1	p2	(CA)7	14	186	199	TATCAGGCCTGTGCAGTCAC
scaffold624789_10.	1	p2	(AT)9	18	303	320	TGCTTTTTGACTTGCTCGAA
scaffold624845_11.	1	p2	(TA)8	16	103	118	GGCATCGTAAGGAACGTTGA
scaffold624860_17.	1	p2	(TA)7	14	1493	1506	TGGCGGTGGAAATAGTAAGG
scaffold624902_10.	1	p2	(GA)7	14	373	386	TCACATGCTGAATGACCAACT
scaffold624988_14.	1	p2	(AT)9	18	46	63	ATCGGTTATTACCGGATCGC
scaffold625007_12.	1	p2	(AT)8	16	1194	1209	GGCGAGGACTGAAATTGGTA
scaffold625011_15.	1	p2	(TC)7	14	873	886	TTTTGCCCCTTCTTTCCTTT
scaffold625063_11.	1	p2	(TA)9	18	47	64	ATCGGTTATTACCGGATCGC
scaffold625214_15.	1	p2	(AG)7	14	1029	1042	CGTATCCATGGTTGAGGTCC
scaffold625237_15.	1	p2	(CT)9	18	184	201	TACACTGAGAGCGACATCGG
scaffold625307_15.	1	p2	(AT)6	12	584	595	GGTCCTGTATGCTGTGGGTT
scaffold625315_13.	1	p2	(AC)7	14	55	68	ACACAGATCTTTCACTGCCG
scaffold625353_18.	1	p2	(TC)6	12	376	387	TTCTGATAAGCCAGGGGATG
scaffold625381_13.	1	p2	(TA)6	12	183	194	AAAGCAAAAGAGGCGATTGA
scaffold625424_16.	1	p2	(AT)6	12	676	687	GGAGATCACTTGCGGAGAAG
scaffold625541_12.	1	p2	(AT)8	16	485	500	AAACTGTAATTCAGGCACCTACG
scaffold625621_12.	1	p2	(AG)6	12	268	279	TTTTCGATGAACCACCACTTC
scaffold625655_17.	1	p2	(TA)6	12	1407	1418	TCAACCTCACAATTTGCTCG
scaffold625681_17.	1	p2	(CT)8	16	186	201	CACAAACGCCACCATTTTTA
scaffold625731_14.	1	p2	(AT)7	14	783	796	TGGTGCTCTTGTTTCGTCAC
scaffold625922_11.	1	p2	(GA)7	14	146	159	TGTGGCAGATCTGAAAAACG
scaffold625937_11.	1	p2	(AG)6	12	250	261	GCATTTTGCTACGTGGTTCA
scaffold625943_14.	1	p2	(GA)8	16	2324	2339	TGCACACAGCAGTTGTCAAA
scaffold626002_16.	1	p2	(AT)7	14	754	767	TGATCATGCTCAACATGCAA
scaffold626022_10.	1	p2	(AT)6	12	324	335	ATTCGGGTAAAAATTGACGG
scaffold626050_13.	1	p2	(CT)6	12	584	595	CGCTAAAACTGGAGTCAGCA
scaffold626097_14.	1	p2	(AG)6	12	2899	2910	ATCAGCCATGTTTGATCAGC
scaffold626277_16.	1	p2	(CT)7	14	187	200	ATTTCATCCCTTGTCATGCT
scaffold626305_11.	1	p2	(TA)7	14	247	260	CTGTTTTCTCAAGGCTCCCA
scaffold626362_14.	1	p2	(CA)10	20	1461	1480	GAAAGGCAAAGATGGGTTCA
scaffold626395_13.	1	p2	(AG)7	14	131	144	CTCTCTCTCAATTGCCACCC
scaffold626399_14.	1	p2	(AT)6	12	100	111	TGGTGTTTATGCTACTTTGAACG
scaffold626406_14.	1	p2	(AT)8	16	748	763	TGGAACACGTACCTTCTGATTC
scaffold626426_12.	1	p2	(AG)7	14	270	283	GATTCTTCGGCTCTTGTGCT
scaffold626565_15.	1	p2	(CA)7	14	188	201	TTTGTACCTGAATGCACCCTT
scaffold626640_17.	1	p2	(CT)8	16	94	109	ACGTTGGACCTGAAAGAGGA
scaffold626683_14.	1	p2	(TC)8	16	871	886	GCCTGAAAATGAACACCGTA
scaffold626778_15.	1	p2	(TA)6	12	113	124	GACATGGAGTTGTGGTGTCG
scaffold626811_13.	1	p2	(AT)10	20	58	77	CTTTTCCGGTCAAAACCAAA
scaffold626844_12.	1	p2	(TA)7	14	475	488	TCGAAAATTTAAAGGCCCAA
scaffold626927_15.	1	p2	(TA)9	18	185	202	GGCTCCATGACCGATAAAAA
scaffold627081_14.	1	p2	(AT)7	14	138	151	GGCAACGACTATCGATCCAC
scaffold627084_16.	1	p2	(CT)7	14	252	265	ATCCAAACACTTCTCACGGG
scaffold627186_18.	1	p2	(AT)9	18	185	202	TTGCAACCGAAGTTTCATTTC
scaffold627418_12.	1	p2	(AG)7	14	367	380	CTCACCGTCGATCAAATCCT
scaffold627438_12.	1	p2	(TC)8	16	51	66	CATGCAAGACCCGAAGAACT
scaffold627490_15.	1	p2	(AT)11	22	774	795	CACACATTTCCTTCCTACCAAA
scaffold627496_16.	1	p2	(AG)6	12	441	452	TTGGATATCGAGATCGAGGG

scaffold627538_10.3	1	p2	(AG)6	12	155	166	TTATGCGATCTGCACGTGAT
scaffold627594_14.0	1	p2	(AG)6	12	239	250	GCATGTGTGTGCTGAGTGTG
scaffold627629_15.8	1	p2	(CT)7	14	2561	2574	TGTATTCATGTGTCAGCGCA
scaffold627743_14.7	1	p2	(CT)9	18	6412	6429	GTGCACTCCTGGAGGTCAAT
scaffold627751_16.6	1	p2	(TC)9	18	1405	1422	GCTCAGCTACAAAACCGGAC
scaffold627796_18.6	1	p2	(TA)7	14	250	263	CCCTCGAATGCACTCAAACT
scaffold627899_10.5	1	p2	(TA)6	12	142	153	TTTCAATCCGGGTCTCTCAC
scaffold627916_12.8	1	p2	(TA)7	14	344	357	TTAATAAATTGTCGCGAACGG
scaffold627950_14.0	1	p2	(AT)6	12	79	90	AAATACTCAGTAAACCAGATGATGAA
scaffold627988_12.0	1	p2	(TA)6	12	69	80	AAGGGGAGTATCACTTGAATGC
scaffold628001_16.4	1	p2	(CA)7	14	43	56	CTAACCTTGGGCTCTGATGC
scaffold628013_10.3	1	p2	(AT)9	18	51	68	CACACTCAATACAATATGAACGACC
scaffold628023_15.0	1	p2	(AT)8	16	263	278	TTTTCGCCTCCGACTAAAAA
scaffold628121_10.4	1	p2	(AT)9	18	66	83	GCATCAACGGCGTGTATTATT
scaffold628174_16.9	1	p2	(TA)6	12	1971	1982	GCATGCAATAGGTTGTGCAG
scaffold628195_11.9	1	p2	(AC)6	12	258	269	GCATATGCAAGCTCAAATTCA
scaffold628210_11.1	1	p2	(AT)9	18	223	240	GATGAGTTCCTGAACCAGCAG
scaffold628230_13.7	1	p2	(TG)8	16	66	81	TGTCGCACAGAATGGTTGA
scaffold628276_12.0	1	p2	(GA)7	14	669	682	GTTCGGTGGTCATCTCACCT
scaffold628286_14.4	1	p2	(TC)6	12	3657	3668	TAACGGGCAGCCTAAGTACG
scaffold628383_15.3	1	p2	(AG)8	16	805	820	AATTTCCCGCATCACACTTC
scaffold628454_13.6	1	p2	(TA)7	14	331	344	CGTTCACGTTCTGCGATTTA
scaffold628509_14.2	1	p2	(CT)7	14	189	202	CACTTTTGGGACCCCTTTTT
scaffold628595_12.8	1	p2	(CT)6	12	283	294	GCAGGTGTGAATGGAGGAAT
scaffold628622_15.9	1	p2	(TA)6	12	166	177	TGTTGCATACGATGTGTAGCAG
scaffold628645_12.0	1	p2	(AT)11	22	2434	2455	TATGGGCCAACTAAAGCGAC
scaffold628726_13.6	1	p2	(AT)6	12	123	134	GGCGTGACATAGTGGATTGTT
scaffold628742_10.4	1	p2	(AC)6	12	324	335	ATAAGTTCGGCGGACAACTG
scaffold628828_16.9	1	p2	(TC)6	12	642	653	GGGCTTATTCCGTCATTTCA
scaffold628903_13.9	1	p2	(GA)7	14	210	223	AAAAATTCGATCTTGGGGTG
scaffold628989_16.8	1	p2	(AG)6	12	422	433	GGTGCTGTAAGGGTTGGAGA
scaffold629007_16.1	1	p2	(TA)6	12	319	330	GCTAGTGTGTTTGCTTGCAACT
scaffold629027_14.4	1	p2	(CT)9	18	587	604	TTTATTTCTTTCCCGCCTCC
scaffold629032_11.5	1	p2	(TA)7	14	621	634	AAAAATGAACTTTATCGGATCTATCA
scaffold629056_12.6	1	p2	(GA)6	12	130	141	CTCGTCTCGGGATCTTTGAG
scaffold629097_13.3	1	p2	(GT)7	14	455	468	GTGTGTGCGTCTGAGTTCGT
scaffold629147_17.8	1	p2	(CT)8	16	187	202	AAAGCCCATGTTTTGTCTGG
scaffold629165_15.9	1	p2	(TC)8	16	91	106	CCCAACTGAAAACTTCCCCT
scaffold629228_13.4	1	p2	(CT)7	14	241	254	CAATCAATCCATCGTCTCCC
scaffold629246_13.7	1	p2	(GT)6	12	124	135	GCACGTGACATCTAACGGAA
scaffold629268_16.8	1	p2	(AG)11	22	181	202	GTCACTAACCCCACCACACC
scaffold629287_10.7	1	p2	(AT)6	12	26	37	TCCGTCAAGGAGATCTTGAAA
scaffold629468_14.7	1	p2	(AT)6	12	460	471	GGGTGGCTTGATTTTGTTCA
scaffold629604_15.0	1	p2	(TG)10	20	49	68	CGGATCGCGACCCTATACAT
scaffold629624_15.2	1	p2	(CT)10	20	273	292	TTAAAGCCTGCCCTTTTTGA
scaffold629652_14.0	1	p2	(AT)6	12	507	518	TGGTAAGTGATAGGTAATGTCAATCC
scaffold629674_12.6	1	p2	(CT)6	12	547	558	CCTATCTTTGCCATACCCGA
scaffold629718_15.5	1	p2	(GA)6	12	192	203	CATGCCCCTAGGGTTTTACA
scaffold629719_18.0	1	p2	(GA)7	14	190	203	GGAGGAAGAAGATTGTGCCA
scaffold629745_16.7	1	p2	(AT)8	16	1047	1062	TGCCTACATCATTTACCCCA
scaffold629831_13.4	1	p2	(AT)8	16	995	1010	GCCAAATCCTAGCCACACAT
scaffold629832_15.5	1	p2	(AC)6	12	1384	1395	TTTGGTGACATGACCACGAC
scaffold629840_17.6	1	p2	(CA)7	14	389	402	CTCACGTTTTTAGCCCAAGC
scaffold629918_16.4	1	p2	(TG)7	14	899	912	TCTTTTATGTGGGGGTGACAG
scaffold630015_13.8	1	p2	(AT)12	24	647	670	TCTCCTTTGCGTGGACAAGT
scaffold630038_14.0	1	p2	(CT)11	22	2022	2043	TGGGGTGTGTGTTCTTGAAA
scaffold630176_15.0	1	p2	(TA)11	22	1945	1966	AGCAAAGAAATGCAGAAGGC
scaffold630205_14.3	1	p2	(TA)12	24	719	742	TGGTTCTCACTAAAACGCGA

scaffold630212_16.	1	p2	(TA)6	12	1123	1134	TCGTTCTTTCTTGCTTCCGT
scaffold630302_14.	1	p2	(TA)8	16	674	689	GGGTTTATGTTTGGTGTTTGC
scaffold630303_11.	1	p2	(TA)6	12	312	323	AGCTCCATCGAGTCAAGCTC
scaffold630342_14.	1	p2	(GA)6	12	622	633	GTGGGAAGATTTGAGGGGTT
scaffold630522_16.	1	p2	(TA)7	14	190	203	ACATCCACTGGCCAAGAATC
scaffold630524_14.	1	p2	(AT)7	14	191	204	CGAAAAACCAAAAACCCTCA
scaffold630545_14.	1	p2	(AG)7	14	54	67	GGCCAGTAACACAAAGGCAT
scaffold630580_11.	1	p2	(TC)10	20	896	915	ATTGTCCTGACGACTCCACC
scaffold630603_17.	1	p2	(GA)7	14	54	67	TGAGAGATCAGTGAGCACGAG
scaffold630717_12.	1	p2	(CT)8	16	52	67	AAGTAACCACCAATAACCGCC
scaffold630718_12.	1	p2	(TA)9	18	757	774	TGTTGATCTTATGAGTGTGAAAACA
scaffold630842_19.	1	p2	(GA)6	12	1845	1856	TGTTCGAAAATGGTGGTTGA
scaffold630856_18.	1	p2	(AG)7	14	120	133	CTGATAACAATGGGCGATCA
scaffold630930_16.	1	p2	(AT)9	18	470	487	CTGGAGAATTGGGAGGCATA
scaffold630957_11.	1	p2	(TC)7	14	251	264	TGGGAATTTTGTGGAGAAGC
scaffold630999_13.	1	p2	(TA)6	12	1265	1276	CATCTGAACAGTGTCAATTTTGC
scaffold631052_17.	1	p2	(TA)6	12	600	611	CGAACCAAAGCAACACAAGA
scaffold631090_15.	1	p2	(AT)6	12	301	312	GCCCTCAACTTTGTACGTGAA
scaffold631137_16.	1	p2	(AG)7	14	191	204	TTGATTCGGAGGCTTGTTTT
scaffold631138_15.	1	p2	(CT)9	18	2037	2054	AAAGAACTCGTCGCCAGTGT
scaffold631153_14.	1	p2	(CT)6	12	240	251	CTCACCCCTCGAGTTTCGTA
scaffold631282_16.	1	p2	(AG)10	20	281	300	GCAAATGCATCAGATTCAGG
scaffold631500_13.	1	p2	(AC)6	12	2198	2209	TAAAGTGAAACGCAGATGCC
scaffold631510_14.	1	p2	(AG)6	12	677	688	GAATTGGTCTTCCTTTGCCA
scaffold631732_15.	1	p2	(AT)6	12	1803	1814	AGGGCAAACTCACCATTGTC
scaffold631774_13.	1	p2	(CT)6	12	87	98	TCACCACGTTCTACGCTCAA
scaffold631778_12.	1	p2	(TA)8	16	49	64	CTCACAGGATTTAGCTGTTCTCA
scaffold631815_10.	1	p2	(CT)6	12	333	344	CCTCTCATGTTTTCCCCAAA
scaffold631818_18.	1	p2	(CT)7	14	333	346	TTCTTTCACCCCTCCCATAA
scaffold631832_12.	1	p2	(AT)11	22	1674	1695	CTCCCAAAATCTCAATCCCA
scaffold631855_16.	1	p2	(TC)6	12	456	467	CCCGTGACATGGAAACTCTT
scaffold631932_17.	1	p2	(CA)6	12	322	333	AGTAGCAGCTGTGGATTCCC
scaffold632014_18.	1	p2	(TC)7	14	1887	1900	ATTTTTGTTTTGCTGCCCAC
scaffold632030_10.	1	p2	(TA)6	12	429	440	AAGAAAAACAGGGGAAAGGG
scaffold632071_10.	1	p2	(TA)7	14	94	107	GGGGGAGGAATGGTAGAGAG
scaffold632124_14.	1	p2	(AG)6	12	415	426	ACTATTGTCGGACACTGGGA
scaffold632245_12.	1	p2	(AT)8	16	590	605	TCGCCTTTAATTCTAGCAACA
scaffold632287_15.	1	p2	(AG)9	18	4321	4338	TCGAGAACTTGCTTGGTGAC
scaffold632471_13.	1	p2	(AG)7	14	650	663	TTTGATCGGTTGACGAATGA
scaffold632518_13.	1	p2	(TA)6	12	765	776	GCAAACATATGGTGGCATTT
scaffold632520_10.	1	p2	(TA)6	12	642	653	TCAACAATTGGAGACAACGC
scaffold632632_16.	1	p2	(GT)7	14	2126	2139	CCCCCAAATTCTCTCCTCTC
scaffold632734_12.	1	p2	(AT)6	12	98	109	CCAACACAAAAACAGGGAAAA
scaffold632824_18.	1	p2	(TA)7	14	192	205	CCTTGTGGGGTACAAGTGCT
scaffold632825_14.	1	p2	(AT)8	16	805	820	AACTTCAAGCACTGGAATGAGA
scaffold632844_10.	1	p2	(AG)8	16	189	204	CTTCCCCAGAAATCGAACAA
scaffold632854_11.	1	p2	(GA)8	16	321	336	CATGCGAGTAGAGCTCGAAA
scaffold632956_17.	1	p2	(CT)7	14	562	575	GAACAAGGGCAACTCGAAAG
scaffold632982_12.	1	p2	(TA)8	16	389	404	ATTTGTGTGGGCATGTTCAA
scaffold633054_14.	1	p2	(CT)7	14	475	488	TTTTGGAGCATCTCCCATTT
scaffold633168_16.	1	p2	(CT)7	14	192	205	TTCCGAAGCTCTTCAAGCTC
scaffold633195_17.	1	p2	(AG)8	16	1788	1803	CCTTCCCAACAGAGGAAAGA
scaffold633227_14.	1	p2	(GC)6	12	269	280	TACCCTAAGGGCATCCACAA
scaffold633239_13.	1	p2	(TC)6	12	877	888	GGCCACTAAAACAGGGATCA
scaffold633263_13.	1	p2	(AG)6	12	400	411	GGGTTTACCTATCCCGTGCT
scaffold633265_15.	1	p2	(CT)6	12	2809	2820	CCTTTGCATAGAGTGCGACA
scaffold633412_17.	1	p2	(CT)7	14	1976	1989	ACTTGTCGAAGGAGACGCAT
scaffold633416_14.	1	p2	(TA)6	12	1506	1517	TTTGGCTCGTATGCAGTCAG

scaffold633455_13.	1	p2	(AT)6	12	267	278	AAAAATGAACATGGCCGAAG
scaffold633490_13.	1	p2	(AT)6	12	431	442	TCGTCACCCTTATCCTACCG
scaffold633514_13.	1	p2	(AG)6	12	103	114	TTGCTTGGAACTTAGCCCAC
scaffold633628_13.	1	p2	(TG)6	12	53	64	CTCATGTACGTTACGATGGCA
scaffold633689_14.	1	p2	(GA)8	16	65	80	TGGTAGCTTGAATACACGTATGA
scaffold633697_15.	1	p2	(AT)6	12	560	571	TTGATATCAGAGCCACTGCG
scaffold633709_17.	1	p2	(GT)6	12	912	923	CAAGGAGTGGAGGTCGGTAA
scaffold633731_14.	1	p2	(CA)6	12	2848	2859	GCTTTTCTTTCGACCCATCA
scaffold633746_11.	1	p2	(TA)12	24	39	62	TTGACGATATATAGTGTTTTGACATG
scaffold633785_14.	1	p2	(TA)8	16	45	60	AAGGAGGTGTTATGAAGGGATT
scaffold633874_10.	1	p2	(TA)8	16	140	155	TCAAGGTAAATGGGTCTAGCAAA
scaffold633962_12.	1	p2	(AT)8	16	796	811	TTTTGGGTAATTGGTGAACCTT
scaffold633964_14.	1	p2	(CA)6	12	6190	6201	AATCGGGTCCTCATCATCCT
scaffold634032_13.	1	p2	(TA)8	16	289	304	AAACAACCCAAGAAAAATACGG
scaffold634113_15.	1	p2	(GA)7	14	1875	1888	AGGGGACTAGGGTTGAAGGA
scaffold634122_15.	1	p2	(GT)6	12	366	377	GTAGAATCCGGCGAGTGAAA
scaffold634208_12.	1	p2	(TC)8	16	54	69	CCTAGAAAGAGAAGAAACAGAGGC
scaffold634212_13.	1	p2	(GA)8	16	1008	1023	CACCATCAGCAGAGAAAGCA
scaffold634219_12.	1	p2	(CT)7	14	120	133	GGTTGGTCAACCAAAACCTG
scaffold634244_10.	1	p2	(TA)9	18	378	395	ATGGACGCTCCAGATTGTTT
scaffold634370_17.	1	p2	(TA)7	14	637	650	TTCCCTCCAAAAATATGGGC
scaffold634375_12.	1	p2	(AT)10	20	590	609	CGTGATAAGAACACTCATGTCCA
scaffold634431_12.	1	p2	(CT)7	14	1153	1166	TACTTCTCACCATCCCCCAC
scaffold634568_11.	1	p2	(AT)10	20	503	522	CCGATTTTTCGGGTATTGAA
scaffold634579_16.	1	p2	(CT)8	16	1732	1747	GCCGGGTAAACTACACTGGA
scaffold634597_10.	1	p2	(AT)9	18	461	478	TAAACGGCTCGGAAAAGACA
scaffold634642_13.	1	p2	(AC)7	14	128	141	AACCATTGAGCAAAAACAATG
scaffold634697_11.	1	p2	(AG)6	12	925	936	CCGGGTTTAAAGCAATCAAA
scaffold634759_20.	1	p2	(CT)6	12	240	251	GGGAGGACAGTCCGTAGACA
scaffold634773_17.	1	p2	(AG)6	12	1837	1848	AATATTCCACCACTGTGGGC
scaffold634784_17.	1	p2	(AG)6	12	638	649	TTTGACTTGCAGCCACTCTG
scaffold634791_18.	1	p2	(TC)6	12	630	641	TCCAACTCCCTCCATTCTTG
scaffold634799_12.	1	p2	(AC)6	12	615	626	CGTGGCTTTGTTGAAACTGA
scaffold634801_13.	1	p2	(TA)11	22	46	67	AAGGGAGTGCTCCCACATTA
scaffold634806_14.	1	p2	(AG)6	12	394	405	TCTTTTTCCACATTTGAAGTTCTTT
scaffold634829_16.	1	p2	(CT)7	14	621	634	TCGCAGCGAAACGTGAAC
scaffold634844_16.	1	p2	(AC)10	20	747	766	CCATCAACAAATGCAATGGA
scaffold634850_18.	1	p2	(TC)8	16	1111	1126	AAAGGAATCAGAGCGCAGAG
scaffold634855_12.	1	p2	(TA)6	12	53	64	ATGGGAAGAGGGGGTATGAG
scaffold634881_10.	1	p2	(AT)10	20	483	502	CCAAACAAACCGGCATACTT
scaffold634890_13.	1	p2	(CT)7	14	292	305	GCACACGTATTAGGACCTCCC
scaffold634931_13.	1	p2	(AT)6	12	251	262	CACCCTGTGACAGATACAGCA
scaffold634934_15.	1	p2	(TA)8	16	563	578	GCGCATGCACCTAATTACAC
scaffold634957_20.	1	p2	(AG)6	12	248	259	CAACAATCAGCAGTGGCAAT
scaffold634960_14.	1	p2	(AT)8	16	2328	2343	TGATCAGCGCAGTCCAGTAG
scaffold635009_16.	1	p2	(AT)6	12	446	457	AGAGCACTGCCAGATCAAAA
scaffold635012_14.	1	p2	(AT)8	16	1165	1180	GGGAAAGTCGATGGTTTCAA
scaffold635134_12.	1	p2	(TA)7	14	332	345	TCCTTTGAGGATGGATTGATG
scaffold635223_15.	1	p2	(AT)8	16	192	207	TCGTTCCTTAAGTCTTCCGC
scaffold635224_14.	1	p2	(AT)6	12	196	207	GCCTTGCAAGCCAGTTTATT
scaffold635267_13.	1	p2	(TA)6	12	906	917	GCCCTCAACGTTGGTATCTT
scaffold635274_12.	1	p2	(GA)6	12	195	206	ATTTGCATGCATAACCCACA
scaffold635290_12.	1	p2	(TA)6	12	192	203	AGGCTTGAGTTTCCTCACGA
scaffold635357_13.	1	p2	(TC)6	12	1473	1484	GCAGAGTTGTCGGGAAAGAG
scaffold635446_15.	1	p2	(AG)11	22	2691	2712	CCGAAAAAGGGTATTGGGTT
scaffold635524_16.	1	p2	(AG)8	16	3225	3240	AGGCTTAAACCAGGACCGAT
scaffold635558_15.	1	p2	(TG)6	12	960	971	GCAACAGTTGTGGTTGATGG
scaffold635611_15.	1	p2	(TG)10	20	1017	1036	TCGAAGCTTTGCTACTGGCT

scaffold635625_16.	1	p2	(CT)6	12	54	65	CAAGATAACCCTTCGATTTAGGAA
scaffold635668_12.	1	p2	(TA)7	14	789	802	ACTGGCCCAATAACCTTCCT
scaffold635685_14.	1	p2	(AT)7	14	1779	1792	CGTAAGGCCTACTCGAGCC
scaffold635695_19.	1	p2	(AT)9	18	499	516	TCTTGGTGGCGGTAGGTAAC
scaffold635724_13.	1	p2	(GT)6	12	118	129	TGTACGACATTGTTTGCGCT
scaffold635771_15.	1	p2	(TC)6	12	110	121	CTAGCCTTTGCCCCTTTTCT
scaffold635893_16.	1	p2	(AG)9	18	907	924	CCCTTTTGATTCTTGCCTCA
scaffold635903_16.	1	p2	(GA)11	22	321	342	TGAAATTCACTTGATCCGCA
scaffold635916_15.	1	p2	(TA)8	16	209	224	TTCGAAATATCGGGGCATTA
scaffold635944_19.	1	p2	(TA)6	12	196	207	TTCCTTGGACCAAAATAGCC
scaffold635963_14.	1	p2	(TA)6	12	1590	1601	TTGTGGTAACCGATTGGGAT
scaffold636040_17.	1	p2	(CT)6	12	312	323	TCAAAGCGATGGAACATAACA
scaffold636047_15.	1	p2	(GA)6	12	141	152	GTGAGAGAGGACCGATTGGA
scaffold636268_13.	1	p2	(TA)8	16	219	234	TGCTGATGTGGGAAAATCTG
scaffold636281_13.	1	p2	(TC)7	14	141	154	GGATTCCCCCTCGAAGTTT
scaffold636287_13.	1	p2	(TA)9	18	48	65	AGGGGGTTATCACTGGATCG
scaffold636510_16.	1	p2	(AT)9	18	1465	1482	CCTTCAATTTTATAACCGAAACA
scaffold636563_13.	1	p2	(TA)7	14	253	266	TCTAAGGAGGTGTTATGATGGGA
scaffold636568_15.	1	p2	(GA)8	16	863	878	ACCTCTTTCCAATCTGGCCT
scaffold636614_14.	1	p2	(AG)7	14	144	157	AGAGAGAGAGAAACGCGAGG
scaffold636619_15.	1	p2	(AT)7	14	2421	2434	AGCGAACCAGAACCGAACTA
scaffold636631_15.	1	p2	(GT)6	12	656	667	GCGTCGAGTACCACTTTTCC
scaffold636757_15.	1	p2	(TA)6	12	1412	1423	TTTTCTCTGGATCACACCCC
scaffold636762_18.	1	p2	(TA)6	12	908	919	GGCGTGGCTCAAGATATCAG
scaffold636789_13.	1	p2	(AT)7	14	342	355	TGCAAAAGTTTTTGTTGGGT
scaffold636846_11.	1	p2	(TC)6	12	129	140	TCTCTCTCCCACTCTTCCCA
scaffold636860_15.	1	p2	(CT)8	16	324	339	AAGCCTTCCCACCGAGTATT
scaffold636892_13.	1	p2	(TG)6	12	565	576	CTCTCCATTCTCTCGCTGCT
scaffold636960_12.	1	p2	(TA)6	12	228	239	CCTCCTTTAACCAAAAATCCG
scaffold636980_15.	1	p2	(CT)6	12	197	208	CCTTCTCTCTCCTTTCCCGT
scaffold636996_12.	1	p2	(TC)6	12	401	412	GGCAACGAGACAGACAAACA
scaffold637101_16.	1	p2	(CA)9	18	2876	2893	AGGCCAATTTTGAAGCAGAA
scaffold637124_11.	1	p2	(AG)6	12	323	334	TTGGGAGGAGGAGATTGTTG
scaffold637128_15.	1	p2	(AG)6	12	713	724	TGGACTGCTGTTCAGAGACG
scaffold637138_16.	1	p2	(TA)12	24	5104	5127	TGTGCCCACTTAAAAATTTGG
scaffold637154_10.	1	p2	(TA)10	20	1030	1049	CTGCAGATCTAAGGGCCAAG
scaffold637163_10.	1	p2	(AT)8	16	1340	1355	GCGACCAAATCAATCACCTT
scaffold637184_13.	1	p2	(AC)7	14	335	348	ATTTGGGTTTTAGGCTTGGG
scaffold637204_16.	1	p2	(GA)9	18	2354	2371	TGCAAGTTCAGACAAACCCA
scaffold637235_14.	1	p2	(CA)7	14	4406	4419	GGTTCAACCTCCCAGATTCA
scaffold637317_13.	1	p2	(TC)6	12	75	86	TGATTTCCTCACCTTGTTTGTG
scaffold637323_13.	1	p2	(TG)6	12	351	362	CCCCCAACTCTTCTTCTTCC
scaffold637388_12.	1	p2	(TA)7	14	362	375	GCATCACCTCAACCCTTGAT
scaffold637390_16.	1	p2	(AT)11	22	684	705	AAGTTGCACAATCCTAATGATTTA
scaffold637393_17.	1	p2	(GA)7	14	1489	1502	TTCCCAATTGCGTAGTCCAT
scaffold637402_16.	1	p2	(CT)6	12	805	816	CCAATTGAATGGAGTCAGGG
scaffold637457_16.	1	p2	(AT)6	12	1467	1478	ATTGTGGGGAAATGATCCAA
scaffold637460_15.	1	p2	(GA)7	14	38	51	CGTGGTTCGATCGTAAATGA
scaffold637591_12.	1	p2	(AG)6	12	346	357	CCCGAAATAAGCTGCGTAGA
scaffold637715_17.	1	p2	(CT)6	12	77	88	ATAACCATACCCACACCCCC
scaffold637807_15.	1	p2	(GA)6	12	4488	4499	CGCTGCTGTAGTCGGAAGTT
scaffold637842_13.	1	p2	(TA)6	12	563	574	GAAGAAAACTGCCGAGTTGC
scaffold637934_14.	1	p2	(TA)8	16	417	432	TTGACCATAATGCCCCTATCA
scaffold637975_10.	1	p2	(AT)11	22	401	422	ATCTCATGCCTTAGAGGGGG
scaffold638050_17.	1	p2	(TC)9	18	3319	3336	CAAACCTAACTGAAATAGGAATGGA
scaffold638095_14.	1	p2	(GA)6	12	456	467	GGAAATTGATGGATTTGGGA
scaffold638134_16.	1	p2	(AG)8	16	1865	1880	TCAAACTTGCCAATCCAAAA
scaffold638179_17.	1	p2	(AT)10	20	122	141	AAATAAGGATGTGTTATGAAGGGA

scaffold638220_16.	1	p2	(CA)7	14	778	791	CCACCCGAATTGGATAATGT
scaffold638221_13.	1	p2	(TA)8	16	193	208	ATGTGTCGGCCTGAATATGG
scaffold638240_16.	1	p2	(AT)6	12	503	514	ATAGTTCCGTCGTCGTTGGT
scaffold638259_14.	1	p2	(TA)8	16	246	261	TGGTGGGTTGAATGCTATGA
scaffold638550_12.	1	p2	(AT)6	12	1084	1095	TTCACAAGCTTGAAAGCAACA
scaffold638568_10.	1	p2	(AT)8	16	95	110	ACGCACTCTCAAGCACACAC
scaffold638709_10.	1	p2	(AT)7	14	71	84	AAAATCAAAGGCCCACATTG
scaffold638816_16.	1	p2	(CT)6	12	554	565	TGTGCATGCCCATATCATCT
scaffold638835_17.	1	p2	(TC)6	12	87	98	CTAGCCTTTGCCCCTTTTCT
scaffold638877_13.	1	p2	(TA)7	14	123	136	TGTATGGGGAGGGTTATCCA
scaffold638895_15.	1	p2	(TG)9	18	223	240	TTGATTTAACTTGCATTCTTTTTCA
scaffold638911_19.	1	p2	(GT)6	12	486	497	GAAGAAGGCGAAGTGGCTTA
scaffold638946_11.	1	p2	(CT)6	12	53	64	CCTAGCTCCTTCCCCTTCAC
scaffold638951_14.	1	p2	(TC)6	12	662	673	ACAAAGTGGTGAGCATTCCC
scaffold639028_17.	1	p2	(TA)6	12	550	561	AGACCAAAAGGTCACGGGTT
scaffold639055_15.	1	p2	(GT)6	12	3074	3085	CCCAAGATTTCCCATAAGCA
scaffold639078_13.	1	p2	(TA)12	24	40	63	TTGACGATATATAGTGTTTTGACATG
scaffold639236_11.	1	p2	(CT)10	20	30	49	CAGATTTTAGGATTTCAGCTCACTG
scaffold639265_19.	1	p2	(GA)6	12	199	210	CTCGGTCCGGATCTTTCAT
scaffold639291_15.	1	p2	(AC)6	12	1222	1233	ATGGAAAACCACGAGTGGAG
scaffold639338_15.	1	p2	(CT)6	12	199	210	GAACCCCTGTGACCATCTGT
scaffold639339_16.	1	p2	(GA)8	16	131	146	TTGGAAATCAAGTAGAACTGAAAA
scaffold639352_14.	1	p2	(TG)9	18	1250	1267	GCCAAACGCCAAAGAAAAAT
scaffold639404_16.	1	p2	(AT)6	12	4321	4332	GCGAAATAGTTGGACATCGG
scaffold639455_11.	1	p2	(AT)9	18	1221	1238	AAAATTTGTTTCCCACCAAATAA
scaffold639471_16.	1	p2	(TA)6	12	195	206	GGATGTGGTCGAGTTTCGTT
scaffold639505_13.	1	p2	(AT)7	14	1235	1248	TCGAGTATTGCTTCGCTTCA
scaffold639543_12.	1	p2	(AC)6	12	216	227	TGCTCACTCCTGCACATTTC
scaffold639560_15.	1	p2	(AG)7	14	1776	1789	GGATTTGACTGGTTGGGAGA
scaffold639606_10.	1	p2	(AG)6	12	183	194	GTGTAGATCGCCATGGTGTG
scaffold639648_15.	1	p2	(CT)13	26	2166	2191	CCCCAAAATTCCCTTTTCAT
scaffold639686_13.	1	p2	(AT)9	18	552	569	CGTCACCCTCAACAAAAGGT
scaffold639697_20.	1	p2	(AT)9	18	67	84	CAAAGGCCCACAATGGTTAT
scaffold639704_13.	1	p2	(TA)6	12	88	99	AACGAATCTTTTCGTGGAGC
scaffold639737_14.	1	p2	(TC)6	12	199	210	TCCGGTTCACCCATTTAGTC
scaffold639761_10.	1	p2	(TA)8	16	242	257	AATTACACATACACGTGGGCT
scaffold639863_19.	1	p2	(AT)12	24	40	63	GGCTAGGCTGGATAAGTTTCA
scaffold639875_13.	1	p2	(CT)7	14	197	210	TGATGGGGTTTAATCATCTGG
scaffold639876_10.	1	p2	(AG)7	14	41	54	CCCATGCATCCATATGAGAGA
scaffold639917_13.	1	p2	(TA)6	12	146	157	AACATTGTTCTCCCCCACAA
scaffold639932_13.	1	p2	(TA)9	18	269	286	CAAAGAGGAAATTCGAACGC
scaffold639967_13.	1	p2	(TC)8	16	194	209	ACTGGTGTTTGTTCATGGCA
scaffold640047_11.	1	p2	(TC)6	12	132	143	GTACTCTCATGCGCTCAGCA
scaffold640055_16.	1	p2	(AG)10	20	144	163	TGCTTTTGACGGAGTGTGAG
scaffold640108_14.	1	p2	(GA)6	12	2360	2371	AATTAAATGAATGGGTGGCG
scaffold640114_11.	1	p2	(CT)6	12	316	327	AGAGATCACACAGGCAGTCG
scaffold640121_12.	1	p2	(AG)6	12	327	338	TCACGGGTTCGAGTTTCAAT
scaffold640167_17.	1	p2	(AT)8	16	307	322	CTAATGGCGAAGTGGATCGT
scaffold640193_11.	1	p2	(TG)8	16	129	144	CATTTTACCGGCATGGTGTT
scaffold640221_13.	1	p2	(AT)6	12	764	775	AACCCACATGCAAGTTTCGT
scaffold640264_14.	1	p2	(AC)9	18	193	210	TCCATCTCCACGTACGACTG
scaffold640287_10.	1	p2	(CT)7	14	433	446	CCCAAGATGAAACGGAGAAA
scaffold640293_11.	1	p2	(GA)7	14	51	64	TCGATTCAGTTTCCCCACTC
scaffold640324_14.	1	p2	(TA)9	18	307	324	TGAATTCGGTCAAGCATCTG
scaffold640329_15.	1	p2	(CT)7	14	824	837	TGGTGTTGGGAAGAATCACA
scaffold640361_15.	1	p2	(TA)7	14	197	210	GCCTTTCGTCACAAACATCA
scaffold640406_15.	1	p2	(AC)6	12	2346	2357	AGAAATTCAAACCCGGAACC
scaffold640497_12.	1	p2	(TA)8	16	773	788	TTCTTCAGTCCCTACCGTCG

scaffold640504_11.	1	p2	(AT)13	26	410	435	GCGATATGCATCTACCGTGA
scaffold640536_15.	1	p2	(TG)6	12	178	189	TTGAAGGGGTCTCTTGGATG
scaffold640550_15.	1	p2	(TA)8	16	47	62	TGCGTTTTGACGATATATAGTGTTT
scaffold640558_15.	1	p2	(CT)6	12	252	263	GGAAGATTCAAACCCCATCA
scaffold640581_14.	1	p2	(CT)10	20	447	466	CCCAAGATGAAACGGAGAAA
scaffold640654_13.	1	p2	(TC)9	18	193	210	TTCCATGTGCATGCAGAAAT
scaffold640691_13.	1	p2	(AG)8	16	1990	2005	GACATGGGCACCTTATTGGT
scaffold640704_13.	1	p2	(GA)6	12	992	1003	TCATGTCGCCGATCATAAAA
scaffold640717_13.	1	p2	(TA)8	16	47	62	AAGGAGGTGTTATGAAGGGATT
scaffold640774_10.	1	p2	(AT)6	12	66	77	ATGAATGGCCCATATTGGTT
scaffold640856_16.	1	p2	(TA)11	22	649	670	TTTACGATTTCGATAGCCCG
scaffold640977_13.	1	p2	(CA)6	12	227	238	GCCCAGTCATTTTGTCCCTA
scaffold640982_17.	1	p2	(TG)6	12	679	690	GAGAGGGTGATTTTGCCACA
scaffold641023_13.	1	p2	(TA)7	14	51	64	TGAGATAAGGGGGTGTTTGC
scaffold641057_18.	1	p2	(GA)7	14	1627	1640	TGGTCTACTTCTATGGCGGG
scaffold641073_17.	1	p2	(AT)10	20	383	402	ATTTGGTTTGCTTGGGATTG
scaffold641108_14.	1	p2	(TA)6	12	394	405	TCCCTTTGATTCCCTTCTCA
scaffold641238_16.	1	p2	(CT)8	16	358	373	GGCTACCCCTCTCGCTCTAC
scaffold641242_13.	1	p2	(AT)6	12	199	210	GCTGATGTCGATTTTCCAGA
scaffold641328_14.	1	p2	(AG)6	12	27	38	CAATTACAATGTTTTTCCAATCCC
scaffold641334_15.	1	p2	(CT)8	16	321	336	CGCATCAAGTTCCCTCATCT
scaffold641399_15.	1	p2	(TA)12	24	1500	1523	TCCCGTATACCTCCAATTTACAA
scaffold641421_11.	1	p2	(TA)7	14	350	363	TCACATGTGGCGTCTTTTTC
scaffold641434_14.	1	p2	(CT)9	18	1208	1225	CTGTGGTGGAAGGGTTGTCT
scaffold641451_18.	1	p2	(AG)8	16	129	144	AACAACTATCTCCAGCCCCA
scaffold641523_12.	1	p2	(TA)6	12	671	682	AGGAAAAGGAGGAGCCAGAG
scaffold641543_11.	1	p2	(AT)9	18	66	83	CAAAGAAACTTGGGACGGAG
scaffold641555_15.	1	p2	(CT)8	16	52	67	AATTCTTCCTCCGGAACACC
scaffold641799_12.	1	p2	(AC)6	12	658	669	CTTCACGGGGTTGTCCTTTA
scaffold641807_16.	1	p2	(TA)7	14	198	211	TGATTCTTGGTGGCAGATTG
scaffold641808_11.	1	p2	(TA)6	12	79	90	CTAGGAGGTTCTCGCATTGG
scaffold641924_15.	1	p2	(TC)7	14	198	211	CTTCAAAATCTAACCGGCCT
scaffold641988_16.	1	p2	(TC)6	12	681	692	GCGAGAGCTATGTGGAGACC
scaffold642088_10.	1	p2	(TA)10	20	261	280	AGGGAGCTGGCACTAGATCA
scaffold642140_13.	1	p2	(AT)9	18	1204	1221	TTGAGATTGCGAATTCAACG
scaffold642208_19.	1	p2	(AT)8	16	1526	1541	GGGTTGGATCAACCACATTT
scaffold642278_16.	1	p2	(CA)6	12	1230	1241	ACACAAGCACACACATGCAA
scaffold642334_10.	1	p2	(TA)10	20	598	617	TTAAACCATGCACGTAGGCA
scaffold642373_10.	1	p2	(GA)7	14	52	65	CCAACTCAGTGTGTGAGTGGTT
scaffold642596_16.	1	p2	(AC)6	12	106	117	CCACAGGATCGAATGAACAA
scaffold642656_15.	1	p2	(TA)11	22	4093	4114	CCATTTGGTGCTGGAGTTCT
scaffold642663_12.	1	p2	(AT)7	14	50	63	GGTTATTAGTTATTACGGATTTAACG
scaffold642707_18.	1	p2	(TC)6	12	172	183	CCCCTTTGTCATCTTAGGCA
scaffold642926_17.	1	p2	(AG)6	12	201	212	CAATAAATTGGGGTCGGCTA
scaffold643009_18.	1	p2	(AT)12	24	43	66	GACTAGAGTTGGTTTCTTAAATGACT
scaffold643031_11.	1	p2	(TA)6	12	526	537	AAGAAAATGGGCAGAAACGA
scaffold643073_10.	1	p2	(AC)6	12	98	109	TCGGGATCTTCACATCTTCC
scaffold643200_12.	1	p2	(TA)6	12	2002	2013	CGAAAACATTTACATACGATGCC
scaffold643221_13.	1	p2	(AT)6	12	261	272	AAAAACGAGCATTTTAGGGTTA
scaffold643357_15.	1	p2	(AG)11	22	2227	2248	CCAGACGACTGCAAAAACAA
scaffold643411_12.	1	p2	(AT)14	28	355	382	TAGGTGTCGGATTTGGGAGA
scaffold643419_10.	1	p2	(TC)7	14	112	125	ATTGTTGCTTTGCCATCTCC
scaffold643444_14.	1	p2	(GA)7	14	407	420	AGAAACAAACGGAATGTCGG
scaffold643448_16.	1	p2	(TA)6	12	1512	1523	GCATGGACCAGAAATTCCAC
scaffold643464_11.	1	p2	(TG)8	16	169	184	CTTGTGGAATGAAAGGGTGG
scaffold643556_12.	1	p2	(AT)9	18	954	971	GGAGGTGAAGATTGGGTGAA
scaffold643665_10.	1	p2	(AT)7	14	573	586	TCCTTCCTTGCTCCTTTTCC
scaffold643730_15.	1	p2	(TA)9	18	244	261	GCGCTTTTTGCCTGATATTT

scaffold643835_16.	1	p2	(TC)9	18	840	857	ACCGCTTACATTCCGATTTG
scaffold643874_16.	1	p2	(GA)9	18	1122	1139	GCAATACTGTTTCCACCGCT
scaffold643881_11.	1	p2	(TC)9	18	330	347	TTCAGCACTCCATCAGCAAG
scaffold643901_15.	1	p2	(CT)9	18	50	67	TGGCCAAAACATCAACTCAA
scaffold643902_15.	1	p2	(AG)7	14	248	261	TAGAGCCGGGTTTAGAGCAA
scaffold643943_12.	1	p2	(TA)10	20	52	71	GGTGACGATGGTGATTGATG
scaffold643944_21.	1	p2	(AT)8	16	198	213	TAGTGAGTAGTTCCGCCCGT
scaffold644011_13.	1	p2	(AT)9	18	301	318	GGCATTTTGGGAAAGACAAA
scaffold644044_16.	1	p2	(TC)6	12	2014	2025	GGATCGGTGACAAAGGGAAT
scaffold644123_15.	1	p2	(CT)8	16	198	213	GATGCAGCTTGGTCTCCTTC
scaffold644303_10.	1	p2	(TA)9	18	217	234	AAAATGGTCCCCTCATGGAC
scaffold644328_15.	1	p2	(TA)6	12	864	875	TGTCCAAATAATTCATCACCAAA
scaffold644391_17.	1	p2	(AC)6	12	2744	2755	CTTCGCCATCTGGTTTTGAT
scaffold644404_15.	1	p2	(CT)9	18	1250	1267	ATAAAATGGGCGATTCCCTT
scaffold644420_18.	1	p2	(GA)10	20	193	212	TTGCTGCCACTACCTGTGAA
scaffold644432_17.	1	p2	(TA)7	14	119	132	ATGGGCTGTCTCTTGGATCA
scaffold644442_14.	1	p2	(AC)6	12	1867	1878	TCCATCCGAAATCCGAATAA
scaffold644469_14.	1	p2	(AT)7	14	1787	1800	TATACAAATGGGCGCATCAA
scaffold644485_15.	1	p2	(CA)6	12	737	748	ATTTTCGCAATCATATCGGG
scaffold644501_15.	1	p2	(CA)6	12	530	541	TCCTCCTTTTCACAACTGGC
scaffold644645_17.	1	p2	(GA)6	12	202	213	GTTGGTTACGGGAATTGCAT
scaffold644655_17.	1	p2	(TA)7	14	1102	1115	AAAATTCAATGACAATTGGAGGA
scaffold644735_15.	1	p2	(CT)8	16	1427	1442	TGGCATTAAATATTAGCCCCC
scaffold644755_15.	1	p2	(AG)8	16	34	49	GCCAATAATTTTTAGCAAGCAA
scaffold644805_15.	1	p2	(GA)6	12	446	457	GAGAAGTGGCGGACTTTCTG
scaffold644826_12.	1	p2	(TC)6	12	747	758	CATGATCCCGTGAGATACCA
scaffold644897_16.	1	p2	(TC)6	12	345	356	AGCGTACAATACAGCCCACC
scaffold644967_17.	1	p2	(AT)9	18	917	934	GGTATGTCAATTTGCCGCTT
scaffold644988_16.	1	p2	(TC)8	16	91	106	CGAATATGCAATCACCAAAGAA
scaffold645028_10.	1	p2	(GA)6	12	81	92	CACGAGATTTACGTGGTTCG
scaffold645087_12.	1	p2	(AT)9	18	88	105	CTGCATGCACCTGATTACAA
scaffold645097_11.	1	p2	(CT)10	20	188	207	TCACCTTCACTTCCTGCTCA
scaffold645177_16.	1	p2	(TG)8	16	946	961	CATGCATTTGTTGTCGTTTTC
scaffold645222_10.	1	p2	(CT)6	12	255	266	ACACACACCGTGGACGTAGA
scaffold645261_16.	1	p2	(CT)7	14	148	161	CCTGTGGAGGGAACTTTTCA
scaffold645374_12.	1	p2	(TA)9	18	838	855	AAAGTGCACAGAAAAATGACTTTG
scaffold645450_15.	1	p2	(AT)7	14	892	905	GGTTGGTAGCTCGGAACAAA
scaffold645454_16.	1	p2	(CT)9	18	1958	1975	CTGCCAACTGAATGAAAGCA
scaffold645511_15.	1	p2	(AT)7	14	2109	2122	CAAACACGGAGATTTCAACAA
scaffold645647_16.	1	p2	(AT)11	22	746	767	GCGCTGTAGATCTAACGGATG
scaffold645652_16.	1	p2	(GA)6	12	1622	1633	ATTTGGGTGTAGAGAGGGGG
scaffold645722_13.	1	p2	(AT)8	16	243	258	ACACGAAACACCACTCCTCC
scaffold645734_15.	1	p2	(GA)6	12	162	173	TTGTTGAAGGGTGGTTGTGA
scaffold645775_13.	1	p2	(CT)9	18	539	556	GTTGCTTAGGGTCTGTTGGC
scaffold645776_13.	1	p2	(CT)7	14	391	404	TTGCTTAGGGTCTGTTTGGC
scaffold645867_12.	1	p2	(TA)9	18	553	570	CGGGGCTCACTAAAAACGTA
scaffold645878_14.	1	p2	(TA)8	16	130	145	TACCCCGCTACCACCAATAG
scaffold645923_15.	1	p2	(AT)7	14	1440	1453	CCTTGATTTCAACTGTCTCCG
scaffold645926_15.	1	p2	(TC)6	12	2656	2667	TTAAAACCGACACCCACTCC
scaffold646078_12.	1	p2	(AT)9	18	146	163	GTTTCGATAGTTTTCATTTCATTTT
scaffold646166_13.	1	p2	(AG)6	12	299	310	GCAATACAAGCGATGTGTGG
scaffold646230_16.	1	p2	(AG)6	12	2747	2758	GGGTAGATGCAACATAGGGG
scaffold646252_10.	1	p2	(TC)7	14	304	317	GAAAGCATCGTTTTTGGCTC
scaffold646272_12.	1	p2	(AT)6	12	341	352	ACAATATGGTGTTGGGTATTAAGAT
scaffold646333_10.	1	p2	(TA)9	18	144	161	TCAGTTTTTGAGTTATGACGTTTG
scaffold646334_10.	1	p2	(AT)7	14	251	264	GAAATATGCATTTGTCGTCACC
scaffold646383_11.	1	p2	(AT)7	14	78	91	CAATTCAAAAATGAGTGAACCA
scaffold646412_12.	1	p2	(AT)8	16	87	102	TTCTCTACACATAGAGACCAATTTTG

scaffold646435_11.	1	p2	(GA)6	12	203	214	CGGACGGGAAGAGATAAACA
scaffold646494_13.	1	p2	(GT)7	14	202	215	CTGCCTCTTTCCACACCATT
scaffold646531_11.	1	p2	(AG)6	12	291	302	GCGACAATAACTGTCTGCGA
scaffold646575_16.	1	p2	(TG)7	14	1706	1719	GCCTCCATAACGAGCTCATAG
scaffold646577_11.	1	p2	(GA)6	12	151	162	TTCTCGATTCCCGATTTTTG
scaffold646596_15.	1	p2	(GC)6	12	158	169	GCACAACGGCTATCTGGTTT
scaffold646693_19.	1	p2	(TA)7	14	202	215	TGGCTCATTCATGACCAAAA
scaffold646721_12.	1	p2	(TC)6	12	156	167	CTACTTGCGTGCTGGAACTG
scaffold646882_10.	1	p2	(AT)10	20	340	359	GGCCATTCAAATTTCAAATCA
scaffold646910_16.	1	p2	(TA)6	12	1381	1392	TTGTCTATTCCTCCGATGGC
scaffold647051_13.	1	p2	(CT)7	14	149	162	GGATCGAAAGGGTGAGTGAA
scaffold647156_11.	1	p2	(TG)8	16	327	342	CCATCTTGATGCAGGTGACA
scaffold647184_17.	1	p2	(AT)10	20	236	255	CTATTTGCCGCTGAAAAAGC
scaffold647209_15.	1	p2	(GA)6	12	838	849	GAGCTGCGACATTTTCAACA
scaffold647349_11.	1	p2	(AT)6	12	627	638	AATTCAAGCATTTTCCGCTG
scaffold647449_10.	1	p2	(CA)6	12	270	281	GCTGTCCACCATCTCCTCTC
scaffold647565_16.	1	p2	(CA)8	16	3764	3779	CCATAGTCCAAGATGTGGTGC
scaffold647873_14.	1	p2	(GA)11	22	44	65	TGGATGGATGGATTAGCAGA
scaffold647905_14.	1	p2	(CT)7	14	368	381	CATTCTTTCTCATCACCCCC
scaffold647910_10.	1	p2	(TA)6	12	204	215	ATGGGAAGAGGGGGTATGAG
scaffold647913_12.	1	p2	(AT)9	18	199	216	TTTTAAAAGGATTTATGGCATGAT
scaffold647914_12.	1	p2	(AT)6	12	54	65	GGAAGAATGGACCCTAATTCAA
scaffold648038_15.	1	p2	(AT)6	12	668	679	CGCTTTCACCAGAATCTTCC
scaffold648061_18.	1	p2	(GA)6	12	189	200	AAGTGTTTTCCCACAGACGG
scaffold648103_13.	1	p2	(TA)7	14	261	274	CGCCAATTAATCATAGCCGT
scaffold648167_16.	1	p2	(CA)6	12	1084	1095	AGGCCATGTGTTCGAGTTTC
scaffold648208_15.	1	p2	(TA)13	26	40	65	AAGGGTTATCACCTGATTTTCTC
scaffold648281_17.	1	p2	(AG)6	12	205	216	GATGGTGGACAAGAGAGGGA
scaffold648306_14.	1	p2	(TA)6	12	53	64	GAAGTGTTATGCGTTTTGACAAT
scaffold648350_12.	1	p2	(AG)7	14	203	216	AGGGGAAAAGAGAGAGGGTG
scaffold648456_11.	1	p2	(AT)7	14	445	458	AAGGGGGAAACAACTGAGAAA
scaffold648465_13.	1	p2	(GT)6	12	127	138	AGTGTGTGTTTGTGCGTGTG
scaffold648480_14.	1	p2	(AG)9	18	415	432	ATTTTTCCTTGTTGGGGTGG
scaffold648481_12.	1	p2	(AT)6	12	357	368	TCCGACCGGTTTTTAAATCA
scaffold648494_16.	1	p2	(TC)6	12	824	835	CGTTTGATTTTTCACTAGAACCA
scaffold648531_11.	1	p2	(AG)6	12	35	46	AACAACACAAAACCCTACAGCA
scaffold648539_14.	1	p2	(AT)8	16	1410	1425	TCCATGCTTGAGCAGTTGAG
scaffold648766_11.	1	p2	(AT)6	12	390	401	TGCAGGGTATGCATGTTTGT
scaffold648790_15.	1	p2	(AG)11	22	3970	3991	AACTCCCTATCCAACTGCGA
scaffold648830_14.	1	p2	(TA)6	12	1444	1455	TGTGGCTTCTGCTGTTATGG
scaffold648834_15.	1	p2	(GA)6	12	200	211	AAATGGGGGAGAAGAAATGG
scaffold648850_14.	1	p2	(AT)6	12	912	923	ATCGCCTTTACTCCATTCCA
scaffold649020_14.	1	p2	(TA)8	16	1172	1187	TTCGTGGAAGGGAGAGATTG
scaffold649132_15.	1	p2	(AT)6	12	1305	1316	TGAGAAGGGTGGGTATGAGG
scaffold649147_13.	1	p2	(AT)10	20	2606	2625	TTTGTCCGTCAATATTAGGGATTT
scaffold649212_16.	1	p2	(TA)11	22	152	173	CGCCCCAAGATTTGATAATG
scaffold649229_16.	1	p2	(TC)7	14	203	216	CAACTCTGCGTCTCCTTTCC
scaffold649262_12.	1	p2	(AT)10	20	1038	1057	ACCAATGCACATTTCCTGCT
scaffold649276_13.	1	p2	(AG)11	22	2020	2041	GATTTCCAGGCATGAGGTGT
scaffold649279_16.	1	p2	(CT)6	12	163	174	TGCTTTCGGGAAAAGCATAA
scaffold649367_10.	1	p2	(GA)6	12	253	264	CTCAAAGCTCCACAAGCTCC
scaffold649579_13.	1	p2	(TC)10	20	250	269	TCCCACCTCCATCTCATCTC
scaffold649617_17.	1	p2	(CT)6	12	69	80	TTTAGACCAATCCCAGATCCC
scaffold649627_11.	1	p2	(TA)8	16	380	395	TGGGAATTGGGTTTTGAATG
scaffold649736_17.	1	p2	(AT)6	12	801	812	TGTCGTAGCATTTTTGTATGTTTTT
scaffold649739_12.	1	p2	(AT)6	12	191	202	TGACGCCTAGAATCATCGAA
scaffold649741_16.	1	p2	(TG)6	12	1493	1504	ATGTCGTATTTGCATTGGCA
scaffold649744_16.	1	p2	(TA)6	12	717	728	GTGCAACGCACGTGTAAAAT

scaffold649746_13.	1	p2	(AT)7	14	442	455	GATTTCAATGGACAGGCACC
scaffold649775_11.	1	p2	(AT)6	12	338	349	AGCCGTTTGTCCGATTTATG
scaffold649780_16.	1	p2	(GA)6	12	3887	3898	CAGGAAAAAGAAGATTGCACC
scaffold649841_15.	1	p2	(GT)6	12	596	607	TCCCTTAATTGGAAGCCAAA
scaffold649845_15.	1	p2	(TA)6	12	878	889	TGCAAGGCATGTGCAATTAT
scaffold649856_13.	1	p2	(AG)6	12	37	48	TGGGGATTTTAGAGAGTATTGTGA
scaffold649889_16.	1	p2	(CT)6	12	332	343	CCCCCTTTCTCTCCCTACAC
scaffold649893_17.	1	p2	(AG)6	12	314	325	GGCCCACTTCTTGGTAAACA
scaffold649972_16.	1	p2	(CT)8	16	201	216	TCGACTTTAACCGTGGGTTC
scaffold649979_14.	1	p2	(TA)8	16	736	751	CACATGGGCATATGTGTCAAA
scaffold650072_10.	1	p2	(TA)6	12	394	405	GGGTTGACATGGCTTCGTAT
scaffold650114_10.	1	p2	(TG)6	12	138	149	CTCCCATTTCTGTGTTCTTCG
scaffold650121_13.	1	p2	(CT)7	14	414	427	GCCTCCTCCTCCCTCTCTT
scaffold650213_14.	1	p2	(TA)9	18	201	218	TTTTTACCCCATTTTGCCCT
scaffold650254_12.	1	p2	(GA)6	12	302	313	GTGAGTACAAGCGGGTGACA
scaffold650419_11.	1	p2	(AT)6	12	154	165	AATTGAGAGTAGCCGACCCC
scaffold650500_17.	1	p2	(CT)7	14	205	218	TTCTCATCTTCAACCCCTGG
scaffold650504_17.	1	p2	(GA)8	16	84	99	GATGAAGTTAGGTGTTGGATGC
scaffold650545_10.	1	p2	(AT)6	12	999	1010	GCATGTATGCATATCCCTGG
scaffold650576_16.	1	p2	(TG)9	18	1313	1330	GGTCGGTAAAAAGTGGCAAA
scaffold650722_10.	1	p2	(CT)6	12	197	208	TCAGGGACTCATTTCCCAAC
scaffold650771_16.	1	p2	(TC)10	20	1385	1404	AGCAATCAGCTCCTGCAAAT
scaffold650789_16.	1	p2	(CA)6	12	547	558	CAATCGGCAGAAGTTTGCTA
scaffold650837_17.	1	p2	(TC)6	12	1440	1451	CGAATGAGCTCGATTTGGTT
scaffold650859_18.	1	p2	(TA)7	14	2820	2833	ACGGGAGACATTGCCATAAT
scaffold650917_18.	1	p2	(TA)11	22	219	240	TTTAACCGAACGAAAATGCC
scaffold650973_21.	1	p2	(AT)10	20	601	620	ATATGGGTTGTCGATCTCGC
scaffold651067_15.	1	p2	(GA)6	12	1592	1603	TATGAATTTTGGCCCTTGGA
scaffold651073_15.	1	p2	(TG)6	12	792	803	AACTTTTTGGTTGGCAAGGA
scaffold651126_14.	1	p2	(GT)7	14	247	260	TTGTGATTCGAAAATTGGCA
scaffold651215_14.	1	p2	(AT)6	12	335	346	TGTTTCCCCAATCCACATTT
scaffold651226_15.	1	p2	(AT)6	12	838	849	GACGACCTTGTCATCCAACA
scaffold651327_16.	1	p2	(CT)6	12	119	130	AGCATCTCTTGCTCTCTCATTG
scaffold651456_18.	1	p2	(CT)7	14	64	77	GGAGATGCACTTCACCCAAT
scaffold651487_16.	1	p2	(AG)8	16	153	168	AGAGGCATTTTGTTTGGAGC
scaffold651544_10.	1	p2	(AT)7	14	299	312	CAAAACCCGTTACATATCTTTGG
scaffold651567_16.	1	p2	(GA)6	12	1676	1687	AGAAGTGGTGGCGGATTATG
scaffold651585_11.	1	p2	(AT)9	18	568	585	ACTGCGATCACGAATTCACA
scaffold651605_14.	1	p2	(AT)8	16	754	769	GGAGGAAGAAGAAGAAAAGGC
scaffold651702_23.	1	p2	(AC)6	12	206	217	TTGGTGCTCCACTATATTGCC
scaffold651841_14.	1	p2	(CT)7	14	152	165	AGATGCCACTAACCCTTGAA
scaffold651923_16.	1	p2	(TC)7	14	991	1004	TACCAGTGAGAATCCTGGGC
scaffold651971_13.	1	p2	(TG)9	18	148	165	GTAACCGTCATGTTCCGGTC
scaffold652029_14.	1	p2	(CA)6	12	1217	1228	TATGAGATGTGGGGGAGAGG
scaffold652045_16.	1	p2	(AC)6	12	2569	2580	TCTTTCCCTCCCAATTCTGTT
scaffold652111_14.	1	p2	(CT)6	12	2134	2145	TCAACGGTGAGTTATGGCAA
scaffold652217_11.	1	p2	(CT)6	12	297	308	TGTTAGAAACAAACGCGGCT
scaffold652248_16.	1	p2	(AG)6	12	1675	1686	GCTTCAATTGAGCAGAAGCC
scaffold652291_10.	1	p2	(GT)8	16	284	299	CGCCCACAATTTGATACCTT
scaffold652307_16.	1	p2	(AG)7	14	515	528	ACAACGTGATACGCTGCAAG
scaffold652331_17.	1	p2	(GA)6	12	402	413	CGTTGCATTCGTCTTTCTCA
scaffold652343_14.	1	p2	(AT)13	26	45	70	ACCATATTTAAGGGTTATCACCTG
scaffold652370_10.	1	p2	(AT)6	12	365	376	CTAAACCTTATCCCCCACCG
scaffold652373_10.	1	p2	(AT)7	14	52	65	CAAAATTTGGAACCTGTCTTCA
scaffold652391_15.	1	p2	(GA)11	22	1206	1227	CCAAGAAAATCCCAGAAGCA
scaffold652468_18.	1	p2	(CT)6	12	311	322	ATATTCTCCCGAACCGACAC
scaffold652486_19.	1	p2	(TC)6	12	330	341	GGAAAATTCCGTTTTTGCCT
scaffold652495_14.	1	p2	(TC)6	12	125	136	CTCTTCATTCCCTCATCCCA

scaffold652583_12.	1	p2	(AG)12	24	48	71	TTCGAAACTGCATGAAAATCA
scaffold652588_17.	1	p2	(AT)8	16	102	117	CACGTGTAAGGGTTGAAGAAG
scaffold652651_15.	1	p2	(GA)6	12	3389	3400	AGCTGAAGAGCTGATGGCTT
scaffold652697_15.	1	p2	(TC)6	12	1215	1226	TGAACTGGCTACTGGCTGTC
scaffold652699_10.	1	p2	(AG)6	12	205	216	GTGTAGATCGCCATGGTGTG
scaffold652723_12.	1	p2	(AT)6	12	156	167	GCGTCGTGGATCAAGGTAAT
scaffold652760_13.	1	p2	(AT)7	14	207	220	ACGGTTACGGGCTGGTATTT
scaffold652798_14.	1	p2	(GA)8	16	1411	1426	GGACAGATCAGAAGCAAGGC
scaffold652882_15.	1	p2	(AT)7	14	1269	1282	AGAGCCACAAATTTTTCTTCAT
scaffold652932_14.	1	p2	(TA)6	12	54	65	TGTGTGTGTGGTTCTATGTTGTG
scaffold652944_16.	1	p2	(AT)7	14	620	633	TTTCAGGCCATAACTCGGTC
scaffold652958_17.	1	p2	(GA)7	14	3164	3177	TGCAGATCAATAAAATGGCG
scaffold653091_12.	1	p2	(AT)6	12	825	836	CGAAATCAAGCAACCAGTCA
scaffold653094_13.	1	p2	(CT)7	14	96	109	CACTCTGCTAGGGTTGGGAG
scaffold653108_15.	1	p2	(TA)7	14	154	167	TCAAGTTCAAATGCCAAGCTC
scaffold653141_13.	1	p2	(AG)7	14	556	569	TATTGCCCATCACTCCCATT
scaffold653167_16.	1	p2	(TC)10	20	322	341	CCCGATTTCTACACCCCTCT
scaffold653179_13.	1	p2	(TG)6	12	486	497	CGCTGCACCTTCAAGTAACA
scaffold653222_11.	1	p2	(GT)7	14	127	140	GACCACCCTAACGGATTTGA
scaffold653233_13.	1	p2	(CA)7	14	677	690	TACAGCAGATGCCTCGTTTG
scaffold653275_11.	1	p2	(AC)6	12	371	382	TTCTTATACCAAAACCTCCACTCA
scaffold653349_16.	1	p2	(TA)6	12	1292	1303	TGTTGGACCCCCTAACTCAA
scaffold653358_12.	1	p2	(GA)6	12	406	417	ATTTGCAAGCCTGTGGTAGG
scaffold653365_10.	1	p2	(TA)9	18	320	337	TCGACAAGAAGCAACACAGG
scaffold653389_16.	1	p2	(TC)12	24	2263	2286	AGAGGAAACCACCACCGTTA
scaffold653405_18.	1	p2	(AT)10	20	1468	1487	TGTGGCATATTGATGATGGTG
scaffold653457_16.	1	p2	(TA)8	16	301	316	TAGTTCCTCGCGGATCAATG
scaffold653581_10.	1	p2	(AT)12	24	583	606	TTCCCCCAGAGAAGTTGTTG
scaffold653582_20.	1	p2	(AT)7	14	208	221	CGCCCCAAAGTGCTTTAATA
scaffold653583_17.	1	p2	(CT)6	12	1396	1407	GTGACAAGCATTCCTCCACC
scaffold653589_14.	1	p2	(AT)6	12	675	686	GCCTTCCTTGGTAGTGGACA
scaffold653603_14.	1	p2	(CT)7	14	652	665	TGACACATAGCCCGATGAAA
scaffold653648_16.	1	p2	(AG)7	14	500	513	AAGCTGAAAAGTCGAGAAAATG
scaffold653667_15.	1	p2	(TC)6	12	557	568	TCGATGAAATAGGGTCGAGG
scaffold653677_10.	1	p2	(AT)8	16	157	172	AAGGAGATTGGGAGGAATGG
scaffold653707_13.	1	p2	(GA)6	12	210	221	ACAGAGCTGAGGAGAGCGAG
scaffold653777_20.	1	p2	(AT)7	14	207	220	AAATGGACCCACGAGATTTG
scaffold653827_14.	1	p2	(AG)6	12	529	540	TTTTTGAGGGAACAATTTGAGAA
scaffold653858_19.	1	p2	(TC)6	12	145	156	TGCAATCACCAATGAACTGA
scaffold653864_14.	1	p2	(AT)6	12	475	486	TTCAATCAGCCAATGGACAA
scaffold653886_17.	1	p2	(CT)6	12	477	488	GAAAATCGGACGTCGAAGAG
scaffold653964_14.	1	p2	(CT)7	14	278	291	CGACTCTCGTTGGCAGATTT
scaffold654011_14.	1	p2	(TA)12	24	114	137	GTTATCACCGGATCGCTACC
scaffold654038_18.	1	p2	(TA)7	14	917	930	CCTTGTCCATGATTTCTTTGG
scaffold654087_12.	1	p2	(AG)7	14	507	520	AAGGGAGGCTCTGCATCATA
scaffold654099_14.	1	p2	(AT)8	16	419	434	AATCCAAACCATCCATTCCA
scaffold654154_14.	1	p2	(AG)6	12	133	144	GCCCACAACTCTGGTTTCTC
scaffold654189_15.	1	p2	(TA)6	12	194	205	GAACTTATGGGAAGGAGAACCA
scaffold654212_14.	1	p2	(AT)6	12	1489	1500	CATAGCGAGGAAGTCCCAAG
scaffold654264_16.	1	p2	(CT)6	12	210	221	GCCTCAAGAATGATCCCAAG
scaffold654315_15.	1	p2	(TC)6	12	160	171	ATCATTACTGACCGCGAACC
scaffold654424_10.	1	p2	(GC)6	12	362	373	TCCAATACGAAGCCCAAATC
scaffold654430_16.	1	p2	(TC)6	12	2110	2121	AAAAAGGGATGAAAAGGGGA
scaffold654437_12.	1	p2	(TA)8	16	206	221	CTGTAGATCAGAGGGCCGAG
scaffold654461_16.	1	p2	(CA)10	20	409	428	GTGTCCGGAGCTATTTCTGC
scaffold654482_17.	1	p2	(AT)6	12	99	110	AGCACACAGGTGAAGACGATT
scaffold654560_16.	1	p2	(GA)6	12	2283	2294	ACTCCCTCCGTCCCATAAAC
scaffold654583_12.	1	p2	(AT)8	16	999	1014	GCATTTTCTCCATGTGGGAT

scaffold654586_17.	1	p2	(CA)8	16	206	221	GCCACTCCAAATTCTTTCCA
scaffold654602_15.	1	p2	(CT)6	12	3906	3917	TCCTCCCGAGGATAGTCTCA
scaffold654608_19.	1	p2	(TC)8	16	317	332	CTGCACTCTCCAGGAATCGT
scaffold654729_12.	1	p2	(AT)9	18	687	704	TGGGGCGCGTATTTAGATTA
scaffold654741_16.	1	p2	(CT)6	12	91	102	CCCACACTCTGCTTTCCATT
scaffold654749_13.	1	p2	(AT)6	12	675	686	TATGCATGGCATGAGTGTGA
scaffold654765_17.	1	p2	(CA)6	12	911	922	ACCGGAGTGTGAAGACGAAC
scaffold654787_15.	1	p2	(AT)6	12	973	984	AATCTGACACGTCGGGAACT
scaffold654839_14.	1	p2	(AT)7	14	1495	1508	TCAGCAATGAGTTGCTCCAT
scaffold654908_17.	1	p2	(CT)6	12	354	365	GGTTGTCGTCTCTTGCCACT
scaffold654938_10.	1	p2	(TA)7	14	160	173	ATGTTCGGATTTTGAAACGG
scaffold654952_17.	1	p2	(GA)8	16	2995	3010	CCTTACTCGAACAGCCCAAC
scaffold654973_11.	1	p2	(TA)11	22	42	63	GCGTTTTGACAATATTTAGTGTTTTG
scaffold655030_18.	1	p2	(TC)6	12	469	480	AATTTCTCACTCTCCGCTGC
scaffold655058_14.	1	p2	(AT)6	12	1404	1415	GAGAGAGAGGTTGTGGCCTG
scaffold655065_10.	1	p2	(GT)9	18	43	60	AAGAGTGTGTGTGTGGGTGTG
scaffold655080_16.	1	p2	(TA)6	12	210	221	CTACGTGAGGCGGTGATTTT
scaffold655084_15.	1	p2	(AG)6	12	55	66	TCACAATACAACTGCCGAGC
scaffold655203_14.	1	p2	(TA)7	14	315	328	TTGACAACCAGGTCACGAAA
scaffold655228_14.	1	p2	(AG)11	22	1099	1120	GTTTTGTTTTCGTTCCCTCG
scaffold655241_14.	1	p2	(TA)10	20	1459	1478	GGACGGCAACAGGAGTTACA
scaffold655260_10.	1	p2	(TA)7	14	240	253	AGGTGGCAACATAATCAGCC
scaffold655303_15.	1	p2	(GA)9	18	3025	3042	GCTCTGCATTAGCAGCTTCC
scaffold655334_17.	1	p2	(TG)8	16	1681	1696	GATTTGGTTGGTCAAGTGGG
scaffold655336_16.	1	p2	(TG)7	14	209	222	TCACATTCACACCTAACGCAA
scaffold655406_16.	1	p2	(AT)6	12	211	222	CTTACCCACTCCACCACCTG
scaffold655500_10.	1	p2	(GA)7	14	208	221	TAAAGGCCGCATCCTATCAC
scaffold655618_13.	1	p2	(TA)10	20	42	61	CGGTTATCACCGGATCGC
scaffold655723_20.	1	p2	(TA)7	14	209	222	CCAAGAATCAGTTAAGCCCG
scaffold655804_13.	1	p2	(TA)10	20	2607	2626	AGGCCAAAAATGAACCACAC
scaffold655946_15.	1	p2	(GA)8	16	1398	1413	TGCTAGGAAGCTGAGGAAGC
scaffold655992_14.	1	p2	(GC)7	14	547	560	CGAGTCGGCAGACCTAAGAC
scaffold656032_14.	1	p2	(CT)7	14	646	659	GCCAGTGTCCATCCATTTCT
scaffold656049_16.	1	p2	(GA)6	12	752	763	GGAGGCATGGAAGAGAATGA
scaffold656095_14.	1	p2	(TA)6	12	304	315	AGTAGAAGCATTTCGTCGGG
scaffold656176_13.	1	p2	(TA)6	12	1325	1336	TTGACATGGTGTAGTCATCAAGG
scaffold656344_14.	1	p2	(CA)6	12	443	454	GTGATTGGCTGGAAGAGCAC
scaffold656386_15.	1	p2	(CA)6	12	2195	2206	TGACGGAACACGTCAGATTT
scaffold656448_18.	1	p2	(TA)6	12	596	607	CATACTTCCACCGCCTTCAT
scaffold656456_16.	1	p2	(CA)6	12	478	489	CAAGCACACCTACACGCACT
scaffold656509_12.	1	p2	(TA)7	14	1033	1046	TTCAGGGAATCTTCGAATAAAAA
scaffold656749_11.	1	p2	(AG)7	14	394	407	TGAGGCTTGTGGTTCAGGTT
scaffold656932_15.	1	p2	(AT)7	14	396	409	GGTTCGGGCATAATGACATC
scaffold656980_13.	1	p2	(AT)8	16	586	601	ATTTGGCCCTTGCAAGTATG
scaffold656991_12.	1	p2	(GA)6	12	657	668	AAAACCAAGGATATCGGCCT
scaffold657127_15.	1	p2	(TC)7	14	211	224	TCTCCCCCGGTAAACAGAAT
scaffold657140_16.	1	p2	(TA)7	14	79	92	ATGTATGGCCCAGATTGGTT
scaffold657167_16.	1	p2	(GC)6	12	180	191	CCCAATATCAGGTAAGGGCA
scaffold657174_10.	1	p2	(AT)7	14	210	223	TGTTGGGATGAAATGTGAGG
scaffold657226_15.	1	p2	(TG)6	12	357	368	GGATATGAAGTGGGAGCCAA
scaffold657239_12.	1	p2	(AT)6	12	587	598	TGCCACCAAAATCAAATCCT
scaffold657300_13.	1	p2	(AT)6	12	265	276	TCAAACCCTGTCATTCACCA
scaffold657457_15.	1	p2	(TA)7	14	123	136	CCCAATTTGCCCTTATATGC
scaffold657464_17.	1	p2	(TA)8	16	381	396	AAAATCAATTCGCGATCACA
scaffold657480_14.	1	p2	(TC)7	14	655	668	TGCTGCAAGCTTAAGAAACAA
scaffold657509_20.	1	p2	(AC)6	12	185	196	TCTTTTTCGAACCGAACCAC
scaffold657551_13.	1	p2	(TC)6	12	97	108	GGGACTGCTGGATAATCCCT
scaffold657567_15.	1	p2	(AT)8	16	176	191	ACTAAACTAGACCGGGCCGT

scaffold657618_15.	1	p2	(TA)6	12	1078	1089	TGATTCTGGGTTTCCAGTCC
scaffold657644_15.	1	p2	(TA)8	16	2350	2365	AACACCAACATGCTGACGAA
scaffold657865_13.	1	p2	(AG)7	14	111	124	AACCTCTCGTGCTCCAACAT
scaffold657937_10.	1	p2	(AT)6	12	303	314	GAATCGTCCCAAATTCCCTT
scaffold657960_15.	1	p2	(TA)13	26	652	677	GTTTGGCCTCACTGGTGATT
scaffold657986_10.	1	p2	(TC)8	16	684	699	TCAAAATTGGCACGATACGA
scaffold658006_15.	1	p2	(AT)7	14	431	444	TCACAACCAAAATCTTGCTCA
scaffold658023_12.	1	p2	(AT)6	12	1149	1160	ACCATTCAACGCAACCATTT
scaffold658056_12.	1	p2	(AG)9	18	1155	1172	ATGCTGCTGTTTTCCATTCC
scaffold658065_10.	1	p2	(TA)8	16	94	109	AAATCATTGCTTGAGCTTGAA
scaffold658104_14.	1	p2	(TA)8	16	393	408	TCAATCCAAACTCTATTTTATCCGA
scaffold658132_19.	1	p2	(TG)9	18	68	85	AGACCTGTCACCGTTTTGCT
scaffold658174_11.	1	p2	(TA)8	16	67	82	TTTTAGTTATCACAGGATCACCC
scaffold658195_16.	1	p2	(GA)10	20	3944	3963	ACTTGGCCCACAAGAACAAG
scaffold658213_16.	1	p2	(AT)6	12	213	224	ACGGCCAATATTTGCTCCTA
scaffold658298_15.	1	p2	(AG)6	12	1011	1022	GTGCTAACGATTTTTCCCCA
scaffold658309_17.	1	p2	(CT)6	12	241	252	CACCGATGTTGAGGCCTACT
scaffold658334_14.	1	p2	(TA)9	18	325	342	CATGGACGAAAATAGCCTCC
scaffold658337_15.	1	p2	(CT)6	12	213	224	GTTTGCTGCTGCTGTTGTGT
scaffold658430_15.	1	p2	(TA)6	12	2110	2121	CCATGCGCGGTCTAAATAAT
scaffold658441_17.	1	p2	(TA)9	18	39	56	TTTAGTGTTTTGACATGATTACTCG
scaffold658444_13.	1	p2	(TC)6	12	96	107	GGACCTCTGGACAATCCCTT
scaffold658485_10.	1	p2	(TG)8	16	153	168	CAGTGTACAACCCCGGAATC
scaffold658489_14.	1	p2	(TA)10	20	63	82	CTACAACATCATGCAAATCAATAGT
scaffold658580_16.	1	p2	(AG)8	16	1536	1551	TATGGATTTAACTCCCCGCA
scaffold658666_18.	1	p2	(AT)8	16	320	335	CAAGAACGAGAGGGTCAAGG
scaffold658747_14.	1	p2	(AT)6	12	154	165	CAGCTCCAAGACATTCCACA
scaffold658755_11.	1	p2	(TA)9	18	384	401	GACAAATGTGGCGTATGCTG
scaffold659005_13.	1	p2	(AT)6	12	430	441	GCATTCCTTTCCCATCTTCA
scaffold659011_13.	1	p2	(AT)6	12	293	304	TGCTCTAATATTCGGCCGTT
scaffold659016_17.	1	p2	(TA)8	16	243	258	TTCGGAGCATGAATTAAGTGG
scaffold659045_14.	1	p2	(AC)6	12	49	60	ATTGGCATATGTCCCCAAGA
scaffold659106_11.	1	p2	(AT)9	18	465	482	TGACCCAGCCTTTTTAGGATT
scaffold659244_13.	1	p2	(CT)7	14	1422	1435	ATCCAACGGATGAAAAGCTG
scaffold659245_11.	1	p2	(TA)10	20	577	596	TTGCAAAAGAAATTGCTTAGCTT
scaffold659261_15.	1	p2	(TC)6	12	882	893	TTTGTGCCTCTGATCCCAAT
scaffold659327_14.	1	p2	(AG)8	16	160	175	TTGCAGCTGGAAATGAAGAA
scaffold659357_15.	1	p2	(TC)7	14	2678	2691	CAACCTTTGAAGACTCCGTCA
scaffold659374_10.	1	p2	(TA)8	16	58	73	ATGGATGGAGTCAAAGCCAA
scaffold659386_13.	1	p2	(TA)7	14	1104	1117	CGAAAATTCGGATCGGCTA
scaffold659439_17.	1	p2	(TG)7	14	212	225	GGTTAGGAATGCATTAAATACCAA
scaffold659440_14.	1	p2	(AT)7	14	1510	1523	ACCATACGTAACGCCCAAAT
scaffold659527_13.	1	p2	(AT)6	12	215	226	TGCATTCATCAATTTTTGGAG
scaffold659558_17.	1	p2	(TC)8	16	210	225	CACTCTCTCACCTTCCATCCA
scaffold659629_16.	1	p2	(CT)6	12	207	218	AGCCTCCCTCTCTTGCTCTC
scaffold659662_17.	1	p2	(TA)6	12	193	204	CGAAGAGCACACACTTTTGG
scaffold659736_14.	1	p2	(TA)7	14	416	429	GATCTCGAGCTCAAATCCCA
scaffold659753_12.	1	p2	(TC)6	12	203	214	AAAGTTTTCCGCATGAATGG
scaffold659805_15.	1	p2	(GT)8	16	1118	1133	AAGGCACTCTGGGCTTGTAA
scaffold659937_10.	1	p2	(TG)8	16	762	777	TCTGTTTCCCCACACAAACA
scaffold660036_15.	1	p2	(CT)7	14	168	181	GTGGGTCGTAGCCTGACTGT
scaffold660056_18.	1	p2	(AG)6	12	2900	2911	TTAGTGCCGAAATCGTAGGG
scaffold660074_12.	1	p2	(AT)8	16	467	482	AAATTAATCAACGATGGGCG
scaffold660140_19.	1	p2	(TA)6	12	496	507	AGATCGACGGTCCGAAATTA
scaffold660174_16.	1	p2	(TA)7	14	335	348	TCAGAGTGGCCATAGCAGAA
scaffold660202_12.	1	p2	(AT)10	20	494	513	CCGAAAATCTAAAGCCCACA
scaffold660241_14.	1	p2	(AC)6	12	2974	2985	GTTCGATGGACCTCGATCAT
scaffold660258_15.	1	p2	(TC)6	12	1240	1251	AGCAGAATGCAGTTGTTGGA

scaffold660285_15.	1	p2	(TA)6	12	80	91	GGAAATAAGGAGGTGTTATGATGTG
scaffold660330_14.	1	p2	(AT)12	24	1748	1771	ATGAACTGCTAGAACGTGCG
scaffold660380_11.	1	p2	(TA)6	12	59	70	TAGGCCGGTCTTTTAGCCTT
scaffold660509_14.	1	p2	(CT)6	12	172	183	TTCAGCATTGTAAGGGGGAC
scaffold660520_17.	1	p2	(TA)6	12	89	100	TTGCACCAATAAAATTTGGC
scaffold660551_15.	1	p2	(TC)9	18	5572	5589	ACAGGGGATTGGTAATGCAA
scaffold660572_14.	1	p2	(TA)6	12	341	352	ATTCCGAATATCAAAGGCCC
scaffold660599_15.	1	p2	(CT)8	16	772	787	GTCACACAAGCTTGACTCGG
scaffold660640_10.	1	p2	(TA)6	12	530	541	CGTAAATTGTTGCAACCGAG
scaffold660778_13.	1	p2	(TG)6	12	644	655	GGTTTTGGATTTTGAGGGGT
scaffold660792_10.	1	p2	(TA)8	16	141	156	AGAGCCCTTCAATGGACAAT
scaffold660953_19.	1	p2	(AT)8	16	163	178	AACGGTACGTTCGGATTTTG
scaffold660956_11.	1	p2	(CA)6	12	692	703	GCCCAACTTATTTGGATATTTGA
scaffold660967_11.	1	p2	(AT)10	20	315	334	CCCAGTTAAGAGCGTTGGAG
scaffold660979_10.	1	p2	(AT)10	20	513	532	CACTTCTCGGAACGAACAAA
scaffold661005_11.	1	p2	(TA)7	14	312	325	TGCTCGTTTTTAACCCGATT
scaffold661093_10.	1	p2	(AC)8	16	525	540	GGGCTCTATGGATGTGGCTA
scaffold661135_14.	1	p2	(AT)9	18	1035	1052	CGTGTCATCCAAACAAATGC
scaffold661140_14.	1	p2	(TC)6	12	521	532	ACCAGAGTCCACCACCACTC
scaffold661177_12.	1	p2	(TA)7	14	338	351	TTGGTCTGATCTGTCCTACCC
scaffold661193_10.	1	p2	(TA)7	14	421	434	ACCTTCCTTTCCGTTCCTGT
scaffold661212_18.	1	p2	(AT)7	14	371	384	CTCCCAAATTTAGCCGATTG
scaffold661257_13.	1	p2	(TA)10	20	417	436	GCCACACATGTCAGAAATGAA
scaffold661277_15.	1	p2	(TC)8	16	1647	1662	ATTTCTGCTCACTGCCTCGT
scaffold661349_15.	1	p2	(CT)6	12	2951	2962	CCAAATTAAGGTCATATTGCACA
scaffold661367_14.	1	p2	(CT)8	16	1011	1026	GCGAAGTCAAACCACCAGAT
scaffold661368_13.	1	p2	(GA)7	14	942	955	CTTCGCCCTTGGATGAAATA
scaffold661496_19.	1	p2	(AT)9	18	640	657	CGAATAGTAGCTTCTGCGGG
scaffold661542_12.	1	p2	(TC)8	16	429	444	ACTTTTGCGCACACAGTCAC
scaffold661555_16.	1	p2	(TC)9	18	317	334	TTCAAATCCCACAAACGTCA
scaffold661572_12.	1	p2	(TA)10	20	142	161	ACGCCCCAGATTGTTTCTTA
scaffold661591_15.	1	p2	(GT)9	18	2562	2579	CACTGGTCCGAGTTCTCCAT
scaffold661625_15.	1	p2	(TA)6	12	217	228	TGAGGAAGTTGATTTGTTGGG
scaffold661702_11.	1	p2	(CT)7	14	215	228	CGCCGCTTTTTACGATACTT
scaffold661748_17.	1	p2	(AT)6	12	164	175	CGAACTAAAGAAATAGGGACGC
scaffold661831_17.	1	p2	(TC)9	18	3161	3178	CTGATAGGCCAACTGTGCAA
scaffold661849_18.	1	p2	(AG)6	12	427	438	TCATGGGGAATTCAAAGAGG
scaffold661862_13.	1	p2	(GC)8	16	333	348	ACGTGTGCTGACTTGTCCAC
scaffold661917_17.	1	p2	(AG)8	16	213	228	TCGACAAAGAAATCATCGGA
scaffold661993_10.	1	p2	(TA)6	12	65	76	GGTTATCACCTGATTTTCTCCC
scaffold662039_16.	1	p2	(AC)8	16	212	227	GCAAATATGATATGCCTGCAA
scaffold662040_15.	1	p2	(AT)7	14	214	227	CAAGGGTAATCCCAAACCTT
scaffold662046_17.	1	p2	(TA)7	14	188	201	AACCACAAAAAGGATAAGTGGG
scaffold662102_10.	1	p2	(TA)11	22	406	427	TGAAACGGACAACAAACGAA
scaffold662152_15.	1	p2	(GA)7	14	5827	5840	TTGCTCTTGCTCCAACACAC
scaffold662159_16.	1	p2	(TG)8	16	1100	1115	CGTTTTCAGACAAGCCCATT
scaffold662316_11.	1	p2	(AG)11	22	594	615	GCTGGCAGCTTCAACAGATA
scaffold662321_18.	1	p2	(AT)6	12	66	77	GGTTTTGATGGTTGTGATTTGTT
scaffold662371_11.	1	p2	(AG)8	16	51	66	AACCTTGGAGTCCCTTCTCC
scaffold662396_13.	1	p2	(TA)11	22	817	838	TGGACCCCCGATTTATAGGT
scaffold662403_14.	1	p2	(TA)7	14	535	548	CCGAAACGTGAATACCCCTA
scaffold662426_14.	1	p2	(TC)8	16	845	860	ATGGCTGTTGGCTTAATTGG
scaffold662496_17.	1	p2	(AG)7	14	994	1007	GCTTTACACTCCCCTCCTCC
scaffold662571_14.	1	p2	(GT)6	12	217	228	CGCGTTTAGAAAAGGGAAGA
scaffold662579_14.	1	p2	(TA)6	12	76	87	TTTATCGTGGTGCATGTTTTT
scaffold662648_16.	1	p2	(AC)6	12	3585	3596	AACTCCCAAGTTTGCGTTTG
scaffold662656_14.	1	p2	(AT)9	18	525	542	TGTGAATTTTCAGATTGTGGTTTT
scaffold662674_14.	1	p2	(AG)6	12	454	465	CCTTCTCAAAGACCGTCTGC

scaffold662838_14.	1	p2	(GT)6	12	282	293	ACATTAAATGCAGCCGCTCT
scaffold662895_16.	1	p2	(TC)6	12	330	341	GCAAATGGTTCACATGGTTG
scaffold662904_11.	1	p2	(AT)10	20	259	278	ACCTCGGCACATTTACCAAA
scaffold662955_14.	1	p2	(AT)8	16	580	595	CAGTTTTGCTATCGTTTATCTTCG
scaffold662973_16.	1	p2	(CT)7	14	283	296	ATTATTTTGCGGTTCCAACG
scaffold662997_17.	1	p2	(AT)7	14	310	323	TCCAGCCCTAATATTGCACA
scaffold663009_14.	1	p2	(GT)7	14	1382	1395	AAACAGGGGTACAAGGGTGA
scaffold663218_17.	1	p2	(AG)6	12	2039	2050	TTTTAACAATGCTGCACTCCC
scaffold663350_18.	1	p2	(TG)10	20	38	57	TGGTTTTGAAAGTGTGATCTGG
scaffold663359_11.	1	p2	(TA)7	14	351	364	AACGGGAGAATCGTGTCATC
scaffold663399_12.	1	p2	(AT)9	18	64	81	TGGATTATCCTGCGGTCAGT
scaffold663403_13.	1	p2	(TG)6	12	484	495	TCCTCAAGATTGTGCAACCA
scaffold663406_17.	1	p2	(TG)7	14	3357	3370	GGCCATCTATCCCTATCCGT
scaffold663423_10.	1	p2	(TC)6	12	347	358	GAGACGCGCAAAAGTAGGAC
scaffold663438_15.	1	p2	(TC)7	14	3286	3299	TGTCCTCCTTTCCTCTGCAT
scaffold663450_18.	1	p2	(GA)7	14	162	175	AATGATAAATCGCGGGTTTG
scaffold663537_13.	1	p2	(CA)6	12	1026	1037	CGGTGTAAAGGAGGGGTGTA
scaffold663564_13.	1	p2	(AG)8	16	91	106	ACTTCTTCCCAAGGCACTCA
scaffold663582_10.	1	p2	(AT)6	12	265	276	TGAATCAATTTAACATCATGCAAT
scaffold663786_15.	1	p2	(AG)11	22	114	135	TGTGAGAGAGTGCGTGTGTG
scaffold663797_18.	1	p2	(AG)8	16	983	998	TTCCTTGCACTGGGAAAAAG
scaffold663905_10.	1	p2	(AG)8	16	218	233	ACATCAACCGTTCACCACAA
scaffold663921_10.	1	p2	(AG)7	14	286	299	GTAGAGGGAGTTGGGGGTGT
scaffold663933_15.	1	p2	(TA)6	12	219	230	TTATTGAGCGCCATTGATGA
scaffold663948_12.	1	p2	(TA)7	14	54	67	ACTTTTAAGGATCAAGGATATTCG
scaffold664014_15.	1	p2	(TA)7	14	217	230	TTGGTCTAAATTGCCCCGTA
scaffold664105_11.	1	p2	(AG)7	14	345	358	AGGGGTGGAGGTAAGAGGAA
scaffold664154_13.	1	p2	(CT)13	26	809	834	ATCCACGCTGCAGAGAAACT
scaffold664159_12.	1	p2	(TC)6	12	531	542	TGACCAATAGGATGTTGCCA
scaffold664160_14.	1	p2	(CA)10	20	6773	6792	CCATGAATGGAAAATGGAGG
scaffold664189_13.	1	p2	(TA)7	14	889	902	AAAAGTCACGCTTGAACCAT
scaffold664247_13.	1	p2	(AG)7	14	1170	1183	CCAATGGGTGACCAGTCTTT
scaffold664315_13.	1	p2	(AT)6	12	169	180	GTTCGAACCGAACCATGAAC
scaffold664326_11.	1	p2	(TC)7	14	1407	1420	ATTGCCATTACCATTCCCAA
scaffold664330_16.	1	p2	(TG)6	12	734	745	GATTTTTGGAGGGTTCTTGC
scaffold664383_17.	1	p2	(TG)8	16	35	50	CAGGAGACGCTCATTCATCA
scaffold664386_14.	1	p2	(AT)9	18	198	215	CATCCACTCTGAAGTTTGAACAG
scaffold664387_15.	1	p2	(AT)6	12	1567	1578	GGACCAGGATTAGCCCAACT
scaffold664457_13.	1	p2	(AT)8	16	1576	1591	TCATAAGGCCCACTTCAACC
scaffold664496_16.	1	p2	(GA)7	14	725	738	GGGGTTTCCCTTACCTTTTG
scaffold664502_15.	1	p2	(AG)8	16	5903	5918	TTTTCGGGAATCTTTCATGC
scaffold664615_11.	1	p2	(AG)8	16	280	295	CAAAAAGGTCCCAGGTTCAA
scaffold664631_16.	1	p2	(AT)9	18	214	231	GGGATTGAACGCACAAAACT
scaffold664766_20.	1	p2	(AT)6	12	1492	1503	AAATGAACGTAGCAAAGGGG
scaffold664869_14.	1	p2	(TC)6	12	46	57	TCTCTCTATCTTTTTGGTTGGTGA
scaffold664897_18.	1	p2	(GA)6	12	154	165	CGGACCGTGAAAGCTCTAAG
scaffold664907_17.	1	p2	(AG)6	12	359	370	ACTAATGGATATGCGGCGAG
scaffold664910_16.	1	p2	(GA)6	12	1241	1252	CAGATTAGGAGATTTGGGCG
scaffold664920_18.	1	p2	(TA)8	16	94	109	GCCGGATTTTGTCCCTATTT
scaffold664926_14.	1	p2	(CT)6	12	219	230	TTTGTGTCCCTGAAAGAGGTG
scaffold664948_14.	1	p2	(AT)8	16	215	230	CACGACAAGAATCCAGCTCA
scaffold665028_13.	1	p2	(AT)8	16	1230	1245	GCCGAGAAGAGGAAGTGTTG
scaffold665075_14.	1	p2	(TA)7	14	1305	1318	AGATTACGAGAAGGAGGCGG
scaffold665117_15.	1	p2	(TA)7	14	366	379	TGACACGTGGCGTAATCTTC
scaffold665132_10.	1	p2	(TC)8	16	167	182	AGAAGACACTTGGGCCTGAA
scaffold665149_15.	1	p2	(CT)8	16	2361	2376	TGGTTCGCATTTCAATCTCA
scaffold665165_10.	1	p2	(TA)8	16	278	293	AAAGGCTGCATGAGAGAGGA
scaffold665219_10.	1	p2	(AC)6	12	262	273	AATGATCCGTTTTTGCCAAG

scaffold665336_18.	1	p2	(GA)8	16	981	996	TGCTCGAAAGTTGCAACAGA
scaffold665356_15.	1	p2	(AC)7	14	392	405	TCCAGCCCATTCTTATTTGG
scaffold665372_14.	1	p2	(CT)6	12	1058	1069	GACGTTGAAAGGAGAGCGAC
scaffold665397_11.	1	p2	(TA)9	18	331	348	TATCCAGCAGCAACATCTCG
scaffold665399_11.	1	p2	(AT)7	14	116	129	AAGGAGGTGTTATGAAGGGAG
scaffold665474_15.	1	p2	(CT)8	16	588	603	TGAAATCCTTTTCGATTCCG
scaffold665507_14.	1	p2	(TC)9	18	819	836	CCAAACCCAGTACCAGCATT
scaffold665527_17.	1	p2	(GA)6	12	2165	2176	CGTCAATCCAGAAGCACTGA
scaffold665568_16.	1	p2	(AG)7	14	73	86	ACGTGGGTTTACTCAGAGCG
scaffold665596_16.	1	p2	(AC)7	14	715	728	CGCAGTAATAGCATGCCAAA
scaffold665636_14.	1	p2	(TC)6	12	293	304	CCTTTCTTCCGACTGCAAAA
scaffold665696_16.	1	p2	(AG)9	18	341	358	CCACCACTCGAAATATGGCT
scaffold665728_15.	1	p2	(GA)6	12	1929	1940	ACCGTGGCATCGAAGATTAG
scaffold665858_15.	1	p2	(AT)6	12	220	231	AAACCAATGCGAGGTAGGTG
scaffold665866_12.	1	p2	(TA)8	16	49	64	TTTTTAAGTTATCGGTGATGACACA
scaffold665915_18.	1	p2	(GA)9	18	4226	4243	GGTCATGGACGATAGCTGGT
scaffold665930_15.	1	p2	(TA)7	14	178	191	CACCCCGACGTAGATTGAGT
scaffold665969_11.	1	p2	(TA)10	20	44	63	GCGTTTTGATGATATATATGTGTTTTG
scaffold665982_15.	1	p2	(CT)8	16	211	226	GTATCGCTGCAAAAAGCACA
scaffold666110_12.	1	p2	(AT)7	14	707	720	TCCACCCAAAAACCGAATAA
scaffold666116_11.	1	p2	(AT)6	12	157	168	CTTTGTGAATGAAATGGTTGCT
scaffold666151_12.	1	p2	(AG)6	12	221	232	CACCCTCCCACACATCAAAT
scaffold666222_12.	1	p2	(TC)6	12	304	315	TTTCCTACGACAACCCTTCG
scaffold666249_11.	1	p2	(GT)6	12	459	470	ACTCCTCGGGACGGTTTACT
scaffold666250_15.	1	p2	(CA)6	12	2556	2567	TGCTCATGCAGGATTAGTCG
scaffold666291_15.	1	p2	(TC)6	12	924	935	AGCTCCGACTTTGTTGTGGT
scaffold666402_15.	1	p2	(GA)9	18	440	457	TGCGACACCGATTAATACCA
scaffold666450_10.	1	p2	(AT)6	12	106	117	TGGGTTTTGTAATTTGACCCA
scaffold666501_10.	1	p2	(TA)11	22	317	338	TAACCCCGAATGCTGTTAGC
scaffold666646_13.	1	p2	(AG)6	12	722	733	CTCAGCTCAGGGTGGAGAAA
scaffold666658_15.	1	p2	(AT)6	12	307	318	CATAAACCCTCACTCCGAGC
scaffold666672_11.	1	p2	(TA)8	16	573	588	GGCCAACTGAAGTTGATCGT
scaffold666700_15.	1	p2	(TA)7	14	241	254	AAAATGCCCTTGTATGCTGC
scaffold666709_17.	1	p2	(AC)6	12	1685	1696	AGCGAAAGACAGAGCAAAGC
scaffold666755_12.	1	p2	(AT)9	18	370	387	AGTTTGGGGGAGGAGAAAGA
scaffold666761_13.	1	p2	(CT)8	16	378	393	ATAAAAATGACACTCGGCGG
scaffold666816_16.	1	p2	(TA)6	12	257	268	GGCAACCAATTTTCTCTCTGC
scaffold666849_19.	1	p2	(AG)6	12	221	232	GGCAAACACAAAGACACGAA
scaffold666869_12.	1	p2	(TA)7	14	495	508	CCCTTATAAATGCGCTTGAA
scaffold666887_13.	1	p2	(AT)10	20	3071	3090	TCTTTTGCGCTTTCGAGAAT
scaffold666913_14.	1	p2	(CA)6	12	257	268	AATGCCTTTTGTTTGCATCC
scaffold667017_13.	1	p2	(AG)7	14	764	777	GTCCTGCCCTCTCATAGCTG
scaffold667029_17.	1	p2	(CT)7	14	2632	2645	TTCTAGTCCACCCGACCAAG
scaffold667096_11.	1	p2	(AG)7	14	110	123	CGTCCACAGTGGTTTGAGAG
scaffold667118_10.	1	p2	(AT)8	16	582	597	GTCGATACGGCATGACACAC
scaffold667119_17.	1	p2	(TC)6	12	3364	3375	AAATCTGGTGGCGATCAAAG
scaffold667137_16.	1	p2	(AT)7	14	581	594	TCGGTCGTGGGATTTTTATC
scaffold667278_14.	1	p2	(TA)9	18	217	234	CGGGTCGAGAGAGGAGAAAT
scaffold667292_14.	1	p2	(TA)8	16	49	64	TATGGGTTATCACCGGATCG
scaffold667335_14.	1	p2	(CA)7	14	1122	1135	CAACGAAAAGAGAGCCTTGC
scaffold667425_16.	1	p2	(AT)7	14	928	941	AAATCAATGGCATCCCACAT
scaffold667434_14.	1	p2	(AT)7	14	894	907	TGGTGCGTGAAGGAGATATG
scaffold667614_13.	1	p2	(CT)6	12	30	41	CTCTATAGCAAGATCTCACGCAG
scaffold667616_20.	1	p2	(GA)6	12	203	214	TGGAGGTGAAGAGAGGGAGA
scaffold667687_12.	1	p2	(TA)6	12	160	171	ATCATCCAACACCCATCCAT
scaffold667728_10.	1	p2	(AC)7	14	103	116	CGCACACACTCTCTGATTCAC
scaffold667853_14.	1	p2	(AG)8	16	395	410	GCGTGGAATTCACCTCAAAT
scaffold667872_12.	1	p2	(AG)6	12	407	418	TCCGGATTCGAATACTCACC

scaffold667876_13.	1	p2	(GA)7	14	508	521	AGTACGGATTGATGGAACGG
scaffold667889_12.	1	p2	(TC)7	14	782	795	TTACGCCCTCTCCATTTCAC
scaffold667971_14.	1	p2	(TC)7	14	49	62	CGTAATGTTTTGGTGGGAAGA
scaffold668030_12.	1	p2	(TA)6	12	69	80	ACACAACTTAGGTGTTCTCATTTG
scaffold668036_14.	1	p2	(TA)6	12	377	388	CTTTCGTCAAACCCTGCTTC
scaffold668050_15.	1	p2	(GT)6	12	690	701	TGAGCGCTATCATGGAGTTG
scaffold668104_13.	1	p2	(TA)8	16	298	313	TGATTGCACCTGAATAAGCC
scaffold668212_15.	1	p2	(AG)7	14	1115	1128	TGGATTATAGATGCACGAGGAA
scaffold668367_12.	1	p2	(TC)6	12	88	99	AAACTTAGGGACCGCTGGAT
scaffold668371_15.	1	p2	(TA)6	12	884	895	GAAATTTGTCGACCACACCA
scaffold668397_11.	1	p2	(AT)9	18	719	736	CATGGACGAAAATAGCCTCA
scaffold668449_11.	1	p2	(AC)9	18	218	235	TCAATCATGACTGCTTTGGTTC
scaffold668465_16.	1	p2	(AC)7	14	3748	3761	CCCCCAAGATATTGCAACTG
scaffold668495_19.	1	p2	(AG)7	14	661	674	AGCACTCGTGTGGGATTTTC
scaffold668537_16.	1	p2	(CT)7	14	417	430	AGGCAATCTAGGCGACAATC
scaffold668553_15.	1	p2	(TG)6	12	171	182	TCGTGTTCTTCACTCATTCCA
scaffold668562_16.	1	p2	(TC)7	14	2757	2770	AAAAAGTGAGGAGCGGTGAA
scaffold668623_13.	1	p2	(AT)6	12	814	825	ACACCGATCCGTTCCTACAC
scaffold668765_17.	1	p2	(TC)6	12	238	249	CCAGCCATTCAAATCAACCT
scaffold668779_12.	1	p2	(TC)7	14	165	178	TGATTAGGCAAGCAGTGGTG
scaffold668788_16.	1	p2	(TG)7	14	2506	2519	CCCTCCGCACCTATTATCAA
scaffold668878_11.	1	p2	(AT)8	16	141	156	TAAGGCAAGCAGTAAACGCC
scaffold668909_13.	1	p2	(AT)6	12	2135	2146	GCAAGGAATCTAACCTGCGA
scaffold669015_10.	1	p2	(GT)6	12	526	537	GTTGGCATTCAAATCAACCA
scaffold669048_16.	1	p2	(TA)6	12	200	211	TCGGGAAGAATATGAGTGCC
scaffold669060_16.	1	p2	(TA)6	12	2048	2059	TCACAATGGCAACTCAAAGC
scaffold669075_17.	1	p2	(CT)9	18	3521	3538	CAACGGTCTACTCAAACGGC
scaffold669255_14.	1	p2	(AG)6	12	437	448	GCCTTTCTTCATGCTTTCCA
scaffold669313_13.	1	p2	(TA)6	12	570	581	TTCGTGAATGACTACCCACG
scaffold669325_15.	1	p2	(CA)8	16	1570	1585	GCACAACGTATATTCCCACTTTC
scaffold669364_10.	1	p2	(TA)7	14	473	486	AAGGCCAACTCAAAAGGGAG
scaffold669386_15.	1	p2	(AC)7	14	3581	3594	TCCATCCCCTGAAATAGCTG
scaffold669405_16.	1	p2	(TG)6	12	509	520	TGCACATTTAGGCTCTGACG
scaffold669471_16.	1	p2	(AC)6	12	214	225	CAACGTTGCTGCGTATGATT
scaffold669491_15.	1	p2	(AT)8	16	220	235	TACCGTGATTTCCTTCCACC
scaffold669505_12.	1	p2	(CT)6	12	923	934	GCATTCTATCTCCTCTCCGC
scaffold669507_13.	1	p2	(TA)8	16	316	331	CATCAACAACACCATCACCC
scaffold669749_10.	1	p2	(TA)7	14	301	314	GACAGCATACGCGCTCATTA
scaffold669837_11.	1	p2	(AT)8	16	173	188	GTTCGAACTGTTGCATGTGG
scaffold669859_15.	1	p2	(TA)6	12	225	236	ACAAAAATGCCCTCGTATGC
scaffold669901_16.	1	p2	(AG)6	12	665	676	GGTGTGCTCGAATTTTTGGT
scaffold669911_16.	1	p2	(TA)9	18	1646	1663	GACAGCCGATATTTGCTCCT
scaffold669928_16.	1	p2	(AT)6	12	495	506	TGTTCTCTACTATATGTCATGTTTTGC
scaffold669944_12.	1	p2	(AG)6	12	458	469	AAGAAAACGGCTGAGCAAGA
scaffold669946_15.	1	p2	(AT)6	12	611	622	AAAGAGCTTCCTCCCACACA
scaffold669985_15.	1	p2	(AT)11	22	344	365	ACCTTAACTTGCATGCACCC
scaffold670069_14.	1	p2	(TA)6	12	91	102	GGACTTGATTCCATGATAACCC
scaffold670087_12.	1	p2	(TA)10	20	218	237	TGCATGCAAGGAAAATGAAA
scaffold670100_16.	1	p2	(AT)6	12	291	302	AAAACCCCATATCTGTGGCA
scaffold670133_13.	1	p2	(AT)9	18	563	580	GAACCTCGAACCGTTGAGAC
scaffold670140_16.	1	p2	(CA)11	22	549	570	AGTCGGGCAAGTCTCCTACA
scaffold670220_13.	1	p2	(AT)8	16	2228	2243	CATCCCGCATCATAACAGAA
scaffold670223_12.	1	p2	(CT)6	12	468	479	AGCATGTGGTCCCTAACTCAA
scaffold670348_14.	1	p2	(AT)6	12	1424	1435	ACGTGTGCGTGTATCCATGA
scaffold670349_11.	1	p2	(AT)8	16	428	443	CATCCCAGTTATGTCAAGCG
scaffold670379_14.	1	p2	(TC)6	12	1890	1901	CCTTGGATTTTGACGCCTTA
scaffold670403_15.	1	p2	(TA)9	18	47	64	TTGGTTATCGCTTGAATGAGA
scaffold670413_15.	1	p2	(AT)11	22	2873	2894	AGCTCCTGCTGACTGAGAGC

scaffold670447_16.	1	p2	(GA)7	14	2392	2405	GTTTTCCTGGAAGGGATGGT
scaffold670575_15.	1	p2	(GT)7	14	1053	1066	TCCTTGTTTTCGGATGTTCA
scaffold670587_16.	1	p2	(TG)6	12	1592	1603	TTCAGATGCTTGTTTTAGGTTCC
scaffold670618_11.	1	p2	(AT)9	18	792	809	AATGGCCGACACTGCTTTAC
scaffold670620_14.	1	p2	(AT)10	20	99	118	TTGTAAAAACTTCCTATACATAACGC
scaffold670635_15.	1	p2	(GT)12	24	188	211	GTCCCGGGAATGAAGAAGTT
scaffold670657_12.	1	p2	(AC)6	12	227	238	TCAAATGTTGATCCAGCAGC
scaffold670659_15.	1	p2	(CT)6	12	1499	1510	CCCTCCATTTCTCAAACCCT
scaffold670749_16.	1	p2	(AT)8	16	2482	2497	ACAAATATCAGTAAAAATGCGCT
scaffold670903_14.	1	p2	(TC)8	16	222	237	CCATTTGTTTCAGCTCGTGA
scaffold670924_11.	1	p2	(AT)10	20	875	894	ACTTGGACCGTGAACACCTC
scaffold671009_17.	1	p2	(CT)6	12	123	134	AACACAAGGAACTTGGGACG
scaffold671066_12.	1	p2	(AT)6	12	122	133	CCCAATTCTCCATCATTATTATTC
scaffold671147_17.	1	p2	(CT)6	12	78	89	CCACTCCATCACCATCACTG
scaffold671158_17.	1	p2	(GA)6	12	733	744	CCGAATCTCGAGCCTTAACA
scaffold671163_13.	1	p2	(TC)8	16	560	575	GTTGAGATTTGGACGGGAGA
scaffold671215_11.	1	p2	(TA)6	12	443	454	CCCCTACTTCCTCGTTCTCC
scaffold671221_16.	1	p2	(TA)6	12	1334	1345	TGCAAGATTTCAAAATCGCAT
scaffold671300_16.	1	p2	(CT)9	18	1043	1060	TGAGGCAAGAAAAGGTTTGTG
scaffold671303_14.	1	p2	(AG)6	12	304	315	TCGGCCAAGAAGAGAGAAAA
scaffold671367_16.	1	p2	(CT)6	12	99	110	TCACATACTCATGCAAGCACA
scaffold671420_12.	1	p2	(TA)7	14	376	389	TCCATCGTGAAAAACCTTCA
scaffold671445_19.	1	p2	(TC)6	12	690	701	GAAGCATGCGAGACATTTCA
scaffold671534_17.	1	p2	(AT)6	12	3132	3143	ACGCAATCGATCTTCCATTC
scaffold671580_10.	1	p2	(GA)6	12	95	106	TCATGGTTACGAACCTCCAA
scaffold671623_13.	1	p2	(TA)8	16	223	238	GTAATCTGTACCGTCCGCGT
scaffold671650_15.	1	p2	(TA)8	16	1278	1293	CCACTTGACATTTTTGCCCT
scaffold671681_16.	1	p2	(TC)6	12	502	513	CTCCTCAACACCACCACCTT
scaffold671694_11.	1	p2	(AT)7	14	369	382	ACCCTAATTGTTTCGGGCTT
scaffold671706_18.	1	p2	(TA)8	16	105	120	TCATTCCAACTTTGTAATCAAGAAA
scaffold671713_11.	1	p2	(GA)7	14	56	69	GTGATGATAATAGGCGGCGT
scaffold671745_17.	1	p2	(TA)9	18	84	101	CCCAAGACCCCAATTTGATT
scaffold671852_15.	1	p2	(AT)8	16	2673	2688	GCAGTGCAACGCATAACAGT
scaffold671918_10.	1	p2	(TG)7	14	152	165	TGAATTGGCGTGAGTGTGTT
scaffold671943_13.	1	p2	(AG)6	12	2757	2768	ACGATGCCTATGATTCTCCG
scaffold671978_17.	1	p2	(AT)8	16	556	571	ATCAGGGACCCAACAACAAA
scaffold672030_15.	1	p2	(TG)6	12	644	655	TGTCATGGCAACAAACCCTA
scaffold672054_14.	1	p2	(AT)6	12	795	806	ATACCGTACCCTTCGCACC
scaffold672080_17.	1	p2	(CT)7	14	71	84	CTCCCTTGAGCAAAGTGGAC
scaffold672088_16.	1	p2	(TC)7	14	1809	1822	GGAGAAGTGCTGAAGGCAAC
scaffold672101_14.	1	p2	(TA)6	12	302	313	AAAATCCAACCATTCACACG
scaffold672112_13.	1	p2	(AT)6	12	524	535	TAGAGGAGGAGAAGCACCGA
scaffold672213_14.	1	p2	(TA)6	12	1458	1469	AGCTTCCTCCACATACACCG
scaffold672220_14.	1	p2	(TG)7	14	52	65	TTGATTGAACTACATTACAACAAGTT
scaffold672287_15.	1	p2	(AG)6	12	228	239	TTGGATTCCCAAGCTTTTTG
scaffold672300_15.	1	p2	(TA)6	12	4800	4811	TGATCCATTTTGTTGGCAGA
scaffold672315_13.	1	p2	(TA)9	18	103	120	GTCTTCCGGAGTACGAGCTG
scaffold672403_16.	1	p2	(TA)6	12	915	926	AATCCTCGTAGCTCCCGTTT
scaffold672414_13.	1	p2	(TA)6	12	53	64	TTCGAATGCGGTTTATCACC
scaffold672512_10.	1	p2	(GT)8	16	320	335	CCGAATACTTTCTTTTGTAGGCTT
scaffold672515_15.	1	p2	(AT)10	20	842	861	CAATGCAGAGATGGACGAAA
scaffold672575_18.	1	p2	(TA)7	14	176	189	TAATGTTGCGTGGGCTTTTT
scaffold672601_16.	1	p2	(AT)8	16	1661	1676	TGATCATCCTGGAGTAAGATTGA
scaffold672615_15.	1	p2	(AG)8	16	149	164	AAATCAGTCTCCATCCGTGC
scaffold672721_16.	1	p2	(AT)9	18	763	780	ACCCTTGGTCGAATTCCATA
scaffold672728_13.	1	p2	(TG)8	16	224	239	GCGCAAAACTTCCCTTTATTC
scaffold672750_13.	1	p2	(TC)10	20	2252	2271	GATGATGATCGGTGGAGGTC
scaffold672758_13.	1	p2	(AG)6	12	229	240	TCCCAATCACCATTCAAGTG

scaffold672763_16.	1	p2	(AC)6	12	43	54	CCAGGATCGAATGGAGGATA
scaffold672764_17.	1	p2	(TA)7	14	95	108	ATTTTCGTTGGAGGAGGGTT
scaffold672768_10.	1	p2	(TA)6	12	436	447	GGCAAGCAAGGGAGTCTATG
scaffold672816_16.	1	p2	(GA)7	14	227	240	GATGGTAGAAGAAGCAGCGG
scaffold672890_13.	1	p2	(AT)6	12	3678	3689	AATTCAGCAAGAATGATAAATCG
scaffold672894_17.	1	p2	(TC)6	12	229	240	CCAAAAATTAAAGGCCCACA
scaffold672967_12.	1	p2	(GA)6	12	3298	3309	CAAACTGTTGAAGATTGTTTACGG
scaffold673055_15.	1	p2	(AG)8	16	372	387	AAAAGGGCACAAACAGCAAT
scaffold673080_12.	1	p2	(AT)9	18	467	484	GTTCGCGCAAACAATGTTAC
scaffold673085_15.	1	p2	(CT)7	14	1074	1087	TAATGGGTGTGGTGCTTTGA
scaffold673093_16.	1	p2	(GA)7	14	401	414	CAAATTGATCCAACGACACG
scaffold673201_15.	1	p2	(GA)6	12	492	503	GTTCATCTCCGCCTTTGTGT
scaffold673210_18.	1	p2	(TC)6	12	353	364	TTTTCAGACACGGGAACACA
scaffold673213_16.	1	p2	(AC)7	14	1455	1468	ATCCATCAAGTTTGCACGGT
scaffold673223_17.	1	p2	(CT)6	12	225	236	TGGACCCAAGTATGCACAAA
scaffold673245_11.	1	p2	(TA)8	16	518	533	ACCTAATCATGTTTTGGGCG
scaffold673261_17.	1	p2	(TC)8	16	599	614	CACCCACCCTTCCCTTTATT
scaffold673289_15.	1	p2	(AG)8	16	1978	1993	GCCAGGGAAATGTTATGGAA
scaffold673306_14.	1	p2	(GA)9	18	1102	1119	AATGATGGTGGAGCTGACCT
scaffold673308_19.	1	p2	(AT)6	12	92	103	TGGGAAGATCTCTCCGTCAT
scaffold673363_13.	1	p2	(TC)6	12	2552	2563	ATTGGACAAGTGGCAATGTG
scaffold673388_13.	1	p2	(AT)9	18	641	658	TCAACCCCCACGTTATCTCT
scaffold673399_13.	1	p2	(AG)6	12	200	211	GTTTTCTGCCGAAGCAAGAG
scaffold673558_15.	1	p2	(CT)7	14	1748	1761	GTGGAAGTGTTTTGTGGGGT
scaffold673583_12.	1	p2	(CA)6	12	686	697	TTTTTGCCGCCTTTGATTAC
scaffold673622_20.	1	p2	(GA)6	12	230	241	TCAAGCCAAGACAAGCAATG
scaffold673792_17.	1	p2	(AG)8	16	742	757	TTAGGGAGGGGAGAATTTGG
scaffold673803_22.	1	p2	(TC)9	18	225	242	TTGAAGCATGTATCACTCTGCAT
scaffold673833_15.	1	p2	(TA)6	12	76	87	TATGGGTTATCACCGGATCG
scaffold673938_12.	1	p2	(AG)6	12	618	629	TCTCACGACAAGAACGTGGA
scaffold674004_14.	1	p2	(AT)8	16	227	242	TCATGATGATTACATTTGTGTTGA
scaffold674108_15.	1	p2	(TG)6	12	832	843	GAAAGGAAACGTCGGAAACA
scaffold674199_13.	1	p2	(AT)10	20	27	46	GAATGACACACGCACACACA
scaffold674318_15.	1	p2	(GA)6	12	1266	1277	AAAAGCCATCAAAACCAACG
scaffold674382_15.	1	p2	(TC)7	14	2094	2107	CTCTTCCTTCTGCGGTGTTC
scaffold674407_14.	1	p2	(AT)7	14	454	467	CCAAAATCAACGTCCCAGAT
scaffold674410_15.	1	p2	(CT)14	28	526	553	CCCGACAACTATGTTCCCTG
scaffold674435_15.	1	p2	(CT)6	12	230	241	TTCATGGCTTTCTGGGTCTC
scaffold674450_10.	1	p2	(AT)7	14	125	138	TGTATGCTGTAAATGAAACTGCTG
scaffold674464_13.	1	p2	(CA)6	12	1126	1137	CACTGGCAAAAATGAATCTCTC
scaffold674517_12.	1	p2	(AG)10	20	600	619	GAAGGGTGAGGCTAGGGAAG
scaffold674598_14.	1	p2	(AG)12	24	4580	4603	GGGCCTTAGTCCATGTCCTT
scaffold674645_14.	1	p2	(AT)6	12	1709	1720	TGACCAACTCCATGTTTCCA
scaffold674703_14.	1	p2	(AT)6	12	774	785	TCAATTAAAAACTTGCTCTCAATCA
scaffold674882_14.	1	p2	(TG)7	14	326	339	GTTTCTGCATTTTGGGAAGC
scaffold674895_10.	1	p2	(TA)8	16	332	347	TTCAGTAGCACAACCACCCT
scaffold674957_14.	1	p2	(AT)8	16	933	948	TGCTATTTTCAGCCCAAACC
scaffold675038_10.	1	p2	(AT)13	26	542	567	GTTGCTATTGCGGGCTTTAC
scaffold675057_10.	1	p2	(TA)8	16	196	211	ATGGGATATGAGGGGAATGC
scaffold675064_15.	1	p2	(AT)6	12	444	455	TTTGAAGTCAAGGGAGCAAA
scaffold675076_15.	1	p2	(TA)8	16	228	243	GCGGATGCTCTTAGTTACGC
scaffold675153_14.	1	p2	(GA)8	16	755	770	TACCTCCCCAATCAATCCAG
scaffold675158_10.	1	p2	(CT)6	12	289	300	AATGCCCCATCTTCAGTTTG
scaffold675207_21.	1	p2	(AG)7	14	104	117	TTATCATGCAAATGAACGGG
scaffold675235_13.	1	p2	(AG)7	14	54	67	AAAGATGGCCAAAACTGTGC
scaffold675279_15.	1	p2	(GA)6	12	974	985	ACGTTGCAAGGTCTACCACC
scaffold675328_10.	1	p2	(TA)9	18	44	61	TGCGTTTTGACGATATATAGTGTTT
scaffold675375_19.	1	p2	(TA)6	12	232	243	AGGTTGCGTACATCTGACCC

scaffold675385_13.	1	p2	(CA)7	14	297	310	TTGCATTGACACAATCAAGTG
scaffold675419_15.	1	p2	(TG)9	18	65	82	GGGCCGAGATTTGTTAGAGG
scaffold675490_15.	1	p2	(CT)8	16	444	459	TATGACTTCGGCATTACCGC
scaffold675502_14.	1	p2	(TA)7	14	230	243	CGTGTCAAAAATCTGTTCATTTG
scaffold675518_13.	1	p2	(TG)8	16	64	79	TCAACTGGATATCAAACGCAA
scaffold675643_16.	1	p2	(GT)6	12	2165	2176	CATCCCTCCACATTTGCTCT
scaffold675648_14.	1	p2	(AT)8	16	178	193	TTTGAATACAATGCTTCATCCA
scaffold675862_10.	1	p2	(AT)7	14	419	432	GAAATGCTGATGTGGCTGAA
scaffold675910_15.	1	p2	(CT)7	14	123	136	CTTGAACATGGCCATCACAC
scaffold675919_14.	1	p2	(GA)11	22	302	323	GTTGTAAGTGGGGGTTGGTG
scaffold675940_15.	1	p2	(TC)7	14	198	211	ATTATTTGCATTGCTTGCCC
scaffold675984_15.	1	p2	(GT)10	20	1011	1030	ATGTGTTGTGATGGGGGATT
scaffold675995_17.	1	p2	(TC)6	12	2779	2790	ATGGATTGCAGAAAGATGGC
scaffold676028_13.	1	p2	(TA)10	20	1194	1213	GAATTCTCCCAAACTGACGG
scaffold676073_14.	1	p2	(TA)7	14	581	594	GTGTTATGCCTATCCCTATCAAGT
scaffold676155_16.	1	p2	(AG)8	16	3993	4008	TTTCTCCTTGAGCCTCTTCAA
scaffold676194_17.	1	p2	(AT)7	14	747	760	ATATCGCGGGCTAAGAACCT
scaffold676221_10.	1	p2	(TA)8	16	798	813	TCCGGAGAAAATGAAGAAGAA
scaffold676277_15.	1	p2	(GA)6	12	405	416	TGGGAACTCGAGAGGAAAGA
scaffold676368_17.	1	p2	(GA)6	12	234	245	TGATTTTGATCCATTGCCCT
scaffold676437_11.	1	p2	(TA)7	14	430	443	GTCGGACGATTAATCACGCT
scaffold676447_20.	1	p2	(TA)7	14	167	180	TGCATTTGATCCCTAGAGTGG
scaffold676523_11.	1	p2	(TG)6	12	101	112	ATTACGTCGATCCAACGGTC
scaffold676551_10.	1	p2	(AT)9	18	48	65	TGAGTGCTAGACTATTGTAAAAACG
scaffold676572_10.	1	p2	(CT)7	14	181	194	TTTATTCCCCACCCTTCACA
scaffold676582_13.	1	p2	(TA)7	14	498	511	ATGATGGCGTCATGTTTTCA
scaffold676686_13.	1	p2	(AT)6	12	847	858	CATTGATTTCATTGCATAATCTGA
scaffold676697_14.	1	p2	(AG)6	12	1426	1437	AATCCACGAAACGGTTTGAA
scaffold676729_12.	1	p2	(CT)6	12	1207	1218	AAACAGCCCATGTGAGAACC
scaffold676731_14.	1	p2	(GA)6	12	288	299	AAACCAATTGGCAACGAGAG
scaffold676751_14.	1	p2	(TA)7	14	317	330	CCGAATTTGGCTCTTTTCCT
scaffold676780_18.	1	p2	(AT)7	14	232	245	ATCTGCTCCTCTCCTAGCCC
scaffold676820_18.	1	p2	(AG)6	12	591	602	GAGGATTTCTTCCCCCAAAA
scaffold676823_13.	1	p2	(TC)7	14	447	460	CTTGAATCCATGACGAGCCT
scaffold676828_16.	1	p2	(TC)6	12	105	116	TCGGTCTCTGGGACCTTTAG
scaffold676963_16.	1	p2	(AT)7	14	15032	15045	GTTGGGCGATTTGAAGCTAA
scaffold676972_16.	1	p2	(CT)6	12	235	246	AGGCAATGGTTTGGTTTCAG
scaffold677015_13.	1	p2	(TA)6	12	435	446	CTTGAGGCCCACACAAGAAG
scaffold677066_15.	1	p2	(GA)6	12	107	118	TATGCACGTGACTTGCTTCC
scaffold677132_17.	1	p2	(AC)7	14	1631	1644	TCCCGGAAATAGTTCCAAAAT
scaffold677153_13.	1	p2	(AT)6	12	146	157	GTTGCATAAACCCTAGGCCA
scaffold677187_13.	1	p2	(AC)6	12	425	436	AGGTCAGTTCCAACCCACAG
scaffold677317_16.	1	p2	(AG)6	12	1230	1241	GGTTTCAAGTGGCAAACGAT
scaffold677320_16.	1	p2	(AT)9	18	1493	1510	CCCTAACCCTAAAGTAAGGACCA
scaffold677391_14.	1	p2	(AT)6	12	1638	1649	TGCACCAGAGTAAGTTGGAATG
scaffold677394_17.	1	p2	(TG)9	18	230	247	GATGAAGATCCTGGACGGTG
scaffold677422_18.	1	p2	(AC)6	12	346	357	TGAAATATCGAGCACCACCA
scaffold677484_11.	1	p2	(AG)6	12	425	436	TGATCCGAGCTTGGAATAGC
scaffold677557_12.	1	p2	(TC)6	12	1191	1202	AAACCTCAAAACCAGGCTCA
scaffold677558_12.	1	p2	(AC)9	18	369	386	CTCCAATCATCGACCGAGTT
scaffold677562_16.	1	p2	(AT)6	12	236	247	TCGAACACCAAACCAATTCA
scaffold677655_15.	1	p2	(TA)6	12	222	233	TGATGGCAACCAAGAACTCA
scaffold677741_16.	1	p2	(CT)6	12	1464	1475	AATTGCATTTGGATGCATGA
scaffold677766_17.	1	p2	(AT)6	12	804	815	GGCTTTTCTGGAATATAAAGCG
scaffold677768_16.	1	p2	(AG)9	18	1539	1556	TTTCTTCCATTGGCTTCACC
scaffold677773_11.	1	p2	(AT)8	16	360	375	GGACATGGGATTGGAGAAGA
scaffold677825_17.	1	p2	(AT)8	16	249	264	TCGAAAACCGGTTAAAGACC
scaffold677854_13.	1	p2	(TA)8	16	536	551	TGAGAAACGAATGCACATGA

scaffold677886_12.	1	p2	(TA)6	12	152	163	GGGCCAAAAGAACAACAAAA
scaffold677929_15.	1	p2	(AT)6	12	2360	2371	TTGTTGTACCATTGTGGAAAGA
scaffold677953_10.	1	p2	(TA)10	20	411	430	AATGATGCTCAAACCCAAGC
scaffold677965_17.	1	p2	(AG)6	12	1109	1120	TCCTGCATGCCCATATACAA
scaffold677968_10.	1	p2	(CT)6	12	398	409	AGAGAGAAAATTGCATCGGG
scaffold678079_13.	1	p2	(TA)7	14	899	912	AATTCGGAACAGACGTCATTG
scaffold678088_15.	1	p2	(AG)6	12	383	394	AAGATCAGCATTCGGTTTGG
scaffold678114_15.	1	p2	(CT)9	18	1347	1364	TGGGGTAATATAAAGGTTCATCC
scaffold678132_17.	1	p2	(CT)6	12	1318	1329	CCGATTCAGATACTCCCCAA
scaffold678179_16.	1	p2	(AT)7	14	333	346	CTCGTGCGCAAAAATTATGA
scaffold678180_15.	1	p2	(TA)6	12	208	219	ACAAAACAGGGGACAAGGGT
scaffold678181_13.	1	p2	(AG)6	12	125	136	TGGAGAGAGAGAAGATCGGC
scaffold678189_10.	1	p2	(AT)8	16	119	134	CAATTGGATTAGTGACATGGCT
scaffold678309_12.	1	p2	(TC)11	22	226	247	CACCAAAGGAAAATTGAATGG
scaffold678316_10.	1	p2	(TG)6	12	347	358	TTCCCTCCTCATTTCCAACA
scaffold678317_10.	1	p2	(TG)6	12	347	358	AAGGTTTTGGTGTTGGGGTT
scaffold678346_13.	1	p2	(AG)6	12	53	64	TCATTGTTTGAAGAGTGGGAAA
scaffold678403_11.	1	p2	(AT)7	14	1099	1112	ATTTTCTTGGCCCAACCTTT
scaffold678444_15.	1	p2	(TA)7	14	1353	1366	CCAACCTGTATCGCTCTTTCT
scaffold678467_16.	1	p2	(AG)8	16	746	761	GGGTCACCTTTGTGATGCTT
scaffold678511_14.	1	p2	(CT)6	12	1240	1251	TGCAAAGATGACAGAAACAAGAA
scaffold678517_11.	1	p2	(AT)9	18	1103	1120	TCGTTGTTCGTGTGAGCAAT
scaffold678565_13.	1	p2	(CT)8	16	1071	1086	AAACCCTCTCAAGAACTCCAAA
scaffold678577_11.	1	p2	(TA)10	20	384	403	CATGTTAAGGAGGGGATCCAT
scaffold678582_13.	1	p2	(TG)6	12	53	64	TGGCTGGCGGTTTTAAATAAT
scaffold678624_10.	1	p2	(TA)8	16	144	159	TTCGGGTCTCAACACATTCA
scaffold678701_14.	1	p2	(TC)6	12	1009	1020	AGGGGGAAACTCGCTAATGT
scaffold678771_12.	1	p2	(TA)6	12	499	510	TCGAAGTCCCACTTCAGCTT
scaffold678936_18.	1	p2	(CT)6	12	730	741	AAATGTGACCGGATTCATCG
scaffold678975_15.	1	p2	(AT)13	26	5282	5307	AGTCTGACCTTCATGGGCAC
scaffold679001_14.	1	p2	(AT)10	20	186	205	TGTTGTGTATAAGGAAGTTTTTCG
scaffold679022_12.	1	p2	(TA)7	14	102	115	TGAAACCTAAGTGGCCTGTCA
scaffold679105_16.	1	p2	(GT)7	14	1691	1704	GAGGTTGATGTTGTCGGGTT
scaffold679179_15.	1	p2	(AT)6	12	238	249	TCGATCAAAGTTATGAATTGGAAA
scaffold679241_16.	1	p2	(GA)6	12	4194	4205	ACCGCTACTTCTCCACGAAA
scaffold679267_17.	1	p2	(CT)6	12	184	195	GCATCTCTTGCTCTCTCGTTG
scaffold679268_13.	1	p2	(TG)7	14	51	64	AGGTCGAGGATTGTCGTCTG
scaffold679319_14.	1	p2	(TA)7	14	485	498	GGTGCCACGTGTCATACTCA
scaffold679377_14.	1	p2	(AT)6	12	333	344	AAATCCTTGCACCTCCTCCT
scaffold679396_15.	1	p2	(TC)7	14	1215	1228	GGATTGGACCTATAATATTGACCG
scaffold679420_16.	1	p2	(TA)6	12	1055	1066	TTGCAGAATCATAAAGTGCAAAC
scaffold679436_16.	1	p2	(TC)7	14	144	157	GGAGAACGCCATTGTTGATT
scaffold679537_17.	1	p2	(TC)7	14	279	292	CATGGCGGATTTACAACTGA
scaffold679720_13.	1	p2	(AT)8	16	1170	1185	TTTGCCCTCTTGTGATACCC
scaffold679746_14.	1	p2	(GA)6	12	3884	3895	TGTAATGAAAGCAGCCGTTG
scaffold679880_15.	1	p2	(CT)6	12	478	489	CTGTTAGCAAGTTCCACGCA
scaffold679898_11.	1	p2	(TA)8	16	235	250	AGCGAAATTGATCTCTGCGT
scaffold679974_16.	1	p2	(CA)12	24	1125	1148	CTGGGAAACCAATCTTGTCG
scaffold679975_14.	1	p2	(AT)9	18	911	928	CAAAGGCCCACAGTGGTTAT
scaffold680003_11.	1	p2	(AT)6	12	67	78	GATGATTGCACCATAACGCA
scaffold680004_14.	1	p2	(TC)6	12	746	757	AGACCCTCAACCTCACCCTC
scaffold680063_13.	1	p2	(TA)6	12	339	350	CAAGAGGAATTGAACCCAGG
scaffold680099_15.	1	p2	(TC)8	16	681	696	GGCAGGAATGAGACACCAAT
scaffold680207_14.	1	p2	(AT)6	12	1173	1184	TGGACAAACAAGCCTCACTCT
scaffold680229_18.	1	p2	(CT)11	22	230	251	CTCGTAGAAGGGCAGTGGAG
scaffold680315_14.	1	p2	(AG)6	12	132	143	ACCTGTCCTGGGTCTGTGAG
scaffold680338_13.	1	p2	(GA)7	14	237	250	TGAATTCAATTGTGTTTTGGGA
scaffold680384_13.	1	p2	(TA)6	12	74	85	ATCCAAGGGTCAATAATGGTT

scaffold680387_14.	1	p2	(AT)8	16	170	185	TGGAGGAGTTCTTCCAGGAG
scaffold680390_20.	1	p2	(CT)6	12	1213	1224	CGAGTATCCTCCCACTCCAA
scaffold680427_12.	1	p2	(AT)10	20	590	609	TACCCCCAGCATCCAATTTA
scaffold680432_15.	1	p2	(TG)6	12	748	759	AGGAGAGATTGTAACGACCCA
scaffold680492_16.	1	p2	(TA)8	16	81	96	CATTATTTAATGTAGGGTGGGTGA
scaffold680548_13.	1	p2	(CT)7	14	534	547	TGCTTCCCTCAATGGTTTTC
scaffold680570_17.	1	p2	(CA)6	12	2675	2686	CTGGCTGCTCTACGCTCTCT
scaffold680574_13.	1	p2	(AT)13	26	461	486	TTGAAGATCCCGGACAGTTC
scaffold680578_11.	1	p2	(GA)8	16	534	549	ATGGACGGCTGTGATTTAGG
scaffold680579_16.	1	p2	(TA)6	12	1549	1560	TTTGGATCACTAGGGCTTGG
scaffold680601_15.	1	p2	(TA)6	12	138	149	CACGTGAGATGCTGAGTAGGA
scaffold680634_13.	1	p2	(TC)6	12	55	66	ACAAGCCCTAGCTCTTTCCC
scaffold680635_11.	1	p2	(TA)8	16	92	107	AGCGGTTATTACCGGATCG
scaffold680683_11.	1	p2	(TC)6	12	950	961	CGCTACTCTTCGAGTGCGTT
scaffold680726_18.	1	p2	(AT)8	16	733	748	ACACCGGTTCCAAGTGATCT
scaffold680734_14.	1	p2	(TA)12	24	290	313	GGAAGGGGAGTTAGCGTATG
scaffold680885_10.	1	p2	(CT)6	12	256	267	ATCCGATGGATGAAAAGCTG
scaffold680905_14.	1	p2	(AC)7	14	378	391	CAATGGCTTGTGTTCCTCAA
scaffold680985_16.	1	p2	(CT)12	24	504	527	AGCCTTTAAGACACGCCAAA
scaffold681070_19.	1	p2	(TA)6	12	240	251	CGCGTGGGTGATATGCTAGT
scaffold681073_15.	1	p2	(CT)12	24	1198	1221	TCCAAAGTCACACTTGCTGC
scaffold681076_14.	1	p2	(CT)8	16	5591	5606	GAATGAGTGATGGCGGATCT
scaffold681093_15.	1	p2	(CA)6	12	171	182	CATTAAAGCCTCACCCCTCA
scaffold681104_11.	1	p2	(CT)8	16	54	69	ATCCTTTGCACAACCCACTC
scaffold681110_13.	1	p2	(TC)6	12	419	430	CAAGAATTCCAAGCTTGCCT
scaffold681119_17.	1	p2	(AT)8	16	1433	1448	GCTACATCACTTCCCCACAAA
scaffold681177_10.	1	p2	(GA)6	12	345	356	CGAAGAAAACACCCGGACTA
scaffold681197_15.	1	p2	(CT)8	16	2095	2110	AAGGGAGCTCCTCAGCCTAC
scaffold681208_16.	1	p2	(TA)8	16	2474	2489	GAGTGAGTTGGCGAGAATCTG
scaffold681216_11.	1	p2	(TA)7	14	1054	1067	TATCCCTACACCGCCTCATC
scaffold681219_16.	1	p2	(GA)6	12	1954	1965	ACGGGAGGAAGACGAAGAGT
scaffold681242_16.	1	p2	(TA)6	12	146	157	TTGGGATTAAGGCTTTGGTG
scaffold681244_10.	1	p2	(TA)8	16	124	139	TCAATTCCTCCCTTAGACACAA
scaffold681257_15.	1	p2	(CT)6	12	197	208	GCATCTCTTGCTCTCTCGTTG
scaffold681304_10.	1	p2	(CT)8	16	183	198	TTTTGACACGTAGCGACACC
scaffold681324_14.	1	p2	(TA)6	12	216	227	TGTGCGTTTTTGGCATAGTG
scaffold681334_18.	1	p2	(CT)7	14	909	922	TTGCAGAGTGATTGTAGGCG
scaffold681341_13.	1	p2	(TG)6	12	241	252	CAATAATGCCCCCTTCATGT
scaffold681470_14.	1	p2	(GA)7	14	240	253	GCGTCTCCAAACAGGAGAGA
scaffold681503_14.	1	p2	(GA)6	12	976	987	CGACGTCGTTCTTGATTCTTC
scaffold681544_16.	1	p2	(AT)6	12	905	916	TACCGTTTCAAGGTGCAATG
scaffold681611_15.	1	p2	(CT)6	12	1497	1508	GCGCTACAAAAACGAGTTCA
scaffold681640_12.	1	p2	(TA)6	12	315	326	AGTAGTTAGCATGGAAGGGGA
scaffold681682_10.	1	p2	(TA)7	14	320	333	TTCGAATTGATGTTTGATCCAT
scaffold681738_13.	1	p2	(GA)8	16	1188	1203	ATCGCATTGCCTCACTTTTT
scaffold681852_15.	1	p2	(TG)6	12	2530	2541	GATTTGGTACATGGATGGGG
scaffold681897_11.	1	p2	(AT)9	18	528	545	TTGAGCCCTGCCAAAATATC
scaffold681915_15.	1	p2	(AG)8	16	330	345	CGAATTTTAGTGGGACATCCA
scaffold681939_13.	1	p2	(TC)8	16	797	812	ATCAATAGGTCACGGGTTCG
scaffold681940_21.	1	p2	(AT)6	12	415	426	GCTATCACGCGAATGGGTAT
scaffold681966_17.	1	p2	(TA)9	18	481	498	AGTCCTAGCCCCACATCTCA
scaffold682001_20.	1	p2	(AT)6	12	243	254	TGCGGGCATAAGACCATATT
scaffold682014_17.	1	p2	(CT)8	16	1064	1079	AGTGGGGAGCCTTACCTTGT
scaffold682217_12.	1	p2	(AT)8	16	2326	2341	AGGCTGTTAAGGTTCGGGTT
scaffold682228_14.	1	p2	(CT)7	14	240	253	AGTCTCCCCATTTGATGCAC
scaffold682235_10.	1	p2	(GA)6	12	144	155	CTTTTGGTCGAGCCAGCTAC
scaffold682271_17.	1	p2	(AG)6	12	242	253	GTTGCTCATTCCCCTTTCAA
scaffold682273_15.	1	p2	(CT)10	20	594	613	CCGAGTTGGAGAGAGAATGC

scaffold682276_17.	1	p2	(CA)8	16	432	447	CCCTGCCTGTAAATCCAGAA
scaffold682319_16.	1	p2	(TC)6	12	2040	2051	TATTTTGATGCCGGGAATGT
scaffold682348_11.	1	p2	(TA)6	12	1004	1015	CACGCTGATATCGCACAACT
scaffold682357_14.	1	p2	(AG)10	20	511	530	ATCCCAGAATGCCTACACCA
scaffold682366_18.	1	p2	(AG)6	12	97	108	TTAAATGCACAGCACAGCTC
scaffold682386_15.	1	p2	(AT)6	12	742	753	TCAACTTATATTTCAGCGACGA
scaffold682390_16.	1	p2	(TC)6	12	243	254	TCAACAACAGCAGAAATCGG
scaffold682445_13.	1	p2	(TG)6	12	693	704	GAATGCTCGTTGTCCCAAAT
scaffold682519_15.	1	p2	(AG)6	12	931	942	CTTTCACGGGTTTGAAGCTC
scaffold682541_14.	1	p2	(TA)9	18	47	64	TTTCATATATCACGTTAAGACATGGA
scaffold682542_17.	1	p2	(AT)10	20	191	210	TAACCCTTGTTAGCCCGTTG
scaffold682556_15.	1	p2	(GA)8	16	239	254	TCAGCCAAATGCAGAGATGA
scaffold682563_11.	1	p2	(AT)6	12	191	202	GCTATAAGGTTGCACCCACG
scaffold682564_12.	1	p2	(AT)12	24	33	56	TCAATTTCTCTAACCTGTAAAATGC
scaffold682565_10.	1	p2	(AT)6	12	405	416	CCCATTCTCTTCATCCCTCA
scaffold682717_12.	1	p2	(AT)6	12	420	431	AATACACCCCAAAGTGGAACC
scaffold682721_14.	1	p2	(TA)10	20	46	65	CCAAATGTTAGGGTTATCACAGG
scaffold682783_19.	1	p2	(CT)6	12	1126	1137	CCTTCATCCCCTGTCTTGAA
scaffold682842_15.	1	p2	(AG)7	14	2487	2500	CTTTGAAATGACATGGGCCT
scaffold683010_12.	1	p2	(AT)7	14	307	320	AAATGCATCATACGGCATACA
scaffold683017_13.	1	p2	(TA)7	14	794	807	TTGATCCTTTTTATGATAACCCAA
scaffold683021_13.	1	p2	(TA)6	12	60	71	GAAAGAGAGTTTAGATCAAGTGTGTT
scaffold683033_14.	1	p2	(TG)7	14	227	240	TTCTTTTTACATTTGGTAGACCATC
scaffold683042_12.	1	p2	(GC)8	16	190	205	CAATTCGAAGCCCAAATCAT
scaffold683083_15.	1	p2	(GA)8	16	329	344	AATGGGTGGGTTATAATGGGA
scaffold683130_14.	1	p2	(TA)9	18	344	361	CACGGGAGGTGAAAATTGAG
scaffold683136_16.	1	p2	(AG)6	12	1377	1388	CGAGCAATATCTTGGGCACT
scaffold683191_13.	1	p2	(AG)9	18	544	561	TCCAACCGCTATTTGAATCC
scaffold683196_13.	1	p2	(TA)9	18	36	53	TTTAGTGTTTTGACATGATTACTCG
scaffold683201_15.	1	p2	(TC)6	12	244	255	TGCTGCTTTAGGTCTTTGCC
scaffold683208_16.	1	p2	(AG)7	14	5578	5591	CACGAACACATGAGGGAATG
scaffold683240_19.	1	p2	(TA)6	12	1081	1092	GATAATGGCAAACCTGCTGC
scaffold683518_12.	1	p2	(AG)12	24	498	521	GGGAGAGAGAAGGGAAGAGG
scaffold683521_14.	1	p2	(AG)7	14	1192	1205	AAGAAAAGGGGGAAAGGTGA
scaffold683598_10.	1	p2	(GA)7	14	678	691	ATTCTAGGTGCACCCCTCCT
scaffold683641_12.	1	p2	(TG)6	12	54	65	TCCCCTTTTACTTTATTCTTTCAA
scaffold683665_12.	1	p2	(AT)9	18	319	336	TAACGATGGACTAGGGGCTG
scaffold683682_15.	1	p2	(TA)10	20	309	328	TCAAGGGGTATTTTTGTCCG
scaffold683718_12.	1	p2	(TC)7	14	405	418	TGTGACTGTCGATGAAGTAAAGG
scaffold683792_14.	1	p2	(TA)9	18	70	87	CGAACGATGACATGCTCCTA
scaffold683848_16.	1	p2	(GA)7	14	243	256	ACTTGCAAAAGACTCCAGGC
scaffold683896_15.	1	p2	(AG)6	12	245	256	ATTCACACCATTTGCCATCC
scaffold683909_15.	1	p2	(AG)7	14	562	575	AATCCCCGCCTATCTAAGGA
scaffold683914_14.	1	p2	(TA)7	14	180	193	TGGATACATGGGTGGATAATATG
scaffold684054_18.	1	p2	(TC)8	16	515	530	ATATTCGGCTCCATCCCTTC
scaffold684061_13.	1	p2	(GA)9	18	2304	2321	ATCTCGCAGTGCAAAATCG
scaffold684070_14.	1	p2	(TG)6	12	571	582	TGTACAGGCATGGGTTTCAA
scaffold684076_13.	1	p2	(GT)7	14	438	451	CAAGACCACGAGCCGTTAAT
scaffold684146_21.	1	p2	(TC)7	14	95	108	CAAAACTCTCATACAGCCAAAA
scaffold684154_15.	1	p2	(TG)6	12	650	661	TGTAATCTGGGATAACGGGG
scaffold684214_15.	1	p2	(TC)7	14	3108	3121	GTAAGCATCGCCCTCCATAA
scaffold684244_14.	1	p2	(TC)6	12	778	789	GGGGCATGAATTGTTACAGG
scaffold684247_17.	1	p2	(AT)10	20	495	514	GGAGCACCTGATTTTCGCTA
scaffold684254_17.	1	p2	(CT)7	14	245	258	AGGGGTTCGAGTGGAAAATC
scaffold684257_16.	1	p2	(CT)9	18	719	736	AGAATTGGAACCCCAAAACC
scaffold684271_14.	1	p2	(TA)8	16	705	720	AGCCCCAAATCACAAACAAC
scaffold684300_11.	1	p2	(TA)8	16	323	338	CCCCTCGTATGCAGTCATTT
scaffold684332_13.	1	p2	(TA)8	16	424	439	TCAGACGAAACATCCCTTCA

scaffold684366_17.	1	p2	(AG)6	12	247	258	TGCTCCTCCTCTTCCTTTCA
scaffold684369_12.	1	p2	(AG)8	16	413	428	TCTCGGCCAGAGAGAAGAAA
scaffold684376_17.	1	p2	(TA)6	12	645	656	TAACCCACCAAATGCTGTGA
scaffold684408_10.	1	p2	(AT)7	14	244	257	GCGTGAGAGATAGCCGAGAG
scaffold684409_16.	1	p2	(AG)6	12	243	254	TTCACCTACCAATTCCAGCA
scaffold684438_15.	1	p2	(TC)9	18	241	258	CACGCGATACCATTCAGTTTT
scaffold684483_20.	1	p2	(TC)6	12	67	78	TTAGCTGCTGGGATTTTGCT
scaffold684488_15.	1	p2	(TC)6	12	1314	1325	CTAGCAATGGGGTGCTTGTT
scaffold684542_12.	1	p2	(TA)9	18	436	453	TGTTTGCTGTCATCGCTAGG
scaffold684580_15.	1	p2	(AT)9	18	761	778	ACAAGAATGGATTGGGTTGG
scaffold684591_17.	1	p2	(AT)6	12	707	718	TTGGATAAATGGGAGGCTTG
scaffold684693_16.	1	p2	(TC)6	12	661	672	ATTGAATACGCGAGACCCAC
scaffold684722_15.	1	p2	(CT)6	12	710	721	GGTCAACCTACAGCACCGAT
scaffold684780_11.	1	p2	(TA)8	16	302	317	TCATGGGGAATGGAAAAAGA
scaffold684848_13.	1	p2	(AT)9	18	776	793	GCCTCCTACCCCACTTCACT
scaffold684864_16.	1	p2	(AG)6	12	1077	1088	AACTTTCAGCCAAGAGCCAA
scaffold684904_11.	1	p2	(TA)10	20	581	600	ACGCGCGTTTTTAGAGTTTA
scaffold684910_13.	1	p2	(TA)12	24	208	231	GTGGCTGGAGGCATACAACT
scaffold685076_14.	1	p2	(TA)8	16	1347	1362	TTTCCGAAACTTCCAATCAA
scaffold685105_15.	1	p2	(AT)6	12	1323	1334	GGTCCCTAAACCCAAATCGT
scaffold685114_14.	1	p2	(AG)7	14	396	409	CATTTGGAGGTGCACACAAC
scaffold685228_13.	1	p2	(TA)9	18	1110	1127	GGAAACCTTATGCGATTGGA
scaffold685230_15.	1	p2	(AT)6	12	3041	3052	TGCTTGAGAGTGGGAGGAGT
scaffold685260_15.	1	p2	(TA)6	12	249	260	CGAATACGTACGGGTGTGCT
scaffold685263_12.	1	p2	(TC)7	14	623	636	ATGCCTTTGCAATTTCTGCT
scaffold685364_18.	1	p2	(TA)8	16	415	430	GGCCAAATCCTAGCCACATA
scaffold685403_12.	1	p2	(TA)6	12	456	467	CTATCAGCGCTTCTTTCCGA
scaffold685431_16.	1	p2	(CT)8	16	561	576	ACTCGTCCTCGTTTCTTTGC
scaffold685461_16.	1	p2	(CT)6	12	1755	1766	TAAATAGTGGCGGATCCAGG
scaffold685484_18.	1	p2	(AT)8	16	751	766	CGCCAAGCACTCACAAACTA
scaffold685559_13.	1	p2	(TA)13	26	40	65	AAGGGGGTTATTAGTGGATCA
scaffold685568_14.	1	p2	(AT)8	16	1449	1464	AGGCTGGTATTTTGGCCTTC
scaffold685656_17.	1	p2	(AT)8	16	2682	2697	TGATAATGCACTTCAATACAAGCA
scaffold685668_11.	1	p2	(CT)6	12	78	89	CATCTCTTCTCCACCAACCG
scaffold685737_15.	1	p2	(AG)7	14	2066	2079	ATCAAGAAATTCACCAGGCG
scaffold685751_11.	1	p2	(TA)9	18	403	420	TACGATTTTTCGGTTTTCGG
scaffold685768_12.	1	p2	(GA)7	14	450	463	CCATCTTCAACCCGTCACTT
scaffold685770_14.	1	p2	(AT)7	14	1070	1083	CGACCTTGGCAATCAACTTT
scaffold685787_13.	1	p2	(CA)6	12	38	49	CCCCCTTCTACTTTGGTCAG
scaffold685796_16.	1	p2	(AG)6	12	3788	3799	AACGAGAAAAGACTGCTGCC
scaffold685799_10.	1	p2	(AT)10	20	71	90	ATCGGTTATTACCGGATCGC
scaffold685838_13.	1	p2	(AT)8	16	1092	1107	CAGGTGCGCCTTATCTCTCT
scaffold685928_11.	1	p2	(AC)6	12	348	359	TGCATGATTTCTTCAATCTTCG
scaffold685955_10.	1	p2	(TA)8	16	831	846	GGGAAAGCCTCAAGTCCAAT
scaffold685983_13.	1	p2	(TA)7	14	819	832	TGTTTTGTTCGACAACGACTCT
scaffold685994_10.	1	p2	(TC)11	22	31	52	TTTTTGTCTCACTAGTGTCGTTTTG
scaffold686016_11.	1	p2	(AG)6	12	107	118	AGTTTTAGCGTGTCAGGCGT
scaffold686045_16.	1	p2	(TC)6	12	108	119	AGGACACGTTGGACCTGAAG
scaffold686111_12.	1	p2	(AT)6	12	578	589	ATCACGATATCCACATTTAGCA
scaffold686144_17.	1	p2	(GA)9	18	869	886	TGCACAGTCCTAATCAAGCG
scaffold686176_17.	1	p2	(AG)6	12	1263	1274	TGAAAGAATTTTTCGGCTGG
scaffold686190_14.	1	p2	(CT)6	12	1004	1015	TTGCGAACTAGTTGTCGTCG
scaffold686197_17.	1	p2	(TA)8	16	247	262	TCCCACTGCCCAAACTTATT
scaffold686260_13.	1	p2	(TA)6	12	530	541	GCAATAACGCTGCAAAATCA
scaffold686315_17.	1	p2	(TA)7	14	1693	1706	CGATAAAAATGGCACCCAGT
scaffold686332_11.	1	p2	(AT)7	14	249	262	CGCTGCTTTCGTGTTTAGTT
scaffold686341_14.	1	p2	(TG)12	24	818	841	GGGGGAGAGTTGGAGATCAT
scaffold686436_14.	1	p2	(CT)8	16	430	445	CAGCGGCTTACTAGCTTCGT

scaffold686476_18.	1	p2	(TC)6	12	153	164	CCCCCAAATCATTCAGCATA
scaffold686478_15.	1	p2	(TA)8	16	501	516	CCCAAGTGGGATATTGTTGG
scaffold686480_16.	1	p2	(TA)11	22	43	64	TCACATAAATAATGGTTTCTTCCTAA
scaffold686487_14.	1	p2	(AG)6	12	579	590	AGTGCGTCAGAAGGTGTCCT
scaffold686517_12.	1	p2	(CT)7	14	124	137	CCCCCGTGCATTAATAAAAT
scaffold686569_13.	1	p2	(AG)7	14	351	364	GGAGGAGAGGCTCTTGGTTT
scaffold686585_17.	1	p2	(GA)6	12	961	972	GCAGCATCGTCTGAGAGTGA
scaffold686586_13.	1	p2	(AT)11	22	876	897	ATTTGGAAACTTGAACCCCC
scaffold686612_15.	1	p2	(AT)6	12	997	1008	TCCACCAACCAAACATTCCT
scaffold686619_17.	1	p2	(CT)10	20	54	73	ACCCATTTCATGTCACCTCC
scaffold686679_23.	1	p2	(AG)6	12	252	263	GGCCACTGCGTTTGTTAGAG
scaffold686682_17.	1	p2	(AG)6	12	251	262	ACTTTTCCTCCCCCATCATC
scaffold686683_14.	1	p2	(GA)7	14	2722	2735	ATCTCCGTCTTTGTTGTGGC
scaffold686695_16.	1	p2	(TC)8	16	1226	1241	CCTCTGCAGCCTAAAACCAC
scaffold686730_10.	1	p2	(CT)6	12	229	240	GACACCTCCACACCCAATCT
scaffold686753_16.	1	p2	(TA)7	14	249	262	GCAAGAAAGCAGTGCACCTA
scaffold686787_13.	1	p2	(AT)8	16	248	263	TTGGCGTAGATTCCACTTGA
scaffold686802_16.	1	p2	(TA)7	14	2933	2946	CACTCATTTGAGGATGGATTGA
scaffold686846_10.	1	p2	(TC)6	12	153	164	GGTGCTTTCTGGTTCATCGT
scaffold686896_12.	1	p2	(AT)8	16	500	515	TGTGGCATGGGTCAAGATAA
scaffold686935_13.	1	p2	(AT)6	12	1276	1287	CGTCATTTTTCAATCCCAGC
scaffold686962_11.	1	p2	(TA)6	12	32	43	ACGTCCTCTAGGTGTCGTCC
scaffold686993_15.	1	p2	(AT)6	12	878	889	GATTCGTTGCAGAAATCCGT
scaffold687046_12.	1	p2	(TA)6	12	2939	2950	CTCACGTGAAAATGCAAGGA
scaffold687051_17.	1	p2	(TC)6	12	88	99	TGATTTCGCTGATTTTGGTG
scaffold687122_15.	1	p2	(TC)9	18	735	752	CTTTCCCATGGAGTTCAGGA
scaffold687124_14.	1	p2	(AT)6	12	65	76	GCTTAATTGTAAACCGTTGTCAT
scaffold687140_19.	1	p2	(GA)6	12	465	476	TGGCACTCAGTTAAGGGTCC
scaffold687162_11.	1	p2	(AT)7	14	454	467	GCGTCGTGGATCAAGGTAAT
scaffold687177_15.	1	p2	(CT)9	18	48	65	TGAATCCTTCCTTGCTAGTCAC
scaffold687185_15.	1	p2	(TA)9	18	498	515	CAATGTATCCAAACATGATGACG
scaffold687190_11.	1	p2	(AT)6	12	373	384	ATCAGGCAAAAACGTGCATT
scaffold687225_15.	1	p2	(TC)7	14	469	482	CAAAGCGGGTAAAGGAACAA
scaffold687276_13.	1	p2	(GA)6	12	1273	1284	TCAGTGCGTGTGATTCTGTG
scaffold687337_16.	1	p2	(AT)9	18	1253	1270	CCACTCACATGGGAATTGTT
scaffold687391_13.	1	p2	(CA)8	16	1130	1145	TCACTAGCCGGACACATCAG
scaffold687426_16.	1	p2	(AT)7	14	3700	3713	AGGGATGTGAATTCGTGCAT
scaffold687429_12.	1	p2	(AG)6	12	415	426	GGCATGTCCGAGTTCTTAGC
scaffold687430_14.	1	p2	(CA)6	12	1026	1037	TTCCATACGACATTGCAAGC
scaffold687435_16.	1	p2	(AG)6	12	899	910	CCAGAACCCAGCTTCTTCAG
scaffold687446_10.	1	p2	(TA)7	14	52	65	TCAACGTACCTATTTTGTTCCTAGTTT
scaffold687461_10.	1	p2	(GC)6	12	276	287	CACACACAAGATTTGGGAGG
scaffold687466_15.	1	p2	(GA)7	14	103	116	GGAGTTCGAGCTTCAGGAGA
scaffold687547_18.	1	p2	(TC)6	12	366	377	GGGGATAATGACGAGACGAA
scaffold687641_12.	1	p2	(TA)9	18	230	247	ATCCTGTCCATCACCCCATA
scaffold687693_15.	1	p2	(TG)7	14	321	334	CAGCATACGCGAAGGGTATT
scaffold687724_16.	1	p2	(AG)8	16	85	100	TCAATAAAATGCTTCCAATCG
scaffold687730_16.	1	p2	(TC)9	18	1122	1139	ATCCAAGGAGCACACCTGAG
scaffold687735_12.	1	p2	(GA)6	12	1003	1014	TGTGTGTTGTGTGTTCACGG
scaffold687752_18.	1	p2	(TA)9	18	46	63	CCAATTTGAATGGTTATCACCTG
scaffold687769_10.	1	p2	(AT)10	20	450	469	ATTTGGCCCTATAAAATGCG
scaffold687786_10.	1	p2	(AT)6	12	165	176	ACCTCGCAGTCATTCCAGAC
scaffold687822_13.	1	p2	(TA)8	16	52	67	GGAGGGGGTATAATTTGAATAGC
scaffold687843_12.	1	p2	(AG)8	16	36	51	TTGAAATTGGATATTTTCAGGAGA
scaffold687858_14.	1	p2	(AG)12	24	242	265	AACCTAACACCAAGGCAACG
scaffold687882_10.	1	p2	(AT)8	16	122	137	CCTCCACCGCCTAACAATAA
scaffold688039_14.	1	p2	(TC)6	12	544	555	CTGCTCCGATGAACCTCTGT
scaffold688055_10.	1	p2	(TC)8	16	715	730	TGACCTCTACGAGGCATACCA

scaffold688116_13.	1	p2	(TA)9	18	171	188	ATAGGGATTTCGGATTTCGG
scaffold688117_13.	1	p2	(TA)8	16	1967	1982	CAACGAATTCCACACCAAAA
scaffold688192_16.	1	p2	(TA)6	12	459	470	AAACTGAGCTCCATAGCCGA
scaffold688218_15.	1	p2	(GA)8	16	271	286	GAAGCCCTTTCTTCCCAATC
scaffold688219_17.	1	p2	(GT)6	12	2934	2945	TGAAACAACACGACCGGATA
scaffold688244_15.	1	p2	(AT)6	12	116	127	CGGATGAATTTCACTTCACG
scaffold688277_17.	1	p2	(AC)6	12	914	925	GTGTCGATGCCTGAAATCCT
scaffold688303_15.	1	p2	(TC)6	12	358	369	ATGGCGAAATCACCAGAAAC
scaffold688304_18.	1	p2	(TG)7	14	31	44	CCGTCAGTTTCAAGACATTCC
scaffold688334_19.	1	p2	(TC)9	18	249	266	AATCCCCCAAACCAATTTCT
scaffold688344_18.	1	p2	(AT)6	12	255	266	CATTCAGTGGGCACATTGTC
scaffold688347_16.	1	p2	(GA)7	14	2000	2013	TGCAGAGAAGGGAAGAGGAA
scaffold688373_11.	1	p2	(TG)6	12	367	378	CGGTTCAACTTCCCATGTTT
scaffold688374_11.	1	p2	(AC)9	18	447	464	TTGACATTGAATCCCCTCATT
scaffold688474_11.	1	p2	(AG)6	12	1613	1624	CTTGCTTGCTGAGGTAAGGC
scaffold688520_15.	1	p2	(AG)9	18	2153	2170	AAGTCCCAGTGAATGATGCC
scaffold688548_13.	1	p2	(AT)7	14	252	265	TAATGGCGCCGCTAATGTA
scaffold688555_10.	1	p2	(AT)11	22	576	597	ACCCCTACACGCAACTCAAC
scaffold688635_11.	1	p2	(AT)7	14	765	778	CCACATAAGCGTCATCTCAAAA
scaffold688663_15.	1	p2	(TA)14	28	35	62	GGGCTGCAGGAATTCAATAA
scaffold688700_13.	1	p2	(AT)9	18	1061	1078	TTTTGCCATCATAAACTCTATTCG
scaffold688722_17.	1	p2	(AT)6	12	136	147	CCATTTCAGCCAAGCTGTTT
scaffold688807_16.	1	p2	(CA)6	12	1163	1174	TCGGAAGGTTTATCCTCAGTG
scaffold688810_16.	1	p2	(TC)6	12	452	463	TAAGCAAAGCGTGCACAATC
scaffold688844_16.	1	p2	(CT)10	20	792	811	CCACTTTCCACAATCCTCGT
scaffold688857_15.	1	p2	(TG)6	12	45	56	TCCTCTCCTCTCTCTCTACTCTCTC
scaffold688943_16.	1	p2	(TA)6	12	477	488	GGGTGGGTCTCCCTTACATT
scaffold688977_13.	1	p2	(TA)6	12	2434	2445	TACCCTCCGGTACACGAAAA
scaffold689002_13.	1	p2	(AT)8	16	422	437	TATTTGACCGTGAATTGGCA
scaffold689015_16.	1	p2	(CT)8	16	1505	1520	TCGCAACTTCACCTTTACCC
scaffold689048_17.	1	p2	(AC)6	12	743	754	ATGTGGAACCAAACGATCAA
scaffold689068_13.	1	p2	(AT)10	20	216	235	TTGGAATAGGTCCTTGGCTG
scaffold689071_16.	1	p2	(TA)7	14	49	62	TTTAGTGTTTTGACATGATTACTCG
scaffold689075_11.	1	p2	(AT)9	18	193	210	GGGTTACCAAATTAGTTCGTCG
scaffold689115_16.	1	p2	(CT)7	14	253	266	TTTTCTTTTCGCTGCATGTG
scaffold689128_11.	1	p2	(TA)7	14	78	91	ATAAGCCACCCAAACAATGC
scaffold689143_15.	1	p2	(TG)10	20	3236	3255	GGATCATCTTCCCTCTCCCT
scaffold689173_15.	1	p2	(AG)7	14	1647	1660	CAAGGCAAGGACCAGATCAT
scaffold689281_16.	1	p2	(AT)8	16	1953	1968	AAGGAGGTGTTATGAAGGGATT
scaffold689286_17.	1	p2	(TA)10	20	248	267	TCCCAAACTGATGGAAGGTT
scaffold689290_19.	1	p2	(AT)7	14	109	122	TGCAAAAGTTATGGTAACAAGATT
scaffold689296_11.	1	p2	(TA)7	14	933	946	GAGTTAATCATGCGCGTCAA
scaffold689432_14.	1	p2	(TA)11	22	48	69	TGGTGAATGATTGACGATGAA
scaffold689502_18.	1	p2	(TA)6	12	74	85	ATCAATGGTCCACATCGGTT
scaffold689544_15.	1	p2	(CT)6	12	56	67	TCTCTCTTGGTTGGTGAAGGA
scaffold689559_13.	1	p2	(AG)6	12	508	519	CGTGGTTGGTGTGAGATTTG
scaffold689571_15.	1	p2	(TC)6	12	1736	1747	TTACGATTCACCAATTCGCA
scaffold689606_15.	1	p2	(GA)7	14	1406	1419	GACGACGTGAAGAGACGACA
scaffold689646_11.	1	p2	(GA)6	12	551	562	GTAGTCGGCAGAACCCAGAA
scaffold689685_20.	1	p2	(CT)7	14	1074	1087	ATCACTGCATTTCGTCCTCC
scaffold689694_10.	1	p2	(TA)9	18	154	171	TGCCTTTATTTTAGCCTCCC
scaffold689704_16.	1	p2	(TC)6	12	2235	2246	ATCCTCACATCGCCAAAAAC
scaffold689732_10.	1	p2	(CT)8	16	52	67	ACCTCATTTTCAACACCCCA
scaffold689793_13.	1	p2	(GC)7	14	214	227	GCTTCTTTGCTACGAGCCAC
scaffold689905_18.	1	p2	(AT)9	18	864	881	AAACCGGGCCTACAAGATTT
scaffold689910_17.	1	p2	(CT)7	14	503	516	ACAAACAGCCCAAGGAAATG
scaffold689943_13.	1	p2	(CT)10	20	568	587	AGGAACAGAGCTTCAACGGA
scaffold690035_15.	1	p2	(TC)8	16	855	870	AAACAATTGGGATGAGCAGG

scaffold690100_14.2	1	p2	(AT)10	20	956	975	CAATGGTGGCCGAAAATTAG
scaffold690112_15.6	1	p2	(CA)8	16	180	195	CTAACCCTAGGTGGTGCCAA
scaffold690133_14.5	1	p2	(TA)9	18	253	270	CCCAGGCATAGAAAGAAAAGAA
scaffold690165_14.7	1	p2	(AT)12	24	1977	2000	CGTCGGTGTATGACCTGTTG
scaffold690190_14.5	1	p2	(AG)7	14	449	462	AACTTGCACCCAAATTCCAC
scaffold690206_14.1	1	p2	(TA)8	16	1194	1209	CAGAACGCTCTTTTGCACAC
scaffold690233_12.7	1	p2	(TA)6	12	397	408	TATCAGTGACCACCCAACCA
scaffold690316_14.9	1	p2	(GA)7	14	257	270	CTAAACCCAGGTGGCAGTGT
scaffold690355_17.0	1	p2	(AG)6	12	532	543	CTGGGAGTGCTGGAGAAGAC
scaffold690369_11.6	1	p2	(TA)8	16	122	137	CGGATCGGAATTTCTCAAAG
scaffold690396_15.8	1	p2	(AT)6	12	576	587	GGGGAAATAAAAGCCCAAAA
scaffold690418_17.1	1	p2	(CT)6	12	256	267	TAGAGGATTCGGCATTGGAG
scaffold690458_18.4	1	p2	(AG)6	12	513	524	GTTGGAAAAAGCCAATCGAG
scaffold690482_14.0	1	p2	(GA)8	16	707	722	TTCCAGGAGCCAGATAGGAC
scaffold690506_15.5	1	p2	(TC)6	12	224	235	CGAAGCCAAACCTAGGAAGG
scaffold690519_15.6	1	p2	(GA)6	12	565	576	TCCATCCACCTCTGCTTTTC
scaffold690523_13.9	1	p2	(AT)9	18	465	482	ATTTGTCCAATGGTGCTTCG
scaffold690546_13.2	1	p2	(GA)6	12	756	767	GGAACCTGAGAATGGGGAAT
scaffold690549_17.0	1	p2	(TA)6	12	1207	1218	CATGTGGATCATACAACAGGG
scaffold690566_13.2	1	p2	(AC)9	18	204	221	TCTACCAAGATCCTGCCTGC
scaffold690576_12.6	1	p2	(AT)8	16	1240	1255	CGACTATTGTTTGTCATCGCA
scaffold690579_18.2	1	p2	(TC)7	14	180	193	GAGGTGCTGGGTCACTGAAT
scaffold690582_15.4	1	p2	(CT)6	12	716	727	GGCAACCCACTTGTGAAACT
scaffold690586_12.3	1	p2	(AT)10	20	85	104	CCGCTCCTCCTTTTCTTTTT
scaffold690632_15.6	1	p2	(TA)9	18	45	62	AAGGAGGTGTTATGAAGGGATT
scaffold690676_15.9	1	p2	(TA)8	16	255	270	GCAGCACATTGTGGTCTTCA
scaffold690704_17.0	1	p2	(AG)6	12	556	567	TTTGGGGGTGCATATTTCTC
scaffold690737_12.8	1	p2	(AT)8	16	466	481	GTGGATCTGGGCTGCATTAT
scaffold690750_13.1	1	p2	(AG)9	18	914	931	TCAACCACACCTCCAACTCA
scaffold690758_15.5	1	p2	(AT)6	12	277	288	TGCAGTTGAGATAAGGGAGGA
scaffold690803_11.5	1	p2	(TA)8	16	116	131	TGAACATGCTCATATTTTAATACACC
scaffold690930_13.7	1	p2	(TC)7	14	217	230	CATCTCCAATGCCAGGTACA
scaffold691001_17.5	1	p2	(CA)6	12	1035	1046	TCGCATTCTTATTCCGATGA
scaffold691018_12.0	1	p2	(GT)8	16	706	721	TTAACTGCTCCTCCACCCAC
scaffold691045_16.1	1	p2	(TA)7	14	911	924	GCCCACCAATTACAACACCT
scaffold691061_16.0	1	p2	(AT)8	16	1116	1131	CGCATGCACATGCATTATTT
scaffold691064_12.3	1	p2	(TA)9	18	48	65	CCCAAGAATGGGTTATTATTTGA
scaffold691091_15.2	1	p2	(AG)6	12	167	178	AGACCGCAATAGCCACTGTC
scaffold691099_12.7	1	p2	(AG)6	12	732	743	CATGATCTGATGAGGCAGGA
scaffold691146_15.0	1	p2	(TC)6	12	219	230	TTAATCGGGCTCTGAGCAGT
scaffold691192_14.8	1	p2	(AG)6	12	1642	1653	GCCAAAAATGACGTTTTGCT
scaffold691213_14.5	1	p2	(AT)9	18	1587	1604	GCTAGAAGCAGCCGTGACAT
scaffold691246_10.7	1	p2	(CT)7	14	316	329	ATTGAATCTACGTCCACGGG
scaffold691268_12.4	1	p2	(AT)8	16	681	696	CCCTTAGTATGCTGTCCGAAA
scaffold691280_10.6	1	p2	(TC)7	14	170	183	AACAATCAAGCCCACCTCAG
scaffold691333_15.5	1	p2	(TA)6	12	918	929	TGAATTTGGTCTCCTTTGGC
scaffold691363_16.7	1	p2	(CT)6	12	508	519	GGAGAAATAATGACGGCCAA
scaffold691407_12.2	1	p2	(CT)7	14	259	272	TCGACCTCCATTAGAGCACC
scaffold691474_16.4	1	p2	(TA)6	12	139	150	ATTGTCCATGCAACCTACGA
scaffold691593_15.6	1	p2	(AT)8	16	258	273	GCAGACAACTGACAATGCAAA
scaffold691646_13.4	1	p2	(AT)6	12	2611	2622	GTGGAAAGAAGCTAACCCCC
scaffold691649_16.3	1	p2	(CT)8	16	258	273	CTAGATTCTTCGTAGCGGCG
scaffold691728_13.9	1	p2	(GA)6	12	857	868	AAGCCAAGTTAGCTCCCAGA
scaffold691762_11.6	1	p2	(TA)6	12	262	273	TTGTTAGAGGTTTTGACGGGA
scaffold691779_11.3	1	p2	(AT)10	20	87	106	ATGAATGGCCCATATTGGTT
scaffold691833_14.8	1	p2	(AT)6	12	514	525	CGAACATGACACAAATTGCC
scaffold691858_16.3	1	p2	(AC)6	12	1739	1750	CCTCCACGAATGGTTTTGAT
scaffold691883_14.2	1	p2	(AT)6	12	1240	1251	CACGGTCATGAATAAAATCGTT

scaffold691914_15.	1	p2	(GA)6	12	571	582	ACTGACCAAGCATCCTCGAC
scaffold691937_18.	1	p2	(GA)6	12	230	241	TGTTTACATGAAAGCGGTGG
scaffold691994_13.	1	p2	(CT)6	12	1111	1122	CTCACCACACATGCACACTG
scaffold691996_14.	1	p2	(TA)7	14	686	699	GCCCATCGTAACATGAAGGT
scaffold692049_13.	1	p2	(AG)7	14	602	615	CTACATGCTGAGATCGAGCG
scaffold692055_16.	1	p2	(TA)6	12	514	525	AAATAAAGGCTGCATGGCAC
scaffold692075_14.	1	p2	(GA)6	12	487	498	GTTGCAGGGCAATACCATTT
scaffold692083_17.	1	p2	(CA)7	14	3530	3543	TCAAATCCACAATTGCCTTG
scaffold692105_12.	1	p2	(AC)7	14	434	447	GTACGCAGAGCTTTCCCAGT
scaffold692141_11.	1	p2	(TA)6	12	452	463	ATGCCCTTTTCTCGAACATC
scaffold692209_16.	1	p2	(TC)8	16	631	646	TCGTGGCTGGTTAAGCTTCT
scaffold692214_11.	1	p2	(AT)7	14	787	800	AAACACATCTCGAGGGATCG
scaffold692246_14.	1	p2	(AT)10	20	46	65	ATGAAGTTAGGAAATAAGAAGGTGT
scaffold692326_14.	1	p2	(CT)6	12	302	313	CCTTGAAGATCAAGACATCTACTCC
scaffold692347_15.	1	p2	(AT)7	14	668	681	AGGGCAATTGATCTTGCCTA
scaffold692365_13.	1	p2	(GA)6	12	2939	2950	AAAAACAAGAACCCACGCAC
scaffold692395_14.	1	p2	(CT)6	12	305	316	AATGAGACCGGAAATGGATG
scaffold692427_18.	1	p2	(GA)6	12	421	432	TGGTGGAGGCTCGGTTATTA
scaffold692439_11.	1	p2	(AG)6	12	520	531	AGCTTCACCAAGCTTTTCCA
scaffold692495_14.	1	p2	(CT)8	16	192	207	CAACCTCCTGCTGCTTATCC
scaffold692496_13.	1	p2	(CT)8	16	260	275	AAAACTCCAAATCCCCCAAC
scaffold692534_14.	1	p2	(CA)7	14	1866	1879	GAAAATGACCAACCATTCGG
scaffold692561_15.	1	p2	(AC)8	16	323	338	TCAGTGATAGAAATTGAGGGGAA
scaffold692606_11.	1	p2	(AT)9	18	573	590	TTACGGGTTGGGCTGTAGAC
scaffold692616_13.	1	p2	(TA)11	22	44	65	GAGGGTTATCATGGGATCAAG
scaffold692643_18.	1	p2	(TA)7	14	209	222	ATGCCGACACCACACATATC
scaffold692655_16.	1	p2	(CT)6	12	613	624	GGTGCACCCTCACTTTTGTT
scaffold692694_11.	1	p2	(AG)8	16	758	773	TAGGGTTCGAATCCCCACTC
scaffold692704_16.	1	p2	(CT)6	12	2480	2491	TTTCCAGCAAAACATTGACG
scaffold692718_15.	1	p2	(TC)6	12	298	309	TGGGAGAATTGGGCTAAGTG
scaffold692734_16.	1	p2	(TA)6	12	136	147	TCCCATTTTGGGATGAATTT
scaffold692766_17.	1	p2	(TC)12	24	1692	1715	GAACTTCTCCATCAGGGCAG
scaffold692777_12.	1	p2	(TA)9	18	399	416	TGATCTCAAAAGATCAACGGTTT
scaffold692785_17.	1	p2	(CA)9	18	6982	6999	TCTACCTAAAGCACGCCAAAA
scaffold692816_13.	1	p2	(AC)9	18	582	599	CGATGGTTGGAAACAAATGG
scaffold692841_16.	1	p2	(AG)6	12	178	189	ATTCATGAACCACAAAGGGG
scaffold692844_16.	1	p2	(CA)6	12	7067	7078	TCACACCAAAGATGCTGCTC
scaffold692873_14.	1	p2	(AT)8	16	261	276	CAAGTATTGGGGCAGCAAGT
scaffold692938_11.	1	p2	(TA)6	12	907	918	AGTGTTGTACGGCGCTAGGT
scaffold692971_12.	1	p2	(AT)8	16	1081	1096	CCACATAATGTTGCGCATGT
scaffold693010_14.	1	p2	(CT)8	16	621	636	CCTGCTCAAACACATCAGGA
scaffold693084_14.	1	p2	(AT)6	12	353	364	TGGCTTCATGCAAATTCAAG
scaffold693116_17.	1	p2	(AC)6	12	842	853	CACGTTAAATCCCTTGCACA
scaffold693176_13.	1	p2	(AG)6	12	456	467	TTTGTGGTATCAGAGCCACG
scaffold693218_10.	1	p2	(CT)8	16	320	335	TGCAACAACAGAAGGATCAGA
scaffold693236_15.	1	p2	(AG)8	16	251	266	TGTACCGTCCTTTGCATTGA
scaffold693248_12.	1	p2	(TC)7	14	2015	2028	AATGCAAAGGATTTGATCCG
scaffold693278_16.	1	p2	(CT)6	12	3142	3153	CCTTCCTTCTTCCTGTTCCC
scaffold693286_15.	1	p2	(AT)8	16	262	277	GGACGCACCAGATTGTTTCT
scaffold693376_16.	1	p2	(CA)10	20	1203	1222	TGTAAGGTGCTCCACCATGA
scaffold693381_17.	1	p2	(AG)8	16	238	253	AAAATCTTCTCCGCATTTCG
scaffold693433_14.	1	p2	(AT)7	14	435	448	ACATCAAAATCGGCATTTCC
scaffold693436_20.	1	p2	(AG)7	14	264	277	AAATGGCACTTCAATAATGGC
scaffold693497_11.	1	p2	(CT)6	12	41	52	TTTCTCAACCGAGCTCACCT
scaffold693576_16.	1	p2	(CT)7	14	3631	3644	TCATGCAGTTGGGAGATGAA
scaffold693603_11.	1	p2	(AC)8	16	55	70	TGATGTGATTAATTCCCACCATT
scaffold693616_16.	1	p2	(TA)7	14	3339	3352	AAGCGTCGTGGGCTTGTAT
scaffold693624_15.	1	p2	(GA)6	12	1340	1351	TGAGCAATAAATCCAGGGAGA

scaffold693634_10.	1	p2	(AG)6	12	200	211	TGCTTATCCAATCTCCGAGG
scaffold693683_17.	1	p2	(AT)9	18	261	278	CGCCACTCCAAACTTCAAAT
scaffold693684_14.	1	p2	(AT)7	14	265	278	GGGCTGGATACAATCCATCTT
scaffold693686_10.	1	p2	(TG)10	20	416	435	GCTGTGCGTCGATTTCTTTA
scaffold693687_12.	1	p2	(TG)10	20	405	424	GCTGTGCGTCGATTTCTTTA
scaffold693737_15.	1	p2	(TC)13	26	456	481	CAGCAAATCACCTCATCCCT
scaffold693788_12.	1	p2	(GC)6	12	53	64	TGGTTAGGTAAATGGGCCAG
scaffold693825_11.	1	p2	(AT)8	16	160	175	GCAGGTTAGCAGGATAAGGG
scaffold693828_13.	1	p2	(AT)9	18	1464	1481	TCTTGCTAAGAATATTGCAGGAGA
scaffold693835_15.	1	p2	(GA)11	22	2494	2515	TCTGGTTTCCAAACAAAGCC
scaffold693839_10.	1	p2	(TA)11	22	639	660	TAACGCGAATATGCTGATGC
scaffold693852_16.	1	p2	(AT)6	12	1262	1273	AATGCCCCACTAATCCCTTC
scaffold693861_17.	1	p2	(AT)7	14	264	277	GGGAAACTCACTACTCTCATTTCG
scaffold693913_15.	1	p2	(CT)7	14	916	929	CTTCCAGGAAACTCCACTGC
scaffold693956_15.	1	p2	(AT)6	12	918	929	TTGTTCGACGTCACAGCTAA
scaffold693972_16.	1	p2	(AT)6	12	108	119	CCGAATCCCGATAACTAAACA
scaffold693987_15.	1	p2	(AG)8	16	271	286	TGCTGCCTTAATCCACACTG
scaffold693990_11.	1	p2	(AT)9	18	452	469	GCTTCAATCCGTCACTCCTC
scaffold694024_13.	1	p2	(AG)6	12	648	659	AACTAATCGATGCACACCCC
scaffold694026_14.	1	p2	(AG)6	12	428	439	AGAAGTGGCGGAGGAGTCTT
scaffold694035_15.	1	p2	(TA)10	20	69	88	GGTTATCACCTGATTTTCTCCC
scaffold694087_10.	1	p2	(TA)9	18	1064	1081	AGGCCTTACATGCCGATCTA
scaffold694088_13.	1	p2	(TG)8	16	1767	1782	ATGAAGGACAATGGAAGGCA
scaffold694106_11.	1	p2	(TA)8	16	263	278	GGCCGATATTTGCTCACATT
scaffold694107_14.	1	p2	(TA)6	12	267	278	GCACCTCTATGGTTGGGAGA
scaffold694124_15.	1	p2	(CT)6	12	268	279	CACTGCGAGTTCAAGGATCA
scaffold694190_14.	1	p2	(AT)6	12	2480	2491	TTTTGTCGCCAATTGTTTGT
scaffold694231_15.	1	p2	(GT)6	12	126	137	TGAGTGAGTGAGCGTGTGTG
scaffold694269_15.	1	p2	(AT)8	16	830	845	CAGCCACGATGATATGACAAA
scaffold694304_11.	1	p2	(CT)9	18	782	799	CTCAATCGCACCGTCACTAA
scaffold694343_18.	1	p2	(AT)12	24	1068	1091	AGAAGCCTTATTGGAAGCCG
scaffold694371_14.	1	p2	(AG)7	14	159	172	TTCTACCACCACCCATCTCG
scaffold694382_14.	1	p2	(TA)8	16	264	279	ACGCGCGCTTTTAGAGTTTA
scaffold694394_18.	1	p2	(AT)6	12	45	56	TTCATTTTTAAATCCTATATCAACGA
scaffold694408_15.	1	p2	(AT)10	20	375	394	CCCAACCAGGCTGAATAAGA
scaffold694438_11.	1	p2	(GA)6	12	319	330	GGTGCTCAAAAATCCGAAAA
scaffold694445_13.	1	p2	(TA)10	20	59	78	CAGATTTGTTATGCGTTTTGACA
scaffold694489_15.	1	p2	(AT)6	12	269	280	TTCGCATGGGAATATAATGGA
scaffold694508_18.	1	p2	(CA)6	12	720	731	TCCTCCACTACCCAAAACAAA
scaffold694509_14.	1	p2	(TA)6	12	492	503	TGGTGAACAGAAACCCTGAA
scaffold694511_15.	1	p2	(CT)8	16	4678	4693	TCCTCCTCCCTTCCTTCAAT
scaffold694527_17.	1	p2	(TG)6	12	469	480	CAACAAAAATGGCACTCTTTCA
scaffold694540_16.	1	p2	(CA)7	14	2304	2317	CTCAGGAGCAATTGGGTGAT
scaffold694572_12.	1	p2	(TC)10	20	877	896	ATGATTTTGTGGTGTGGGGT
scaffold694600_16.	1	p2	(GA)6	12	187	198	AGGGCTGTCTCTCACTCCTG
scaffold694613_12.	1	p2	(TA)7	14	501	514	TTCACACATGCACCTCACCT
scaffold694620_18.	1	p2	(AG)6	12	1213	1224	ACTGCACTCAACCACAACCA
scaffold694632_16.	1	p2	(AG)8	16	622	637	CCTACCCTCTGTTCCGACAA
scaffold694649_14.	1	p2	(CT)7	14	868	881	GGCCTTTCCATTTTCCTCTC
scaffold694670_17.	1	p2	(TA)11	22	46	67	GGGTGTTTTGACAATATCGC
scaffold694728_15.	1	p2	(GA)8	16	1319	1334	CCCTTTGGTATGAGAAGCCA
scaffold694789_15.	1	p2	(TC)8	16	330	345	GCTCTTCTCCCCCAACTACC
scaffold694792_14.	1	p2	(TG)7	14	725	738	TATGCAGACGAAAAAGCGTG
scaffold694882_15.	1	p2	(AT)8	16	266	281	GCAAGGATTGTAGCAAAGGG
scaffold694884_17.	1	p2	(AT)6	12	1137	1148	TAGCAATCAAGTCCCTTCGG
scaffold694907_13.	1	p2	(CT)6	12	402	413	CATTGCTTTCCGACTGTTCA
scaffold694909_10.	1	p2	(AT)8	16	403	418	TCCTTCCTTGCTCCTTTTCC
scaffold694936_10.	1	p2	(AT)8	16	156	171	TCGATGAATGATGAGAAGCA

scaffold694945_13.	1	p2	(AT)11	22	1051	1072	AACCGAAAAAGAAACCTTTCAA
scaffold695017_13.	1	p2	(TA)9	18	264	281	GGTTTGCGTTAGATATGCCC
scaffold695023_16.	1	p2	(TA)6	12	627	638	ACTTTGATTTCTTGGTGGCG
scaffold695091_15.	1	p2	(CT)6	12	442	453	CCGTAATTTCTCGACACCGT
scaffold695092_16.	1	p2	(TA)6	12	267	278	GTGCTTCCTGAGTACCCTGC
scaffold695097_16.	1	p2	(TC)7	14	311	324	AAACTGAGTGATGCCAGCCT
scaffold695143_10.	1	p2	(TA)10	20	499	518	AAGGCGACATGTTTCAATCC
scaffold695259_18.	1	p2	(TC)9	18	264	281	AGAACCCATGGACATGGAAA
scaffold695306_15.	1	p2	(TA)6	12	1337	1348	TCGTGGAGCAAAAACATCAA
scaffold695328_12.	1	p2	(AT)7	14	269	282	CTTGTGAGCCATGTTGTTGG
scaffold695340_11.	1	p2	(AT)6	12	363	374	CTGTGATGCCACTGCTGTCT
scaffold695375_14.	1	p2	(AT)8	16	768	783	TCAAACCTTGTGACTCTGCAA
scaffold695514_14.	1	p2	(AT)6	12	555	566	CATCTAATGTCCATTTTTGCCA
scaffold695519_15.	1	p2	(CT)6	12	39	50	TTTCTCAACCGAGCTCACCT
scaffold695577_16.	1	p2	(GA)6	12	685	696	CCATCCTGCACCATCATACA
scaffold695582_15.	1	p2	(GA)6	12	1297	1308	AAATTGCACCTCGTCGACTC
scaffold695583_14.	1	p2	(AT)8	16	554	569	GGACTTGTTCCCACTTCCAA
scaffold695589_14.	1	p2	(AT)9	18	988	1005	TTTGGATCCATAACATGAAAAA
scaffold695611_13.	1	p2	(GA)7	14	887	900	GCCAACTTTCTTCATCCGTC
scaffold695629_15.	1	p2	(TC)8	16	1766	1781	TCACCTTCAGGGGACAAAAC
scaffold695676_15.	1	p2	(TA)8	16	49	64	ATGGGTTATTACCGGATCGC
scaffold695714_16.	1	p2	(AT)7	14	285	298	TGTTGCGATTTTCATTTTCC
scaffold695758_14.	1	p2	(TC)6	12	1433	1444	TTCGTCAGTGGATCTTGCTG
scaffold695765_15.	1	p2	(GA)7	14	219	232	AATGAATGGAAACGAGGTGC
scaffold695857_18.	1	p2	(TC)7	14	952	965	AACCACAACCCTTCTCCCTC
scaffold695895_18.	1	p2	(TC)6	12	54	65	CAGAAATTGCCTTGGTTGTTC
scaffold695899_15.	1	p2	(GA)7	14	813	826	CTCTTCAATTTCTCCGCTCG
scaffold695900_15.	1	p2	(GA)7	14	271	284	CGCCAAAAACACAAACAAGA
scaffold695928_16.	1	p2	(AT)6	12	92	103	GAAACCCCCAATTGTCTCAA
scaffold695933_14.	1	p2	(TA)9	18	266	283	ATGTTTTCAATCTTGGCCGT
scaffold695939_12.	1	p2	(TA)6	12	273	284	GCACCGGATTGTTTCTCATT
scaffold695952_13.	1	p2	(TA)9	18	1836	1853	GATTTATCGATCAACCATTTCTTTT
scaffold695977_12.	1	p2	(TA)7	14	51	64	CCAATTTGAATGGTTATCACCTG
scaffold695991_16.	1	p2	(CT)9	18	267	284	GGGTTGCAAGAAACCTTTGA
scaffold696009_16.	1	p2	(AG)6	12	940	951	TTCAGAGGCGAGAACCAACT
scaffold696017_14.	1	p2	(AT)8	16	908	923	TGGTTTCACCAAAAACCGAT
scaffold696040_15.	1	p2	(TA)8	16	649	664	TGATTTGCATGCGTACTTGA
scaffold696041_15.	1	p2	(AC)6	12	605	616	AGGGAAACGTTTTGGTGTTG
scaffold696116_15.	1	p2	(AG)7	14	184	197	ATACATGGCACAAAGCGACA
scaffold696118_13.	1	p2	(TA)9	18	639	656	CGGATCACCTAGGTTTTGGA
scaffold696155_14.	1	p2	(CT)7	14	136	149	ATTCTGCTTTCCACGTGCTT
scaffold696185_14.	1	p2	(CA)7	14	494	507	CTTTGGAGTTAATCCGCTGC
scaffold696222_15.	1	p2	(TC)8	16	807	822	CAGCTGCACCACAGAAGAAA
scaffold696259_21.	1	p2	(TA)7	14	88	101	CACATGAATGGATGTGATTTGTT
scaffold696282_19.	1	p2	(AT)10	20	107	126	CCATTTGCAATGGACAAAAA
scaffold696299_13.	1	p2	(AT)9	18	488	505	CAACAGGGAGAGATTGAGATTG
scaffold696313_16.	1	p2	(CT)7	14	271	284	TCATGTCTCTTGGCCTTGTG
scaffold696314_16.	1	p2	(TC)6	12	359	370	GGCAAAACCATCCTTTACGA
scaffold696328_13.	1	p2	(TA)9	18	267	284	AAAGGCTTGCTAGTGGTTGG
scaffold696364_14.	1	p2	(TG)7	14	1178	1191	ATCGAATGCACACACTTCCA
scaffold696392_15.	1	p2	(AG)9	18	705	722	GTGCTGTGTTGAAACCCCTT
scaffold696393_16.	1	p2	(CT)6	12	274	285	CCCCAAATTGATGGTTTCAT
scaffold696405_20.	1	p2	(GA)6	12	190	201	CCTTCCCTTGACGACTTACG
scaffold696407_12.	1	p2	(TG)7	14	287	300	TTCCACTTCTTGTTGTGATTGC
scaffold696457_11.	1	p2	(CT)9	18	672	689	GCATGCGGGGACATAATCTA
scaffold696458_14.	1	p2	(TA)7	14	969	982	GCTTATGAGGGTGAGTTGGC
scaffold696459_16.	1	p2	(TA)7	14	974	987	TGGCCGAAAATTAGAGATGG
scaffold696479_19.	1	p2	(TC)6	12	888	899	GCCTTCTCTCAAATAAGGGTG

scaffold696512_17.	1	p2	(TC)7	14	319	332	TCCACGTTTCCATCTTCCTC
scaffold696581_17.	1	p2	(TA)6	12	370	381	AGTCCGAGGATAACCCTTCC
scaffold696598_16.	1	p2	(GA)6	12	101	112	GCAGAAAGACATTGATAACCACC
scaffold696695_10.	1	p2	(TC)6	12	412	423	AAATCGAGACACCGACGAAC
scaffold696710_14.	1	p2	(AT)7	14	179	192	CCCCTCCTCTCGAACTCTTT
scaffold696750_11.	1	p2	(TA)9	18	44	61	TTTAGTGTTTTGACATGATTACTCG
scaffold696759_12.	1	p2	(AT)10	20	356	375	AAACTGGACTGGGTATCAACAA
scaffold696762_16.	1	p2	(TC)8	16	270	285	CTTTTTGGCAATTCCCTTCA
scaffold696792_11.	1	p2	(TA)8	16	252	267	CAACAACACATGCTTCGACA
scaffold696857_18.	1	p2	(AC)8	16	270	285	ACGTGCCAAGACTCAAAACA
scaffold696911_15.	1	p2	(AT)7	14	1055	1068	CTGAGCCCTTCTTATTCATGTT
scaffold696927_18.	1	p2	(CA)7	14	2114	2127	TCTGGCTGTGTTCGTTCTTG
scaffold696941_11.	1	p2	(CA)7	14	344	357	CGGCCAAACCAATAAATACG
scaffold696975_15.	1	p2	(AG)6	12	519	530	ACACACCCCAAAAGAAGACG
scaffold696980_13.	1	p2	(AG)10	20	1623	1642	CTTCAGCTTCATTTGCCCAT
scaffold697029_16.	1	p2	(AG)6	12	1626	1637	GCACATCAACACTCGCAAAT
scaffold697073_15.	1	p2	(AG)6	12	3398	3409	CCGTGACAGGTCAAAACCTT
scaffold697080_18.	1	p2	(GA)8	16	762	777	TCAGCTGAAGGAGGAGGAAG
scaffold697094_15.	1	p2	(TG)7	14	3606	3619	CTCCAACTCTCACCCAGAGC
scaffold697124_13.	1	p2	(AT)6	12	104	115	TCATGCAATCACTATTAAGACTCCA
scaffold697131_15.	1	p2	(TC)6	12	322	333	CAGCGTTCTGTCGAAATCAA
scaffold697132_12.	1	p2	(AT)6	12	502	513	CCAAGGCCGTACCTACTCAA
scaffold697140_14.	1	p2	(CT)8	16	777	792	AGAAAAATGCACACTCGCAA
scaffold697194_15.	1	p2	(TG)6	12	868	879	GGTCTTGCCGGATTCATCTA
scaffold697224_12.	1	p2	(AC)8	16	3087	3102	CTGCATTAACCCCGCTTAGA
scaffold697232_15.	1	p2	(CT)6	12	395	406	TCCCTTCTCTCCCACTCATC
scaffold697267_13.	1	p2	(TA)10	20	675	694	CCTTTTCTTAGGCGTTCTTGC
scaffold697295_15.	1	p2	(TC)8	16	2837	2852	CCCTCGATTGTCTTAATCGG
scaffold697300_13.	1	p2	(AT)7	14	239	252	GCGTGAGTCGGTGAGTGTAT
scaffold697323_16.	1	p2	(GA)9	18	233	250	GCTGAGGGGAGACTACATGG
scaffold697413_12.	1	p2	(TA)7	14	835	848	CGTTGGCAAGGTATCGATTT
scaffold697448_10.	1	p2	(AT)10	20	1384	1403	GGATGGAATGGATGTTTGGA
scaffold697449_18.	1	p2	(GA)6	12	593	604	TCCATTTAATATGTCGATGACCA
scaffold697462_17.	1	p2	(CA)6	12	93	104	CTAACCTTGGGCTTTGATGC
scaffold697511_10.	1	p2	(CT)7	14	488	501	GGGGGAGGAGAAGATAGCTG
scaffold697522_12.	1	p2	(TA)6	12	404	415	CTAAGGCTGATGGGGTTCAG
scaffold697531_15.	1	p2	(CA)6	12	169	180	CCTTATCCAACGCTCCGTTA
scaffold697547_14.	1	p2	(GA)6	12	4832	4843	TTGAGATTCCGTGAGGACTG
scaffold697582_18.	1	p2	(AT)6	12	772	783	AAAACTTGACCCGATCATTG
scaffold697623_18.	1	p2	(CT)6	12	655	666	CAGCAAAATCCTTCACCTCAG
scaffold697638_13.	1	p2	(AT)10	20	330	349	GCACCAAAAAGGAAAAATAATCC
scaffold697661_11.	1	p2	(AT)8	16	498	513	TTACCTCTGTTGGTGCAACTT
scaffold697701_13.	1	p2	(AG)8	16	186	201	TTTCTTTGTTACCATGGGGG
scaffold697715_16.	1	p2	(TA)6	12	625	636	GGACAAAACGGGAAATAGCA
scaffold697751_16.	1	p2	(TA)7	14	94	107	CCCGTATACACACCACGGAT
scaffold697798_15.	1	p2	(TA)9	18	271	288	CGGCATGTTCCTCAACTACA
scaffold697842_13.	1	p2	(GA)10	20	692	711	TAGACGAAGGTCGAAATGGG
scaffold697898_15.	1	p2	(TC)6	12	268	279	GTGTTGGGCCGTGTTCTACT
scaffold697926_13.	1	p2	(AT)6	12	144	155	GTAGCTTCAAACTCCCGCTG
scaffold697965_15.	1	p2	(TA)9	18	2628	2645	TGAGTAAAAGCACGATTTTGGA
scaffold697991_13.	1	p2	(TC)6	12	452	463	AATTTCGTCCAGCCATTCAC
scaffold698043_15.	1	p2	(AT)7	14	276	289	TGCAAGCACACTCAGACACA
scaffold698057_14.	1	p2	(CT)6	12	585	596	GAGGCAAAGCAAGGCATAAG
scaffold698059_14.	1	p2	(GA)12	24	3524	3547	CGAGTTCTTGATGCTGGTCA
scaffold698107_12.	1	p2	(AT)7	14	166	179	CGATTAAAAACCAGACCGGA
scaffold698124_13.	1	p2	(AT)11	22	1711	1732	ACTTACCGTCATTTCCGTCG
scaffold698138_12.	1	p2	(CA)7	14	1517	1530	CACACTAAATTGGTGATGGATGA
scaffold698179_10.	1	p2	(AT)9	18	430	447	GGCCTAGGTTTCGAGGTAGG

scaffold698215_10.	1	p2	(AT)8	16	891	906	TTTTCCCATGAAGCCAAAAC
scaffold698296_15.	1	p2	(TG)6	12	690	701	GCGCTCAAACTTAAGCATCC
scaffold698324_12.	1	p2	(TA)6	12	337	348	AAATATCGGCCGTCAGATTG
scaffold698332_16.	1	p2	(AG)8	16	868	883	TGCACTCTGTGATGGGAAAA
scaffold698336_15.	1	p2	(TC)8	16	715	730	GTGCAGCAAAATTGCTTTGA
scaffold698341_14.	1	p2	(TA)9	18	576	593	GCCTTCCATTCCAAAAATCA
scaffold698395_15.	1	p2	(CT)6	12	2276	2287	AGTGAGGGAAAGTGAAGCGA
scaffold698414_15.	1	p2	(TA)8	16	46	61	TGAAGTTAGGAAATAAGGAGGTGTT
scaffold698467_15.	1	p2	(AG)7	14	308	321	TTCGTATTTGTCTAGCGCCC
scaffold698479_17.	1	p2	(AC)8	16	961	976	CTTGAAATTCGCAACAGCAA
scaffold698504_12.	1	p2	(AT)7	14	278	291	AATCTGACGGCCGATATTTG
scaffold698513_11.	1	p2	(CT)6	12	174	185	TGGTGCAACCATTGGAGATA
scaffold698532_17.	1	p2	(GA)6	12	1267	1278	AGTCAGCGGAACCGTATCAC
scaffold698554_13.	1	p2	(AT)9	18	75	92	TGAAGTTAGGAAATAAGGAGGTGTT
scaffold698565_14.	1	p2	(TG)7	14	618	631	AATTTAAAGCCTTGTGCCCC
scaffold698587_14.	1	p2	(TA)7	14	905	918	TTTGATGGCTTGAGTTTCCC
scaffold698596_12.	1	p2	(AC)6	12	599	610	CGAAAAGACACGCACACACT
scaffold698639_16.	1	p2	(TG)6	12	1399	1410	ATCACAACTAGGGCTGACCG
scaffold698705_18.	1	p2	(AG)6	12	203	214	TTTCATTTGGATTTCCGAGC
scaffold698714_14.	1	p2	(CT)6	12	427	438	TCTTCCCTCTCTCCCCATTT
scaffold698744_15.	1	p2	(TG)6	12	907	918	AACTCAAGATTCTGCATCGGA
scaffold698748_17.	1	p2	(TA)8	16	151	166	CTGTGTGATGTGGAGTTGGG
scaffold698749_16.	1	p2	(AT)6	12	3614	3625	ACAGGAATTCGCTTTCTCCA
scaffold698759_14.	1	p2	(TA)10	20	273	292	TCACCCGGACCTCTTCTTAG
scaffold698799_13.	1	p2	(AT)11	22	1285	1306	ACTGTCAACCCCTCCCTTCT
scaffold698822_15.	1	p2	(TA)6	12	280	291	CGAAATTGAGCTTTTTGGGA
scaffold698829_14.	1	p2	(AG)7	14	390	403	ACCACCCCAACACACAAAAT
scaffold698845_16.	1	p2	(AC)7	14	357	370	TATATGGGCCGTTAGATCGC
scaffold698906_17.	1	p2	(TC)8	16	1052	1067	AAGCATTTCATTGGGCAGAG
scaffold698943_15.	1	p2	(CT)8	16	520	535	TAGCGTGCCTATTGCACATT
scaffold698972_12.	1	p2	(AT)10	20	2017	2036	AACGCCGTCTGGATTTTATG
scaffold698973_14.	1	p2	(TA)10	20	645	664	AAACCCTGTCGTATCTCATATTACAC
scaffold698996_14.	1	p2	(TC)6	12	340	351	ATCACGAGTTTTTCCCTTAAAA
scaffold699029_14.	1	p2	(AT)9	18	211	228	CACCGGTGAATGGAAAAATC
scaffold699067_12.	1	p2	(TA)6	12	208	219	TCACATTAAATTTGGCGCAG
scaffold699077_13.	1	p2	(AT)8	16	741	756	GATTAGCAAATTTCGGGACG
scaffold699082_14.	1	p2	(GA)7	14	492	505	ACAACAATCAGCACACGGAT
scaffold699096_12.	1	p2	(TA)8	16	712	727	TCATGATTTGGCTTTAGGGC
scaffold699102_17.	1	p2	(AT)7	14	164	177	ATGAACAGAGCATTCCGTCC
scaffold699164_15.	1	p2	(AG)10	20	273	292	AGTGCAAGGACAAATGGGAG
scaffold699181_16.	1	p2	(CT)8	16	138	153	AAGTTGACGCCTCACTTCGT
scaffold699189_14.	1	p2	(TG)6	12	74	85	CAAGAGTTGAAAATCCTCCCA
scaffold699279_13.	1	p2	(GA)6	12	418	429	TAGGGTCCCACCACCTAACA
scaffold699298_16.	1	p2	(TC)6	12	281	292	TGCTCCGTTTTCGATTCTCT
scaffold699304_12.	1	p2	(TA)10	20	45	64	ATCGGTTATTACCGGATCGC
scaffold699331_15.	1	p2	(CT)6	12	968	979	AAAGTGCAGCCCACCATTAC
scaffold699389_13.	1	p2	(GA)8	16	77	92	TCTCAGATGTTTGGTCGGAA
scaffold699394_14.	1	p2	(CT)8	16	279	294	TGGGTTTCATCAAGATTGGA
scaffold699411_12.	1	p2	(TA)9	18	1127	1144	AGTGGTAGGCCGAGTTCAAA
scaffold699458_12.	1	p2	(CA)6	12	164	175	AGTTGGGTTGGAGCATTGAG
scaffold699486_15.	1	p2	(AG)8	16	1039	1054	TCAAGAAAGAATGTGGAGCAAG
scaffold699491_14.	1	p2	(AT)6	12	2703	2714	GCACATAGCGTCTTCGTCAA
scaffold699495_16.	1	p2	(CT)7	14	68	81	TTCCTTTCTTGCTTGTTTCTTTC
scaffold699501_13.	1	p2	(TA)6	12	776	787	GCACATTTTATTTTGGGGGA
scaffold699523_13.	1	p2	(CA)6	12	434	445	TTTCCACCATGATATCGACAC
scaffold699527_10.	1	p2	(TC)6	12	41	52	GGCAACGGAATACCATTTGT
scaffold699550_16.	1	p2	(TG)6	12	5903	5914	CAAGAGCGCCTCAAAAATTC
scaffold699573_13.	1	p2	(AT)10	20	110	129	AGGTTAGCACGATAAGGGCA

scaffold699579_15.	1	p2	(GT)6	12	337	348	CGTGTCCATTGAGTACCTCG
scaffold699582_14.	1	p2	(TA)11	22	1316	1337	CTATCCTTTGCTTCAACCGC
scaffold699608_14.	1	p2	(TA)7	14	50	63	TGAAGTTAGGAAATAAGGAGGTGTT
scaffold699617_15.	1	p2	(AT)8	16	631	646	TTAGGACCCATAATCTGCCG
scaffold699694_16.	1	p2	(TA)6	12	1864	1875	GTGGTTTAGGTGAACCCCTG
scaffold699728_16.	1	p2	(AT)6	12	365	376	GGTTCAAAACCATGATTCCA
scaffold699746_16.	1	p2	(CA)6	12	4086	4097	GCGGTACAGTTGAACCACAC
scaffold699762_13.	1	p2	(TA)8	16	128	143	AGCACTGAAAACCCAGCCTA
scaffold699765_17.	1	p2	(TG)8	16	279	294	AACAGTTCGCTGCAACAGG
scaffold699767_14.	1	p2	(TA)7	14	281	294	CGTAGGAACTTACACAAAGTTGG
scaffold699770_13.	1	p2	(AT)6	12	53	64	AAGGGCATTGTTGTACATTGG
scaffold699781_12.	1	p2	(GA)7	14	73	86	TTCAAATTTGTTATTGATACCGATG
scaffold699784_11.	1	p2	(TC)6	12	574	585	TCCTTCCACATCTCTCCGTC
scaffold699796_16.	1	p2	(AT)6	12	284	295	ATCAAGTTCCTGCCCCTTCT
scaffold699799_14.	1	p2	(AT)6	12	864	875	CGTGAATACACCAAACGCAC
scaffold699836_17.	1	p2	(CT)6	12	555	566	CTGTCTCCTCCACCTCTTCG
scaffold699854_15.	1	p2	(AT)6	12	141	152	GGCTAGCACAAATCTCTGGC
scaffold699868_18.	1	p2	(TC)8	16	1826	1841	ATCCTTTATGGCGTTTGCAG
scaffold699932_11.	1	p2	(TA)7	14	215	228	TCACGCGGAAATAAATCCAT
scaffold699968_19.	1	p2	(AT)6	12	760	771	GCACCTTTCCTGAGACCAAT
scaffold699989_14.	1	p2	(CT)6	12	364	375	GTTGCTTTGCAGACCCTCTC
scaffold700021_18.	1	p2	(GT)8	16	106	121	CGGAGATCCAATCTCGTTTC
scaffold700025_13.	1	p2	(AT)6	12	83	94	CATCCCTATCAACTCTTTCGATG
scaffold700058_12.	1	p2	(TA)8	16	328	343	TCAAATGCACTTCATAAGCCC
scaffold700123_12.	1	p2	(TA)7	14	283	296	TTGAACACACAGTTCATGCCT
scaffold700129_13.	1	p2	(AT)7	14	283	296	GAAATTCTAGGTCCGCCTCC
scaffold700130_16.	1	p2	(CT)7	14	644	657	TCGAAGCAAAGTCCTCATCC
scaffold700153_12.	1	p2	(TA)10	20	518	537	TGACGCCCCAGATTGTTTAT
scaffold700155_15.	1	p2	(AT)8	16	562	577	GAGCAACACAACCACGTGAC
scaffold700161_13.	1	p2	(TA)6	12	1033	1044	TGGGTTTTACACATTGGCATT
scaffold700191_16.	1	p2	(GA)9	18	3351	3368	AATTGCGGACGTAGTTGACC
scaffold700269_15.	1	p2	(TA)6	12	119	130	GATCATTTCCAAAAACAATGATG
scaffold700275_12.	1	p2	(AT)6	12	284	295	GGAACTACCATTTTTGAATTGGA
scaffold700290_11.	1	p2	(TA)7	14	458	471	AAATCATGAGCGTCCGTCTT
scaffold700300_10.	1	p2	(GA)6	12	618	629	ACCCTTTCCATCGTGAGAGA
scaffold700303_11.	1	p2	(TA)7	14	161	174	TCCATTCCGAAAATCAAAGG
scaffold700392_17.	1	p2	(TG)9	18	980	997	ACCACCACAGTTCACTGCAA
scaffold700399_17.	1	p2	(CA)6	12	1299	1310	GGTGTCAGGCATGTTTGTTG
scaffold700408_16.	1	p2	(AT)6	12	337	348	CCAGTTCACTCGAATCTCACC
scaffold700435_15.	1	p2	(AC)8	16	730	745	ATCGTGTCCTTCTGGCATTC
scaffold700446_13.	1	p2	(GA)8	16	73	88	TTCAAATTTGTTATTGATACCGATG
scaffold700452_15.	1	p2	(AG)7	14	284	297	CAGACCATTCGAAAACAGCA
scaffold700474_14.	1	p2	(AT)9	18	116	133	GATGTCTTTTGATCAGTTGGTGA
scaffold700522_16.	1	p2	(TG)6	12	2329	2340	AACCGAGAGCATAACCTGACA
scaffold700534_16.	1	p2	(TG)7	14	1299	1312	TGCATTATCGCATCAGGAAA
scaffold700643_16.	1	p2	(TA)10	20	43	62	TTTAGTGTTTTGACATGATTACTCG
scaffold700675_16.	1	p2	(TG)7	14	519	532	AAAATAAAGCTGGGCTGCTG
scaffold700676_13.	1	p2	(AT)8	16	564	579	AACTTCATTATTTGGGGGTGC
scaffold700709_14.	1	p2	(AT)9	18	2037	2054	CCTCCTCAACAGAGGATATAGGA
scaffold700733_13.	1	p2	(TA)10	20	540	559	CCACTCTTTGACTCCCCAAA
scaffold700829_15.	1	p2	(TA)10	20	572	591	GTCGGACGAAACCATGAAAC
scaffold700973_15.	1	p2	(CT)6	12	659	670	CCCTAACTCTTGCCCCTTTC
scaffold700996_16.	1	p2	(AG)10	20	565	584	CGAGCCTCAGCCAAAATCTA
scaffold701008_13.	1	p2	(TA)7	14	497	510	TCCACATCACATGACCTTCTG
scaffold701035_15.	1	p2	(GA)8	16	590	605	TCTCATCTGCTTGTCGTTGC
scaffold701119_22.	1	p2	(GT)6	12	489	500	GTAGGGGGCAGACATTAGCA
scaffold701120_15.	1	p2	(AG)6	12	426	437	AGAATTGAGACCCATGCACC
scaffold701150_16.	1	p2	(AT)6	12	1545	1556	GAAATTGCTAGTTCGGGCCT

scaffold701172_11.	1	p2	(AT)6	12	74	85	TTACGCTAGTCCGTGGGTTT
scaffold701181_11.	1	p2	(TA)8	16	49	64	TGAAGTTAGGAAATAAGGAGGTGTT
scaffold701205_11.	1	p2	(TA)13	26	754	779	TGCATGCATTTTAGCTTTGG
scaffold701296_14.	1	p2	(TA)9	18	282	299	GGATTAGGTGGACATTTGGG
scaffold701333_17.	1	p2	(TA)8	16	177	192	AAAATGCCCTTGTATGCTGC
scaffold701353_18.	1	p2	(AT)7	14	139	152	ATAAAAATGGCACCTGGCTG
scaffold701393_13.	1	p2	(AC)7	14	1012	1025	TGATTCACCTCCCATGATCC
scaffold701399_12.	1	p2	(AG)6	12	376	387	ATGGGTTCGAGTCTCAATGG
scaffold701445_11.	1	p2	(AT)9	18	406	423	TCCCGAAATCCGAATAAAAA
scaffold701452_13.	1	p2	(TA)6	12	1491	1502	TGGTGATTGATCCACCTACG
scaffold701459_18.	1	p2	(TA)6	12	422	433	AAGAGACAAACAAGCATGGGTT
scaffold701464_13.	1	p2	(AC)6	12	241	252	GCTTTAGAGATGGGAGCACG
scaffold701485_16.	1	p2	(CT)14	28	680	707	CATTCATATGAGGATGGCCC
scaffold701490_10.	1	p2	(TC)7	14	490	503	CGGTACGGTAACGGTAAGGA
scaffold701516_14.	1	p2	(CT)6	12	94	105	TCTTCACCACCTGAAGAGGG
scaffold701541_15.	1	p2	(TA)6	12	80	91	ATTTGCTTGATCCAACGGTC
scaffold701583_11.	1	p2	(TA)6	12	53	64	CCAATTTGAATGGTTATCACCTG
scaffold701631_15.	1	p2	(GA)8	16	551	566	CAGAGGAGCCTCAAGATTGC
scaffold701680_16.	1	p2	(CA)6	12	638	649	TCAGAGTGCTCAAAACCAAGAA
scaffold701744_15.	1	p2	(AT)7	14	1248	1261	CGAAACCCTCTCTAATTTGATTGA
scaffold701747_14.	1	p2	(AT)8	16	1157	1172	GGGTTATTATTTGATCACCTCCC
scaffold701749_16.	1	p2	(TA)10	20	738	757	ATAAAACGTGGAGCGAGCAT
scaffold701775_18.	1	p2	(CT)6	12	1601	1612	CTGCGAGTCATGCTCGATTA
scaffold701814_16.	1	p2	(TC)6	12	290	301	TTTGCATGAGACGCCAATAG
scaffold701909_16.	1	p2	(GA)7	14	502	515	AACACCAAAATATCGTCCCG
scaffold701924_13.	1	p2	(AT)7	14	534	547	TGAAGAAGATTCTCATCCCACA
scaffold701930_17.	1	p2	(TG)7	14	528	541	ACATTGTATTGGGCTGCTCC
scaffold702003_16.	1	p2	(TC)6	12	782	793	CCACTCGATTTTGCTGGTTT
scaffold702100_15.	1	p2	(AC)7	14	1620	1633	TAAAAGTTGATGATCCCCGC
scaffold702171_15.	1	p2	(AG)8	16	1031	1046	TGATTCAGAATTTCTCCAGATGC
scaffold702185_12.	1	p2	(AG)8	16	119	134	TGTGAGGGACACAATTCTTGA
scaffold702196_16.	1	p2	(AC)7	14	3659	3672	AAATTCCAATGGTGGCCTCT
scaffold702232_14.	1	p2	(AT)8	16	1014	1029	ATGCAAGTTTTGCTTCCCAA
scaffold702260_18.	1	p2	(AG)6	12	28	39	GAGCAGGGAGATAAGAGAGAGAA
scaffold702277_12.	1	p2	(GA)6	12	2226	2237	TGCATTCTTGGAACCACTTG
scaffold702324_12.	1	p2	(AT)6	12	490	501	GGAGTTTCCGGTGTTGAAGA
scaffold702329_18.	1	p2	(CT)7	14	1354	1367	CCACAATTTCGATCTCTCCTC
scaffold702355_15.	1	p2	(AT)8	16	942	957	GGTAAACATGCACAGGTATAGACG
scaffold702425_13.	1	p2	(CT)12	24	3604	3627	AGACCCAAAAAGTAGGCCGT
scaffold702488_14.	1	p2	(TA)6	12	292	303	CAACCATTGATTCCCGAGAT
scaffold702519_17.	1	p2	(CT)7	14	2282	2295	TCAATCCTTGTCACCAACCA
scaffold702561_16.	1	p2	(AT)7	14	291	304	GGACACGCGGATCAGTATCT
scaffold702579_12.	1	p2	(AG)12	24	1220	1243	TGCATTTTAAAGGTCCCAGAA
scaffold702581_14.	1	p2	(CT)6	12	1015	1026	GAAATGGGAGAGCCAAACAA
scaffold702602_16.	1	p2	(AG)7	14	867	880	CCCAGAAGCAGATCCATGTT
scaffold702605_19.	1	p2	(TC)7	14	291	304	TCCTTGACCGCGTAAAGATT
scaffold702683_14.	1	p2	(AT)8	16	288	303	TTCATGCATTCACCATACGAA
scaffold702692_16.	1	p2	(TC)9	18	2966	2983	AGCACCGTGTACTCTGCCTT
scaffold702733_16.	1	p2	(TC)6	12	1338	1349	TCGCTACCACGAACTAACCC
scaffold702762_14.	1	p2	(GA)10	20	2652	2671	ATTTGGTCCCGTACAAGCAG
scaffold702813_16.	1	p2	(AC)6	12	2850	2861	CGTTTCTTCCCTCATTTCCA
scaffold702828_15.	1	p2	(CA)6	12	293	304	GACTTGCTTGCAAGAACATACA
scaffold702846_14.	1	p2	(AT)6	12	2332	2343	CCACTTCAAGCAGTGCAGTC
scaffold702865_10.	1	p2	(TA)8	16	421	436	GAATCTCAGCCACAAAATTCG
scaffold702867_16.	1	p2	(TA)8	16	49	64	GGGTTATCATGGGATCCATTC
scaffold702908_15.	1	p2	(TA)7	14	291	304	AAGAAGCAATGGTCGCAAGT
scaffold702923_15.	1	p2	(CA)7	14	397	410	TCCAACTGGTTTGGTGGTTT
scaffold702947_15.	1	p2	(GA)11	22	51	72	GGAGGAAGCATTGGACTTTG

scaffold702958_17.	1	p2	(TA)6	12	2745	2756	CCTTTTTGCTTTATTAGAAACCTG
scaffold702968_14.	1	p2	(CT)6	12	690	701	TTTTCGGTTTGTCTCATCCC
scaffold702997_17.	1	p2	(AT)7	14	108	121	GGCGTGACACCATGTAAAAG
scaffold703028_14.	1	p2	(AT)7	14	808	821	TTTTTGGTGGCGGTAGGTAG
scaffold703079_12.	1	p2	(TC)8	16	640	655	TTTTGTTTCCCTTTCGATGC
scaffold703095_13.	1	p2	(AG)6	12	544	555	CATTGATGGACCTGCTCTCA
scaffold703124_13.	1	p2	(AT)10	20	2027	2046	TCTACTATACCCTTGCAAATTATCAG
scaffold703139_15.	1	p2	(AC)8	16	164	179	TTTGCATCGAGACCAGTTTG
scaffold703140_14.	1	p2	(TA)6	12	294	305	TTCACAAGATTGTATGGTCCTTG
scaffold703148_14.	1	p2	(AT)6	12	1082	1093	TATACACCCCGCATCCATTT
scaffold703157_16.	1	p2	(TA)9	18	205	222	TCCAATTTGCCCTTTTATGC
scaffold703180_17.	1	p2	(AT)6	12	2353	2364	AAGTTAGGCCTGCCATTGTG
scaffold703225_18.	1	p2	(TA)9	18	71	88	TTCCAAATGAAATGAAAACCG
scaffold703256_14.	1	p2	(AG)7	14	292	305	AAAATGGCGGTCAACTCAAG
scaffold703292_14.	1	p2	(GA)7	14	1159	1172	ACATGACTCGAGCCTGTCCT
scaffold703348_15.	1	p2	(GA)7	14	1022	1035	CCTACGAAGAAATACTGCGCTT
scaffold703349_16.	1	p2	(AT)6	12	1071	1082	TCTTTGTGGGGAAGAACAGC
scaffold703360_22.	1	p2	(CT)6	12	540	551	CACCTCCATCTCTGCTCCTC
scaffold703362_10.	1	p2	(AG)8	16	41	56	CATGCATGAGCAAGAGACAGA
scaffold703371_15.	1	p2	(AG)6	12	295	306	TTCCATTTCGTGATTCCTCC
scaffold703402_16.	1	p2	(GA)6	12	62	73	CAACCATTATTATTCCAATCGAAC
scaffold703406_13.	1	p2	(GA)6	12	624	635	CATGCATTCGCAAAGAAGAA
scaffold703428_15.	1	p2	(AT)8	16	2617	2632	CTTTTCCCCCAGATGTCTCA
scaffold703442_16.	1	p2	(CA)7	14	3063	3076	GGTCGAACACTCAGCAGTCA
scaffold703448_10.	1	p2	(TA)7	14	149	162	TTTATGCGGCATTCATGTGT
scaffold703463_15.	1	p2	(TC)9	18	289	306	CTGCATTTTCTGCTGGTTCA
scaffold703489_15.	1	p2	(TA)6	12	909	920	ACGAAAACAAAAGGTACGGA
scaffold703502_15.	1	p2	(TA)7	14	153	166	TGCAATGCATGGAGGAAATA
scaffold703586_18.	1	p2	(AT)7	14	2880	2893	GGCGTTTGAATTAGCCTTGA
scaffold703621_12.	1	p2	(TA)6	12	717	728	CGGTTTGAGAACCAATGACC
scaffold703629_14.	1	p2	(AC)6	12	4470	4481	ATCTTTCTTGGGGCCATCTT
scaffold703634_14.	1	p2	(AT)9	18	559	576	TGGCACACTCTCATTGCTTC
scaffold703650_10.	1	p2	(CT)6	12	310	321	TGGAACACATGCCCAGAATA
scaffold703673_13.	1	p2	(AG)12	24	33	56	GTAGATGCGTGTGGTCGATG
scaffold703695_13.	1	p2	(AT)7	14	1036	1049	TTTCCCTATGAAAACCGTGC
scaffold703697_13.	1	p2	(AT)6	12	162	173	GGAATAAACGGCCAATTCAA
scaffold703698_18.	1	p2	(CT)7	14	93	106	ACAAAGCCACCGTCAGAGTC
scaffold703701_17.	1	p2	(AG)6	12	1771	1782	CTGCTTTGTCCAGCATTTCA
scaffold703706_19.	1	p2	(TA)8	16	434	449	AATTGTGCATGCCTGTTCAT
scaffold703716_13.	1	p2	(AT)8	16	189	204	GATTCCGGTTTCAAATCCAA
scaffold703717_15.	1	p2	(TC)6	12	1646	1657	TTCATTATCATCCGCCTTCA
scaffold703743_13.	1	p2	(TC)6	12	949	960	ATGGACCAATGCACCAAAAT
scaffold703754_14.	1	p2	(AT)6	12	88	99	ACAATTTGCTGTGGCTGATG
scaffold703779_15.	1	p2	(AG)6	12	204	215	AATAGGCGCTTCGAGAAGGT
scaffold703824_17.	1	p2	(TG)7	14	1588	1601	CATGTTTGCCTGTTTTGTGG
scaffold703847_13.	1	p2	(AC)6	12	296	307	TGCATCGATGATCTTGAAGG
scaffold703877_13.	1	p2	(TA)9	18	69	86	TTGAGCGACGTATCTCCTTG
scaffold703881_14.	1	p2	(AT)13	26	2014	2039	AGGAAAATGTGATAGCAGCG
scaffold703903_12.	1	p2	(TA)6	12	340	351	TCATATCATTGTTTCCGCGA
scaffold703910_16.	1	p2	(TA)8	16	469	484	ATCCGGATCTGATTCGATTG
scaffold703922_16.	1	p2	(GA)6	12	403	414	TCCACAGAGATTTCCCACATC
scaffold703968_16.	1	p2	(TA)7	14	52	65	GGTGACGATGGTGATTGATG
scaffold703979_17.	1	p2	(CT)6	12	298	309	TCCAGAACATAAACACCGCA
scaffold703985_11.	1	p2	(AT)10	20	322	341	CTGGTACGTGCGACGTATTG
scaffold704017_13.	1	p2	(CT)11	22	588	609	TGACTTGGTGAGTGCAAGAGA
scaffold704024_13.	1	p2	(TA)7	14	894	907	ACTCAAGTGGGGGATTGTTG
scaffold704079_14.	1	p2	(AT)9	18	292	309	TGATGATGATGGATTTAGCGA
scaffold704103_13.	1	p2	(TA)12	24	874	897	GAAGACTCAATCATGGGCGT

scaffold704106_19.	1	p2	(CT)8	16	864	879	TTGGTGATGTGCGTTTTGAT
scaffold704125_11.	1	p2	(AT)7	14	365	378	GCTGGTCGGTTAATTCCTCA
scaffold704226_14.	1	p2	(TA)7	14	94	107	ATCCAAGCCATTAATTCCGA
scaffold704345_13.	1	p2	(GA)7	14	968	981	GGAAGACTCATTGCCCAAAA
scaffold704372_15.	1	p2	(AG)6	12	622	633	GCATCTCTCCCATCTTCTGC
scaffold704400_18.	1	p2	(TC)6	12	460	471	AGTGTTTTGATCGAGTCGCC
scaffold704406_12.	1	p2	(TG)7	14	108	121	TTATGATATTTCCATAAGTCACACCT
scaffold704428_15.	1	p2	(AG)6	12	300	311	AATGCAGAGACTGAATGGGG
scaffold704466_15.	1	p2	(GA)9	18	594	611	CACTGGGATTTCAGACAGCA
scaffold704492_20.	1	p2	(TA)6	12	97	108	AATGGCAAGCGTCTTTGTTT
scaffold704496_15.	1	p2	(TA)14	28	132	159	CTTTAGGGCCCTTGATTTCC
scaffold704517_16.	1	p2	(AG)7	14	1598	1611	GGAACTTTCTCTGGGGCTCT
scaffold704541_10.	1	p2	(AT)8	16	480	495	TAGGTAACCGGTTCGACCTC
scaffold704601_15.	1	p2	(TA)8	16	296	311	CTCTTCATACGAGAAGGGCG
scaffold704625_16.	1	p2	(AG)7	14	673	686	AGGTGGGCCTAAAGTTTGGT
scaffold704725_14.	1	p2	(CT)7	14	1673	1686	ACATTGAACGCTCCAAAACC
scaffold704821_16.	1	p2	(TC)6	12	1080	1091	CCCCTCAATCATCCTCCTTT
scaffold704875_12.	1	p2	(AT)8	16	340	355	GTTTGGGCCTTTTTATTCCG
scaffold704878_13.	1	p2	(TA)8	16	1023	1038	ATACTAGTGCCTTGCCCGAG
scaffold704880_11.	1	p2	(TA)6	12	177	188	TTCTAAAGGGGAAACGACAAA
scaffold704923_14.	1	p2	(GA)7	14	1601	1614	ATAGTACACGTGGCGGAACC
scaffold704962_16.	1	p2	(GT)6	12	1124	1135	AACGCCTTTCACCCCTAAAT
scaffold704967_16.	1	p2	(GA)8	16	328	343	GCTACCCATTTCCCAGCATA
scaffold704974_14.	1	p2	(AC)6	12	1148	1159	TGCAAGGCAGAGTCACATTC
scaffold704977_15.	1	p2	(AT)7	14	667	680	AAACCACGAAATCAAGCAGG
scaffold704987_16.	1	p2	(CT)7	14	200	213	TCCCATCAACCCTCAGTTTC
scaffold704992_13.	1	p2	(TA)6	12	301	312	CAATAGCTGGCCACCCTCTA
scaffold705010_17.	1	p2	(AT)6	12	2755	2766	GGGAGATGGGTTGAAACAGA
scaffold705023_14.	1	p2	(AC)7	14	1729	1742	ATCGAACCATTCCTGCTTTG
scaffold705066_19.	1	p2	(TC)6	12	606	617	CACTTACTTAAAGTCAACTCCCCTG
scaffold705067_10.	1	p2	(TA)9	18	754	771	AATTTTTGCTCTTTTGCATCA
scaffold705103_19.	1	p2	(AG)7	14	300	313	AAAAGAGAAGCCCTCCAAGC
scaffold705167_16.	1	p2	(AC)7	14	1458	1471	CGGCAAAGAGTTATTCGGAG
scaffold705175_11.	1	p2	(TA)8	16	368	383	GCAAGCTGGAGACGAAGATT
scaffold705187_13.	1	p2	(TG)9	18	4016	4033	TGATTTGGGACACTCACAACA
scaffold705189_13.	1	p2	(TA)6	12	112	123	TGAATTGAATAATCCCAAATCAAA
scaffold705210_14.	1	p2	(AT)7	14	100	113	TCACCGAAAAGATATGAAAATCAA
scaffold705259_11.	1	p2	(AC)8	16	51	66	TGCCAATACAAAACCAACCA
scaffold705383_13.	1	p2	(TA)11	22	43	64	GCGTTTTGACGATATATAGTGTTTTG
scaffold705436_14.	1	p2	(GA)8	16	4127	4142	GACTTCTTTTCGAACGTCGC
scaffold705524_16.	1	p2	(AT)6	12	2902	2913	GCAATCGGTGACCTTTTCTT
scaffold705526_16.	1	p2	(AG)6	12	2658	2669	TATCAGTTGGCAGGGGAGAG
scaffold705546_11.	1	p2	(AT)6	12	342	353	CAAGTCCAGGTCGTTTGGAT
scaffold705547_19.	1	p2	(AG)9	18	1186	1203	TGATGCTGCATTTTGTGTGA
scaffold705563_13.	1	p2	(TG)7	14	1275	1288	CTTCAATCCCACCACCAAGT
scaffold705564_11.	1	p2	(AC)6	12	122	133	TGGATGTCATACCGGACTCA
scaffold705572_15.	1	p2	(AT)8	16	5412	5427	GAGCAGGATTCTGTGGAACC
scaffold705655_13.	1	p2	(TG)7	14	834	847	GGCAGCTCACAAATCTCTCC
scaffold705684_11.	1	p2	(GA)11	22	415	436	TCCCCAGCACAGTTATTTCC
scaffold705699_15.	1	p2	(TA)8	16	113	128	AAAAGTGGCATTTTGCCCTA
scaffold705700_11.	1	p2	(AT)11	22	62	83	GGAAATAAGGGGGTGTTATGA
scaffold705822_11.	1	p2	(CT)9	18	591	608	GGACCAACTATGGCACAACC
scaffold705861_13.	1	p2	(TA)7	14	1760	1773	CACTTTTCATCTCCAACCCAA
scaffold705864_10.	1	p2	(CT)6	12	76	87	TCGGCTCTTTTTCTTTCTCG
scaffold705867_16.	1	p2	(AT)10	20	1024	1043	TTATGCAGCAAAAATCCGAG
scaffold705898_17.	1	p2	(GT)7	14	1995	2008	AGGAGAACCACGCATTTACG
scaffold705906_16.	1	p2	(CT)7	14	5092	5105	CCATTCCTGAGACCAAAAGG
scaffold705912_14.	1	p2	(TA)7	14	1684	1697	GGAATGATTTCCCTGAGCAA

scaffold705915_14.	1	p2	(CT)6	12	210	221	TGTCCATTGGCAGTTAGCAG
scaffold705937_13.	1	p2	(TC)6	12	247	258	CCAATAGTTCTTCGGTCCCA
scaffold705997_15.	1	p2	(GA)6	12	736	747	GCACTCGTTTCTTTCTTCGC
scaffold706009_11.	1	p2	(AT)6	12	312	323	TGAAATTCAATGATCGGACAA
scaffold706021_15.	1	p2	(AT)7	14	866	879	CTGCCTTAGGTGGCTTTGAG
scaffold706118_14.	1	p2	(TG)6	12	275	286	TTTTACGTGTTTGGATTTGGG
scaffold706119_15.	1	p2	(AT)6	12	113	124	CATTACCCTGGCCAGTCAGT
scaffold706151_14.	1	p2	(TA)9	18	860	877	TCCGATTTCAAACGAAAACC
scaffold706156_16.	1	p2	(GA)8	16	820	835	ATTTTCCCCTCAAAACGAGC
scaffold706174_15.	1	p2	(AT)8	16	524	539	GTGGAGAATGAAAGTGTGCG
scaffold706175_17.	1	p2	(CT)6	12	721	732	TCTTATTCTCCCTCTCGCCC
scaffold706218_10.	1	p2	(GA)6	12	185	196	CCTTCTTGCTCCTTGCTACG
scaffold706267_16.	1	p2	(GA)6	12	1061	1072	CTTCAGATGGTGTCAAAACCC
scaffold706282_13.	1	p2	(TA)6	12	1095	1106	TGTAATAAATCTTTAAAATGGGAATG
scaffold706298_13.	1	p2	(TA)7	14	734	747	CTCAGAATCCACTCCTGCAA
scaffold706369_18.	1	p2	(AT)6	12	411	422	GGTGTGGTACTTGGGACAGG
scaffold706386_16.	1	p2	(CT)8	16	302	317	TTTTAGCCACTTTCTTGCCC
scaffold706409_14.	1	p2	(TA)11	22	98	119	ATGGGTTATCACCGAATCGC
scaffold706451_13.	1	p2	(AG)8	16	1724	1739	CCGACCTTACATAGCGGAAA
scaffold706470_15.	1	p2	(TA)6	12	307	318	GAGAAATGGCCCATGACTGT
scaffold706471_12.	1	p2	(AT)8	16	128	143	GCCTCCTTTCATGCAATGTT
scaffold706486_16.	1	p2	(GA)8	16	398	413	GAGAAACCCGACATGCAAAT
scaffold706549_15.	1	p2	(TC)6	12	53	64	CTCCTTCTGCGCACTTTTCT
scaffold706550_15.	1	p2	(CT)9	18	251	268	GTAGGAACCGTGCAGCACTA
scaffold706560_16.	1	p2	(TC)7	14	502	515	AACCGCGTCTCTTAGTTTTATGA
scaffold706612_10.	1	p2	(AC)7	14	979	992	ATGTTGCACGAATGGTTTGA
scaffold706622_12.	1	p2	(TA)8	16	1081	1096	TCATTTTGATTACTTTTACTATTCGTG
scaffold706642_14.	1	p2	(TC)6	12	843	854	AGTCGATTTTCTGCAACCGT
scaffold706670_16.	1	p2	(CA)7	14	776	789	TGCAGCGAAAACATGGAGTA
scaffold706671_14.	1	p2	(CT)6	12	68	79	TTTCTCAACCGAGCTCACCT
scaffold706689_17.	1	p2	(TA)7	14	1343	1356	AATGCAATCCTTTCACTGCC
scaffold706701_16.	1	p2	(TA)10	20	256	275	TTGTTCGGGTTGATTTGACA
scaffold706728_15.	1	p2	(TG)8	16	1932	1947	TTGGCAACTATCCCTAACGG
scaffold706744_17.	1	p2	(AT)6	12	309	320	TCAAAACGGTCAAACGATGA
scaffold706772_15.	1	p2	(CT)6	12	1514	1525	ATGATAGGGCATGGCATTTT
scaffold706832_15.	1	p2	(TA)6	12	610	621	AAGCAGGAAGTCATGCCACT
scaffold706837_14.	1	p2	(AG)9	18	1009	1026	AGCAATTTGTGAAAGTGGGG
scaffold706839_15.	1	p2	(AT)8	16	117	132	TTCGAGTTTTGATGGGAACA
scaffold706841_16.	1	p2	(TC)9	18	3580	3597	AGAGGACTGGTCCGAGGAAT
scaffold706862_14.	1	p2	(AT)6	12	116	127	CCTCTTTTCGACCTTAATAAGCC
scaffold706873_12.	1	p2	(TA)10	20	96	115	TGAAGGTAGGAAATAAGGAGGTG
scaffold706887_14.	1	p2	(AC)6	12	485	496	CTTGCATTATCCGGTCGATT
scaffold706898_12.	1	p2	(AT)7	14	307	320	CGGTTTTTCACCGATTTTTG
scaffold706901_14.	1	p2	(CT)6	12	166	177	CGAAGAGAACGATGTCGTGA
scaffold706909_17.	1	p2	(CT)8	16	139	154	AACAACCGGCCTAATCCTTT
scaffold706914_13.	1	p2	(TA)10	20	45	64	TGCGTTTTGATGATATATAGGTGTTT
scaffold706982_16.	1	p2	(GA)8	16	1518	1533	ATGTTGCATGAGTGAGCTGC
scaffold707083_14.	1	p2	(TA)9	18	202	219	ACCACGAACAATGACGAACA
scaffold707092_12.	1	p2	(TA)11	22	203	224	TATGGGTTATCACCGGATCG
scaffold707098_16.	1	p2	(AT)8	16	91	106	GGAATTGTGATTAGTGACGGC
scaffold707099_16.	1	p2	(TA)6	12	896	907	GTTACTCGTGGAGGTGCCAT
scaffold707130_13.	1	p2	(AG)6	12	243	254	TGCAAGAATGGTGAGAGTGG
scaffold707177_17.	1	p2	(CT)7	14	1209	1222	CCCACGCCATATTCTCTCTC
scaffold707198_15.	1	p2	(AT)6	12	1072	1083	ACCACTCATCAAAGGAGGGC
scaffold707199_17.	1	p2	(AG)6	12	472	483	TCGGATTGTTGATTGGTTGA
scaffold707207_13.	1	p2	(AT)9	18	1112	1129	TGATGATGGTGGTGGTGAGT
scaffold707224_15.	1	p2	(GA)7	14	3055	3068	TGAATACGGAGCAAGAACCC
scaffold707307_15.	1	p2	(GA)6	12	1495	1506	ACCGGATGCTAATTTGTTCG

scaffold707338_13.	1	p2	(AT)6	12	669	680	TCGAGGAGTTTACACGGAAGA
scaffold707351_14.	1	p2	(GA)8	16	308	323	GGTTCAAAAATCGGACTGGA
scaffold707370_15.	1	p2	(AT)7	14	782	795	CAAGATGCGATCTATTTTGGC
scaffold707385_12.	1	p2	(TC)9	18	306	323	CTTGGAAACCTTTTACCCCA
scaffold707412_12.	1	p2	(AT)9	18	597	614	TGCACGTAGGCATGTTCAAT
scaffold707413_12.	1	p2	(TC)6	12	1208	1219	CGAGGTTGCCCAAACTCTTA
scaffold707428_13.	1	p2	(AG)8	16	308	323	TGGTGGTCTGGTGACTGAAA
scaffold707451_19.	1	p2	(AT)6	12	311	322	AGGTGCACTAAGCCAGCACT
scaffold707472_13.	1	p2	(TA)8	16	85	100	GCTACATATTTTGATGCATACGG
scaffold707551_14.	1	p2	(GA)7	14	743	756	CAGCACACGAACAGCTTCAT
scaffold707578_14.	1	p2	(AT)9	18	591	608	CCTAACCCTTGACTGCAAGC
scaffold707586_15.	1	p2	(CT)6	12	418	429	CAACTCCCAAATCCTCCAAA
scaffold707613_15.	1	p2	(TC)6	12	312	323	ACAAATTGGTTTTGGCGTTC
scaffold707617_15.	1	p2	(AT)6	12	1306	1317	ATGAATCCACACAAGTGGGC
scaffold707632_18.	1	p2	(TC)6	12	2235	2246	CAAAATTGGAACGACTTGCAT
scaffold707641_11.	1	p2	(TG)11	22	63	84	ATGGGAAGGGGAGTTAGCAT
scaffold707689_12.	1	p2	(CT)7	14	51	64	CAAACAACAATTCAGCAAATACC
scaffold707720_12.	1	p2	(TC)11	22	1573	1594	CTCCTTCTGTTGATCCCCAA
scaffold707737_14.	1	p2	(CT)7	14	874	887	TGAAGCAATTGTGCAAGGAC
scaffold707745_13.	1	p2	(AT)6	12	56	67	CGTTTCTCATCTGATTACCGC
scaffold707757_14.	1	p2	(TA)9	18	48	65	AGAGGGTTATCATGGGATCAA
scaffold707767_12.	1	p2	(AT)9	18	123	140	ATATATGGGTTATCGCCGGA
scaffold707776_15.	1	p2	(CT)6	12	313	324	CTGACTCGTGCCCTTATGGT
scaffold707804_15.	1	p2	(TA)8	16	117	132	TTCGAAATCTAACGATCCGC
scaffold707869_12.	1	p2	(AT)8	16	471	486	GGATCGAGTCCATGCCATTA
scaffold707877_15.	1	p2	(TG)7	14	193	206	TACGTGTATGATGGAGGCCA
scaffold707878_15.	1	p2	(CT)6	12	338	349	ACCACTGCATCACACCAAAA
scaffold707905_16.	1	p2	(TC)8	16	1360	1375	GCCACCCCTAGTTTTGATGA
scaffold707928_13.	1	p2	(TA)9	18	303	320	ACCAAACCAAACCAAGCAAC
scaffold707940_10.	1	p2	(GA)6	12	117	128	GGGGACCATCTCAAATGTTTT
scaffold707958_16.	1	p2	(AG)8	16	30	45	GCAAAGTGCCACCAACACT
scaffold707963_15.	1	p2	(GA)6	12	2952	2963	TGGTTAGGATTTCTCTTTGCC
scaffold707964_15.	1	p2	(TC)9	18	2779	2796	AAATGGCTGCAACGAAGAGT
scaffold707995_16.	1	p2	(TA)6	12	635	646	GAGCATTCGGGGTGCTATAA
scaffold708052_19.	1	p2	(AC)6	12	360	371	TCTCCTCCCTTCGTCTCTCA
scaffold708079_15.	1	p2	(AT)6	12	4207	4218	CATTCATGCATCCAATCTGC
scaffold708095_16.	1	p2	(TA)8	16	2090	2105	GTTCTCGCGCGACATTATTT
scaffold708097_14.	1	p2	(AT)7	14	469	482	TTCATGGATTCAAAAGGGGA
scaffold708126_14.	1	p2	(GA)6	12	272	283	TTTGATCCTTGCTTTGCCTT
scaffold708143_16.	1	p2	(AT)9	18	95	112	TTCAGTTGGCCGAATGATTT
scaffold708146_15.	1	p2	(AC)6	12	2903	2914	TAAGGCAGCTCAAAAGGGAG
scaffold708156_14.	1	p2	(TA)6	12	252	263	CGATCTAACGGCCCAGATT
scaffold708161_16.	1	p2	(AG)9	18	569	586	CAACGGTTTATCTGCGGAAT
scaffold708185_16.	1	p2	(AG)6	12	922	933	CCGGACATGCTAACGAGACT
scaffold708217_12.	1	p2	(TA)7	14	1221	1234	TTTGCACTAGATCACTCCCCTT
scaffold708218_15.	1	p2	(CT)14	28	3268	3295	GGCGTCGGTTGATAGATTGT
scaffold708219_15.	1	p2	(GT)6	12	309	320	CGAACTCCAGACACCACCTT
scaffold708236_14.	1	p2	(AT)6	12	411	422	TGCAGTCTTACAGCCCAACA
scaffold708270_14.	1	p2	(TA)10	20	1042	1061	CAACCAAAATGATGGCGATA
scaffold708291_16.	1	p2	(GA)6	12	147	158	TTAAGGAACACACTTGGCCC
scaffold708301_14.	1	p2	(AT)10	20	530	549	GATCTCGCGGATCAGAAGAC
scaffold708344_14.	1	p2	(AT)6	12	161	172	GCAAGTAATGCGGAGCTAGG
scaffold708351_10.	1	p2	(AT)13	26	491	516	ACCACTTCTTTCGCTACGGA
scaffold708362_13.	1	p2	(AG)7	14	314	327	AGTGTTGAGCAAAAGGGCAG
scaffold708367_16.	1	p2	(TC)10	20	4311	4330	TCTTTGCCTTCTTCCATGCT
scaffold708409_16.	1	p2	(AT)6	12	712	723	CTCGGCCTTGGAACTTGTAG
scaffold708420_11.	1	p2	(GA)6	12	547	558	ACGTTTGAATGCATTGGGTT
scaffold708427_15.	1	p2	(TA)11	22	3435	3456	CCCCAACTAGGTACCGTGAA

scaffold708443_15.5	1	p2	(TC)6	12	115	126	CATCCCTTAATCCCCATCCT
scaffold708457_17.7	1	p2	(GT)6	12	650	661	AAAGTGATTGTGAAACCGGAA
scaffold708476_16.5	1	p2	(CT)7	14	1133	1146	TGTTTTTCCACAACTCAACCC
scaffold708483_15.3	1	p2	(TA)8	16	1409	1424	TGTCAGCTACCTAACAGCTGGA
scaffold708537_13.3	1	p2	(AT)6	12	1989	2000	CTTTCCCCATGCATCATCTT
scaffold708559_15.2	1	p2	(AT)7	14	2305	2318	CCTTATGCGTTCCAAAATGG
scaffold708578_17.2	1	p2	(TC)6	12	405	416	TGAGGCGGTTAGGAGTTGTC
scaffold708587_18.0	1	p2	(TA)7	14	614	627	ACCGGAATGAAAATCGGATA
scaffold708720_20.5	1	p2	(TA)8	16	474	489	TCTTTGTTTTCAACGCCTCC
scaffold708724_13.1	1	p2	(TA)9	18	130	147	GGAAAAAGAAACCCACATGC
scaffold708731_11.3	1	p2	(AT)6	12	161	172	GCAAGTAATGCGGAGCTAGG
scaffold708736_15.7	1	p2	(GA)6	12	646	657	GGACCAGAAATCCCAGTTGA
scaffold708778_12.6	1	p2	(GA)6	12	177	188	TTGCGAGAACCAACTCTGTG
scaffold708779_13.1	1	p2	(TA)9	18	590	607	ATGACACGCATAAAGGGACC
scaffold708802_15.4	1	p2	(TA)6	12	471	482	TGATGATTGCCCCCAGTTAT
scaffold708809_18.4	1	p2	(TA)10	20	202	221	CGGGGTCGGATTATACCTTT
scaffold708833_11.3	1	p2	(AT)8	16	313	328	TAAATACCAAGCTCCGCCTG
scaffold708864_13.3	1	p2	(GA)6	12	683	694	CTGTATAGGCGTGGCCAACT
scaffold708898_15.5	1	p2	(AG)6	12	2545	2556	TTCTTTGGTGACCTGTTGGA
scaffold708907_12.0	1	p2	(TC)6	12	706	717	GCCCACCACCTGATAACAAA
scaffold708957_13.6	1	p2	(TA)7	14	316	329	TGCATTTTTAATTTATTTTCCTGA
scaffold708972_15.0	1	p2	(TC)7	14	316	329	AATTATGTGGCCGAGGACAG
scaffold708989_16.1	1	p2	(CT)7	14	3719	3732	TGAAAATGGACCCCTCTCTC
scaffold709008_11.6	1	p2	(TA)9	18	47	64	AGGTTTTGACCATATTTACTGTTTTG
scaffold709023_14.1	1	p2	(AC)9	18	312	329	TCATAATGGTCTCCATCGCA
scaffold709053_15.5	1	p2	(AT)8	16	704	719	GGATTCATGAGATCGACGGT
scaffold709065_13.3	1	p2	(TA)9	18	134	151	GCATATGCATTAAAATAACTTGAGAC
scaffold709114_13.2	1	p2	(CT)8	16	1372	1387	ACAAAACAAAATGTTGGCCC
scaffold709115_14.0	1	p2	(AT)8	16	2627	2642	TTTTATGCATCGTGCCAAAG
scaffold709119_17.0	1	p2	(TC)9	18	2208	2225	GGAAGCGCTCTTTTTACACG
scaffold709122_15.1	1	p2	(AG)6	12	319	330	GAACGTCCAGTGCCAAAGTT
scaffold709144_15.4	1	p2	(TA)8	16	50	65	GGTTATCACCGGATCGCTAC
scaffold709198_16.4	1	p2	(AG)11	22	1673	1694	CGTAGGTTCAGATCATGGCA
scaffold709208_13.9	1	p2	(AT)8	16	465	480	AAAATCAAAGGCCCACAATG
scaffold709211_12.5	1	p2	(AT)7	14	408	421	GCACCAATATTAGGCCATCG
scaffold709246_14.2	1	p2	(AT)6	12	6809	6820	CAGCGTTTGCTTTGAGACAA
scaffold709260_14.5	1	p2	(TA)6	12	104	115	AATCTCGAAAATGGATGACCC
scaffold709301_15.4	1	p2	(CA)6	12	1384	1395	ATGGCATCCCACAAGTATCC
scaffold709311_18.7	1	p2	(AG)6	12	141	152	GCGAAATTCGTTGGTTTGAC
scaffold709363_14.8	1	p2	(TA)7	14	1040	1053	TATGCATGGATTGATGTGGG
scaffold709380_12.7	1	p2	(TA)10	20	313	332	TTTTTGGATGGAAAACCACT
scaffold709381_16.1	1	p2	(AT)7	14	67	80	GAGTTATCATTGGAGTAAGCCCC
scaffold709397_15.3	1	p2	(TA)8	16	1473	1488	AACTTTTCCGGCCTCTCATT
scaffold709399_11.3	1	p2	(AT)6	12	1127	1138	CGCAAATTAGTGGCTTGCTT
scaffold709457_15.5	1	p2	(GA)11	22	616	637	ATTTGGGTCTCTTCGACACG
scaffold709476_14.6	1	p2	(GA)6	12	274	285	AAGCCAGCACATGCATACAC
scaffold709491_10.5	1	p2	(TC)9	18	315	332	CCTCCAGGACACAAGACGAT
scaffold709510_15.3	1	p2	(TA)9	18	169	186	GATTGAAGACCGCCTCGATA
scaffold709517_12.4	1	p2	(TA)8	16	621	636	TTCATATTCACTTGAAGACTTGAAAA
scaffold709534_15.8	1	p2	(TA)6	12	1304	1315	TCTCACCTTCGGTCAAAACC
scaffold709557_16.5	1	p2	(TA)10	20	107	126	CCGGGGTATGCTATAAACGA
scaffold709564_11.2	1	p2	(TA)7	14	319	332	TCGTGAAACACTTCAACCCA
scaffold709580_16.7	1	p2	(AC)11	22	311	332	TGGACCATGTTTTAACTGTATGC
scaffold709591_15.6	1	p2	(TC)6	12	321	332	TTAACTCAAAGCACGAGGGG
scaffold709622_14.7	1	p2	(TC)6	12	641	652	ATTTCTGATGGTCAGGCCAA
scaffold709636_12.2	1	p2	(TA)9	18	855	872	TTCCAATTTCTCTTGGCAATG
scaffold709638_12.6	1	p2	(AT)8	16	90	105	AAATAGTTCGGGTTTTCGGC
scaffold709674_16.9	1	p2	(TA)6	12	1064	1075	GACGGCAACGTTTTACGTCT

scaffold709678_17.	1	p2	(GA)6	12	734	745	TAGAAATGGAGGTTGGGTGG
scaffold709748_15.	1	p2	(GA)8	16	414	429	CTCCACTTCACCGGCTTTTA
scaffold709760_17.	1	p2	(TA)6	12	493	504	AATACCCTTGTATGCTGCGG
scaffold709767_17.	1	p2	(CT)6	12	630	641	CACAGCCCCCATAACCAGTA
scaffold709794_10.	1	p2	(TC)7	14	651	664	TAAATACCGACAACCCCCAA
scaffold709811_15.	1	p2	(AT)6	12	488	499	AAACAAGCAAGCAATCAGCA
scaffold709867_10.	1	p2	(AG)6	12	819	830	TGTGATCCGTTGAGGAATGA
scaffold709873_11.	1	p2	(AT)8	16	517	532	TCTACCCCTCAGAATCCTCG
scaffold709874_10.	1	p2	(AG)6	12	189	200	AAGAAGCAGCACTAAACCCG
scaffold709878_17.	1	p2	(GA)8	16	1466	1481	GAAAGTTGCAGCCCAGTGAG
scaffold709918_13.	1	p2	(AC)6	12	973	984	AGTTTTGCATCCAGGGTACG
scaffold709928_11.	1	p2	(GA)8	16	433	448	CTGTCCGTCACGTTGAACC
scaffold709929_14.	1	p2	(GA)7	14	661	674	TTCAAATTGCGGATGGATTT
scaffold709956_16.	1	p2	(TA)7	14	72	85	GAAAATCAAAGGCCCACAAA
scaffold709966_16.	1	p2	(CT)6	12	2429	2440	TGCACTTGTTTTCCCAATATCA
scaffold709975_11.	1	p2	(AT)6	12	323	334	TTTAAGTCGGCGAAGGAAAA
scaffold709991_14.	1	p2	(AT)7	14	321	334	GGAAAAACCATCACAAAAATTG
scaffold709998_10.	1	p2	(TC)6	12	171	182	CAATTCGACGACCAAATCCT
scaffold710033_12.	1	p2	(CT)10	20	2855	2874	GCACAGAGCAACCAATCTGA
scaffold710043_15.	1	p2	(AC)6	12	634	645	AAAATGCCGAACTTCCAAGA
scaffold710063_12.	1	p2	(AC)6	12	376	387	TCAGATCGCTATCGTGTTCG
scaffold710074_11.	1	p2	(TA)12	24	657	680	CTATGCAGCCTCCAGCTTCT
scaffold710093_13.	1	p2	(AT)6	12	1221	1232	GAATAAATATGAACGAAAGCACAAA
scaffold710095_15.	1	p2	(CT)6	12	920	931	TTCGTGGTGTAATGGCAAAA
scaffold710125_11.	1	p2	(AG)8	16	488	503	GTATCCCAGGCCGAATTTTT
scaffold710135_17.	1	p2	(AT)6	12	637	648	GCATTACTTTCTGTTTGAGAGGAA
scaffold710151_15.	1	p2	(CT)9	18	2238	2255	CTGTTGCTGGGAGAGGACAT
scaffold710157_14.	1	p2	(AG)6	12	649	660	GGCATTGTCAGACGACGTAA
scaffold710166_16.	1	p2	(GC)6	12	1873	1884	ATATATTGTGCAGGCAGGGC
scaffold710182_17.	1	p2	(AT)6	12	498	509	TTGGACTTGTGCTTGCGTTA
scaffold710192_19.	1	p2	(CA)6	12	1042	1053	ACCTGGCAAGATTCATCGAC
scaffold710204_13.	1	p2	(AT)10	20	66	85	TATGATGGGAAGGGTGGGTA
scaffold710224_15.	1	p2	(GA)10	20	3056	3075	ATTTTCATCGGAAATGCTGC
scaffold710229_16.	1	p2	(TG)10	20	832	851	GCCTTCATTCCAGCTGTCTC
scaffold710263_14.	1	p2	(CA)12	24	1977	2000	TCCATGAAGGAGGAACAAGG
scaffold710266_13.	1	p2	(TA)6	12	132	143	ACTCAATCTGCAAGCGTGAC
scaffold710281_15.	1	p2	(AT)10	20	539	558	GGTCAAATCGTGGTCCATTC
scaffold710295_13.	1	p2	(TG)7	14	2165	2178	ACCAGAACCAACAAGCAAGC
scaffold710305_13.	1	p2	(AG)7	14	524	537	TTCATTACCCCCACCCACTA
scaffold710335_15.	1	p2	(AT)6	12	1985	1996	GAAAGCAATGATGACGACGA
scaffold710363_17.	1	p2	(AT)8	16	118	133	TCCGCCTTAATCCATCAAAC
scaffold710364_12.	1	p2	(AT)7	14	722	735	GATAGTCCATGCCCCATGAT
scaffold710392_12.	1	p2	(AT)6	12	685	696	TGATTCCTTTATGGCGTCTG
scaffold710402_12.	1	p2	(CT)7	14	1212	1225	CTCGCCAACGTACCTCTCTC
scaffold710403_14.	1	p2	(AG)6	12	1222	1233	AAGCAGGACAGTAACAGCCG
scaffold710404_11.	1	p2	(AT)11	22	44	65	TTCATAACATTTCTATCGGTATTTGC
scaffold710418_18.	1	p2	(TA)7	14	77	90	TTTGCACCTGAGGAGGTGTT
scaffold710431_14.	1	p2	(TA)6	12	841	852	ATTGCGGTAAAGACCACGAC
scaffold710471_16.	1	p2	(GA)7	14	1220	1233	CACGTTGTCCTGGAACATTG
scaffold710474_15.	1	p2	(TG)6	12	2329	2340	TCTCACATATTCCCATTGCG
scaffold710517_10.	1	p2	(GC)6	12	271	282	GGACCATGAGTCACGAGCTT
scaffold710570_14.	1	p2	(GA)7	14	1123	1136	TCCGGTCTATTCTCACCTCAA
scaffold710574_14.	1	p2	(CT)8	16	582	597	TGCTACTTTGTCCCGGATCT
scaffold710588_14.	1	p2	(TA)8	16	2600	2615	GGAGACAATGCACAGCTCAA
scaffold710662_17.	1	p2	(GA)7	14	324	337	GGCACCTAACACCAATGCTT
scaffold710673_16.	1	p2	(CT)6	12	334	345	TCGAAGGTGGATGTCTTTCC
scaffold710695_13.	1	p2	(AG)6	12	537	548	GACGAAGAAAAGGATGTCCG
scaffold710696_16.	1	p2	(AC)6	12	2023	2034	GAAAGCAGTGACGAAGGGTC

scaffold710722_11.	1	p2	(TA)7	14	476	489	TCATCCTTAATTGGCTGCAA
scaffold710773_15.	1	p2	(AG)8	16	693	708	TGGTTGGTCACGAAAGATGA
scaffold710778_16.	1	p2	(CT)11	22	1200	1221	CTGGAAAAGACAGCCATCGT
scaffold710825_14.	1	p2	(TC)6	12	2276	2287	CTAGTGTGCTGGCTGCTTTG
scaffold710844_15.	1	p2	(TA)6	12	162	173	TGGCATCATATATGCGGTTG
scaffold710853_13.	1	p2	(TA)8	16	50	65	TCGTGTTAAAGCACGGTATCA
scaffold710861_15.	1	p2	(AT)10	20	788	807	TAATGGACGTCATGACCGAA
scaffold710884_21.	1	p2	(AG)8	16	537	552	TACCAATGGACCACAAGCAA
scaffold710896_14.	1	p2	(CT)10	20	316	335	CCCTTCAATCCCAAGGTTTT
scaffold710964_15.	1	p2	(GA)6	12	787	798	GCTGTTTTCCATTTGATCTGC
scaffold710965_14.	1	p2	(AG)6	12	221	232	CAGTCTGAAGCTTGGGGAAG
scaffold710971_12.	1	p2	(GA)8	16	742	757	CAAGGTGGCTTCACACACAA
scaffold710990_12.	1	p2	(TA)7	14	321	334	ATTCAATGGCAATCTCCTGG
scaffold711003_16.	1	p2	(AC)8	16	1176	1191	CCCCAATGGTTAAGGTGACA
scaffold711010_15.	1	p2	(AT)9	18	81	98	AATTGAATGGCAAGGATTGG
scaffold711029_15.	1	p2	(TA)10	20	159	178	TGTGGTATCAAATCCAGCCA
scaffold711053_16.	1	p2	(TA)8	16	3090	3105	CCAAGGGCATTACACTCGAT
scaffold711073_13.	1	p2	(TC)8	16	324	339	CCCCGACAATCATCACTCTT
scaffold711094_14.	1	p2	(CT)7	14	904	917	TGTCCCAATTGAAACTCGAA
scaffold711106_10.	1	p2	(TA)9	18	1634	1651	TGATGCTAATCCAAACGATCC
scaffold711112_13.	1	p2	(GA)6	12	1757	1768	TGTATTTTTCCCGTGAAGCAC
scaffold711116_15.	1	p2	(AG)12	24	196	219	GCATTTTCCAAGGCAGACAT
scaffold711137_13.	1	p2	(CA)6	12	1138	1149	TCCAGGTCCAAATGAAAAGG
scaffold711191_14.	1	p2	(AG)6	12	815	826	CGCACTCTGCAACACTGAAA
scaffold711224_14.	1	p2	(AT)7	14	328	341	TTCTCTCCGCACAATTCCTT
scaffold711240_15.	1	p2	(TG)7	14	1759	1772	CCCAATAGTTCAGCACCATC
scaffold711245_14.	1	p2	(TA)6	12	1108	1119	TGTCAATCGAATTAAACCGTACA
scaffold711249_14.	1	p2	(GT)6	12	316	327	TGCATCTGATTCTGACGAGG
scaffold711263_16.	1	p2	(AT)9	18	2824	2841	AAGGGGAGAGCAGGAAAATC
scaffold711286_14.	1	p2	(TG)6	12	393	404	TTTGTTCAATCGCTTTGCTG
scaffold711287_15.	1	p2	(TC)6	12	675	686	CGTGATAAGCACCCTCCAAT
scaffold711342_11.	1	p2	(AG)7	14	53	66	GAGAAAGGGAGGAGGAGGAG
scaffold711375_15.	1	p2	(GA)9	18	179	196	AGAGCATGGAGCCAAAAGAA
scaffold711422_16.	1	p2	(AT)7	14	2831	2844	GATTGAATCTCCCACTTCCG
scaffold711426_16.	1	p2	(GA)8	16	2330	2345	GACTGCTCTCCTCATCTGGG
scaffold711439_13.	1	p2	(AT)7	14	711	724	CCGGCTATCTCACTCCAGAC
scaffold711480_10.	1	p2	(AT)6	12	776	787	ATCCCGTATTCTCACCCCTC
scaffold711534_17.	1	p2	(TA)9	18	2717	2734	CAGTCACAAAAGGGGGAAAA
scaffold711556_15.	1	p2	(CT)7	14	2103	2116	CCTCCGGTTCAAAATCAAGA
scaffold711559_15.	1	p2	(AG)8	16	419	434	ATTTCAGTCCCATCAGCCAG
scaffold711569_14.	1	p2	(TA)10	20	1021	1040	AATGCGCTTTCTGCAAATCT
scaffold711578_10.	1	p2	(AT)9	18	401	418	TCAATTTGATAATTTGAAGCTCTATCC
scaffold711621_11.	1	p2	(TA)10	20	604	623	ACGTCAGCTTCTTCCCACTG
scaffold711666_17.	1	p2	(AG)9	18	198	215	AAACGTGCGAGGAAAACATC
scaffold711737_16.	1	p2	(CG)6	12	46	57	TATGGTGGTATGGTGTGGGG
scaffold711758_13.	1	p2	(TA)10	20	658	677	TGAGGGGAATGCACCACTAT
scaffold711771_15.	1	p2	(AT)8	16	1273	1288	GCCTTTGACATCCAGGACAT
scaffold711775_17.	1	p2	(GA)6	12	5545	5556	TCAGTTGGCACCAAAATTGA
scaffold711861_17.	1	p2	(TC)6	12	332	343	GCCGTTCTTCCCTTCTCTCT
scaffold711865_19.	1	p2	(CT)8	16	329	344	TTTACGCACATACCCCCATT
scaffold711866_14.	1	p2	(CT)6	12	333	344	CAGGAGCAACCATTTTGTGA
scaffold711870_11.	1	p2	(CT)9	18	972	989	TCACCCATTTCCACCAAGAT
scaffold711885_15.	1	p2	(AG)6	12	2907	2918	CCTGAGCGGATAAATCCAGA
scaffold711922_15.	1	p2	(TA)7	14	50	63	AAGGAGGTGTTATGAAGGGATT
scaffold711972_12.	1	p2	(AT)9	18	1059	1076	CATCATGTAGGAAAATGTTTACAGA
scaffold712010_16.	1	p2	(TA)11	22	2925	2946	TTGACACGCATGCTTACACA
scaffold712013_15.	1	p2	(TA)12	24	91	114	TCAAACTCATTGTTGTTTCACAAA
scaffold712061_17.	1	p2	(AC)7	14	376	389	TCACCTAACCCCTCTCTTGG

scaffold712090_15.	1	p2	(AT)6	12	1034	1045	CTCTTCGGTGATCAAGCGTT
scaffold712111_15.	1	p2	(AG)9	18	7876	7893	GATCAAAACCCCTCCATCAA
scaffold712121_16.	1	p2	(AG)6	12	860	871	GCTGAAGCAATCGAGAAGGT
scaffold712150_11.	1	p2	(TA)7	14	778	791	TACAGCGTGGACGGTACAGA
scaffold712186_10.	1	p2	(TA)6	12	129	140	TAGTGGGGGATGATGTGGAT
scaffold712243_17.	1	p2	(AT)7	14	114	127	AGGCCTAATTGCCGTCCTAT
scaffold712254_15.	1	p2	(TC)7	14	2195	2208	ACAAGAAGGTGGCCATGAAC
scaffold712274_16.	1	p2	(AT)8	16	652	667	GAAACACAAAAATTAGCATACAACG
scaffold712288_16.	1	p2	(TA)11	22	453	474	CAACAAAAATCCTAGTCCATCCA
scaffold712312_16.	1	p2	(GT)7	14	738	751	CCTTCCCACATTCCACATCT
scaffold712339_15.	1	p2	(GA)10	20	1671	1690	ATCTCTGCGATGCCTTTCAT
scaffold712385_15.	1	p2	(TC)6	12	549	560	ATGTTGCCACCTCAGCTTCT
scaffold712389_14.	1	p2	(AT)12	24	2018	2041	TCATGACTCACGAGATGGGA
scaffold712395_15.	1	p2	(AG)6	12	118	129	CCCAAGCATTAAAGCCCATA
scaffold712398_14.	1	p2	(AC)8	16	510	525	TCCAAACTTGATCCGAGAGG
scaffold712411_15.	1	p2	(CA)6	12	134	145	CCCGTTATGATTCGTTAAATCG
scaffold712423_16.	1	p2	(CT)7	14	274	287	TCAGACCAAATCAGAAGGCA
scaffold712434_14.	1	p2	(GT)6	12	1724	1735	TGAGGGATGATGCATACGAA
scaffold712452_18.	1	p2	(AG)6	12	1096	1107	ATCACAAAATTCACACCCCG
scaffold712532_10.	1	p2	(GA)6	12	872	883	GGGCTAAAATGGTGTTGGAA
scaffold712582_11.	1	p2	(TG)8	16	1508	1523	TTCCTGGAGGATCTGCATTC
scaffold712584_13.	1	p2	(GA)8	16	1647	1662	CTCTCTCATGCGTGGTGAAA
scaffold712639_15.	1	p2	(AG)8	16	333	348	TCAAGCTAACCAGCCAACCT
scaffold712655_17.	1	p2	(CT)8	16	295	310	ACACAGACAACCCATGGAGA
scaffold712692_17.	1	p2	(AG)7	14	5486	5499	CCGTGGAAGACAAGGGATAA
scaffold712728_12.	1	p2	(TC)7	14	1144	1157	AACGCAAACACATACGCAAA
scaffold712738_18.	1	p2	(AT)8	16	1196	1211	ACGATGTCGTGTAGGGAAGG
scaffold712780_16.	1	p2	(TA)6	12	2918	2929	CGAACATTGTCACCGTCAAC
scaffold712783_15.	1	p2	(CT)7	14	1005	1018	TTGGCTCTGGTTTGTTACCC
scaffold712784_12.	1	p2	(GA)9	18	863	880	ACGTAAGGGTGATGGGTGAA
scaffold712789_16.	1	p2	(TC)8	16	907	922	AATCCAAGGTACCCCACTCC
scaffold712812_18.	1	p2	(AT)6	12	872	883	TGAAATTGTGTTGCAGGCTC
scaffold712814_15.	1	p2	(AG)6	12	152	163	CGAACGCAATGCAATAAATG
scaffold712841_14.	1	p2	(AT)6	12	3034	3045	GCAAAAGAAACAAACGGGAA
scaffold712854_11.	1	p2	(TA)6	12	100	111	GCAAAATTGGTCTCTATGTGTAGAA
scaffold712896_14.	1	p2	(CT)7	14	1099	1112	AAAGGAGGTGGATCGGTTCT
scaffold712904_15.	1	p2	(TA)8	16	545	560	GAGAAATCAATCTCAGCCGC
scaffold712911_16.	1	p2	(TA)6	12	191	202	CCGGTTATCCAATCCATTTC
scaffold712920_13.	1	p2	(TA)10	20	734	753	TCCTCCTAAAATAACGGCCA
scaffold712941_11.	1	p2	(AG)7	14	675	688	CGTGGGTGTAGTGATGGATG
scaffold712968_14.	1	p2	(AT)7	14	612	625	GTGGCATCGTGAGGAGTGTT
scaffold712993_10.	1	p2	(AG)6	12	282	293	AAAGTCCTACATGCCGGTTG
scaffold713006_14.	1	p2	(AC)7	14	2096	2109	ACCCCCACTTCCTCTGTTTC
scaffold713008_16.	1	p2	(TA)6	12	2511	2522	TGCATGAGAAATGAGCGGTA
scaffold713053_12.	1	p2	(TA)13	26	660	685	ATGAGTTATCACCGGATCGC
scaffold713061_16.	1	p2	(CT)8	16	525	540	CGAGAATTAGCTGCCACTCC
scaffold713078_15.	1	p2	(GA)7	14	337	350	CCGGCTCCGATCTATACAAA
scaffold713091_14.	1	p2	(TC)6	12	507	518	AAAACCTCCAATCCCTCCAC
scaffold713129_13.	1	p2	(GA)7	14	702	715	GCATTGGCGTTTGAAGAAAT
scaffold713147_16.	1	p2	(CT)6	12	309	320	ATCCGCCAAACCTTCTTCTT
scaffold713157_12.	1	p2	(TA)9	18	46	63	GAACCACCGAGTACCAAGTGA
scaffold713163_12.	1	p2	(AG)6	12	640	651	AAACAATGTAGGGCAAACGG
scaffold713171_14.	1	p2	(TA)9	18	47	64	GGTTATCACCGGATCGCTAC
scaffold713175_15.	1	p2	(AC)6	12	692	703	TGGCTCTTTCAACTCAGCAA
scaffold713262_16.	1	p2	(AT)6	12	603	614	TGTGGGTCAGCTATGCATGT
scaffold713304_16.	1	p2	(CT)6	12	2752	2763	TAGCGTAGATATGCCAGGGG
scaffold713308_17.	1	p2	(CA)7	14	627	640	AATGTTGCGAATGGAAGAAA
scaffold713321_11.	1	p2	(AT)10	20	224	243	GTGCGTGGCTCAATCCTATC

scaffold713396_14.	1	p2	(TA)10	20	631	650	AATTACATTGGGCCATCCTG
scaffold713405_14.	1	p2	(AG)6	12	341	352	ATATTCGGATCAGGAATGCG
scaffold713440_19.	1	p2	(TA)7	14	339	352	TCCAAATGCAACTGGTGAAA
scaffold713444_15.	1	p2	(TA)7	14	431	444	TGAGTAACGCATCAAGCCAC
scaffold713454_13.	1	p2	(TA)8	16	539	554	TTCTCGGGATTTAACGTCCA
scaffold713458_10.	1	p2	(AT)12	24	217	240	AGCTTAAAAGGCCGGTCAAT
scaffold713469_15.	1	p2	(AT)6	12	341	352	CCCAGATAATTTTATATGTGGTGAAA
scaffold713481_10.	1	p2	(AT)9	18	536	553	GTGATTGGTGGTTTTGTGGA
scaffold713488_14.	1	p2	(AT)6	12	917	928	GGCTTCTTCTCTACCCAATCG
scaffold713497_17.	1	p2	(CT)7	14	362	375	CTCTCCAAAAACAGTCCCTCTC
scaffold713502_18.	1	p2	(GA)6	12	410	421	GAACTTCACCGCTTGGACAT
scaffold713510_14.	1	p2	(CT)7	14	892	905	AGGCGTCAAAGAGGAAGACA
scaffold713592_19.	1	p2	(TA)6	12	2482	2493	TTCGTTCATTGCATGTGGTT
scaffold713638_14.	1	p2	(AT)8	16	932	947	CCCATCTCGAACATTCCTGT
scaffold713670_16.	1	p2	(CT)8	16	338	353	CATGCAGGTTTTGTCCAATG
scaffold713708_12.	1	p2	(TA)9	18	755	772	GCCGCAATATACATGGCTTT
scaffold713710_14.	1	p2	(TA)9	18	2439	2456	TTCTTTTTGCATTAGCCTTTGA
scaffold713862_14.	1	p2	(TA)7	14	510	523	TAGCAAATTTCGGGATGAAA
scaffold713868_14.	1	p2	(AT)14	28	33	60	GGAGTTTTGACCTAATTAAGACCC
scaffold713877_16.	1	p2	(CA)6	12	1549	1560	CTGGAAAACGCTGATGGATT
scaffold713944_14.	1	p2	(AC)8	16	1023	1038	GCAAATTGTCACTCCCTTTCA
scaffold713953_13.	1	p2	(TG)8	16	725	740	TGTTGCCTTGCAAATTATTTCT
scaffold713965_13.	1	p2	(TC)7	14	342	355	GCAAAGAAGAGTGGAGGCAC
scaffold713990_14.	1	p2	(TA)8	16	86	101	TTTCGTGTTTCTTTTGATTTTTCA
scaffold714016_17.	1	p2	(TA)8	16	341	356	ACTCAATGGACACATGCCAA
scaffold714042_19.	1	p2	(CA)6	12	345	356	CGCAACCTCTAGAAACCCAC
scaffold714055_16.	1	p2	(TC)9	18	818	835	CGTCTTAGATCCCTCCCACA
scaffold714065_11.	1	p2	(AT)8	16	1040	1055	GGCCTGGGCCTACATAAGTT
scaffold714078_13.	1	p2	(AT)8	16	934	949	CCAACATCACACTCGACCAC
scaffold714104_16.	1	p2	(CT)7	14	465	478	CCATTCAGCAATAATAGGCCA
scaffold714107_14.	1	p2	(TA)8	16	48	63	TGGTTATTAGGGGATGGTGA
scaffold714116_14.	1	p2	(TA)10	20	1627	1646	TTTCAAACGAGATCTCAGGG
scaffold714119_10.	1	p2	(TA)9	18	339	356	ATTCCAAAAATCAAAGGCCC
scaffold714124_14.	1	p2	(TA)12	24	1294	1317	GGAATTCAATTGTTTATTTGTTGC
scaffold714162_16.	1	p2	(TC)7	14	1891	1904	TGTGTCGTGTTCGTGTCAAA
scaffold714265_13.	1	p2	(GA)10	20	1319	1338	CCTCACTGGAGGAAGGATCA
scaffold714282_14.	1	p2	(CT)6	12	607	618	GGCAACCCACTTGTGAAACT
scaffold714290_12.	1	p2	(AT)6	12	332	343	TTTGATATTCTCACCATCCTACTCA
scaffold714293_17.	1	p2	(AT)10	20	1520	1539	TGGGACCCTAATACACCATCA
scaffold714306_13.	1	p2	(CT)7	14	345	358	CCAAAATTGGCGGATAACTG
scaffold714357_17.	1	p2	(AG)7	14	63	76	GAGCGCACTCGAAAAGTAGC
scaffold714369_11.	1	p2	(TA)7	14	643	656	AATCCAACGGTAAAACAGCG
scaffold714431_14.	1	p2	(CT)14	28	102	129	GGCCTCTTGACAAAAAGCTG
scaffold714445_14.	1	p2	(AT)8	16	599	614	GTGTGCGTGTTGAATATCGG
scaffold714479_14.	1	p2	(TA)9	18	128	145	AATCATAGCCATCCATTCCG
scaffold714482_13.	1	p2	(AG)9	18	831	848	ACACACACCCAGAGAGAGGG
scaffold714483_11.	1	p2	(AT)7	14	664	677	CCAGGCTTGTGCAAGCTATT
scaffold714491_18.	1	p2	(TC)7	14	784	797	AATCACCAAACGTCACACGA
scaffold714495_14.	1	p2	(CT)10	20	2133	2152	CAGAAAGAGCCCATAGCCAC
scaffold714497_15.	1	p2	(TA)6	12	348	359	TCAGCATGTTGCCATTAGGA
scaffold714501_15.	1	p2	(TA)10	20	46	65	AAGGAGGTGTTATGAAGGGATT
scaffold714513_15.	1	p2	(TA)7	14	3013	3026	CTCTTCTTCTGCCCCACCTA
scaffold714530_10.	1	p2	(AT)7	14	719	732	TCACGCACTCTCACTCATCC
scaffold714540_14.	1	p2	(AT)11	22	646	667	ATGGGGTTCTTCTCCTTTCC
scaffold714544_11.	1	p2	(TG)7	14	378	391	GAGGTGGCTTCTTTAGGGCT
scaffold714545_15.	1	p2	(AG)6	12	292	303	TCAGCATGTTCCATGTTCAAG
scaffold714551_15.	1	p2	(CT)6	12	121	132	TATCTCTCATTTCCTCCGCC
scaffold714553_17.	1	p2	(AC)6	12	661	672	TTGGCCTCACGATAGCTCTAC

scaffold714558_14.	1	p2	(TA)8	16	742	757	GTGCCTGAACCACCAACTTT
scaffold714562_17.	1	p2	(TC)6	12	426	437	ACGGCTAGATTCGATCCTGA
scaffold714615_16.	1	p2	(AG)7	14	479	492	CACCTTTTTCTTCCCCAGGT
scaffold714619_14.	1	p2	(TA)6	12	1670	1681	CACAACGAATTCCTACGGGT
scaffold714626_13.	1	p2	(CT)10	20	75	94	TTCAAACCTTTGCCACTTCC
scaffold714655_15.	1	p2	(AC)6	12	2838	2849	TCAACGAGGAAATCGCTTCT
scaffold714676_17.	1	p2	(AC)6	12	3529	3540	TGGAACCAACTCGTCAGACA
scaffold714683_11.	1	p2	(CT)7	14	995	1008	AGAAGCAGTTGGGATGATGG
scaffold714692_16.	1	p2	(TA)6	12	153	164	ATGCCCATCTCATTTCAAGG
scaffold714694_13.	1	p2	(TA)9	18	1029	1046	AAGGGATGGTATCATTTGATCG
scaffold714699_16.	1	p2	(CT)10	20	3692	3711	TCTTATTGGGTTGTCCGAGG
scaffold714740_17.	1	p2	(AG)9	18	344	361	AAAGAGAGAGTGCATGCGTGT
scaffold714751_12.	1	p2	(TG)8	16	35	50	TGAGTGTGTGTCTCGTGTGTG
scaffold714756_16.	1	p2	(AG)6	12	349	360	TTTGAAGGAAAACTCGTCCC
scaffold714781_16.	1	p2	(AG)7	14	348	361	GTGCCTGCTCCACTTTCTTC
scaffold714824_12.	1	p2	(GA)6	12	827	838	CTTCCATACTAGCTTCGCCG
scaffold714835_12.	1	p2	(AT)10	20	1037	1056	TGCAAGTTCCGAGTTCAAGTT
scaffold714878_15.	1	p2	(TA)6	12	1875	1886	TCTCAGCTCGATAAGTGGCA
scaffold714887_13.	1	p2	(TA)6	12	287	298	CATATCCTTTGAACCGGCAC
scaffold714908_17.	1	p2	(CT)7	14	349	362	TCGATCTGGGCTCTCTTGTT
scaffold714948_18.	1	p2	(AG)7	14	324	337	GTGGAGAGTGAGGAAGCAGG
scaffold714956_14.	1	p2	(GA)8	16	3692	3707	TTGGAAGAGGAAAGTGGGTG
scaffold714965_14.	1	p2	(TA)6	12	685	696	CCACGATGATTTCGATACACA
scaffold714981_16.	1	p2	(TA)8	16	683	698	ATTCACAGCCCTTCATCTCG
scaffold714990_11.	1	p2	(TA)8	16	67	82	GGTCCATAAGTGTTTTGAGTTATGA
scaffold715022_20.	1	p2	(AT)6	12	966	977	TTGGTCTTGGTCACGATTCTC
scaffold715072_11.	1	p2	(GA)6	12	460	471	CGGAGAGATTTGTGGGGTTA
scaffold715088_16.	1	p2	(TC)6	12	661	672	TTGGTGAAACCAAGCATGTG
scaffold715100_14.	1	p2	(AG)6	12	110	121	CTGGACGCATTAGTGGGTTT
scaffold715124_12.	1	p2	(TA)10	20	885	904	TATAAGGATCAACCGCCTGC
scaffold715127_14.	1	p2	(TG)9	18	1286	1303	GGGGCTTCAGATGAAATCAA
scaffold715128_14.	1	p2	(GA)7	14	349	362	AGCATCAGACCAATGTGCAA
scaffold715180_14.	1	p2	(TC)6	12	1116	1127	TGGTGCAGATGTCCTGGTTA
scaffold715184_16.	1	p2	(AT)7	14	1330	1343	CTACGCAGGGGCGTATGTAT
scaffold715227_15.	1	p2	(AG)7	14	3053	3066	GTGATCGCTGGTTCTTTCGT
scaffold715253_15.	1	p2	(GA)6	12	3360	3371	AGGTTGCGTCAGATTGGAAG
scaffold715292_17.	1	p2	(GT)6	12	621	632	AGTATGCTTTGGCCGATCC
scaffold715301_12.	1	p2	(TA)10	20	717	736	AATGATGTTAATCCAGCGGC
scaffold715305_11.	1	p2	(TC)6	12	697	708	GCCACTCCATCACCATAACC
scaffold715329_17.	1	p2	(AG)7	14	2663	2676	GCAGCAACATCTCTCGTGAA
scaffold715360_14.	1	p2	(AT)6	12	185	196	TGCGAGTATCAAAACCGAGC
scaffold715374_14.	1	p2	(AG)8	16	216	231	GTGGGAACGTGTAGTCGGAG
scaffold715418_13.	1	p2	(TA)12	24	252	275	TCATATCATTGTTTCCGCGA
scaffold715443_18.	1	p2	(AG)7	14	1517	1530	TTCCACCTCAAAAACAAATGG
scaffold715478_15.	1	p2	(TC)8	16	901	916	AATCACGCGAGGAAATCAAC
scaffold715479_15.	1	p2	(TA)6	12	3963	3974	GGGTGGAATGGTGGTGTTAC
scaffold715575_14.	1	p2	(CT)8	16	3504	3519	GCATTGGAGATGGAGCAAAT
scaffold715590_14.	1	p2	(TC)9	18	999	1016	GGTGGTGTTTGCCTGTCTCT
scaffold715599_14.	1	p2	(CT)7	14	352	365	CCCAACTGGAAAAGTCCAAA
scaffold715605_11.	1	p2	(TA)10	20	333	352	CGCAGATCCCAGATTTGTTC
scaffold715640_14.	1	p2	(TA)6	12	1113	1124	TGAAATTGTGTTGCTTGATCG
scaffold715650_17.	1	p2	(TA)6	12	705	716	TGAAGTTAGCACCTGAGGATGA
scaffold715713_16.	1	p2	(GT)8	16	135	150	CAATGAGGTGTCTGCCCTCT
scaffold715742_17.	1	p2	(AT)7	14	1970	1983	CCCGAACTCCGAGTACAAAA
scaffold715746_15.	1	p2	(GA)6	12	80	91	TGCTGATCTATTTACATGCTTTTCA
scaffold715755_16.	1	p2	(AG)6	12	481	492	AGGAGAGTGCAGCTGGTCAT
scaffold715758_14.	1	p2	(CT)9	18	687	704	AGATTGAAGCTCGGATGGTG
scaffold715820_15.	1	p2	(TC)7	14	1431	1444	TCACGTGGTGGAGACAAAAA

scaffold715836_14.3	1	p2	(AT)6	12	357	368	TGGTTTGAGCAAATTGATATTTTA
scaffold715840_16.2	1	p2	(AT)9	18	1081	1098	TTGTTGTCCATACATTTTGGAAT
scaffold715876_14.8	1	p2	(AT)7	14	2339	2352	ACCCAACTGGGTAAACCCTT
scaffold715902_16.9	1	p2	(AC)7	14	580	593	CTGGGGATGGATTGATGAAG
scaffold715953_17.0	1	p2	(TC)7	14	603	616	AAAATCCTTTCCACAACCCC
scaffold715989_16.6	1	p2	(GA)9	18	828	845	GATGTGGGTGGTTTGCTTCT
scaffold716007_22.9	1	p2	(GA)9	18	50	67	AGGGGTCCAAAAGCAGAAGT
scaffold716031_10.7	1	p2	(AT)7	14	224	237	TTGACATCGCAATCAACCAT
scaffold716048_15.6	1	p2	(AT)10	20	329	348	TTTCTGCACAGATTTGATGGTC
scaffold716057_16.1	1	p2	(GA)7	14	1010	1023	AACCGGGCAAGAAGAAAACT
scaffold716124_16.8	1	p2	(AT)6	12	565	576	TGAATTTCCTGTCATGCGTT
scaffold716130_16.7	1	p2	(TC)6	12	1021	1032	GCTTCGATGTTGATGCTTGA
scaffold716133_15.0	1	p2	(TC)8	16	1252	1267	TTTTGCCATGTGTATCGTTGA
scaffold716153_10.8	1	p2	(TA)11	22	43	64	CCCAAAAATGGGTTATTATTTGA
scaffold716155_16.0	1	p2	(CT)8	16	827	842	CCCATACACACAAGGCAGTG
scaffold716180_15.9	1	p2	(CA)8	16	2317	2332	ATTGATGCCCTGGTTACAGC
scaffold716229_15.6	1	p2	(CT)6	12	1858	1869	TGCCAGAACTTACCGACCTAA
scaffold716249_10.8	1	p2	(AT)12	24	936	959	CCAAATTTTGATCAATTTCCAA
scaffold716250_12.3	1	p2	(TA)8	16	1001	1016	CTCTGTGTGTGATTTCCGCT
scaffold716251_14.2	1	p2	(AG)8	16	1152	1167	ACGAGGGGTTTCTCTCGTTT
scaffold716269_14.2	1	p2	(AT)10	20	549	568	ATCTTGCATCGGCAAGAGAC
scaffold716273_21.7	1	p2	(TA)8	16	83	98	AAAATCGATATTGAATTAAAGGCTC
scaffold716275_15.8	1	p2	(AT)6	12	1709	1720	TTCACAAAGGGCTTTTCAGAC
scaffold716279_14.5	1	p2	(AG)10	20	134	153	TTGGGTGGAATAGACTTGGG
scaffold716307_14.7	1	p2	(TA)7	14	32	45	TCAACATCATCATCAACATACCC
scaffold716341_16.0	1	p2	(AG)6	12	848	859	AGCACTGCAACGCAACATAC
scaffold716344_17.6	1	p2	(AG)6	12	1019	1030	GGGCCGTACTTTCTGTCAAA
scaffold716365_16.2	1	p2	(TA)10	20	45	64	TAAGGGCGGTATCACCTGAA
scaffold716403_16.0	1	p2	(AG)7	14	2575	2588	TGAACCGAAAATTGGGTAGG
scaffold716461_16.4	1	p2	(AG)8	16	835	850	TCAAAACCGGTGATTAACTGC
scaffold716462_16.3	1	p2	(GT)8	16	694	709	TCTGATCATTGAGGAAGGGG
scaffold716518_17.8	1	p2	(AG)7	14	452	465	TGTTTTCGTTCTGAGAGGGG
scaffold716564_13.9	1	p2	(TC)6	12	475	486	GGTTCCCAGTTGGCATGTAA
scaffold716609_14.7	1	p2	(GC)6	12	240	251	CCGAAGCCCAAAAACAAATA
scaffold716610_17.0	1	p2	(CT)6	12	724	735	AAGTCCATTTCCACCCCTTC
scaffold716635_15.9	1	p2	(CT)6	12	233	244	GTTTCACAGGAGGCGGTTTA
scaffold716657_14.2	1	p2	(AG)10	20	1253	1272	CAGATTCAAAGACGGCGTTC
scaffold716687_17.7	1	p2	(CT)7	14	2466	2479	AGATGCTGAAACCTGGCATT
scaffold716768_17.4	1	p2	(CA)7	14	173	186	CGTGGTTGTAGGTCGGAGTT
scaffold716774_17.2	1	p2	(AG)6	12	362	373	ATCGAACAATTCCTTCCACG
scaffold716781_12.9	1	p2	(AT)7	14	1698	1711	CGCGAGATTCGATGGTAGAG
scaffold716808_12.2	1	p2	(TA)9	18	177	194	ACTTCGATCACTTCGTTCCC
scaffold716883_20.0	1	p2	(AT)6	12	626	637	ATATGTTGCAGGCCGAGAAG
scaffold716924_15.5	1	p2	(AT)7	14	2042	2055	CCCACACACAATGCAAGAAT
scaffold716938_17.4	1	p2	(GA)6	12	1175	1186	ACCCCTTTTACCCTTTCCCT
scaffold716979_15.8	1	p2	(GA)8	16	836	851	AGTCAGCACGCAATTTCTCA
scaffold717043_12.9	1	p2	(TA)6	12	467	478	TCAGACATTTCGATCCCAGA
scaffold717124_15.3	1	p2	(CT)10	20	1653	1672	AAGTTCCACTTGTTCACGGC
scaffold717140_15.3	1	p2	(CT)6	12	1536	1547	CAAGCCCAAATCAAGGAAAA
scaffold717150_11.1	1	p2	(TC)6	12	54	65	CTCCTCTTTCTCCCTCTCCTC
scaffold717156_17.9	1	p2	(TA)6	12	626	637	GTTCCCTGGAAACCATTTCA
scaffold717164_13.5	1	p2	(GA)8	16	817	832	AGGGAAAGATCCCTGCTTGT
scaffold717169_12.7	1	p2	(GA)6	12	575	586	TCAATTCCCAAACCATATCCA
scaffold717207_15.5	1	p2	(AG)7	14	544	557	TCAGCTTGTTAGTGTTCAGTTTGA
scaffold717256_11.6	1	p2	(AT)11	22	81	102	CCTGCATGTGCAAATTGAAA
scaffold717265_16.9	1	p2	(GA)7	14	1964	1977	GCAGCATTGATCTAGAGGGC
scaffold717281_16.0	1	p2	(AT)10	20	663	682	TGTTGCGTCTTGTATTGGAGTT
scaffold717327_12.1	1	p2	(TG)6	12	342	353	TCAAAACATTTATTTATGCACACATTT

scaffold717353_17.	1	p2	(TG)9	18	3424	3441	CCAATGATGGGTAACGGAAT
scaffold717361_14.	1	p2	(TA)7	14	867	880	GTTTATGTTGCGAAATCGGC
scaffold717363_12.	1	p2	(AT)12	24	1000	1023	TTCGCACAAATACAAATCGC
scaffold717381_16.	1	p2	(AC)6	12	367	378	ACATGCAATGAAAATGCCAA
scaffold717500_14.	1	p2	(CT)6	12	368	379	ATTCTATGGTGCCCCCTCTC
scaffold717502_13.	1	p2	(CA)6	12	1529	1540	CACGAAAATTTTGCATATCGG
scaffold717528_16.	1	p2	(CT)8	16	279	294	GAATGATGCATGCTCTCACC
scaffold717532_16.	1	p2	(AT)7	14	447	460	GAAGGTGACGTGTTGCAGAA
scaffold717571_14.	1	p2	(AT)6	12	205	216	GGATCTTCTCATTCCATCGAG
scaffold717637_18.	1	p2	(AC)8	16	730	745	CAGCAGCACCATACCAGAAA
scaffold717700_15.	1	p2	(TC)6	12	321	332	AATCTGCTGGTGTTCCTTGG
scaffold717733_11.	1	p2	(AT)7	14	368	381	GAATGAGGGTTTTTGTGGGA
scaffold717737_15.	1	p2	(AG)6	12	1744	1755	CTTTCCCTGCGTTGCATAAT
scaffold717739_15.	1	p2	(TC)9	18	355	372	TCCCTGACCACCATCAATTT
scaffold717774_13.	1	p2	(AT)9	18	891	908	TGAGTGGATATATTGGGAAGGG
scaffold717801_15.	1	p2	(CT)7	14	1336	1349	ATCTACCGGTTTTCCCCATC
scaffold717845_14.	1	p2	(AG)6	12	2152	2163	CGATTTTGTTTGCCGAAAAT
scaffold717847_13.	1	p2	(GT)6	12	334	345	AAGCGATGCTCCAACTTGAT
scaffold717880_16.	1	p2	(AT)7	14	1227	1240	ACTGTTGATGCAGATGGTGG
scaffold717884_16.	1	p2	(TA)6	12	709	720	AGAGAGAACTGGGGTCAGCA
scaffold717932_13.	1	p2	(CT)7	14	756	769	TCTCTCCCTTCTTCTGCTTCA
scaffold717936_16.	1	p2	(GA)7	14	226	239	GAAAGAAAAGTGTTGGGGGC
scaffold718021_14.	1	p2	(CA)6	12	570	581	CAAGATGGCATCATCCATTG
scaffold718114_16.	1	p2	(TA)6	12	601	612	ATAAGCAGCATTTGGCCTTG
scaffold718123_16.	1	p2	(TA)7	14	670	683	TGTTCTTGTCCGTCGGATTT
scaffold718173_15.	1	p2	(TA)9	18	45	62	CCAATTTGAATGGTTATCACCTG
scaffold718188_16.	1	p2	(AG)7	14	2607	2620	CGGGTAAATTTGAGGTGGAA
scaffold718304_15.	1	p2	(CA)6	12	509	520	TATGCTCGCTGGATTACGTG
scaffold718336_15.	1	p2	(TC)7	14	337	350	CTTGCAGTTTCCTCACCTCC
scaffold718348_18.	1	p2	(AC)7	14	372	385	AAACAACGATGGCAACAACA
scaffold718362_18.	1	p2	(CT)6	12	2439	2450	TCATAGATTTGGGCATGCAA
scaffold718389_17.	1	p2	(CT)6	12	67	78	GCACAACCACTCCACAAAGA
scaffold718410_11.	1	p2	(TA)10	20	963	982	TTTTGATAATGGTTTTGTACACATTTT
scaffold718424_10.	1	p2	(TA)6	12	67	78	TCTAAGGGCCGAGATTTGTT
scaffold718446_16.	1	p2	(TC)6	12	1427	1438	TGGATATTGAGAGGCTGGCT
scaffold718451_16.	1	p2	(TA)8	16	586	601	GGAGCTCGAGAGATATTGCG
scaffold718482_15.	1	p2	(TC)6	12	632	643	TGCTTTATGCCTTGCCTCTT
scaffold718486_13.	1	p2	(AT)11	22	178	199	GGGGTGTTTTGACAATATTACGA
scaffold718500_14.	1	p2	(GT)7	14	64	77	GGCAGTCGTTTTGAGACGTT
scaffold718511_13.	1	p2	(TA)7	14	260	273	TCGCGGGAATCAACTTTATC
scaffold718570_17.	1	p2	(AT)6	12	1277	1288	CGGCACGTGACTCACTTAAA
scaffold718622_16.	1	p2	(TC)6	12	1819	1830	TTCCTGAGTTGGTGAAAACG
scaffold718625_14.	1	p2	(GA)6	12	2462	2473	TGGGGAAGAAAAGGAGAGGT
scaffold718629_12.	1	p2	(AC)8	16	492	507	TTGCTATTGAGAGGAAGCGA
scaffold718636_12.	1	p2	(TC)6	12	989	1000	CTTTGGCAAATCAGGCGTAT
scaffold718639_15.	1	p2	(TG)6	12	3020	3031	AGGCGCTTCTCTCAGGTGTA
scaffold718648_14.	1	p2	(AT)10	20	101	120	CGGAAACCGCCATAAAGTT
scaffold718652_14.	1	p2	(TC)7	14	792	805	CCAGACAAAATCCCCTCTCA
scaffold718662_16.	1	p2	(CA)6	12	1620	1631	TTCACATGATCTTGGATGGG
scaffold718667_16.	1	p2	(TA)13	26	1349	1374	TTTTCTGCATGATTTGGATGA
scaffold718678_22.	1	p2	(CT)10	20	340	359	AAACGATTTTTGATCGTGGC
scaffold718682_16.	1	p2	(AT)10	20	2035	2054	TTGAGCTGGTTGATTCATTTTG
scaffold718698_16.	1	p2	(AT)6	12	87	98	GTGGGCGCAAGTAAAGAGAG
scaffold718715_17.	1	p2	(TG)6	12	2252	2263	TTGAACTTGTTTCAAATCCATGA
scaffold718726_16.	1	p2	(AG)6	12	970	981	TTTGCTCTCTCACACATGCC
scaffold718757_14.	1	p2	(CT)6	12	378	389	CAGTGCGTGTGTGTGTCAAG
scaffold718777_15.	1	p2	(CT)6	12	845	856	ATCACCCCCTCTCCAAGAAT
scaffold718782_14.	1	p2	(GA)6	12	72	83	TTCGAACTTCCATCCTGCTT

scaffold718786_15.	1	p2	(GA)7	14	1403	1416	ACCGCCGTCTGTAATAATGC
scaffold718804_16.	1	p2	(CT)7	14	123	136	AATTGCCTTGTGTTTCTGGG
scaffold718817_14.	1	p2	(CA)6	12	2597	2608	TGCTGTGGAATACCTGGGTT
scaffold718827_19.	1	p2	(AG)6	12	854	865	GAGAGGAGGAGGAGAATGCC
scaffold718856_13.	1	p2	(GT)6	12	263	274	GCTGAGATATACGCGGTGGT
scaffold718893_14.	1	p2	(CT)8	16	33	48	TGATTCTATTCTGTGCTTCGGA
scaffold718902_14.	1	p2	(AT)9	18	1327	1344	GTTCTGCCGAGATGAGGAAG
scaffold718905_10.	1	p2	(AT)10	20	189	208	CTATGCTGCCAAGTGCTCAA
scaffold718933_11.	1	p2	(CT)7	14	503	516	TGGGCCAAACCCTATATCAA
scaffold718943_12.	1	p2	(GA)8	16	1385	1400	ATGTCCGAGTTGTTCCCAAG
scaffold718963_14.	1	p2	(TG)6	12	1389	1400	AGATCTCGAGCAGCCAACAT
scaffold718990_16.	1	p2	(AT)8	16	954	969	GGTTGATCGTAATGGGATGG
scaffold719002_14.	1	p2	(GA)6	12	1622	1633	CTCCTTCCGTTTGTTGAGGA
scaffold719044_15.	1	p2	(AG)6	12	529	540	AGTTTGGAGGCCTGTCAATG
scaffold719046_14.	1	p2	(AT)6	12	1603	1614	AATTGTTCAACCTCTCCGCT
scaffold719064_12.	1	p2	(AC)6	12	1327	1338	CATGTGGTTGAATTTCGTTCA
scaffold719079_17.	1	p2	(GA)8	16	4814	4829	CGCAAAAGCAAGACACAAAC
scaffold719090_13.	1	p2	(TA)7	14	378	391	GAATCAACATTTCATCGCCA
scaffold719091_16.	1	p2	(TA)10	20	372	391	CATTGTGATAGGGTTCCGCT
scaffold719132_12.	1	p2	(AT)9	18	294	311	CACATATAATCAGGGGCGGA
scaffold719152_12.	1	p2	(TA)6	12	668	679	AGCGCAAACCAAACAAAAAC
scaffold719157_15.	1	p2	(GA)7	14	924	937	TGGGTGGGAGATAAGAGGTG
scaffold719203_16.	1	p2	(TC)9	18	2585	2602	AAAAACCAGCACCAATCCAG
scaffold719206_15.	1	p2	(AT)9	18	276	293	CCCCTAGGCATGGATTATCA
scaffold719243_14.	1	p2	(CT)6	12	1000	1011	TCATCCAAGTTCATGCAAGG
scaffold719277_15.	1	p2	(TA)6	12	2461	2472	CAACTGGCTATGTTGCTCCA
scaffold719304_11.	1	p2	(GA)11	22	373	394	AATAATGGCGGGTACGTTGA
scaffold719358_17.	1	p2	(CA)6	12	3927	3938	TCAACTGCTGCAAATGATCC
scaffold719361_15.	1	p2	(TC)8	16	221	236	GCGTCTCACCTAACCTCACC
scaffold719370_17.	1	p2	(AT)6	12	382	393	TCCCCAGAGCTTGAGAGAGA
scaffold719390_12.	1	p2	(TA)10	20	42	61	TTTCCATGTAATAAAAAGTTTCCCA
scaffold719407_15.	1	p2	(CA)10	20	286	305	GGTCCAGATCATGGGTCACT
scaffold719443_13.	1	p2	(AT)9	18	68	85	TCCGATGGTTGTAGTGGAGTT
scaffold719448_15.	1	p2	(AT)7	14	125	138	GTCGGCGTTTTCAGCACT
scaffold719457_12.	1	p2	(TC)6	12	262	273	CCCTTCACAAGTGGTGACAA
scaffold719460_15.	1	p2	(TA)6	12	201	212	ATATGGGATTTTGCATGGGA
scaffold719497_15.	1	p2	(AT)8	16	379	394	AATGACTCAGAATTTGGCCG
scaffold719498_17.	1	p2	(TC)8	16	4573	4588	ATGGCATGACTCTTGAGCCT
scaffold719535_14.	1	p2	(TA)9	18	2305	2322	TTCTGATATGGAAATGCCCC
scaffold719545_15.	1	p2	(AG)8	16	1542	1557	GACGTGGTTTGCAGGCTATT
scaffold719565_13.	1	p2	(TA)7	14	125	138	GGTTTCCCTCCCAAAAACAT
scaffold719586_13.	1	p2	(AT)6	12	1018	1029	CCTGAGATTGGTCGAGGGTA
scaffold719616_14.	1	p2	(CT)6	12	431	442	TTCAGACTCCAAAAACAAAGCA
scaffold719641_15.	1	p2	(AT)8	16	380	395	CTAGCCATCCATTCCGAAAA
scaffold719648_15.	1	p2	(TC)7	14	93	106	AGAAAGTTGCAGGCTGGCT
scaffold719703_16.	1	p2	(TC)8	16	381	396	CCACCATTTTTATTCCCCCT
scaffold719733_15.	1	p2	(AT)6	12	1800	1811	TCCAAACTCCAACCTCCATAA
scaffold719739_16.	1	p2	(TA)6	12	1158	1169	GCATGATCAAAGAGGCCATT
scaffold719759_16.	1	p2	(TC)6	12	849	860	TCCTTGGCATACATTCTCTCTC
scaffold719777_14.	1	p2	(CT)6	12	519	530	AGCAACCAGCTGCATTAACC
scaffold719794_16.	1	p2	(TC)8	16	846	861	TCCCACCACCTCTACCCATA
scaffold719805_12.	1	p2	(CT)6	12	1093	1104	GGAATGTGATTGGGGAAGAA
scaffold719807_17.	1	p2	(TA)7	14	52	65	CACAGCTGTCAATCAACAAGAA
scaffold719813_18.	1	p2	(TC)8	16	382	397	CTGTCTCAGTCACCGTCGAA
scaffold719821_10.	1	p2	(TA)11	22	358	379	TTACACTGCAGTACGTCGCC
scaffold719856_17.	1	p2	(AT)6	12	1432	1443	GACTTCTGGTGGACGACGAT
scaffold719898_16.	1	p2	(AG)6	12	526	537	AGTCGCGAGTCTCTCTCTCG
scaffold719933_14.	1	p2	(TG)12	24	368	391	TTCGCCATATCCATGTTTCA

scaffold719943_13.	1	p2	(CT)13	26	34	59	CCACCCTCCATTGCTCATAA
scaffold719956_18.	1	p2	(CT)9	18	2164	2181	TTTGCCTTTGATCGACACTG
scaffold719988_15.	1	p2	(CA)9	18	723	740	CCCGGTCTATCTATGGGGAT
scaffold719999_12.	1	p2	(TA)10	20	2000	2019	ACGCGTGTGACATGTTCCTA
scaffold720024_15.	1	p2	(AC)9	18	615	632	CGCGAGACATGAACGAATAA
scaffold720031_11.	1	p2	(TC)6	12	556	567	TTTGGCCTTGTCCTCGTATAA
scaffold720053_15.	1	p2	(AT)6	12	1975	1986	TCGATTGTATTTAAGCACGCA
scaffold720067_15.	1	p2	(TA)6	12	280	291	TGTCACTGCACTACGAGATGAA
scaffold720078_11.	1	p2	(GT)7	14	1113	1126	ACCCCTTTGTCGATTCTCCT
scaffold720087_17.	1	p2	(TC)6	12	374	385	CCCATAAACCACACTAAAGATGG
scaffold720091_12.	1	p2	(TA)8	16	899	914	CAAGGCAAGACTTGTGGTCA
scaffold720162_17.	1	p2	(CT)6	12	361	372	TCCCGTGAGGTAAACATCCT
scaffold720163_15.	1	p2	(TC)6	12	180	191	CCGACATTCAGCAGATGAGA
scaffold720170_14.	1	p2	(CA)6	12	1717	1728	GAACCTTCGGACAGCTCTTG
scaffold720176_14.	1	p2	(TC)7	14	388	401	AGTGATCACACCTGCCCATT
scaffold720209_13.	1	p2	(TA)6	12	390	401	AAACATGGAATGAGTTAAGGGAA
scaffold720219_14.	1	p2	(TC)7	14	388	401	GGTGTGCCTTGTCCAATTTT
scaffold720224_18.	1	p2	(TC)8	16	494	509	AAGAGGGCCAGGAACAAAAT
scaffold720255_15.	1	p2	(AG)7	14	1741	1754	CACGCTGGCCATATACCATA
scaffold720298_15.	1	p2	(TA)6	12	786	797	TCAAACCATTATACCTACCGCA
scaffold720305_15.	1	p2	(TG)9	18	984	1001	CTGCTTATCTTTTCGGGCTG
scaffold720313_12.	1	p2	(TC)8	16	613	628	CTACGTAGCTCGGTTCTCCG
scaffold720358_13.	1	p2	(AT)8	16	230	245	CTTTCTCCTCACGCTCTGCT
scaffold720386_16.	1	p2	(GA)6	12	223	234	GAGTGGAGGATTCGGTGAAA
scaffold720477_16.	1	p2	(AG)6	12	3070	3081	TGGAGCAGATCCCAGTCTCT
scaffold720499_17.	1	p2	(GA)7	14	6856	6869	TGAGGCCAATTCCTCAGTGT
scaffold720502_11.	1	p2	(CT)9	18	121	138	ACTACCACCAGCACCTCCAC
scaffold720507_11.	1	p2	(TA)9	18	171	188	AACAAACGAAAGGGACCACA
scaffold720519_14.	1	p2	(GA)8	16	855	870	TCAGCAGCCATTGAGACATC
scaffold720581_14.	1	p2	(AT)6	12	689	700	ACAAAACAAAACAGGGGCAA
scaffold720585_14.	1	p2	(TG)6	12	37	48	CGAACCACGTTAAATCTCTGTG
scaffold720594_17.	1	p2	(TC)8	16	923	938	AGCTCAATGCACTTCCCAAT
scaffold720600_16.	1	p2	(CT)7	14	159	172	TAATCGTGTTGCATTGCCTC
scaffold720617_12.	1	p2	(GA)6	12	359	370	AGGAGTCGGAGTGAAAAGCA
scaffold720619_14.	1	p2	(AT)9	18	724	741	TTTGGCGATATGCAATCAAA
scaffold720658_14.	1	p2	(TA)8	16	1694	1709	AAATCCGTCCCAATATTCCC
scaffold720698_15.	1	p2	(TC)8	16	820	835	TGCTGAGACAGTGGAAGGTG
scaffold720701_16.	1	p2	(AT)7	14	1458	1471	GCGTGGTTGTGAGCGTATAA
scaffold720705_16.	1	p2	(GA)7	14	191	204	CTGCTTTGTGTTGCGTGTTT
scaffold720706_17.	1	p2	(CT)8	16	2734	2749	CATGGCAGTTTCACATTTGC
scaffold720716_17.	1	p2	(TA)9	18	388	405	TTTACAAGATCAATGGTCCCAA
scaffold720794_15.	1	p2	(TA)10	20	80	99	ACGGCTGCAAAAGTTTCCTA
scaffold720839_14.	1	p2	(AT)6	12	1458	1469	TCGACGTCTACAAAACGCAC
scaffold720850_16.	1	p2	(GT)6	12	768	779	AGGAGGACGAGTGTGGTGAC
scaffold720886_17.	1	p2	(TA)8	16	1738	1753	CATTTTTAATTGCAAAATTAATCCA
scaffold720915_14.	1	p2	(AT)7	14	1270	1283	TGCATGTTCAATTGGGAAAA
scaffold720924_15.	1	p2	(TA)9	18	44	61	AAGGGTTATCACCTGATTTTCTC
scaffold720941_14.	1	p2	(TC)6	12	2816	2827	TAGCAAAAACGAAGCCACCT
scaffold720958_17.	1	p2	(TA)6	12	592	603	CCCAAAATCAACGTCCAGAT
scaffold720960_16.	1	p2	(TG)8	16	3737	3752	ACGATCATCAAAGAATCGGC
scaffold720978_15.	1	p2	(GA)12	24	737	760	TTGCCTCTGCAAGAATTGTG
scaffold721021_16.	1	p2	(TA)10	20	3781	3800	ACAAACCACTGAATCGCACA
scaffold721023_19.	1	p2	(TA)7	14	237	250	TCTGCGTTACTTGCTTTCCA
scaffold721025_12.	1	p2	(TA)7	14	521	534	TGAATATTGATTGGTCCATGC
scaffold721030_16.	1	p2	(GA)6	12	1696	1707	TCTGCTTTCACACCAAGTCG
scaffold721084_15.	1	p2	(AG)7	14	3577	3590	ATGTGCACAGCGAGGTATTG
scaffold721100_18.	1	p2	(AC)6	12	931	942	AGGCCAGAAACTGCTCAAAA
scaffold721103_15.	1	p2	(GT)6	12	2092	2103	CCCCTATGAAGCCCAGAAA

scaffold721114_15.	1	p2	(TC)7	14	143	156	ATCACTTCCGATCGAACCAC
scaffold721167_13.	1	p2	(TC)7	14	647	660	ACTACGGCCACATGAGCTTT
scaffold721191_19.	1	p2	(TC)6	12	1026	1037	ATTTGTTCACCCTGGACGAT
scaffold721203_17.	1	p2	(AT)6	12	109	120	AGATTCTCACGCCATTCTCAA
scaffold721213_14.	1	p2	(TC)8	16	627	642	GCGTGGCATATTTCTGATGA
scaffold721226_14.	1	p2	(CT)6	12	722	733	TCTGGACAAGAAGCCATTGA
scaffold721287_14.	1	p2	(AG)8	16	1473	1488	CTGTTTCCTGTCCAATTCCC
scaffold721307_13.	1	p2	(TA)9	18	513	530	TTTTCATTATTTATTGCAAGTTTTCG
scaffold721352_16.	1	p2	(GA)8	16	848	863	GTCGGCAATTTCTTGATGCT
scaffold721357_13.	1	p2	(AT)6	12	585	596	TTGTTGAACGTCTCCAACTCC
scaffold721399_14.	1	p2	(AG)10	20	1360	1379	GGGAGTTGAGGGATCACAAA
scaffold721428_14.	1	p2	(TG)6	12	644	655	GAGCAGAAACTTGCGGAGTC
scaffold721463_15.	1	p2	(CT)9	18	984	1001	CCGTGGTGATTCTTTGGACT
scaffold721466_12.	1	p2	(TA)10	20	654	673	GTTAACCTTGCAAGCTGCCT
scaffold721496_11.	1	p2	(GA)7	14	728	741	CTTGCTCCTAATCGTCGGTC
scaffold721498_14.	1	p2	(CT)7	14	898	911	GCCATGAACTATATTGATTTTCCA
scaffold721576_15.	1	p2	(GA)6	12	6102	6113	GCCTCAAAATATCTGCTCCAA
scaffold721578_11.	1	p2	(TA)6	12	347	358	ATTGGTTTGGCAAAAGCCTC
scaffold721635_11.	1	p2	(AT)9	18	1972	1989	TCCTTTCTCAAATGAAGAGAAACA
scaffold721671_13.	1	p2	(AG)7	14	871	884	TGCAGAGATTTGTGGCAGAC
scaffold721673_10.	1	p2	(AT)6	12	402	413	TTTTCAGTGGTGTTTGTTGTTT
scaffold721676_11.	1	p2	(AT)7	14	1133	1146	TATAAAAATGCAGCCAGGGG
scaffold721688_15.	1	p2	(AG)9	18	3466	3483	TGCATTTTTCAGCATTTCCA
scaffold721720_14.	1	p2	(AT)12	24	1403	1426	AAAAACGCGGAAATCACATC
scaffold721725_16.	1	p2	(AG)7	14	1123	1136	GTCGTCGTTTCCACCTCTGT
scaffold721728_14.	1	p2	(CT)7	14	402	415	GCGGCTCTGCAACTTTTAGT
scaffold721781_16.	1	p2	(TA)8	16	1424	1439	GCCTTGTCCGTTGTCAGAAT
scaffold721823_14.	1	p2	(CT)12	24	1036	1059	GCCATTCTCCTTCAAAACCA
scaffold721828_13.	1	p2	(AG)9	18	398	415	GCCCAAGATACTCCATCCAA
scaffold721837_16.	1	p2	(CA)7	14	3259	3272	AGGCATTGGTTTGTTGGAAG
scaffold721852_17.	1	p2	(TA)9	18	47	64	AAGGAGGTGTTATGAAGGGATT
scaffold721854_14.	1	p2	(GA)9	18	3391	3408	CGCTTGTTCCTTGGTAGGAG
scaffold721863_18.	1	p2	(GA)6	12	105	116	GGTTGATGTCATCGTCATGG
scaffold721872_13.	1	p2	(AT)9	18	202	219	ATTTTGACGGGATTCAGGTG
scaffold721878_13.	1	p2	(GA)10	20	3282	3301	CAAGCAAGAAAAAGCGAACC
scaffold721888_15.	1	p2	(TG)6	12	925	936	TGAAAGGTAGGGTTTTCGCA
scaffold721889_15.	1	p2	(TA)6	12	656	667	TGCAAGTAAAATCGTCGTGC
scaffold721919_16.	1	p2	(AG)6	12	6480	6491	TGAAGTTGACGAAGAAGATGACA
scaffold721938_15.	1	p2	(TA)6	12	627	638	CCTAAAATTGCCCCATCCTA
scaffold721941_10.	1	p2	(TA)8	16	566	581	TTGAATCTCCGGCTGAAACT
scaffold721958_14.	1	p2	(AG)7	14	404	417	TTGGCCACAAATTAAAAGGG
scaffold721962_16.	1	p2	(AT)6	12	2942	2953	TGAAACTCTCAACAGATTCCCA
scaffold721978_16.	1	p2	(TA)9	18	47	64	CACTTAAGGGGGTTATTAGTGGA
scaffold721979_16.	1	p2	(GT)6	12	106	117	TGGGAACACTCTTCAGGACA
scaffold722010_14.	1	p2	(AT)8	16	1086	1101	TTTTCATTGGAGTTGTGCCA
scaffold722011_14.	1	p2	(TA)6	12	54	65	CAGATTTGTTATGTGTTTTGACAAT
scaffold722019_12.	1	p2	(CT)12	24	36	59	TGGTGGCTGAAATGCTTGTA
scaffold722025_16.	1	p2	(CT)6	12	407	418	TTCTGCCCTTAAGGCTGTTG
scaffold722040_16.	1	p2	(AT)6	12	4010	4021	TTCTAAAGCTCCACCACACG
scaffold722078_15.	1	p2	(TC)7	14	504	517	GAGTCATCAAGAAGGCCAGC
scaffold722135_14.	1	p2	(TA)6	12	65	76	GACCAAAAATCCAATCCAGG
scaffold722149_17.	1	p2	(GA)6	12	1223	1234	GGAGAAATCAAGAGGAGGGG
scaffold722186_14.	1	p2	(TC)6	12	190	201	AGCCTGTACGACTCCGACAC
scaffold722203_14.	1	p2	(GA)6	12	170	181	ATTTGAGGGGGAAAGGAGAG
scaffold722210_13.	1	p2	(AT)8	16	972	987	GGCATAGGTTTGGGTTTCAA
scaffold722226_18.	1	p2	(GA)6	12	294	305	GAGGATCTGTGGGGTGGTAA
scaffold722235_13.	1	p2	(AT)7	14	286	299	GGAATTCCAGCAACCTCTTG
scaffold722249_16.	1	p2	(TG)6	12	3548	3559	TTCGAGGCGTTTTCTAGGTG

scaffold722281_13.7	1	p2	(AT)9	18	351	368	GTGTCAAATTCGCAACGAAG
scaffold722292_14.9	1	p2	(TA)6	12	1388	1399	TTTGATGGGATGGTATGTTTATG
scaffold722294_12.0	1	p2	(AC)9	18	328	345	AACCAACATCCCATCTCCAT
scaffold722304_14.8	1	p2	(TA)6	12	77	88	AAAAATCAAAGGCCCACAAT
scaffold722334_18.7	1	p2	(CT)6	12	860	871	GCCATCAAAAGAGGAAACGA
scaffold722337_14.6	1	p2	(TG)6	12	156	167	CACGAATGAAACAAGTTGGG
scaffold722361_14.2	1	p2	(CT)6	12	633	644	TGATTTCAGTTGGTAGCAGGAA
scaffold722379_15.9	1	p2	(CA)7	14	1476	1489	ACATGGCGTGCTACAATCAA
scaffold722386_15.7	1	p2	(TA)7	14	388	401	CTTCTTCCCAGTTTCCCCTC
scaffold722407_20.0	1	p2	(AT)6	12	358	369	GGGTTATCATTTGAACGCGA
scaffold722415_15.4	1	p2	(CT)8	16	148	163	CCCAAGCAAAAGACGACACT
scaffold722421_11.6	1	p2	(GA)6	12	800	811	AGCTTCTGACATCCACGCTT
scaffold722433_13.7	1	p2	(AG)7	14	525	538	ATTTCGTGAATTGGCTACGG
scaffold722436_13.8	1	p2	(AG)7	14	507	520	TCTTTTGCAGCCCTCCTTTA
scaffold722446_16.1	1	p2	(TC)6	12	840	851	GAAAAATGTATGGGGTCGGA
scaffold722452_14.4	1	p2	(TA)7	14	1722	1735	AGGGACTTAACAAGCCATCG
scaffold722457_12.0	1	p2	(TA)6	12	53	64	TTTCTCATACAAAAAGACATTTCTCA
scaffold722459_18.0	1	p2	(CT)8	16	313	328	TGCTCACAAGCAACCAAAAC
scaffold722466_16.8	1	p2	(AG)7	14	3130	3143	ACCTTAGCAACGAAGGAGCA
scaffold722515_13.8	1	p2	(AT)6	12	1711	1722	GCAAGTCTGGTACTTGGGGA
scaffold722542_11.7	1	p2	(AT)7	14	746	759	TTGACTGTCATTTTACCTCTTTATGA
scaffold722581_14.7	1	p2	(CA)9	18	4301	4318	CATAGCTTGCTCACCAACCC
scaffold722606_12.8	1	p2	(TA)8	16	567	582	CGGTTCTGACCACTAAACGA
scaffold722629_15.0	1	p2	(AT)10	20	86	105	TTTGGATCTGTTTGTCGAGTTG
scaffold722630_17.1	1	p2	(TA)6	12	2291	2302	GATAATCACCGGAAAAGCGA
scaffold722640_19.6	1	p2	(TA)6	12	1614	1625	CCCACACCTCATCAACCTCT
scaffold722663_15.7	1	p2	(TA)10	20	44	63	AAGGAGGTGTTATGAAGGGATT
scaffold722664_15.4	1	p2	(CT)9	18	671	688	ACATGGGCAATAAGTCAGGC
scaffold722678_10.5	1	p2	(TA)9	18	233	250	GAAAATCTGCAGTGGGGTGT
scaffold722691_17.1	1	p2	(CT)8	16	714	729	ATGGGAGCTCATGAACGAAC
scaffold722702_14.7	1	p2	(CT)10	20	993	1012	ATACGGGGCATAAGCTGTCA
scaffold722716_16.4	1	p2	(TA)6	12	413	424	CCCAGCATCCGTTAGTTACAA
scaffold722717_14.0	1	p2	(TA)7	14	411	424	CAAATCGATTCGGAGTTTGAA
scaffold722730_16.2	1	p2	(GC)6	12	168	179	TATAGGCACTTCCACCAGGG
scaffold722757_16.7	1	p2	(TC)7	14	2450	2463	TCACCTTCTTTCCCCTTCCT
scaffold722758_13.4	1	p2	(TA)8	16	829	844	GCGAAATAGGATCGCCAATA
scaffold722765_14.5	1	p2	(GA)11	22	3864	3885	TAGCGCTGCAGAATTCAAGA
scaffold722777_16.0	1	p2	(TC)6	12	746	757	GTAAATCACGAGACCGCCAG
scaffold722792_15.7	1	p2	(AT)6	12	415	426	AGAAATCCAGCAACCAATCG
scaffold722872_10.5	1	p2	(AG)6	12	1119	1130	TGAGGAATGAGAGCGTAGGG
scaffold722877_14.3	1	p2	(TA)6	12	320	331	CGTGCAAAATAGCACCAAGA
scaffold722890_14.9	1	p2	(TA)9	18	215	232	TCCAGCGCCCTATAATGTTC
scaffold722916_11.8	1	p2	(AT)7	14	673	686	CGTTGTCTGCCTTGGAATTA
scaffold722938_14.7	1	p2	(AT)8	16	332	347	TAATGGCCCTGAATCTTTCG
scaffold722980_14.0	1	p2	(GA)6	12	1165	1176	ACAACAAGATCCCCTGCAAT
scaffold722985_14.2	1	p2	(CT)7	14	782	795	TGGGTGCTTTTCTTGCTCTT
scaffold722998_15.1	1	p2	(AG)7	14	985	998	GCCCATTGATGAAAGTTGGT
scaffold723014_13.9	1	p2	(TC)7	14	930	943	AAGAGGGAGAGAATGGGAGC
scaffold723021_11.0	1	p2	(AT)12	24	692	715	CAGAGCGCACTCGAAGAGTA
scaffold723059_15.0	1	p2	(AT)6	12	649	660	TTCCCCCTTTTATGGTCAAA
scaffold723080_15.3	1	p2	(TA)7	14	2396	2409	TATGCAGCCATCAGACCAAG
scaffold723082_17.7	1	p2	(AC)6	12	2012	2023	CAAAAATGCCACTGCTTGAA
scaffold723105_11.0	1	p2	(TA)9	18	275	292	TTTGAGGAAGGATTTGAGGC
scaffold723108_16.6	1	p2	(TA)8	16	48	63	GCGGTTATCACCGGATCG
scaffold723119_16.3	1	p2	(TC)7	14	3796	3809	TTGCTGCTGACACCAATCTC
scaffold723130_16.2	1	p2	(TA)7	14	1114	1127	TCAACAACGGTAAGTTGCTCTT
scaffold723149_15.9	1	p2	(AC)7	14	1456	1469	CATGTGCGACTTTGGAGGTA
scaffold723159_17.4	1	p2	(AG)7	14	3584	3597	TCAAGAATCCCTTTAGCCGA

scaffold723162_13.	1	p2	(TC)9	18	97	114	CCCCATTACCATCTTTCTCG
scaffold723187_14.	1	p2	(AG)6	12	275	286	AGGGAGTTGCTAGGGTGTGA
scaffold723218_17.	1	p2	(AT)6	12	977	988	CATGCAGGGCTGAGTACAGA
scaffold723219_16.	1	p2	(CT)6	12	947	958	CTTCCCCTTCGCTCCTACTC
scaffold723225_10.	1	p2	(AT)9	18	173	190	TCAAAAACCGAAAACCGAAC
scaffold723245_14.	1	p2	(GA)6	12	841	852	TATTGTAGCGGCCCAATACC
scaffold723249_11.	1	p2	(TA)7	14	1108	1121	GCATCGTAAGGAGCGTTGAT
scaffold723263_15.	1	p2	(AG)7	14	417	430	AAATCAGCACCCAACCAAAG
scaffold723290_19.	1	p2	(TC)6	12	419	430	GAGTGCTTCGAAAAGGTTGC
scaffold723294_18.	1	p2	(TC)7	14	1344	1357	GTTAGGGTTTTTGTCGGGGT
scaffold723295_14.	1	p2	(TC)6	12	419	430	GATATTCACCGACGTGCCTT
scaffold723300_13.	1	p2	(TC)6	12	62	73	TAAGAGTTGTCCGGAGTCGG
scaffold723305_13.	1	p2	(CT)8	16	415	430	CTTGTTGAGAGGTGGCTGTG
scaffold723308_14.	1	p2	(TA)9	18	322	339	TCAATCATCCAACACACCAA
scaffold723360_11.	1	p2	(TC)7	14	829	842	ACGCGAGGGTTGTGATAAAC
scaffold723469_14.	1	p2	(CT)7	14	2275	2288	TGGTATCAGGGTTTCAGCTTC
scaffold723480_14.	1	p2	(AT)9	18	575	592	TCCACCACTGTCAGAAAGCA
scaffold723507_12.	1	p2	(AC)10	20	248	267	GAACCAGCTGACCATGTGAA
scaffold723517_13.	1	p2	(CT)7	14	62	75	AATTTCTTGCTCCAAACCTTTA
scaffold723546_16.	1	p2	(TA)9	18	1117	1134	AATCAAAGAGCAATGAGCCG
scaffold723552_16.	1	p2	(GA)6	12	174	185	GCAACAAATGCCAACGCTAT
scaffold723561_13.	1	p2	(AT)6	12	514	525	TTGATGTGAGATGGGCTTGA
scaffold723566_16.	1	p2	(GA)11	22	35	56	CCTACCTAAGGAGGGAGGGA
scaffold723603_16.	1	p2	(AC)10	20	630	649	CCCTACGCACTCGTTTTTCT
scaffold723608_14.	1	p2	(AT)6	12	423	434	CCTGCTGTTGATTTGATGGA
scaffold723613_15.	1	p2	(AG)7	14	422	435	AAATGGAATGTGGCGAAGAC
scaffold723723_14.	1	p2	(TG)9	18	203	220	GAAAAATTCGTAAGTGGCCG
scaffold723752_15.	1	p2	(CA)6	12	165	176	GTAACTCAAGGCCCATTCCA
scaffold723759_12.	1	p2	(CT)6	12	727	738	CCCAACAATTTCGGTTTGAC
scaffold723771_18.	1	p2	(TA)6	12	426	437	ACCAAACCCATTCTTGTCCA
scaffold723772_14.	1	p2	(AT)11	22	708	729	TTGATGGATTTTTCAAGCCC
scaffold723781_17.	1	p2	(CT)8	16	897	912	TTTCTTCAAATTTGGGGTGG
scaffold723790_18.	1	p2	(TA)6	12	425	436	TGCAAGCAAAAAGACGAAAA
scaffold723810_17.	1	p2	(AG)6	12	1340	1351	GAGGGAGCTGCAACAAGAAA
scaffold723824_11.	1	p2	(TA)9	18	602	619	TTATGGCCCTTGGATTTGAG
scaffold723831_17.	1	p2	(AC)8	16	25	40	TGTGACCTCAATTGCAAAAC
scaffold723864_10.	1	p2	(TA)8	16	595	610	ACTGGACCGGACCGTTTT
scaffold723882_10.	1	p2	(AT)9	18	1099	1116	TTGGCAAAGTCCCCTATTTG
scaffold723935_19.	1	p2	(CA)6	12	370	381	AGCTGCAGCATTTCTCACAA
scaffold723948_15.	1	p2	(AG)6	12	278	289	GGTCAGTTTCTTGCTTGCAG
scaffold724018_11.	1	p2	(AT)10	20	1415	1434	TCGTGCATTACTCGGTTACTTG
scaffold724043_14.	1	p2	(CT)7	14	3112	3125	GGAACCAATCTGGTGCATTC
scaffold724057_10.	1	p2	(TA)7	14	269	282	TCAGATCACCACCGGACATA
scaffold724073_15.	1	p2	(CT)8	16	1601	1616	CGCACACACCATCTGTGAAT
scaffold724092_15.	1	p2	(TA)6	12	219	230	TTCCTCTTGAATTTGGTGGG
scaffold724093_15.	1	p2	(CT)6	12	428	439	GGGAACCAGATACGAGGACA
scaffold724126_16.	1	p2	(TC)6	12	2129	2140	TGGAAATGGAATCCGAAGAC
scaffold724130_15.	1	p2	(AT)6	12	660	671	CTTCAAGGATTTGAGCCGAG
scaffold724163_12.	1	p2	(AG)7	14	57	70	GCTTCTTCTTGCTGTGAGTGG
scaffold724170_12.	1	p2	(GA)13	26	495	520	TGAAATCATGCTGGTTGCAT
scaffold724171_13.	1	p2	(AT)8	16	1510	1525	GCCTGTTTGCCACTCAAAAT
scaffold724173_12.	1	p2	(AT)8	16	426	441	ATTGTCACATGGTCCGCATA
scaffold724175_17.	1	p2	(AT)10	20	1849	1868	TGTGCCTTGATTCATTGAAAA
scaffold724197_15.	1	p2	(CA)6	12	737	748	TCAAGATTTTGTGTGGCTGC
scaffold724202_17.	1	p2	(AG)7	14	428	441	CACCCCTGAAACTCCATCAT
scaffold724206_15.	1	p2	(AT)8	16	743	758	GACGACGATGAAAATCGTGA
scaffold724216_17.	1	p2	(TA)9	18	267	284	AACGCGCATTTTAGGGTTTA
scaffold724238_17.	1	p2	(TC)6	12	51	62	TGTCGGTGGACTGATTTGTG

scaffold724242_13.	1	p2	(TA)7	14	126	139	CGTGAGAAGCGTTGATATGG
scaffold724282_13.	1	p2	(AT)6	12	552	563	CCTCTCACATGTCTCCACGA
scaffold724302_17.	1	p2	(TA)6	12	383	394	GGATCTGCGTCCATTTCACT
scaffold724320_12.	1	p2	(AT)7	14	1697	1710	CGAGACATGGAATTAGGGCT
scaffold724339_15.	1	p2	(GA)9	18	834	851	CACCAAATGTATGTGCATGAGA
scaffold724386_13.	1	p2	(AT)6	12	197	208	GGGGATGGGGGTAAGTAATG
scaffold724392_15.	1	p2	(TA)6	12	431	442	TGACCGAAAAATCCAACGAT
scaffold724424_13.	1	p2	(AG)7	14	156	169	ATCAGCTGCCAAACCAAGAT
scaffold724457_13.	1	p2	(AG)9	18	638	655	AAAGGTCCCTCACCAGTCAA
scaffold724460_15.	1	p2	(AG)7	14	940	953	GCTGCTCCTGTCTCTTTGCT
scaffold724500_16.	1	p2	(GA)6	12	723	734	GGTGCTGCAACTGAACTGAA
scaffold724512_14.	1	p2	(CT)6	12	426	437	CTGTCACGTCTCTTCCACCA
scaffold724530_14.	1	p2	(AG)10	20	553	572	TGGCTATAGGACATCGAGGG
scaffold724562_11.	1	p2	(GA)7	14	432	445	TTTGCATGGAATAAGAATTTTGAA
scaffold724567_13.	1	p2	(CT)7	14	430	443	TTAACCGCCAAACTCAAACC
scaffold724572_15.	1	p2	(AG)8	16	1553	1568	GGGCTATTGTCATTTCGACC
scaffold724573_17.	1	p2	(CA)6	12	4009	4020	CCTCTGGCTGTTCTGGATTT
scaffold724593_11.	1	p2	(GA)8	16	736	751	CTCCACTGATGTGTGGATGC
scaffold724601_14.	1	p2	(AG)8	16	242	257	CATGAATTTTTGGGAAGCTGA
scaffold724637_15.	1	p2	(TC)8	16	3806	3821	TTCATGCAAACTGCTGGAAC
scaffold724645_14.	1	p2	(AT)6	12	1104	1115	TCTGTTCAGAGAATGCTGGG
scaffold724779_16.	1	p2	(AG)7	14	1348	1361	CATGACCCAATCAATGCAAC
scaffold724796_14.	1	p2	(TG)6	12	518	529	TGAAAAAGAAAAACGCGTCA
scaffold724813_14.	1	p2	(AG)6	12	51	62	TGTACGTGCGTACGTGTGTG
scaffold724814_14.	1	p2	(GA)6	12	991	1002	TCCTGTTTGATGAAATGCCA
scaffold724824_14.	1	p2	(GT)8	16	51	66	GTCTGAGCGAGAGTGTGTGC
scaffold724856_15.	1	p2	(AT)7	14	378	391	CAAATGAGATTGGTTCGAGCTT
scaffold724867_15.	1	p2	(AT)9	18	1173	1190	CATACATGTTGAATTGCGGC
scaffold724885_15.	1	p2	(AT)6	12	758	769	AAGCTCGGGCCTGAACTATT
scaffold724891_18.	1	p2	(TA)6	12	407	418	ACTCAGAAATCCATCCCACG
scaffold724903_17.	1	p2	(CA)6	12	1705	1716	AGAAACCCATGTGCAACTCC
scaffold724972_16.	1	p2	(CT)7	14	2949	2962	CGCCTTTGCATCTCCTGTAT
scaffold725058_13.	1	p2	(AT)11	22	53	74	CATTAAAATGTGTATGCACCTGA
scaffold725061_18.	1	p2	(TG)7	14	1887	1900	TGTGCATTTCAACTTGGGAA
scaffold725088_13.	1	p2	(TC)6	12	1059	1070	CAAAGGGGGAAAAGAAAAGG
scaffold725140_14.	1	p2	(AT)6	12	537	548	CGGTGGAGATGTGGAGTACA
scaffold725167_15.	1	p2	(TA)12	24	81	104	CATTGTGGGCCTTTGATTTT
scaffold725236_13.	1	p2	(CT)7	14	1713	1726	TAAAAATGGGAGATGAGGCG
scaffold725238_15.	1	p2	(AT)7	14	617	630	GCGGCCAGTTCAATACAAAT
scaffold725254_12.	1	p2	(AG)7	14	606	619	AGAGAGAAAAAGCTTCGGGG
scaffold725256_13.	1	p2	(GA)6	12	750	761	AAAAACATCAACTGGGACCG
scaffold725257_14.	1	p2	(TC)6	12	2289	2300	ACCGATCCATCTCTCGTGAC
scaffold725262_13.	1	p2	(TA)8	16	49	64	AGACCGGACCGTTAGGTAAT
scaffold725264_17.	1	p2	(AG)8	16	881	896	ACCTCCCTCCTCCTCAGTGT
scaffold725271_16.	1	p2	(CT)7	14	439	452	CCAAGATGAATAAATGAAAGGGA
scaffold725283_11.	1	p2	(CT)6	12	359	370	GCAAGAGAAGCCCTCACAAC
scaffold725285_15.	1	p2	(GA)6	12	255	266	ACGCAGCTCCCTTTTTACTG
scaffold725298_12.	1	p2	(CT)6	12	1385	1396	CGGATTTAACCCCCAAATCT
scaffold725309_15.	1	p2	(TA)6	12	4479	4490	TCGAAAGTCCAATTTCCACC
scaffold725325_18.	1	p2	(GA)7	14	440	453	GAACTGAGAACTGCTGCGTG
scaffold725353_17.	1	p2	(CT)8	16	439	454	TGCTCCCCTCATCTTTTGAC
scaffold725361_14.	1	p2	(AT)6	12	132	143	CTTTGATTCCCCACCTTCAA
scaffold725362_17.	1	p2	(TA)6	12	835	846	TGTTCGTGTTCTCGAACGAT
scaffold725430_16.	1	p2	(CT)6	12	670	681	ACCTGGTGCTGTCCAATAGC
scaffold725451_15.	1	p2	(AT)6	12	720	731	AAACTTCCGATGGAATGCAG
scaffold725452_14.	1	p2	(AT)8	16	115	130	CAACGCGTCTTTGAGAAGTG
scaffold725458_15.	1	p2	(GA)6	12	2508	2519	ATTCATTGCAGGTTTGGAGC
scaffold725465_13.	1	p2	(CT)8	16	544	559	GGGATTGGACCCTCATTTTT

scaffold725467_14.	1	p2	(TC)6	12	841	852	AAACTCGGTTTGGGCTTTTT
scaffold725470_15.	1	p2	(TC)6	12	874	885	CGCTTGTCCTGAGTTGTGAA
scaffold725474_15.	1	p2	(TA)10	20	2012	2031	AGTTGCCGATTGGTAAGCAC
scaffold725500_13.	1	p2	(TA)10	20	706	725	TATGAGAAGGGCATTTTCGG
scaffold725505_15.	1	p2	(TC)6	12	1756	1767	AACACATGTCATGATAGCAGTTAGA
scaffold725522_16.	1	p2	(CA)8	16	169	184	ATGTCAGTCTGCCAAAGGCT
scaffold725540_15.	1	p2	(CT)9	18	634	651	TTTCACGAACCCACATTTTT
scaffold725551_11.	1	p2	(TA)7	14	444	457	TCGTAAAACATGAACTTCTTTGGA
scaffold725602_12.	1	p2	(GT)10	20	1213	1232	TACGCAAAATACGCCAATCA
scaffold725613_12.	1	p2	(AT)6	12	411	422	GAGGCTATCGAGGCTTTTCC
scaffold725617_12.	1	p2	(AG)11	22	109	130	TCCACCTTGAAGCTCTCGAT
scaffold725634_15.	1	p2	(GT)7	14	717	730	CTCTGCTGATCCCCTTTTTG
scaffold725638_16.	1	p2	(GA)6	12	731	742	TCCACAGACAGATTTCCCAA
scaffold725684_13.	1	p2	(AT)7	14	1177	1190	TATACACGTTTCCCTCGCCT
scaffold725707_16.	1	p2	(CT)6	12	7547	7558	CCTCCTATACCCCTTCTCGC
scaffold725715_16.	1	p2	(CT)6	12	801	812	AAGAAACCCCCATTGAAACC
scaffold725716_16.	1	p2	(AG)6	12	449	460	CCACAATGTAAGGAGCACAAA
scaffold725727_12.	1	p2	(GT)6	12	534	545	TGCAAACAGAAACAAGGCAC
scaffold725734_17.	1	p2	(TC)7	14	920	933	CCTGGTCATAAGTACAAGAACCG
scaffold725735_13.	1	p2	(TA)6	12	1332	1343	CATTTTCGACCGTCATGAGA
scaffold725756_16.	1	p2	(AC)7	14	1031	1044	AATTGCCTGCACCTCCAAT
scaffold725776_15.	1	p2	(TC)7	14	447	460	GAGAAATGGAGCAGCCTACG
scaffold725783_15.	1	p2	(AT)7	14	928	941	GACGTACGACTCATGCGACA
scaffold725784_16.	1	p2	(CA)6	12	1158	1169	CCAAATTTCCAATACAAGGCA
scaffold725787_16.	1	p2	(TC)6	12	643	654	TCGACATATTTTCTTCCGCC
scaffold725811_11.	1	p2	(TA)7	14	156	169	GCGGGGTTGTTAAAGAAGAG
scaffold725845_14.	1	p2	(CT)6	12	449	460	AAATTCAACCTTGGATGCTACA
scaffold725865_15.	1	p2	(CT)7	14	437	450	CCGGTTTGCACCAATTCTAT
scaffold725895_14.	1	p2	(TA)6	12	360	371	TGGGTCAATTCCAATTCAAAA
scaffold725896_16.	1	p2	(AT)8	16	512	527	CAAATCTTGTTGCCATGCTG
scaffold725945_16.	1	p2	(TA)9	18	1105	1122	ATTGCATGCCACAATTTCAA
scaffold725946_14.	1	p2	(AG)9	18	1095	1112	TGATATTCATTGCCTTTGCG
scaffold725982_14.	1	p2	(AT)9	18	232	249	TCAATTGGCCATATTAGCACA
scaffold725984_18.	1	p2	(AG)6	12	835	846	GGCAAGAAATAACAGCATACCA
scaffold725997_14.	1	p2	(TA)6	12	810	821	CCCCCACAGACATATTGACTC
scaffold726014_14.	1	p2	(TC)8	16	409	424	TGCAAACATGGGACTAATATGAA
scaffold726020_19.	1	p2	(AG)7	14	1728	1741	ACCGCTTCAAACAAAAGCAG
scaffold726027_17.	1	p2	(AG)6	12	764	775	TGCAAAATGGAATGGACTGA
scaffold726060_15.	1	p2	(CT)7	14	473	486	ATCTTGTTCCGTGCATTTCC
scaffold726083_14.	1	p2	(CT)9	18	1516	1533	AAACCCAAACCTTAATGCCC
scaffold726094_14.	1	p2	(CT)7	14	356	369	CGATTTACGAGCATCCCATT
scaffold726101_10.	1	p2	(TC)6	12	148	159	CTCCACCCTTTAATGTCACCA
scaffold726107_17.	1	p2	(CT)7	14	836	849	AATTGCCCATGTTGGTTAGC
scaffold726109_14.	1	p2	(GA)7	14	909	922	AGCCAAGAAATGGAGGGAAT
scaffold726132_14.	1	p2	(CT)6	12	103	114	GGCCTCCAACGTTTTCAATA
scaffold726150_13.	1	p2	(AT)9	18	360	377	CGTCGTTGGTGCTATACCCT
scaffold726157_14.	1	p2	(TA)9	18	3852	3869	GGAACGCAGAGGATCAATTC
scaffold726163_14.	1	p2	(AT)6	12	206	217	ATCTGGGCTACCGATTTGTG
scaffold726176_15.	1	p2	(TC)6	12	231	242	AAGTACATTCCCCCGAAAGG
scaffold726185_13.	1	p2	(TA)6	12	454	465	TACCCCATGCCTCAAGAATC
scaffold726193_14.	1	p2	(CT)8	16	253	268	CAACGAGAAGTCGAGAAGGG
scaffold726233_15.	1	p2	(CT)8	16	1373	1388	CTCCATCCCTGCTCTCTCAC
scaffold726248_14.	1	p2	(AG)8	16	1770	1785	TTGATGGGTGGAATGTAAAGG
scaffold726278_18.	1	p2	(CT)6	12	87	98	ATTAACGCACACACGTGACA
scaffold726298_13.	1	p2	(AT)6	12	403	414	GTGTGGCCTACCAAACACG
scaffold726309_14.	1	p2	(TA)7	14	1059	1072	TTAAAATGAATGAAGGGCGG
scaffold726352_15.	1	p2	(TA)7	14	1427	1440	GGTTCTCATTTGAACGCACC
scaffold726353_16.	1	p2	(TC)7	14	710	723	TGGGCTGCTAAGAAAGGAAA

scaffold726415_14.	1	p2	(AG)7	14	311	324	CAAATTTGCTGATGCCATTG
scaffold726436_16.	1	p2	(CA)6	12	299	310	CCGAATTCCGACCTAACAAA
scaffold726437_17.	1	p2	(GA)6	12	1322	1333	AAGGAGAGTGCAGCGACAGT
scaffold726458_13.	1	p2	(TA)6	12	2329	2340	TCAATCGGCAAATTCAGGAT
scaffold726461_16.	1	p2	(CT)6	12	1629	1640	TCGGAAAAAGATTCCCATTG
scaffold726471_17.	1	p2	(AT)9	18	1217	1234	GGGGCTGAAAAATCAAAGGT
scaffold726472_18.	1	p2	(AT)7	14	455	468	CATGGCAGTATTGGCATCAC
scaffold726482_16.	1	p2	(TC)7	14	2785	2798	TTGATGGTCCAACACAATGG
scaffold726498_13.	1	p2	(CA)6	12	130	141	TTGGTGCTGACTTCCAACAA
scaffold726526_12.	1	p2	(TA)9	18	325	342	TAATAGCGGCCGATCTGAAG
scaffold726529_13.	1	p2	(TA)9	18	935	952	ACGTCCTACTCGCCCACTT
scaffold726548_15.	1	p2	(GT)8	16	3789	3804	GCAGGTTTCCATATGTCGCT
scaffold726559_15.	1	p2	(AC)7	14	2481	2494	GTGAAAAGTGGCCAACATGA
scaffold726560_11.	1	p2	(AG)10	20	483	502	TCCACCCACTGTCCCTAGTC
scaffold726617_13.	1	p2	(AC)6	12	743	754	ATACATATGGACGCCCCAGA
scaffold726639_14.	1	p2	(GA)9	18	107	124	TTGCCTTGCTTTCTCTCTCC
scaffold726664_17.	1	p2	(TG)6	12	339	350	CGTTCGGGATCATAAAAACG
scaffold726675_10.	1	p2	(TA)6	12	120	131	TCATGTCCATTGATCTGAAACA
scaffold726677_16.	1	p2	(AG)6	12	122	133	CCAAACCAGGTGAAAAGGAA
scaffold726700_21.	1	p2	(AG)7	14	878	891	TTCTGAAAGCATGAACGGTG
scaffold726707_15.	1	p2	(GT)10	20	453	472	GTTGTGATGGGGGATTTGAT
scaffold726721_17.	1	p2	(GA)6	12	797	808	GCATGACCAATGCAGTACCA
scaffold726731_13.	1	p2	(TA)7	14	1024	1037	TTGTTGGAATACGTGGGAAA
scaffold726739_12.	1	p2	(AT)7	14	1143	1156	CGAAATCTTGTCCCTTCACG
scaffold726746_16.	1	p2	(TA)6	12	51	62	ATGGGTTATCACCGGATCG
scaffold726749_14.	1	p2	(AG)11	22	2049	2070	CGAAACCAATTTTTCATCCG
scaffold726753_15.	1	p2	(AT)6	12	879	890	TCTGCCCATAAATTGTGTATGA
scaffold726765_16.	1	p2	(CA)9	18	64	81	TTTTCTTTTGGGCAGCAACT
scaffold726774_17.	1	p2	(CT)8	16	458	473	TTTGCCAAACTGAAGAGCCT
scaffold726807_15.	1	p2	(CG)6	12	1698	1709	ACAAACGGAGTGTTCAAGGG
scaffold726814_15.	1	p2	(TA)7	14	111	124	ATGAGTTTGCACCTGTGGAG
scaffold726817_10.	1	p2	(AT)7	14	130	143	TGGAATCCAAAGCTATTAGACCA
scaffold726837_10.	1	p2	(TC)9	18	456	473	GGGCTGAAGCTCCTTTCTTT
scaffold726839_14.	1	p2	(CT)6	12	233	244	AAAACGGGAATCGGAATCTT
scaffold726842_13.	1	p2	(AT)7	14	1073	1086	GAACCAAATCCACAAATCGC
scaffold726860_13.	1	p2	(TA)10	20	883	902	CATTCGGGCCTCTCTGAATA
scaffold726873_18.	1	p2	(AG)6	12	329	340	GAGAATGGAACTTGCCTCCA
scaffold726887_13.	1	p2	(AG)11	22	567	588	GAGGATTGCACACTCCCACT
scaffold726894_13.	1	p2	(AC)6	12	464	475	AAACTAGAAACCCGTGGCAA
scaffold726981_13.	1	p2	(CT)7	14	1058	1071	TGGTCCCAATACGTGTCTCA
scaffold727026_13.	1	p2	(TA)9	18	43	60	GAAATAAGGAGGTGTTATGAAGGG
scaffold727049_15.	1	p2	(TC)6	12	838	849	AATTTGATCAACACGTCCCC
scaffold727064_15.	1	p2	(TG)6	12	363	374	AAATTGACACACGCATGCAC
scaffold727066_15.	1	p2	(GT)10	20	458	477	GCACATGTTCAAACACGCA
scaffold727087_14.	1	p2	(TA)8	16	747	762	AAAATGCCCTTGTATGCTGC
scaffold727100_16.	1	p2	(TC)10	20	414	433	AGGCATGAGTTGTCACTCCC
scaffold727103_15.	1	p2	(AG)6	12	4452	4463	CTTATGCAGGGATCGTGACC
scaffold727108_12.	1	p2	(TC)6	12	1045	1056	AGCCAGTGGTCCAGAGAGAA
scaffold727117_13.	1	p2	(TA)9	18	240	257	GCCACAAATGTCACAAATCAA
scaffold727122_16.	1	p2	(AG)8	16	1513	1528	GAATTGAGTTCATCCCGGTG
scaffold727152_16.	1	p2	(CT)6	12	669	680	TGCAAGAAAATGATCCACCA
scaffold727157_13.	1	p2	(AT)9	18	169	186	TGTGCAATTTGTAAGAAACACG
scaffold727158_14.	1	p2	(CT)6	12	466	477	TTATGAAGGAGGCGTGGAAC
scaffold727179_15.	1	p2	(TC)7	14	684	697	TAGCACGTCTGCACTTGGAC
scaffold727200_16.	1	p2	(CT)9	18	250	267	TTTTCCTGCATTTTGCATTTC
scaffold727201_13.	1	p2	(TA)8	16	922	937	ACAACTCGCGAGCGTAAATC
scaffold727212_15.	1	p2	(CT)12	24	6482	6505	TGTTAACGATGGGAGCATTG
scaffold727223_15.	1	p2	(TA)9	18	47	64	CGGATTTAAGGGTTATTACCTGATT

scaffold727225_14.3	1	p2	(AG)9	18	86	103	GGTTGAGAACAAGGGGTTGA
scaffold727236_16.2	1	p2	(TC)7	14	1527	1540	AATCATACCGCTTCTCGCTC
scaffold727241_14.7	1	p2	(AG)6	12	2569	2580	GATTTGGGTTGTTTGATGGG
scaffold727262_16.5	1	p2	(AG)6	12	195	206	GCACGCCCTTTTCTCTACAC
scaffold727263_17.0	1	p2	(AG)6	12	710	721	CGGGAAAAAGTCTCACAGTTG
scaffold727326_15.7	1	p2	(AT)8	16	466	481	GCAACTGGCGTGATTATTGA
scaffold727331_16.0	1	p2	(AT)6	12	63	74	TATGCCCGGATTTTTGTTTT
scaffold727352_13.2	1	p2	(TA)8	16	1062	1077	GTGCCCACCAACTTGTTCA
scaffold727385_16.6	1	p2	(GA)6	12	154	165	AGTTTAAAGGGGCCTTGCAT
scaffold727386_17.8	1	p2	(AT)7	14	468	481	TTGATCATAATTTTCGCGCTT
scaffold727390_14.9	1	p2	(AC)7	14	1084	1097	AACAATAGGACCTTCAGGCAA
scaffold727409_13.6	1	p2	(TA)11	22	545	566	TCCGTCATATAAATGCCACAA
scaffold727423_13.7	1	p2	(AG)11	22	58	79	TCGTTGGTCAAGGATAGCAA
scaffold727426_16.9	1	p2	(CA)13	26	43	68	AACACTCACGCCTTCCAAAC
scaffold727474_12.6	1	p2	(AT)13	26	436	461	TTCACCAAATCAATGCTCCA
scaffold727477_17.2	1	p2	(TC)6	12	243	254	CTTTTGAGGGCGCAGTCTAC
scaffold727480_13.5	1	p2	(TA)6	12	1163	1174	CCATTTCCTAGGTCGCGATA
scaffold727497_14.3	1	p2	(TA)9	18	673	690	AAGGCCCTTGGATTTGAGAT
scaffold727528_15.3	1	p2	(AG)10	20	464	483	TTGGAGCTGCATTTCTTGTG
scaffold727581_14.3	1	p2	(TG)6	12	1556	1567	TCACAAAGAGCATGTTCACG
scaffold727593_15.6	1	p2	(AT)9	18	467	484	AAAAGCTATGGGGAAGAACACA
scaffold727599_18.2	1	p2	(TA)8	16	916	931	GAACCAGACTGCACGTTTCA
scaffold727612_16.6	1	p2	(AG)6	12	510	521	GTGGACTGGTTTCAGGTGGT
scaffold727615_17.8	1	p2	(TA)6	12	154	165	TCTCTACAAAACGAGACCAATCTTT
scaffold727618_17.2	1	p2	(AG)6	12	1754	1765	TCTCTCCCTCTCCAACTCCA
scaffold727646_12.0	1	p2	(AG)9	18	987	1004	GCTGTCGTACACGGTGCTAA
scaffold727659_11.5	1	p2	(TA)6	12	422	433	TCAAATGACTTGGGCATGAA
scaffold727670_13.1	1	p2	(AT)7	14	965	978	TCATCCAAAAGCAAAGGAAAA
scaffold727671_17.7	1	p2	(AT)8	16	1015	1030	TGCGTTTGTTAGCTTTGGTG
scaffold727672_16.3	1	p2	(TC)9	18	302	319	CGAAGATTTATGCGGGGTTA
scaffold727707_15.0	1	p2	(AT)7	14	1031	1044	TGGATAAACAAAATTGATGGTTTG
scaffold727714_15.9	1	p2	(GA)7	14	5143	5156	GCGGAACAGTAGTTGGGATG
scaffold727727_18.0	1	p2	(AT)8	16	2120	2135	GAGAAGCAGCGGTAGGTGAT
scaffold727746_16.5	1	p2	(AG)6	12	1063	1074	CGTCCAAAATACCTTTTATTCCA
scaffold727757_17.7	1	p2	(AG)10	20	1216	1235	ACCCAGAAACAGCACAATCC
scaffold727769_16.1	1	p2	(AC)6	12	1714	1725	GATACCGTGGGCAACCTAAA
scaffold727771_16.4	1	p2	(TA)6	12	1676	1687	GCCATGGATGCGATAAAAGT
scaffold727773_14.9	1	p2	(TA)7	14	187	200	ATCTAGGGGCCGAGATTTGT
scaffold727806_16.3	1	p2	(AC)7	14	9455	9468	CGATTGTTGCGTGCATAAAC
scaffold727809_11.4	1	p2	(AT)6	12	518	529	CCCAAGCCATGGAGTAGAAC
scaffold727817_14.8	1	p2	(AG)6	12	1120	1131	TGAAGTCTAAAGGGAGACGGG
scaffold727849_14.8	1	p2	(AT)6	12	110	121	CTTAAGCAAATTGCAAGCCA
scaffold727852_14.5	1	p2	(TA)9	18	305	322	AGTTGGCACCGTATCACTCC
scaffold727861_17.2	1	p2	(TC)6	12	1284	1295	TTTGAAAGGTATGATTTGGCA
scaffold727889_15.6	1	p2	(AG)11	22	2768	2789	AAGCAAACATTGTTCCAGGG
scaffold727890_16.1	1	p2	(TA)6	12	1320	1331	GGTACCCCACATGAGAATCAA
scaffold727923_16.2	1	p2	(TC)6	12	479	490	GGCTCAATTATTTAGGCCCAT
scaffold727929_15.0	1	p2	(TA)10	20	1865	1884	AATTGGACCGGACCATTAGTT
scaffold727932_15.7	1	p2	(TA)10	20	45	64	GGGGTTATCATGGGATCAAG
scaffold727940_13.3	1	p2	(CA)7	14	203	216	GTTCTCTTCTTCTGCCACCG
scaffold727944_15.5	1	p2	(TG)7	14	1735	1748	GTGTGGATCTAGGGCACGTT
scaffold727947_14.6	1	p2	(AT)9	18	2409	2426	GAGTTGATCGTCGGTGCATA
scaffold727966_11.8	1	p2	(GA)6	12	1018	1029	CCCTTGGTATCAAAAGGGGT
scaffold727970_13.1	1	p2	(TA)9	18	474	491	TTTTTACCATTTTGCCCCTG
scaffold727977_15.4	1	p2	(GA)7	14	850	863	CAAATGCAAATCTTCTGGCA
scaffold728007_11.5	1	p2	(AG)6	12	552	563	TGGAACTGCATGCTAAGTGG
scaffold728008_15.4	1	p2	(GA)9	18	592	609	GAAGAAATCCCTGCCTTTCC
scaffold728011_15.8	1	p2	(AT)8	16	731	746	ACACAAGGATTGTTTTCCCG

scaffold728031_14.7	1	p2	(TA)10	20	780	799	CCTATTGCTTAAGACGACATGC
scaffold728033_17.0	1	p2	(AG)7	14	479	492	CTCCATTGGTGGAACGAGAT
scaffold728047_15.4	1	p2	(TA)6	12	983	994	GGCCCAAGCAAAATAAGTCA
scaffold728064_16.0	1	p2	(AT)9	18	299	316	TGCAATTTATATGCTTTTGCAC
scaffold728083_17.3	1	p2	(AT)10	20	188	207	CATAACAAGTGGCGAAAGGG
scaffold728097_15.6	1	p2	(CA)9	18	2099	2116	TGCAAGCAATAATAAGCCCC
scaffold728098_15.6	1	p2	(GA)7	14	134	147	CTGGCAATTTGACGGGTAAT
scaffold728120_18.9	1	p2	(TA)9	18	625	642	TGCACAATCGATTTACGTGG
scaffold728132_17.5	1	p2	(AT)6	12	580	591	GTTTCGCAAGGCAAATAACC
scaffold728137_15.0	1	p2	(AG)7	14	481	494	TCATCAAGGCCTCACATTCA
scaffold728155_17.2	1	p2	(AC)7	14	2004	2017	AAACAGCAGAGAAGCCCAAA
scaffold728201_17.3	1	p2	(CT)7	14	1573	1586	GAATTCGGGGTGTTTTGAGA
scaffold728210_14.4	1	p2	(AT)7	14	263	276	TGCGTTGTTTTACCATTGGA
scaffold728212_18.0	1	p2	(TC)6	12	249	260	CTCGTCCAGGACAAATCCAT
scaffold728223_14.1	1	p2	(TC)7	14	2660	2673	CATTGCCGCAAGATCAAGTA
scaffold728226_12.7	1	p2	(TC)6	12	689	700	ATCTGCATGTCTACGTCCCC
scaffold728229_18.0	1	p2	(TA)7	14	143	156	TCCCAACCCCATTTACAAAA
scaffold728235_12.9	1	p2	(AT)10	20	93	112	GTGGGTTTACCTAGAGCGCA
scaffold728248_13.2	1	p2	(GA)7	14	640	653	GGAATGAAGTATGTGGAGGAAGA
scaffold728256_15.0	1	p2	(AT)6	12	927	938	CGCCCTTTTAGTTAAAACCTTG
scaffold728266_15.8	1	p2	(TG)9	18	354	371	ACAATGGGTTCATTTGCCAT
scaffold728281_18.4	1	p2	(AT)6	12	203	214	CTATGTTGACTTCGCCGTGA
scaffold728304_16.0	1	p2	(AT)6	12	3210	3221	TCCTCCAGCGAGTCGTAGTT
scaffold728309_13.7	1	p2	(TC)9	18	721	738	TGTGAGTTGCCACTCTCCAC
scaffold728317_15.9	1	p2	(TA)6	12	741	752	CCATGAATTTCACCAGCAAT
scaffold728320_17.0	1	p2	(GT)8	16	3415	3430	TTCTTGATGGAAAGGCAAGG
scaffold728324_15.5	1	p2	(CT)6	12	1845	1856	GGCCAGAAACTGCCATAAAA
scaffold728325_13.7	1	p2	(TA)8	16	481	496	AAGACTCGGGTCCATGACAG
scaffold728329_16.5	1	p2	(TA)7	14	983	996	GTAACAGTAGCTGCCTGCCC
scaffold728349_16.9	1	p2	(AG)7	14	953	966	CCTTGAGCAATGTGGAGCTT
scaffold728356_16.6	1	p2	(TC)6	12	257	268	GTTAGGCTTCCCATCCCACT
scaffold728360_16.8	1	p2	(TG)6	12	2767	2778	TTCGCTCTGATATCCCCATT
scaffold728369_14.8	1	p2	(AG)8	16	1453	1468	TATTCCCGGTATGTAGCCCA
scaffold728388_16.1	1	p2	(AC)6	12	1799	1810	TCTCTCTGCTTCACACACGC
scaffold728394_13.9	1	p2	(TG)7	14	1327	1340	CCACAAAGCTCTTGGAAATAGG
scaffold728405_16.2	1	p2	(AT)8	16	193	208	TAGTATTGGAGGTTGGGGGC
scaffold728408_16.2	1	p2	(AG)11	22	1397	1418	CTCACGCTGGTAAAAGAGCC
scaffold728433_13.0	1	p2	(AT)6	12	397	408	TCGTTCCTACTTTGTGGTGG
scaffold728434_16.3	1	p2	(AT)6	12	1203	1214	GCAGTATCGGGAGTGAGAGG
scaffold728436_15.5	1	p2	(AG)7	14	1742	1755	GATTTGGGGTTTCGGAGATT
scaffold728458_16.2	1	p2	(TA)7	14	56	69	CCCTACCCATTTACCCGTTT
scaffold728478_13.4	1	p2	(TA)13	26	614	639	ATGGTCGTGATTGTATGCGA
scaffold728487_15.7	1	p2	(TA)7	14	132	145	CCTAGCCACACACGGAATCT
scaffold728494_15.5	1	p2	(AT)6	12	1431	1442	CCAATTTAAGTTCGAATGAGTTTTC
scaffold728495_14.8	1	p2	(CT)6	12	599	610	AACCGGTTTGACCGATTTTC
scaffold728514_18.8	1	p2	(AC)6	12	633	644	CTGCACCGGATAATACAGCA
scaffold728518_16.1	1	p2	(AG)6	12	390	401	CCACAAGATCAGCTTTTCCC
scaffold728533_16.8	1	p2	(TA)10	20	37	56	AAGTTTATATCAATAGTTTTGTGTCGG
scaffold728574_15.9	1	p2	(TA)10	20	972	991	TGCAGGTTGAGCAGGTGTAG
scaffold728575_12.4	1	p2	(AT)8	16	486	501	GGAGTTTGAGAGGGGCAAGT
scaffold728595_15.6	1	p2	(AC)6	12	2528	2539	TTTCATTGCTGCTGCAGTTT
scaffold728628_13.8	1	p2	(TA)6	12	1089	1100	AGTGTTTTCAGGCGTTCACC
scaffold728640_13.6	1	p2	(AT)7	14	746	759	ATTCCTCACGGACCTCACAC
scaffold728687_12.3	1	p2	(GA)6	12	2022	2033	GGTTGAGGCGGATAAAGTCA
scaffold728722_16.4	1	p2	(AC)6	12	3361	3372	GTTCGTACCGAACAACACCC
scaffold728724_14.8	1	p2	(AT)6	12	1043	1054	CAAAGCTCAGCCGACCTAGT
scaffold728729_15.6	1	p2	(CT)9	18	41	58	TGCAAGAAAAACAAGCCCTC
scaffold728738_16.0	1	p2	(GT)7	14	781	794	TTGTCGCTGGACACGATAAG

scaffold728740_15.	1	p2	(AT)7	14	286	299	TCGACTGAAAATTTTGGCTAATC
scaffold728767_16.	1	p2	(TG)6	12	2242	2253	CTTATGCCACTCCCCACTGT
scaffold728785_16.	1	p2	(GT)9	18	118	135	CACGAGCTGTTAATCACCACA
scaffold728809_13.	1	p2	(TA)8	16	292	307	TGGTTAACTCAATCTCAGCCG
scaffold728836_12.	1	p2	(TC)11	22	482	503	TTAATCAGATGAGGGCAGGG
scaffold728845_13.	1	p2	(AT)6	12	369	380	TGGACCACACCTATCATAACCA
scaffold728874_15.	1	p2	(GA)6	12	1609	1620	TGTGGGCGTCAGATCTCATA
scaffold728875_16.	1	p2	(AT)12	24	2156	2179	TGTTGGATTGGACATTGGGT
scaffold728888_18.	1	p2	(TG)7	14	493	506	CACTCCTGTATGTAGTGACACGAA
scaffold728902_15.	1	p2	(TC)9	18	794	811	TTTGGTTTTTGGTTTGCTCC
scaffold728907_16.	1	p2	(TA)9	18	46	63	CCAATTTGAATGGTTATCACCTG
scaffold728951_13.	1	p2	(AT)6	12	1777	1788	CCTGGGCTTTGTTCACAGAT
scaffold728957_15.	1	p2	(GA)6	12	1197	1208	TGAGAGTTTCTGCGTTGGTG
scaffold728958_16.	1	p2	(TC)6	12	183	194	GTTGGCTTTTTGTTGCCACT
scaffold729004_15.	1	p2	(AT)7	14	2507	2520	CATCTTGATGTCCCCATTGA
scaffold729039_20.	1	p2	(TC)6	12	239	250	GCTTCAGTTCTGTGGCATCA
scaffold729050_16.	1	p2	(TA)6	12	693	704	TCATCAGCAAACTTCCCACA
scaffold729056_14.	1	p2	(TC)7	14	564	577	TGGATTTAGCCGATTCCAAG
scaffold729057_15.	1	p2	(AT)8	16	495	510	CACTTGTCGTCATGGGAATG
scaffold729059_11.	1	p2	(TA)13	26	169	194	GCACTCTCCAGCAATGTTGA
scaffold729063_13.	1	p2	(TC)9	18	492	509	TGGTGAAGAAAGTGGGCTTC
scaffold729077_14.	1	p2	(TA)9	18	1325	1342	AGCAGTGGAACGAGGAAGAA
scaffold729100_12.	1	p2	(CT)12	24	183	206	CGCATTTCATCTGCTTTTCA
scaffold729103_16.	1	p2	(AT)7	14	186	199	GGGGGTGCAACATCATATTC
scaffold729105_12.	1	p2	(AT)7	14	1231	1244	TTTGTTGGGTCTTGGGCTAC
scaffold729118_14.	1	p2	(AT)6	12	741	752	CACCGAATATTCCCAACTCAA
scaffold729126_15.	1	p2	(TG)6	12	918	929	CCTTCCCTTAAGCCCATCTC
scaffold729136_10.	1	p2	(AC)8	16	735	750	GATAGCTCTGAGGCTGGTGC
scaffold729138_13.	1	p2	(AT)6	12	576	587	CCACTTCTCCCATTTGCATT
scaffold729141_15.	1	p2	(TA)6	12	31	42	CCGTAGCTGTTATTGATGGAA
scaffold729154_16.	1	p2	(TA)6	12	267	278	CACCAGAATTTAGGCGGAGA
scaffold729176_16.	1	p2	(TG)8	16	496	511	CCCGAATATCCCCCAACTAA
scaffold729179_15.	1	p2	(AG)7	14	592	605	GAAGCCGAAGGAATCATCAC
scaffold729200_13.	1	p2	(AC)7	14	3490	3503	TCTGAGCATTTGCAAGGATG
scaffold729229_18.	1	p2	(TC)6	12	1272	1283	TAAGCAATCCCCATTTTTGG
scaffold729235_11.	1	p2	(TC)9	18	1056	1073	CACAAGCTCGGAAGGGTAAA
scaffold729303_17.	1	p2	(GA)6	12	1795	1806	CTGCAAAACTGGAGGAGAGG
scaffold729309_13.	1	p2	(AT)6	12	502	513	ATCGATTAGGTCGCACAAGG
scaffold729316_15.	1	p2	(GT)6	12	1465	1476	GCGCTGTAACCAACAACAGA
scaffold729337_20.	1	p2	(AT)9	18	1171	1188	CAAAGCCCAATGGGAAACTA
scaffold729384_16.	1	p2	(AT)13	26	217	242	GCAACTCGACATCAACGTCA
scaffold729414_16.	1	p2	(TC)7	14	2087	2100	CGTCCCAAGAAATGTGACCT
scaffold729431_13.	1	p2	(AT)10	20	490	509	TGGTTGATTAGATTACCGCTACAA
scaffold729441_18.	1	p2	(TA)7	14	503	516	TCTCACGAGGATTTTCGATGT
scaffold729462_14.	1	p2	(AT)11	22	933	954	AAAGGGCCTATATCCAATATGAAA
scaffold729473_16.	1	p2	(TC)8	16	3224	3239	TGCGAATTTGGAATTATCTGC
scaffold729479_13.	1	p2	(TA)6	12	62	73	GGGGTTATCATGGGATCAAG
scaffold729500_12.	1	p2	(AT)10	20	180	199	AACGCAGATCTGATGGCAC
scaffold729504_17.	1	p2	(CT)7	14	4612	4625	ACGGACCGTGTACTCTACCG
scaffold729518_13.	1	p2	(AT)6	12	506	517	AACAATGCAGTAGCTGGTTGG
scaffold729545_14.	1	p2	(AT)9	18	1109	1126	GGTGATTTTTGATTATAGGAATATGG
scaffold729628_21.	1	p2	(AG)14	28	46	73	GGAACAAAGACACCATTGATAAAA
scaffold729648_15.	1	p2	(TA)8	16	81	96	TTTGATAACGTCAAATCCAACAA
scaffold729654_15.	1	p2	(AG)10	20	1294	1313	CATTCCAATCATTCCCCAAC
scaffold729657_15.	1	p2	(TA)7	14	654	667	TGACCCATTTCTCATCATTGG
scaffold729658_16.	1	p2	(AT)9	18	1340	1357	TTTGTGCCTAAAATGCCCTC
scaffold729671_17.	1	p2	(CT)7	14	143	156	TCCCAACTCACAATCCATGA
scaffold729676_14.	1	p2	(AT)10	20	157	176	TTCTGCATGCATTTATTGGG

scaffold729678_12.	1	p2	(AT)7	14	1232	1245	ACAAATGAACACTCCGGCAT
scaffold729682_13.	1	p2	(GA)6	12	1502	1513	AGGCAGAAAAGAGGAGGGAC
scaffold729688_15.	1	p2	(TA)9	18	1012	1029	GGATCCACGTCCACTATGCT
scaffold729692_17.	1	p2	(AC)7	14	2941	2954	CTCGTTAGCAAGCAATGCAC
scaffold729700_11.	1	p2	(TA)9	18	295	312	GGCTCCACAACCATCTTCTT
scaffold729701_15.	1	p2	(GT)7	14	3029	3042	GCTGAAGAGGTCCAGCAATC
scaffold729706_15.	1	p2	(AG)7	14	672	685	TCATGTGAGGATATGGCGAA
scaffold729707_16.	1	p2	(CA)6	12	827	838	CAATGTCAGAGTGGTGGTGG
scaffold729761_11.	1	p2	(AT)6	12	1350	1361	TCTTCTCGCATACCAAAGGT
scaffold729782_15.	1	p2	(GA)9	18	503	520	GCGTGGGGAATAATGAGAGA
scaffold729810_14.	1	p2	(TC)7	14	1091	1104	CCCAAGAAGCCCTTCTCTCT
scaffold729813_14.	1	p2	(AT)6	12	1607	1618	AAATGGATGCTGATAAATGGA
scaffold729818_17.	1	p2	(GA)7	14	1328	1341	CGAGAGAGCTTTTCCTTGACA
scaffold729824_15.	1	p2	(AT)9	18	1244	1261	GGAAAAGAACTGCCAGAACG
scaffold729825_14.	1	p2	(CT)10	20	317	336	TTTCCCCTCCCTCATTTACC
scaffold729839_13.	1	p2	(AT)9	18	787	804	CCATTCCGTCGTTGTAGGAA
scaffold729896_13.	1	p2	(AG)9	18	1755	1772	TGGCCTCAGATAGTTGGTCC
scaffold729897_14.	1	p2	(AT)11	22	4285	4306	TGCAACGTGAGTAGTGACTCG
scaffold729919_15.	1	p2	(TA)7	14	1204	1217	AAGGTACAAGTGGGTTCCCC
scaffold729940_15.	1	p2	(AC)6	12	1953	1964	ATACCCAGACCCAAAGCAAA
scaffold729959_16.	1	p2	(GA)6	12	582	593	CAACAAAAGCGTGTTCATGG
scaffold729977_14.	1	p2	(GA)8	16	931	946	GTGCCAGAGATCGGAGAAAG
scaffold729991_14.	1	p2	(AT)10	20	1643	1662	CACCACAAAGCAATTGGAAA
scaffold730036_14.	1	p2	(GT)6	12	1297	1308	TGGGTGCCATTTCTATCACA
scaffold730050_19.	1	p2	(TC)7	14	514	527	CTTAATGAGGGGCCACAAAG
scaffold730061_17.	1	p2	(TA)6	12	602	613	TGATCTGGAAGTAAGGAATCCTAGA
scaffold730064_15.	1	p2	(TC)9	18	2331	2348	GCAAAGACCATTCTTGAGGC
scaffold730069_15.	1	p2	(TC)7	14	822	835	TTGGGTTGCATCAGAAAACTC
scaffold730102_12.	1	p2	(CT)12	24	505	528	GATGAGAGAGAGAGCGGTGG
scaffold730113_17.	1	p2	(GA)6	12	518	529	ACTCTCACGCACCGGAATAC
scaffold730123_17.	1	p2	(AG)6	12	518	529	AAGTTGCATGCCATTTACCA
scaffold730145_15.	1	p2	(GA)6	12	1614	1625	AATGCCCTCCTATTATGCCC
scaffold730159_16.	1	p2	(TA)11	22	820	841	TATGGGTTATCACCGGATCG
scaffold730170_17.	1	p2	(GA)6	12	430	441	GGGCGAAGTGATCGAGAATA
scaffold730186_14.	1	p2	(TA)7	14	517	530	GGATTTTGGATTGGTCGAGA
scaffold730190_15.	1	p2	(TC)9	18	170	187	CAATGTTGGTGACGTCTTGC
scaffold730222_14.	1	p2	(GA)8	16	2582	2597	CACAGCTGGCATAACCAAGA
scaffold730227_15.	1	p2	(GA)6	12	132	143	TCACGGATTCACCAACTGAA
scaffold730229_16.	1	p2	(AC)6	12	2395	2406	TTGCAAACTTAATTGGTGCG
scaffold730230_13.	1	p2	(AT)8	16	1207	1222	GCCCCCGATTTTTCAAAGTA
scaffold730246_15.	1	p2	(AT)6	12	1189	1200	AATGCCACCATTGTTGGTTC
scaffold730256_16.	1	p2	(AG)6	12	926	937	CTGGGTTGGTAGTTGCCAGT
scaffold730274_11.	1	p2	(AT)13	26	67	92	AGAATTTCAAGGTAATGGGGA
scaffold730279_15.	1	p2	(AG)8	16	103	118	GCACGTCTCTCGGACATACA
scaffold730290_14.	1	p2	(TA)8	16	1056	1071	TCGAATTTGTGAACTCCGAA
scaffold730292_15.	1	p2	(TA)9	18	2814	2831	TTTGCACTTAAGAGGAGTTTTGAA
scaffold730306_14.	1	p2	(AG)6	12	1178	1189	GCATTGCAAGCTTCGATACA
scaffold730314_18.	1	p2	(CT)6	12	955	966	GACCAGCGAGTCACACTCAA
scaffold730329_11.	1	p2	(TA)6	12	118	129	GCGAAGCTAATGCATTCTGTC
scaffold730343_15.	1	p2	(AT)8	16	469	484	GTTAAAGCCAAAAGTCGGGC
scaffold730347_13.	1	p2	(AG)10	20	3547	3566	CAGCAGCAAGCAATAACGAG
scaffold730361_18.	1	p2	(CT)6	12	1181	1192	CGAATGCTTTTTCTTCCACC
scaffold730364_12.	1	p2	(CT)9	18	1002	1019	TTGCACTTCCTGGAGAACCT
scaffold730371_17.	1	p2	(TC)6	12	516	527	ATTTTGTCGCAGTTGATCCC
scaffold730372_14.	1	p2	(TA)6	12	2931	2942	CACACATGGAAAAGATCTCCAA
scaffold730402_16.	1	p2	(TA)6	12	1242	1253	CTCCCAATTATGGACAGGGA
scaffold730417_14.	1	p2	(TA)6	12	2652	2663	TAGTGGGGCAAGAAACAAGC
scaffold730418_12.	1	p2	(TA)7	14	522	535	AACACATTTCTTCAACATTCATCA

scaffold730423_13.	1	p2	(TA)9	18	110	127	ATCAACGGTTCACATCGGTT
scaffold730425_15.	1	p2	(GT)6	12	731	742	TGGAGAACTCATTCTTACTGCG
scaffold730435_11.	1	p2	(AT)7	14	959	972	ACGAACACACACGCACTCTC
scaffold730479_11.	1	p2	(TA)7	14	1155	1168	GGCCAGATTTCGTCCCTATT
scaffold730494_12.	1	p2	(TA)7	14	81	94	TGTTTGCACGTGAATAAGCC
scaffold730556_17.	1	p2	(AG)6	12	143	154	GGTTCAACCATTTTGTTGGG
scaffold730579_12.	1	p2	(AT)10	20	1000	1019	CGCCGACCAATCATGTAGA
scaffold730599_15.	1	p2	(AT)8	16	3333	3348	TTGTGGATGCCCTAACCAAT
scaffold730607_13.	1	p2	(TC)8	16	1581	1596	CCAAGCTTAAGCAAGCAAGC
scaffold730631_15.	1	p2	(CT)6	12	530	541	TCTTTGACGTTAATTTTCGGAGA
scaffold730633_15.	1	p2	(TA)7	14	2579	2592	CCTGAAAGAATTTGGGGGAT
scaffold730660_14.	1	p2	(AG)6	12	953	964	ATCTCTGCCCCCATCTCTCT
scaffold730663_15.	1	p2	(AC)6	12	4254	4265	ACCCTCCACCCTTTCTCTGT
scaffold730667_15.	1	p2	(GA)7	14	715	728	CATGTCGTGTCGTGTCAGAA
scaffold730668_16.	1	p2	(AG)7	14	4517	4530	GTACCTCTGTCCTTGCAGCC
scaffold730672_13.	1	p2	(TG)6	12	55	66	TTGTGTGATCGAACCACGTT
scaffold730678_12.	1	p2	(CT)11	22	1385	1406	GTCTAGCCGGCATCGATAAT
scaffold730713_15.	1	p2	(TA)6	12	2400	2411	AAAAGAGATGCGTGCAAGGT
scaffold730761_16.	1	p2	(AC)8	16	1365	1380	ACGGTGTCTCCGCAATTAAC
scaffold730768_16.	1	p2	(TC)6	12	146	157	GGCTATGGGTGGTAGGACAA
scaffold730806_14.	1	p2	(CT)7	14	615	628	CAATAAAGCCCGTCACGTTT
scaffold730834_15.	1	p2	(TC)6	12	533	544	GTGGTGCGATGATAACGATG
scaffold730836_11.	1	p2	(AT)11	22	35	56	AGCCGTGAGATTTACTTTTAACTT
scaffold730862_15.	1	p2	(TA)11	22	43	64	GCGTTTTGACAATATATAAGTGTTTTG
scaffold730881_16.	1	p2	(GA)10	20	1189	1208	CCAAACCAAAACTCATCAACC
scaffold730884_17.	1	p2	(AG)7	14	533	546	TCTCCCAACACACCTTTTCC
scaffold730888_16.	1	p2	(AG)9	18	1153	1170	GAGGATAACTGGCCAACCAA
scaffold730906_13.	1	p2	(AC)8	16	1969	1984	CAACTCCCCCGTAGTTTTCA
scaffold730910_15.	1	p2	(GA)6	12	2403	2414	GTTGGTGTTTGCTGGGATTT
scaffold730911_16.	1	p2	(TC)8	16	1259	1274	TCGAGCTGAACGAAAGAGGT
scaffold730916_18.	1	p2	(CT)10	20	525	544	CCCCACCTTAGCGTTAAACA
scaffold730932_15.	1	p2	(AG)9	18	530	547	ACCCAAAACAAAATGCATGA
scaffold730934_14.	1	p2	(TC)6	12	506	517	TATGGCAAAAACACCAACGA
scaffold730942_17.	1	p2	(TC)7	14	534	547	ACTCAACTCTGATCGGTGGG
scaffold730951_18.	1	p2	(AT)6	12	660	671	GGAGATGGAGGGTTCAAGGT
scaffold730956_15.	1	p2	(TA)6	12	318	329	GGTTTATTGTGGCGAATGCT
scaffold730964_14.	1	p2	(AT)14	28	1099	1126	GGTGTTGGGAGGTGAACAAT
scaffold730982_17.	1	p2	(CT)6	12	554	565	CCAATAGGCCCATTCAAAGA
scaffold730992_15.	1	p2	(AG)6	12	1496	1507	CTCAATGCGTAGGCTTCTCC
scaffold731000_16.	1	p2	(TA)8	16	1095	1110	AAACCGCACTTTAGCTCGAA
scaffold731007_11.	1	p2	(TA)8	16	534	549	AAATTCCCTTGTATGCTGCG
scaffold731011_15.	1	p2	(AC)7	14	831	844	AGTTTCGATTCGATTGACGG
scaffold731028_15.	1	p2	(AG)8	16	2523	2538	GATTCTAGCATCGTGAGGGC
scaffold731029_13.	1	p2	(TA)9	18	913	930	TTCCAACAATCTCAGCATCA
scaffold731034_14.	1	p2	(TA)9	18	918	935	AAGTATTGATCGACGTGGGA
scaffold731049_15.	1	p2	(CT)6	12	198	209	AACACAGGTCCGCAAATAGG
scaffold731054_15.	1	p2	(GA)8	16	1529	1544	CTGCCTCCCTTGTTCTTACG
scaffold731082_14.	1	p2	(CT)7	14	793	806	TCCCTAATCATCTCCCCTCC
scaffold731100_16.	1	p2	(CT)8	16	561	576	CCTAGAGCACACTCGAAGGG
scaffold731114_15.	1	p2	(CA)7	14	2804	2817	CCTCCTTCCATAGCAGCAAA
scaffold731121_16.	1	p2	(AT)9	18	3464	3481	TGATCAAAATCCACACCTCG
scaffold731137_12.	1	p2	(TG)7	14	537	550	CAGAGTTTGTTTCGCAACCC
scaffold731143_12.	1	p2	(TC)6	12	77	88	ACTGGTGGAAACTGGATTGC
scaffold731172_16.	1	p2	(AG)6	12	541	552	CCACCTCTCTGCTCCACTTC
scaffold731183_14.	1	p2	(TA)10	20	255	274	TTTGAACCCAAACCTCAAGC
scaffold731192_14.	1	p2	(AT)9	18	385	402	AGGAAGCGAGGTAGGCTTTC
scaffold731196_14.	1	p2	(CA)8	16	235	250	GCCAGATTCTCTTGGTGGAG
scaffold731223_15.	1	p2	(AT)6	12	54	65	CCTTTCTCCATGGGCATCT

scaffold731236_15.	1	p2	(AG)8	16	1299	1314	TCGTACGTACTGTGATCCGC
scaffold731260_13.	1	p2	(TC)8	16	1979	1994	GGACAAAACGACCAAAAGGA
scaffold731278_15.	1	p2	(TA)6	12	1195	1206	TCTCTCACCTCCTCCCATGA
scaffold731299_17.	1	p2	(TG)9	18	362	379	ATCCAAGCAACAAAAATGGC
scaffold731307_14.	1	p2	(AT)7	14	253	266	GCATATGCATGGTTCTCACG
scaffold731352_16.	1	p2	(CA)8	16	542	557	TGTTGGTCCACCATTCTTTT
scaffold731383_14.	1	p2	(TA)7	14	52	65	GAAATTAGATTAAAGAAAAGATGGT
scaffold731391_16.	1	p2	(AG)8	16	2519	2534	TGGGGTGAATCAGTTCAACA
scaffold731405_14.	1	p2	(TA)11	22	129	150	CGAGTTAGGAAATAAGGAGGTGC
scaffold731434_16.	1	p2	(AC)8	16	544	559	GCAGCTCAAAAAGACAGTCCA
scaffold731439_14.	1	p2	(TA)12	24	402	425	CACTTTTTGTGAAACCCCTCA
scaffold731450_12.	1	p2	(AT)9	18	1165	1182	GGGGATTCCTGCAATTTTCT
scaffold731515_15.	1	p2	(TC)7	14	316	329	ATTCAAACCGCTAGTGTGGC
scaffold731518_16.	1	p2	(GA)6	12	549	560	TCCCCATTAATCCCATCAGA
scaffold731525_15.	1	p2	(GA)8	16	1204	1219	CCGGTTTCTTTCCATTTTCA
scaffold731528_17.	1	p2	(AT)8	16	147	162	TTCCGTGTGCGTATTCTTGA
scaffold731554_17.	1	p2	(GA)9	18	545	562	AAATTATTCAACTTGGATCACTCAT
scaffold731567_15.	1	p2	(TG)9	18	545	562	ACTTGTCAATGCCGGTAAGC
scaffold731570_16.	1	p2	(TA)8	16	916	931	TCACAACGGGGTCAAATGTA
scaffold731618_13.	1	p2	(CA)7	14	935	948	ATCAGGCTCGAGTCCATGTC
scaffold731620_10.	1	p2	(GA)6	12	552	563	CGGCATGAGATGAGATGAGA
scaffold731632_16.	1	p2	(AG)8	16	319	334	AACAGAGCAAGACGAGGCAT
scaffold731664_17.	1	p2	(AG)6	12	1411	1422	CTGCTTGAGTTGCTCTGCTG
scaffold731683_15.	1	p2	(TG)7	14	68	81	GCCAATCACTAACCAACACG
scaffold731705_16.	1	p2	(TA)8	16	1496	1511	TCCGCCCTCGTGTTTTATTA
scaffold731706_15.	1	p2	(TG)6	12	469	480	TTCATTCATGGTCGTAGGCA
scaffold731712_17.	1	p2	(TG)6	12	2533	2544	CATTGCCATTGCAGAAGCTA
scaffold731717_14.	1	p2	(AT)9	18	548	565	TTAAGGTGTCAGAGGCGGTT
scaffold731721_16.	1	p2	(TG)6	12	2460	2471	TGTACATGATGCATTTTCCCA
scaffold731735_14.	1	p2	(CA)6	12	2317	2328	ACCAACCAGCTTAGCGAAAA
scaffold731752_16.	1	p2	(AG)7	14	1630	1643	CAAACCCAATATCACAGCCC
scaffold731757_15.	1	p2	(TC)8	16	1864	1879	AAAAAGTCCCCAGCCAATCT
scaffold731767_16.	1	p2	(TA)6	12	445	456	CCACTAACCTTGTCTCCCCC
scaffold731805_17.	1	p2	(AG)6	12	847	858	GGTGTGCTCGGATCTTGATT
scaffold731809_17.	1	p2	(TA)6	12	557	568	AAGATTCTCTCTTGTAGGTTGTCCA
scaffold731830_12.	1	p2	(CT)6	12	753	764	GCCCTAGGGTTCCTGATTTC
scaffold731831_20.	1	p2	(GA)6	12	1298	1309	CGCAATGATAGACCACAACG
scaffold731834_15.	1	p2	(CT)7	14	127	140	AATCCCCCACCACTTTCTCT
scaffold731879_16.	1	p2	(TC)11	22	5994	6015	AGTGCATTGACATCGAGACG
scaffold731896_15.	1	p2	(AT)6	12	1370	1381	AATCGTGAAATCAAACCAGAA
scaffold731906_11.	1	p2	(TA)8	16	555	570	CCACCCGTTTACCTTTTTCA
scaffold731933_16.	1	p2	(TG)7	14	2089	2102	AGAAGCTTGTTGTCCGCTGT
scaffold731939_13.	1	p2	(AT)9	18	201	218	GAATTGTTCCTGCTCGTGGT
scaffold731949_15.	1	p2	(AC)7	14	152	165	CACTGGATCTGCCGATGTTA
scaffold731954_14.	1	p2	(AC)8	16	295	310	CCATATGATGCTGATGCGAT
scaffold731998_14.	1	p2	(AT)8	16	704	719	AGTCACGTCTATTCATCATTGACA
scaffold732005_16.	1	p2	(AG)6	12	1075	1086	TCTCACAAATCCACACCCAA
scaffold732031_16.	1	p2	(TA)13	26	92	117	TTTAAGATGTGCATGCATTTGA
scaffold732039_14.	1	p2	(CA)7	14	3809	3822	CGCAAACGATGGCAATAAT
scaffold732054_14.	1	p2	(TA)6	12	749	760	ATTTTGCACCGCCATATCAT
scaffold732066_16.	1	p2	(CT)6	12	185	196	AACGCGAAGTAGCATGGTTT
scaffold732086_14.	1	p2	(CT)7	14	250	263	ACGACGCAAAAATGGAAAAC
scaffold732089_14.	1	p2	(GT)6	12	627	638	ATGCCACCACTTCCCTGATA
scaffold732130_13.	1	p2	(AT)10	20	2229	2248	CCAGATGTGAGGAGCAAACA
scaffold732131_15.	1	p2	(TA)6	12	309	320	TTCTAACGGCCCAGATTTTG
scaffold732154_13.	1	p2	(TA)11	22	185	206	CAAAAATCTAACGGGCCAAA
scaffold732173_16.	1	p2	(AT)9	18	399	416	CCACGCTTCATTATCAACCA
scaffold732187_13.	1	p2	(AT)13	26	753	778	TGCTCTCAATTAAATACACCCG

scaffold732233_14.	1	p2	(AG)9	18	561	578	GCCAGCAGTAAAGAGGGTGT
scaffold732238_13.	1	p2	(TA)9	18	657	674	AGATCAACGGATGGTATCGG
scaffold732257_15.	1	p2	(AC)7	14	1162	1175	TGCCATTATGGTGCATTGTT
scaffold732273_14.	1	p2	(TC)6	12	1440	1451	TCCACTCTCTTGCGCTTTTT
scaffold732279_16.	1	p2	(TA)8	16	2394	2409	CAAGATGATGAGGGCCAAAT
scaffold732288_16.	1	p2	(TC)7	14	664	677	GGAGACCAATTCTTGGCTGA
scaffold732298_16.	1	p2	(AT)7	14	2647	2660	CAATAAATTGGGGTCGGCTA
scaffold732299_12.	1	p2	(TA)7	14	50	63	TGGTTATTACTGGAACGCGA
scaffold732309_16.	1	p2	(CT)8	16	454	469	CGGCCTATCGTCTTCCTACC
scaffold732346_16.	1	p2	(TC)7	14	5937	5950	TGCAATGCTAATGGCAACTC
scaffold732348_14.	1	p2	(GA)8	16	566	581	TGCAACCACCACTGGAGATA
scaffold732355_14.	1	p2	(TA)6	12	570	581	GCAAAAGTGCCTACTTCACCA
scaffold732357_14.	1	p2	(AT)6	12	744	755	AAACCAACTATCTCGGTGCG
scaffold732360_13.	1	p2	(TC)7	14	1008	1021	GACCTGGTGTCCCATCTCTC
scaffold732372_14.	1	p2	(CT)6	12	608	619	GCAATCTATCCCATACAAGGC
scaffold732380_15.	1	p2	(TC)6	12	198	209	TCTTCTCTCAGGTGGGGGAT
scaffold732386_16.	1	p2	(TC)7	14	569	582	TGCATCAAGAGAACAACTACATCA
scaffold732408_13.	1	p2	(AT)7	14	1297	1310	TCCGGATCATTGACATTTGTT
scaffold732420_15.	1	p2	(TA)10	20	989	1008	ATCTGTCTCCTGCCCATGAC
scaffold732423_17.	1	p2	(TA)6	12	783	794	ACAGTGGCTAAAATGCACCG
scaffold732452_16.	1	p2	(AC)9	18	2435	2452	GGGCTTTGTTGCTGGAGTAT
scaffold732460_14.	1	p2	(CA)7	14	572	585	CCTGCATCACAAAAGCAAAA
scaffold732478_16.	1	p2	(TG)11	22	49	70	TTTCTTGACTGTGGATTTCCAAT
scaffold732503_13.	1	p2	(CT)8	16	637	652	TGTTGGTTTGTGAGGTCAGC
scaffold732512_18.	1	p2	(AG)8	16	1274	1289	CGTTGTCTCCGCTACTGTTG
scaffold732521_17.	1	p2	(TA)6	12	5132	5143	ATCGGATTCTGGGGGATAAC
scaffold732547_15.	1	p2	(AG)7	14	1831	1844	GCATGCAAAGTTGCAAACAA
scaffold732557_15.	1	p2	(TA)9	18	938	955	GCAGCAACACCAAAACTCAA
scaffold732558_13.	1	p2	(GA)6	12	679	690	TGAAGGCACAGAGCATCATC
scaffold732576_15.	1	p2	(GA)6	12	147	158	GGTAGAGGAGCTGATGTGGC
scaffold732594_14.	1	p2	(TA)7	14	628	641	CATATGGTGTCAGGTTTGGG
scaffold732613_17.	1	p2	(TA)7	14	651	664	ACATCAGTTGTAGCTGGGGG
scaffold732627_14.	1	p2	(AT)6	12	535	546	ACATGCCCTAAAAACCGATG
scaffold732630_14.	1	p2	(CT)6	12	381	392	AGACCAAACCTCAAGCATGG
scaffold732637_15.	1	p2	(TG)6	12	1250	1261	TTGAGCCCCTTTTATGGAAA
scaffold732645_15.	1	p2	(TA)6	12	1617	1628	TCCAACAGCTCAAACAGCAT
scaffold732661_15.	1	p2	(GA)6	12	755	766	GGTGGAACTGATTGGGAGAA
scaffold732695_16.	1	p2	(AG)6	12	579	590	TGCCTTGTGTGTCACGAGTT
scaffold732738_19.	1	p2	(AG)6	12	581	592	TCCCTTCTTACATATGGCCC
scaffold732748_16.	1	p2	(AC)8	16	577	592	CTGAGTACCCCGTCTTCCAA
scaffold732749_15.	1	p2	(AG)7	14	2771	2784	CCATTATGTGTGCGAGTGGT
scaffold732754_15.	1	p2	(CT)9	18	568	585	AAAACCACGTCGTTCTTGCT
scaffold732764_15.	1	p2	(AC)7	14	1066	1079	CCAATGTATCATCCCTCGCT
scaffold732767_12.	1	p2	(TA)7	14	1690	1703	CTGCTCCTCTCATGGTCAAT
scaffold732782_16.	1	p2	(GT)6	12	247	258	AAAATCCAATTCGAATCCCC
scaffold732792_18.	1	p2	(TC)6	12	2321	2332	TTGATTCCATGAACACCCTTT
scaffold732810_13.	1	p2	(TC)8	16	119	134	CAGGGGATCTCAAGCCTGTA
scaffold732833_12.	1	p2	(CT)7	14	565	578	CCCGACTCCAAAATGAAGAA
scaffold732856_12.	1	p2	(AG)7	14	381	394	CAGCTGAACCAACCATCCTT
scaffold732859_13.	1	p2	(TA)8	16	349	364	CCACCATGATTTCGACACAC
scaffold732862_15.	1	p2	(CT)7	14	254	267	GCGAGCAGACCAGAAGTCA
scaffold732869_15.	1	p2	(AT)10	20	599	618	GGAAGGGAAGAATCCTCGAA
scaffold732903_11.	1	p2	(AT)7	14	903	916	TCGTGAGAAATTAATGGAACAAAA
scaffold732909_15.	1	p2	(TA)8	16	1474	1489	CACTTGCTTGGAAAAAGGGA
scaffold732928_15.	1	p2	(CT)6	12	586	597	TTCGGGAAAATGAACTCACC
scaffold732938_14.	1	p2	(TC)6	12	2551	2562	GCCAGTTCTTTTTCATGGGA
scaffold732954_15.	1	p2	(CT)6	12	918	929	GATCAAACACGCATCACCAC
scaffold732962_14.	1	p2	(GA)7	14	1415	1428	ACAACACGGAACCACTAGGC

scaffold732966_15.	1	p2	(CA)8	16	90	105	GCCGGACTTTGATTGAGTTC
scaffold732975_15.	1	p2	(AG)8	16	1312	1327	ACCTGATCACTTGTCCGAGG
scaffold733003_17.	1	p2	(AT)7	14	2227	2240	AGTGAACCATGGGTCCGTTA
scaffold733011_15.	1	p2	(AG)6	12	1344	1355	TTCAGCAACAGCTTGACCAC
scaffold733020_13.	1	p2	(GA)8	16	2452	2467	TCTCCGATAGGCAAAACGAC
scaffold733058_12.	1	p2	(AT)11	22	79	100	GAAAAACCGAAAACCGAACA
scaffold733065_10.	1	p2	(AT)9	18	1179	1196	AGAGCAACACATGCCAACAT
scaffold733087_14.	1	p2	(TA)6	12	53	64	TCATTTGTTAGAGGTTTTGACCA
scaffold733098_14.	1	p2	(TA)10	20	565	584	ACATCGGCTCAAACTCCAAA
scaffold733100_12.	1	p2	(TA)9	18	233	250	CATGAGCCATTATGTGCTGG
scaffold733128_14.	1	p2	(TA)11	22	41	62	TTTGATGATATATAGGTGTTTTGACC
scaffold733148_14.	1	p2	(TA)6	12	259	270	TTGGGGTATGGGAATAGCTT
scaffold733172_15.	1	p2	(AG)9	18	6201	6218	GTCACCTGTCACCAGAGCAA
scaffold733187_15.	1	p2	(TG)11	22	583	604	GAAAGCCCCCTTTTCTCAAC
scaffold733216_18.	1	p2	(AT)7	14	2493	2506	TTGCACAGTACATGCGTTCA
scaffold733238_15.	1	p2	(AT)9	18	2470	2487	CGGACAAACACGACAACATC
scaffold733247_16.	1	p2	(AT)6	12	595	606	GATTCTGCTGAGGGTCGTTT
scaffold733264_16.	1	p2	(TC)6	12	222	233	TACTGCTCCATCTTCAACCG
scaffold733267_14.	1	p2	(GT)6	12	54	65	CAAGAGTAGAGAAAATCCTCCCA
scaffold733276_14.	1	p2	(CT)13	26	270	295	GGAGTGGAGTGTGAGTGGGT
scaffold733302_13.	1	p2	(CT)6	12	2219	2230	CAACTGACCAACAACAGCCA
scaffold733306_14.	1	p2	(GA)8	16	186	201	TTTCTCTCTCCTCTCGCTGC
scaffold733348_16.	1	p2	(CT)6	12	206	217	ATCTCGGCCTAGCTGGATTT
scaffold733360_11.	1	p2	(TA)11	22	292	313	TAGACCCAGGCTTCGAGGTA
scaffold733374_12.	1	p2	(CT)6	12	598	609	ATTCCATCACCCAACTCTCG
scaffold733396_12.	1	p2	(TA)11	22	1967	1988	AGCAACCATGCAATTAAGGG
scaffold733402_14.	1	p2	(GA)8	16	1668	1683	TCATCAACGAAGAAACGCTG
scaffold733450_17.	1	p2	(AG)7	14	1959	1972	GATGCCCTCCACATCAGATT
scaffold733457_16.	1	p2	(AT)6	12	741	752	GTAGTTTACCTGGCTGGCGT
scaffold733479_12.	1	p2	(AT)10	20	1172	1191	TGTGAAGGCCTACGAACTGA
scaffold733507_14.	1	p2	(TA)8	16	201	216	ATCTTGACCGCTGATTTTGG
scaffold733509_16.	1	p2	(TG)6	12	9357	9368	TTCGAGGGGATTAATGATGG
scaffold733510_16.	1	p2	(AT)6	12	1895	1906	ATTGGCAATTTTTGAAACGC
scaffold733540_11.	1	p2	(AT)11	22	1131	1152	GAAGCAACCTTCCTCTGCAT
scaffold733556_17.	1	p2	(AT)6	12	2655	2666	TTCCATCCCTCTCCAATGAG
scaffold733573_18.	1	p2	(TA)6	12	603	614	AGCAATGAGCAACATTCAGC
scaffold733575_17.	1	p2	(CT)6	12	34	45	TTTTAATTCACGCACAATTACATTT
scaffold733588_12.	1	p2	(AT)11	22	429	450	TGTTGAATGTTGTGCCTCGT
scaffold733595_16.	1	p2	(AG)8	16	203	218	TACAAGCACAACAACACGCA
scaffold733610_16.	1	p2	(CA)6	12	2608	2619	TCAAACACTGCGCTTCAGTC
scaffold733613_16.	1	p2	(GA)6	12	815	826	GGTTGCACCTCTGTTTTCGT
scaffold733617_13.	1	p2	(AT)7	14	254	267	CCAACTACGTGGGTGGTTTT
scaffold733647_16.	1	p2	(AG)6	12	384	395	CCATCTGGCATTAGTTGCCT
scaffold733669_16.	1	p2	(AG)6	12	484	495	TGTTGCAAAATGCTGGTGAT
scaffold733671_17.	1	p2	(TC)10	20	149	168	TGTGTTGGTCTGAGAGGCTG
scaffold733674_12.	1	p2	(TC)8	16	971	986	AGGTTTTTCAAGGAGTGCCC
scaffold733679_15.	1	p2	(TC)8	16	1324	1339	GAGGACAGGAATGTTTCTGGA
scaffold733719_14.	1	p2	(CT)6	12	607	618	TAAAGAATGCCCACTCCCAG
scaffold733745_18.	1	p2	(TC)7	14	607	620	AGCAGAAGGCACCGAACTTA
scaffold733751_14.	1	p2	(TC)7	14	5101	5114	CATGTCTCCCCTACTTGCGT
scaffold733770_15.	1	p2	(AT)8	16	1226	1241	TGAAAAGGCCATTCGAGACT
scaffold733778_17.	1	p2	(GA)10	20	2343	2362	GCTGACGAAAGGAGTGGAAC
scaffold733802_14.	1	p2	(GA)9	18	1493	1510	ATGGCTTCACCAACCTTTTG
scaffold733820_16.	1	p2	(AT)8	16	66	81	CGGCTTGGATTATTTCCTATTTC
scaffold733843_14.	1	p2	(TA)8	16	52	67	TTAGTTAGTACCGATTTCAGGGTT
scaffold733849_15.	1	p2	(CT)6	12	45	56	CCGAAAATACAGGCGCATA
scaffold733858_15.	1	p2	(TG)6	12	951	962	GGTTTCCTTAACTCTGCGAAA
scaffold733864_11.	1	p2	(AT)9	18	70	87	CAAAAACAACTTCAATATGGATCTC

scaffold733882_15.	1	p2	(TC)6	12	1828	1839	TGGCTTCTGCACTTTCCTTT
scaffold733884_17.	1	p2	(AG)6	12	80	91	CCAATTTTCTCTTCGGGCTA
scaffold733888_16.	1	p2	(CT)6	12	133	144	ACCCCGTGATTGTACGAAAA
scaffold733893_11.	1	p2	(TC)7	14	610	623	GGCCAAATTGCAAGTTCATT
scaffold733896_13.	1	p2	(TC)12	24	900	923	TCATTTTCGCCCGATACTTC
scaffold733907_16.	1	p2	(AG)6	12	1206	1217	TCTGATAGGATTGGCTCGGT
scaffold733910_17.	1	p2	(CT)10	20	606	625	GAAGGTTCTGCAACGGAAAG
scaffold733913_17.	1	p2	(CT)6	12	1794	1805	AGCACGTGTTGAGGCTTCTT
scaffold733920_16.	1	p2	(AC)7	14	1673	1686	ACTGTGGATGGAGTTCGGTC
scaffold733958_15.	1	p2	(AG)6	12	1549	1560	AAATTGAGAGGCTCCAACGA
scaffold733976_14.	1	p2	(AT)6	12	323	334	CCATGCACGTAAGCATGTTC
scaffold733977_14.	1	p2	(CT)10	20	2187	2206	TATTAGGCCACCCCCTAACC
scaffold733986_14.	1	p2	(TC)6	12	8369	8380	GCTTGCTCTTGCAACCTCTT
scaffold734001_14.	1	p2	(AG)9	18	876	893	CCCAACAAACCCTTTCTCAA
scaffold734012_13.	1	p2	(CT)7	14	1745	1758	AGTACGGCAGTGGTAGGTGG
scaffold734024_17.	1	p2	(GA)6	12	1305	1316	AGATGCATAGGTGTCTGCCC
scaffold734026_19.	1	p2	(AG)6	12	2732	2743	CTTCCATTCCATTCCACACC
scaffold734054_14.	1	p2	(TA)8	16	1020	1035	CCCAAAAATGGTTTCACACA
scaffold734072_15.	1	p2	(TA)7	14	377	390	ATCCGACCTAATGAAAGCGA
scaffold734086_12.	1	p2	(GA)8	16	344	359	GTGAGGTGGGCAGAGTCAGT
scaffold734094_16.	1	p2	(AG)6	12	4040	4051	TCCAACCAACATCAAATGGA
scaffold734103_16.	1	p2	(AG)9	18	440	457	CAAATGGGAATCCATGAAGG
scaffold734105_16.	1	p2	(AG)8	16	836	851	CCGACAATAAGAAGAGAGGCA
scaffold734148_14.	1	p2	(TA)11	22	166	187	AGCCACTGAACCAAGTGACC
scaffold734151_16.	1	p2	(TA)7	14	620	633	ACAATGATATTCGCGAAGGC
scaffold734170_15.	1	p2	(CT)6	12	623	634	TGGCCTCTAATCAGTTCGCT
scaffold734173_15.	1	p2	(GA)11	22	3527	3548	TCCAAAAAGAGGATCCCAGA
scaffold734193_16.	1	p2	(TA)6	12	667	678	GGGTTTCTTACCCGAGCTTC
scaffold734200_14.	1	p2	(GA)6	12	1650	1661	ATTCAAAAGCTGGGATGGTG
scaffold734202_12.	1	p2	(AG)6	12	958	969	GAGATTTAGTGCGCGAAAGG
scaffold734203_13.	1	p2	(GA)6	12	3018	3029	TGGAAAAGGCATATTGTGGG
scaffold734208_13.	1	p2	(GA)7	14	248	261	ATGGGAAGATGTGATGAGGG
scaffold734228_15.	1	p2	(TC)6	12	1184	1195	GCACCACCCTACCCTTCTTT
scaffold734235_16.	1	p2	(TC)8	16	2817	2832	GACAAGCAAAGGGTTGGTGT
scaffold734240_13.	1	p2	(AC)6	12	283	294	TTGTCAACCAACACCTGCAT
scaffold734253_17.	1	p2	(AC)6	12	1160	1171	CCAATGTGCCCAGAGAAGTT
scaffold734269_12.	1	p2	(AG)7	14	425	438	TTTCTCGCATTGGTCAATCA
scaffold734309_14.	1	p2	(AT)12	24	116	139	GGTGCTGTGTGATGATGGAG
scaffold734349_12.	1	p2	(TA)6	12	446	457	GCTCGCTTTCATTTCACACA
scaffold734350_16.	1	p2	(TG)7	14	1316	1329	CTCTTTTGTTTTCCATGCCC
scaffold734352_15.	1	p2	(GA)6	12	1114	1125	TTGTGTGAAGCGGAGAGATG
scaffold734354_16.	1	p2	(AC)8	16	1286	1301	GAGCTCTTCAGTGGCGAAAC
scaffold734356_14.	1	p2	(TA)7	14	1492	1505	TGTTAAACGGACTGGCCAAC
scaffold734360_17.	1	p2	(GA)7	14	865	878	CGTGTAGAATCGCCTTCCTC
scaffold734380_15.	1	p2	(AT)6	12	2005	2016	TTTGGGTTGGAGATGGTTTT
scaffold734392_14.	1	p2	(AT)8	16	520	535	CAAACGAAAAATTATCAACTGTAGG
scaffold734402_15.	1	p2	(AT)6	12	4939	4950	ACCAAGTTGAGGGCATTGAA
scaffold734463_14.	1	p2	(CT)8	16	2282	2297	TGACCGGATCTCTCACTCCT
scaffold734469_14.	1	p2	(CT)6	12	3323	3334	ACAAAACCATCAGCCACCTC
scaffold734481_14.	1	p2	(AT)6	12	1328	1339	GGGGACTTTTTAACCAACCAA
scaffold734484_17.	1	p2	(AC)9	18	29	46	TGTGAGTGTGTGTGCAATGA
scaffold734507_16.	1	p2	(AG)7	14	631	644	AGGGAATATCAGGGGAATGG
scaffold734517_16.	1	p2	(AG)12	24	617	640	TTGAATCGAACTGGAGGAGG
scaffold734524_15.	1	p2	(AG)7	14	402	415	GGAAATCCAAGGCTACACGA
scaffold734541_14.	1	p2	(AT)6	12	2147	2158	ACAGGATAACGGATGCCTTG
scaffold734571_14.	1	p2	(CT)6	12	1945	1956	GGGGTGGTCCTCATTCTAAA
scaffold734592_16.	1	p2	(TA)8	16	1527	1542	TCGCGTGTCATTCTAGACCA
scaffold734597_15.	1	p2	(TA)9	18	630	647	GGCCTTCAAGCAAAATCAAA

scaffold734629_15.	1	p2	(AG)7	14	5793	5806	GTCATCGAGCCTAATCGAGC
scaffold734634_15.	1	p2	(GA)11	22	55	76	GCGATTTTAACAAAAACGGG
scaffold734642_16.	1	p2	(CT)6	12	1126	1137	CATTTTCCCAAACCCACAAC
scaffold734646_15.	1	p2	(CT)7	14	468	481	GGTGACAAGTGGCATGTTTG
scaffold734648_15.	1	p2	(GT)9	18	631	648	CATTCAAAAGCTTGCTTCCC
scaffold734651_16.	1	p2	(GA)9	18	576	593	TCCCCACGGTCTAATGTAGC
scaffold734656_13.	1	p2	(GT)7	14	633	646	CGCATTTGTCTCTCACCTCA
scaffold734657_15.	1	p2	(CT)9	18	632	649	AGACTGCACCTGCGGTAACT
scaffold734677_16.	1	p2	(TG)7	14	1785	1798	CCTGGTGTCCACTGTGTTTG
scaffold734684_17.	1	p2	(GA)6	12	569	580	CGGTTGATATTTGTTTGGGG
scaffold734695_14.	1	p2	(CT)11	22	1060	1081	TGATGTGGAGCTTCTTCACG
scaffold734734_16.	1	p2	(CT)12	24	1965	1988	CAAGGTCTGACGAAGTCGC
scaffold734745_16.	1	p2	(AC)7	14	1923	1936	CAGCCCTTGGCTCTTTTAGA
scaffold734760_16.	1	p2	(AG)8	16	868	883	TTGCACTCTCCTTTGTGTGG
scaffold734771_15.	1	p2	(TA)6	12	2903	2914	TTTGCAGTCATACTCCTCGG
scaffold734813_14.	1	p2	(AT)6	12	341	352	CCAAGCAAACTACAAACCCA
scaffold734817_15.	1	p2	(TA)9	18	88	105	TCTTCCAACGTCAAAGTTGCT
scaffold734834_17.	1	p2	(TA)7	14	985	998	TTGTCTATGCCGGTTTTTGA
scaffold734870_14.	1	p2	(GA)6	12	670	681	AATTTCGGTTACATGGCAGC
scaffold734895_15.	1	p2	(AT)9	18	50	67	TTGTTAGAGGTCTTGACGGGA
scaffold734911_13.	1	p2	(TA)10	20	439	458	TTTGGGGAGGAGAAAAGAGAA
scaffold734917_15.	1	p2	(TA)7	14	49	62	CTTATCCAACTCAATTTATATGATCG
scaffold734921_11.	1	p2	(CA)6	12	1076	1087	ATGCGATGTGTGGTCGAATA
scaffold734937_14.	1	p2	(AT)7	14	70	83	GGGTTATCACCTGATTACTACCCT
scaffold734940_16.	1	p2	(AT)10	20	1243	1262	TCGTGCGATGTATGATGTGT
scaffold734951_15.	1	p2	(CT)7	14	647	660	GGGAGGAAGATGCAACTCAG
scaffold735003_14.	1	p2	(GA)8	16	2237	2252	AAAGGCCACGTGTTAATTGC
scaffold735037_15.	1	p2	(TG)7	14	927	940	TTTCCTTTATGATCCCCTGC
scaffold735043_15.	1	p2	(GA)6	12	349	360	TTGCTAGGGTTTCGTTTTCG
scaffold735067_15.	1	p2	(AC)9	18	647	664	ATGCATTGCGACCATTATCA
scaffold735091_15.	1	p2	(AG)7	14	652	665	ACTAGGTTGTTGTGGCGGAG
scaffold735092_15.	1	p2	(AG)7	14	2309	2322	TCATATATGTTCCTGGCGGC
scaffold735150_16.	1	p2	(AT)7	14	2192	2205	TCGATCGGGAGTCAGAAATC
scaffold735156_14.	1	p2	(AT)6	12	246	257	GATCGGTTGGGAAAAAGTCA
scaffold735168_15.	1	p2	(CT)7	14	105	118	ATGTGGCTTGCTTGCTTCTT
scaffold735178_18.	1	p2	(CT)6	12	367	378	CTACATCCCATCATCACCCC
scaffold735190_13.	1	p2	(AT)8	16	591	606	TTTGATTTTTAATGGGGCAAA
scaffold735196_14.	1	p2	(CT)11	22	1937	1958	GCTCAATTCTTGGACCTTGC
scaffold735207_16.	1	p2	(AC)6	12	1261	1272	GGACTCTGCAGCATGTTCAA
scaffold735212_17.	1	p2	(AT)6	12	661	672	GCTCATGATTTGGCCAGTTT
scaffold735235_17.	1	p2	(TC)7	14	1109	1122	AATTTGTGTTGGCTTCAGGG
scaffold735254_14.	1	p2	(AG)8	16	1656	1671	GCGATCATTCTCGTGAAGAAA
scaffold735260_16.	1	p2	(TC)8	16	432	447	GCTTGTACCCGTAGCGTGTT
scaffold735276_14.	1	p2	(GA)6	12	1242	1253	AGTAGAGGGCGAGAACGACA
scaffold735290_15.	1	p2	(TC)6	12	1222	1233	ATCTCCCACGCTCACACTCT
scaffold735292_15.	1	p2	(TA)7	14	568	581	TTCCCACCATGACTTCAACA
scaffold735313_16.	1	p2	(GA)9	18	384	401	CCCCCAAATCTACAAAAGGG
scaffold735314_16.	1	p2	(TC)6	12	632	643	CAATCGAGCAATCTGTAAGGTG
scaffold735318_14.	1	p2	(GA)6	12	961	972	ATTCGTAACGTAACACGGGC
scaffold735320_13.	1	p2	(TA)9	18	1530	1547	ACCCACCCTTCTTTTTGCTT
scaffold735345_15.	1	p2	(AT)6	12	259	270	CTTCAACGGAGGGGAAGATT
scaffold735377_15.	1	p2	(CT)8	16	1294	1309	GTGTGGTCTGCAAAGTGTGG
scaffold735386_10.	1	p2	(AT)6	12	352	363	AATCGCTGAACTGTTTTCCG
scaffold735395_15.	1	p2	(TA)9	18	1234	1251	CACACCTACTTTAATGACGCACA
scaffold735398_17.	1	p2	(TG)6	12	2186	2197	GGCCAACATGATTAGCATCC
scaffold735404_14.	1	p2	(TG)6	12	1613	1624	CTTGTCAGCGCGTTTAATGA
scaffold735409_15.	1	p2	(TC)6	12	667	678	GATGCTGGAAATTCTGGGAA
scaffold735420_16.	1	p2	(AG)6	12	5753	5764	AAATTTAACGGGACACCACG

scaffold735428_15.	1	p2	(AT)8	16	681	696	GAGACATCAGCTGAGGGGAG
scaffold735430_15.	1	p2	(CT)6	12	667	678	GCTAAACTCCAGCGCAAAAC
scaffold735438_16.	1	p2	(CT)6	12	113	124	CTCGCTCGGAAAAGCAATAC
scaffold735496_16.	1	p2	(TC)9	18	2309	2326	GATTGTTGGGTTTTCCGATG
scaffold735529_17.	1	p2	(CT)6	12	1368	1379	TCTTTGGGATTCCTCTCGAA
scaffold735531_15.	1	p2	(GA)7	14	669	682	ACCTCGGACGCCTAAAGAAT
scaffold735543_17.	1	p2	(TG)8	16	1303	1318	TCCTTCGAGACTCCATCGTT
scaffold735555_15.	1	p2	(AT)6	12	626	637	TTTGAACTCCGTAGCAACCA
scaffold735600_17.	1	p2	(AG)6	12	675	686	CCATGTCTTCCTCTTCGAGC
scaffold735624_16.	1	p2	(TC)6	12	906	917	CTCACCTGCATCGTCTTTCA
scaffold735629_15.	1	p2	(CT)10	20	668	687	CTGCTCTCCAGAAGCAAACC
scaffold735630_14.	1	p2	(GA)9	18	1437	1454	CGGAGGCTGAGGCATTATAG
scaffold735638_16.	1	p2	(AG)9	18	670	687	CGCAGGATTGTACGGTTGTA
scaffold735704_17.	1	p2	(TA)9	18	44	61	TGAAGTTAGGAAATAAGGAGGTGTT
scaffold735717_16.	1	p2	(AG)8	16	1340	1355	TGTTGGCATGGTTGATGAGT
scaffold735720_12.	1	p2	(TC)6	12	680	691	GGATTCGAGTTTTTGAAACCA
scaffold735741_15.	1	p2	(GA)6	12	132	143	TGGTTGAAAGATGAGGGAGAA
scaffold735748_11.	1	p2	(TA)7	14	678	691	TCGATTAACTTGACAAGGTTTGAA
scaffold735749_15.	1	p2	(AG)6	12	3685	3696	AGGCGTGTTTTGTTTGGAAG
scaffold735750_16.	1	p2	(CT)7	14	129	142	GAGAGACGAGCTCACGCATA
scaffold735755_12.	1	p2	(AT)10	20	348	367	TGGTTATCATTTTGTCACAGTTTTT
scaffold735763_14.	1	p2	(AG)12	24	841	864	GGCCCACCATACCACAATAC
scaffold735767_14.	1	p2	(CT)6	12	120	131	TAGCCTTGGCCCCTAAGTTT
scaffold735775_16.	1	p2	(CT)6	12	78	89	AGCAACAGCGGAAGAAGAAG
scaffold735778_15.	1	p2	(TA)6	12	2311	2322	CATGATACCTCACTGGGGCT
scaffold735781_16.	1	p2	(CT)6	12	68	79	ATTTGTTCAAAATCCGCGAC
scaffold735794_13.	1	p2	(AT)8	16	679	694	AAACTTTGGAATCGACATTGC
scaffold735796_16.	1	p2	(AG)7	14	1791	1804	GTCGAGCAACAGCAGGTGTA
scaffold735801_18.	1	p2	(AT)9	18	63	80	GGTTTACCCATAGCGCACTC
scaffold735814_16.	1	p2	(AT)7	14	681	694	TTCTCCTCACAATGCTTCCA
scaffold735819_18.	1	p2	(TG)6	12	183	194	GCTTTGTGATGGGTGAAGGT
scaffold735826_14.	1	p2	(TC)6	12	858	869	TCCCAAGAATGAAGCCACTC
scaffold735830_13.	1	p2	(GA)8	16	848	863	AAGCTCAGTAGCGTTCTCGC
scaffold735834_16.	1	p2	(TC)6	12	857	868	CTTGATGCCCCGTTAAACAT
scaffold735835_15.	1	p2	(GA)7	14	1042	1055	ATGATTCCTCCCCTTCCATT
scaffold735880_15.	1	p2	(TA)6	12	558	569	CCGGTACATTCGGTAGATGG
scaffold735886_15.	1	p2	(GT)8	16	755	770	TTGAGCATTGATACAGTGGAGA
scaffold735917_16.	1	p2	(AT)6	12	1692	1703	TCTCGATTCAACTCATCGGA
scaffold735926_17.	1	p2	(CT)7	14	5030	5043	CTCATTTCGGAAGGAGCAAC
scaffold735953_14.	1	p2	(AC)7	14	2378	2391	TGTTAATGAAATTTACGCACACA
scaffold735955_16.	1	p2	(CT)8	16	1791	1806	GTGTAACCGTGGATCAGGCT
scaffold735956_15.	1	p2	(AG)6	12	221	232	GGGCTGTACTTCAGAGGCTG
scaffold736006_14.	1	p2	(AG)12	24	1980	2003	CGGGAAGTGGAGAGAGAGTG
scaffold736018_15.	1	p2	(AC)8	16	3000	3015	GAATGAGGGATCGGGTGATA
scaffold736064_14.	1	p2	(TG)6	12	203	214	AGCGATTTTAACCTCCCGTT
scaffold736071_14.	1	p2	(TC)6	12	529	540	CGGGGAGTAGATGAATCGAA
scaffold736072_21.	1	p2	(AT)7	14	348	361	TGTGTGCGAATTTGGAAAAG
scaffold736080_15.	1	p2	(GA)8	16	460	475	GGGGAAAGATTGCAAATTCA
scaffold736083_16.	1	p2	(CT)7	14	3936	3949	CATCTTCACCGGCTTCTCTC
scaffold736117_15.	1	p2	(CT)8	16	1458	1473	CATTTCAGCCACCATCTCCT
scaffold736122_14.	1	p2	(AT)6	12	2246	2257	TTTCCGACCATCTAAGTCGC
scaffold736131_14.	1	p2	(TA)6	12	698	709	GTGGCTTGTGTTTCCTTGGT
scaffold736139_16.	1	p2	(TG)7	14	3153	3166	GAATTTTTGAGATCGACGCC
scaffold736154_18.	1	p2	(TA)6	12	285	296	TTGATTCTCGCCATGTACAAA
scaffold736159_11.	1	p2	(GA)6	12	699	710	ATGTGCAGCCCCTGAGTAAG
scaffold736177_16.	1	p2	(AC)6	12	74	85	GGCGTGCATGTTTTATCTGA
scaffold736179_14.	1	p2	(AG)13	26	347	372	CCATGTGTCGTCAAGATGCT
scaffold736180_16.	1	p2	(TG)6	12	564	575	GATTTTGGCAATTCAACGGT

scaffold736182_16.	1	p2	(CT)6	12	4509	4520	CGCTTCGCCATTGTAATTTT
scaffold736200_17.	1	p2	(CA)8	16	528	543	ATGCCAACCCACGCTAATAA
scaffold736209_21.	1	p2	(AT)6	12	703	714	TGAGAGCGAGCAAGGGTTAT
scaffold736215_13.	1	p2	(TG)6	12	684	695	TGATTAAAAACTGAACCGGACA
scaffold736223_16.	1	p2	(CT)6	12	1491	1502	AAATTGGTGGGAATGCAGAG
scaffold736243_16.	1	p2	(AG)6	12	921	932	CACCGCCTCGTATCTTCATT
scaffold736251_14.	1	p2	(AC)8	16	700	715	GGGCTTGGTCAGAAAATTGA
scaffold736262_15.	1	p2	(TA)9	18	2535	2552	GGCCTGATCTTACCTAGGGG
scaffold736264_15.	1	p2	(AT)8	16	701	716	CGTGATTCATGCCATATTTGA
scaffold736278_16.	1	p2	(AG)7	14	3352	3365	GGATCCCGGTCATATACGTG
scaffold736310_14.	1	p2	(TC)7	14	704	717	GCTCCTCCTATCCACATCCA
scaffold736320_14.	1	p2	(TA)8	16	1202	1217	TTGGATGCGTTGATTGAAAG
scaffold736342_13.	1	p2	(CT)7	14	432	445	TTTCACCCAAATCACGAACA
scaffold736345_14.	1	p2	(AG)14	28	1260	1287	AACCCTGATCACCAAACGAG
scaffold736350_16.	1	p2	(AT)8	16	2785	2800	TCGGTTGGTGAAGTTGTTGA
scaffold736375_15.	1	p2	(TA)7	14	683	696	ACACGGATCGGAAATCCATA
scaffold736414_16.	1	p2	(AT)6	12	710	721	TCCAACGGAAATCCTTATACTCA
scaffold736426_15.	1	p2	(CT)6	12	844	855	AACCCACTTCCACAGAATGC
scaffold736503_15.	1	p2	(GT)7	14	714	727	TGCACATGCAAAGCTAAAGG
scaffold736522_17.	1	p2	(TC)6	12	1323	1334	CGATCACTGTAAGAACCGCA
scaffold736538_15.	1	p2	(CT)6	12	340	351	CACCCATGTTTGTTTTTCCC
scaffold736558_17.	1	p2	(CA)9	18	1111	1128	TCGTTTTGTCGAACTGTTGC
scaffold736606_16.	1	p2	(AG)6	12	717	728	CGAGCAGTTTGAATTGGTGA
scaffold736650_16.	1	p2	(AG)6	12	644	655	GGCTTATTTCCATCCCGAAT
scaffold736653_14.	1	p2	(AC)7	14	718	731	GTGTTGGTGCTTGATGGCTA
scaffold736682_19.	1	p2	(AC)7	14	723	736	TGCCATTTGATGGAGAATCA
scaffold736701_10.	1	p2	(AT)10	20	344	363	CGAATCCAGGTAAGGCTTGA
scaffold736712_15.	1	p2	(GA)7	14	723	736	GGGCAGAAAAGGTGAAACAA
scaffold736713_14.	1	p2	(GA)6	12	4841	4852	TCTCTTTCCCCCTCCTTTTG
scaffold736724_15.	1	p2	(CT)10	20	71	90	CTCCCCACTTTCCTTCAACA
scaffold736726_15.	1	p2	(TC)11	22	1256	1277	GCCATTGCACTTATGCTCCT
scaffold736750_14.	1	p2	(AG)7	14	518	531	TAGTTTTCACCATTGCGACG
scaffold736774_15.	1	p2	(AT)8	16	887	902	CGTTTTCCACCTTCAAGACA
scaffold736787_16.	1	p2	(AT)6	12	250	261	AACTCAATGGGGACATCAGG
scaffold736819_14.	1	p2	(TG)11	22	1558	1579	TGCAACTGCATGGGATAGTC
scaffold736826_16.	1	p2	(TC)6	12	2415	2426	GGAGGAACTCCATCTCCCTC
scaffold736850_15.	1	p2	(AT)6	12	3308	3319	GAGACAAAAAGCATTTGCCC
scaffold736876_14.	1	p2	(TC)6	12	151	162	AATGGAGATCCGTGCTTCAC
scaffold736882_14.	1	p2	(CT)7	14	733	746	GGTGAAAGGCCATGTGAACT
scaffold736884_15.	1	p2	(TC)6	12	1211	1222	TACACCAAATCTTGGCTCCC
scaffold736888_14.	1	p2	(AT)7	14	1433	1446	TTTCGACCAATGAGAAAGGC
scaffold736900_14.	1	p2	(AC)6	12	218	229	TGGTCTGCCTAATTTACTGCAA
scaffold736907_15.	1	p2	(AG)6	12	1645	1656	AGAGACTGTTCAAGGGCAGC
scaffold736936_15.	1	p2	(TA)13	26	763	788	TTGTCTTGACGCTGACAACC
scaffold736945_14.	1	p2	(GA)7	14	4078	4091	CGAAGAAAAGCAGGTTTTGG
scaffold736970_15.	1	p2	(GT)6	12	1265	1276	CCAAGCACATCAGCTGAAAA
scaffold736996_16.	1	p2	(CT)6	12	960	971	TTCCTGCTTTTCATCGCTCT
scaffold737011_14.	1	p2	(AT)13	26	1843	1868	GAGAGGAGACGCACAGAAGG
scaffold737021_15.	1	p2	(GA)11	22	2325	2346	TGCACTAAGTGGTGCTTTCG
scaffold737037_14.	1	p2	(CT)8	16	4765	4780	CACGTGGGACTACTGACCCT
scaffold737056_15.	1	p2	(AC)6	12	347	358	TTTTAAGTCGTGTTGCGTGC
scaffold737064_15.	1	p2	(AG)9	18	1124	1141	TGTCAGCAGACATAGCAGGG
scaffold737100_15.	1	p2	(AT)8	16	447	462	CCAGTCGAACCGACAAGATT
scaffold737106_14.	1	p2	(CT)6	12	117	128	TCGAACCCAAACAAATTTCC
scaffold737118_14.	1	p2	(TC)6	12	1282	1293	GGCTGTTGTAAAACCCTTGC
scaffold737130_16.	1	p2	(AG)8	16	38	53	AAAGCAATCAGTCAAAGGGG
scaffold737138_18.	1	p2	(CA)7	14	747	760	GAGAGCAAGCAACAATCCAA
scaffold737185_16.	1	p2	(TA)6	12	1518	1529	GAGTGAGTTGGCGAGAATCTG

scaffold737211_16.8	1	p2	(AT)6	12	1335	1346	CTATATAGGTCCCCCGTCCC
scaffold737252_15.7	1	p2	(TA)8	16	2012	2027	CCTGCGTGGTTTTTCTTTTG
scaffold737275_14.5	1	p2	(TC)7	14	5085	5098	TATATCGTCCAGCTCCGACC
scaffold737280_15.4	1	p2	(TA)6	12	516	527	GGAGGTTGAGATTTTGGAGGA
scaffold737296_17.4	1	p2	(GA)7	14	3113	3126	TGAGAGGAAAATGGTTTGGG
scaffold737300_14.6	1	p2	(CA)9	18	753	770	GGTAGACATGCAAACCGTGA
scaffold737312_17.0	1	p2	(TC)10	20	4403	4422	TATGACAAGCAGCAGTGCCT
scaffold737326_14.4	1	p2	(TA)9	18	40	57	CGGATTTAAGGGTTATTACCTGATT
scaffold737327_15.2	1	p2	(AT)10	20	1491	1510	TTTGGCTTGAACAGCACTTG
scaffold737330_15.6	1	p2	(AT)8	16	757	772	TTTTGGAGCCGAGAAGAGAA
scaffold737338_13.4	1	p2	(AG)6	12	128	139	TTGATTAGAGGAAACTGCGGA
scaffold737345_14.6	1	p2	(AT)6	12	1499	1510	GAATGTGGGCGATCTTGACT
scaffold737369_17.5	1	p2	(CA)6	12	841	852	GCTGCATATAAACCCGGAAA
scaffold737392_18.6	1	p2	(AT)10	20	756	775	CACTTTCCATCCAAAATGCAC
scaffold737393_13.8	1	p2	(AC)10	20	1844	1863	GCACAAATTTTCAATTCACGTT
scaffold737452_15.2	1	p2	(TA)10	20	2132	2151	TGAGAGGATGATGGTGTTGC
scaffold737479_17.0	1	p2	(AT)6	12	597	608	CCATTTAATTTCCAAAGGGTT
scaffold737494_13.6	1	p2	(TC)8	16	562	577	GCTTACGTGTTTCAGGGCTC
scaffold737504_15.7	1	p2	(CT)7	14	121	134	CCTTGCATATGATGGTTAGCA
scaffold737506_14.0	1	p2	(TA)10	20	1466	1485	GCGCAAGAGCTTTTTCTGAG
scaffold737509_19.4	1	p2	(GA)9	18	765	782	CACATTCTTTAAGCCATGGGA
scaffold737526_15.1	1	p2	(TA)6	12	753	764	GATCCACGTTAGAACCCCCT
scaffold737531_18.1	1	p2	(TC)6	12	1260	1271	TCCGATCTCTGTTTCGATTTG
scaffold737532_15.6	1	p2	(AT)6	12	1495	1506	TGCAAATGGTACTAGGGACG
scaffold737543_14.6	1	p2	(AG)6	12	177	188	CATTTTGAGCCATTGGACCT
scaffold737550_15.7	1	p2	(AG)8	16	1976	1991	CTGAATGCAATCAATGGGTG
scaffold737556_15.1	1	p2	(TA)10	20	895	914	TGTAAAGCCCATTTGAACCC
scaffold737575_15.6	1	p2	(TA)11	22	1303	1324	CGAGTGCCTCAAGTATGCAA
scaffold737576_17.8	1	p2	(TG)6	12	697	708	CCTCAATTTCTGCAGCCTTC
scaffold737583_14.0	1	p2	(AG)6	12	1256	1267	TGGATGGGTTACTGGATCAAT
scaffold737585_16.5	1	p2	(TA)7	14	298	311	ATATTTTATGGGACGGGGGA
scaffold737600_15.6	1	p2	(CT)7	14	4885	4898	GTGCGTTTTCGTCCAGAAAT
scaffold737636_14.2	1	p2	(CT)10	20	2027	2046	ATTCGATGAATGTGCTGCAA
scaffold737650_17.4	1	p2	(CT)8	16	1527	1542	TTAGAGGTGTCCAACAGGGG
scaffold737678_15.4	1	p2	(TC)8	16	1614	1629	CCACGCGCTCCTTAACTTAC
scaffold737685_14.8	1	p2	(GA)8	16	777	792	TTGATGGCATCGATGAGGTA
scaffold737691_13.3	1	p2	(TC)6	12	1465	1476	AGGCACGGCCAAGATAATAA
scaffold737699_15.3	1	p2	(TC)7	14	1736	1749	TCTCCGAATTCCGAAAAGAA
scaffold737713_14.3	1	p2	(AT)10	20	743	762	GTAGGTCGGGGTAGGGTTGT
scaffold737716_10.8	1	p2	(TC)6	12	1119	1130	AATTCATCACCACCTCACCC
scaffold737727_16.7	1	p2	(TA)8	16	203	218	CGTCCTCTCCCTTTCCTTTC
scaffold737729_15.3	1	p2	(TA)6	12	405	416	GACACTCACGATTTACCGCA
scaffold737734_15.0	1	p2	(TG)6	12	3259	3270	TTCACGTCATGGTCGTTTGT
scaffold737753_14.8	1	p2	(CT)9	18	222	239	TGGCAGAGTGGACTTCTCAA
scaffold737773_14.4	1	p2	(TA)6	12	4558	4569	TTGTATTTGATCCGCAGCCT
scaffold737780_16.6	1	p2	(AG)8	16	562	577	TAGGTTTGGATACCCGTTCG
scaffold737787_15.0	1	p2	(CT)6	12	1204	1215	GGAAGAAATTAAAAACCCCCA
scaffold737807_15.9	1	p2	(TC)8	16	194	209	TATGGATTCTGGGATGGGAA
scaffold737808_14.9	1	p2	(AT)11	22	779	800	AATCCTCAAAGCAATAACGC
scaffold737811_15.6	1	p2	(AC)7	14	786	799	TGTTTCATAATTTGGGCATGA
scaffold737827_15.6	1	p2	(AT)6	12	790	801	TCAGGCTTACAGCCATCCTC
scaffold737833_15.3	1	p2	(GA)6	12	480	491	TCATCCATTCCCAGTTCTCC
scaffold737852_16.3	1	p2	(TA)6	12	1968	1979	CTCGCAGTAGGTAAAAGGCG
scaffold737854_14.9	1	p2	(TA)14	28	1876	1903	CACAAAAGGATGGGAATTGG
scaffold737862_15.9	1	p2	(CA)7	14	790	803	ACATTTTCAACGGCACGATT
scaffold737870_13.6	1	p2	(CT)6	12	2083	2094	AGAAAAAGGAACGCCTCCAT
scaffold737877_15.8	1	p2	(TA)8	16	2389	2404	CCTTGACAGATGCAAAGACG
scaffold737885_15.3	1	p2	(CT)6	12	793	804	ACCATTGATAGCATGCGTGA

scaffold737907_17.	1	p2	(CA)6	12	1844	1855	AGGTGGGATTGTTTGCTTTG
scaffold737924_16.	1	p2	(AG)13	26	32	57	TTGCTAATCTTCGATGTATCAACC
scaffold737926_16.	1	p2	(TG)7	14	270	283	TACTGTCCAGCCTTGCATTG
scaffold737951_14.	1	p2	(AG)12	24	25	48	TGACAGATGCACTGATCCAAA
scaffold737956_16.	1	p2	(AT)6	12	1536	1547	TGCATGTGTGCATGTTTGTT
scaffold737977_17.	1	p2	(TC)8	16	2089	2104	GGATGCTATGATATGGTGATGC
scaffold737988_15.	1	p2	(TG)6	12	1797	1808	CGTCAAATTCTGGTTTATCATTCC
scaffold737993_15.	1	p2	(AC)9	18	1238	1255	CCGCAGCCTGAGTTGATTTA
scaffold737995_15.	1	p2	(GA)6	12	1996	2007	TGTGATGGAACGAGGATTTG
scaffold738001_16.	1	p2	(AC)7	14	3296	3309	TGAAGATACGAATCCTGGGC
scaffold738016_14.	1	p2	(CA)6	12	1379	1390	CGCATGAACCATGAAATCAG
scaffold738017_17.	1	p2	(CT)8	16	962	977	AAACGTCATTTCCTGCTGCT
scaffold738057_17.	1	p2	(AT)9	18	799	816	AATATGGGGTTTTGCCATCA
scaffold738072_15.	1	p2	(CT)6	12	180	191	TTCTGCCCATTCTTCCACTC
scaffold738080_17.	1	p2	(AT)7	14	611	624	TTTTATAGGACTGGGCCACG
scaffold738092_17.	1	p2	(GA)7	14	416	429	TGAGAGAGAGAAAGATAATCCTAAA
scaffold738095_16.	1	p2	(TA)6	12	1178	1189	ACACCGAAATCGGAGTTAGC
scaffold738113_16.	1	p2	(AC)8	16	312	327	GCATAGGGAGATTTGCGGTA
scaffold738129_16.	1	p2	(TG)10	20	82	101	TTCGGTGTATTTAGCCCCTT
scaffold738148_13.	1	p2	(TA)10	20	753	772	TCGGTCAATCCACAACTTCA
scaffold738164_15.	1	p2	(TA)8	16	4419	4434	TTTGGCCGGACTAGTTATGG
scaffold738172_13.	1	p2	(CA)10	20	934	953	TCTATTCTCTTTGCCACGCC
scaffold738186_15.	1	p2	(GA)8	16	5354	5369	GATTGGAAAAGGGTGGGTTT
scaffold738204_17.	1	p2	(AT)6	12	361	372	ACCCACAATCAACTTGCACA
scaffold738227_14.	1	p2	(GA)7	14	42	55	AGAGATCACTGATTATCTTTTCAATTT
scaffold738260_17.	1	p2	(TC)6	12	2145	2156	GGCTATTGTGGCATGGAGAT
scaffold738262_15.	1	p2	(CT)7	14	2125	2138	GATAAAGGTCGGCGTCAAAG
scaffold738329_16.	1	p2	(AT)6	12	1471	1482	TCGAATTGACATCTTCGTGC
scaffold738385_15.	1	p2	(AT)6	12	1664	1675	TTTGTGCCAAACCACTCTTG
scaffold738426_15.	1	p2	(CT)8	16	2033	2048	TTCTCATGCCCCTTCAAATC
scaffold738454_19.	1	p2	(TA)6	12	115	126	ACATGGTGGTGGGTTCAGAT
scaffold738456_13.	1	p2	(AT)7	14	787	800	GTCTCGATTGAATTTTCGCC
scaffold738461_14.	1	p2	(TC)6	12	1887	1898	CAATGAGACCATGTTGGTGC
scaffold738492_15.	1	p2	(CT)6	12	2326	2337	AACATTGGCTGGATTTCAGG
scaffold738494_16.	1	p2	(GA)6	12	5115	5126	GCACCTTCACCAACCATCTT
scaffold738495_13.	1	p2	(TC)10	20	2260	2279	CATCAGCCACCATTTTCCTT
scaffold738499_15.	1	p2	(CT)7	14	814	827	TCCCCAGTCAATTTCACACA
scaffold738504_19.	1	p2	(AC)7	14	484	497	CAGCGTTTTTGAGTCCATCA
scaffold738511_14.	1	p2	(TA)6	12	833	844	CGGTGGTGGAAAAGATGACT
scaffold738516_16.	1	p2	(TG)6	12	428	439	TGCATTGAAATTGACAGGGA
scaffold738525_12.	1	p2	(TC)6	12	70	81	TTTCCTAGAAATGCTCTCTTTCTGA
scaffold738555_14.	1	p2	(TC)8	16	324	339	TGCTAACATACGCATGAGGC
scaffold738572_14.	1	p2	(CT)12	24	176	199	ACCTGCTTGATTTTGTTGGA
scaffold738579_15.	1	p2	(GA)8	16	834	849	CGACTTGCGCTAGAATCGTT
scaffold738591_15.	1	p2	(AT)9	18	2033	2050	CCCCCATGATTTTCTTTCCT
scaffold738595_17.	1	p2	(TG)6	12	512	523	AAGTCCTGGACCTATGTTTGGA
scaffold738596_15.	1	p2	(CA)6	12	1921	1932	CCGGCTCAAGTCATTTTCTC
scaffold738613_17.	1	p2	(CT)6	12	337	348	CCTTCACCACCTCTTGCATT
scaffold738618_16.	1	p2	(TG)6	12	4968	4979	CATCCTACGCATTAAACCCA
scaffold738621_16.	1	p2	(CT)8	16	4122	4137	GCCCCTGGTTTTGGTCTATT
scaffold738634_14.	1	p2	(AC)7	14	410	423	CATCTGCTGCTTTGTTTGGA
scaffold738639_15.	1	p2	(GA)6	12	121	132	AATCGCTTCCGCATTTAAGA
scaffold738652_14.	1	p2	(CT)6	12	1927	1938	ACCTGAGGGAGTTGATGTGG
scaffold738656_13.	1	p2	(AG)6	12	1610	1621	TGACAGCAAGCCAGATTGTC
scaffold738658_16.	1	p2	(TC)6	12	621	632	TATTTGAAGGGAGTGCCCAG
scaffold738679_16.	1	p2	(GA)7	14	846	859	CCTGCAGATGACTGGCTACA
scaffold738694_14.	1	p2	(AC)6	12	2967	2978	TCATTTCAAGCAAAATCGCA
scaffold738708_15.	1	p2	(TG)6	12	914	925	TTGGCAATTTATGGTCACCT

scaffold738736_19.	1	p2	(AC)9	18	846	863	GCTCAGGCTTACATGGGTGT
scaffold738743_13.	1	p2	(AT)9	18	5646	5663	AGCTACACCTGAGAGTGCCC
scaffold738761_16.	1	p2	(CG)6	12	93	104	CTTATGGTGGTATGGTGTAGAGG
scaffold738763_16.	1	p2	(TA)9	18	199	216	GCGGGTCAAGTTGAGGAATA
scaffold738768_19.	1	p2	(CT)7	14	463	476	TCCCAGAATTTGCCTTCAAT
scaffold738769_15.	1	p2	(TA)6	12	3283	3294	TGATTTTTGGAACCGTAGGC
scaffold738792_16.	1	p2	(AC)6	12	1401	1412	TGGTGGTGAATAGGGGACAT
scaffold738810_14.	1	p2	(GA)6	12	1284	1295	TGGTATGAGTTGGCTTTTTGG
scaffold738811_17.	1	p2	(GA)6	12	240	251	GGCAGGTCTCAGCCAAATTA
scaffold738820_17.	1	p2	(CT)6	12	804	815	CGAAACGAGAATAACCGGAA
scaffold738823_16.	1	p2	(CA)6	12	1141	1152	GGTGGAAAACATGCACACAG
scaffold738845_15.	1	p2	(GA)6	12	7006	7017	GGAACCACAACCCATCACAT
scaffold738846_13.	1	p2	(AT)10	20	197	216	TAACGATGGACTAGGGGCTG
scaffold738861_17.	1	p2	(TC)7	14	10508	10521	AACGAAATAAACCCCCAACC
scaffold738872_12.	1	p2	(TC)6	12	185	196	CCAAGTCCCTTCGTTTTCAA
scaffold738886_16.	1	p2	(AT)6	12	923	934	TTGCTTTGGTCATACAAACATT
scaffold738895_14.	1	p2	(TA)7	14	864	877	TTGGGTATTGTTAGCTCGGG
scaffold738899_16.	1	p2	(CA)6	12	1813	1824	TGGAACCTATTTCCTCCACG
scaffold738915_14.	1	p2	(GA)6	12	171	182	TCACTGGGGACAATCTCACA
scaffold738920_15.	1	p2	(AG)10	20	3020	3039	GCTTTGTGCCTGCATTATGA
scaffold738955_17.	1	p2	(AT)6	12	615	626	GGGACGTGGTTAGCAGATGT
scaffold738956_14.	1	p2	(CT)6	12	2247	2258	ACAGCTGGCCTTGGATGATA
scaffold738970_14.	1	p2	(AG)9	18	2899	2916	CAATGGAGCAGAAAGAGGGA
scaffold738973_13.	1	p2	(AT)8	16	683	698	AGGTCGGGTTTTCAGCCTTA
scaffold738978_15.	1	p2	(AG)7	14	928	941	AGTCAGTGCTCACCGGATCT
scaffold738979_15.	1	p2	(TG)7	14	1227	1240	TCCATTTATCGGAGTTACGGTT
scaffold738980_12.	1	p2	(TG)11	22	1812	1833	GGTTTATTGGTGCTGGTGCT
scaffold738987_13.	1	p2	(AT)9	18	300	317	TTTCTTGTTGAGGAATCGGG
scaffold738995_15.	1	p2	(TC)6	12	4019	4030	AATAAGCCTCCACACCCCTC
scaffold739003_14.	1	p2	(AT)6	12	164	175	TGAACCAAACACCCCCTAAG
scaffold739020_12.	1	p2	(AT)11	22	361	382	GCCATGTGGAGGTTGATTTT
scaffold739037_15.	1	p2	(GA)6	12	675	686	TTGGTGAAGATTCGATTCCC
scaffold739043_16.	1	p2	(CT)6	12	176	187	TTTACTCCGCCACGGTTAAG
scaffold739048_17.	1	p2	(CA)6	12	3540	3551	CAAATCGTCAAATCCCCCTA
scaffold739066_15.	1	p2	(AT)11	22	872	893	GAAAATGTCGTGAATGCCAA
scaffold739073_14.	1	p2	(TC)8	16	1087	1102	TGTGTTGATGCAAGTTTGGAC
scaffold739077_15.	1	p2	(TG)11	22	2600	2621	CGATTTACGCCGAGTTAGGT
scaffold739086_15.	1	p2	(TC)8	16	103	118	AAGCCTCCCAAGTCTCCAAT
scaffold739089_17.	1	p2	(AG)6	12	90	101	AGCCCCGAAAAAGTAATGGT
scaffold739092_14.	1	p2	(TA)8	16	2386	2401	TTGCGCAAATAAACCAACAA
scaffold739095_17.	1	p2	(GA)6	12	200	211	TTGGGGTGGAGAGAAGTGAG
scaffold739106_16.	1	p2	(CT)7	14	2441	2454	AGTGGTGTTGGACTTGGGTC
scaffold739142_13.	1	p2	(AT)6	12	33	44	TCAGTCTGCACAGCTGACAA
scaffold739157_14.	1	p2	(AG)7	14	880	893	ACGATGGCTTTGCTGTTCTT
scaffold739167_18.	1	p2	(TC)6	12	1703	1714	GGCGTGCCTAATGGTATTTC
scaffold739182_17.	1	p2	(TC)10	20	270	289	TGAAGCCCATGTTGAATCTG
scaffold739195_15.	1	p2	(TC)6	12	2029	2040	TTTCTGGGGAGTTCATGTCC
scaffold739201_19.	1	p2	(TA)7	14	67	80	GGGGTTATCATGGGATCAAG
scaffold739205_15.	1	p2	(AG)11	22	135	156	GGCCAGGAGATGAGTCAGAA
scaffold739208_17.	1	p2	(TA)8	16	169	184	CCAAGATCAATGGTTCCTAAGTG
scaffold739213_15.	1	p2	(CT)6	12	188	199	GAATGGCTTCGAGCTTACCA
scaffold739237_16.	1	p2	(GA)8	16	4349	4364	AGATGAGCCGAGGAGCAATA
scaffold739254_16.	1	p2	(TC)7	14	1768	1781	TCCAATTCCGATACCTGACC
scaffold739261_18.	1	p2	(AT)8	16	482	497	GGCTGCAAACATTTGAGGAT
scaffold739270_15.	1	p2	(CT)10	20	364	383	TTTATGAAAAATGGCCCCAA
scaffold739320_16.	1	p2	(TA)9	18	897	914	GTTCCGATACGTCTGAAGGC
scaffold739321_22.	1	p2	(TA)6	12	166	177	GGTAGGAACTGCATGACCAAA
scaffold739323_12.	1	p2	(TA)13	26	78	103	CAGGATAATCCAGAATCAACACA

scaffold739345_17.	1	p2	(GA)7	14	2746	2759	GGCCATGACCTCTTCCTGTA
scaffold739346_15.	1	p2	(CT)9	18	1846	1863	TCAACATTCAGCCGATCAAA
scaffold739349_16.	1	p2	(AG)8	16	5503	5518	TTTCTTCCACGCCTTTCAAT
scaffold739352_14.	1	p2	(AT)9	18	1964	1981	GCAGGACAAAGCAGATAGGG
scaffold739374_13.	1	p2	(AG)7	14	907	920	AAGAGGGCAGAAAGAGGAGG
scaffold739380_14.	1	p2	(GA)6	12	1437	1448	TGACGCTCGCAGTATTTTTG
scaffold739386_16.	1	p2	(AT)8	16	120	135	TTGAGTTGTGATGTTTGCATTTT
scaffold739391_18.	1	p2	(AT)9	18	2487	2504	GCTAGAGCCAAGGACATGAAA
scaffold739398_15.	1	p2	(AT)7	14	3597	3610	TATGAGATCTCGCCATGACA
scaffold739406_15.	1	p2	(AG)7	14	2426	2439	AAAATCGCCCCTCAAAACTT
scaffold739410_14.	1	p2	(GA)10	20	943	962	AAATATGAGTTTCCTCTTCCATGA
scaffold739440_14.	1	p2	(CT)8	16	743	758	TCAATCAAATCAAGGGGAGC
scaffold739447_15.	1	p2	(CT)6	12	190	201	GCCATCTATCTTGTTCGTGACA
scaffold739449_14.	1	p2	(TC)10	20	2325	2344	TAATGCCCACATGAGGAATG
scaffold739470_15.	1	p2	(CT)11	22	906	927	TATCCGAGTTTTGCCAGGTC
scaffold739480_14.	1	p2	(GA)6	12	2792	2803	AGCTTTTTCCGATGATCCCT
scaffold739491_14.	1	p2	(TC)6	12	36	47	TCCAGTCTTCTGCCAATCAA
scaffold739505_15.	1	p2	(GA)7	14	654	667	TGCTTTCGTTCAGGACTGTG
scaffold739518_15.	1	p2	(AG)7	14	2630	2643	CCCCAGCAATCCTCTCTACA
scaffold739531_16.	1	p2	(TA)6	12	1733	1744	TCAAAGCAAAATCGGCTAAA
scaffold739533_16.	1	p2	(TG)6	12	300	311	GGTCAGAATCACGGCAGTTT
scaffold739535_15.	1	p2	(AT)7	14	2176	2189	GTTTGATGACGTGGTTCGTG
scaffold739564_15.	1	p2	(TG)6	12	3104	3115	TGTACGCGTTATTTGCCAAC
scaffold739569_16.	1	p2	(CT)6	12	1099	1110	TACCAGCAACCATGTGGAAG
scaffold739572_15.	1	p2	(TC)8	16	2173	2188	GAGAGAAGGGGTGGGGATAG
scaffold739573_14.	1	p2	(GA)7	14	292	305	CTGTCTCCAGTGTCTTGCCA
scaffold739602_16.	1	p2	(AG)11	22	1785	1806	GCGTCCTCATTTATGATCGG
scaffold739627_16.	1	p2	(AG)6	12	931	942	CCATACGTTGGTAATGCAACC
scaffold739645_15.	1	p2	(CA)6	12	410	421	TGCAGGCAGTATTTCGACTG
scaffold739647_15.	1	p2	(AG)7	14	1509	1522	CCACTGCATCACAACCATTC
scaffold739654_14.	1	p2	(GA)8	16	834	849	CAAGGTCGTACTAGCCAGCC
scaffold739670_14.	1	p2	(TC)7	14	757	770	ATGTGGGGTTGAGATCTTCG
scaffold739682_15.	1	p2	(CA)7	14	910	923	TGAGTCGTTTTCATGATGGC
scaffold739695_13.	1	p2	(AT)6	12	121	132	TCTCCTCTCCTCAAAAGCCA
scaffold739705_14.	1	p2	(TA)8	16	50	65	AAATATGTGCTCTCATTTGATTACACT
scaffold739718_17.	1	p2	(TC)8	16	2078	2093	TCATGCAATACGGCTAGCTT
scaffold739750_15.	1	p2	(CT)11	22	618	639	TGATGATTTTTGGCCTTTGTC
scaffold739795_16.	1	p2	(GA)7	14	3211	3224	ACAGATTGCATTCTCCCGTT
scaffold739807_18.	1	p2	(AG)11	22	1929	1950	TTACAATTACGAACGCGTGG
scaffold739812_15.	1	p2	(AT)8	16	1802	1817	CATTCAGTTCATCATTTTCATGG
scaffold739826_14.	1	p2	(TA)10	20	292	311	TTGACCGTCCAACAATTCAA
scaffold739833_16.	1	p2	(GA)14	28	565	592	TGAAACTGAAGCTTGCATGG
scaffold739834_16.	1	p2	(CT)6	12	1475	1486	CCACGACCAATTCTTACAGC
scaffold739841_15.	1	p2	(CT)8	16	357	372	ATTCTCTCCAGCCCCTTCAT
scaffold739842_16.	1	p2	(CT)10	20	398	417	CCGGTTTATGGATGAGGAGA
scaffold739868_15.	1	p2	(CT)7	14	455	468	TAATATCCAAAACGCGCACA
scaffold739879_15.	1	p2	(TA)6	12	1505	1516	TCATCATGTGATGCAGACCA
scaffold739880_13.	1	p2	(TA)9	18	2247	2264	TGCCTGTATGAAAAAGCATCA
scaffold739934_15.	1	p2	(AT)9	18	437	454	TGAATGGAACACACACACCA
scaffold739939_14.	1	p2	(TA)6	12	2102	2113	TTCGGTAGGCCTGAATTGAC
scaffold739946_17.	1	p2	(CT)13	26	954	979	AGCTGCTTCGAGATGAGAGC
scaffold739958_17.	1	p2	(TA)8	16	96	111	AGGCATTCGAAAAGCTCATT
scaffold739970_15.	1	p2	(TC)6	12	3875	3886	TCCTCTGGTTTCTGTTTGCC
scaffold739996_15.	1	p2	(AT)7	14	126	139	GGCTAATTGTTGGCCTTTGA
scaffold740004_15.	1	p2	(GT)6	12	2056	2067	GGGAATGATGGAATGGTGAG
scaffold740012_14.	1	p2	(TA)6	12	441	452	TTGCAAAACAAAGCACGATT
scaffold740016_15.	1	p2	(GT)10	20	617	636	AGTACAAGGTGGCGGTTGAC
scaffold740017_17.	1	p2	(AT)6	12	399	410	AAAAACAAGTCATCCATGTCCC

scaffold740023_17.5	1	p2	(AG)6	12	1189	1200	CTCTCTCCCCCTTTCTTGCT
scaffold740028_15.0	1	p2	(AT)9	18	1913	1930	TTACCTGCGTGTTTTACAACTG
scaffold740029_18.1	1	p2	(GA)7	14	293	306	GCCACAGTGGAAGAACCAAT
scaffold740032_13.7	1	p2	(AT)9	18	59	76	GGCCATTGGGCTTATCCTA
scaffold740059_14.4	1	p2	(GA)6	12	1186	1197	TCAGTCGTCAGTAAACCCGA
scaffold740062_17.9	1	p2	(AG)6	12	316	327	GCCTCGCATGCTATTGCTA
scaffold740072_15.7	1	p2	(AT)6	12	115	126	GCTTGAGTGTGGCACATTTAGT
scaffold740077_16.4	1	p2	(AG)8	16	2818	2833	CTGTATCAGATGTCCGGCCT
scaffold740089_16.7	1	p2	(TG)6	12	977	988	TGTCCTGAGAGGCAGGAAAT
scaffold740116_17.0	1	p2	(TC)6	12	991	1002	TGGAATCGTTTGTCCACTTTT
scaffold740121_17.4	1	p2	(AG)7	14	3023	3036	CTTTGCTGTTCGTGGTTCAA
scaffold740124_16.7	1	p2	(AC)7	14	988	1001	CCATAGAAAACGGCCAGAAA
scaffold740151_17.2	1	p2	(AG)8	16	2037	2052	AATTTTTAGCCATGGTCCCAC
scaffold740158_13.6	1	p2	(CT)6	12	815	826	CTTCGTCTTCTCCAACTCGC
scaffold740176_20.9	1	p2	(CA)7	14	302	315	TTCACTGAATTTGCCTGAAAAA
scaffold740180_15.4	1	p2	(TC)8	16	336	351	ACCACTAATCCAACCCCCTC
scaffold740192_13.6	1	p2	(AG)7	14	1023	1036	GGGAGTTCTTGTGCATGGTT
scaffold740200_16.0	1	p2	(CT)6	12	1892	1903	TCGCAAAAGTGATCTTCGTG
scaffold740202_13.9	1	p2	(TC)7	14	714	727	ATGCGTGGGCGATATTATGT
scaffold740209_16.1	1	p2	(TG)9	18	4240	4257	TCAACACCCATCAAGATGCT
scaffold740212_15.3	1	p2	(GA)6	12	277	288	CTACCTCAGCCTCGCCATAG
scaffold740216_15.3	1	p2	(GA)6	12	1087	1098	GACCCAAACGGAGCATCTAA
scaffold740219_13.6	1	p2	(AT)6	12	1252	1263	CCAGAAGCAGTGAAGCACAA
scaffold740223_15.5	1	p2	(AT)7	14	5027	5040	TTTTCCACAGAAATGTTGGCT
scaffold740230_17.4	1	p2	(CT)8	16	4219	4234	TCGTCTTCATGCTCACTTCG
scaffold740237_16.6	1	p2	(AT)8	16	1972	1987	ATCAATGATGAGCCATGCAA
scaffold740242_16.7	1	p2	(AT)8	16	2378	2393	CTGTCACGGTCAGCACTTGT
scaffold740265_16.2	1	p2	(GT)8	16	1006	1021	CGGGGGAATAATAAGGGAAG
scaffold740281_17.6	1	p2	(TG)9	18	3386	3403	TGGGTTTAGGGATTAGCTGC
scaffold740284_17.5	1	p2	(CT)6	12	2361	2372	GCACTGAAAAAGGGATCCAA
scaffold740288_16.5	1	p2	(CT)8	16	2607	2622	GTGACGAGTTTGCGTGAGAA
scaffold740294_13.8	1	p2	(CT)6	12	1088	1099	CAAACACCCATTCAAACCCT
scaffold740309_16.4	1	p2	(AT)8	16	1083	1098	TTCCTTGAATCAGCCACACA
scaffold740311_17.7	1	p2	(AG)6	12	2268	2279	TGTGGATTCGTGTCGGATTA
scaffold740321_13.0	1	p2	(TA)10	20	1825	1844	GAACCTCCTCGTTAGCTCCC
scaffold740335_13.2	1	p2	(CT)7	14	1565	1578	TTATGCCCTCCATTCTCTGC
scaffold740353_18.5	1	p2	(AT)6	12	336	347	TTCTTTTATGGGCCATGAGG
scaffold740355_16.2	1	p2	(GA)9	18	2270	2287	TTTGGAATTCAAGGACTGGG
scaffold740378_16.4	1	p2	(TA)8	16	1072	1087	TTCGGTCAGATTATGTGGGG
scaffold740382_13.6	1	p2	(TA)6	12	1410	1421	TGCTTCATGAACCGACAAAA
scaffold740424_15.3	1	p2	(GA)6	12	1906	1917	GGAACTGAGCTTTGAGGGTG
scaffold740448_15.5	1	p2	(CA)6	12	1226	1237	TGGTTTACACTTTCCGGGTC
scaffold740452_18.1	1	p2	(TC)7	14	665	678	CACAGGAAAAGGAAACGGAA
scaffold740457_16.5	1	p2	(AT)6	12	387	398	ATGCACACCAACTGCCATAA
scaffold740485_15.3	1	p2	(GT)8	16	3885	3900	TGTCAAGTAACCATTCAGGGC
scaffold740524_14.0	1	p2	(TC)7	14	1328	1341	ACCACCTGCCCAACTATCTG
scaffold740534_16.0	1	p2	(TA)6	12	91	102	CAACAAGGTACTCGAAGAACACA
scaffold740536_17.0	1	p2	(GA)8	16	1816	1831	GCCTGGTTCCAAATTTTCCT
scaffold740542_17.7	1	p2	(AG)9	18	259	276	CCTCATTGCTGTCGCTATCA
scaffold740573_14.9	1	p2	(TG)6	12	577	588	ACAATCGGAGTGCCATTTTC
scaffold740580_13.2	1	p2	(TC)11	22	1410	1431	ACAGGAACAAGCCCATCAAC
scaffold740581_13.2	1	p2	(TA)9	18	963	980	TCAGCCCTGAGTGGTTTTTC
scaffold740585_15.4	1	p2	(GA)6	12	384	395	GAGAGGGGTGTTTGGTGCTA
scaffold740594_14.3	1	p2	(AC)7	14	632	645	TAGACAGTTGCACCCAGCCT
scaffold740607_16.4	1	p2	(TC)6	12	8655	8666	TTGGCTTTAATCAGGGCATC
scaffold740610_14.5	1	p2	(AT)9	18	1053	1070	AGTCGGGAGAAATCTCGTTG
scaffold740614_14.7	1	p2	(AT)6	12	522	533	CGAAACAGCAATCAAAAGCA
scaffold740619_15.0	1	p2	(GA)7	14	3302	3315	AGAATGGGACTCACTGGTGG

scaffold740657_18.	1	p2	(GA)6	12	413	424	GCAGTGGAAGAACGAATATGG
scaffold740675_16.	1	p2	(AT)12	24	49	72	GGAGGTGTTATGAAGGGATTACC
scaffold740683_15.	1	p2	(GA)6	12	1882	1893	GAGGTAAATGTGGAAGCCCA
scaffold740689_15.	1	p2	(CA)10	20	2043	2062	GCCATGATGCCTGTGAAGTA
scaffold740690_15.	1	p2	(AT)9	18	475	492	GGAATTTAGACGATTGATCCGA
scaffold740726_15.	1	p2	(TA)6	12	1372	1383	TTCCACCAGATACGGAGACC
scaffold740736_15.	1	p2	(TA)9	18	46	63	CGGATTTATTGGTTATTACCTGA
scaffold740747_13.	1	p2	(CT)6	12	616	627	CGACACATACGAATTGCCAC
scaffold740759_16.	1	p2	(TC)8	16	3536	3551	GATACCCTGGTGGTCCATTG
scaffold740767_15.	1	p2	(TC)6	12	186	197	TGAAATTTGGCTTGCATTTG
scaffold740768_16.	1	p2	(CT)6	12	1071	1082	TGCTTTATGCAATGTCAGTGTG
scaffold740789_18.	1	p2	(GA)6	12	1016	1027	ATGCAAAAATTGGTCCAACG
scaffold740812_17.	1	p2	(TG)8	16	2619	2634	AGAAGGGGGATTGTTGCTTT
scaffold740818_14.	1	p2	(TC)7	14	664	677	AGGTCTTTCGAACCCCCTTA
scaffold740819_14.	1	p2	(AG)6	12	337	348	TGGGAGCTTTATGATTTGGC
scaffold740821_14.	1	p2	(TC)6	12	345	356	CCACACCATAGCTGGTCGAT
scaffold740844_16.	1	p2	(CT)10	20	783	802	TCCCTTTTTCTCAAGGGAGG
scaffold740854_14.	1	p2	(AG)7	14	220	233	AGCTTGGCGAATTCATCATC
scaffold740855_16.	1	p2	(AG)6	12	1301	1312	GCATGTTCATGGCTATCATTTG
scaffold740862_15.	1	p2	(GA)8	16	1094	1109	CAGGAGAATTTGGATTCGGA
scaffold740865_17.	1	p2	(AG)8	16	256	271	GTGACCGGTGGTTGTCTTCT
scaffold740876_16.	1	p2	(TA)8	16	1095	1110	CTAAACTCCGCCAACTGCTC
scaffold740880_14.	1	p2	(CT)8	16	118	133	CTGACATGGAAAGCACCCTT
scaffold740902_18.	1	p2	(AT)6	12	890	901	AAGAATACCACCGCCAACCT
scaffold740923_13.	1	p2	(AT)6	12	2314	2325	GAGGGTATCACCAATCTGCAA
scaffold740949_16.	1	p2	(AG)6	12	1604	1615	CCCCTAGGGTTTCCCATTTA
scaffold740958_14.	1	p2	(AG)8	16	1111	1126	GTTTGCTTTGGTGTGGGATT
scaffold740971_14.	1	p2	(AT)8	16	87	102	ATTACGTCGATCCAACGGTC
scaffold740986_16.	1	p2	(TC)6	12	1598	1609	TCCTCAGGAGTAAGAGGGCA
scaffold740988_17.	1	p2	(AC)6	12	1996	2007	CTTTTCCATTTCCGATCCAA
scaffold740991_14.	1	p2	(TA)8	16	3268	3283	TTAAACCATGCACGTAGGCA
scaffold740996_12.	1	p2	(CT)9	18	2450	2467	AGATGTGCATTCAGAGGGTG
scaffold740999_16.	1	p2	(TA)8	16	476	491	CATCGTTAATGTTGATTTTTATTCG
scaffold741004_13.	1	p2	(AC)7	14	1973	1986	AGCCCTCCACGATAACATTG
scaffold741019_15.	1	p2	(TG)7	14	759	772	ATGACATGGCCATAACGAGG
scaffold741029_16.	1	p2	(AG)14	28	487	514	GAGACTGCAGCACTCACAGC
scaffold741032_15.	1	p2	(TG)6	12	1568	1579	GGTGGTGGTGTTGAATAGGG
scaffold741043_15.	1	p2	(TC)13	26	75	100	CACGTATGGATAAGGCTAAAGATG
scaffold741061_14.	1	p2	(AG)8	16	565	580	CCGAAATCCGGGTTTTATTT
scaffold741082_15.	1	p2	(AT)10	20	2274	2293	CTGTGTGCCTCCTCCTTTGT
scaffold741093_13.	1	p2	(TC)13	26	618	643	TTTTATGCCAAAGCAAAGGC
scaffold741100_14.	1	p2	(AT)8	16	1146	1161	TCGATTCTTGTCATCCATGC
scaffold741101_17.	1	p2	(AT)7	14	1147	1160	GCCTAGCCGGTCAGTTACAC
scaffold741103_14.	1	p2	(AC)9	18	1641	1658	TTTCTGATGGGGTTGAGGAG
scaffold741105_18.	1	p2	(GA)6	12	3879	3890	CTGAATGCCTGTTGGTTCCT
scaffold741110_16.	1	p2	(TC)9	18	591	608	TCAGAAACCACTCCCTCACC
scaffold741121_12.	1	p2	(AT)8	16	1676	1691	GGGCAGCAACACCTTAAAAA
scaffold741122_13.	1	p2	(AC)7	14	1932	1945	CACATTTCCATTTCCATTGGT
scaffold741129_13.	1	p2	(AC)10	20	369	388	CACGCTTGCTAGACAACGAC
scaffold741138_15.	1	p2	(CT)8	16	419	434	AAGAGAGGTCAAAGCTGCCA
scaffold741154_15.	1	p2	(GA)10	20	3712	3731	GAAGAAGGAGAGGAGGCCAT
scaffold741157_12.	1	p2	(TA)12	24	2783	2806	ATGGCGGTAGGTAGTTGTCG
scaffold741167_15.	1	p2	(AT)8	16	1263	1278	AACCGAAGTGATTCGGGTTA
scaffold741185_15.	1	p2	(GT)7	14	2428	2441	TTTGCTGAGCATGTCATGTG
scaffold741196_17.	1	p2	(CT)7	14	5709	5722	GAGCAAAGAAGCCTCGAATG
scaffold741201_14.	1	p2	(AT)6	12	511	522	TGGATGATGTCTGGGACTTTC
scaffold741212_18.	1	p2	(AT)7	14	4661	4674	AGCTTCATCTCTGCGTCCAT
scaffold741213_16.	1	p2	(GA)7	14	339	352	CATCCAGGTCACCCTTTTGT

scaffold741223_14.	1	p2	(AG)6	12	2117	2128	AGGCCTCGATAAATCCGTCT
scaffold741235_17.	1	p2	(CA)11	22	1163	1184	CTCAGCAATTGCCAAAGACA
scaffold741258_13.	1	p2	(AT)9	18	1503	1520	TCCCATTCAGGCTTGAGGTA
scaffold741277_18.	1	p2	(CT)7	14	49	62	TTTAATCGGGATCCGGGC
scaffold741279_13.	1	p2	(TA)8	16	2305	2320	GGCTCCATGGAAATGACAGA
scaffold741294_16.	1	p2	(AG)9	18	2969	2986	AGCCTCCTCAAATGCAGAAA
scaffold741303_15.	1	p2	(CT)6	12	523	534	GTTGCTGTCACTGTGCCACT
scaffold741305_15.	1	p2	(AG)7	14	1621	1634	CATTGGTGTTCGGAATAGGG
scaffold741316_13.	1	p2	(AC)7	14	143	156	TCCGACCGGTTTTTAAATCA
scaffold741339_15.	1	p2	(GA)8	16	495	510	TCAACTAGTGCTGCGAATGC
scaffold741351_13.	1	p2	(AC)6	12	3829	3840	AACTTAGTGCCCCAGTCCCT
scaffold741354_14.	1	p2	(GA)10	20	708	727	AAGCAGCCTCACACAAGTCA
scaffold741356_17.	1	p2	(AG)6	12	189	200	CCAACGCATCCATATCATCA
scaffold741380_16.	1	p2	(TC)13	26	2454	2479	GAATCTGTTGCGTCGTCTGA
scaffold741383_16.	1	p2	(GC)6	12	270	281	AAGTGCACTCGCTACGACCT
scaffold741386_21.	1	p2	(TA)7	14	52	65	CACCACATTTAGTGGTTATCATTTG
scaffold741411_16.	1	p2	(CT)6	12	2345	2356	GGAGGAGAGATGGCATGGTA
scaffold741426_15.	1	p2	(TC)9	18	1220	1237	ATTGGTCTCTCAAGCACGGT
scaffold741443_15.	1	p2	(TC)6	12	632	643	AATGAAACGGAATCCAGTCG
scaffold741448_14.	1	p2	(AT)10	20	214	233	CTTTTGGCTATCTCGCTTCG
scaffold741459_17.	1	p2	(AT)9	18	464	481	TGCACTTGCAAATTTAAGCTG
scaffold741462_16.	1	p2	(AT)8	16	1229	1244	CAGAGAGAAAATCGGTGGGA
scaffold741472_16.	1	p2	(TG)6	12	134	145	ACGACTCCATGTTCCGACAC
scaffold741476_13.	1	p2	(GA)6	12	2346	2357	TGTTGGAGACCCTTCTTTGC
scaffold741477_14.	1	p2	(AT)7	14	71	84	CCAGACTTTTGGTCTCAATATATCC
scaffold741510_17.	1	p2	(CT)8	16	1239	1254	TGCGCTCTTGTTCTGATTTG
scaffold741512_16.	1	p2	(AG)6	12	959	970	TACCAACCGGTTCCCTTGTA
scaffold741518_16.	1	p2	(CT)6	12	1063	1074	GGAACTGCAAAATTCTGGGA
scaffold741532_13.	1	p2	(CT)8	16	2003	2018	TTGGGTCTTGAAGAAGACGG
scaffold741535_15.	1	p2	(CA)11	22	5578	5599	AAGCACACCACCTCTGCTCT
scaffold741555_15.	1	p2	(TC)11	22	2399	2420	GGATCTTCGAGGAGTGGTGA
scaffold741584_15.	1	p2	(AT)10	20	1249	1268	CTATGCAATGCCACCACAAC
scaffold741589_16.	1	p2	(TG)6	12	1258	1269	TGTCGGAGTTTTGTGAGCTG
scaffold741592_13.	1	p2	(CT)10	20	3778	3797	TCAATGATGTTGTGGGTGCT
scaffold741602_16.	1	p2	(GA)6	12	1875	1886	TGTGTTCAGACCGAGTCAGC
scaffold741671_15.	1	p2	(TC)11	22	631	652	TATGATGCTGGACAAGTCGG
scaffold741680_16.	1	p2	(GT)7	14	2974	2987	TTAAGCCTGTAATGGGGCAC
scaffold741683_15.	1	p2	(CA)11	22	9540	9561	TCTTTGATTTGGCTGCTTTG
scaffold741697_16.	1	p2	(AT)6	12	1445	1456	TCTGGGATTGGGCTTTATCA
scaffold741700_15.	1	p2	(CT)7	14	4196	4209	TGTTGGTGTGATGGTTTTGG
scaffold741701_14.	1	p2	(CA)7	14	660	673	AAGCAACAAATGGCAGCTTT
scaffold741706_16.	1	p2	(AG)7	14	3517	3530	TAAGCAACCGAAAAGATGCC
scaffold741716_16.	1	p2	(GA)7	14	1758	1771	TTGCAGCAAATGGATCTGTC
scaffold741720_14.	1	p2	(CT)8	16	2281	2296	TCTTCTGCCGTTGATGTCTG
scaffold741727_15.	1	p2	(CT)6	12	2677	2688	CAAAGAAACCGGAAGGTTGA
scaffold741733_15.	1	p2	(TC)6	12	1303	1314	AGCGAAAACTAGATGCCGAA
scaffold741738_13.	1	p2	(TC)8	16	887	902	CGATGTTTCTCGTCTCACCA
scaffold741759_11.	1	p2	(GA)6	12	2383	2394	TGCTTTGCCTAGGCCTATTAAG
scaffold741788_17.	1	p2	(CT)10	20	391	410	ATCTTGCCGCTGTTAAGGAA
scaffold741810_16.	1	p2	(AT)12	24	2652	2675	GTTTCCGGTCAATGATGTCC
scaffold741811_15.	1	p2	(CT)7	14	1322	1335	ACAATCTTGGTGGTTACGCC
scaffold741812_15.	1	p2	(CA)6	12	2882	2893	TCTGCTTGTCAAAGTCGCAC
scaffold741826_18.	1	p2	(TC)6	12	1330	1341	CAAACCCCGAGTCTGATGTT
scaffold741843_14.	1	p2	(TC)6	12	1491	1502	GACCCCTCAGCAGTGACAGT
scaffold741868_15.	1	p2	(GT)6	12	2298	2309	ATTGCTGAATGTTGATGGCA
scaffold741872_14.	1	p2	(TG)8	16	1118	1133	CCGATAAGAATGGATGTGGG
scaffold741875_17.	1	p2	(AT)7	14	4062	4075	AAACAAGGGCAAGCATATCG
scaffold741890_16.	1	p2	(TA)7	14	122	135	TCGTTAGAGGTTTTGACGGG

scaffold741899_22.	1	p2	(CA)6	12	3451	3462	TGGTGAATATAGAAGGGCGG
scaffold741903_16.	1	p2	(AG)6	12	4178	4189	AAGCGCCAAATGTAAAATCG
scaffold741910_14.	1	p2	(TA)6	12	116	127	CACACGCTGGAACTGCTTTA
scaffold741912_15.	1	p2	(AC)7	14	1873	1886	CCTCACAATTTCCCCCTTTT
scaffold741913_16.	1	p2	(AG)6	12	3485	3496	ATCGTCTCAATAGTTGCCCC
scaffold741920_17.	1	p2	(AT)6	12	2814	2825	ATAAAGTAGTAGGCCCGCCC
scaffold741926_14.	1	p2	(AC)6	12	3793	3804	ACAAGAAACGGTGAGAACCC
scaffold741941_19.	1	p2	(GT)8	16	1365	1380	CTGATGCAGATGCAGACAGT
scaffold741948_15.	1	p2	(AG)7	14	5572	5585	TTCGTGCTCTTGAACGTGAC
scaffold741958_18.	1	p2	(GA)8	16	719	734	AAATGAAGTTGGGCAGTTCG
scaffold741971_18.	1	p2	(AG)6	12	2330	2341	GGCATGCAATTTGTCAAGAA
scaffold741984_14.	1	p2	(AT)11	22	3995	4016	CCAAAGAGTGACGACCGAAT
scaffold742012_17.	1	p2	(GT)6	12	3487	3498	TCGTGTTCTCAGGATGTTGC
scaffold742020_16.	1	p2	(TC)6	12	63	74	GTGCAATGTGAGTGGACGTT
scaffold742021_15.	1	p2	(TA)7	14	2840	2853	GGTTCGAGTTTCGATGAGGA
scaffold742032_15.	1	p2	(GA)6	12	2682	2693	TCCGAACAAAATGCACAAAA
scaffold742035_17.	1	p2	(CT)6	12	3224	3235	CCAAGAAATCAAGGATCGGA
scaffold742061_16.	1	p2	(AC)9	18	4743	4760	GATGCCAAGGAACCTGTTGT
scaffold742070_16.	1	p2	(TA)9	18	1416	1433	ACAGGATCTGCAGGTGGAAC
scaffold742080_16.	1	p2	(AG)8	16	1429	1444	TGACTTTTGGGGTTTTCGAG
scaffold742085_15.	1	p2	(TA)7	14	777	790	TGTTTGTGGTTGAGTACGCC
scaffold742090_14.	1	p2	(TC)8	16	3293	3308	CTTCTGTTGAAACCCCGGTA
scaffold742133_15.	1	p2	(TA)6	12	2241	2252	TGTTCTTCAAATGGGATGTCA
scaffold742154_17.	1	p2	(TA)7	14	1465	1478	TGTGTTGCCAAAAACACGAA
scaffold742165_15.	1	p2	(AC)10	20	4075	4094	TGAGCTGGACGGACATTGTA
scaffold742174_14.	1	p2	(AG)7	14	2635	2648	CAAGGCGTTGGAAAAATGAT
scaffold742179_15.	1	p2	(TG)8	16	696	711	TTTTGCTTCCACTGCTTGAA
scaffold742192_14.	1	p2	(CT)11	22	1672	1693	TAGTACCATCGCCACCCTCT
scaffold742197_15.	1	p2	(GT)7	14	1513	1526	ATGGAGACTTATGGAGGGGG
scaffold742198_16.	1	p2	(GA)13	26	2640	2665	AGAGCGTTAGCTCTTTCGCC
scaffold742211_16.	1	p2	(AG)6	12	5152	5163	AACCTGTATTGGGACATCGC
scaffold742218_15.	1	p2	(AG)7	14	3402	3415	GTTTATCTTCGGCTTGCTGC
scaffold742221_17.	1	p2	(CT)7	14	2119	2132	TGCTCTTATTCATGGTCCCC
scaffold742223_13.	1	p2	(TA)6	12	1682	1693	TCAGTTTTCGAGTTATGAATTTGC
scaffold742236_16.	1	p2	(CT)6	12	2902	2913	AAGCAGCAATCTCTGCCATT
scaffold742248_16.	1	p2	(AC)6	12	587	598	GTGTGGATGTCCATCACTGC
scaffold742253_16.	1	p2	(TA)7	14	3250	3263	AAATCTGCATGCACCTGTTC
scaffold742279_15.	1	p2	(TG)7	14	856	869	TGTTCAAACTTTTGTGGGCA
scaffold742280_15.	1	p2	(GA)8	16	3022	3037	CACCACAGAAGAGGGAGAATG
scaffold742293_15.	1	p2	(CA)9	18	83	100	CTCGAACGGGATCTTGATGT
scaffold742300_16.	1	p2	(CA)7	14	1214	1227	AAGCAAACACCACAACACCA
scaffold742309_16.	1	p2	(CT)6	12	270	281	ATATATTGTGAGCCCTGGCG
scaffold742329_15.	1	p2	(AT)7	14	206	219	GCAGTGCTTCAAGAGGGAAC
scaffold742332_17.	1	p2	(TC)9	18	997	1014	TTCAATTTGCCTGTGGAAGA
scaffold742343_16.	1	p2	(AG)7	14	1193	1206	TCGCCTCTCAAGATTGTGAAT
scaffold742351_17.	1	p2	(CT)7	14	155	168	AACACGCACTCTTTCACACG
scaffold742357_16.	1	p2	(GA)6	12	819	830	GATGGTAATTGGGAACGGTG
scaffold742366_17.	1	p2	(AG)9	18	1945	1962	GAATAAACGGCGGTAATGGA
scaffold742411_17.	1	p2	(CT)6	12	211	222	CGTCATCGTATTGGCTTCCT
scaffold742422_15.	1	p2	(AT)6	12	2737	2748	CTTTTGGACCTCCCTTCCTC
scaffold742423_14.	1	p2	(AT)10	20	4316	4335	TCTCCTCCGTGGACGTAGAT
scaffold742424_17.	1	p2	(TA)6	12	167	178	GCTCTGATGCCAAACTGTTG
scaffold742447_14.	1	p2	(AG)7	14	1433	1446	GTGGCAAATGAGGAGATGGT
scaffold742451_15.	1	p2	(TC)9	18	2661	2678	CAATGAATGACCAGCCGTAA
scaffold742452_13.	1	p2	(TG)6	12	1347	1358	TGAGTTGTTCATTTCAGATGTTGTT
scaffold742455_15.	1	p2	(AT)9	18	1436	1453	CAGTTTTTGAGTTATGATGCTTTCA
scaffold742465_19.	1	p2	(GA)7	14	32	45	TCTCTCTCTAACACACAAACAGAGA
scaffold742467_17.	1	p2	(CT)6	12	813	824	AGCGACCAACAGGTAACGAT

scaffold742475_15.	1	p2	(TC)6	12	3959	3970	CATTTTGCTTTGCAGGAACA
scaffold742477_15.	1	p2	(TC)6	12	2147	2158	ACACTATTACGCCTGGCTGC
scaffold742494_14.	1	p2	(TC)8	16	2622	2637	AAGCTGATGCCATATCCTCG
scaffold742495_14.	1	p2	(AT)10	20	4171	4190	GGCTCGAACCCAAAATATCA
scaffold742517_15.	1	p2	(TA)6	12	5860	5871	CCGAATCCTTTCATAGAGCG
scaffold742539_17.	1	p2	(TC)6	12	6158	6169	CCGATCCCAATCTCTCCATA
scaffold742546_14.	1	p2	(AG)7	14	104	117	GTCCGTTGGTTTACCCAGAG
scaffold742556_16.	1	p2	(AT)6	12	624	635	CAAGGAAGGAGGAGTGGTTG
scaffold742557_14.	1	p2	(AT)10	20	1150	1169	GAGTGGGTATGAGGGGAACA
scaffold742558_15.	1	p2	(TC)12	24	2355	2378	AAAGGCAATCCCACCTTTCT
scaffold742560_15.	1	p2	(AT)7	14	2082	2095	CAAAGGTTCCAAGCCGTTTA
scaffold742566_16.	1	p2	(TA)10	20	46	65	GGGGTTATCATGGGATCAAG
scaffold742587_15.	1	p2	(CA)6	12	6974	6985	ACTTGCGTAGCATCATCCAA
scaffold742595_18.	1	p2	(CA)7	14	2364	2377	TCGATGCATACTTGTTGGGA
scaffold742597_15.	1	p2	(GA)9	18	1982	1999	TAAACCTGGAGGAATTGCCA
scaffold742625_14.	1	p2	(CT)8	16	1869	1884	TCGTCACGTGCGATTTTAAC
scaffold742629_14.	1	p2	(TA)6	12	1333	1344	CCCAGTTCGTCGAGAAAGTC
scaffold742640_17.	1	p2	(GA)6	12	542	553	CAGACCATCTGGGAACTAATCA
scaffold742651_16.	1	p2	(CT)9	18	902	919	TGGAGCGCAGGCTATAAGAT
scaffold742666_15.	1	p2	(CT)6	12	2880	2891	AACAGCACTGACTGGCTTCA
scaffold742690_16.	1	p2	(AG)12	24	1122	1145	GCAAGAACGAAGATTCCAGC
scaffold742699_15.	1	p2	(AT)8	16	759	774	TGCAATAAAAAGACCTTGCATTT
scaffold742709_16.	1	p2	(GA)9	18	1367	1384	TCTCTTCCACAATCACGCTG
scaffold742713_15.	1	p2	(AT)7	14	1855	1868	CCAGGAAGACTCATTCGATCC
scaffold742725_15.	1	p2	(TA)8	16	197	212	CTCACACCCACATCCATCAG
scaffold742727_16.	1	p2	(AT)7	14	1868	1881	ACCTATTGAAAGCCTCCCGT
scaffold742742_14.	1	p2	(TA)7	14	793	806	GACGGCTTTCTCAACACCTT
scaffold742753_14.	1	p2	(TC)10	20	2651	2670	AGCAGACTGGTTCCAAAAGC
scaffold742756_18.	1	p2	(CT)8	16	423	438	GGGGCTGCTTTCTCTTCTCT
scaffold742761_16.	1	p2	(AG)10	20	2999	3018	TACTGCAAATTCCGCCTCTT
scaffold742763_16.	1	p2	(TG)6	12	5372	5383	TGGGTCTCAGATTCTTGGTCA
scaffold742766_16.	1	p2	(AG)6	12	855	866	TATGCATCGCTCAGATTTCG
scaffold742776_16.	1	p2	(AG)8	16	730	745	GGTACTGGTGGAACTGCCAT
scaffold742777_17.	1	p2	(AT)9	18	9078	9095	AATGTTTCCTGCCACTCAAA
scaffold742780_15.	1	p2	(AG)6	12	8006	8017	CCATACAAGCAGTGGCAGAA
scaffold742781_15.	1	p2	(CT)7	14	1034	1047	GGAAACAAACTATCCCATTTGC
scaffold742797_15.	1	p2	(TA)6	12	519	530	ACCTCAGAAACCAGTGGTCG
scaffold742816_14.	1	p2	(TG)6	12	2611	2622	CTTCAGTACTTGGCCCACTTG
scaffold742848_15.	1	p2	(CT)8	16	2119	2134	CCATTTTCTTATCTCGCCCA
scaffold742852_16.	1	p2	(TG)6	12	1600	1611	TGCTGACAGGATTAATTGATGG
scaffold742877_16.	1	p2	(CT)9	18	441	458	GTTGAATCGATTGTACCGCC
scaffold742908_17.	1	p2	(CA)6	12	728	739	GGCCACATGCTCAATTACCT
scaffold742937_15.	1	p2	(TA)6	12	51	62	TGAAGTTAGGAAATAAGGAGGTGTT
scaffold742941_15.	1	p2	(TC)10	20	7420	7439	GATCCTTCCTCTCGTTATGGC
scaffold742946_14.	1	p2	(TG)7	14	2203	2216	TCGCGTAAACAACACGATCT
scaffold742952_18.	1	p2	(CT)6	12	319	330	TTATCGGCTGTACTCTCTCGC
scaffold742993_16.	1	p2	(AT)7	14	2079	2092	TCCTACAACTCCGGTTCCTG
scaffold742996_16.	1	p2	(AT)9	18	2273	2290	AAGATTTTTGTCCAGTCGGG
scaffold743002_16.	1	p2	(TC)8	16	312	327	ATCCCTCGCGCTCACTACTA
scaffold743011_17.	1	p2	(TC)9	18	297	314	TATGGGATTGGGTCTTTTGC
scaffold743032_16.	1	p2	(AG)6	12	4618	4629	ATTAAAGCACCTTTCGCGTG
scaffold743041_13.	1	p2	(AT)7	14	2380	2393	GGGGAAAAACCTTTCCAGAG
scaffold743047_16.	1	p2	(AG)8	16	181	196	CTGGTCCATTCAAACCTGCT
scaffold743049_14.	1	p2	(AT)6	12	4783	4794	CCGCATCTTCTAACGAGAGG
scaffold743051_16.	1	p2	(TC)8	16	3302	3317	AAGATGTCGCCGTCTCTCAC
scaffold743055_15.	1	p2	(TC)12	24	1462	1485	AGGCCCAAGACCTTACGAGT
scaffold743065_15.	1	p2	(AG)6	12	5227	5238	CTCGAGGAAGTAATCGCAGG
scaffold743066_15.	1	p2	(TA)11	22	93	114	TTTTCGAGTTATGAAGTTAGCACC

scaffold743076_15.	1	p2	(TA)8	16	350	365	CCCTCCCTTAAAATCGGAAA
scaffold743078_23.	1	p2	(TA)8	16	228	243	GCCAAGTTCACTAACCTTTTTCTC
scaffold743085_16.	1	p2	(AT)7	14	1049	1062	AACCAACATGCACAACCAAA
scaffold743101_16.	1	p2	(GA)6	12	2997	3008	GGGTTCCTGCGTCATAAAAA
scaffold743107_16.	1	p2	(GA)6	12	47	58	GGAGAGAGAGTGTTGGGTAGAGA
scaffold743132_15.	1	p2	(TA)7	14	2359	2372	ATATCAGAAAGCCACACGGC
scaffold743175_16.	1	p2	(AT)10	20	48	67	CGCCGGTGCCTATCATATT
scaffold743185_14.	1	p2	(AG)8	16	6900	6915	GAACACCTCTCCAGAGCCAG
scaffold743191_16.	1	p2	(CT)6	12	3218	3229	CAGCAAATACTCTGCACCGA
scaffold743198_16.	1	p2	(TC)6	12	1295	1306	TATTCCGAGTTTCATTCGGG
scaffold743205_16.	1	p2	(AT)10	20	2391	2410	GGAAATTGAAGCTGTTGCCT
scaffold743207_15.	1	p2	(TA)6	12	87	98	CAGATGCTCGAACAAGTCCA
scaffold743212_16.	1	p2	(AC)7	14	1887	1900	TTACGGATATGGCCGGTTTA
scaffold743221_14.	1	p2	(TC)7	14	1824	1837	TTTCATCGTCTGCAACAAGC
scaffold743224_14.	1	p2	(AT)6	12	2443	2454	GGTTTGTGGGACAAAAGGAA
scaffold743226_16.	1	p2	(GA)11	22	3727	3748	GATCAATGTCTTTGGGCGTT
scaffold743241_16.	1	p2	(GA)6	12	328	339	TTTTCCTAGAGAGGGAGGGG
scaffold743246_15.	1	p2	(GA)10	20	2160	2179	TCACTGTTTATCCCCCTTGC
scaffold743251_14.	1	p2	(AT)6	12	674	685	GGAGAAAGTTGATTTGTTGGGA
scaffold743261_16.	1	p2	(AT)6	12	1763	1774	TTGTTGCCTTCTGATGCTTG
scaffold812_14.6	1	p3	(ATT)5	15	903	917	GGCCAACCCATTTGACTTTA
scaffold1098_16.9	1	p3	(ATC)5	15	248	262	GGGTGGTATGGTGGAAGAAA
scaffold1208_14.5	1	p3	(CTC)5	15	689	703	CATTCACCACATGAGATGCC
scaffold1331_10.4	1	p3	(ACA)5	15	334	348	CCCTTTGAGAATAATGACATTGG
scaffold1455_15.6	1	p3	(ATT)5	15	316	330	CGAACCGGAATCGTAGTTGT
scaffold1511_11.7	1	p3	(ATG)5	15	193	207	GCGACATCCACATAACATGC
scaffold1599_16.9	1	p3	(ATT)7	21	721	741	CTATTTGGGAGTGGGTGGAA
scaffold1761_16.1	1	p3	(TCA)6	18	424	441	GCCTTCAAAAACCATGCAAC
scaffold1840_16.0	1	p3	(CCA)5	15	821	835	GGTGTTGATTCCAGCAGCTT
scaffold2512_10.9	1	p3	(TGA)8	24	235	258	CCCAAGACCCCAATTTGATT
scaffold2627_15.0	1	p3	(ATT)5	15	104	118	TCTTTCGTTGCCAGGGTAAA
scaffold2962_15.4	1	p3	(AAT)5	15	237	251	TTCCGTTACCCTCGACTTTG
scaffold3235_12.9	1	p3	(CGG)5	15	184	198	AGTTGCAGCAGCATTCCTCT
scaffold3590_15.1	1	p3	(TCT)8	24	1917	1940	TCTGATCAAAACTGCTTCGG
scaffold3649_15.8	1	p3	(CGG)6	18	622	639	AGACCCACAATTCCAACCAC
scaffold3663_17.9	1	p3	(ATG)5	15	103	117	TCGAGTAAGCGGAAATCAAGA
scaffold3668_15.3	1	p3	(CTA)5	15	1452	1466	TGCATCAATCTCATTTCCCA
scaffold4159_16.1	1	p3	(GAC)5	15	905	919	TAAAATGGAGAAAATGCGCC
scaffold4441_14.6	1	p3	(GAT)5	15	5068	5082	GCCATTACATGCAGGGTTCT
scaffold4575_14.6	1	p3	(TCA)6	18	726	743	GCTCATGTCAACGTTTTCTGG
scaffold5211_16.6	1	p3	(ATT)5	15	1169	1183	CTGATCCCATGTTTTCTGCAT
scaffold5479_13.8	1	p3	(TTA)5	15	486	500	TCCCTATAACCGATACACCG
scaffold5712_14.7	1	p3	(CCG)5	15	121	135	CTTTTTGTATGGGTCGCGTT
scaffold6097_16.9	1	p3	(ACA)5	15	591	605	TGGAAGTTATGGTCGCAACA
scaffold7149_14.2	1	p3	(TTC)5	15	428	442	ATCGGGTGGAGATTGTTACC
scaffold7235_13.8	1	p3	(CAC)5	15	135	149	ATCACCGGCAGCAGATTAAG
scaffold7350_12.3	1	p3	(ATT)5	15	178	192	ATAAAGTGGCGGAGCTAGGG
scaffold7927_17.0	1	p3	(GAT)5	15	3619	3633	AGAGGAAAATGGAAAGGCGT
scaffold7953_13.9	1	p3	(TTA)6	18	147	164	CCACAGCATTGACATTAGGG
scaffold8247_15.0	1	p3	(CCG)5	15	1548	1562	CTGAAATCCCATTCGCATCT
scaffold8307_13.8	1	p3	(TGT)5	15	46	60	ATGTAGCCGACCCCAATTTA
scaffold9587_14.7	1	p3	(TTA)5	15	525	539	CGTTTTATCTGCGGATTTCAA
scaffold9866_15.2	1	p3	(AAT)5	15	2561	2575	ACAAGTTCGAAACCTGGACC
scaffold9883_12.9	1	p3	(TGA)6	18	43	60	CCCAAGACCCCAATTTGATT
scaffold10562_15.0	1	p3	(AAC)8	24	1636	1659	AGTATGACGGCCATGGGTAA
scaffold10985_16.8	1	p3	(AAG)5	15	52	66	TCAATATCTTACAATATCACAATGGC
scaffold11170_10.4	1	p3	(AAT)7	21	211	231	TGTTCGGACTGAACTGGTGA
scaffold11593_14.0	1	p3	(ACA)5	15	138	152	CGAGGCTGAATTTATGGCAC

scaffold12446_16.1	1	p3	(CCA)5	15	4411	4425	AACATTCCGCCACAGATAGG
scaffold13512_13.6	1	p3	(AAT)5	15	131	145	GGATGATGGATTCGAGTGGA
scaffold14589_16.6	1	p3	(CCG)5	15	1974	1988	GATTTTGCGGCGTTTGTATT
scaffold14724_15.1	1	p3	(GAA)5	15	52	66	GCTTCTCACGATTCTTGGTGT
scaffold14863_12.8	1	p3	(ATC)7	21	223	243	TGCAACACTTGAGCTTATGGA
scaffold14883_16.8	1	p3	(ACA)7	21	1620	1640	TGTTCGGTGAATGTTTTGGA
scaffold14889_13.5	1	p3	(GGA)5	15	430	444	AGCAATGCGAGGATGAAGAT
scaffold14944_10.2	1	p3	(ATA)5	15	52	66	CTACCTCGCCTCGCTATTTG
scaffold15105_16.5	1	p3	(ATC)6	18	1106	1123	TTTATTAGAATGCCGGGGAA
scaffold15303_14.0	1	p3	(TTA)5	15	115	129	GAAAAAGATGGTAAAAACCTTCCA
scaffold15875_18.9	1	p3	(GCA)6	18	31	48	CAGCCAAACATTGAGCAGTT
scaffold15940_14.7	1	p3	(TTC)5	15	970	984	AATGCCTTATTTTCCCACCC
scaffold16359_14.2	1	p3	(AAT)6	18	315	332	CAGAGCGCACTCGAATAACA
scaffold16669_13.0	1	p3	(AAC)6	18	286	303	TTCGAACCTTCTGCAAAATATAA
scaffold16827_11.6	1	p3	(TAA)5	15	58	72	AAGAACATTTATGGCAAACAACA
scaffold16963_18.3	1	p3	(GTG)5	15	539	553	CTACCACTGCCGGAAAACAT
scaffold17092_16.0	1	p3	(ATA)5	15	5841	5855	TTGAAGAGAGGCAACGAGGT
scaffold17138_15.2	1	p3	(ACT)5	15	1688	1702	TCTAGCCCACAACTTGGCTT
scaffold17836_16.5	1	p3	(ATG)5	15	380	394	TCATTGAGCATGCTACGACC
scaffold18172_21.9	1	p3	(ATG)5	15	37	51	CCTGAAACGAGTGATGCTCC
scaffold19294_14.7	1	p3	(AAC)5	15	1911	1925	CCGAACCGGAAAAGTCACTA
scaffold19396_18.2	1	p3	(TTA)5	15	757	771	CCACCTACAGGTGCACAAGA
scaffold19406_16.1	1	p3	(CGG)5	15	1370	1384	TTGGCTATCGGTTACTTGGG
scaffold19923_16.4	1	p3	(ATA)5	15	12235	12249	ACCTTCTTGCAACCAACGTA
scaffold20611_15.9	1	p3	(ATA)5	15	2540	2554	ATCGAACCGTGAACACCCTA
scaffold20806_11.9	1	p3	(GAA)5	15	270	284	CTCCTGCTTCACCTCGATTC
scaffold21294_13.9	1	p3	(GAC)5	15	53	67	ACAAAAATCCAACAAACCCG
scaffold21378_21.3	1	p3	(TAA)6	18	751	768	TGTGATTTCATTCGCATGTTC
scaffold21743_14.8	1	p3	(TGT)7	21	1398	1418	TGTCTTCTATTCATCTGGCCG
scaffold21825_14.7	1	p3	(TAT)8	24	653	676	TTGTACTGTGTTGGCTTCATGTT
scaffold21902_15.6	1	p3	(GTT)5	15	53	67	TGGTTTTAATTGTGGGCTCTC
scaffold21940_12.3	1	p3	(AGA)5	15	53	67	TTTTTCACGGTTGGAAAGGA
scaffold22365_15.4	1	p3	(ATC)6	18	61	78	TCAATCACCAATCAACACTTGAA
scaffold22515_13.1	1	p3	(ATT)5	15	504	518	TGGTTGAAAACCAAGGTGATG
scaffold23725_14.0	1	p3	(TGT)6	18	41	58	CCAATTTATTGGGATTAAGGC
scaffold23989_13.8	1	p3	(TTA)5	15	526	540	CAGCAAAACAACTTCATGTACGA
scaffold24715_16.6	1	p3	(TCA)5	15	852	866	CAGGCACTCCAAAATCAGGT
scaffold24965_16.0	1	p3	(CTT)5	15	81	95	CGCCGTTAGCAAAGGAATTA
scaffold25050_11.6	1	p3	(TGT)5	15	47	61	TGTAGCCGACCCCAATTTAT
scaffold25213_12.5	1	p3	(GAT)5	15	118	132	TACAAATCAAGCACGCAAGC
scaffold25814_11.1	1	p3	(ATT)5	15	229	243	TGAATTGGGTTTGACAATCG
scaffold25849_12.3	1	p3	(TTC)5	15	114	128	GGCGATTGTCAACTTGGTTT
scaffold25865_17.8	1	p3	(ACC)7	21	1329	1349	TGTCTGAAATAGCTTGGCCC
scaffold25889_18.4	1	p3	(TTC)5	15	786	800	TCATCACTCCACCTGCTCAC
scaffold26004_13.0	1	p3	(CAT)6	18	868	885	CCACAAGTTATCACACCCCC
scaffold26245_16.2	1	p3	(TTA)6	18	327	344	TTTTACGTTGTACGAATCCTATCTTT
scaffold26323_10.2	1	p3	(AAT)5	15	70	84	ACATCGCATACGTGTATGTTTAAT
scaffold26655_15.0	1	p3	(ATG)6	18	1001	1018	ATCCCAAGATGACCATGAGC
scaffold26685_12.9	1	p3	(TAT)6	18	2097	2114	ACGTGGGACCTTTCAGTCAC
scaffold27208_17.2	1	p3	(ATA)5	15	227	241	AATGCTGGAAATTCGATTGG
scaffold27305_15.1	1	p3	(CAC)6	18	2093	2110	TCTCCATGATTCCATCGTCA
scaffold28279_12.8	1	p3	(TTC)5	15	189	203	ATTTCGGGTCAACCTTTGAA
scaffold28381_14.5	1	p3	(ATC)5	15	64	78	GTGATGCCATAACATCGTCG
scaffold28526_13.0	1	p3	(TTA)5	15	224	238	TTTAAAAATCGGACCGGAGA
scaffold28775_13.4	1	p3	(AAT)5	15	233	247	TCGTGCAATAAAACTCGTGC
scaffold29076_18.7	1	p3	(CAG)5	15	466	480	ACATGTTGAGTCCGAGTCCC
scaffold29092_12.0	1	p3	(ATT)5	15	150	164	TGAAGGACCCGTCATACAACT
scaffold30000_12.6	1	p3	(TAT)5	15	700	714	ATTTGGTGCTCAGTGGTTCC

scaffold30204_15.3	1	p3	(AGC)6	18	128	145	TACGGCCGGGTAAATTACAT
scaffold30252_15.9	1	p3	(GAG)5	15	2987	3001	ATGGCCAGAGGAAGTAAGCA
scaffold30258_11.0	1	p3	(AGA)5	15	435	449	GATTGTTGAAGGCCGACAGT
scaffold30697_15.9	1	p3	(TGT)5	15	75	89	CATGTAGCCGATCCCAATTT
scaffold30714_14.5	1	p3	(ATG)5	15	684	698	TGGCAACTCAAAAATGCTCA
scaffold30745_12.4	1	p3	(CCG)5	15	235	249	AATACCGATACCCACTCCCC
scaffold31031_15.0	1	p3	(CCA)5	15	1588	1602	CCAGCAGAACAAGAACACCA
scaffold31088_10.2	1	p3	(GTG)7	21	733	753	GGATTTGGGAATGGAACTTG
scaffold31311_10.3	1	p3	(GCT)5	15	329	343	CCCAGTTTTGGTCGTACTGG
scaffold31601_14.9	1	p3	(ATC)5	15	407	421	ACCGTCCACGTCAGTATTCC
scaffold31994_14.6	1	p3	(ATA)7	21	516	536	CTTGCTTCCTCGCTTGTCTC
scaffold32356_16.6	1	p3	(CAT)5	15	382	396	TGTTGAAAGAGCCTCCATCC
scaffold32738_15.2	1	p3	(ACA)6	18	431	448	TAGTGTAGGACCCCTCACGC
scaffold32880_15.8	1	p3	(TTA)5	15	1877	1891	TTACCAGGTGGCAACATTCA
scaffold32930_16.0	1	p3	(TTG)5	15	227	241	ACCCTACATAGCGGGGAAAG
scaffold33369_12.1	1	p3	(GGC)6	18	245	262	GAGGGGGAAAAGAGAGGATG
scaffold33812_16.0	1	p3	(GCG)5	15	711	725	CGTTACTTCCATTGACCGCT
scaffold33872_13.8	1	p3	(GGC)5	15	267	281	TCGACCCAAATAGAAGACCG
scaffold33961_10.0	1	p3	(TGA)5	15	450	464	TGTTGTGTATTGACCCCCAA
scaffold34135_16.6	1	p3	(ACA)6	18	1568	1585	GTGGTCCACTCTAATGCCGT
scaffold34209_16.6	1	p3	(TTC)5	15	330	344	GCTGAGTACCCCATCTTCCA
scaffold34421_12.0	1	p3	(AAT)5	15	701	715	TGGAGGAATAAAGGCTGGTG
scaffold34893_10.5	1	p3	(GGC)5	15	233	247	ATCTTCTTCTGGATGCGGTG
scaffold35049_10.4	1	p3	(TGG)6	18	160	177	AACATCCAAGTTATTCACGGA
scaffold35083_15.4	1	p3	(CAA)5	15	140	154	ATTCGCCGACAAGATAATGG
scaffold35166_18.5	1	p3	(GCA)5	15	1645	1659	GTAGACGCCAGCCAGTTAGG
scaffold35388_12.1	1	p3	(CAA)5	15	310	324	ATCAAACACGCCAATCATCA
scaffold35477_15.4	1	p3	(GAT)5	15	246	260	CGCAACCATTTCATTGTGAC
scaffold35574_12.5	1	p3	(AAT)6	18	398	415	AATGCGTAACCCTTGTTTGC
scaffold35645_15.1	1	p3	(TAT)5	15	2047	2061	GGGTTTGAATTTTGTGGCAT
scaffold35846_10.7	1	p3	(TTA)6	18	222	239	TTTGTGTCGATCAACTTGTGTG
scaffold36287_19.6	1	p3	(GCT)5	15	286	300	GCCAGAACCGAGAGCACTAC
scaffold36382_13.1	1	p3	(TAA)5	15	1342	1356	CATAAATGCCGAAATGGAGA
scaffold36497_17.3	1	p3	(GCT)5	15	433	447	CAATGACGAATAGCAGCCAA
scaffold36522_15.9	1	p3	(AAT)7	21	221	241	CCGGATATCCAGTTTCATCC
scaffold36721_15.0	1	p3	(ATC)5	15	928	942	CAGCGAATCAATACGTGCAT
scaffold36722_16.1	1	p3	(TCT)5	15	642	656	CGCCGAAGTCATTAGGTCTC
scaffold37851_14.3	1	p3	(GAT)5	15	115	129	ACGAGCAAGAGGATGAGGAA
scaffold37987_13.4	1	p3	(AAT)6	18	1384	1401	CTTTCGTTGATCGATTGGGT
scaffold38130_15.7	1	p3	(CAT)5	15	1739	1753	TAAGGTTGGCTGTAATGCCC
scaffold38136_13.2	1	p3	(TGA)5	15	111	125	CCCAAAACCCCAATTTGATT
scaffold38205_12.6	1	p3	(TAT)5	15	213	227	TTTTTCCACCACTTATTCTTTTGA
scaffold38441_21.3	1	p3	(TAA)5	15	159	173	TTCGAATGTTGCTGCTCAAG
scaffold38600_15.0	1	p3	(GGC)5	15	1119	1133	AGAAGAGGGAAAAGCCCAAG
scaffold39144_18.3	1	p3	(TGA)5	15	43	57	CCCAAGACCCCAATTTGATT
scaffold39186_10.0	1	p3	(ATC)6	18	89	106	TTTCATGGGTACACATTTGAGC
scaffold39431_14.6	1	p3	(GAA)5	15	195	209	GGGAAGGGGACAACATTTCT
scaffold39471_13.4	1	p3	(GTG)5	15	376	390	ATCCACTTTTCTGCTTTGGC
scaffold39673_14.5	1	p3	(ATT)5	15	190	204	TTGATCACACACGAGTCCATT
scaffold39682_16.5	1	p3	(TCA)5	15	495	509	CGTTGGTGAAGAACAACTTTGA
scaffold39754_13.6	1	p3	(TAT)5	15	710	724	GTTTGGAGGTCAGGTGTTCG
scaffold39984_17.0	1	p3	(AAT)6	18	471	488	ATGGCCTCCCACCTTCTATT
scaffold40059_13.1	1	p3	(TGT)7	21	50	70	TTTGGTTCATTTAGCCGACC
scaffold40407_12.7	1	p3	(ATA)5	15	386	400	TCTCTCTTGCCCAGCATCTT
scaffold40412_17.5	1	p3	(ATG)5	15	37	51	AGGAGGATGACGACGATGAT
scaffold40525_19.1	1	p3	(GAA)5	15	199	213	CCACCAATGACAGCAATCAG
scaffold40587_13.6	1	p3	(CGG)5	15	50	64	CCACCATCGTCGTCTCATC
scaffold40594_12.2	1	p3	(AAT)5	15	328	342	ACGTTTACGCTCTGCGATTT

scaffold40686_10.2	1	p3	(AGA)5	15	68	82	TCTACTTAGAGCAGGGCCGA
scaffold40769_15.6	1	p3	(TCG)5	15	563	577	TTTTGTTGTTTGCTGCTTCG
scaffold40883_17.9	1	p3	(CTT)5	15	2833	2847	TTCGAAGCTTGGAGAACGAT
scaffold41212_10.4	1	p3	(ATC)5	15	867	881	CAAAACCTTGGTGAACAGGC
scaffold41535_13.9	1	p3	(TGT)7	21	39	59	TGTAGCCGACCCCAATTTAT
scaffold41659_15.8	1	p3	(TCT)5	15	886	900	TGGGGGAGAAGTATGTGAGG
scaffold41863_14.8	1	p3	(GAA)5	15	605	619	CCGTCAAGCTCTATGCTTCC
scaffold43211_15.3	1	p3	(CCG)5	15	4494	4508	AATCACAAACAAATTCCGGC
scaffold43343_13.9	1	p3	(ATG)6	18	102	119	TGGCTCGAATTACAAAAACCA
scaffold43373_16.5	1	p3	(ATT)6	18	725	742	TGCACTGCTTATCAGATTCAAG
scaffold43915_17.7	1	p3	(GAT)5	15	329	343	AGTTGAAATGCTTGCATGGG
scaffold44026_10.4	1	p3	(CTC)5	15	452	466	TGCCTCAGACTCTTCCACCT
scaffold44112_12.7	1	p3	(CCT)5	15	303	317	GCTCCTCCACCTCTGTTCTG
scaffold44366_18.4	1	p3	(ACA)6	18	1943	1960	GGTTGTGTGCCATCATCAAG
scaffold44479_13.6	1	p3	(CTT)5	15	175	189	GGCACAAACTTGTGACTCCA
scaffold45283_16.6	1	p3	(TTA)5	15	188	202	TTCTCATCTCCAGTCTCCATGA
scaffold45418_17.1	1	p3	(CAA)7	21	3618	3638	AGAGGTTGGAGCAATGAGCA
scaffold45616_16.5	1	p3	(CCG)5	15	502	516	CAGTCGTCAGCCGTCACTTA
scaffold45710_12.2	1	p3	(CCA)5	15	204	218	CACCCCTATTCTTTTTGCCC
scaffold45763_16.7	1	p3	(CGC)5	15	295	309	AAGAAGATTTTTGCCACCCA
scaffold45971_10.9	1	p3	(AAT)5	15	107	121	TTCCATGACCCTCGACTTTG
scaffold46072_15.4	1	p3	(AAG)5	15	866	880	TGCTGTCTCTGGCTCTTTCTT
scaffold46129_10.0	1	p3	(TTA)6	18	49	66	TTGCCCACTCCACCACTT
scaffold46353_16.5	1	p3	(GCC)6	18	1115	1132	AATGCAGGTTGGAAAAGGTG
scaffold46716_15.8	1	p3	(CAA)6	18	2651	2668	GCTTTCGTTGCACATCTTGT
scaffold46869_13.9	1	p3	(ACA)6	18	64	81	CACATGTTGTCAAATAGATTCACTAG
scaffold46945_12.2	1	p3	(ATG)5	15	947	961	CAATCGGTCATGAGTTCGAG
scaffold47006_15.0	1	p3	(AGG)7	21	1884	1904	GCCCCAACTATTGGTGTTGT
scaffold47721_10.5	1	p3	(TGT)5	15	38	52	TGTAGCCGACCCCAATTTAT
scaffold47809_14.2	1	p3	(AAT)5	15	400	414	TCGGATTCTATTAGTGATTCAAGA
scaffold48162_11.6	1	p3	(CAT)6	18	368	385	TCAAAATCATCACTCTCCACTCA
scaffold48290_13.9	1	p3	(ATA)6	18	1993	2010	TGGCTCATTACACAAAAACG
scaffold48400_16.2	1	p3	(AAC)5	15	1566	1580	CCTTGCAGAAAAAGGCTTAGG
scaffold48497_12.7	1	p3	(TTA)5	15	265	279	TGGCAAGATTTGTTTTGACAGT
scaffold48597_10.9	1	p3	(CAA)5	15	98	112	ATTCAAGGCCAACAATCCAG
scaffold48673_14.0	1	p3	(CAT)5	15	1313	1327	TCACACATGGAGAACGAAGC
scaffold49007_14.1	1	p3	(AAT)8	24	100	123	TTGTGATGGAGTAGAGGGGC
scaffold49118_17.3	1	p3	(TAA)5	15	2258	2272	TCAGGCCTGTTTACACCCTT
scaffold49163_15.2	1	p3	(TGT)6	18	39	56	ATGTAGCCGACCCCAATTT
scaffold49196_10.8	1	p3	(CGC)6	18	336	353	TTTCCGATGTTCGATTTTCC
scaffold49741_14.8	1	p3	(CAT)5	15	361	375	CGTACATCCCCAAAGTCCTG
scaffold50181_15.0	1	p3	(CAG)5	15	2843	2857	TCAGCAGCAACTGATCCAAC
scaffold50200_13.6	1	p3	(TGA)5	15	140	154	GAGAATGTACCTTGGGTCGC
scaffold50278_12.6	1	p3	(TGA)5	15	45	59	CCCAAGACCCCAATTTGATT
scaffold50981_15.0	1	p3	(TGA)8	24	2952	2975	GACCCCAATTTGATTGGAAA
scaffold51188_16.8	1	p3	(TTA)5	15	884	898	TTGCTCGCAACGATGTTAAA
scaffold51276_12.6	1	p3	(CCG)5	15	287	301	ACGGCTGGCATTTGTTAGAG
scaffold51281_17.3	1	p3	(CAT)5	15	477	491	ACCATATGCAAACATGCGAA
scaffold51290_14.6	1	p3	(ATC)5	15	1537	1551	AAATTGGGGTTTTCCTCTGG
scaffold51751_17.2	1	p3	(ATA)5	15	2341	2355	TGCATGAAACTTTGTAAAACCA
scaffold52070_10.8	1	p3	(GAA)5	15	181	195	GATACCACGTCAAGCAACCC
scaffold52203_15.9	1	p3	(ATA)5	15	445	459	AGGATAAAAGAGGCAGGGGA
scaffold52548_14.9	1	p3	(AAC)6	18	895	912	TGTAGCACGAGTGATGAGGC
scaffold52992_10.3	1	p3	(CAG)5	15	175	189	CGATCATCCCTCATCTGACA
scaffold53144_11.2	1	p3	(ATA)5	15	86	100	CACTTTGACGCTGCTTGAAT
scaffold53154_11.3	1	p3	(TCT)6	18	142	159	CGGAGGTGATCTCAAATGGT
scaffold53238_14.3	1	p3	(CAT)5	15	90	104	CAAACCATGAATAAGCAATCCA
scaffold53460_11.3	1	p3	(TTA)5	15	73	87	TTTGCTTACGGAAACAGCAA

scaffold53553_14.5	1	p3	(CCA)7	21	350	370	TTTTCCCCCTCCTCTCATCT
scaffold53693_18.1	1	p3	(GGT)5	15	1617	1631	ATGTGTTTTCGGATGGAAGC
scaffold53828_18.4	1	p3	(GGA)6	18	1754	1771	TGCTGGTGATGCTCAAAGAC
scaffold54151_11.8	1	p3	(AGA)5	15	281	295	CCCAATTTTCCGCATTTTT
scaffold54459_15.7	1	p3	(ACA)5	15	63	77	ATGTCCTTGAAGATGCTGGC
scaffold55038_13.4	1	p3	(GCT)6	18	227	244	AAAGCATACGGGTGAAGTGG
scaffold55284_14.2	1	p3	(ACA)5	15	1537	1551	CATCTCGGGATTCAGTGGTT
scaffold56112_20.0	1	p3	(GGC)5	15	283	297	ATATTCTCGCTTCTTCGCCA
scaffold56324_11.3	1	p3	(CAT)5	15	135	149	ACGTCGCGACTCCTCTCTAA
scaffold56338_16.5	1	p3	(TGA)6	18	2306	2323	TGGAGATTCCGGAGTTCTTG
scaffold56544_15.7	1	p3	(TTG)6	18	1022	1039	TCTGAATGTGCTTTGATGGC
scaffold57252_11.8	1	p3	(GCA)5	15	45	59	TGGGCAGCCAAATATTGAGT
scaffold57542_17.4	1	p3	(AAT)7	21	776	796	TCGACTTTGTTTGGTTCGGT
scaffold57553_15.3	1	p3	(GAA)7	21	2973	2993	TGCTTGCATCCCATAAATCA
scaffold57632_17.5	1	p3	(AAT)9	27	8943	8969	TTTGTCTTTCCCTTTGATGCT
scaffold57850_15.4	1	p3	(TGT)6	18	39	56	TGTAGCCGACCCCAATTTAT
scaffold58069_16.9	1	p3	(AGC)5	15	1677	1691	CTTTCGGAGTCACAGAAGGC
scaffold58175_12.0	1	p3	(ATT)5	15	471	485	GAATGCGTCGGAAAAGTTGT
scaffold58274_12.4	1	p3	(TTG)8	24	387	410	TCCATATAGCCGACCTCACA
scaffold58279_12.6	1	p3	(AAC)8	24	577	600	CAAAATCGATCTGCAACCCT
scaffold58280_11.6	1	p3	(CAT)5	15	64	78	GCATTCGTATAAAGAAAATCGCA
scaffold58361_14.2	1	p3	(TGC)5	15	220	234	CGATCTCGTCGGGTATGAGT
scaffold58539_18.6	1	p3	(TTA)5	15	326	340	GCTTGTGATGTAGAGAAATGAAGG
scaffold58591_13.0	1	p3	(CGG)6	18	348	365	TGTCGAGGGTATAAGGGACG
scaffold58797_13.8	1	p3	(GAA)5	15	148	162	TTCGAAGGTGTTGATCCCAT
scaffold58906_16.6	1	p3	(ATG)5	15	940	954	GCACAAAATGTTGCTGCTCA
scaffold58938_14.2	1	p3	(CGG)5	15	190	204	CCAAGATTTCCGAAACCAAA
scaffold59137_11.2	1	p3	(AAG)5	15	242	256	GGTGAGTTTGAAGCATTGCATA
scaffold59182_16.1	1	p3	(GAT)6	18	2602	2619	GGCCCAAAGATCTCAAACAA
scaffold59514_16.8	1	p3	(CAT)5	15	1294	1308	ATTGTCTGCAAACCCGAAAG
scaffold59534_14.4	1	p3	(CGC)5	15	347	361	TCCTATCTATTCCGCGTGCT
scaffold60035_15.5	1	p3	(CAT)5	15	548	562	TCTCAAATATACGAAAAACGGTGA
scaffold60232_12.0	1	p3	(ATC)5	15	64	78	TCCAATTAATACAGTCAGCATTTCA
scaffold60240_11.2	1	p3	(TAT)7	21	281	301	AAGGAGCATCCTTGGTTGAA
scaffold60631_16.9	1	p3	(GTT)5	15	50	64	ACCCTTGAGCTTGCATCTGT
scaffold60646_12.1	1	p3	(GGC)6	18	53	70	GTCGGTGACGAGGTGGAGT
scaffold60981_14.0	1	p3	(AAT)5	15	466	480	TGGAACCATTGCAGTCAAGA
scaffold61087_15.5	1	p3	(TGT)5	15	50	64	TGTAGCCGACCCCAATTTAT
scaffold61124_16.7	1	p3	(TTA)5	15	506	520	TGTGTACGTAGTTGAGCATGTTG
scaffold61228_15.5	1	p3	(ATC)6	18	763	780	AATGTCACGAGTTGCAGCAG
scaffold61379_19.6	1	p3	(TAT)5	15	1347	1361	GGTGCAGGCTAAAAATGTTG
scaffold61507_14.5	1	p3	(TGT)6	18	43	60	ATGTAGCCGACCCCAATTTA
scaffold61600_13.1	1	p3	(TTA)5	15	365	379	CGATGGTTGATCTTGATTGTTG
scaffold61680_19.1	1	p3	(AAT)7	21	533	553	GATTAGCAAATTTCGGGACG
scaffold62820_11.9	1	p3	(TGG)5	15	77	91	TGATGGATCGAATATTCTCACG
scaffold63009_14.7	1	p3	(TTG)6	18	2035	2052	ACAATGTGGGAAAAATGGCT
scaffold63068_16.5	1	p3	(TTG)5	15	5738	5752	ACTTGAGCAGAATGGGCAAT
scaffold64028_10.5	1	p3	(GCT)5	15	452	466	TGGCAGTCCATTCATCTGTC
scaffold64138_10.5	1	p3	(TGA)5	15	134	148	AGCAGCCCCTCTTTTGAAAT
scaffold64143_10.8	1	p3	(AAT)5	15	369	383	GAATCTGATTTAAACATGGTGGC
scaffold64355_10.8	1	p3	(CAT)6	18	63	80	TCTTGTGAGACTGTTGTTCTGGA
scaffold64588_16.3	1	p3	(TGA)6	18	43	60	CCCAAGACCCCAATTTGATT
scaffold64589_19.3	1	p3	(TGA)6	18	43	60	CCCAAGACCCCAATTTGATT
scaffold64591_20.3	1	p3	(TGA)6	18	43	60	CCCAAGACCCCAATTTGATT
scaffold64626_10.4	1	p3	(TTA)5	15	508	522	GATGGATGAAAACCCACACC
scaffold65362_12.5	1	p3	(TGA)7	21	41	61	CCCAAGACCCCAATTTGATT
scaffold65612_11.4	1	p3	(TGT)6	18	268	285	ATGTAGCCGACCCCAATTTA
scaffold65679_14.7	1	p3	(ATC)7	21	64	84	ATGATCGGATTTTGTTGGAGA

scaffold65777_18.1	1	p3	(ATC)7	21	3098	3118	TTAAACTGGCACCCATCAAA
scaffold66407_13.4	1	p3	(ATT)5	15	1206	1220	TCTTCCCTCGTTTGTTCCAC
scaffold66509_18.6	1	p3	(CAT)5	15	63	77	TGCATAGAGGAAATTGCATAGC
scaffold66719_23.0	1	p3	(CGG)5	15	797	811	CCTATAATTGAAGCCGCCAA
scaffold66929_16.1	1	p3	(CGG)5	15	3451	3465	GGAGGAGATCGAGAGTGACG
scaffold67462_17.3	1	p3	(TCA)5	15	65	79	TTGCAAAAGTGATGTGACCG
scaffold67857_11.3	1	p3	(CAG)5	15	60	74	GGGCAGCCAAATATAGAGCA
scaffold67895_12.0	1	p3	(TGA)5	15	46	60	CCCAAGACCCCAATTTGATT
scaffold68015_14.7	1	p3	(CAT)8	24	1566	1589	CTCAACTTTCCAACTGATGGC
scaffold68071_10.9	1	p3	(GCT)5	15	101	115	AGCTGTGTCTCCAAACTCCC
scaffold68075_14.8	1	p3	(TTA)7	21	1683	1703	AGCTGAAGGAGAGGAGGAGG
scaffold68572_16.1	1	p3	(TGT)5	15	54	68	CAACGGTTTACAAGTGTTGTTG
scaffold68631_10.1	1	p3	(CGA)6	18	54	71	GCTTAAAGGTGGAGGATAGTGG
scaffold69004_15.2	1	p3	(TAT)6	18	288	305	CGTTTTTGTCAATGCGTCTG
scaffold69128_10.7	1	p3	(TGA)5	15	46	60	CCCAAGACCCCAATTTGATT
scaffold69200_12.3	1	p3	(GGT)6	18	192	209	CTCATCCCTCGCACATTTCT
scaffold69821_15.6	1	p3	(CAT)7	21	64	84	TGGGGTCTACAACAAACTGAA
scaffold69862_13.8	1	p3	(CAT)5	15	67	81	CATATCATAAAGATAAAGACAGCTTC
scaffold69961_17.0	1	p3	(TTC)5	15	66	80	CGAGCTGCATCGAGCTTT
scaffold71059_10.8	1	p3	(TGA)5	15	46	60	CCCAAGACCCCAATTTGATT
scaffold71060_10.8	1	p3	(ATC)5	15	64	78	TATCAACCCAGCAACCATCA
scaffold71063_15.5	1	p3	(TCA)5	15	65	79	CAATTAAGTTCTACGAATTCATTTTTG
scaffold71275_15.0	1	p3	(ACA)5	15	1996	2010	ATCTTTGCGGTGATTTCCTG
scaffold71474_17.2	1	p3	(GAG)5	15	344	358	ATTCGTTGATTTGGCTCCAG
scaffold72269_18.2	1	p3	(TAA)5	15	108	122	TGCAACACAATCATTATGGCT
scaffold72723_10.7	1	p3	(GCA)6	18	422	439	ATAACCCTCCCTCTGGTGCT
scaffold73439_14.3	1	p3	(ATC)6	18	270	287	GCTGAAATTTCGTCCCAAAA
scaffold74073_17.1	1	p3	(CTG)5	15	900	914	GAAATTTGGAAGTGCCTGGA
scaffold74105_15.8	1	p3	(TGG)5	15	1550	1564	TGATTTTGGATTTTAGGCGG
scaffold74279_12.2	1	p3	(AAT)6	18	64	81	AATGAATAAGTTTGCATTTAAGAGG
scaffold74361_15.0	1	p3	(AAG)5	15	471	485	GCTCGTGTCCAAATCAAACA
scaffold74425_15.8	1	p3	(CTT)6	18	5667	5684	GCAATGAACACTTAGCAGCG
scaffold74977_15.4	1	p3	(TAT)5	15	84	98	TCAGGTTTGACTTTCATTCTCG
scaffold75789_14.4	1	p3	(TTG)5	15	740	754	ACCGAAATTAACGTGGAGGA
scaffold76051_14.8	1	p3	(GTG)5	15	76	90	TCACAAACCGCTGTTGTTTC
scaffold76374_11.6	1	p3	(ATC)5	15	50	64	GCCCGAGGTTGAAGATGATA
scaffold76597_13.8	1	p3	(TCA)6	18	267	284	TGTGTTGTTTGATGTCTTTGTGA
scaffold76665_12.0	1	p3	(TTA)6	18	43	60	TTTCTTTTTCCTCAACAATTTCG
scaffold76679_16.1	1	p3	(CCG)5	15	1005	1019	TTTGGGAGTTCTCCTCCCTT
scaffold76719_18.3	1	p3	(CAT)5	15	668	682	TGTGTTTTCTTGCCCTTTCC
scaffold76983_10.2	1	p3	(TCA)5	15	65	79	TGAATATGCGGGAAGAAAGC
scaffold77149_15.6	1	p3	(GAG)5	15	1733	1747	CATGTCATGGCTGAGAGGAA
scaffold77206_15.4	1	p3	(GGC)5	15	1046	1060	TGCTGAGATGGAACTTGACG
scaffold77233_15.9	1	p3	(CCG)5	15	447	461	CACGATCACAATCAAGGTGG
scaffold77300_13.5	1	p3	(TAT)5	15	1123	1137	CCAGCCCAATAGAGGTGAAA
scaffold77510_13.1	1	p3	(TTG)8	24	1689	1712	TATGATCGTACACGATGGCG
scaffold77569_13.7	1	p3	(TCA)5	15	65	79	GCAACGAGGTGTGTGTTCAA
scaffold77653_17.0	1	p3	(CAT)5	15	859	873	TCAGAACCAGCACGAAATCA
scaffold77932_17.3	1	p3	(TGG)5	15	3344	3358	CGATTGTGGTGACGAAGATG
scaffold78015_15.9	1	p3	(TTG)8	24	526	549	ATCGTTGTGAATTTGGGGAA
scaffold78522_11.1	1	p3	(TCC)5	15	213	227	TTCGGTGCGGAGCTATTATC
scaffold78812_13.1	1	p3	(TCA)6	18	66	83	TTGGCATAACAAGCTAGGACAT
scaffold79180_11.5	1	p3	(TGT)6	18	39	56	TGTAGCCGACCCCAATTTAT
scaffold79857_16.9	1	p3	(TTC)7	21	2157	2177	CGGTGGTTTAATGGAGTTGC
scaffold79982_13.4	1	p3	(ATA)5	15	806	820	GGGCAAAAGCCAATGAAATA
scaffold80009_16.0	1	p3	(ATA)6	18	2316	2333	AACGAACGAAGCTGAGCAAT
scaffold80115_14.4	1	p3	(TGA)6	18	43	60	CCCAAGACCCCAATTTGATT
scaffold80122_12.0	1	p3	(TGT)6	18	43	60	ATGTAGCCGACCCCAATTTA

scaffold80398_11.9	1	p3	(ATA)5	15	789	803	ATGCAAAATTCGGCAGATTC
scaffold80612_12.6	1	p3	(ATC)5	15	63	77	AAATTTACTCGCTGGTCTATCTATG
scaffold80725_11.4	1	p3	(TCA)6	18	80	97	ACCTGAGGTTCAGGGTCCAT
scaffold81012_15.5	1	p3	(GCA)5	15	388	402	GATGAGATTCCCGAGGTTGA
scaffold81318_13.5	1	p3	(ATC)7	21	64	84	GAAATGCAAAGACCAAGAACAA
scaffold81500_14.8	1	p3	(ATA)6	18	694	711	TGTCAACCATAATATATGCATCGAG
scaffold81525_13.9	1	p3	(TGA)6	18	45	62	CCCAAGACCCCAATTTGATT
scaffold81673_17.5	1	p3	(TGA)5	15	810	824	CCCAAGACCCCAATTTGATT
scaffold82205_14.3	1	p3	(TCA)7	21	65	85	GCGAACACAGTTTTTCAGCC
scaffold82517_15.7	1	p3	(CAA)6	18	64	81	TCTTGAAATTTTCTTATTGTTCCC
scaffold83000_12.3	1	p3	(GAT)5	15	1632	1646	TTGTGTCAGACTTGTTCGGC
scaffold83214_11.7	1	p3	(CTT)7	21	716	736	CCCCCAAACTTATTGACAAATG
scaffold83533_12.6	1	p3	(AAG)5	15	504	518	GTCAGCGAATTGTTGCAGAA
scaffold84374_15.8	1	p3	(AAT)5	15	5001	5015	TTGCATTTTTCATAGCCCAA
scaffold84394_15.9	1	p3	(GCC)5	15	749	763	CCTCCTCAACCAGAGTCTCCT
scaffold84645_14.2	1	p3	(ATG)5	15	1977	1991	GTATTCCACCACGCTCCTTA
scaffold84849_15.6	1	p3	(TGA)6	18	46	63	CCCAAGACCCCAATTTGATT
scaffold85214_13.8	1	p3	(CTG)5	15	801	815	AAGAAGGGGGCAAAGTGAAT
scaffold85521_16.7	1	p3	(TGC)7	21	900	920	GAGAGCAAAGAGTTGGCACC
scaffold86132_14.8	1	p3	(TAT)6	18	32	49	GATGGATGGATCAGAACCGA
scaffold86415_16.5	1	p3	(TTA)5	15	2711	2725	CAATTCGTGTCATGGTCGAG
scaffold87418_11.4	1	p3	(TTA)6	18	149	166	CTTGCGGTCTTGAACATGAA
scaffold87509_10.0	1	p3	(TCT)5	15	653	667	GCAGATTCCCTTGATTTTGG
scaffold87966_14.5	1	p3	(ATT)5	15	45	59	CAGAATGATTGAAGCAAACATCA
scaffold88286_14.8	1	p3	(CAA)5	15	667	681	TGGGACGATAAGGGATAGTG
scaffold88293_17.4	1	p3	(ATA)5	15	178	192	TGAGATTTTTGGTGTCAGTGG
scaffold88414_12.5	1	p3	(AAT)6	18	239	256	CCCGGTTTGATCTGTGAACT
scaffold88416_10.0	1	p3	(AAG)5	15	134	148	CCGGTTAATGACCCATTTGT
scaffold88719_15.2	1	p3	(TAA)5	15	1512	1526	TGGAATTCAACATCAATGGTTC
scaffold88797_17.5	1	p3	(ACA)5	15	2315	2329	TCGAGATGTGAAGATTGAGGC
scaffold88946_12.6	1	p3	(CTT)5	15	223	237	ATACCTCGGCCTTTGATGTG
scaffold89061_15.8	1	p3	(TAA)5	15	1116	1130	TACGCAAAGGCACTTCTCAA
scaffold89296_12.3	1	p3	(CAG)5	15	44	58	GAAGTACCTGCCTACTCGTCTGA
scaffold89991_17.3	1	p3	(TAT)5	15	297	311	GAGGGAGGCACTAAGAAATGG
scaffold90266_13.4	1	p3	(AAG)6	18	259	276	TCAACAGTTACCCCGAAAGG
scaffold90337_18.2	1	p3	(GCC)7	21	1899	1919	CGCAATTCATCACAACTGCT
scaffold90348_15.7	1	p3	(GCT)5	15	2684	2698	CCCAGAAGCAGAAGAGGTTG
scaffold90729_12.5	1	p3	(TCT)5	15	415	429	CGAGATTGGGAAATTGGAGA
scaffold90829_16.4	1	p3	(TGT)5	15	45	59	ATGTAGCCGACCCCAATTTA
scaffold91432_12.8	1	p3	(CTT)5	15	237	251	CAGCCGAGAACATCATCAAA
scaffold91636_14.0	1	p3	(ATA)5	15	272	286	GGTGGATTAGTTGTCGTTTTGA
scaffold91781_19.5	1	p3	(GAT)6	18	35	52	TGTATATTCCTGAAGACGATGGC
scaffold91968_13.2	1	p3	(CAT)5	15	999	1013	GCATGCATAATGTGACACCC
scaffold92678_11.1	1	p3	(TAT)7	21	77	97	TGATGATTGAGTAAAAACGACAAAA
scaffold93016_16.3	1	p3	(CAT)5	15	3939	3953	ACACATGCACATTTCACGGT
scaffold93225_12.5	1	p3	(CAT)5	15	63	77	CCGTATCAAGCCACCAAGTA
scaffold93244_12.9	1	p3	(GAG)5	15	389	403	TCGAGGAAGGAGAGGTGTTG
scaffold93468_14.2	1	p3	(TGA)5	15	48	62	CCCAAGACCCCAATTTGATT
scaffold94449_14.9	1	p3	(AGA)8	24	734	757	TCTTTGCGATGAGCTCCTTT
scaffold94746_13.7	1	p3	(CCA)5	15	246	260	TTATCCCATCCCCCTTAACC
scaffold95065_16.0	1	p3	(CAT)7	21	64	84	ATAAACTGTTACTCCTGGGTGC
scaffold95204_17.6	1	p3	(ATT)6	18	2054	2071	CTGCCACCGATTTGAACATT
scaffold95447_11.1	1	p3	(TTA)5	15	411	425	GACGCTTGGTTGGATAGCTT
scaffold95703_14.2	1	p3	(AAG)5	15	3336	3350	CCGCCTCCGTAAATAAACAA
scaffold95841_15.2	1	p3	(TGT)5	15	203	217	GATTCGCTACCGTGTGGAGT
scaffold96180_15.5	1	p3	(TGA)5	15	56	70	CGGACAGAAGGATGGCTTTA
scaffold96335_17.1	1	p3	(TCA)5	15	65	79	TTGTTTTATTGTGTCTTTGTCATTGT
scaffold96336_14.1	1	p3	(TCA)5	15	65	79	CATAAACCACTTCGAACGGC

scaffold96721_13.6	1	p3	(TGT)7	21	42	62	ATGTAGCCGACCCCAATTTA
scaffold96772_13.9	1	p3	(TTA)5	15	483	497	GCTCGATGGAAAGCAGAAAA
scaffold96914_15.8	1	p3	(AAT)5	15	657	671	TGCCACAACTTAGAATCGCA
scaffold96984_13.8	1	p3	(TAA)5	15	398	412	TGATGTTAAGAAACATTAAAAAGGG
scaffold97121_10.4	1	p3	(AAT)7	21	367	387	GCCAAAAGATACTAAACTTCCAAA
scaffold98102_16.3	1	p3	(CAC)5	15	4818	4832	AATGGAAAAGCATGTCAGGG
scaffold98266_17.6	1	p3	(ATG)5	15	117	131	CCAATGTGCTGCTTATGAGG
scaffold98421_14.9	1	p3	(GGA)5	15	901	915	GAAAACGGAATCGAAGGTGA
scaffold98706_10.7	1	p3	(CGG)6	18	197	214	GAAGGATGAGCGAAATGAGG
scaffold98827_16.5	1	p3	(GCC)7	21	8105	8125	AGTGTGAAGGCCATGATTCC
scaffold98865_16.1	1	p3	(GGC)5	15	142	156	TTCAGCCCAGCCCAATAATA
scaffold99241_17.2	1	p3	(ATC)6	18	722	739	CTAGGGCTAGCAGCTCCAGA
scaffold99256_11.4	1	p3	(TAT)7	21	90	110	GGGCCGATCCTATCACTACA
scaffold99551_10.5	1	p3	(CAG)6	18	94	111	ATTCCCGAGACTGAGATGGA
scaffold99744_15.0	1	p3	(TTC)5	15	554	568	TCTGGTGGAGTTCATTGAGATG
scaffold99800_10.3	1	p3	(AGA)5	15	56	70	TTCTCTCTGTGCTGATCGAAA
scaffold100302_14.	1	p3	(GAT)5	15	4695	4709	GAAATGTAACAGCCTCCCCA
scaffold100451_13.	1	p3	(TGA)5	15	47	61	CCCAAGACCCCAATTTGATT
scaffold101371_19.	1	p3	(CGC)5	15	1428	1442	CTATAGGCACGCCGAACAAT
scaffold101828_15.	1	p3	(TGT)5	15	48	62	ATGTAGCCGACCCCAATTTA
scaffold102165_10.	1	p3	(CAT)5	15	65	79	CCCTTTAAGATAAAAATGAATATTGG
scaffold102526_13.	1	p3	(ATC)5	15	45	59	GCCCGAGGTTGAAGATGATA
scaffold102969_17.	1	p3	(ATC)5	15	1337	1351	CAATCCCAATTGTATCCGCT
scaffold103057_14.	1	p3	(ATC)5	15	60	74	CCAACTCATTTTGCCCACTAA
scaffold103106_16.	1	p3	(TAA)5	15	646	660	GATTAGCAAATTTCGGGACG
scaffold103110_12.	1	p3	(AAT)5	15	351	365	ATTTGGGAGTGTTCGGACTG
scaffold103198_13.	1	p3	(AAT)5	15	101	115	AAAAATCAGACCAAAACTTTTCAA
scaffold103594_16.	1	p3	(TAA)7	21	1150	1170	TGGAGCTAGTGAGGGTGGTT
scaffold103833_16.	1	p3	(CGG)7	21	595	615	CTGACCTCGTGTAACTGGCA
scaffold104959_14.	1	p3	(ATG)5	15	998	1012	TTCCATGGGTACAGAGGAGC
scaffold104971_16.	1	p3	(TTA)5	15	233	247	GGAAGATGAAAAGACAAGCGG
scaffold105270_11.	1	p3	(TCA)6	18	65	82	TGAAGAATTATGCATCAGGCAA
scaffold105354_13.	1	p3	(ACA)6	18	1165	1182	AGCAGCTACAACGGTAAGGC
scaffold105850_14.	1	p3	(CTG)6	18	1219	1236	CCAGCAGTGCACTCGTAAAA
scaffold106554_15.	1	p3	(GCG)5	15	1004	1018	TGGTTATGGAGGAGACGGAG
scaffold106916_15.	1	p3	(ATT)5	15	2700	2714	GAGTGGATAGGCTCCGTTTG
scaffold106951_12.	1	p3	(AGA)5	15	314	328	TCCCAAGCATGGAATCAAAT
scaffold107049_10.	1	p3	(ACC)6	18	178	195	ATTCACACCTGCTCCAGTCC
scaffold107966_14.	1	p3	(TAA)8	24	1475	1498	TGGGATCTATTTGATGAGGGA
scaffold108012_13.	1	p3	(CTT)5	15	577	591	TGGGTTGTTAAGCCTTGGTC
scaffold108125_14.	1	p3	(AAG)5	15	392	406	TTATTTCCGCATCTTTTGGG
scaffold108237_16.	1	p3	(ACA)5	15	3230	3244	ATTTGGCATCAACCTCCAGA
scaffold108252_16.	1	p3	(CGC)5	15	774	788	CTTGATCGGGTCCGACTTTA
scaffold108350_14.	1	p3	(GGA)5	15	2788	2802	CCTCCGGAACTCTCCTAACC
scaffold108594_15.	1	p3	(CCG)5	15	204	218	AAATTAAATAACCTCGCCGGA
scaffold108742_14.	1	p3	(AAT)5	15	1872	1886	GGCTCGCCAAGGTAGATAAA
scaffold108933_14.	1	p3	(TGC)5	15	634	648	GAAATGAAGCCAAACCCTCA
scaffold108955_19.	1	p3	(AAG)5	15	1052	1066	CGCACACTTGGAGTTGAAAA
scaffold109303_19.	1	p3	(AGC)5	15	49	63	TTGTGGAGAAAGGAATGGGA
scaffold110026_10.	1	p3	(ATC)5	15	82	96	CCATGTAAGAAAAGTGGAAGGG
scaffold110229_12.	1	p3	(GGC)5	15	207	221	CAAAATTAAAAATGCCCCCA
scaffold110992_16.	1	p3	(AAC)6	18	384	401	TGAAGGATGGGTAGAATCGG
scaffold111120_13.	1	p3	(TAG)7	21	870	890	CTCATTGAACTTGGCAAGCA
scaffold111374_15.	1	p3	(TCG)5	15	577	591	CATGAGGCTGCTGAACTCAC
scaffold112284_16.	1	p3	(TGT)6	18	42	59	TGTAGCCGACCCCAATTTAT
scaffold112656_14.	1	p3	(TAA)5	15	441	455	CGGGGTTCGAGTTCATATTG
scaffold113320_16.	1	p3	(GGC)5	15	790	804	TGCTGCCACACTCTCTCTGT
scaffold113395_12.	1	p3	(TCA)6	18	1028	1045	AACATCATCCCCATCACCAT

scaffold113495_13.	1	p3	(AAT)5	15	69	83	TGGTTGAGCTAAAATCTTTGAGAA
scaffold113771_14.	1	p3	(GAG)5	15	3007	3021	TGGTGGTTTTTGGATGATGA
scaffold114539_16.	1	p3	(ATA)5	15	498	512	TGCTAAACGATGAGCTTGGA
scaffold115034_17.	1	p3	(AAT)6	18	403	420	CGTCGTCGCTACATGAAGAA
scaffold115356_17.	1	p3	(GAG)5	15	1275	1289	GCCGTAGAGTAGATCGGTGG
scaffold115775_15.	1	p3	(TGA)5	15	47	61	CCCAAGACCCCAATTTGATT
scaffold116107_13.	1	p3	(CAA)8	24	2140	2163	CAAATGCGAAACCGATCTTT
scaffold117130_14.	1	p3	(ATT)5	15	1205	1219	CGTGGAGCCTATTTGGATGT
scaffold117230_15.	1	p3	(GAC)5	15	82	96	CAAAAACCCCGAATTCATTG
scaffold117330_15.	1	p3	(GAA)5	15	307	321	TATGCCCGTGAAAAAGAAGG
scaffold117477_15.	1	p3	(GGC)7	21	306	326	AAATGGAGTCGAAGCAGCAT
scaffold117583_15.	1	p3	(CAT)5	15	57	71	GGCGTCTCAAACGTATCTCC
scaffold117956_17.	1	p3	(GCA)5	15	1272	1286	TTTGAAGCAAAAGTTTGGGC
scaffold117988_16.	1	p3	(CAT)6	18	971	988	TGTGGCTGTTCATTCTTGGA
scaffold118044_10.	1	p3	(TGT)6	18	41	58	TGTAGCCGACCCCAATTTAT
scaffold118564_16.	1	p3	(GCG)5	15	399	413	GTGGTAGAGGCGGTTATGGA
scaffold118788_15.	1	p3	(ATA)5	15	673	687	TTTTCAATCATATAGAATCTGCTCTTG
scaffold120841_11.	1	p3	(ACA)5	15	434	448	AATATGAGAAGAGCAAACCCACA
scaffold121154_11.	1	p3	(AAT)6	18	121	138	TCAACGTGATTTGTCATTTGTG
scaffold121498_12.	1	p3	(GAG)6	18	265	282	TCATGGATTTAGACTGCCCC
scaffold122425_10.	1	p3	(AAT)5	15	382	396	TAAAGTGACCAGTTTGCCCC
scaffold122659_16.	1	p3	(GGC)5	15	2221	2235	TTTTGGGGGTTGAAATGGTA
scaffold122741_16.	1	p3	(CAC)5	15	379	393	TGAAACTCCCCACAATCTCC
scaffold122902_13.	1	p3	(TTA)7	21	895	915	ACACACGCATACACACACGA
scaffold122929_17.	1	p3	(ATC)5	15	2314	2328	TGTGTGAAACCTCCTTCATGG
scaffold123274_10.	1	p3	(AAT)6	18	561	578	TTGCCTCTAATTTTGGCTCC
scaffold123912_13.	1	p3	(GTG)5	15	49	63	TCTGGTCAACATCAATCTGAGC
scaffold124017_16.	1	p3	(TAA)5	15	615	629	CGTTGGCCAGTCGGTTAAT
scaffold124181_11.	1	p3	(ACA)6	18	479	496	AATTGCAAAAGCGCAAAAAT
scaffold124338_14.	1	p3	(CCG)5	15	301	315	ACCATTCATCCATAGCGGAG
scaffold124641_14.	1	p3	(CAA)6	18	66	83	TCCAGCCTTTACCTCTTTTTG
scaffold125218_15.	1	p3	(TGA)5	15	50	64	CCCAAGACCCCAATTTGATT
scaffold125899_14.	1	p3	(ATC)7	21	470	490	CCCAAGAATGACTGGGGTAA
scaffold126032_12.	1	p3	(ATT)7	21	224	244	CTCTATCACAACCCAAGGCG
scaffold126241_13.	1	p3	(TGT)9	27	38	64	TGTAGCCGACCCCAATTTAT
scaffold126926_15.	1	p3	(TAG)5	15	690	704	GGTTCGTCTTCAACCACGAT
scaffold126957_16.	1	p3	(ATT)6	18	318	335	TAGCAGGGCATGAACAAACA
scaffold127101_14.	1	p3	(ATA)7	21	1625	1645	GAATGGCATTTTAACTTTGATCATT
scaffold127442_12.	1	p3	(TGT)7	21	39	59	TGTAGCCGACCCCAATTTAT
scaffold128061_13.	1	p3	(TCT)5	15	113	127	CAGCCGAGAACATCATCAAA
scaffold128316_17.	1	p3	(TAT)5	15	672	686	GCATGAAACTTGGAATGGAAA
scaffold129273_17.	1	p3	(GGC)5	15	3353	3367	AGATTTGGCCGTGTACGAAG
scaffold129468_14.	1	p3	(TAA)5	15	3946	3960	ATAAAATGGGAGCGGAGAGG
scaffold129614_13.	1	p3	(AAG)5	15	174	188	ATGGCATGAAACGGAATAGC
scaffold129760_16.	1	p3	(CGC)5	15	509	523	GCCGGACATCTATACCAGGA
scaffold129887_17.	1	p3	(CAT)5	15	163	177	TCTTGGGTTCTACCTTGGACA
scaffold130032_17.	1	p3	(AAT)6	18	1954	1971	TCTTGTTGTCGCGTTTAATGA
scaffold130071_12.	1	p3	(CGG)5	15	533	547	TGCATGAAATCAAACTCCCA
scaffold130338_18.	1	p3	(CAT)5	15	67	81	AAAAACCAACTGAATTGCAAAA
scaffold130503_15.	1	p3	(AAT)6	18	189	206	CCGATTCGTGGAAACCTGTA
scaffold130545_13.	1	p3	(GAA)6	18	436	453	TTAAGACGGAAATCCACACG
scaffold130677_13.	1	p3	(TTA)6	18	203	220	GACAGGGGTCTCGCAAGATA
scaffold130768_10.	1	p3	(TTA)5	15	409	423	ATCGTATTCCACCGGATCAA
scaffold130853_17.	1	p3	(TTA)5	15	354	368	TGTTTGTTGTGTGTCTCCCA
scaffold130999_11.	1	p3	(GAA)5	15	195	209	TCAAAACTCGGTCTTGCACA
scaffold131057_13.	1	p3	(GAT)5	15	22	36	AGTCCGTGTTCCGATGAGT
scaffold131383_12.	1	p3	(TCA)6	18	257	274	CTTGTACCACTGGCCTCCAT
scaffold131514_12.	1	p3	(TAA)6	18	414	431	GCAACCTGAAAATTGAACATTG

scaffold131570_12.	1	p3	(CTT)5	15	156	170	CAGGTCAACTGAAATCTGAAAGAA
scaffold132139_13.	1	p3	(AAT)5	15	888	902	TCCATATTCCCTTCGTCGTC
scaffold132189_14.	1	p3	(TTC)5	15	632	646	ACGAGAACCCTCACATCACC
scaffold132972_18.	1	p3	(TGA)5	15	217	231	ATTGGTGCAAAATGTGTTGA
scaffold133008_14.	1	p3	(GAT)5	15	39	53	TACAGTCCGTGTTCCGATGA
scaffold133080_14.	1	p3	(CGC)5	15	347	361	TCCCACATAGGAAAAACAAAAA
scaffold134661_14.	1	p3	(ATA)6	18	562	579	CCTTGATCATTCCCGAAAAA
scaffold134875_18.	1	p3	(TTG)5	15	675	689	GTCTTGAATGCCACCCACTC
scaffold134996_16.	1	p3	(TTG)6	18	530	547	TGGTTCATATAACCGACCCC
scaffold135665_17.	1	p3	(ATC)5	15	2784	2798	TTCCCACTAATTTCACCTGGA
scaffold135855_15.	1	p3	(CAT)5	15	1712	1726	TACCTTGGGCTCCACCTCTA
scaffold135861_17.	1	p3	(TAA)5	15	2190	2204	TTGTGCATATTGTTGGGGAA
scaffold135922_14.	1	p3	(GAC)5	15	1258	1272	CGAGTGGCTGCTACCTGAAT
scaffold136436_12.	1	p3	(GCA)6	18	349	366	TTGATGAGCCATAACCCTCC
scaffold136732_16.	1	p3	(ATT)5	15	586	600	TCCTTGTCACAATCTGCTGC
scaffold137401_11.	1	p3	(ATT)8	24	1146	1169	TGGTTTGACCATCATTGCTC
scaffold137593_17.	1	p3	(ATG)5	15	477	491	TGGATGGGTGCACATAATTG
scaffold138160_12.	1	p3	(AAT)6	18	182	199	TTGGGCAACTTGAAGATTAAAA
scaffold138190_14.	1	p3	(CTT)6	18	110	127	CCCCCAAACTTATTGACAAATG
scaffold138293_12.	1	p3	(TTA)6	18	200	217	CGGGAGAGAAAATGCAGAAG
scaffold138380_17.	1	p3	(GCC)5	15	1092	1106	TGCAGCAGCCAAGACTTAGA
scaffold138473_16.	1	p3	(ATT)5	15	287	301	TCCAATCCATAGCAACCAAA
scaffold138946_12.	1	p3	(TAT)5	15	1049	1063	GTAACCATGGGCCAAAAATG
scaffold139070_14.	1	p3	(CAA)6	18	66	83	TCTGTCGACTGAAATGCAAA
scaffold139657_16.	1	p3	(CTC)5	15	725	739	CCAAATGTGATTGCCCTTTT
scaffold139767_14.	1	p3	(CTC)5	15	1633	1647	CAGTACGACCAGGGAAAAGC
scaffold140269_10.	1	p3	(TTA)6	18	248	265	CGTACGGAAATCTGATAGGAAAA
scaffold140486_16.	1	p3	(ATC)6	18	64	81	CCAAATTTGTAAATGCAAACAAAC
scaffold140839_13.	1	p3	(TGT)6	18	2223	2240	CCAATGGGTGAAAGAATATGG
scaffold140896_14.	1	p3	(TGT)6	18	47	64	TGTAGCCGACCCCAATTTAT
scaffold141213_10.	1	p3	(ATA)5	15	177	191	TACTCCCTCCGTCTCACTCC
scaffold141449_17.	1	p3	(CAG)5	15	1468	1482	CATTTGTGCCAGATCCATTG
scaffold142004_15.	1	p3	(ATT)5	15	6987	7001	CCCTGTTGAGCATACACCCT
scaffold142275_11.	1	p3	(AGA)5	15	103	117	TCAGTTCCGTCTAGGCTTCAA
scaffold142836_11.	1	p3	(AAT)5	15	172	186	ATCAGAGCCAGCGTTTGAGT
scaffold142847_17.	1	p3	(AAG)5	15	998	1012	AGGTCATGTGTTCGAGTTTCAA
scaffold142901_15.	1	p3	(ACA)5	15	549	563	TGTATTGAATCCGGTGGGTT
scaffold143093_12.	1	p3	(GCG)5	15	305	319	CCTTTTATACGGGTCGGGTT
scaffold143192_11.	1	p3	(TTA)5	15	609	623	CGGAGATTCGCAAGTTCAGT
scaffold143399_17.	1	p3	(CTT)5	15	110	124	CGTTGGCTCGACGTTATCTT
scaffold143454_13.	1	p3	(GAT)5	15	213	227	GGTGGCGGTAGTTTCAAAGA
scaffold143463_17.	1	p3	(GAT)7	21	1520	1540	GCAACGGAAACAACCTCTTT
scaffold143491_11.	1	p3	(TTC)5	15	180	194	CTGGCCTGATCTACAGCCTC
scaffold143500_10.	1	p3	(CCG)5	15	144	158	TCTGCTCAGCCCCTTCAG
scaffold143579_14.	1	p3	(TTG)6	18	357	374	GCTGTAGCTGACCCCAATTT
scaffold143952_14.	1	p3	(TTA)7	21	8338	8358	GATGCGTTTGAAGGGAAAAA
scaffold144015_15.	1	p3	(TGA)6	18	1162	1179	CCGAAGAGCATAGTTCAGCC
scaffold144406_13.	1	p3	(ACC)5	15	653	667	ATAAGGATTCCGGGTTTTCG
scaffold144410_11.	1	p3	(CGC)5	15	146	160	GGTTATTTATTAAAGTTGGAGGTGGA
scaffold144522_12.	1	p3	(ATT)5	15	37	51	AAAATTGCGTCTCCTATGGC
scaffold144670_17.	1	p3	(CAT)5	15	2538	2552	ACCTATGCATGTTGCCGTC
scaffold145156_10.	1	p3	(GGC)5	15	876	890	CACAACGGTCATCTGCTTTG
scaffold145660_15.	1	p3	(TTA)5	15	1313	1327	TCAGTCACAAGAGCACCCAC
scaffold146323_14.	1	p3	(TGA)5	15	91	105	TTTGATTGGGAATAATTGGG
scaffold146343_12.	1	p3	(ATT)7	21	230	250	CCCAACCCTAACCCGTTTAT
scaffold146883_14.	1	p3	(TCA)5	15	113	127	TCGCATCTGGGATAATGAAA
scaffold147220_16.	1	p3	(TGA)5	15	138	152	CAATTTGATTGGGAATATATTGGG
scaffold147347_15.	1	p3	(ATT)6	18	1108	1125	CCACACCCCTTTTGACTGAT

scaffold147453_17.	1	p3	(TTA)5	15	500	514	GGCATGTATTTATTATTGGACCAT
scaffold148028_17.	1	p3	(ACA)5	15	5993	6007	CCTCGTGCAAGCATTACAAA
scaffold148504_11.	1	p3	(TAA)6	18	311	328	TTCAAGGTTCTCGCTCTAATCC
scaffold148855_15.	1	p3	(TCT)5	15	148	162	GCATTATGTAAGCTCAAATAGGCT
scaffold148911_16.	1	p3	(TAA)6	18	133	150	CTCAAGATGCGAAGCAAACA
scaffold149734_15.	1	p3	(GTG)6	18	2399	2416	AAGTCACGAAGACGGCAAGT
scaffold150286_14.	1	p3	(TAT)5	15	59	73	TCGCTTTGATTATTAAATCTTCTTGA
scaffold150918_15.	1	p3	(AAG)5	15	526	540	GAAAGAAGCTCCCGAAGGAC
scaffold151048_15.	1	p3	(TGA)5	15	202	216	CCAAGACCCCATTTTGATTG
scaffold151259_17.	1	p3	(TCA)5	15	29	43	CACCGGTTGGACCGTCTT
scaffold152047_12.	1	p3	(ATG)5	15	39	53	TCCTGATGGAGGTGATGATG
scaffold153681_10.	1	p3	(CAA)5	15	224	238	ATGTGTTGGTTGCAGGTTCA
scaffold153738_14.	1	p3	(AGT)5	15	667	681	CAGTTGACACTTGGGGGACT
scaffold153827_13.	1	p3	(CGG)7	21	1343	1363	CCATGCTAATTTCAGGGGAA
scaffold154407_15.	1	p3	(GCA)5	15	161	175	CAGAGGATGAAATTCCCGAG
scaffold154628_14.	1	p3	(TCT)5	15	2125	2139	TGTGGAACCAACACGATTTT
scaffold154673_11.	1	p3	(CCT)5	15	115	129	GGGCTTCTTGTTGGAATTGA
scaffold154678_14.	1	p3	(AAG)5	15	678	692	CGGATCTTACGGAGTTGAGC
scaffold154855_11.	1	p3	(TCA)5	15	65	79	ATAGTGCAAAGTTGGTGCCC
scaffold155754_12.	1	p3	(CCG)5	15	450	464	CCCCAAGCTATTCTCCAACA
scaffold155810_11.	1	p3	(TAT)5	15	475	489	GTTTGGAGGTCAGGTGTTCG
scaffold155880_10.	1	p3	(AAT)5	15	263	277	CCTTGTGCAAATTAATCCCG
scaffold155986_16.	1	p3	(CGG)5	15	724	738	TAGGGAAAAGTCATCACGGC
scaffold156571_10.	1	p3	(GCT)5	15	191	205	TTGAATATCGGCGAAGTGCT
scaffold156646_16.	1	p3	(TGT)6	18	43	60	ATGTAGCCGACCCCAATTTA
scaffold157088_14.	1	p3	(ACA)6	18	2032	2049	ACATCCATCATCATCAGCCA
scaffold157281_14.	1	p3	(ATC)6	18	206	223	CTTCACATCAACACCCGATG
scaffold157353_16.	1	p3	(AAT)5	15	1340	1354	ATTATTGAATGGGCCCAAAA
scaffold157360_12.	1	p3	(CGC)5	15	65	79	TGGCTATCCTCAGCTGCTCT
scaffold157595_13.	1	p3	(GGC)5	15	6078	6092	TATATGTGGCCTTCTTCCCG
scaffold158421_16.	1	p3	(CTT)5	15	619	633	CACTGGACACACCTCTCCCT
scaffold158649_10.	1	p3	(GAT)5	15	435	449	CATTGGCAGCAGCAAAACTA
scaffold158758_18.	1	p3	(TAT)7	21	727	747	TAGCTCTGTTGCAGCCGATA
scaffold158879_10.	1	p3	(ATC)5	15	69	83	AAGCCAATTTTGGTGGGTTT
scaffold159071_14.	1	p3	(ACA)6	18	2584	2601	TCCAATCACTTACCAAATGCAC
scaffold159673_11.	1	p3	(CCG)6	18	45	62	AATTACCTTGCCGGAAATTG
scaffold160644_15.	1	p3	(TCA)5	15	2340	2354	CTTTCCCCAGCATCAACATT
scaffold161086_13.	1	p3	(CCA)5	15	961	975	AGAACTCGAGCTTGACCCAC
scaffold161700_15.	1	p3	(TCT)5	15	107	121	TCAGAAGGGGTTATGTCCTCA
scaffold161708_13.	1	p3	(ATC)6	18	65	82	CAAGTTCTTTCAAATTGGTGGA
scaffold161765_17.	1	p3	(CAG)5	15	1295	1309	CACATGGCTCAGACGACACT
scaffold162708_16.	1	p3	(TTG)6	18	135	152	GCCAACCCTCCTCCTTTATC
scaffold163455_20.	1	p3	(CAA)5	15	311	325	GGTACAACATCATGCCACCA
scaffold163819_16.	1	p3	(AGT)6	18	1929	1946	AACCTCTGCCGTGAAATCTG
scaffold163874_11.	1	p3	(TTG)6	18	64	81	TGACCCTAGTGGTAACACGG
scaffold164227_10.	1	p3	(CAA)5	15	39	53	CAGCCATGAATGAGAGTGGG
scaffold164578_11.	1	p3	(CCG)6	18	147	164	CTGTTCTCGCTTACCAAGCC
scaffold164722_10.	1	p3	(CCG)5	15	90	104	ATAAAACCTGCCGGAATCGT
scaffold165540_14.	1	p3	(TCT)5	15	1489	1503	TGGAGATCGGAAAATTGGAG
scaffold165855_16.	1	p3	(CTC)5	15	4658	4672	CCAAAATGGGGAGATGAGTG
scaffold165914_14.	1	p3	(ACC)5	15	503	517	GGGGGCCAAACAAATATACA
scaffold166272_17.	1	p3	(TCT)5	15	1435	1449	TGTACTTGTTCGTGTTGCCC
scaffold166432_16.	1	p3	(ATA)5	15	273	287	ATGGGTTCGAGTCTCAATGG
scaffold167500_17.	1	p3	(ATC)7	21	3474	3494	GCATTATGTCATGGTTCCCC
scaffold167676_16.	1	p3	(AAT)5	15	773	787	TGCAAATGAAAAAGGGGTAGA
scaffold168439_14.	1	p3	(CAA)5	15	370	384	TATGGTAGCTGGCTCGACCT
scaffold168792_15.	1	p3	(AAT)5	15	276	290	TCTCGCCAACTTCCTCTGAT
scaffold169730_12.	1	p3	(CCA)5	15	93	107	GCCCGAATTTTCCCTAACTC

scaffold169924_13.	1	p3	(ACA)6	18	424	441	GTGGGCACCCAACAAAATTA
scaffold170018_19.	1	p3	(ATC)5	15	136	150	CGTCGGGTAGACCAATGACT
scaffold170983_10.	1	p3	(CAA)5	15	170	184	AGAAATACATGCAGGGCTGAG
scaffold171005_15.	1	p3	(TGT)5	15	713	727	ACCAAGGGTGCGAGAATATG
scaffold171064_12.	1	p3	(CCG)6	18	312	329	TCCTCTTGGGTTGTTTCACC
scaffold171088_16.	1	p3	(TCA)6	18	174	191	AGAAAAAGAAGAGGGAGCGG
scaffold171367_19.	1	p3	(TCA)6	18	261	278	CTTGCCAATGCTCCACACTA
scaffold171500_15.	1	p3	(CAT)5	15	39	53	ATCATCATCATGTCCACCGA
scaffold171588_12.	1	p3	(GCG)5	15	575	589	AGGAGGAGGAAGAGGAGTGC
scaffold171913_16.	1	p3	(AGG)5	15	576	590	GCTTTGCAACACACATTTGG
scaffold172165_14.	1	p3	(GCC)6	18	734	751	ATAAATCGAACCTCCCCACC
scaffold172672_18.	1	p3	(CAA)5	15	657	671	TGCAGCAATTATGCAACCAT
scaffold173246_15.	1	p3	(TTA)5	15	582	596	AGTCAGAAAAGCCCACCTCA
scaffold173742_17.	1	p3	(TCA)5	15	169	183	TAAGGCCGTATTAACCGTCG
scaffold173758_14.	1	p3	(TCT)5	15	36	50	GCTACATCCAATGCTGGTGA
scaffold174008_14.	1	p3	(TAT)6	18	1008	1025	CCGATATTTTGGCCTTCGTA
scaffold174265_14.	1	p3	(AAC)6	18	1414	1431	AATGTCCCCATTGAGACTCG
scaffold174627_17.	1	p3	(CAA)6	18	634	651	CGATTTTGCCCAAGAATACC
scaffold174841_17.	1	p3	(GGC)5	15	3859	3873	ACCAACTTCACCGATCCAAG
scaffold175543_16.	1	p3	(AAC)7	21	7296	7316	GTTTGGTGGATCAAGCACCT
scaffold175822_13.	1	p3	(TCA)5	15	249	263	GGTGGTCGAGTTGGTTGAGT
scaffold177700_13.	1	p3	(CAT)6	18	778	795	TATTGTGGCACTCTCCCCTC
scaffold178448_16.	1	p3	(TGC)6	18	1070	1087	TGGAAGATGGAAGAGGATGG
scaffold178466_16.	1	p3	(TCA)6	18	367	384	CACCTCAGCCACCCTAGAAG
scaffold179974_16.	1	p3	(TTC)6	18	243	260	GATCGTGTTCGTGTCGTGTC
scaffold180284_13.	1	p3	(TGA)5	15	107	121	ATGAGTCGGTTTGTTGAGGC
scaffold180318_11.	1	p3	(CCA)5	15	282	296	GAAAGACCACGGCGATTTTA
scaffold180842_13.	1	p3	(ATA)5	15	306	320	ACAAATTCCCGTTCCATCAA
scaffold180990_11.	1	p3	(ATC)6	18	139	156	ACCTGTATTAGTACGGCGGC
scaffold181055_10.	1	p3	(ATT)6	18	590	607	ACATGCAAATCCATTACCCA
scaffold181231_14.	1	p3	(TGT)6	18	358	375	AACGTGGAGGACAGTGGTCT
scaffold181269_14.	1	p3	(ATT)5	15	229	243	ATTTCCCAACACTCACTCGC
scaffold181536_11.	1	p3	(TTA)5	15	58	72	CAGAAGATTCATATTGATTTTGAGG
scaffold181738_15.	1	p3	(ATT)6	18	834	851	AAGGCGGTGTATTATGTCGG
scaffold182831_16.	1	p3	(AAC)5	15	367	381	TGATCTCTCCCGTGAAAACAT
scaffold183025_18.	1	p3	(CAA)5	15	1014	1028	CCTTTTCGGGTGCTTTACAA
scaffold183197_18.	1	p3	(AGG)6	18	246	263	ATGCAGGATGAGGAGGAATG
scaffold183546_13.	1	p3	(TCA)5	15	116	130	TTTCCAACAATAACCCCGTG
scaffold183680_16.	1	p3	(AAG)5	15	36	50	CTCGCTGGATCCCTAGAAGC
scaffold184885_11.	1	p3	(ATT)6	18	38	55	TTGAAAACCGATTTCCCTT
scaffold184963_10.	1	p3	(TTC)5	15	284	298	TTCCAAGCATTTGATGCAAG
scaffold185898_16.	1	p3	(TTA)5	15	1209	1223	TGAGGTTCCAATTATATCCTTATGC
scaffold186381_11.	1	p3	(TTA)7	21	166	186	TGTGATTTGGATGATGTGTAAGC
scaffold186842_16.	1	p3	(AAC)6	18	3267	3284	TTTTTGAATGGCCGTTTACC
scaffold186906_10.	1	p3	(TAT)5	15	96	110	TTGTCAAGATTGGCTTCGTG
scaffold187133_12.	1	p3	(TAA)5	15	543	557	TCGGCTTTTGTTACATGCTTT
scaffold187166_15.	1	p3	(CAT)5	15	35	49	AAACATGCCCAACATTCAGC
scaffold187551_14.	1	p3	(AAT)6	18	932	949	CTTCCAAAATAGGGGGTTCC
scaffold187703_10.	1	p3	(AAT)6	18	37	54	TTTTGAATTAAATGGTGAGAAATGA
scaffold187795_14.	1	p3	(TTA)5	15	242	256	GGGTTTATGTGTTTATCACGTTG
scaffold188397_14.	1	p3	(AAT)7	21	734	754	CCGGTATCTTACTTTTGCCG
scaffold188707_14.	1	p3	(TAA)5	15	134	148	TCTCCCTACTCTTTCGTTGCTC
scaffold189167_15.	1	p3	(CGC)5	15	1236	1250	GCCAACTTTGCTTGCATTTT
scaffold189187_10.	1	p3	(TAA)5	15	343	357	AAATGTATCCGCCGTGATTG
scaffold189617_16.	1	p3	(TAT)6	18	91	108	TTTGAAGATCCGGAAATTTGT
scaffold190073_14.	1	p3	(GAA)5	15	34	48	GGATCGTAAAGCCTGGTGAA
scaffold190114_13.	1	p3	(AAT)6	18	222	239	GACGCCCAATGATCAAAAAT
scaffold190771_14.	1	p3	(AAG)5	15	50	64	ACAGTGGAGGAGCTCGCA

scaffold191178_12.	1	p3	(TAT)6	18	439	456	CTCGAACACGAGACCTCCAG
scaffold191414_12.	1	p3	(TAA)5	15	195	209	CGGACCAGACTCCAACTTTT
scaffold192041_13.	1	p3	(TTG)6	18	600	617	TATAGCCGACCCCACGTAGT
scaffold192964_15.	1	p3	(CAT)5	15	262	276	GGGCATCAAAACCTCCAGTA
scaffold193012_15.	1	p3	(TAA)6	18	102	119	CTTCATAGTACGCCACCCGT
scaffold194068_11.	1	p3	(ATC)5	15	67	81	TTCCTCAATTTTGGGACCAG
scaffold194374_13.	1	p3	(CTC)5	15	209	223	GATGTACGCACTTGGTGGTG
scaffold194512_14.	1	p3	(ATT)5	15	299	313	GGGGCGTGACAATATCAAAG
scaffold194558_12.	1	p3	(GAG)6	18	453	470	GTCGCCACAAGAACGAAAAT
scaffold194772_14.	1	p3	(ATT)5	15	1343	1357	GGATTCACGGATTGAGCCTA
scaffold195714_10.	1	p3	(CTT)6	18	378	395	AGGCCAACTGACATCTGGAA
scaffold195808_16.	1	p3	(TCT)5	15	3274	3288	TCGGAGGCGATTTACATAGG
scaffold196105_15.	1	p3	(GCA)5	15	3922	3936	GGGGTTTTGCTGCTACACAT
scaffold196261_14.	1	p3	(ATG)5	15	87	101	TTTCATGTGTGCTTATTGTTTTCA
scaffold196288_17.	1	p3	(ATG)5	15	94	108	TGCAATGGCTTTTCATTGTT
scaffold196384_11.	1	p3	(ATT)8	24	272	295	TCATTGTTGGAAATAGGGGC
scaffold196393_12.	1	p3	(AAT)7	21	662	682	TCACCACGCTCCCTAAGTGT
scaffold197059_15.	1	p3	(ATT)5	15	1201	1215	CGTGAAAATCCGATTAGGGA
scaffold197372_17.	1	p3	(GCG)5	15	1337	1351	CCAGCGAGTCTTCTGAGCTT
scaffold197513_15.	1	p3	(TGA)5	15	672	686	TTGTTCGCGATTTGCATTTA
scaffold197773_16.	1	p3	(CAT)5	15	67	81	CCCTGCTCAGTAGATTCCTTTG
scaffold198329_16.	1	p3	(TCA)6	18	2570	2587	GGCAAATTCGTCGTCAGACT
scaffold198789_10.	1	p3	(TAA)5	15	1018	1032	TGCTGTTGAGAATAGCGAGC
scaffold199206_17.	1	p3	(GGA)5	15	658	672	TTGGCCAAACTGATCAACAA
scaffold199703_10.	1	p3	(ATG)5	15	298	312	CCCGCTATCAATGTTCCACT
scaffold200363_15.	1	p3	(ATT)6	18	1396	1413	GTGTCTACGGCTGCCTCTTC
scaffold201027_11.	1	p3	(ACA)5	15	360	374	GGAGAGGATTGGATGGACAA
scaffold201126_15.	1	p3	(TCT)5	15	755	769	GACGTATGCCAAGCATTTCA
scaffold201387_15.	1	p3	(ATC)6	18	525	542	ATTGTGGAGTTGCCCATCA
scaffold202062_18.	1	p3	(ATG)5	15	1261	1275	GTGCATGCAGCTGAAGATGT
scaffold202174_12.	1	p3	(CGG)5	15	75	89	GGAGGTATACTTTGCTGCAGGT
scaffold202779_10.	1	p3	(CAT)5	15	46	60	TTCAGCAAAGAGTAGTTTCCCA
scaffold203553_11.	1	p3	(GGC)5	15	90	104	GTTCGGAGTTGGGTAGTTGC
scaffold204264_15.	1	p3	(TCA)8	24	2514	2537	AAGTTGTGGCCAGCAGAAAT
scaffold205423_15.	1	p3	(TAA)5	15	1539	1553	CGGTAATATGGTTGGATGGG
scaffold205615_10.	1	p3	(CGC)5	15	437	451	ACACCTCCTTCCATGCAAAC
scaffold205832_12.	1	p3	(CTT)6	18	211	228	GCCTTTGGTCTTGTCCGTAA
scaffold206820_15.	1	p3	(CCG)5	15	1728	1742	TTCTCCACCACCTCCTCCTA
scaffold207002_12.	1	p3	(TAA)5	15	322	336	GAAGCTGAGCAACGAGAAGG
scaffold207037_17.	1	p3	(ATT)5	15	1198	1212	AAGGTAGGTCTGCCCCTGTT
scaffold207385_12.	1	p3	(TTC)6	18	77	94	CGTCTCTCCCTATTCCCTCTC
scaffold207395_15.	1	p3	(ATC)5	15	419	433	TGGTTTTGGAGCATCATCAA
scaffold207641_10.	1	p3	(CGC)5	15	148	162	CCTCGCCTCTTACATCTGCT
scaffold208184_20.	1	p3	(ACA)5	15	1491	1505	TCTGTTGATCGACATCCCTG
scaffold209780_14.	1	p3	(TAT)5	15	779	793	CGAAAATGATCAGTGCAACG
scaffold210867_16.	1	p3	(AGA)5	15	2535	2549	AATCCCTTGGGAAATGAACC
scaffold211281_16.	1	p3	(AAT)5	15	232	246	TGGGTCTAAAGATGTTGCCTC
scaffold211472_13.	1	p3	(CAT)5	15	191	205	CACAAACCAAAGGTGCATGT
scaffold211884_15.	1	p3	(ACA)6	18	2487	2504	TACTTTAGCTGGCAGGCACC
scaffold211964_11.	1	p3	(GGC)5	15	58	72	ATTTTGAACGGTAACAGCCG
scaffold212278_16.	1	p3	(TTC)5	15	1713	1727	CGCAAACACAGAACAGCATT
scaffold212860_10.	1	p3	(TAT)8	24	275	298	TCAATGTTACGTTCAGGCCA
scaffold213189_14.	1	p3	(CAG)5	15	2261	2275	AGCATTGGCTTCAGCTGTTT
scaffold213237_14.	1	p3	(GAT)5	15	181	195	GAGAAAGTCAGTCCACGCCT
scaffold214027_10.	1	p3	(TAT)7	21	683	703	TGATGGGCCTCTTCATTTTC
scaffold214139_14.	1	p3	(TAT)6	18	510	527	CCCTACTCCCCCGTAAATTC
scaffold214306_12.	1	p3	(CAG)5	15	74	88	GGGCAGCCAAATATAGAGCA
scaffold214402_11.	1	p3	(ATT)5	15	855	869	CGGGAACAATAAATGCCAAG

scaffold214491_13.5	1	p3	(TTC)5	15	72	86	GGCCAAAACCGTGTAGTTTG
scaffold214746_11.4	1	p3	(ATA)5	15	436	450	ACTCCGTGTTCACCTTCTGC
scaffold215089_15.2	1	p3	(ATT)5	15	61	75	TGGAGTAATTGCATTACATTCGAG
scaffold215240_19.2	1	p3	(GCC)5	15	148	162	TGAACATTAAAGAATATCTACTCAGC
scaffold215520_11.4	1	p3	(TAA)5	15	183	197	GAATATTATGGCACCATGGGTA
scaffold215830_14.2	1	p3	(TTG)5	15	2314	2328	TAGCCGACCCCATTTTATTG
scaffold215960_12.5	1	p3	(GAT)5	15	206	220	CAAAACCATGGCATTTTTGA
scaffold215985_17.6	1	p3	(CGC)5	15	919	933	TATGGATTCACCTCCTTCGC
scaffold216198_17.0	1	p3	(ATT)5	15	1141	1155	CGTATCATTTGGTGAGCTTGAA
scaffold218216_15.0	1	p3	(ATT)6	18	872	889	TAGGCTTGATGGTTGTTGCC
scaffold218381_18.7	1	p3	(TTA)6	18	51	68	AATTGGGGTGTTGGAACTTG
scaffold218972_11.2	1	p3	(CCG)5	15	270	284	GAAAAAGGGAATAGGGCCAG
scaffold219240_12.7	1	p3	(AAT)5	15	51	65	GTACGCAATCATGCATCACC
scaffold219726_16.1	1	p3	(ACA)6	18	857	874	GGCGTGTGTTTGCCTTAGTT
scaffold220421_14.6	1	p3	(ATC)5	15	337	351	TTCTTGGTCTCCAAAGTCCG
scaffold221256_16.7	1	p3	(TAT)7	21	92	112	TTTGAAGATCCGGAAATTTGT
scaffold222115_10.9	1	p3	(TAT)6	18	230	247	TATTTTCCGGCGATTTTGAG
scaffold222377_10.8	1	p3	(TTA)5	15	321	335	GATTGAGATTGAGCCCGAAA
scaffold222464_11.2	1	p3	(CAA)5	15	358	372	TGGTCAATGAACCAAAGCAA
scaffold222611_10.2	1	p3	(TAT)6	18	180	197	GTAAGTAAGGCGGTGGCAGA
scaffold222940_12.0	1	p3	(CCT)5	15	103	117	CTTTCGATGCTCCTCTCGAC
scaffold222996_12.0	1	p3	(ATG)6	18	250	267	CTCCTGATGAACCCCACATC
scaffold223478_12.9	1	p3	(AAC)7	21	227	247	GCTCCAGAGCAAGATTCCAG
scaffold224095_10.5	1	p3	(TTC)7	21	37	57	CTTTGCCCTCTCTCCATCTG
scaffold224185_11.9	1	p3	(TGT)6	18	62	79	TTTGGTTCATGTAGCCGACC
scaffold224350_13.5	1	p3	(CCA)5	15	105	119	TGCAGAAGCATTATTCATCGTC
scaffold224356_15.3	1	p3	(TCT)5	15	258	272	CAGCCGAGAACATCATCAAA
scaffold224711_11.0	1	p3	(GCT)6	18	137	154	AGCAGCTAATCGCCTCTCTG
scaffold224875_16.2	1	p3	(TCT)5	15	377	391	TTTTCCAAATGCTCCAAAGG
scaffold224926_11.3	1	p3	(ACC)5	15	294	308	GGCTTAAACTCGATTGGCAC
scaffold227230_19.4	1	p3	(TCA)5	15	297	311	TTTCCCCAACCTCAACATTC
scaffold228260_13.1	1	p3	(GAA)5	15	150	164	GAGGATTCAGAGGAGGACCC
scaffold228855_17.2	1	p3	(GAA)5	15	335	349	TCAAATTGAATGGCTTGGTG
scaffold229187_14.0	1	p3	(TCT)5	15	101	115	TCAGAAGGGGTTATGTCCTCA
scaffold229472_14.5	1	p3	(CGT)5	15	223	237	GATCCCCTGCAAGTGTGACT
scaffold230308_15.9	1	p3	(TAT)6	18	861	878	GCATCTAAGGAACATGGATACTG
scaffold231319_11.7	1	p3	(CGG)5	15	116	130	CCGGAAGAAAGAGTGGGTTT
scaffold231826_17.3	1	p3	(TAA)6	18	41	58	CAATATAAGAACATTTATGGCAAACA
scaffold232245_16.8	1	p3	(ATT)5	15	246	260	TTGTGATTCGTTGTGTTTTGC
scaffold232891_16.7	1	p3	(CAT)5	15	661	675	TCCCAAACTTGAATCCTTCG
scaffold233919_13.7	1	p3	(AGC)6	18	767	784	ACATTCCCATTTGCAAGCTC
scaffold234028_13.0	1	p3	(CAA)5	15	429	443	TAACTGTGATCACGAAATGCG
scaffold234814_13.9	1	p3	(TTC)5	15	67	81	GATGCAGCAACTTCCTCTCC
scaffold235450_20.3	1	p3	(TTC)5	15	404	418	GGTTCTCCCTACTCCCCCTC
scaffold235518_10.4	1	p3	(AAG)5	15	199	213	GTGCCCACACTGCTCAACTA
scaffold235758_13.3	1	p3	(CAT)5	15	157	171	GGGAGCATCATCAACGTTCT
scaffold236079_10.7	1	p3	(TGT)6	18	47	64	ATGTAGCCGACCCCAATTTA
scaffold236162_16.5	1	p3	(CCG)5	15	659	673	AATCCGTACCAAATCCCTCC
scaffold236638_18.1	1	p3	(TTC)5	15	106	120	CTCGCTGACTTCAATCCACA
scaffold237160_12.0	1	p3	(TGT)5	15	134	148	TTGGCAATTTCTTGGAGGAG
scaffold237457_15.6	1	p3	(GGT)6	18	119	136	TTAACGTCAAATGCGAATGG
scaffold237867_13.3	1	p3	(CAC)7	21	103	123	CCGAAGTGCTAGACCCAAAG
scaffold238321_14.6	1	p3	(CTT)6	18	254	271	CCCCAAACTTATTGACAAACG
scaffold238467_11.6	1	p3	(TCA)5	15	172	186	GCAGTACTTGAACCTTCGCC
scaffold238544_16.6	1	p3	(ACC)5	15	93	107	CTAAAACTTGAAAACGCCGC
scaffold239061_10.7	1	p3	(TGA)5	15	281	295	AAATTTATTTTGAGCCGGGG
scaffold239487_16.3	1	p3	(ACA)5	15	317	331	ACGTTTTCTTGCCCACAAAC
scaffold240471_16.7	1	p3	(AAT)6	18	371	388	CAGAAAGGGGAACACTCGAA

scaffold240556_16.	1	p3	(TTA)6	18	1737	1754	CACTATGTGGACCATCAATCTCA
scaffold241245_17.	1	p3	(GAT)5	15	185	199	CTCGAGCGCACAAAACATT
scaffold241498_16.	1	p3	(CAA)5	15	3575	3589	GCAAAAGACAATGAAGGGGA
scaffold241682_10.	1	p3	(ATA)7	21	152	172	GTCCTTTGTGGAGCGATGTT
scaffold241953_16.	1	p3	(TCT)5	15	533	547	CGAACTAGCAAACCGGCTAC
scaffold241989_16.	1	p3	(TGC)5	15	544	558	ATACGGGTGAAGTGACCAGC
scaffold242060_14.	1	p3	(CCG)5	15	94	108	TCCCCTTTCTCTCTCTCTTCG
scaffold242167_15.	1	p3	(CAA)5	15	113	127	ACCACTCAAACCCACAAAGG
scaffold242495_15.	1	p3	(ATT)5	15	825	839	AGCCGCGCCTAAATAGTTTT
scaffold242545_16.	1	p3	(GCA)6	18	826	843	ACATTCCCAAGGCTGAGATG
scaffold244774_16.	1	p3	(TCT)5	15	276	290	TAATTCGCTGAAGCAGCAAC
scaffold245132_13.	1	p3	(AAT)5	15	455	469	TGCAGAAACCATGTATTTACTTTGA
scaffold245188_17.	1	p3	(GTG)5	15	562	576	TCCACTTTTCTGCTTTGGCT
scaffold245530_12.	1	p3	(CAG)5	15	50	64	CTGGGCAGCCAAACATAGAG
scaffold246144_14.	1	p3	(TTA)6	18	571	588	GAAAGCATTTAACCGCCAAA
scaffold246368_13.	1	p3	(TAA)5	15	1575	1589	GCACAGGTAGTGTTGCATGG
scaffold246939_15.	1	p3	(AAC)5	15	899	913	TCAAAGGGTTTGAATGGCTC
scaffold247019_12.	1	p3	(TTA)5	15	576	590	AGATCGAGCGATTTGTACGG
scaffold247375_12.	1	p3	(GAC)5	15	80	94	CAGAGAGGCACTATACAGTTCGG
scaffold248400_12.	1	p3	(ATC)7	21	47	67	TTTTAATTCCCCATATTACCAACA
scaffold249059_18.	1	p3	(TAT)5	15	481	495	AATGGGACAACTCATCCTCG
scaffold249220_10.	1	p3	(ATT)5	15	139	153	GATAGCCGTTGGTGGTTGAT
scaffold250518_14.	1	p3	(ACC)7	21	635	655	CGTCTCTTTTCCGTCGACTC
scaffold250584_18.	1	p3	(GTG)5	15	131	145	TCGGATCCACTTTTCTGCTT
scaffold250649_13.	1	p3	(CTC)5	15	361	375	GGAACCCCTTCAGGATTCTC
scaffold251316_16.	1	p3	(AAC)6	18	4158	4175	CGTTGGACAATCTGTAGCCA
scaffold252132_14.	1	p3	(TTA)5	15	95	109	TGCGGCTTCCATTTAGATTT
scaffold252319_12.	1	p3	(GCC)5	15	68	82	CTTCACTCGCCGGAAAAAT
scaffold253256_16.	1	p3	(CCG)5	15	197	211	CCAGATCTGCCAACGTTTTT
scaffold253263_10.	1	p3	(TAT)5	15	274	288	TTTTCTTTTCCTTTTATGCTCG
scaffold255159_16.	1	p3	(AAC)6	18	2397	2414	TATAAGGCAATTTGCGAGGC
scaffold256100_10.	1	p3	(AGA)5	15	110	124	TATCCTTCATCAGTTCCGCC
scaffold256515_14.	1	p3	(TCA)5	15	446	460	TTTGGGTCCTCCACAAGAAC
scaffold256590_14.	1	p3	(TCT)6	18	88	105	GTCTTCGGAAGCGATCTCAA
scaffold256830_12.	1	p3	(CCA)5	15	119	133	GTCATACCAGAGGAGCAGGC
scaffold259633_12.	1	p3	(TCA)6	18	1912	1929	CATCACGTCCCATTGTTCTG
scaffold259748_17.	1	p3	(TAT)5	15	444	458	CTGCGACAATTGCTCAAAAC
scaffold259833_15.	1	p3	(TTG)5	15	2497	2511	TGACCCACATAGTGGGAAAGA
scaffold260297_13.	1	p3	(GAA)6	18	73	90	GATGCAGATGAGGACGTGAA
scaffold260857_14.	1	p3	(GGC)5	15	477	491	TTCTTCGCTACGGCTACGAG
scaffold260910_16.	1	p3	(TAT)7	21	480	500	AAAGGTTGAGAACCATGATGA
scaffold261491_12.	1	p3	(TTA)6	18	942	959	ATGCCGTGATTGAAACACAA
scaffold262041_13.	1	p3	(GAA)5	15	431	445	GGCTCTGCAAGAATTTGAGC
scaffold262207_16.	1	p3	(CGC)5	15	49	63	CCCTCCTCCTTCTTGCTCTT
scaffold262507_17.	1	p3	(CAT)5	15	46	60	GAATCAAGTATCTGATCTGAGCCA
scaffold262904_10.	1	p3	(TCT)5	15	99	113	TGCTGCTGCTTTCTTCATTG
scaffold263023_17.	1	p3	(GGC)5	15	46	60	GAAAACAAAAGATAGATGGAGCAA
scaffold263605_17.	1	p3	(CTC)5	15	934	948	TTGCAGAATCCAACTGCAAG
scaffold263663_18.	1	p3	(CCG)5	15	216	230	ACGGTTATTGGGAAATGCAA
scaffold263979_16.	1	p3	(GAT)5	15	358	372	GATTGCGACCACCCTTACAT
scaffold264197_12.	1	p3	(TGT)6	18	485	502	TGCGATTAAGGCTTTGGTGT
scaffold264535_10.	1	p3	(GGC)5	15	418	432	GGCGAAAGTGTAGATCTGGC
scaffold265184_12.	1	p3	(GGC)5	15	317	331	GCCAGTCGTATCTAACCCGA
scaffold265537_18.	1	p3	(TTA)6	18	1112	1129	TGTTCATCGGTGAAGACCAA
scaffold266411_13.	1	p3	(GGC)5	15	198	212	TGTGTGATCCCTCAACAGGA
scaffold266886_17.	1	p3	(ATC)5	15	733	747	TTTCTGGAAATAGGGGGACC
scaffold266915_10.	1	p3	(TGT)6	18	51	68	GGTTCATGTAGACGACCCCA
scaffold266976_17.	1	p3	(GTG)6	18	837	854	CGATCTCGTTGTGTTTCGTG

scaffold266982_15.	1	p3	(ATA)5	15	960	974	CCTCTTCCTCGTACTCGGTG
scaffold267446_16.	1	p3	(TTG)5	15	1185	1199	TGGCTCCACAATTCATAGCA
scaffold267951_17.	1	p3	(TAT)6	18	1442	1459	TCGTAGTTTGTTGGCTCAAGG
scaffold268532_16.	1	p3	(ATC)5	15	150	164	GAACCTGTGGTAGTACGGCG
scaffold268972_16.	1	p3	(TTG)5	15	3261	3275	GCCATGCCTTCAGTTTTGAT
scaffold269307_15.	1	p3	(AAT)5	15	2142	2156	TTGCACGAACAAAATTCGAC
scaffold270782_11.	1	p3	(TTC)6	18	296	313	TCGAATCAAATCCATCAGGA
scaffold271156_13.	1	p3	(TAT)5	15	2199	2213	AGCATCAACTGCGGCTAACT
scaffold272205_15.	1	p3	(ATG)6	18	38	55	GATGATGATGCCACTCTTGG
scaffold273462_17.	1	p3	(TAA)5	15	460	474	GGATTGGGGCGTGATAAATA
scaffold273485_23.	1	p3	(TAA)5	15	1011	1025	ATGTTTTCGCGCCTTATTTG
scaffold273576_17.	1	p3	(GAA)5	15	327	341	AGCCGATTCTGAAGTTCCAA
scaffold273832_10.	1	p3	(GGT)5	15	657	671	AAATCTGCCCCAACACTCAC
scaffold274250_10.	1	p3	(GCA)5	15	168	182	CCGTGCTATGATGAGCCATA
scaffold275742_10.	1	p3	(ATA)6	18	394	411	ACACCCCGTATTTTCGAATG
scaffold275832_16.	1	p3	(TGA)5	15	3842	3856	GAGAGAGTTGTGCATTGGCA
scaffold276474_14.	1	p3	(TCA)7	21	1163	1183	GGCTTAATGGATCGTGTCGT
scaffold277111_17.	1	p3	(TAC)5	15	824	838	GATGTGGGCTTTTTCCGTTA
scaffold277585_14.	1	p3	(ACC)6	18	75	92	GCGACGACTCTCCGTCTATG
scaffold277947_14.	1	p3	(TCC)6	18	371	388	ATCTTGATCATGCAGCTCCC
scaffold278106_12.	1	p3	(TCT)5	15	266	280	TGGGTGGGTACCGATTAAAA
scaffold278683_16.	1	p3	(CCG)5	15	170	184	AAATTCAATTACCTGCCGGA
scaffold279140_13.	1	p3	(GCT)5	15	51	65	ATGACGTCGGCGGTGATT
scaffold279692_14.	1	p3	(ATT)5	15	386	400	CTAGTTTCATTGGAGGCGGA
scaffold279735_15.	1	p3	(CCG)6	18	1083	1100	CATCCTTTCAATGGCAATCC
scaffold279736_11.	1	p3	(TTA)7	21	859	879	GGTGGGAGTAGCCTCATCAT
scaffold280046_15.	1	p3	(GGC)5	15	49	63	GAGAACAAACAAAGAAGAGAAAAC
scaffold280177_11.	1	p3	(ATG)5	15	470	484	AACATGTTTTCAATCTTGACCG
scaffold280767_18.	1	p3	(TAT)5	15	660	674	TTGCACAGACATTATCGCATC
scaffold280832_16.	1	p3	(TAA)5	15	234	248	AAACCTCCACCAGAAATTAAAGA
scaffold281345_13.	1	p3	(TCC)6	18	301	318	TGCGTTAACGTACACAACTTCA
scaffold282108_10.	1	p3	(AAG)5	15	188	202	GGTCCCAAGTAAGGTCGGTT
scaffold282240_19.	1	p3	(CAG)5	15	111	125	GAGGACGAATCCTTTCCAGC
scaffold282444_14.	1	p3	(AAT)5	15	577	591	TTCCCTACCCCAAATTTTCC
scaffold282574_10.	1	p3	(AAT)5	15	212	226	GGCAAATAATTGATCGCCTT
scaffold282915_12.	1	p3	(AAT)5	15	113	127	GCATTTCAGGATATTAAAAACCAA
scaffold283481_15.	1	p3	(AAC)5	15	714	728	TCGTTCATGGCATATTCAGG
scaffold283870_13.	1	p3	(TGA)5	15	161	175	ACGCTATGTACCTTGGGTCG
scaffold283926_10.	1	p3	(TCT)5	15	219	233	CAAGGATCATGTCGCAGAAA
scaffold284069_12.	1	p3	(GAG)5	15	179	193	TCATGGATTTAGACAGCCCC
scaffold284440_17.	1	p3	(TTC)6	18	418	435	CGGGGAATTATATAAGTATGTCTTGA
scaffold284611_14.	1	p3	(CAC)5	15	82	96	ACGAGGGTGATGTTGGAGAG
scaffold285080_10.	1	p3	(ATT)6	18	292	309	TCAATGCTTTGCCTATGTTCA
scaffold286131_11.	1	p3	(ATC)6	18	37	54	TGTACCGGTATCATCCCCAC
scaffold286954_14.	1	p3	(CAA)5	15	206	220	TGCTCCAGTTTGTCGTGAAG
scaffold288377_15.	1	p3	(GAA)5	15	542	556	CAATTGGTTGACAAGACCCC
scaffold288502_17.	1	p3	(AGG)6	18	484	501	ACGATCATCCATCCATCCAT
scaffold288737_11.	1	p3	(TTC)5	15	673	687	TCAACGAATACCTGCTACCAA
scaffold289957_18.	1	p3	(TGT)5	15	528	542	TGACGGTGTACCAGAAGCAG
scaffold291053_17.	1	p3	(CGG)6	18	47	64	CCACCATCGTCGTCTCATC
scaffold292048_16.	1	p3	(AAT)5	15	1774	1788	TAGAAATGTCAGGGTTGGGG
scaffold292215_14.	1	p3	(TAT)5	15	1760	1774	ACGTGGGTTCCATTTTTGAG
scaffold292334_12.	1	p3	(ATG)6	18	114	131	GATGATGATGCCACTCTTGG
scaffold292844_13.	1	p3	(CAG)5	15	85	99	GTGGGGCAGCCAAATATAGA
scaffold293464_11.	1	p3	(TCA)6	18	79	96	GCGTCCGACTCCTCAACTAT
scaffold293507_15.	1	p3	(CTT)9	27	298	324	TTTGTTGGGAAGGTCGTAGC
scaffold293811_16.	1	p3	(ATT)5	15	239	253	CGTAGGCCTAGTTGGCTCTG
scaffold294318_10.	1	p3	(ATA)5	15	367	381	CATCGGTTAGTTCTCCCACC

scaffold294595_10.	1	p3	(CTT)5	15	114	128	ATGGTTGCCTTTGTTTGGAG
scaffold295174_10.	1	p3	(AAT)5	15	696	710	GCTCTAACGATGCCTTTTCG
scaffold296016_11.	1	p3	(TCT)5	15	101	115	ACACTCCACCAAGCCAACTC
scaffold296860_17.	1	p3	(TGA)8	24	431	454	GGGAAATCCAAGTCCCAACT
scaffold297356_17.	1	p3	(GAA)5	15	591	605	GAAGGTGTGTCGGAATTCGT
scaffold298144_15.	1	p3	(ATG)5	15	1133	1147	CCCCCAATACCCAAATTAGA
scaffold298858_13.	1	p3	(ATT)5	15	370	384	CAGTGTGGGTTTCGGTGTTT
scaffold299091_13.	1	p3	(CGG)7	21	1197	1217	ACACAAGTTATTGGCGAGGG
scaffold299353_16.	1	p3	(AAC)7	21	351	371	TCTCGAACCAAATTTCAGCC
scaffold299863_17.	1	p3	(CAT)5	15	747	761	AAGGAGGAAAAGAACCTGCC
scaffold300774_16.	1	p3	(TCA)5	15	750	764	CATGAGGGGAACTGGTTCAT
scaffold301696_13.	1	p3	(GAA)5	15	680	694	GGTTTTTGGTGGGAGGAAGT
scaffold301952_13.	1	p3	(TTA)5	15	277	291	CTCTATAGCCGCCTGCATTT
scaffold302025_16.	1	p3	(AAT)5	15	2557	2571	AACCCTCTTAGGGTGGCAAT
scaffold302455_13.	1	p3	(TGG)5	15	890	904	TGGAGTTGCATAAATTGTGG
scaffold302573_17.	1	p3	(GGC)5	15	123	137	ACAATGAATAAACGGGGCTG
scaffold302805_14.	1	p3	(CCG)5	15	1085	1099	AATATGGCAAAGGCTGCTGT
scaffold303551_12.	1	p3	(GAT)5	15	67	81	GCTAGGAAGGCTCTTGGGAT
scaffold303804_12.	1	p3	(TCT)5	15	40	54	GCAGCAACTTCCTCTCCTTC
scaffold304525_14.	1	p3	(CAT)5	15	268	282	ATCATCAATGTCTCCTGCCC
scaffold304604_14.	1	p3	(AAC)6	18	980	997	ATGACTGCAGGAGATTCGCT
scaffold306052_15.	1	p3	(TTC)5	15	2485	2499	CGAAAAATGGGATGCTGAGT
scaffold306230_19.	1	p3	(TAA)5	15	160	174	GAACTAACTGCTGCAAGGAAAAA
scaffold306253_18.	1	p3	(CTC)5	15	336	350	TGGGACAAGCTCTTGTGTTG
scaffold306528_11.	1	p3	(CCT)6	18	80	97	CTTCTCAGCCTCAGCCTCTG
scaffold306586_15.	1	p3	(TAA)5	15	415	429	TTGCTTTGGCTCACAGTACG
scaffold307222_10.	1	p3	(CTT)7	21	1220	1240	ATTTGCAGGAATTGGTGAGC
scaffold307589_16.	1	p3	(CGC)7	21	5006	5026	CGAGTTGCCTGACACTGAAA
scaffold307773_13.	1	p3	(AAG)5	15	166	180	CCGGGTTGAGACCTTTGTAA
scaffold308185_15.	1	p3	(TTA)5	15	71	85	GGGAGTGGGTTATCGGTTTT
scaffold308307_16.	1	p3	(ATT)5	15	32	46	GGAACTTGATTATGTATCTGATGATG
scaffold308739_10.	1	p3	(AAT)5	15	416	430	AGCCCACCTTATTGTTCGAG
scaffold309330_12.	1	p3	(GAG)6	18	335	352	CGCGAAGGTGACTGACATAG
scaffold309954_10.	1	p3	(TGA)5	15	86	100	CATCACGACGAGGAGCATTA
scaffold310146_11.	1	p3	(GCC)5	15	67	81	CCTTCCCTCTATTTCCGACC
scaffold311109_14.	1	p3	(AAG)5	15	72	86	TCCAAGGACTTGTCGGTTCT
scaffold313403_15.	1	p3	(AAG)5	15	482	496	GCTCGTTGCAAGCATATGAA
scaffold313707_16.	1	p3	(GGA)5	15	50	64	AGTTGGGAGTTGGGAGTCCT
scaffold314284_10.	1	p3	(ACA)5	15	494	508	GATCCATGTGTCCACGTGTC
scaffold314514_11.	1	p3	(ACC)6	18	180	197	CTCACTCTCTCCCTCCCTCC
scaffold314863_10.	1	p3	(GCA)5	15	52	66	CTTCAGCTTGGTTCTGGAGG
scaffold314882_16.	1	p3	(ACC)6	18	679	696	GGGTCCATCATTCCCTTTCT
scaffold315255_14.	1	p3	(AAC)7	21	408	428	TTTGCCAAGCTATCCAAAGG
scaffold316231_12.	1	p3	(AAT)5	15	379	393	GCTGGATCACTATTTGGTGG
scaffold317633_10.	1	p3	(TAT)5	15	512	526	ACCCGAACCGGAATACAAAT
scaffold317793_12.	1	p3	(TGA)5	15	245	259	ACGGCACCCACAATAAATTC
scaffold318316_15.	1	p3	(CAA)5	15	105	119	TACAACCTTCGATCCATCCC
scaffold318417_18.	1	p3	(GAA)6	18	29	46	TCCTTACTGAATTTGGGGTTG
scaffold318907_13.	1	p3	(GAA)5	15	232	246	CTCCTGCTTCACCTCGATTC
scaffold319802_11.	1	p3	(GGC)7	21	154	174	CAGAGGTTTTGGAGTTTCCG
scaffold321117_17.	1	p3	(CTT)5	15	239	253	TTCTCCTCCCTTGTGATTGG
scaffold321268_12.	1	p3	(GCG)5	15	181	195	GCGGAGGCAATAGACAGAAG
scaffold321664_11.	1	p3	(CTC)7	21	37	57	TCATCCTCGGAAGCAATCTC
scaffold321826_15.	1	p3	(TAA)5	15	932	946	AGTACCATTTCGGCCATTTG
scaffold322064_14.	1	p3	(CGT)5	15	45	59	CGTCGACCACCATCTTAACAC
scaffold322137_17.	1	p3	(GAG)5	15	156	170	CTTGACGGTGAAGAGGGTTG
scaffold323396_17.	1	p3	(TTA)5	15	101	115	TTTTCGTTTCTGGTTTCGCT
scaffold324512_18.	1	p3	(TCT)5	15	1196	1210	AGACCTCGAGTCGGAGATGA

scaffold324909_15.	1	p3	(CAA)5	15	2544	2558	CTCGGGGGTCAACACTACAT
scaffold325026_14.	1	p3	(AAT)5	15	2623	2637	AAACGAGGGCGAACTGTAGA
scaffold325899_16.	1	p3	(TGT)5	15	46	60	ATGTAGCCGACCCCAATTTA
scaffold325900_16.	1	p3	(ATC)5	15	5101	5115	TTTCCCTCCAAAGCCAGTAA
scaffold326079_12.	1	p3	(AAT)6	18	435	452	TGTTGCAATTCGTGTTAAATCTT
scaffold326219_13.	1	p3	(TGC)6	18	157	174	CGCCCAGTTCTGGTCATACT
scaffold326522_15.	1	p3	(CAC)5	15	568	582	TCACCAACATGCCCGTATAG
scaffold326671_11.	1	p3	(ATT)6	18	436	453	TTCCTCTCGATCCTCGTTACA
scaffold327243_14.	1	p3	(ATC)5	15	357	371	GGCTTGCATTTGAAAGTACAGA
scaffold327621_16.	1	p3	(GTT)5	15	366	380	CGATATGAACGAATGCGATG
scaffold327776_15.	1	p3	(ATC)5	15	22	36	ATTGCCACCATCCGAACA
scaffold328875_18.	1	p3	(CTT)5	15	1227	1241	CTTTGCTCGATCTATTCGGC
scaffold329574_14.	1	p3	(AGT)5	15	1063	1077	AGCTTCTTTCAATCGCCTCA
scaffold329965_11.	1	p3	(CGC)5	15	64	78	TTCAAAATTATACCTGCCGGA
scaffold330161_10.	1	p3	(CTG)5	15	67	81	ATAATTCCCGGCGTCATCAT
scaffold330313_15.	1	p3	(TAA)5	15	418	432	GTGTCCAGTCCGAGCAAAAT
scaffold330377_11.	1	p3	(TAA)7	21	752	772	ATTTTCCCATTGCACCAAAA
scaffold330386_13.	1	p3	(AGA)6	18	392	409	GGGGATCTTGGGAAGTGATT
scaffold330605_15.	1	p3	(TTA)6	18	3737	3754	CCCGTGGAGACGAGGTATTA
scaffold331266_15.	1	p3	(TTA)5	15	773	787	CGTGGTGCACTTGCATACTT
scaffold332699_15.	1	p3	(TGA)6	18	163	180	AGCAGATATGGGAGTGGTGG
scaffold333040_14.	1	p3	(GTT)5	15	269	283	GGTGGAGCAAGGTTTGTGTT
scaffold333453_12.	1	p3	(ACA)5	15	954	968	CGAGACTCATCCACTTGCAG
scaffold333557_20.	1	p3	(CAA)5	15	189	203	GTCAGACCAGCTCTCCTTCG
scaffold333877_12.	1	p3	(GAT)5	15	30	44	GAACAAAATAAAAATTTGGGAGGA
scaffold334955_15.	1	p3	(ATG)5	15	489	503	AAGGGGCACTGGTAAGGTCT
scaffold335564_13.	1	p3	(ATA)5	15	71	85	TTGCTTCCGTGTTTTATCCA
scaffold335872_18.	1	p3	(GTT)5	15	1313	1327	TCTAGACTGCGGGGTCAATC
scaffold336179_12.	1	p3	(CGG)6	18	776	793	AAGAAGAAGCTCCTCCCACC
scaffold336211_11.	1	p3	(GAG)5	15	93	107	GTTGGGGGTGACGTAGTCG
scaffold336425_15.	1	p3	(ATA)5	15	620	634	ATGTGTGTGGCCATTTTCAA
scaffold336918_13.	1	p3	(TAA)5	15	1272	1286	TGCGTCAGAAGATCCATTACA
scaffold337007_12.	1	p3	(TCT)5	15	114	128	GATGCAGCAACTTCCTCTCC
scaffold337462_15.	1	p3	(TAT)6	18	3218	3235	AAGACGTTCACCCACTGGAG
scaffold337500_11.	1	p3	(GTT)5	15	175	189	GGGAGAGTTCTCTGGGGAAG
scaffold337517_10.	1	p3	(ATA)5	15	314	328	CAGTTCAGCAGCGGAATTTT
scaffold337542_13.	1	p3	(TTA)5	15	390	404	CATGAAGTCCTTCCCCTTGA
scaffold338225_15.	1	p3	(CGT)5	15	3772	3786	GCGGAATAGCATTCACGTTT
scaffold339547_14.	1	p3	(AGC)5	15	835	849	AAACCATGCAATGAACACGA
scaffold339616_15.	1	p3	(AGA)5	15	2908	2922	GGCGACATCAAACACAACAA
scaffold340330_17.	1	p3	(TGA)5	15	1659	1673	GTCGCCAATTATTGATGCCT
scaffold340842_15.	1	p3	(TTA)5	15	853	867	ACAGGCCATTAGTTGGCAAT
scaffold340866_10.	1	p3	(GTT)5	15	286	300	TGGTTCCCTTCTTGTCCTTG
scaffold341209_10.	1	p3	(TGA)5	15	82	96	GCGGTTTCGATGGACATAAC
scaffold341636_15.	1	p3	(ATA)5	15	491	505	TCCATTTTTCTTCGTGCATTT
scaffold342387_10.	1	p3	(CTT)5	15	48	62	ATCGTTCTGCAGGAGCTTGA
scaffold343217_11.	1	p3	(CAG)6	18	153	170	CGATCATCCCACATCTGACA
scaffold343336_18.	1	p3	(AGC)5	15	263	277	AAACTGCTTCAAATGGACCG
scaffold344047_13.	1	p3	(TAA)5	15	242	256	TCTTCAAACTTTGTTCCGCA
scaffold345357_16.	1	p3	(TGA)5	15	109	123	GGTAAGGTTGCGTACATCCG
scaffold345620_15.	1	p3	(ACA)5	15	2464	2478	CGTGTGAAAATGAAATCGCA
scaffold346340_16.	1	p3	(ATC)5	15	1068	1082	TCCCCTTTCTCCACATTTCA
scaffold346586_18.	1	p3	(TCG)5	15	911	925	CGATCGAATGATCCCTGAGT
scaffold346770_14.	1	p3	(CAA)6	18	1327	1344	TATAGGTGCTGGGGCTAACG
scaffold346875_18.	1	p3	(TGA)5	15	1389	1403	TTCCACGAACCAACCAAAAT
scaffold347121_14.	1	p3	(AAC)5	15	450	464	TCCTCGCTCCTAACTTGCAT
scaffold347206_14.	1	p3	(TGA)5	15	1834	1848	AAACCGAGTGTTTTTGCCTG
scaffold347630_13.	1	p3	(TAT)5	15	258	272	TGTTTAAAGTCCATTCGGGC

scaffold348055_13.	1	p3	(GGT)5	15	785	799	AGGCAAAAATGGAGGTGTTG
scaffold348394_10.	1	p3	(CTT)5	15	33	47	AGGTGCACGTGACTCCAAC
scaffold348692_16.	1	p3	(ATG)5	15	567	581	CCCTCCCCCTCTCATATTTT
scaffold349508_13.	1	p3	(CTT)5	15	944	958	CATACCTCGGCCTTTGATGT
scaffold350182_20.	1	p3	(GAA)5	15	51	65	CATTGAAGAGCTCGCTGGAT
scaffold351426_14.	1	p3	(AAG)5	15	117	131	TGAGGTCGCTCACAGATGAC
scaffold352549_18.	1	p3	(ATT)5	15	1952	1966	ATTTGGGAAGGCCTTTGTTT
scaffold352687_13.	1	p3	(CCG)5	15	1944	1958	TAGTACTGCAGGCGAAGCG
scaffold352962_17.	1	p3	(CTT)5	15	108	122	CCTTTAGAACTTGCTCCACCA
scaffold354674_15.	1	p3	(ATT)6	18	281	298	GTTCGATTCTCCTTGGGGAT
scaffold354863_11.	1	p3	(GGC)5	15	177	191	CGATACTGGGCTTCTTCGAC
scaffold355579_12.	1	p3	(TTA)5	15	1307	1321	CCCCTTAGGGTTCCTCATGT
scaffold355825_18.	1	p3	(GAG)5	15	200	214	CGAAGTATGTGTCCGTGGTG
scaffold356260_12.	1	p3	(TTA)5	15	409	423	TGATGTCGAGCTGGATTGAG
scaffold357485_13.	1	p3	(GAA)5	15	49	63	GAGGTATTGGGGGATTTGAG
scaffold357571_13.	1	p3	(CGG)5	15	215	229	AAATCTCTCAATCTTGCGTCG
scaffold358333_13.	1	p3	(GAG)6	18	329	346	TAACTGAGCTGGCGGACTCT
scaffold358846_13.	1	p3	(TAT)5	15	198	212	GTCGTCGAGAGAAGCTCACC
scaffold359058_11.	1	p3	(GAG)5	15	47	61	GTTTAGACGTCACGCACAGC
scaffold360691_10.	1	p3	(GCT)5	15	112	126	CTGTGTCTCCAAGCTCCCAT
scaffold361262_15.	1	p3	(TTG)6	18	1178	1195	CATATGCTCCATACAGCCGA
scaffold361783_17.	1	p3	(CGG)5	15	28	42	GCGGCTCCTCCTATGTAAAA
scaffold361832_11.	1	p3	(AAT)5	15	819	833	GGTCCGATTGAGGAGATGAA
scaffold362263_13.	1	p3	(TGG)6	18	473	490	GGGGTTTTCTGAAATCGTGA
scaffold363199_13.	1	p3	(GGC)5	15	615	629	ACATCTTGGCCGTCGTAAAC
scaffold363512_11.	1	p3	(AAT)5	15	230	244	AAATTGTTCTTCGTGGACCG
scaffold363652_16.	1	p3	(CAT)5	15	705	719	CCCGCTTCGATATCATTTGT
scaffold363706_10.	1	p3	(TAT)6	18	734	751	GTGCGGGCTAAAAATGTTG
scaffold363984_15.	1	p3	(CCG)5	15	207	221	CGCTGCCTCTGTCAACAAT
scaffold364254_16.	1	p3	(ACG)5	15	736	750	CTGTATCGAACGAGCATCCA
scaffold364668_17.	1	p3	(ATT)5	15	151	165	CCAAATATTACAATAGCTCACAACAA
scaffold364863_15.	1	p3	(CAT)5	15	212	226	GTGAGAAAGTTTGCTTCGGG
scaffold365149_12.	1	p3	(ATC)5	15	88	102	TTTTAATACCCCATTTTACCAACA
scaffold365741_11.	1	p3	(CAC)5	15	117	131	CCGAAGTGCTAGACCCAAAG
scaffold365823_11.	1	p3	(TTC)5	15	236	250	GGAGTCACTCACGCTCTTGC
scaffold366054_12.	1	p3	(GAA)5	15	189	203	TCAGCATGCAATACCAAACAA
scaffold366156_11.	1	p3	(TCA)6	18	85	102	AGCTCCCTTCCTCATCATCA
scaffold367038_10.	1	p3	(TAT)5	15	209	223	TCCATACTTGGCATCGGTTT
scaffold367064_15.	1	p3	(TGT)6	18	44	61	TGTAGCCGACCCCAATTTAT
scaffold367414_15.	1	p3	(TTA)5	15	33	47	TTTTCTTAAGTTGTGATTTGTCCA
scaffold367531_14.	1	p3	(TTA)7	21	1214	1234	TTTGTCATATGCGAACAGCA
scaffold367865_12.	1	p3	(AGA)5	15	199	213	TTGAGCTGCACTTGTTTTGTC
scaffold368139_15.	1	p3	(ATG)6	18	928	945	ACGTACCCCAGCACTACTCG
scaffold368384_13.	1	p3	(ATT)6	18	718	735	GATGGGACCCACACAATTTC
scaffold368453_15.	1	p3	(ATT)5	15	1541	1555	TCTCCTTTTCCTCCACAAATTC
scaffold369065_12.	1	p3	(TCC)5	15	89	103	ATCAGGCACATCACCATCAA
scaffold369933_14.	1	p3	(AAT)5	15	188	202	TTTATTCCGTGACCCTCGAC
scaffold370153_21.	1	p3	(TAT)5	15	797	811	TGAAAGTAATGCCCATGGAA
scaffold370868_13.	1	p3	(GTG)5	15	721	735	GCGATGGGAAGTGCATATTT
scaffold371046_14.	1	p3	(CTT)5	15	311	325	GGTTAATACCGCTGATGGCA
scaffold371152_16.	1	p3	(ATT)5	15	111	125	CACGTGCATTAATTATTGTTTTCA
scaffold371327_14.	1	p3	(AGA)5	15	72	86	TAGCAGGCCAAAGAGGAAGA
scaffold371613_15.	1	p3	(TTA)5	15	604	618	TCTCCCAAGTTCAATCCATGT
scaffold372311_16.	1	p3	(TTG)5	15	1738	1752	TTTCCTCTCTGAGCCTTCCA
scaffold372498_14.	1	p3	(TTA)5	15	884	898	ATGCCTTATATGCCGGACAC
scaffold373173_10.	1	p3	(TCT)5	15	184	198	CATTCTCTAAATGGTTTCCATTCC
scaffold374074_16.	1	p3	(GAT)7	21	1138	1158	GATCTCGATCGTGACCCAAT
scaffold374595_10.	1	p3	(GGA)5	15	305	319	GGGAGTTTCGTTTGAGCAAG

scaffold374606_11.5	1	p3	(AAT)5	15	252	266	ATAAATTGGGGTCGGCTACA
scaffold375106_16.7	1	p3	(AAG)5	15	313	327	TAGTGTGCGTGATCGAGGAG
scaffold375993_16.9	1	p3	(TCT)5	15	178	192	CACTAATGAATCTCCTAGCGGG
scaffold376324_14.5	1	p3	(CGC)5	15	341	355	GTAGCTCCCTTCCCAACAGA
scaffold376579_14.3	1	p3	(TTA)8	24	2311	2334	TTTTCAATGTCCACACCCCT
scaffold377319_14.2	1	p3	(CAT)5	15	192	206	ATGTCCTCAATCGATCCCAG
scaffold378423_17.0	1	p3	(CCG)6	18	4114	4131	CTCACGGTTGGAAGAAGAGC
scaffold379011_13.7	1	p3	(AAC)5	15	2761	2775	TCCAACCGCTTTTGCTTAAA
scaffold379895_16.6	1	p3	(GAT)5	15	950	964	CCGGATTACTCCGATGATGA
scaffold380032_15.6	1	p3	(GTT)5	15	457	471	ATTTCCCTGATTGGCTTCCT
scaffold380162_15.6	1	p3	(TCT)5	15	1942	1956	CGAAGTTGTGCAAACCAATG
scaffold380508_18.3	1	p3	(AGA)5	15	79	93	TTGAAAGAGCATCGTGCAAC
scaffold381524_10.6	1	p3	(CAA)5	15	46	60	GTGGCTTCTATGGGCAATGT
scaffold381536_14.3	1	p3	(AAG)5	15	441	455	GGGGTCAGTCGTGACAGATT
scaffold381572_14.3	1	p3	(TTG)6	18	46	63	TGTAGCCGACCCCAATTTAT
scaffold382019_17.7	1	p3	(TGG)6	18	732	749	ATGGCCTGCTCATACAGCTC
scaffold382035_12.2	1	p3	(ATT)5	15	492	506	CGGATGAATTTTTGTTCGCT
scaffold382318_11.5	1	p3	(AGA)5	15	51	65	GAGCACGTTATTGGCTGGAG
scaffold382656_11.6	1	p3	(AAC)5	15	243	257	CCTTGGAGTTGTCCAGCATT
scaffold382837_15.4	1	p3	(ACA)5	15	684	698	GCTCAACACCTGGGAGGTTA
scaffold382894_12.7	1	p3	(GAA)5	15	99	113	AGGGGGAGAGTTCTCTTGGA
scaffold382918_11.6	1	p3	(AAG)5	15	137	151	GAGTCTTCCGACAAACCGAG
scaffold384020_13.8	1	p3	(TGT)5	15	30	44	ATTGGGATTAAGGCTTTGGT
scaffold384289_16.3	1	p3	(TTA)5	15	727	741	CCCACTCGAAATTAACCACG
scaffold384495_17.6	1	p3	(TGA)8	24	39	62	CCCAAGACCCCAATTTGATT
scaffold385073_16.8	1	p3	(GAT)5	15	2131	2145	GGTCCTATATTGTGGTTTCCG
scaffold385714_14.5	1	p3	(CTT)7	21	375	395	AAACCTTAACGCCCTCACCT
scaffold386196_14.8	1	p3	(GGA)7	21	1195	1215	ACTCCGACATGGAGAACACC
scaffold386951_16.1	1	p3	(CCG)7	21	945	965	CCCCCTTTCCTCCTTTCTTT
scaffold387017_13.2	1	p3	(TAT)5	15	606	620	CCATTTTCCAAGAAAGGTTGTT
scaffold388081_14.0	1	p3	(TTC)5	15	616	630	TACACACCCCAAATATCCCG
scaffold388171_18.7	1	p3	(AAT)5	15	305	319	CGATGATCACGTCAAAAACCT
scaffold388181_15.2	1	p3	(AAC)5	15	323	337	TCGGTTCCGATCTTCACTTC
scaffold388480_14.9	1	p3	(ATG)5	15	42	56	CCTGAAACGAGTGATGCTCC
scaffold388544_11.2	1	p3	(GGC)5	15	154	168	GAGGTGAAACTGCCCTGAAA
scaffold389074_18.6	1	p3	(GTG)5	15	460	474	GAAGTTGGCGTGGTGGTAGT
scaffold389353_15.6	1	p3	(TTG)5	15	2863	2877	GTTTGCTGTTGGATGGGTTC
scaffold390641_15.4	1	p3	(ATG)5	15	84	98	TCCTGAAATGAGTGATGCTCC
scaffold390837_15.1	1	p3	(TGA)5	15	4209	4223	GAAGAGGAATGTGTTGGCGT
scaffold391802_19.9	1	p3	(CGC)5	15	73	87	ATGGTAGTATGGTGTGGGGG
scaffold392126_11.7	1	p3	(AAT)6	18	183	200	CTCCATCAGGTTTGTCCTCC
scaffold393743_17.7	1	p3	(TCA)5	15	1073	1087	TGGACCTTCTGATTTCGAGC
scaffold394131_18.0	1	p3	(CCT)5	15	2334	2348	GGGCTTCATCTTACCACCAA
scaffold394748_18.5	1	p3	(ACA)7	21	260	280	AGACAACGGGACGGAAGATT
scaffold394799_13.2	1	p3	(TGA)7	21	973	993	GATCTGCAGCCATGTTGAAA
scaffold395217_16.5	1	p3	(CAC)7	21	104	124	CCGAAGTGCTAGACCCAAAG
scaffold395267_11.0	1	p3	(TGA)5	15	447	461	AATGGTGGTGATGTCTGTGC
scaffold395887_15.9	1	p3	(ATA)5	15	2237	2251	TTTGCTTTGACTTTCGGGTC
scaffold396402_16.7	1	p3	(TCT)6	18	2002	2019	ATCTCCTGCAACACTCCCAC
scaffold397498_16.9	1	p3	(GAT)5	15	1796	1810	GATACGCGTCGTTGTCATTG
scaffold397875_17.1	1	p3	(CGG)5	15	366	380	TCTCCGCACACTGAATAACG
scaffold398183_12.0	1	p3	(GGC)5	15	154	168	TGTCACCCAACTTATAAAAGAAGAA
scaffold398509_10.0	1	p3	(TTG)5	15	391	405	AATTTTCTTTTGCCGACACG
scaffold399013_16.1	1	p3	(ATG)6	18	353	370	TGTGATGTGATTGGGAGAAATC
scaffold399959_10.6	1	p3	(CCA)5	15	473	487	GCCACATGCTTTGTGTGAGT
scaffold400179_11.9	1	p3	(TTA)8	24	699	722	CCCATAATTTTATTGGGGGA
scaffold400195_16.3	1	p3	(CAA)5	15	302	316	AGTTTGTTGCTCATAGCGGG
scaffold400346_14.1	1	p3	(TTA)8	24	3220	3243	CAATACAAGGGTTCTCGCGT

scaffold400467_12.	1	p3	(TGT)6	18	51	68	TAGCCGACCCCAATTTAATG
scaffold400994_13.	1	p3	(ATA)5	15	231	245	CAAGATGTTTGGCGATTGAA
scaffold401163_12.	1	p3	(ATC)5	15	2352	2366	GCTGCAGATGCAAAACTCAA
scaffold401196_15.	1	p3	(CGC)5	15	1640	1654	ACCACAAATTCCTCAACCCA
scaffold401353_14.	1	p3	(CGC)5	15	701	715	TAAAATTGCCCTATTGCGCT
scaffold401617_20.	1	p3	(TCC)5	15	217	231	TATCATCCTCGGAGGCAATC
scaffold402051_14.	1	p3	(TCA)7	21	63	83	CATGAAACATTTCAAAATATCATCC
scaffold402182_11.	1	p3	(TAT)6	18	220	237	GTGGTCCCGTAACTCGAAAA
scaffold402417_14.	1	p3	(TGT)6	18	143	160	AACGTAAAGAGGGGTAGGGG
scaffold402720_10.	1	p3	(CAA)7	21	99	119	TGAATCAGAAAATCCCCTGC
scaffold402745_14.	1	p3	(ATA)6	18	4819	4836	TTCCCATCACTTCGAGGAAC
scaffold402881_16.	1	p3	(AGA)5	15	118	132	TCACACCTCACTAATTTCTTGTTT
scaffold402964_10.	1	p3	(CAG)5	15	357	371	ATTTACAGCTCGGTTTCGGA
scaffold403092_10.	1	p3	(GCT)5	15	197	211	TCTGAAAATTGGTGCTGCTG
scaffold403381_16.	1	p3	(AGA)5	15	45	59	CAGATGTAGGAGGCGAGGAG
scaffold403562_11.	1	p3	(GAA)5	15	533	547	CGTGGTTCAACTGTTGCTTG
scaffold403578_16.	1	p3	(ACC)5	15	5471	5485	CAATCTCCTCAGACATCGCA
scaffold404047_15.	1	p3	(TTG)5	15	2237	2251	CCCTCCTTTCACATGTTCGT
scaffold404086_14.	1	p3	(TGA)5	15	607	621	TCAACAATTTACGGGCTTCC
scaffold405201_12.	1	p3	(ATT)5	15	206	220	CTGATGAAGAAGACGAGGGC
scaffold405553_15.	1	p3	(TTC)5	15	323	337	ACCCCAAAACCACATCAGAC
scaffold405946_11.	1	p3	(GCA)5	15	186	200	AGTAATCCTGACCACCGTGC
scaffold406857_15.	1	p3	(AAC)5	15	1807	1821	TTTAACGGATATGCTTGGGA
scaffold407079_15.	1	p3	(TGT)7	21	695	715	TGTAGCCGACCCCAATTTAT
scaffold407082_14.	1	p3	(TAT)5	15	162	176	TGGGACAAGGTGACATAAAATG
scaffold408521_10.	1	p3	(ATA)7	21	231	251	TGGTGTCGAGCAGCCTATCT
scaffold408554_15.	1	p3	(CTC)6	18	952	969	CTCTTTCGCAGCCTCCTCTA
scaffold408727_12.	1	p3	(CAC)6	18	79	96	AGCCATGAGCAATAACAGCC
scaffold408752_17.	1	p3	(TTA)5	15	79	93	CCGAAATCTTCAAGCCACAT
scaffold408779_15.	1	p3	(TGT)6	18	42	59	TGTAGCCGACCCCAATTTAT
scaffold408957_16.	1	p3	(ATA)5	15	1121	1135	TCCACCATCTATGTGCCGTA
scaffold409454_14.	1	p3	(TGA)6	18	41	58	CCCAAGACCCCAATTTGATT
scaffold409460_11.	1	p3	(ATT)5	15	119	133	GGGCATTACATTTACGTTGGA
scaffold409635_15.	1	p3	(ATG)5	15	667	681	CAGCCTCAGGACTCCTCATC
scaffold409658_13.	1	p3	(TTA)9	27	192	218	ATCAGAGCCATGGAAAAGGA
scaffold409673_13.	1	p3	(ATC)5	15	641	655	TTATTTGGCGGGTTAATGGA
scaffold409800_10.	1	p3	(CCG)6	18	276	293	TCCCGCCCTCTACCTTTATT
scaffold409930_16.	1	p3	(TCA)5	15	881	895	CCTTCAAAAACCATGCCACT
scaffold409975_13.	1	p3	(AAT)5	15	581	595	GACCCAAATTTTCCCCAACT
scaffold409986_11.	1	p3	(ACA)7	21	957	977	ACAGCTTCGGCAGATCACTT
scaffold410299_14.	1	p3	(GCT)5	15	910	924	GCTTTGAGGGTCAAACCAAG
scaffold410669_15.	1	p3	(CCG)5	15	634	648	ACCCCCTTCTCCGTTTCTAA
scaffold410673_15.	1	p3	(ACA)5	15	344	358	GTTTCTGCCACGTGCATTC
scaffold411399_15.	1	p3	(TCA)5	15	305	319	CGCTTTGCTAGATTTTTGCC
scaffold411453_15.	1	p3	(GCT)5	15	4650	4664	GGATGCATTCCAGAGTTGCT
scaffold411723_15.	1	p3	(GTG)5	15	52	66	ACCGTAACCGCCAAACAC
scaffold411825_16.	1	p3	(TCA)5	15	813	827	AAGAACTGCTCCCTCAACAAA
scaffold411854_13.	1	p3	(GGT)5	15	1615	1629	TTTGGCAGAATTGGATTTGG
scaffold412060_16.	1	p3	(CTT)7	21	193	213	TCACCGGAAACAAATACATCA
scaffold412118_11.	1	p3	(GAT)7	21	45	65	TTCTTCTGTACAATTAATGTCCAAGTC
scaffold412129_14.	1	p3	(ATA)6	18	378	395	GTCCGTTGGGTGTTTGACTT
scaffold412312_16.	1	p3	(ATA)5	15	399	413	ATGGGTAGCCAGTTTCACCA
scaffold412628_15.	1	p3	(ACA)5	15	967	981	CCCAGTTCGCCACTAACAAT
scaffold412640_13.	1	p3	(CGG)6	18	755	772	ATGCTGTGTTTGAGCGACTG
scaffold412823_14.	1	p3	(CGG)5	15	39	53	CCACCATCGTCGTCTCATC
scaffold412941_12.	1	p3	(TTA)7	21	629	649	TGTGATGAGATCGTGAACCTG
scaffold413335_11.	1	p3	(TTA)5	15	549	563	TCCATTTAATCCCCCTTCTTC
scaffold413370_12.	1	p3	(TTA)7	21	936	956	CTTGGCATTCTCTTTCTCGG

scaffold413822_15.4	1	p3	(TGT)5	15	1717	1731	AGTTATGTAGCCGACCCCAA
scaffold414264_15.3	1	p3	(GGT)5	15	903	917	AAGTGATATTTTCGGCGGTG
scaffold414770_16.7	1	p3	(TCA)7	21	2582	2602	TTTTCAAGATAACCAGCGCC
scaffold414925_15.9	1	p3	(AAG)5	15	399	413	CAAGGCAGAGAAAAAGCCAG
scaffold414928_17.3	1	p3	(GGC)5	15	1237	1251	TCCGCTGCTAATTTGCTTTT
scaffold414970_14.8	1	p3	(GAT)5	15	1017	1031	TTCAGGTTGAAGTCTTGGGC
scaffold415281_11.3	1	p3	(CGG)5	15	192	206	GGTTTTTGCTTGCACTTTCC
scaffold415387_13.3	1	p3	(AAG)5	15	1891	1905	TTGTATGGCACGAGTTCTTGA
scaffold415496_16.6	1	p3	(TCC)7	21	55	75	CTCGTCCTCCGTGGATATGT
scaffold415606_15.2	1	p3	(TAA)5	15	937	951	GCGCAGTTGCCAAACTTATT
scaffold415671_17.2	1	p3	(ACA)5	15	466	480	GCAGGTTGCAATAAAGCACA
scaffold415740_15.9	1	p3	(GGC)6	18	4949	4966	GAATCCGGAGAGTGAGACGA
scaffold415975_13.9	1	p3	(AGA)7	21	224	244	CGGAAGAAGCACAGACAACA
scaffold416035_15.9	1	p3	(TGA)7	21	3954	3974	GCCGACTCTTTCTTCCTTCC
scaffold416239_14.0	1	p3	(AAT)5	15	609	623	TAAACGTTCGTCACGTCAGC
scaffold416585_15.5	1	p3	(TGT)7	21	40	60	TGTAGCCGACCCCAATTTAT
scaffold417083_13.9	1	p3	(TGG)5	15	64	78	TGATATTTTCAATGATGGATCG
scaffold417533_16.1	1	p3	(TGA)5	15	4263	4277	TCAAATGCAAATCTACCTGGG
scaffold418366_16.5	1	p3	(ACA)5	15	855	869	TTCGACGCGGAAGTAAATCT
scaffold418822_16.3	1	p3	(TTA)5	15	2291	2305	TTGCCCATGCATACACATTT
scaffold418937_14.6	1	p3	(ATT)5	15	1097	1111	TTTTCGGTTACCATGTCGTT
scaffold419570_13.8	1	p3	(AGA)6	18	196	213	GAGCGGAGGCTTAAGGATTT
scaffold419756_15.3	1	p3	(GGC)5	15	638	652	TCGAAATTCAAGCACACGAG
scaffold419868_17.0	1	p3	(AAT)5	15	1053	1067	GAGAAAGAATCAACTGCGGC
scaffold419934_14.8	1	p3	(CGG)5	15	832	846	ACAAAAATCCCTCAGCAACG
scaffold419945_15.4	1	p3	(AGA)5	15	837	851	TTGGTTACTCTGGGAATGGC
scaffold419978_14.4	1	p3	(AAG)6	18	1206	1223	TTCTTGGATTGGAAGGCATC
scaffold420332_19.6	1	p3	(AAG)5	15	2411	2425	CGAGAAGATCTTGAGGTCGC
scaffold420462_13.8	1	p3	(TGT)5	15	49	63	TTGGTTCATGTAGCCGACCT
scaffold420574_12.9	1	p3	(ATC)7	21	737	757	ACGGAGAAATTCGACTCAGG
scaffold421484_16.0	1	p3	(GCG)5	15	765	779	CCACCATCACCGTTATTTCC
scaffold421527_13.3	1	p3	(TGT)5	15	121	135	CGGAGAAATGGTTTCTGCAT
scaffold421531_13.9	1	p3	(ATG)6	18	601	618	ATGAGGATGATGACGAAGCC
scaffold421606_15.0	1	p3	(GTC)5	15	1496	1510	TTTTTGCACCAAAATGGACA
scaffold421806_11.9	1	p3	(CGG)6	18	215	232	AATCATGTACACCCGGTTCG
scaffold422137_16.2	1	p3	(GAT)7	21	495	515	GAAAGTGGGGGTTGATTGAA
scaffold422920_15.4	1	p3	(CGG)5	15	248	262	ATAACCTGGAAATCGGGGTC
scaffold423260_13.3	1	p3	(GGC)7	21	988	1008	TGAAAATCCAACAAGCCACA
scaffold423275_16.9	1	p3	(ACA)6	18	1683	1700	TTGCACAAGCTCTTGCACTC
scaffold423536_15.5	1	p3	(ATG)6	18	404	421	TTTCTTGATTCCGTCGTTCC
scaffold423772_10.8	1	p3	(ATC)7	21	74	94	GATTTTACACCTGCAAGGGC
scaffold423946_15.9	1	p3	(TGA)7	21	1113	1133	TATGACACAATGTCCCGTGG
scaffold424283_16.9	1	p3	(CTC)5	15	689	703	TATTGGCTCCAACCAGGAAC
scaffold425527_15.6	1	p3	(AAT)6	18	241	258	CACGCTTGGATGTGATACGA
scaffold425572_12.0	1	p3	(TAT)6	18	76	93	CCTTTCTCCAATTGCTTTTCG
scaffold425691_12.9	1	p3	(ACT)5	15	1078	1092	ATAGATCCGGAATGATCGGA
scaffold425760_13.1	1	p3	(ATT)6	18	656	673	ACATACCGACGTGACCGTTT
scaffold425780_16.8	1	p3	(GGC)5	15	381	395	GTTCATCAATTCCCACCACC
scaffold425787_15.6	1	p3	(TGG)5	15	5747	5761	TGATCTACTCCGTCCCCAAG
scaffold425896_16.2	1	p3	(CAT)6	18	2496	2513	TGCAAGAGAAAACACATCCG
scaffold425909_19.8	1	p3	(GGC)5	15	645	659	ATGGTGGAAACCAAGGCAT
scaffold426298_12.3	1	p3	(AAT)5	15	204	218	GCTGTAAATGAAACTGCTGTATGC
scaffold426331_15.3	1	p3	(AAT)5	15	61	75	CAGAGCGCACTCGAAGAGTA
scaffold426861_12.7	1	p3	(TAT)6	18	114	131	TTGTCATATGAATCATGAAATTTTG
scaffold426888_15.2	1	p3	(CTT)5	15	871	885	GTTCGCTGAGGCAACAACTT
scaffold427405_14.8	1	p3	(ATA)5	15	527	541	TGACTGCGCGACTTTGATAC
scaffold429243_15.3	1	p3	(AAG)5	15	1172	1186	ACTCTAACCCCTACTCCGGC
scaffold430246_15.3	1	p3	(AAG)6	18	123	140	ATGCAGCTCATGTCTGATGC

scaffold430283_16.	1	p3	(ACA)5	15	400	414	AGCAAAAGGTCGTCCTGCTA
scaffold430401_12.	1	p3	(TAA)5	15	403	417	TTTAGGCCAAGTTGTACCCA
scaffold430477_13.	1	p3	(CAT)7	21	1046	1066	GATTCAGGGGAAATTCACGA
scaffold430483_17.	1	p3	(TTG)5	15	181	195	CTTTATGATGGAGGCGGATT
scaffold430561_14.	1	p3	(GGC)6	18	294	311	GATCCCAGATCCGAATCCTC
scaffold430942_13.	1	p3	(ATT)6	18	63	80	TTCCAAAGTTGGACTTATGTAAAAA
scaffold431025_15.	1	p3	(GAC)5	15	1013	1027	TGAGCAACTGCCAAAACGTA
scaffold431685_16.	1	p3	(CAC)5	15	533	547	AGTTATCTTCCTCCGGCGTC
scaffold431814_16.	1	p3	(TCA)5	15	77	91	CATTGCGTCATACGATGTATTAAA
scaffold432461_12.	1	p3	(TAT)6	18	120	137	CTAGCCCAGCATATTCCCAC
scaffold432493_16.	1	p3	(ATT)5	15	177	191	ATCCCAAGCCATTACCATCA
scaffold432842_17.	1	p3	(ATC)6	18	1401	1418	CTTTGAGCACCGAGTGGTTT
scaffold433340_16.	1	p3	(GTC)5	15	845	859	CCTTCGACTTTTGACTGGGA
scaffold433423_14.	1	p3	(CAT)7	21	734	754	AGCGAATCGAGATAGCCAAA
scaffold433438_14.	1	p3	(TTA)8	24	519	542	AGCCACTGACAGCCACAGTA
scaffold433805_17.	1	p3	(CCG)5	15	394	408	TCACACTCTCGCTCCCTCTT
scaffold434033_13.	1	p3	(GGC)6	18	309	326	GCAAAATTAAAAATGCCCCA
scaffold434149_14.	1	p3	(CTT)7	21	50	70	CCCTAAGTTTGCATCTCCCA
scaffold434661_17.	1	p3	(ATA)5	15	1088	1102	AGACGTAAATGGGCGTGAAT
scaffold435475_16.	1	p3	(TTC)5	15	37	51	CCTATTACTTCCTCGACTTTAATGG
scaffold435553_16.	1	p3	(ATG)5	15	751	765	GATATGCAAGCAGCCAGTGA
scaffold435580_20.	1	p3	(GAG)5	15	206	220	TGGTACCGATCTGGTGCATA
scaffold435621_13.	1	p3	(AAC)5	15	161	175	CTAGAGGGCGGCACATTTAC
scaffold436624_16.	1	p3	(ATA)5	15	134	148	TCTTCCGCTTGCTTGTTCTT
scaffold437143_10.	1	p3	(ATT)5	15	403	417	GCTCTGGGTAAACTCACGGA
scaffold437378_17.	1	p3	(ATA)5	15	441	455	TTCCATGCAATAAGCATCTATGA
scaffold437400_17.	1	p3	(AAT)6	18	513	530	TCACCAAAAATCGAACACACA
scaffold437468_16.	1	p3	(CAT)5	15	2717	2731	GGCTACAAAGGGACATCCAA
scaffold438063_15.	1	p3	(ATC)5	15	75	89	CCACATTTTCCACCTTAGCC
scaffold438124_11.	1	p3	(CCG)8	24	376	399	CTCTCCTGCCTCCGACTATG
scaffold438443_14.	1	p3	(TCA)5	15	191	205	AGGCGGGTACACCACACTAC
scaffold438464_13.	1	p3	(TGA)5	15	485	499	AAGATTACGACGGCGATACG
scaffold438570_15.	1	p3	(ATC)5	15	775	789	CTCCCATCATCCTTTTTCCA
scaffold438846_16.	1	p3	(GGA)6	18	269	286	TATGCGACCACGATCAAGAG
scaffold438946_13.	1	p3	(ATA)5	15	278	292	CTCTAAGGGATGAATGCACG
scaffold439137_16.	1	p3	(ATC)6	18	50	67	CATGCGCTCAGCATAAAGAA
scaffold439238_17.	1	p3	(TTC)5	15	30	44	GGATCAGCAGTGGCTTTCTC
scaffold439445_17.	1	p3	(TGT)5	15	2634	2648	TTGGGATTAAGGCTTTGGTG
scaffold439623_11.	1	p3	(ATT)6	18	444	461	AAACTGCCAAGTGCCAACAT
scaffold439781_11.	1	p3	(ATG)5	15	485	499	AACCGTCTCAGTTGTTCGCT
scaffold440287_13.	1	p3	(ATC)5	15	975	989	CAAGACCTTTTTGTTCGCTT
scaffold440641_17.	1	p3	(AAG)5	15	2298	2312	AGGTTCGAGCTACCGAAACA
scaffold440740_11.	1	p3	(CAA)8	24	382	405	TTTGCTGGATACCGCAAGTA
scaffold440859_14.	1	p3	(GGT)5	15	515	529	GAGGGAGAGAGAGGGGAAGA
scaffold440912_11.	1	p3	(AAT)5	15	1127	1141	GCACATATTCGTTCCCGACT
scaffold440998_15.	1	p3	(TAT)6	18	4517	4534	TTACGCGGGAACCTACAGAC
scaffold441003_12.	1	p3	(GCG)6	18	1062	1079	ATGGAGGAGGAGGAAAAGGA
scaffold441074_16.	1	p3	(TGT)5	15	2694	2708	TCGTTCAATTCACACACGTTC
scaffold441075_17.	1	p3	(GCG)5	15	412	426	TGAGGGTTAGAGATCGGTGG
scaffold441392_13.	1	p3	(TTG)7	21	157	177	GGTGGCTGAAGATAGGAATGA
scaffold442095_16.	1	p3	(AGG)5	15	1363	1377	AGCAGAGTTTGTTCGTCGGT
scaffold442546_20.	1	p3	(ATC)5	15	703	717	TGCGGAAGTAGCTTTGATGA
scaffold442620_12.	1	p3	(TAT)6	18	955	972	GAGCCATTGATGGCATTTTT
scaffold443169_17.	1	p3	(ACA)5	15	1165	1179	CAGAAAGCGCTTCGAGAACT
scaffold443522_17.	1	p3	(GCA)5	15	794	808	TCGGTTTCGGAGGTATTGAG
scaffold443807_13.	1	p3	(TAA)7	21	72	92	TGTTTGGATTTCATGAATTAGTATTTT
scaffold444527_20.	1	p3	(ATT)7	21	428	448	TCAAGCTTGGGTGTTGATGA
scaffold444570_15.	1	p3	(GCA)6	18	1519	1536	CTGACCACCATCTTCTCCGT

scaffold444771_14.	1	p3	(TCC)5	15	84	98	CGCTCCTCCAAGAACAACTC
scaffold444925_17.	1	p3	(GGC)5	15	388	402	GCTGTTTATCACGACGAGCA
scaffold445355_18.	1	p3	(ACG)5	15	467	481	ACTAGCGAAAAACGGACGAA
scaffold445537_12.	1	p3	(TTG)5	15	510	524	AAGGTCAATATGCGGTGGAG
scaffold445576_21.	1	p3	(TCC)5	15	126	140	CTCCTTCCAAATCCAATCCA
scaffold445580_11.	1	p3	(CTA)5	15	67	81	CCAACCAAATTGGACTTGTG
scaffold445586_14.	1	p3	(CCA)5	15	2638	2652	CCTTTCAGGCTTGAATCTCG
scaffold445852_17.	1	p3	(TGA)6	18	45	62	CCCAAGACCCCAATTTGATT
scaffold445868_17.	1	p3	(CAT)5	15	2146	2160	CGCCTCTTGATTAACCTCCA
scaffold446294_11.	1	p3	(TCT)6	18	324	341	GTTTGGTCCCTTTCGAATCC
scaffold446309_10.	1	p3	(AAC)5	15	81	95	GGGTTAGTTATGGAACGATGC
scaffold446925_17.	1	p3	(ATT)5	15	384	398	CATGTCACAACATGGAATCTCA
scaffold446948_14.	1	p3	(ATC)6	18	1968	1985	CAGGATGGTTTGAAATGAGG
scaffold447024_11.	1	p3	(CGG)5	15	230	244	TAATTTATCGATGGCGGACG
scaffold447151_19.	1	p3	(TAT)5	15	67	81	TTGATTGCTTTAAATCCGGC
scaffold447256_11.	1	p3	(AAT)5	15	117	131	TTTAAAGTTGCCATTTCAGCC
scaffold447391_19.	1	p3	(TTA)5	15	214	228	GCCAAAATCTGTATACCCCG
scaffold447611_12.	1	p3	(ACA)5	15	379	393	AACCTTTTTGAGCTCCGCTT
scaffold447880_17.	1	p3	(CTT)6	18	4038	4055	CATGCATGACTTGGTGCTCT
scaffold448140_14.	1	p3	(TTG)8	24	970	993	TTTGGTTCATGTAGCCCACC
scaffold448185_10.	1	p3	(GCG)5	15	76	90	CGCTGAACGAGCTAGAACTTG
scaffold448317_20.	1	p3	(AGA)5	15	40	54	AAGGAGAGGAAGATACGATTTGAA
scaffold449108_14.	1	p3	(AAT)5	15	1335	1349	CCTCTCCATTCTGAATCCCA
scaffold449245_14.	1	p3	(GGC)5	15	500	514	TTCTTTGTCGTGGTTTCGTG
scaffold449422_15.	1	p3	(ATC)6	18	3391	3408	ACAGGAATTGAAATGACGGG
scaffold449695_17.	1	p3	(TAT)6	18	46	63	TGCACAAAAATGTTTTAAAATTGC
scaffold449707_15.	1	p3	(GGA)5	15	420	434	TAAGGATGGGTTTCCGAATG
scaffold449988_15.	1	p3	(AAT)5	15	6175	6189	TGGATTTGGAATCGGTTTTC
scaffold450110_10.	1	p3	(CAA)5	15	39	53	CAGCCATGAATGAGAGTGGG
scaffold450155_17.	1	p3	(TGT)8	24	39	62	TGTAGCCGACCCCAATTTAT
scaffold450191_10.	1	p3	(ATA)5	15	412	426	TCATTTATTTCCTTTTTATATGTGCAA
scaffold450206_16.	1	p3	(TAA)6	18	177	194	TTCAAGTGTGCTTCCACCAA
scaffold450450_15.	1	p3	(TTG)6	18	2128	2145	TAGCATTCGTGTTTCCAGCA
scaffold450521_11.	1	p3	(TGA)6	18	40	57	CCCAAGACCCCAATTTGATT
scaffold451740_13.	1	p3	(TAT)6	18	311	328	CCGATCCATTTTAGGAACGA
scaffold451795_15.	1	p3	(TCA)5	15	319	333	GGCCAGTGTTGAGGTCAAAT
scaffold452041_16.	1	p3	(GTG)5	15	191	205	AGGTTTGCCAATCGTTCTTG
scaffold452151_17.	1	p3	(GAT)6	18	708	725	TTGATAAGCCAGCCACTTGA
scaffold452177_17.	1	p3	(TTC)5	15	842	856	TGGGTAATGGCTTCAACTCC
scaffold452335_17.	1	p3	(ATC)7	21	1164	1184	GTGCCACCTTTTAGCACCAT
scaffold452593_13.	1	p3	(ATT)5	15	212	226	ACTGCATGGGCTATTTCCAC
scaffold452598_16.	1	p3	(GAG)5	15	255	269	AGTAGAGGTGCCTGTGGTGG
scaffold453322_15.	1	p3	(TAT)5	15	660	674	AAAGCAGTTAATAACGAAAAACCA
scaffold453374_16.	1	p3	(TTC)5	15	276	290	ATTGTTGTTGCTGCTGTTGC
scaffold453474_20.	1	p3	(ATA)6	18	48	65	ATGTTCCACCTCCCAAGGTT
scaffold453495_10.	1	p3	(ATT)5	15	393	407	GACGGGTGTGGGCTAAAAAT
scaffold453707_10.	1	p3	(ATA)7	21	376	396	CGTGTGCATGTGAAATTTTTAT
scaffold453730_16.	1	p3	(GGT)5	15	173	187	TCCAAATCGCTCAAACATTG
scaffold453796_11.	1	p3	(TTA)5	15	678	692	CCTAGACTCCGACGAAAAGC
scaffold453864_19.	1	p3	(CTC)5	15	26	40	CACTCTCCTCAATGGCGTC
scaffold454028_14.	1	p3	(TCA)8	24	2864	2887	TTGAGACTCAGATGAAATGTAGCC
scaffold454119_13.	1	p3	(TAC)5	15	225	239	TTTATGCATTGCCGTGAAAA
scaffold454125_15.	1	p3	(ATG)5	15	36	50	ATCAGGATCGAGTAAGCGGA
scaffold454537_12.	1	p3	(AAT)5	15	790	804	ACTTGTGAGACAAAGAGAACAAAA
scaffold454628_19.	1	p3	(AAC)5	15	565	579	TCCCTCATCACTACCCAACC
scaffold454729_15.	1	p3	(ATC)5	15	86	100	TTCACATTTACAACCTACATCGG
scaffold455048_14.	1	p3	(ATA)6	18	1881	1898	TTTTCGATTTGATTTGGGTTT
scaffold455436_17.	1	p3	(CTT)6	18	412	429	TTATATGCCACTCTTCCCGC

scaffold455903_15.	1	p3	(TGT)5	15	2580	2594	CCATCTTTCGAATGGTCGTT
scaffold456021_14.	1	p3	(ATT)7	21	3164	3184	CAACGGCCTTTCTTTAGCAG
scaffold456170_13.	1	p3	(CAT)5	15	1702	1716	ACATTTCTCTTGGGTGCCAG
scaffold456201_10.	1	p3	(TAT)5	15	189	203	GCTAGACCATTGTAGGGCGA
scaffold456544_11.	1	p3	(TAA)8	24	249	272	GCATTGGAAAATATTACTGGGG
scaffold456844_18.	1	p3	(ACA)6	18	576	593	TACTTGGGACGGGATGGTTA
scaffold457138_16.	1	p3	(GAG)5	15	3359	3373	GGCGAAGAATGCACACTACA
scaffold457617_14.	1	p3	(TTC)5	15	3736	3750	TGTCGTCGTGGACAAGAAAA
scaffold457630_12.	1	p3	(TTA)5	15	433	447	TCTTCTATACATAGTGCTTCCGGT
scaffold457709_13.	1	p3	(ATA)5	15	323	337	GTTCGGTTCCGGTTTCAAAT
scaffold457714_15.	1	p3	(CAT)5	15	608	622	CTTCCACAGGCATTGGGTAT
scaffold457742_11.	1	p3	(CCG)5	15	62	76	CAAATCACCAATCAACAAAACC
scaffold458651_17.	1	p3	(TGA)5	15	44	58	CCCAAGACCCCAATTTGATT
scaffold458875_17.	1	p3	(GAA)5	15	1646	1660	ATGGTGAAAGGCTCCCTGTA
scaffold459137_13.	1	p3	(TTG)5	15	362	376	GGTTGAGTTGAGGGGAATCA
scaffold459290_15.	1	p3	(ATA)5	15	384	398	AACCCTCAGCAATATGCCAA
scaffold459314_12.	1	p3	(TAA)5	15	639	653	CGACAGAGTTGCAAAGAAGTTG
scaffold459341_14.	1	p3	(TTC)5	15	118	132	AATCCCACTCTTTTTGCTGC
scaffold459397_14.	1	p3	(TTA)5	15	201	215	TCACGAGTTGGCTCTTTGTG
scaffold459510_18.	1	p3	(GGC)6	18	234	251	CACCCTTCGATACTCCGAAA
scaffold459758_16.	1	p3	(GAA)5	15	4141	4155	AGAAGGCAGAGACCGTGAAA
scaffold459783_10.	1	p3	(AAT)6	18	46	63	CCGACTAGGACTAAGGGTCCA
scaffold459935_16.	1	p3	(CAA)5	15	1435	1449	AAAGGCCATGCTGACAAAAC
scaffold459940_10.	1	p3	(AAT)5	15	256	270	CAGCAACCACCAAATACTCTTG
scaffold459978_16.	1	p3	(TAT)5	15	602	616	AAGATCAGGGAAAAGGGAGC
scaffold460000_16.	1	p3	(GCA)5	15	80	94	CAGCTTGGTTTTGGAGGTGT
scaffold460486_16.	1	p3	(ATA)5	15	445	459	ACGACCTGTCAAGACCCAAT
scaffold460616_14.	1	p3	(TTG)6	18	66	83	TCCAAAATTAGTACAAGCATCAAAA
scaffold460921_12.	1	p3	(CAT)5	15	127	141	TCGCCTTCTTTTGCAGCTAT
scaffold461024_15.	1	p3	(TAA)5	15	4187	4201	TGTAAGCAGCACGCCAACTA
scaffold461087_18.	1	p3	(GTG)5	15	283	297	ATGATCTCGACCTCCCTCCT
scaffold461143_17.	1	p3	(TTC)5	15	3749	3763	CTGCACACCTGTATGTTCGG
scaffold461587_14.	1	p3	(ATT)5	15	667	681	TGCTTGAAATGAGTTGGAATG
scaffold461764_10.	1	p3	(ATA)5	15	397	411	GTCAGCGAGGCGAACTCTAC
scaffold461785_15.	1	p3	(GAT)6	18	256	273	TTTCAAGGAAACATCCCAAAA
scaffold461811_17.	1	p3	(CAC)5	15	681	695	TGTGACGTCTAGCTCGATCC
scaffold461839_12.	1	p3	(TAA)5	15	427	441	TTTCCACAAAGCGTCGTACA
scaffold462337_17.	1	p3	(TTG)5	15	280	294	GGGTTGGGTTTTCTCCATTT
scaffold462507_15.	1	p3	(TCC)6	18	4338	4355	CAGATGGTGAATGGAGGGAG
scaffold462817_14.	1	p3	(GGC)6	18	10495	10512	GAGAGTAGGATTGGGGGAGG
scaffold462866_18.	1	p3	(TTG)5	15	520	534	CACCGGTTTCAAGGGTAGAA
scaffold463049_17.	1	p3	(ACA)6	18	181	198	TGCTTGCGGTATTGTTTTGA
scaffold463389_17.	1	p3	(CAC)5	15	579	593	AAACCTCACCACAAACGGAG
scaffold463414_11.	1	p3	(GTT)5	15	69	83	TGTTGTTGAAAAAGGCGACA
scaffold463990_16.	1	p3	(CGG)5	15	4440	4454	TAGGGCTTTTGTGTGGTTCC
scaffold464123_10.	1	p3	(AAT)6	18	378	395	GTCTCAATGGGGACATCTGG
scaffold464261_10.	1	p3	(CGC)5	15	247	261	TTGAGCAAGAAGGGTGTTGA
scaffold464272_10.	1	p3	(ATT)6	18	169	186	CCCAAATTTTCTTAAGCCCTG
scaffold464462_12.	1	p3	(TGT)5	15	50	64	TGTAGCCGACCCCAATTTTA
scaffold464577_16.	1	p3	(ATC)5	15	648	662	ATCCATCCATGCATTTTGGT
scaffold464717_15.	1	p3	(CCG)5	15	2017	2031	ACCCATGGATCCAACTTCAA
scaffold465065_14.	1	p3	(TGT)6	18	48	65	TGGTTCATGTAGCCTACCCC
scaffold465180_10.	1	p3	(ATC)5	15	85	99	GAATGTCAAGATGAGAGATGGAAA
scaffold465220_20.	1	p3	(ATT)6	18	911	928	CCGAACAACACTCAACTCCA
scaffold465291_13.	1	p3	(CAA)6	18	68	85	GGGGTTGAGGCCACTATATC
scaffold465589_15.	1	p3	(TTC)5	15	369	383	TTACTCCTCGAAAACAGCCG
scaffold465615_15.	1	p3	(AAT)6	18	601	618	CGAAGCAATACACTTTTGAAGAA
scaffold466368_14.	1	p3	(TCT)5	15	459	473	AGTTGGGATATTCGGGAAGG

scaffold466499_15.	1	p3	(AAT)5	15	185	199	GCTCTTTCAATAAACAGAATCCA
scaffold467167_13.	1	p3	(CGC)5	15	1360	1374	GCAGCGCATAACAAGTGTCT
scaffold467173_14.	1	p3	(ATC)6	18	2783	2800	CTGGCAATTCAGCCAAAAGT
scaffold467192_15.	1	p3	(GAA)5	15	1011	1025	TTCAAATTCCACAAACACGG
scaffold467223_15.	1	p3	(AAG)5	15	1027	1041	ATACCGCAGATCCCTTTCCT
scaffold467260_14.	1	p3	(AAT)5	15	81	95	TTGAATTCGGACATGAGCAA
scaffold467863_21.	1	p3	(TTA)5	15	278	292	ACGTAGGCGGCTTTACTGTG
scaffold468075_13.	1	p3	(TAT)6	18	281	298	CAGAAAGGTGTTGGTGGGAT
scaffold468474_13.	1	p3	(TGA)5	15	50	64	CCCAAGACCCCAATTTGATT
scaffold468552_12.	1	p3	(CAT)5	15	228	242	ATTTTATCCGGACGGGTTTC
scaffold468607_18.	1	p3	(TTC)5	15	215	229	TCTGTTCCCCATAGGCACTC
scaffold468781_15.	1	p3	(ATT)5	15	587	601	TTGTTACTAAGGGTTGCGGG
scaffold469198_15.	1	p3	(AAT)5	15	132	146	TCATTTTGGGACGGAGGTAG
scaffold469397_19.	1	p3	(GCG)5	15	805	819	AGAAAAACGAACCGCATTTG
scaffold469846_13.	1	p3	(ATA)7	21	357	377	TGATATCCCACCCGATCACT
scaffold469870_14.	1	p3	(ACA)6	18	89	106	GCACAAATTGAAAGCACACAA
scaffold469987_11.	1	p3	(CTC)5	15	575	589	TTGGTATGATGGAATGGGGT
scaffold469988_15.	1	p3	(TGA)6	18	40	57	CCCAAGACCCCAATTTGATT
scaffold470735_12.	1	p3	(GTA)6	18	286	303	CAGCTGCTGTCATCATCGTT
scaffold470842_12.	1	p3	(ATA)5	15	259	273	AGTTCCCCATTGCTGTTTTG
scaffold470965_17.	1	p3	(CGG)5	15	492	506	TGAGCCTACATCTGTGCTGG
scaffold471329_15.	1	p3	(GCT)5	15	315	329	GCCGGTTAATATGCATTTGG
scaffold471508_17.	1	p3	(CGC)5	15	280	294	CGGAGAGCTCGGTAAATGAG
scaffold471609_16.	1	p3	(TAT)5	15	126	140	AAGGAGCAGCTGTCTTTTGTG
scaffold471673_15.	1	p3	(ACA)5	15	934	948	TCTGCGGGAAAGGTGTAATC
scaffold471755_18.	1	p3	(AGG)5	15	1843	1857	GATTGGTTCAGCTATTCCGC
scaffold472169_18.	1	p3	(CAT)5	15	3196	3210	GCTGGATTCTTGAGGTGAGC
scaffold472376_16.	1	p3	(CTC)5	15	205	219	GAAGTAAGCCCGACCTCCTC
scaffold472958_16.	1	p3	(TGC)5	15	131	145	TCGCAACTATCTGCACCATT
scaffold472961_13.	1	p3	(TAT)5	15	87	101	ATGTTGAGCCCAACCCAAC
scaffold473050_13.	1	p3	(TTA)6	18	761	778	AATCATTCGATTTGGCAAGC
scaffold473101_14.	1	p3	(AGA)5	15	159	173	GGGAGGTTTCGTCACACAGT
scaffold473158_16.	1	p3	(TGA)5	15	105	119	GCAACGGAAACAACCTCTTT
scaffold473194_15.	1	p3	(AGT)5	15	1696	1710	AGCAGGTGAGGGTGAAAATG
scaffold473246_15.	1	p3	(TAA)5	15	655	669	AAACAAGGCAATTGTGGGTT
scaffold473296_18.	1	p3	(ACA)5	15	119	133	GCAGATAATCACGATTTAGTTGG
scaffold473333_11.	1	p3	(CTT)5	15	368	382	CTAGCTCTGAGATCCCGGC
scaffold473869_14.	1	p3	(TAT)6	18	80	97	CCATTGAGACTCGAACCCAT
scaffold474017_14.	1	p3	(TAT)5	15	5132	5146	ACGTCGGCATTGCTAAAATC
scaffold474186_12.	1	p3	(AAG)5	15	132	146	GAAGCCAGGGAAAGAATGAA
scaffold474266_13.	1	p3	(AGG)5	15	520	534	AAGAAGTCCCTGGCTTGGAT
scaffold474294_12.	1	p3	(ATT)7	21	378	398	TTGATGGCGTCGGTATGTTA
scaffold474449_16.	1	p3	(AAT)6	18	328	345	ATTTTCGTCGCCCCTCTTAT
scaffold474608_14.	1	p3	(TGA)5	15	67	81	GTTGCGTACATCTGACCCC
scaffold475012_15.	1	p3	(TTA)5	15	1041	1055	GCGGGACCTAGAATGTTGAA
scaffold475614_16.	1	p3	(TCT)5	15	172	186	CTGCCCTTAGCCGTTAGATG
scaffold475675_16.	1	p3	(TCA)6	18	2766	2783	CCTTCTCACTGACCTGCACA
scaffold475690_15.	1	p3	(CAG)6	18	287	304	TAATTTACGGCTCGGTTTCG
scaffold475886_17.	1	p3	(TCA)6	18	2055	2072	AAATGGCCGAAGAGATTCCT
scaffold476073_19.	1	p3	(GAA)6	18	257	274	GGTTTCAAATTGGCCAAACA
scaffold476219_16.	1	p3	(AAG)5	15	536	550	ACGTGCCCTGTTCTCTCACT
scaffold476431_10.	1	p3	(AAT)7	21	511	531	CCAAGTCCTCATCTCGTGGT
scaffold476465_10.	1	p3	(ACA)8	24	1122	1145	TTCCTTGTGAAGCACAATCCT
scaffold476622_11.	1	p3	(TTA)5	15	64	78	CCCATACATTTGTGGGGATAG
scaffold476894_13.	1	p3	(ACA)5	15	855	869	ATCGTGACCAACCCAAACAT
scaffold477057_14.	1	p3	(AGC)5	15	712	726	ACGATGTTTTGTTGCGATGA
scaffold477122_15.	1	p3	(CGC)5	15	35	49	GTCTACCCCGCCAGATCC
scaffold477874_14.	1	p3	(CCG)6	18	350	367	AACTCACCCACCTTCTCCCT

scaffold478116_16.	1	p3	(CAG)5	15	233	247	AAAATGAACGAGCATCCAGC
scaffold478184_12.	1	p3	(CTC)5	15	413	427	TTAGGTTTTGCCCAGGATTG
scaffold478253_12.	1	p3	(AAT)5	15	339	353	CCAAAATCTCGGCTTCAATC
scaffold478539_12.	1	p3	(AAG)5	15	257	271	AGTGTGCGCGATAGAGGAGT
scaffold478567_12.	1	p3	(TCT)5	15	298	312	GGGTTATATCCCCGTCTACCC
scaffold478817_15.	1	p3	(CAT)7	21	5804	5824	TGACTTATGCGTGCATGTGG
scaffold479031_10.	1	p3	(TAT)5	15	199	213	CCCAGCGGAGAGCTATACTG
scaffold479032_15.	1	p3	(TTA)6	18	43	60	TCACTCCGGATCAAATAGGC
scaffold479178_15.	1	p3	(AAC)5	15	741	755	TCCATGACATTGCCTACGTT
scaffold479188_14.	1	p3	(GAA)5	15	199	213	GATAAGCGGCTGAAGGTGAA
scaffold479586_10.	1	p3	(TCT)5	15	119	133	TGCAGCAACTTCCTCTCCTT
scaffold479607_17.	1	p3	(TAA)5	15	1877	1891	ATCCTGTGGTGGCATGTTTT
scaffold479648_14.	1	p3	(AAT)6	18	835	852	TGAGCGCACTCGAAAAGTAA
scaffold479791_15.	1	p3	(TAT)6	18	309	326	CAACTTTAGTCGTCGTCATCATC
scaffold479935_11.	1	p3	(GAG)5	15	365	379	TTTCGCAGTATGCCTCAGTG
scaffold480413_18.	1	p3	(CGG)5	15	447	461	TTCGATAACAAAAGGCCAGG
scaffold481031_13.	1	p3	(ATC)8	24	712	735	CCATTCCGTTGAACATCAAA
scaffold481610_14.	1	p3	(GGT)8	24	1645	1668	CAGCAGGAGTGGTGCAGATA
scaffold481762_11.	1	p3	(ATT)6	18	201	218	TCTAACATGCCATGGAGCAG
scaffold481907_13.	1	p3	(CAT)5	15	92	106	GGGTAACTGAGCCGAGTCAT
scaffold482065_10.	1	p3	(ATA)5	15	341	355	CACTCCATCGGATCCAAGAT
scaffold482080_15.	1	p3	(TTC)5	15	295	309	TGATGTTTAGGCTGCAGGAA
scaffold482589_18.	1	p3	(AGC)5	15	134	148	CAAGAAGCTTGCCAACATCA
scaffold483159_16.	1	p3	(GAA)7	21	444	464	TCAATTGATTTTCGTAATCCTGG
scaffold483495_15.	1	p3	(CCG)5	15	458	472	TAGGACGATAATTCCCACGC
scaffold483745_15.	1	p3	(CAG)5	15	1699	1713	GCATTAGTCCTGGTGGCATT
scaffold484141_11.	1	p3	(AAT)6	18	130	147	ATGCAGTTGGAAAGCACCTT
scaffold484554_14.	1	p3	(AAT)5	15	1298	1312	GTGGGGCCTTACACCAACTA
scaffold484643_13.	1	p3	(CGG)5	15	57	71	CTCAATTTTTCCGGCGAAT
scaffold484733_17.	1	p3	(CAA)6	18	247	264	GGACTGTGATGGGCTAGGAA
scaffold484775_18.	1	p3	(GAG)5	15	685	699	TGCGGATTAGGGTAGCTTTG
scaffold484921_16.	1	p3	(GGC)6	18	59	76	AAGAAACCAGCGACACATTG
scaffold484989_15.	1	p3	(TAT)5	15	108	122	CACAAATGGGGTTGACTTCC
scaffold485281_14.	1	p3	(CCA)5	15	166	180	ACCAAACGATGCAGATTTCC
scaffold485673_16.	1	p3	(TCT)5	15	1877	1891	CAAATTTGATTGGCTCTGTGA
scaffold485799_19.	1	p3	(GAA)5	15	2402	2416	GCCCTTACAAGACCATCCAC
scaffold485867_16.	1	p3	(ATA)5	15	309	323	ATGCCGGATCGAATAATCAG
scaffold485980_17.	1	p3	(CTC)5	15	297	311	CCAATATCTTCCTCCCCTCC
scaffold486634_12.	1	p3	(TAA)5	15	741	755	TGTATGCCCTGCAAAACAAA
scaffold486696_16.	1	p3	(AAG)6	18	3251	3268	TAGGCACAAATCTATCCGGG
scaffold486850_16.	1	p3	(TGT)6	18	33	50	CCAATTTATTGGGATTAAGGCA
scaffold486856_11.	1	p3	(AAT)6	18	390	407	CCTCATTTTGAACCCGAATG
scaffold487310_13.	1	p3	(AAG)6	18	2433	2450	TCCCAATTCAGACATGCAAA
scaffold487539_15.	1	p3	(ATA)5	15	1116	1130	GAAGCTGAGCAACGAGAAGG
scaffold487685_16.	1	p3	(AAT)5	15	1529	1543	CGTTTCCAACACCGACCTAT
scaffold487987_12.	1	p3	(GAT)5	15	113	127	CATTGGAGATGCCCTTAGGA
scaffold488314_16.	1	p3	(ATT)6	18	3792	3809	ATTCCGAAACCTGCTGTTTG
scaffold488353_10.	1	p3	(GCG)5	15	307	321	TGCAAGATTGAGCGAGATTG
scaffold488371_10.	1	p3	(ACA)6	18	206	223	GCTAGGTTTGTCTTCTGGCG
scaffold488624_16.	1	p3	(TAA)5	15	261	275	TCCTGAATGTCCCCACTGAT
scaffold488980_14.	1	p3	(TTG)6	18	912	929	TCATCCAAACCTCAACCAGA
scaffold489047_15.	1	p3	(ATA)5	15	344	358	TTCATGCCTGTATTTCAATCG
scaffold489629_15.	1	p3	(TAA)5	15	3362	3376	AAGTGGGCCTTATCTTGCCT
scaffold490478_16.	1	p3	(TTC)6	18	4033	4050	TAGGCCTCTTCTTCAGCAGC
scaffold490516_12.	1	p3	(TAT)5	15	639	653	GAATATATCTTGCCGTTGCCA
scaffold490615_16.	1	p3	(CTT)5	15	385	399	ATTTCACGTTTCACGCTTCC
scaffold490670_18.	1	p3	(TAT)6	18	364	381	CGGACCAGCCTAGAATTTGA
scaffold491260_17.	1	p3	(CAG)5	15	366	380	AGAATGGCGAAGAAGTGGAA

scaffold491581_13.	1	p3	(TAT)6	18	35	52	CGAACCATAGTTGTTGGACG
scaffold492617_18.	1	p3	(ATT)5	15	215	229	TGTCATGCATAATCGAACTGG
scaffold492647_14.	1	p3	(TGG)6	18	272	289	CCCATGGACCAAAACTATGC
scaffold492671_13.	1	p3	(AAT)5	15	190	204	GTGCCACCAAAAATCACACA
scaffold493036_11.	1	p3	(CGG)5	15	314	328	CAACGAATTCCGCCATAACT
scaffold493080_14.	1	p3	(TAA)5	15	444	458	CATGACAACCCTCTAGTTCGC
scaffold493265_12.	1	p3	(TCT)5	15	68	82	TGTGGAACTCATCATCTAATCCA
scaffold493275_14.	1	p3	(GCA)5	15	1000	1014	GCACAAATTGTTCCCATTCA
scaffold493357_14.	1	p3	(TTA)5	15	632	646	TCGTACAAAGGAACTTGGGC
scaffold493381_14.	1	p3	(CTT)5	15	227	241	ATCCCCCTACCCCAAACATA
scaffold493505_16.	1	p3	(GCC)6	18	1046	1063	GGGTTTTACCGCCGTTATTT
scaffold493735_12.	1	p3	(CTT)5	15	165	179	TGATTTCGCACGAGTGTTGT
scaffold493770_17.	1	p3	(GAT)5	15	861	875	CCATTTCCGGTGGAAGAGTA
scaffold493776_10.	1	p3	(GGT)7	21	368	388	TCTGGTGGGAGATCAAAAGC
scaffold493825_15.	1	p3	(TAA)5	15	387	401	AGCAAGGCTTGGATCAATGT
scaffold494013_16.	1	p3	(CCG)5	15	1152	1166	AGGCTTTGCATAGCTGTCGT
scaffold494083_13.	1	p3	(AAC)6	18	305	322	TTCGATTCAAGGTCTCACGA
scaffold494386_15.	1	p3	(AGA)5	15	1021	1035	GAAAATGGGTGTGACTTGGC
scaffold494669_12.	1	p3	(CAA)6	18	398	415	GCGGTGGATTTAGGATTTCA
scaffold494685_16.	1	p3	(TGA)5	15	74	88	TTACAAGGGAAAGGTTGCGT
scaffold494750_14.	1	p3	(TTA)5	15	61	75	CAAATACAAATTCAAGGATTATACAC
scaffold495384_15.	1	p3	(ATA)6	18	2154	2171	TTAAGTTGAAGGCCGCAATC
scaffold495568_10.	1	p3	(ATT)6	18	67	84	AATTAAACCCAAACCAAACTCTT
scaffold495571_16.	1	p3	(TTG)5	15	51	65	TTGGGATTAAGGCTTTGGTG
scaffold495606_15.	1	p3	(AAG)5	15	4174	4188	GTTGCAAAACGACTGGGAAT
scaffold495626_17.	1	p3	(ATT)6	18	204	221	ACCACAGCGACCGATAATTC
scaffold495979_15.	1	p3	(ATC)6	18	4760	4777	TCCTCTTTCTTGGGTGATGG
scaffold496061_17.	1	p3	(ATT)5	15	323	337	TTAGTCCGTTTAATCCGCCA
scaffold496109_15.	1	p3	(TCT)5	15	1413	1427	GGCACACAATCATGGTGAAG
scaffold496403_15.	1	p3	(AAT)5	15	3562	3576	GGGAGAGAGAGGGGAGTGTC
scaffold496428_12.	1	p3	(ATT)5	15	531	545	ATCGCAATCTCTCGGACACT
scaffold496437_16.	1	p3	(TAT)5	15	235	249	ATTGGGCCTGAGTTTTGATG
scaffold496453_15.	1	p3	(AAT)5	15	188	202	CGCGGTTATTTATGTCCGTT
scaffold496818_11.	1	p3	(TTC)5	15	968	982	GTCTAGCATCCTTTGGCAGC
scaffold496985_12.	1	p3	(TGT)7	21	41	61	TGTAGCCGACCCCAATTTAT
scaffold497224_12.	1	p3	(ACC)5	15	130	144	GGGTTTGTTCTAGTTCATCCCA
scaffold497349_15.	1	p3	(GCA)5	15	99	113	GGCTGAGATGGACTACGAGG
scaffold497442_15.	1	p3	(ATA)5	15	1809	1823	GGTGTTGAATGAAGGGAGGA
scaffold497624_17.	1	p3	(ATA)5	15	265	279	TGATGGGTGAGTTTTATATGATGC
scaffold497651_14.	1	p3	(ATC)5	15	1459	1473	AGCTGCAGATCACAGAGCAA
scaffold497753_14.	1	p3	(ATT)5	15	360	374	TTGTAATCCTTCCCACCTCG
scaffold497814_14.	1	p3	(TTG)5	15	345	359	ATGTAGCCGACCCCAATGTA
scaffold497819_13.	1	p3	(CAA)6	18	195	212	CCCCCATTACTCACATCAGAA
scaffold497842_15.	1	p3	(TAT)7	21	619	639	TGAAACCTTCTGCCCTCAAT
scaffold498002_14.	1	p3	(AAT)5	15	173	187	AGCATGAGTACATACATTTCTAGCAT
scaffold498003_15.	1	p3	(AAT)5	15	5763	5777	TTGGTGTAATTTTGGAAGGGA
scaffold498440_11.	1	p3	(TCA)6	18	89	106	AAATCCCCAAAAGAACATGG
scaffold498448_13.	1	p3	(GAG)5	15	138	152	AGCCTTTTGTGAATGATGGC
scaffold498544_15.	1	p3	(TCT)7	21	2575	2595	ACTGCTTTCTCACAACGCCT
scaffold498821_12.	1	p3	(GAA)5	15	183	197	GGATTCGATGTCTGCCAACT
scaffold498874_20.	1	p3	(TAA)5	15	527	541	GGTTCATCGGGTCCTGAGTA
scaffold498926_10.	1	p3	(ATT)6	18	398	415	ACTCAATATGCCCAAGGTGG
scaffold499225_11.	1	p3	(GAG)5	15	67	81	GGGTCGTCGATTTGGACTC
scaffold499541_14.	1	p3	(GAA)5	15	1046	1060	ATCCAAGGGCTCGATTCTCT
scaffold499777_14.	1	p3	(GGC)5	15	942	956	GCAGAAAGCGTTTTAGGTCG
scaffold500183_17.	1	p3	(TTC)5	15	213	227	TTGTCCAAGTGGGAGATTGTT
scaffold500383_17.	1	p3	(TTC)5	15	478	492	TGGATGAAGGGGTTGTTGAT
scaffold500570_12.	1	p3	(TTA)5	15	115	129	TTTCAAATACCTTGACCAACGA

scaffold500689_17.	1	p3	(GCA)5	15	481	495	CAAGGCATATAAGCTGGGGA
scaffold501061_13.	1	p3	(ATA)5	15	1172	1186	GCTTGTAGACGCTTTACGCC
scaffold501094_15.	1	p3	(ATT)5	15	166	180	TGTGTTGTATGCGTTCATGACT
scaffold501158_15.	1	p3	(TAA)6	18	310	327	CACCGCCTTAATTTCTCCAG
scaffold501233_12.	1	p3	(TTG)5	15	190	204	CTTTATGATGGAGGCGGATT
scaffold501294_15.	1	p3	(CTT)7	21	365	385	CTCGACACAGTTCATCGGAA
scaffold501366_17.	1	p3	(ATC)6	18	2102	2119	TGCCTCATGTAATGGTGGAG
scaffold501811_15.	1	p3	(CAT)5	15	4343	4357	TGCCTGTAACAAGGGTGGAT
scaffold502014_15.	1	p3	(ACA)5	15	1163	1177	GTCGGGGTAATCCGACCTAT
scaffold502577_15.	1	p3	(ATT)6	18	3775	3792	TTGACCGTACTGGTGATGTACC
scaffold502663_14.	1	p3	(TCT)6	18	833	850	TGAAAACTCCGGTTCCATTC
scaffold502895_14.	1	p3	(CTT)7	21	242	262	TCATCGAATCAAATCCATCAA
scaffold503301_14.	1	p3	(TCT)5	15	928	942	CCATTTTCCCATCAACATCC
scaffold503573_15.	1	p3	(ATT)5	15	183	197	TTACTATGCGGACTGGGACC
scaffold503629_13.	1	p3	(ATT)6	18	151	168	AAGGGAGCTACAACCTTTCATC
scaffold503774_16.	1	p3	(GGC)5	15	530	544	GGAGACAGCGGCTAGTAACG
scaffold503777_15.	1	p3	(TGT)5	15	212	226	GCTACGAGGCAGATAAACGG
scaffold503861_18.	1	p3	(GCA)5	15	718	732	TAGTACCGTGGGGCAGATTC
scaffold503994_13.	1	p3	(AAT)5	15	386	400	GTTTGTCGATCATTACGCCC
scaffold504271_12.	1	p3	(AAT)5	15	729	743	TTCATGTTTCGCGATTCAAC
scaffold504489_19.	1	p3	(ACA)6	18	1120	1137	CATAGGGTTGCTGATGCAGA
scaffold504850_14.	1	p3	(TCA)5	15	51	65	GAATGGCATGTGGATCTGTG
scaffold504868_15.	1	p3	(ATA)5	15	343	357	ATTTGTTCAAAATCCGCGAC
scaffold505305_11.	1	p3	(AGC)5	15	67	81	TTACAGCTTGGTTTCGGAGG
scaffold505480_14.	1	p3	(ATT)8	24	1007	1030	GCATAGGATATTTATTACACCACGG
scaffold505906_15.	1	p3	(TCC)6	18	4062	4079	GCCCTCAAATCTGACCAAAA
scaffold506257_10.	1	p3	(ATC)6	18	543	560	TCATCACCACCACCATCATC
scaffold506391_15.	1	p3	(CGG)5	15	926	940	CAATTTGATTGTGCGATGGT
scaffold506560_13.	1	p3	(GAA)5	15	205	219	CAATTCCCTTGGATCCTGAA
scaffold507037_18.	1	p3	(ACA)5	15	212	226	AATTGGCCCTCATTTCCATT
scaffold507173_19.	1	p3	(CAG)5	15	86	100	TGCTCATCAAAAAGTTCCCA
scaffold507338_15.	1	p3	(TGA)6	18	991	1008	ACCCCCTGTTTCTGGATCTT
scaffold507379_10.	1	p3	(TAT)5	15	316	330	TGTACGGTGTAATGCTTGTGC
scaffold507492_16.	1	p3	(ATA)5	15	475	489	CTTGTAATCCGCATCCTCGT
scaffold507582_14.	1	p3	(ACA)7	21	438	458	CACGAGATGGGGACTCTTGT
scaffold507627_19.	1	p3	(CGG)5	15	507	521	ACAAGTATCCACCACTCGCC
scaffold507780_10.	1	p3	(GAA)5	15	29	43	CCTCCTCTATTGCTGATTTAAGGA
scaffold507899_15.	1	p3	(GTT)6	18	545	562	GGCGTTTCTTTGTTGAGAGC
scaffold507988_16.	1	p3	(TCA)1	30	1005	1034	AATTGTGCTCCATTTCCCAG
scaffold508421_16.	1	p3	(CTT)5	15	405	419	TCATCGAATCAAATCCATCG
scaffold509085_13.	1	p3	(AAG)5	15	245	259	CTGGTCCACTTCCAGCTTTC
scaffold509152_14.	1	p3	(GAG)5	15	254	268	ATTCTACGGTGATTCGTCGC
scaffold509447_16.	1	p3	(ATC)6	18	1028	1045	AGGCTTGCTCAACCAAATCA
scaffold509521_12.	1	p3	(GAG)6	18	437	454	CTTTTCAGGCCCATTTCTCA
scaffold509722_15.	1	p3	(TGA)5	15	49	63	CCCAAGACCCCAATTTGATT
scaffold510321_12.	1	p3	(AAT)5	15	470	484	TTCTCAGTGCTATTTTGTTCCG
scaffold510335_14.	1	p3	(CGC)5	15	300	314	AGGAGAAGAAAGCCGAGGAG
scaffold510527_17.	1	p3	(GAA)6	18	352	369	AGGAGTTTTCCTCTTTCCGC
scaffold510692_14.	1	p3	(ATT)5	15	769	783	CATGCAAGACAACAAGGCAC
scaffold510895_15.	1	p3	(TAT)5	15	396	410	TCCATCTGTCATCTCATCCA
scaffold511001_16.	1	p3	(AGG)5	15	476	490	GCAGCCACGATTCTCAAGAT
scaffold511248_13.	1	p3	(ACC)5	15	636	650	CGTTCTAAGGCGTGCGTATT
scaffold511303_13.	1	p3	(TGG)5	15	58	72	AGCTTTGGTTCATGTAGCCG
scaffold511557_11.	1	p3	(GCG)6	18	489	506	GGCCAGCTATACAAATTCGC
scaffold511714_10.	1	p3	(ATT)6	18	343	360	ACCCTAATCAACATCTGCCG
scaffold511725_15.	1	p3	(GCT)5	15	52	66	CGTCATCGTGACGTCTGC
scaffold511745_19.	1	p3	(CCA)5	15	417	431	CTCGTGTCACCAGGTCAAAA
scaffold511889_17.	1	p3	(TTG)5	15	52	66	CGACCCACATAGTGGAAAA

scaffold512814_11.	1	p3	(TGC)5	15	36	50	TCTCTTCCATCCAATAATTCCTGT
scaffold512912_15.	1	p3	(ACA)5	15	445	459	TGTGACTGCATAAAGGCCAA
scaffold513228_11.	1	p3	(TAA)5	15	408	422	CCACCAAGAATTTGTGCCTT
scaffold513615_11.	1	p3	(CCT)7	21	1189	1209	TGTTTCCCTTTCCCTTCCTT
scaffold514041_16.	1	p3	(TCC)6	18	104	121	TTTCAAAAGATGAGCTACTAGCAA
scaffold514110_15.	1	p3	(CGG)5	15	357	371	CCTTTAACCAAAAGTGCCCA
scaffold514195_16.	1	p3	(CTG)5	15	1399	1413	GATTCTTGCTAACATCTCTGCG
scaffold514417_16.	1	p3	(ATT)7	21	3253	3273	GCCACAATAACTTGTGAAACCA
scaffold514430_10.	1	p3	(TAT)5	15	172	186	ACCACGTTGGGATCTTGGTA
scaffold514431_10.	1	p3	(ATC)6	18	631	648	CCTTTTTCTGTTTCTTGCGG
scaffold514552_17.	1	p3	(ATA)5	15	605	619	TGGGAAAAGAAAATGGGAAA
scaffold514739_14.	1	p3	(TAA)5	15	376	390	TGTTGTATGGTGAAGCGTCC
scaffold514975_10.	1	p3	(GAA)5	15	326	340	GCTGAAAGAACTGAGGACGG
scaffold515030_19.	1	p3	(ATA)5	15	1129	1143	TGTTCACACACCCCACCTTA
scaffold515492_15.	1	p3	(ATC)6	18	980	997	CATTTCAACACAAGGCAAGC
scaffold515548_12.	1	p3	(AAT)6	18	477	494	CGTGGATATAACTCGGCCAT
scaffold515701_17.	1	p3	(TCT)5	15	1658	1672	CCCCATATGAATCCTTTCCA
scaffold515886_12.	1	p3	(TGT)6	18	43	60	ATGTAGCCGACCCCAATTTA
scaffold516263_16.	1	p3	(ATC)6	18	2304	2321	TGTACAATGACCGTGCCTGT
scaffold516296_12.	1	p3	(CCG)5	15	225	239	TGTTGAGGAGTAGGGTTGGG
scaffold516472_14.	1	p3	(GTG)5	15	365	379	GGGGTCCTTGTCGTATAGCA
scaffold516483_19.	1	p3	(TGC)6	18	509	526	TGCCTTCTGAATGATGGACA
scaffold516719_12.	1	p3	(TTC)5	15	239	253	GTCGCTGTTGATGTTCCAGA
scaffold517207_15.	1	p3	(TCT)5	15	99	113	TTGATGTAGATATGGAGCGATTTT
scaffold517279_16.	1	p3	(ATG)5	15	1638	1652	ATCAAGGGCCAGTCTGCTTA
scaffold517431_17.	1	p3	(CCG)8	24	595	618	ACAGTGGAGACGGAATCGAC
scaffold517761_16.	1	p3	(AGA)5	15	1178	1192	TTGGGAAGTTTCGTCACACA
scaffold518022_16.	1	p3	(AGC)5	15	2047	2061	GGTAGCCGAGCAGCTTCTAA
scaffold518273_16.	1	p3	(CGG)6	18	6007	6024	TTCGGAGGGCAACTCATAAC
scaffold518294_15.	1	p3	(TCA)6	18	65	82	CGATGAAGCTCGGAGAAGTT
scaffold518433_15.	1	p3	(CAT)5	15	1547	1561	TCCTGCAGTTTTTGTGGTTG
scaffold518493_10.	1	p3	(TGG)5	15	258	272	TTTGGAGGGGTTTAGGTTCA
scaffold518587_14.	1	p3	(TTA)5	15	277	291	TCGGGCTTTGATTTCAAGAT
scaffold518679_17.	1	p3	(CAG)5	15	2219	2233	TGCAATTTCAGGCACATCAT
scaffold518703_14.	1	p3	(GGT)5	15	1275	1289	TCTGGTTCGGATTGACATGA
scaffold518821_15.	1	p3	(AAT)5	15	71	85	TTCAGAATCATTTACTTCCAAGTTT
scaffold519098_11.	1	p3	(GAA)6	18	181	198	CTCCTGCTTCACCTCGATTC
scaffold519185_12.	1	p3	(CGG)5	15	282	296	AGAGAGAACAGATGCGAGGG
scaffold519345_17.	1	p3	(CTT)5	15	1253	1267	GTTGCCACAATTTCCTGCTC
scaffold519913_14.	1	p3	(GGC)6	18	64	81	GGTGTAGATCTGGCGGGTAG
scaffold520527_13.	1	p3	(TTA)8	24	258	281	TCCGAGGTCAGCAATTCTTC
scaffold520626_11.	1	p3	(AAT)5	15	269	283	CAAAAAGGAACGCAAAAACAA
scaffold520840_20.	1	p3	(CGC)7	21	140	160	TATCAAAACTGGATTGGCCC
scaffold521749_15.	1	p3	(TTC)5	15	342	356	GGCGATTGTCAACTTGGTTT
scaffold521811_12.	1	p3	(AAG)5	15	1468	1482	ACATGCAAGGAGTGAAAGGC
scaffold522153_15.	1	p3	(ATT)5	15	222	236	GGGGCGTGACATTAACACTA
scaffold522367_10.	1	p3	(TTC)6	18	90	107	GCCGGAAGAAAAGACACAAG
scaffold522523_13.	1	p3	(CAG)5	15	314	328	ATCCGCAGTCAAAACGTACC
scaffold523135_16.	1	p3	(CCG)6	18	391	408	CCCAACCTTTTACTCCTCCC
scaffold523314_10.	1	p3	(TGA)6	18	76	93	CCCAAGACCCCAATTTGATT
scaffold523389_17.	1	p3	(TTA)5	15	1009	1023	CGCAAGATGTTTCAGGGATT
scaffold523450_15.	1	p3	(CAC)5	15	709	723	AATGTTTCTACGCATTGGGG
scaffold523632_14.	1	p3	(AAT)5	15	66	80	GCAAAATCTCAATTGTAGTGCC
scaffold523640_13.	1	p3	(CAT)5	15	328	342	ACATGTGGTGGCAGGTTACA
scaffold523697_10.	1	p3	(CAT)5	15	297	311	TAGCCTGCTCAGCCTCTCTC
scaffold523770_16.	1	p3	(GGC)5	15	216	230	ATACTGGGCTTCTCCGACCT
scaffold523794_16.	1	p3	(GGT)5	15	648	662	TGAATCGGGACAGCATGTTA
scaffold523975_15.	1	p3	(GCG)6	18	2329	2346	TGTAGCCCGTGACTGTACCA

scaffold524247_16.2	1	p3	(TAT)5	15	44	58	ACCCTCACTAGTTTCGGTTAGA
scaffold524451_15.1	1	p3	(AAT)6	18	872	889	ACAACCAAGCAGGTCCAAAA
scaffold524470_19.1	1	p3	(TCA)5	15	112	126	CGATACCCATAACGGGTGAG
scaffold524568_13.8	1	p3	(TTC)5	15	168	182	CATGGTTTTGGGAGGAGAGA
scaffold524730_19.3	1	p3	(CCT)6	18	432	449	TGTCAATGCATCTGCCTCTC
scaffold525239_10.0	1	p3	(TAT)5	15	134	148	AGAAAATGCTGGAAATGAGGA
scaffold525242_17.0	1	p3	(TGG)5	15	1278	1292	ACGGCTAAAATCAGGAGCTG
scaffold525365_16.1	1	p3	(TCA)8	24	855	878	TAAATCCTTCGAGGTCACCG
scaffold525366_10.2	1	p3	(GGA)5	15	77	91	GAATCAGTGCTTGCCGATCT
scaffold525873_11.7	1	p3	(AAG)5	15	273	287	GTGGAAGCATCAAAGCAGGT
scaffold526130_10.1	1	p3	(GCT)5	15	52	66	GCGTTATCGTGACGTCGG
scaffold526931_18.7	1	p3	(TTA)5	15	2679	2693	CTTTTTGTTTTGGAGTGGGG
scaffold527008_17.0	1	p3	(TAT)7	21	2541	2561	AATGCGATAGCCTTGCCTTA
scaffold527011_11.4	1	p3	(CAA)5	15	135	149	CCCGGATCCACTACAAGTTC
scaffold527183_15.1	1	p3	(CCG)7	21	1230	1250	TGCATCTGAATACACGAGGTTC
scaffold527231_16.1	1	p3	(GAT)7	21	995	1015	AATGCCAACACAACCAAACA
scaffold527324_16.7	1	p3	(AAT)6	18	1894	1911	ATGTTCATCAATTGCAGCCA
scaffold527554_12.8	1	p3	(ATT)5	15	347	361	TTCGACCCCAACTCAATAGC
scaffold527633_14.2	1	p3	(TGT)5	15	519	533	TAGCCGACCCCAACTTATTG
scaffold527876_17.8	1	p3	(CAT)5	15	467	481	TGAAACCCCATGATTTCCAT
scaffold527938_15.0	1	p3	(CTC)5	15	1180	1194	TGCACATTTTCCATTGAAGG
scaffold527943_13.5	1	p3	(TTA)6	18	136	153	TGTAAAATTTCCAAGGCAGAGA
scaffold527991_15.3	1	p3	(TCT)5	15	474	488	AATTGGCATTTTGTAGGCTCA
scaffold528041_17.1	1	p3	(TTG)5	15	57	71	AGCTTTGGTTCATACAGCCG
scaffold528206_10.6	1	p3	(TAA)5	15	1509	1523	CACCCGGAACTCGAAAAAT
scaffold528233_14.3	1	p3	(ATC)5	15	2989	3003	ACAAAAGCAAACCGCTAACC
scaffold528814_16.4	1	p3	(TCA)5	15	610	624	ACCGGACACAATACTGCACA
scaffold528816_13.6	1	p3	(TGT)5	15	45	59	ATGTAGCCGACCCCAATTTA
scaffold528832_12.1	1	p3	(TGA)5	15	51	65	GACCCCAATTTGATTGGAAA
scaffold528844_16.8	1	p3	(CAC)5	15	309	323	GCGAACTGACAACGAGATCA
scaffold528912_19.8	1	p3	(CCA)6	18	271	288	GTTGGTTCAGGGTTAGCAGC
scaffold528994_12.6	1	p3	(TTG)6	18	49	66	TTGTATTGTCTTGATTGCAGGAA
scaffold529027_17.5	1	p3	(GAT)6	18	51	68	GGTACGTTACTGTAAAACCCTGA
scaffold529220_18.1	1	p3	(AAT)5	15	51	65	CAGAGCGCACTCGAAGAGTA
scaffold529222_15.4	1	p3	(TGA)5	15	4189	4203	CAGAGGCACAGATTAGCAGC
scaffold529239_18.9	1	p3	(TCC)5	15	686	700	TACTGCTGATTCAAGTGGCG
scaffold529245_11.8	1	p3	(ATT)5	15	53	67	GCTAACCATTTACTTGCACATTTT
scaffold529357_15.6	1	p3	(ACA)5	15	297	311	AAAGCATTCACGTAACGGGT
scaffold529509_13.2	1	p3	(TCA)5	15	2543	2557	AACACTATCCCACAAATCACCA
scaffold529541_11.9	1	p3	(TTA)6	18	98	115	TCGATGTATTGTTTGGATAATATGCT
scaffold529672_17.1	1	p3	(AAT)6	18	399	416	ATTCGGATTGCATCCAAGAA
scaffold529862_16.1	1	p3	(GGC)5	15	1815	1829	TCCGTCATTTTCCCACTCTC
scaffold529953_15.0	1	p3	(TTG)5	15	59	73	TGCATTCAACATCATTACAAAGTC
scaffold530361_13.5	1	p3	(AAT)6	18	47	64	GGACTTTGGTGTGAGAAAATTG
scaffold530424_12.5	1	p3	(AAG)5	15	96	110	TGAATTTCACCAATCGGGAG
scaffold530500_13.9	1	p3	(TGT)7	21	214	234	TGAGATTCCCGCATCCTATC
scaffold530557_16.7	1	p3	(CAT)6	18	1936	1953	CGCCCGACTGAATTATCATC
scaffold530719_16.6	1	p3	(GAT)6	18	749	766	TGAAGATTCGTGCGATGTGT
scaffold530838_15.4	1	p3	(GAA)5	15	531	545	AGGTTTTCGGCGGAGATTAT
scaffold530931_15.4	1	p3	(TGA)7	21	43	63	CCTCAAGACCCCAATTTGAT
scaffold531584_17.2	1	p3	(AAT)5	15	1172	1186	TCCCAAATGATTTCAAAATGG
scaffold531681_16.5	1	p3	(AAT)5	15	823	837	GCAGAAGAGAAGGTGGGAGA
scaffold531990_12.9	1	p3	(TAT)5	15	107	121	CGAGAGAGAGAATGAGTGGTGA
scaffold532019_14.9	1	p3	(TCA)5	15	104	118	CCCAGGCTCAAATTCCTACA
scaffold532201_10.0	1	p3	(TTC)5	15	399	413	TTGTTGATGGTTGAGAGGTGTC
scaffold532317_15.8	1	p3	(TTG)5	15	891	905	AGAATCACAATGCTCCTGGC
scaffold532581_13.6	1	p3	(ATT)6	18	413	430	AAAATGATGATTCCGGGTCC
scaffold532616_17.2	1	p3	(AAT)5	15	622	636	TCAATATGAATTGATCGCCG

scaffold532628_14.	1	p3	(TAA)8	24	399	422	ATTGCTCGATCCACCTCTTG
scaffold532879_16.	1	p3	(TAT)6	18	412	429	TCAAATTGTGTCGAGGCTAATG
scaffold532982_16.	1	p3	(GTG)6	18	3291	3308	GTCTAAAATTCGGCAGCGAC
scaffold533052_16.	1	p3	(CCG)5	15	1171	1185	GGACTCCCATCGTCTCCATA
scaffold533134_10.	1	p3	(AAT)5	15	282	296	GAGCTGAGCAATGAGAAGGG
scaffold533461_15.	1	p3	(TTA)7	21	43	63	TGAAGTTTCGAAGACTGGAAGA
scaffold533689_11.	1	p3	(AAT)7	21	424	444	TCACCGTTGTCATAGCCAAA
scaffold533873_16.	1	p3	(CGC)5	15	516	530	AATATTGGCTTCCCCAAACC
scaffold533989_15.	1	p3	(TGT)5	15	46	60	ATGTAGCCGACCCCAATTTA
scaffold534026_12.	1	p3	(AAT)5	15	335	349	TGAAAACGATTTAAACGTGGG
scaffold534232_15.	1	p3	(TGT)5	15	4596	4610	CAAATCATGGAAACAGCACG
scaffold534588_20.	1	p3	(TCT)6	18	890	907	AGGTCGGCCCTGTAGAATTT
scaffold534628_17.	1	p3	(TTG)5	15	914	928	TGCATACCAAGTTATTGGCG
scaffold535278_12.	1	p3	(TCT)7	21	1028	1048	CAAAACGCCTCCAATTTTGT
scaffold535391_16.	1	p3	(ATG)5	15	842	856	CATCGACTTCCACGACAAGA
scaffold535480_10.	1	p3	(ATC)6	18	66	83	CTGCCATCTGGTACAACTGC
scaffold535533_17.	1	p3	(TTG)5	15	1159	1173	CACCGGTTAGGTGGGTAGAA
scaffold535844_16.	1	p3	(AAT)5	15	341	355	TGTGTTGCTGAAGGAGTTCG
scaffold535895_15.	1	p3	(TGT)5	15	47	61	TGTAGCCGACCCCAATTTAT
scaffold535965_17.	1	p3	(TCA)6	18	107	124	TGATCACAAACTTAGCGGACA
scaffold535992_16.	1	p3	(AAT)6	18	639	656	TGCTTATTTGGATTGGCCTC
scaffold537445_15.	1	p3	(TAT)5	15	1046	1060	ATTGATCGAGACCGAACCAC
scaffold537507_20.	1	p3	(GAT)5	15	78	92	AGTTCTAGTAGCCCGGAGCC
scaffold537543_17.	1	p3	(TCA)5	15	247	261	CATTGCAAGACAGAACCGAA
scaffold537561_17.	1	p3	(TTG)5	15	208	222	GCAGACCTAACATAGTGGAAAA
scaffold537678_13.	1	p3	(CCA)5	15	70	84	ATCCTCCTCCACCCGTCTAC
scaffold537876_11.	1	p3	(ATT)5	15	435	449	CGAACCCATTAAGCCTCAAA
scaffold538028_15.	1	p3	(CAT)7	21	1287	1307	AGGCTGGCTCTTTCAATCAG
scaffold538060_10.	1	p3	(ATT)5	15	234	248	CTGCAGAAATGAGAGGAGGG
scaffold538209_12.	1	p3	(CAT)6	18	63	80	TTGGCCTAGACTTCACATTTTTC
scaffold538494_15.	1	p3	(ATT)7	21	919	939	AATGCTTGCAAGGGTGTAAGA
scaffold538554_11.	1	p3	(ATC)5	15	54	68	GTACCGATATCATCCCCACC
scaffold538858_13.	1	p3	(TAA)5	15	529	543	AGGTCAGATCGAAGGTCTCG
scaffold538885_15.	1	p3	(TCA)5	15	202	216	ACTGCATCTGGATCCTCCAC
scaffold538967_14.	1	p3	(ATA)5	15	3343	3357	GGAGCTTGGGATTATAGGGC
scaffold539049_16.	1	p3	(TAT)6	18	3048	3065	AGGGAAGTGTGGGGAAGAAG
scaffold539270_15.	1	p3	(ACC)5	15	760	774	ATCCCAATTTGGCAACTCAT
scaffold539640_18.	1	p3	(GAG)5	15	409	423	GTGATCTTGAAGGAGCTGGC
scaffold539738_13.	1	p3	(TGA)7	21	545	565	CAGAGCGAGGGGTACTCAAG
scaffold539829_15.	1	p3	(TTA)5	15	583	597	TTCAGTCATTGCGTGCACTT
scaffold539843_13.	1	p3	(ACA)5	15	82	96	CAGAAATGACAAAATTCATGGC
scaffold540156_14.	1	p3	(GCC)5	15	85	99	AGTCTCCCTCGCCAGAAAAT
scaffold540632_15.	1	p3	(AAG)5	15	1110	1124	CAAACATTATGCACCAAGCG
scaffold540721_13.	1	p3	(AAT)6	18	287	304	GAAAGGGGTGACCAAGTTGA
scaffold540883_10.	1	p3	(GCC)5	15	439	453	TGAGAGAACCTCCCCCTTTT
scaffold541049_16.	1	p3	(GTC)5	15	1405	1419	CTCATGCCGGAGTTAGGAAG
scaffold541502_13.	1	p3	(GAA)5	15	199	213	TAGGAAGCCAACAATGGAGG
scaffold541693_11.	1	p3	(TGT)5	15	46	60	TGTAGCCGACCCCAATTTAT
scaffold541823_13.	1	p3	(TAA)5	15	518	532	GCCTTCTCGAATTTGTCTGC
scaffold541975_17.	1	p3	(TGT)6	18	43	60	TGTAGCCGACCCCAATTTAT
scaffold542130_16.	1	p3	(ACA)6	18	1089	1106	CCGCAATTTGATTGGGAATA
scaffold542271_13.	1	p3	(TAA)5	15	244	258	TCACGGGTTTGGGAATTAAA
scaffold542322_15.	1	p3	(AAC)5	15	4564	4578	GGTAGCCCCTAACCACACAA
scaffold542396_14.	1	p3	(ATT)5	15	992	1006	CCCAGCTCACGTTTACCCTA
scaffold542423_12.	1	p3	(TCC)5	15	204	218	TTTTATCTTCGGTGCGGAAC
scaffold542447_13.	1	p3	(TCA)6	18	217	234	TTCATCTGTAACGGGTGGGT
scaffold542685_12.	1	p3	(TAT)5	15	152	166	ATCAGGTTGCCCTCCTTTTT
scaffold542744_13.	1	p3	(CGC)5	15	50	64	GGTGGTATGGTGTGGAGGAC

scaffold542992_17.	1	p3	(CTC)6	18	208	225	TCTTCGTGTTTGTCCATTCG
scaffold543113_15.	1	p3	(AAC)6	18	955	972	CGCCATTTCGTGTTTAATGA
scaffold543610_11.	1	p3	(TTA)5	15	509	523	AATCTGAGGCATGTTACCGC
scaffold544059_10.	1	p3	(ATA)5	15	100	114	CACAATTTGAGGTGTATGGCA
scaffold544152_11.	1	p3	(ATT)6	18	453	470	TATTAGGGCATGCAAAAGCA
scaffold544633_14.	1	p3	(ATA)5	15	575	589	ATCATCCCCAAAGCAAAAAT
scaffold544880_17.	1	p3	(TGA)7	21	89	109	GTTCGTAAAGAATGGGCTGG
scaffold544988_15.	1	p3	(ATT)5	15	448	462	TTTTTGCAACGTGGTCTTCA
scaffold545383_15.	1	p3	(TCT)5	15	1024	1038	CAACTGTCCTTGGAAGAGGG
scaffold545439_13.	1	p3	(CGC)5	15	531	545	GTGTGGAAAAGGGAGTGCAT
scaffold545557_12.	1	p3	(GGT)5	15	656	670	CCACCTGCGAACCATAAAAT
scaffold545657_15.	1	p3	(ACA)7	21	338	358	TTGGATTGCAACCTCCTTTT
scaffold545774_15.	1	p3	(AAT)5	15	923	937	CAAAATGTACCCCGAAATGG
scaffold545872_15.	1	p3	(ATA)6	18	957	974	GGCCTACAAACTGCCCATAA
scaffold545934_13.	1	p3	(AAT)6	18	391	408	AAATCCAGAACGCAGGTTTG
scaffold546127_18.	1	p3	(GGC)6	18	592	609	CATATCGATTTTGCCTGGCT
scaffold546421_10.	1	p3	(ATC)7	21	333	353	TTTGTGCTCACACTTCTCTCG
scaffold546929_13.	1	p3	(AAC)5	15	336	350	AAGCCCACCTTATTGCTTGA
scaffold547013_16.	1	p3	(AAC)5	15	922	936	CCCCGCACATAGTCAAGAAT
scaffold547073_15.	1	p3	(TAC)5	15	2902	2916	TGTCCGGTGTCGTTTTAATG
scaffold547631_15.	1	p3	(TTA)5	15	615	629	GAAGGCATGGGTTTTCTTGA
scaffold547644_17.	1	p3	(GAG)5	15	145	159	AGAATGGAGCGGAGGTTCTT
scaffold547685_13.	1	p3	(CGG)5	15	46	60	GGGAGGGAAGAGAGGAGAAA
scaffold547858_11.	1	p3	(AAT)6	18	98	115	TTGACCAAGATACACCTTGCAT
scaffold548207_16.	1	p3	(ATA)5	15	2746	2760	TGGAATGATGAGGTGGGTAAA
scaffold548235_16.	1	p3	(CTG)5	15	783	797	ATTTGCTCTAACCAATGGCG
scaffold548319_10.	1	p3	(GCC)5	15	55	69	ATCCCCCTTTCCTAGGGTTT
scaffold548443_10.	1	p3	(ATC)6	18	457	474	TACTGCTCTCTGGGGCATCT
scaffold548567_19.	1	p3	(AGA)5	15	957	971	CTGTTGGGAGGTTTCGTCAT
scaffold548636_16.	1	p3	(CCA)5	15	283	297	TTTTTGCCCTATTTTTCCCC
scaffold548772_18.	1	p3	(ATC)5	15	97	111	TGGCCCAACCTCAATATTCT
scaffold548861_15.	1	p3	(ATG)6	18	1271	1288	GCGTGATACCAATGGATGTG
scaffold549199_17.	1	p3	(TTA)5	15	258	272	TTCTCAATCAAATCGGGGTC
scaffold549288_18.	1	p3	(TTC)5	15	67	81	CGGTTTTCCCTACTCTCCCT
scaffold549328_15.	1	p3	(ATT)5	15	5240	5254	TTTAGCTTCTGGTGGGCTGT
scaffold549506_16.	1	p3	(TTA)7	21	245	265	TTTGCCGATCATCCACTACA
scaffold549669_19.	1	p3	(CGC)5	15	41	55	TTCTGTCAATTTATGTGTTAACTTCTG
scaffold549719_17.	1	p3	(CGG)5	15	103	117	AATTTTTCCAACTCATCCGC
scaffold549806_14.	1	p3	(ATC)5	15	310	324	TAGCCGAATTCTCCTCGAAA
scaffold549808_12.	1	p3	(TCT)5	15	916	930	GGGGGTTTTGGATGAACTTT
scaffold549921_18.	1	p3	(TCC)5	15	2436	2450	CATCCACCTTCACACCATCA
scaffold549955_17.	1	p3	(CGG)6	18	57	74	AATAATTTACCGGCAATGGTG
scaffold550847_16.	1	p3	(CGG)6	18	152	169	GAAAACTGAGCCAACCCAAA
scaffold551119_15.	1	p3	(TTA)5	15	217	231	TTCCGGTAATTCAACAAAACG
scaffold551203_15.	1	p3	(AAT)5	15	1673	1687	CCACGAATATGACGACAACG
scaffold551651_15.	1	p3	(AAT)5	15	1989	2003	CGATCCAAGGAGAAAATCCA
scaffold552101_15.	1	p3	(CAC)5	15	1399	1413	TGCCTTCTTTAACAGCCCAT
scaffold552626_16.	1	p3	(AAT)6	18	925	942	TATTTCCTTCTCGTGGGTGC
scaffold552656_18.	1	p3	(ATT)5	15	2265	2279	TCCCACGAGGAATTTGAGTC
scaffold552657_12.	1	p3	(CGG)5	15	505	519	GATGAGACCACCGAGAGGAA
scaffold552834_11.	1	p3	(TCC)5	15	339	353	ACAACTCGTCTTCCGTGGAT
scaffold553078_10.	1	p3	(GCC)7	21	100	120	CAGAGCCAGCCTATCTCCAG
scaffold553245_13.	1	p3	(TTC)5	15	242	256	GCATGGGGTTATTCAAGAGG
scaffold553457_13.	1	p3	(GAA)5	15	284	298	TTAGCATCCAAAAGGGTTGG
scaffold553531_13.	1	p3	(ATA)5	15	330	344	AGTTTGGGTATCCGCTCCTC
scaffold553555_15.	1	p3	(TTG)5	15	1746	1760	AAAGCCGAATTCGTTACAACA
scaffold554172_18.	1	p3	(TTA)5	15	176	190	TTCCGGTAATTCAACAAAACG
scaffold554280_16.	1	p3	(ATC)5	15	1057	1071	GACCGTCACAGTTAGTGCCA

scaffold554654_14.	1	p3	(AAT)6	18	756	773	AACGCATACCACATAAGCCA
scaffold554843_15.	1	p3	(AAC)7	21	521	541	AAATCCAGCAGCAAATCGAC
scaffold554858_19.	1	p3	(ATC)5	15	241	255	CCGAGAGATGTCTCCCAGAA
scaffold554905_12.	1	p3	(CAT)6	18	108	125	TTTCGGGAATTCAAAGCATC
scaffold555104_14.	1	p3	(CTT)5	15	807	821	ACCTTGCTCGTGTACCCATC
scaffold555414_14.	1	p3	(ATA)5	15	121	135	TGGGAGCAAATTTCAAGAGTC
scaffold555451_11.	1	p3	(TTC)6	18	76	93	AAAATTGGTGCGGATGTCTC
scaffold555629_18.	1	p3	(TAT)5	15	620	634	CAAACCGACAGGGAAACACT
scaffold555829_14.	1	p3	(TCA)6	18	109	126	ATTCGGTTGCTTTTGTCACC
scaffold555887_11.	1	p3	(TTC)5	15	237	251	CCACTGTTGTTGCTGCTGTT
scaffold555897_12.	1	p3	(CTC)6	18	685	702	AAACAGTTTCCCTGCAATCG
scaffold555931_16.	1	p3	(ATG)5	15	3819	3833	GACGACTCAGCTTGACCACA
scaffold555958_12.	1	p3	(CAT)5	15	425	439	ATGCTTTTGCAGGATTCAGG
scaffold556179_12.	1	p3	(TTA)5	15	434	448	TGCAGCAATGGAGGTAAGAA
scaffold556392_15.	1	p3	(TCA)6	18	1951	1968	TGTGAACTTCCTCCAACAACA
scaffold556563_18.	1	p3	(TCA)5	15	1726	1740	CCACCAGTACCAAAACCACC
scaffold556620_11.	1	p3	(CTT)5	15	135	149	GAATTTGGCCAAGTCGATTC
scaffold557096_16.	1	p3	(GTG)6	18	5557	5574	AGCTTGCAAGTAGGAGGCAA
scaffold557514_13.	1	p3	(ATT)5	15	450	464	TGTTGAGGCATGGCTATGAA
scaffold557542_14.	1	p3	(ACA)6	18	3229	3246	ACAGTTCAGCTCCACAACCC
scaffold558103_14.	1	p3	(ACA)5	15	797	811	CATGTGCATCAAACGGAAAC
scaffold558176_17.	1	p3	(TGA)5	15	1063	1077	TGCTTACCTCCGGAATTTTG
scaffold558197_12.	1	p3	(CTT)7	21	109	129	TCAACGCTCACCTTCACATC
scaffold558378_14.	1	p3	(CAA)5	15	2605	2619	ACTTCCCAGACCTTGTTCCA
scaffold558565_14.	1	p3	(TAT)5	15	3395	3409	TCTTCTTGACCAATAATAAAGAAAAC
scaffold558863_13.	1	p3	(TAT)5	15	126	140	CCAAACCAACCTCGCTCTTA
scaffold558921_11.	1	p3	(GGC)6	18	90	107	AAGAGATAGGGGAAGGAGCG
scaffold558930_11.	1	p3	(GGC)5	15	273	287	CAAACATGGGAGGGTTTTGT
scaffold558979_10.	1	p3	(GAA)5	15	86	100	CCAGACATCGAAGAAGCTGTT
scaffold559187_16.	1	p3	(TGA)6	18	152	169	AGGAGCCACCTGATGAACAC
scaffold560033_16.	1	p3	(CAC)5	15	1682	1696	GCTTGTCCTCCACTTGAAGC
scaffold560655_12.	1	p3	(AGA)5	15	411	425	GGGAGGTTTCGTCACACAGT
scaffold560980_10.	1	p3	(TGT)7	21	43	63	TGTAGCCGACCCCAATTTAT
scaffold561081_11.	1	p3	(ATA)5	15	292	306	ACCAGTTGGGTTCGAGAAGA
scaffold561251_12.	1	p3	(TTA)5	15	90	104	CCTAAGCAATTGATAGTGCCAA
scaffold561708_13.	1	p3	(AGA)5	15	307	321	GTTTTCCACCAAGGTTGCAT
scaffold561791_17.	1	p3	(GGT)5	15	1657	1671	TTTTGGGTTTGGAGACGAAC
scaffold561809_11.	1	p3	(TTA)7	21	244	264	TTCGGTTTATACAATAACCAATTTAC
scaffold561884_14.	1	p3	(TGT)5	15	216	230	TGACATTCCTTTCCATTGGC
scaffold561954_15.	1	p3	(TCA)5	15	112	126	AGTCACGGGTTCGAATTTCA
scaffold562123_14.	1	p3	(GGC)5	15	159	173	GCGAGTTTCTTGAGGTCGTC
scaffold562240_14.	1	p3	(TCT)5	15	532	546	GTTGTCGGTGGTCATGTTGA
scaffold562470_18.	1	p3	(TAT)5	15	294	308	TCGTGCAAGTTTTCAAGATCA
scaffold562739_17.	1	p3	(TGA)6	18	994	1011	AGGTTGCGTACATCTGACCC
scaffold562848_15.	1	p3	(TGT)5	15	3391	3405	AGGTGCTAGCAGCATGGAAT
scaffold563062_12.	1	p3	(TTA)5	15	354	368	TCACGATCCTTCTGTCCCTT
scaffold563311_16.	1	p3	(TCA)5	15	399	413	CTTGCAATTGTCGTGCAAGT
scaffold563459_13.	1	p3	(ACA)6	18	667	684	ACCGTTGTGGTTCGGATTAC
scaffold563860_15.	1	p3	(ATC)6	18	514	531	TCAATTCAAAATCAAACCATGC
scaffold564042_14.	1	p3	(ATA)5	15	590	604	TGTTCACGGCAGAAGCATAG
scaffold564084_12.	1	p3	(TTG)5	15	158	172	TTGATACTACACGGTGGCGA
scaffold564090_12.	1	p3	(TAT)5	15	372	386	TGGTTAATGCATTTTGCCTG
scaffold564132_15.	1	p3	(TTG)5	15	2203	2217	ACTTGGCACGATCCAATTTT
scaffold564273_10.	1	p3	(CTT)5	15	926	940	ATCCCATGGCTGTTGTTCTT
scaffold564423_16.	1	p3	(TTA)5	15	487	501	TCTCCTGTACTTCGTTTAGACATCA
scaffold564426_11.	1	p3	(TTG)5	15	439	453	ATTGATCGTACACGATGGCA
scaffold564466_15.	1	p3	(ATT)5	15	236	250	ATGTTCATGTTGGGTGCTGA
scaffold564720_14.	1	p3	(TTA)7	21	937	957	GGGATCCAAACCTCGACATA

scaffold564738_18.	1	p3	(CCG)5	15	841	855	CCAAGGTGCAACTTACAGCA
scaffold564825_13.	1	p3	(AGA)5	15	54	68	AGCTTATGTTGCATGGAGGG
scaffold564826_14.	1	p3	(ATA)6	18	155	172	TTGGAAAATGGAAAAGGCTG
scaffold565954_16.	1	p3	(CTT)5	15	1230	1244	CCATGCATTTCAGGTTTTCC
scaffold566056_16.	1	p3	(AGA)5	15	2474	2488	CTCCAAAAGCTTGCACACAA
scaffold566411_14.	1	p3	(ATG)5	15	608	622	GGGCTGTTTTTGAATCGAGA
scaffold566510_10.	1	p3	(CAT)5	15	345	359	TGACATTGTGACCTTCAGGC
scaffold566582_13.	1	p3	(ATC)5	15	116	130	AAGGCTACAACCACATACCGA
scaffold566718_14.	1	p3	(TAT)6	18	3291	3308	AGATTGCACATATAGCCCCG
scaffold566731_16.	1	p3	(GAT)6	18	385	402	AAAATCTTTTGGGGCGTTCT
scaffold567634_14.	1	p3	(TAA)5	15	750	764	GGAATTCAATCCAAGGACCA
scaffold568056_17.	1	p3	(CAT)7	21	2364	2384	TCAAACTGGAAACCGAAACC
scaffold568120_18.	1	p3	(TAA)5	15	1266	1280	CTTCCCTAACCGTCCCTTGT
scaffold568134_10.	1	p3	(TGT)5	15	334	348	TTCTGATTTGCAGCAGGTTG
scaffold568234_16.	1	p3	(TGA)7	21	479	499	ACAAAACACAACAACCCCGT
scaffold568426_14.	1	p3	(ATA)6	18	645	662	ATGCGGATGTTGTGGGTAAT
scaffold568459_15.	1	p3	(TTG)7	21	716	736	TGTCAAGCTCTTGCATAGCAGT
scaffold568554_14.	1	p3	(ATT)6	18	1673	1690	AATAAAAGGCGGATTGACCC
scaffold568577_14.	1	p3	(TTG)5	15	1294	1308	TGGAGCTCTTGGATACCTGG
scaffold568934_18.	1	p3	(GCA)5	15	1034	1048	AAGCGTTGAAGCAGCAAAGT
scaffold568981_15.	1	p3	(AAT)5	15	398	412	CCAACCTCAGAATCATCTTTCA
scaffold569142_18.	1	p3	(CAT)6	18	369	386	TTGATCTCAGTCAGCCATGC
scaffold569219_14.	1	p3	(ACA)5	15	53	67	TCAAAACATTTAGTTGGCACAAT
scaffold569381_11.	1	p3	(TGC)6	18	403	420	TCTCCATCCTCAACCGATTC
scaffold569388_10.	1	p3	(ATT)5	15	108	122	ATATAGGCCCAAATCTGGCA
scaffold569451_12.	1	p3	(TTG)5	15	73	87	CTATCGGTACTCGGATGGGA
scaffold569925_18.	1	p3	(AAT)5	15	3147	3161	AGCATATGCCTTGCTTGCTT
scaffold570026_13.	1	p3	(AAT)5	15	492	506	TGAAAAATCCGAATCCGAAC
scaffold570065_16.	1	p3	(CAC)5	15	123	137	CAATGGACAACCAAGCCTTT
scaffold570249_16.	1	p3	(TCA)8	24	2131	2154	TGCCCAGTATTGGTCATTCA
scaffold570796_16.	1	p3	(GGC)5	15	436	450	GCGTCTTTATAGTCGCCGAG
scaffold570844_19.	1	p3	(TTC)5	15	686	700	TCTCGCAGAGGAGGTCAAAT
scaffold571167_15.	1	p3	(GAT)5	15	560	574	AAGAAAGACGAAGCATGGGA
scaffold571251_15.	1	p3	(ATT)5	15	1235	1249	ATCAAAACTGGTAATGCGGG
scaffold571590_16.	1	p3	(CGG)5	15	2042	2056	TAGACACATGCCAACTCCCA
scaffold571630_17.	1	p3	(ACG)5	15	764	778	ACGACGACGGAAAGATTGAG
scaffold571631_13.	1	p3	(TTA)5	15	1227	1241	GGGACAACGGGTTCTGATAG
scaffold572154_13.	1	p3	(CCA)5	15	216	230	CCAGCAGACACGAAACAGAA
scaffold572157_14.	1	p3	(TCA)5	15	198	212	GGTCTCAACTTCGCGATCAT
scaffold572424_10.	1	p3	(TGA)6	18	96	113	TGGTTTGGGAATAATTGGGT
scaffold572654_18.	1	p3	(CAC)5	15	953	967	CGTTAAGGACACAAACCCGT
scaffold572788_11.	1	p3	(CAT)6	18	114	131	GGGTGGTTTATGGCCTTTTT
scaffold573085_10.	1	p3	(TAT)5	15	68	82	CATTTGGGGGTATTACAATTTTT
scaffold573220_15.	1	p3	(TCT)5	15	359	373	GCGTTTCTTAAACTGCCTGC
scaffold573256_12.	1	p3	(AAT)7	21	82	102	GACAGCTGCACGACATGATT
scaffold573328_17.	1	p3	(TTG)5	15	331	345	GAAGGGGGAGACCGAAATTA
scaffold573394_17.	1	p3	(AAG)6	18	122	139	ATGTTGGAGTCGGGAAGATG
scaffold573538_12.	1	p3	(CTT)6	18	736	753	CTCCCACGACCTTTTGTTGT
scaffold573938_10.	1	p3	(GGT)5	15	322	336	ATTTGTACACCGGTGGTGGT
scaffold574103_11.	1	p3	(ATA)6	18	186	203	CGTTTGAAGCCGAGTTGAAT
scaffold574201_10.	1	p3	(ATA)5	15	572	586	AAAATATGGTGTGCATAACGAGA
scaffold574226_11.	1	p3	(CGG)5	15	248	262	TGCGCCACAAAATTTCAGTA
scaffold574250_10.	1	p3	(ATT)5	15	891	905	GTTTGGATTGACAAGTCGGG
scaffold574770_15.	1	p3	(ATC)5	15	1993	2007	TTGTTCTTGGGATTGGTGGT
scaffold574853_10.	1	p3	(GAG)6	18	989	1006	GTGCAGATGTGTCTGTCGCT
scaffold574922_14.	1	p3	(AAT)5	15	1892	1906	AAGAGGCCACCGAAACTCTT
scaffold574931_14.	1	p3	(ATA)6	18	221	238	AAAGAGGTTGTTTCCGTTGC
scaffold575088_15.	1	p3	(AGG)6	18	3022	3039	TCGTAATGATGCCACAGGAA

scaffold575473_14.3	1	p3	(TTC)5	15	548	562	CGTTGACTGCTGGAGAATGA
scaffold575600_15.8	1	p3	(ATC)5	15	1555	1569	CTGACCCAAGGTCCCAAGTA
scaffold575839_17.7	1	p3	(ACC)5	15	749	763	ACCTGCACCACCACCAAGT
scaffold575991_11.8	1	p3	(ACA)5	15	426	440	TCTTGCAAAATGATTGGGTG
scaffold576448_14.8	1	p3	(TAC)5	15	3270	3284	TTGACGGCTCATGCTTACTG
scaffold576766_15.9	1	p3	(TTA)5	15	1175	1189	AAAAAGGTCCCCTTTCCAAG
scaffold576805_10.6	1	p3	(TTA)6	18	219	236	GAAACCTGACACCGTAGGGA
scaffold577334_18.0	1	p3	(CCA)7	21	158	178	CCCATCTCTTGTTTTCTTCATCA
scaffold577475_11.3	1	p3	(CTC)5	15	413	427	CCGGATCACATTTCGAGTCT
scaffold577618_16.2	1	p3	(CAT)5	15	902	916	AGGCTTGCGGGTCTTACTTA
scaffold577659_13.2	1	p3	(CAT)6	18	1029	1046	ATACTTCCGTATTGCCGCAC
scaffold579121_17.0	1	p3	(TGA)5	15	2049	2063	CTTGCAATGTGGCATTCATT
scaffold579269_12.5	1	p3	(TCT)5	15	136	150	TTTGCTGAATTTTCTTCGCA
scaffold580205_15.1	1	p3	(TTC)5	15	2456	2470	CAAGCACAAAATAGCGAATCA
scaffold580233_17.0	1	p3	(CTT)5	15	85	99	TAGTGGGGGTCAGAACATGC
scaffold580663_15.0	1	p3	(CAT)6	18	132	149	CCACAACTGGTCGGTATGGT
scaffold580920_10.3	1	p3	(ATG)6	18	51	68	GCAGCAGCAACATACAAACC
scaffold581086_18.3	1	p3	(CCG)5	15	2245	2259	TCTCCGCCATCAAATTCTTC
scaffold581284_17.3	1	p3	(CAA)5	15	1664	1678	TTTGTTGTGGAGTTTCAGGTG
scaffold581372_20.4	1	p3	(TTA)5	15	290	304	ATTGCCTCCACAAGAATTGG
scaffold582178_16.4	1	p3	(CCA)5	15	484	498	GCAAGACTGTCGTCCTCCTC
scaffold582190_12.7	1	p3	(TGA)5	15	45	59	CCCAAGACCCCAATTTGATT
scaffold582229_18.5	1	p3	(AGA)5	15	453	467	TGTTGTGCGTGCTTTTCTTC
scaffold582394_10.0	1	p3	(TGT)5	15	45	59	TGTAGCCGACCCCAATTTAT
scaffold582449_17.4	1	p3	(ATT)7	21	218	238	TCGAACTCCACTGTTCCATTT
scaffold582782_16.1	1	p3	(ACA)5	15	2113	2127	CATGTCACACTTCGCTCACC
scaffold582785_12.1	1	p3	(AAT)6	18	1185	1202	AATTATGGCGTTGGGTGAAC
scaffold582866_15.1	1	p3	(TGT)5	15	51	65	TTCATGTAGCCAACCCCAAT
scaffold582893_13.8	1	p3	(ATC)6	18	183	200	GCTACCTCTCCCTCTCTCCC
scaffold582985_13.9	1	p3	(ACA)5	15	1401	1415	CCATAGTTTAAGCAAGGGCA
scaffold583212_14.4	1	p3	(TGA)5	15	102	116	AGGTTGCGTACATCTGACCC
scaffold583580_15.2	1	p3	(GAA)5	15	1288	1302	GATGGGGTTGCAGAAGGTAA
scaffold583927_13.2	1	p3	(TAT)6	18	1197	1214	CCCCACAATGTCTCGTCTTT
scaffold584134_15.9	1	p3	(GTG)5	15	255	269	AAGTGGACCATTATCGGACG
scaffold584289_13.0	1	p3	(CGC)6	18	356	373	CGCCTTCTTTGCACCTACTC
scaffold584291_12.8	1	p3	(TGC)6	18	913	930	GGATTTGGCCCTGTGTGTAT
scaffold584633_12.1	1	p3	(GGC)6	18	112	129	GTTGGCAACTGGATGTAGGG
scaffold584733_14.7	1	p3	(ACC)6	18	1126	1143	GTTTCCAACGAAGTTCCCAA
scaffold584739_12.2	1	p3	(TGA)5	15	103	117	CCAAGACCCCAATTTGACTG
scaffold584751_11.0	1	p3	(ATA)7	21	608	628	TAGATGGCTGGGAAAATTCG
scaffold584786_10.7	1	p3	(CTT)6	18	284	301	ATTGTCAAACCAGCGAGAGC
scaffold584787_13.2	1	p3	(CTT)6	18	274	291	ATTGTCAAACCAGCGAGAGC
scaffold584892_13.5	1	p3	(GAA)5	15	165	179	CGACCGAATAATCCTGTGGA
scaffold585028_15.8	1	p3	(ATT)5	15	317	331	CAGTGCTGTCCAAACCTCAA
scaffold585298_15.8	1	p3	(TCT)5	15	1144	1158	AGAAGGAAATGGGAATGGCT
scaffold585565_15.3	1	p3	(TAT)6	18	164	181	AAAATGGTGGCTTTCTTCCC
scaffold585983_17.6	1	p3	(TGA)7	21	2812	2832	CTATGCCGTCGATTCTGACA
scaffold586096_14.2	1	p3	(GGA)5	15	101	115	CATGTACCCCACAGAGGGTC
scaffold586300_14.5	1	p3	(CTT)5	15	1307	1321	TTTCCTCCAACATTGCTTCC
scaffold586545_16.5	1	p3	(TAA)5	15	955	969	CCAAGTCACCCAAGAATTGC
scaffold586802_16.0	1	p3	(ATT)5	15	233	247	TTTGTTGTGGGTTACCCGAT
scaffold586870_15.7	1	p3	(TGT)6	18	44	61	ATGTAGCCGACCCCAATTTA
scaffold586888_13.9	1	p3	(GAA)5	15	321	335	CTTTTCACGTCGGGATTGTT
scaffold587106_12.3	1	p3	(CGG)5	15	2609	2623	CGGAGAAGGAAATAGGACCC
scaffold587823_16.2	1	p3	(ATC)7	21	2237	2257	ATCATGTCAAGGGCTCAAGG
scaffold587828_10.5	1	p3	(AAG)5	15	318	332	GGATTTGTGTGACTGCATGG
scaffold587892_10.0	1	p3	(AAG)5	15	609	623	ATGAGCGAAACAAAATTGGG
scaffold587969_10.5	1	p3	(TAA)7	21	129	149	GTTTACCTGGCTGACGTGGT

scaffold588057_16.9"	1	p3	(AAT)5	15	711	725	TATCCGTTCGGCTGTACCTT
scaffold588111_12.2"	1	p3	(AAG)5	15	211	225	GTCAATGGGAACAACCGTCT
scaffold588157_16.2"	1	p3	(TAT)6	18	2732	2749	ATTGCAAGCAAAATCATCCC
scaffold588355_12.0"	1	p3	(ATT)6	18	320	337	ACCCCATCTCAACCAAATGA
scaffold588723_16.1"	1	p3	(TTA)5	15	815	829	CCAATCATACATGCAAAGTGC
scaffold588991_15.5"	1	p3	(AAT)6	18	1756	1773	ACCATGACCGACATGCAGTA
scaffold589399_16.1"	1	p3	(GGA)6	18	1119	1136	GCTGCTCCTCATTGTCATCA
scaffold589484_13.9"	1	p3	(AAC)6	18	1815	1832	CCGTAAATGCCTGTCAACCT
scaffold589549_13.8"	1	p3	(CGG)6	18	80	97	AATCATGTACACCCGCTTCG
scaffold589822_12.6"	1	p3	(CGG)5	15	49	63	CAGCACCACCAGCGAGAA
scaffold589885_10.6"	1	p3	(GTT)5	15	226	240	TTGCGGATAATACAATGGAGC
scaffold590321_16.4"	1	p3	(GCT)5	15	338	352	TGGCAAATATGGATGTGGAA
scaffold590370_13.7"	1	p3	(TCT)5	15	103	117	GGAAAACTTTATCATTTCCCTTGA
scaffold590530_16.3"	1	p3	(ATT)5	15	170	184	TGGCCTTTTAATAGGATGCG
scaffold590710_16.0"	1	p3	(ATG)5	15	4215	4229	TTGGGAATTTCTTTCCATGC
scaffold590887_17.4"	1	p3	(CAA)6	18	273	290	TTTGACCAAACGGAACAACA
scaffold590909_13.8"	1	p3	(AAT)7	21	84	104	GTCCAAAAGCTTATCGGCTG
scaffold590966_10.6"	1	p3	(ATT)8	24	501	524	TGAAATCCCTCAAATCTTACCAA
scaffold591125_12.7"	1	p3	(CGC)5	15	244	258	GAATCTTAGGACGCGACGAG
scaffold591654_10.1"	1	p3	(ATC)5	15	247	261	ACGAGTGAGGCTGGAAAGAA
scaffold591698_14.2"	1	p3	(TGG)6	18	1363	1380	CCCATCATAGGGAAAGGGAT
scaffold592654_16.7"	1	p3	(GTT)7	21	4824	4844	CCGACCCCACTTAGTGAAAA
scaffold592719_17.1"	1	p3	(AAT)5	15	1622	1636	ATGATGAGCCGTCAATCTCC
scaffold593051_12.8"	1	p3	(TTG)5	15	2869	2883	TGGTTTATGTAGCCAACACAATTT
scaffold593064_18.3"	1	p3	(TTC)5	15	977	991	GGTTCCCCATTCTCCTCTTC
scaffold593654_20.0"	1	p3	(TTG)5	15	232	246	AATTAGCGCACCCACAAATC
scaffold593761_13.3"	1	p3	(GGT)5	15	1250	1264	GATCCTTTGCTGGAGGTTCA
scaffold594136_13.6"	1	p3	(ATT)5	15	974	988	TCGTCTTGATTTTGTTCTGCAT
scaffold594378_18.1"	1	p3	(CCG)6	18	168	185	CCCGACTTCGTCTCTACGAC
scaffold594466_13.5"	1	p3	(GGA)5	15	620	634	TCACAGACTCACAGTGTTGGC
scaffold594517_17.2"	1	p3	(TAT)5	15	2359	2373	TTGGATGATGGAAGAAAATCG
scaffold594557_15.3"	1	p3	(ATT)5	15	1014	1028	AAAGGGAAAAGCCCCTATTTT
scaffold594591_12.6"	1	p3	(ATG)5	15	257	271	TCATTTCTAAACCGGAACGG
scaffold594592_10.0"	1	p3	(ATG)5	15	256	270	TCATTTCTAAACCGGAACGG
scaffold595066_12.5"	1	p3	(AAT)5	15	76	90	TCCCTTTAAAAACACAAACCTTTT
scaffold595279_17.3"	1	p3	(CGG)5	15	1470	1484	CGTCAGATGAGGGTCAGGAT
scaffold595313_13.0"	1	p3	(ATA)6	18	1079	1096	ACAGTTTGAGATCCATCGCC
scaffold595453_17.1"	1	p3	(TCA)5	15	2053	2067	GCTTCAACCATAGCACCCAT
scaffold595480_16.9"	1	p3	(TTG)5	15	48	62	TGTAGCCGACCCCAATTTAT
scaffold595499_16.6"	1	p3	(TGT)5	15	172	186	TGTAGCCGACCCCAATTTAT
scaffold595523_18.7"	1	p3	(TAG)5	15	2434	2448	AATGGTACCCCAACTTCACG
scaffold595590_10.5"	1	p3	(CAT)5	15	247	261	CGAGATTTATGAGAGCCCCA
scaffold595658_17.4"	1	p3	(TCT)6	18	684	701	AGGTTGGTGGATTTTGGGA
scaffold595808_14.0"	1	p3	(ATA)5	15	2715	2729	TCTCGTGTAACGAACAAGCAA
scaffold596212_22.3"	1	p3	(AGG)6	18	163	180	CGTTGCAGAAGTTTGCTTGA
scaffold596462_11.7"	1	p3	(TTC)5	15	163	177	TCTTTGCCTTTGTCTGGAGC
scaffold596958_17.9"	1	p3	(AAC)5	15	474	488	AACACCACAAGCGACAAGACT
scaffold597084_16.0"	1	p3	(CCT)7	21	578	598	TAGCAGTTGGTGTTGAAGCG
scaffold597091_17.5"	1	p3	(AGA)5	15	912	926	TGGAGCTCTGAAGCTCAACA
scaffold597322_15.3"	1	p3	(AGA)5	15	1240	1254	GGATACCCATGAACTGGTCG
scaffold597404_10.5"	1	p3	(CTG)5	15	86	100	GTCCCTTTTTCCTGAGGACC
scaffold597727_14.5"	1	p3	(CAA)5	15	231	245	GGATGATGATGTTCAGATGGG
scaffold597864_15.6"	1	p3	(CCA)5	15	538	552	CATCCTTGCCAATTTCCATT
scaffold597990_16.2"	1	p3	(ATA)5	15	24	38	ACCCCTTGCGGGGTAATA
scaffold598690_14.1"	1	p3	(TTG)5	15	1749	1763	CACGAACACCCCTGCATATC
scaffold598725_15.6"	1	p3	(GCC)6	18	206	223	GCTTATCTGGACAACCCCAG
scaffold598813_17.4"	1	p3	(CGA)5	15	906	920	GGCAACCTCAATGTCCAAAA
scaffold598951_16.2	1	p3	(AAC)5	15	386	400	TATGGAGAAAATCCCTCCCC

scaffold598988_17.	1	p3	(GCT)5	15	2196	2210	AATCCGAGGTGTGTTGCATT
scaffold599052_15.	1	p3	(AAT)5	15	592	606	TGCAATTATTGGGTTCCAAAG
scaffold599197_14.	1	p3	(GCA)5	15	1006	1020	GGGAGAATAAACAGACGGCA
scaffold599292_13.	1	p3	(ATT)6	18	1581	1598	TGCATTTTCACGTGCATTTT
scaffold599293_14.	1	p3	(AAT)5	15	134	148	TTCGAAGCTGGAGATGTGACT
scaffold599323_15.	1	p3	(TTA)6	18	383	400	GGCAACGTGATTCAGTTCAA
scaffold599519_13.	1	p3	(CGG)7	21	199	219	GCCGAGGGTGAAATAGATGA
scaffold599762_18.	1	p3	(AAT)5	15	65	79	TTCCACGTTTCCTTAAAATATGG
scaffold599913_17.	1	p3	(TTA)5	15	862	876	GGCCGTTTGGAATAGGATTT
scaffold599957_17.	1	p3	(TCA)6	18	188	205	TAATCCATGGAAGGCTCCTG
scaffold600030_11.	1	p3	(TGA)6	18	107	124	TTGGTACTCACAAAACCCCC
scaffold600150_16.	1	p3	(ATC)5	15	490	504	ATATGCGACGTGAATCCCAT
scaffold600283_16.	1	p3	(TCA)5	15	741	755	TCGCAATTTTCACTGATGGA
scaffold600495_15.	1	p3	(GAA)5	15	615	629	GGTTTCTTGCAGGAGAATGC
scaffold600778_13.	1	p3	(AAT)5	15	371	385	TGGAATGTCTTCCATTAAGTGC
scaffold601102_15.	1	p3	(ATA)6	18	3597	3614	GGACGGTTCACCAAAAATGA
scaffold601406_15.	1	p3	(TTC)5	15	515	529	TAATGGGGAAGTCCTAGGGG
scaffold601870_13.	1	p3	(AAT)7	21	502	522	ATACTGGCGGACAATATGGG
scaffold602035_10.	1	p3	(GGT)5	15	317	331	GCTACGAGGGCGAGATGTAG
scaffold602147_17.	1	p3	(GAA)5	15	1429	1443	GCCCTGCCCTAAGACTATCC
scaffold602169_10.	1	p3	(TAT)6	18	60	77	TTGCAAGAAAATTGTCCCGT
scaffold602364_16.	1	p3	(CGC)5	15	593	607	ACCACCACCACCGTACAAAT
scaffold602868_13.	1	p3	(TTG)6	18	382	399	ATCCATACAGCCGACCTCAC
scaffold602978_16.	1	p3	(CCA)5	15	545	559	TAATTTCCCCCAATTTTCCC
scaffold603033_16.	1	p3	(ATC)5	15	1788	1802	CTCACTCGAACTCGTCTCCC
scaffold603152_15.	1	p3	(CGC)5	15	756	770	GCCTAAGAAGCCCAAATTCC
scaffold603326_15.	1	p3	(ATA)5	15	72	86	TGAAGTCCGGATCAACTTACG
scaffold603510_15.	1	p3	(TCT)5	15	458	472	CAGCCATGCTTCTTATGCAA
scaffold603581_11.	1	p3	(ATC)5	15	106	120	CAGCGAAGTGACAACCTTGA
scaffold603611_11.	1	p3	(ATT)5	15	371	385	TGCAAAATCAAGTATACGTTTGG
scaffold603777_11.	1	p3	(CCG)5	15	318	332	AAACACTGTGGCTCCAGCTT
scaffold603892_13.	1	p3	(AAT)5	15	972	986	ACGTGGAAGAGGGACATTTG
scaffold603894_17.	1	p3	(TTG)5	15	1913	1927	ACTGGCGACCTAGCAAAATG
scaffold604078_15.	1	p3	(TTA)5	15	301	315	ACATTAACCACAATGGAGGC
scaffold604197_13.	1	p3	(TTC)5	15	1486	1500	GCCCTGCATTTAGTTGAGGA
scaffold604210_13.	1	p3	(AAT)5	15	888	902	GGATGCCATTTCTTCTCCAA
scaffold604338_11.	1	p3	(TAT)5	15	576	590	CCGATTTTCTCGGATTCCAT
scaffold604354_11.	1	p3	(ATC)5	15	204	218	TGCTTTCAAAACCAGCACAC
scaffold604513_16.	1	p3	(CAT)5	15	761	775	GTTTCTTGGACAAAGCAGCC
scaffold604644_10.	1	p3	(CCG)5	15	57	71	ATCGGATGAAAGTTGCGATT
scaffold604717_16.	1	p3	(TGA)5	15	123	137	GCTTTTGAGCCCTCTGTTTG
scaffold604976_14.	1	p3	(CAA)6	18	536	553	GGCAGCGAAAAATCAGCTAC
scaffold605010_15.	1	p3	(AAT)7	21	1877	1897	AAGGCAATGAGGCAAGAAAA
scaffold605122_16.	1	p3	(TTC)6	18	960	977	TCAATACATGGCATTGGTGG
scaffold605778_16.	1	p3	(AAG)5	15	1443	1457	TCTGCAATCAATCAGCAAGC
scaffold605900_19.	1	p3	(CAT)5	15	134	148	CTTGTGGTTGTTGGTGTTGC
scaffold605995_18.	1	p3	(TAA)6	18	481	498	TAGCACCCGTAGTTGCTGTG
scaffold606069_15.	1	p3	(GAA)6	18	2233	2250	GCCACACCTGGAGTTTCATT
scaffold606126_14.	1	p3	(TGT)6	18	32	49	CCAATTTATTGGGATTAAGGC
scaffold607064_12.	1	p3	(AAT)5	15	651	665	TCGCCCATTTTGAATTAACAC
scaffold607093_12.	1	p3	(GAA)5	15	74	88	CGGAAGGCATGAAGAAGAAG
scaffold607264_13.	1	p3	(TAA)9	27	822	848	CACGCCACGTCAACTTCTAA
scaffold607314_11.	1	p3	(CGG)6	18	174	191	CCAATCATCGGCCTTTTCTA
scaffold607448_17.	1	p3	(AGC)6	18	290	307	TTTTGGGGACACATCACAGA
scaffold607488_15.	1	p3	(AAT)5	15	926	940	GAGGTGAGGTTCCATCTCCA
scaffold607727_15.	1	p3	(GAT)7	21	657	677	GTCAATTGCGGGGATACAAT
scaffold607758_18.	1	p3	(CCA)5	15	176	190	AGTTTATGACCATCAGCCGC
scaffold608052_16.	1	p3	(CAA)6	18	3576	3593	CTTGGCCATGAACCTCATTT

scaffold608081_20.9	1	p3	(ATT)6	18	1880	1897	AAAAATGTTTCTGTAGTGGTTGTTG
scaffold608155_16.5	1	p3	(CGC)6	18	600	617	GTAACTCCATGATGCCGACC
scaffold608360_15.9	1	p3	(AAG)5	15	49	63	AACATGGACTGGAAGTTGCC
scaffold608879_13.0	1	p3	(GTT)5	15	541	555	CGCATTAAACGGATACGACA
scaffold608974_13.6	1	p3	(AAT)6	18	328	345	TTTATTCCGTGACCCTCGAC
scaffold609203_15.0	1	p3	(CCG)5	15	176	190	GATTGGATTTAATTCCCCCG
scaffold609402_10.0	1	p3	(TGG)5	15	940	954	TGATGATGATAACGAAGGCG
scaffold609553_15.0	1	p3	(TTA)6	18	1641	1658	TGTTGCACCAATGTCTGGAT
scaffold609634_20.3	1	p3	(GCA)6	18	381	398	TTGGTCCCAAATCCCTACAA
scaffold609768_15.2	1	p3	(AAT)6	18	709	726	CCAAGTTACGTGGCGTAGAA
scaffold609931_12.7	1	p3	(TAA)5	15	1263	1277	TTTGAACTCGATTTGTCCCC
scaffold610032_14.4	1	p3	(CCT)5	15	2418	2432	TCCCACTCCCATTCAACTTC
scaffold610073_13.9	1	p3	(AAT)5	15	612	626	TATCGCTTTAGGCCCAGCTA
scaffold610287_18.5	1	p3	(AAG)5	15	480	494	ATTCCACAGACCAAAACCCA
scaffold610373_17.4	1	p3	(CAA)5	15	10010	10024	GGTCATTGCCTCGGATTAAA
scaffold610467_11.6	1	p3	(ACA)7	21	465	485	GCTTTTCCAGTGAAAATCCG
scaffold610492_16.3	1	p3	(CGC)5	15	895	909	TGGGACTTGGAACTAGGGTG
scaffold610547_11.2	1	p3	(CAT)5	15	63	77	TGATTCATCCTCCGTTGTGT
scaffold610913_15.2	1	p3	(GAT)5	15	64	78	TGATGATAATGAGGTTGCTGG
scaffold610961_16.0	1	p3	(TAT)5	15	3973	3987	TTTTGAAAAAGTGTTGCCCC
scaffold611117_15.1	1	p3	(GAG)5	15	305	319	TGAAGCAGTGGAGACAGGTG
scaffold611323_14.0	1	p3	(TAT)6	18	235	252	TTAGAGGTGTCAAAACGGGC
scaffold611553_10.8	1	p3	(TTA)6	18	432	449	GCAAGGGGACAACCTTTGTA
scaffold611568_17.5	1	p3	(CGG)5	15	39	53	GGACTGGAGCAGGTGTGAAT
scaffold611615_13.0	1	p3	(CCA)5	15	252	266	CAATCAACAAAACAAGCCCC
scaffold611796_15.2	1	p3	(ATT)6	18	1937	1954	AATCACCCTCGAATCAGTTTG
scaffold611986_16.8	1	p3	(TTG)5	15	585	599	AGCCGACTTCAATTTATTGGG
scaffold612222_12.7	1	p3	(ATC)8	24	101	124	GTTTGGGTGAGAACGAGGAG
scaffold612273_14.9	1	p3	(GGT)5	15	320	334	GCAAACATCTCAATGGGGAC
scaffold612278_17.0	1	p3	(ATT)6	18	850	867	AAAACGGAATCTACTTAGGGGA
scaffold612505_17.0	1	p3	(ATG)5	15	209	223	GATGTGGCTTCTGATGACGA
scaffold612637_13.0	1	p3	(AAG)5	15	1198	1212	ACTAGAAGCATTTGGCGCTC
scaffold612799_13.0	1	p3	(CGG)5	15	165	179	ATGTACACCCACTTCGGCTC
scaffold612954_10.3	1	p3	(TCA)6	18	77	94	CGTTGGATTGGATTCCTCAT
scaffold613146_15.9	1	p3	(ACA)5	15	179	193	TTGAAGATGATACGTTGAACCC
scaffold613201_13.4	1	p3	(ATT)5	15	2640	2654	TGTAGTTAAGGCGGTGGTGA
scaffold613263_15.9	1	p3	(ATA)5	15	803	817	CCAAAAGGAACAAGAGTTGAGG
scaffold613467_14.4	1	p3	(GAA)5	15	167	181	TGAAGAAGAAGGGGAGGACA
scaffold614029_13.7	1	p3	(AAT)6	18	168	185	GGGGTCGACTACATGAACCA
scaffold614204_15.0	1	p3	(CGG)6	18	274	291	ATCCTCAACTCCATCGCTTG
scaffold614207_12.6	1	p3	(CGG)6	18	291	308	CAAATTCCGTGACCAAATCC
scaffold614208_11.6	1	p3	(CGG)5	15	297	311	CAAATTCCGTGACCAAATCC
scaffold614232_10.5	1	p3	(AGG)5	15	210	224	ATTAACTCGGGGTGCAGTTG
scaffold614368_20.5	1	p3	(CCG)5	15	52	66	AGCAAACCCTAATCGGCAGT
scaffold614683_14.2	1	p3	(ATT)7	21	654	674	TAGAAGCAGCAGCAGTTTGC
scaffold614691_16.0	1	p3	(TGT)5	15	48	62	ATGTAGCCGACCCCAATTTA
scaffold614748_13.3	1	p3	(ATC)5	15	213	227	TGCTCAAGAAAATGAGAGCAAA
scaffold614838_14.3	1	p3	(TAA)5	15	465	479	TTCCATGCACTCTTTTGTGC
scaffold614906_11.0	1	p3	(ATA)5	15	456	470	GCGTAATCCCCTATTTGCCT
scaffold615182_18.8	1	p3	(TCA)5	15	1379	1393	TCACCCTCAAACATTCCACA
scaffold615246_10.5	1	p3	(GGC)6	18	250	267	TCTGTTTTGTGCGAGTCTGG
scaffold615292_11.5	1	p3	(ATC)5	15	135	149	TCATGTTCAAATCTGTGAAGGC
scaffold615412_13.4	1	p3	(AAT)5	15	68	82	TCCATGAAACATAAATCTTGCC
scaffold615492_16.9	1	p3	(GGT)5	15	1105	1119	TAGGTCACACTTGCAGTGCC
scaffold615500_17.1	1	p3	(TAT)5	15	1141	1155	TGTGAAAATCTCGGTTAATCCAT
scaffold615740_11.7	1	p3	(TTG)5	15	691	705	GGGTCAGATGTACGCAACCT
scaffold615785_20.0	1	p3	(GTT)5	15	27	41	TGGGTTCAATGCATTTACTTCTT
scaffold615818_19.0	1	p3	(TTG)5	15	962	976	ATATAGCCGACCGCACAAAG

scaffold615877_15.	1	p3	(ATT)6	18	65	82	TGAAATTGAAAACCTTAAAAATGAA
scaffold615988_15.	1	p3	(ATC)6	18	2954	2971	TTCCTTTTCAAGGTGCTTCA
scaffold616009_11.	1	p3	(CCT)5	15	440	454	GAGGACCTTCAAGGGTGTCA
scaffold616057_17.	1	p3	(GAA)5	15	965	979	AGATTGCTGTGATGTGGGTG
scaffold616160_13.	1	p3	(CGG)5	15	957	971	TATTCGACGAGGATTCCGAC
scaffold616351_13.	1	p3	(TTG)5	15	77	91	ATCCAGAGGAGCTTGCTGGT
scaffold616426_12.	1	p3	(CTC)7	21	489	509	AATGATCATCCAACGGTTTCA
scaffold616617_13.	1	p3	(ATC)5	15	837	851	GACCGGGACTGTAATCCTCA
scaffold616704_15.	1	p3	(TCA)8	24	1255	1278	TGTGGATGGTCTGAATGGAA
scaffold616715_11.	1	p3	(TTA)5	15	359	373	GCATCAAAACATTTCAGCCA
scaffold617145_10.	1	p3	(GAA)5	15	216	230	AGGGTAGGAAGCCCAAAGTG
scaffold617365_13.	1	p3	(AGA)5	15	172	186	CCATCAGTTCCTTCTAGGGC
scaffold617701_14.	1	p3	(TTG)6	18	240	257	TGTAGCCGACCCCAATTTAT
scaffold617751_10.	1	p3	(ATA)5	15	160	174	CTCGCACCAAATGGGTTAGT
scaffold617757_19.	1	p3	(AGG)5	15	201	215	CGTTGCTGGTGATGAAGAGA
scaffold617941_15.	1	p3	(TCA)5	15	295	309	TCTTCAACATTCCTGGGCTC
scaffold618157_15.	1	p3	(ATT)5	15	611	625	CATCGGGTGCAATGATTAAG
scaffold618488_16.	1	p3	(TGA)5	15	47	61	CCCAAGACCCCAATTTGATT
scaffold618503_16.	1	p3	(AAT)5	15	862	876	TAACGGGAGAAATGGTCCAA
scaffold618510_18.	1	p3	(CGC)5	15	290	304	TGATGGTATGGTGTGGAGGA
scaffold618779_11.	1	p3	(GGC)5	15	239	253	GGTGTGGAGGAGCAATTCAT
scaffold618970_15.	1	p3	(TTC)7	21	355	375	ATCCTCCACAGAAATGCCAC
scaffold619060_12.	1	p3	(TCA)6	18	139	156	ACATGGGTTTAGGGTTTCCC
scaffold619065_12.	1	p3	(AAT)7	21	64	84	GTTTCATACCCCCACCACAC
scaffold619194_14.	1	p3	(TTC)5	15	489	503	GAACACATTGCTGAGAGCACA
scaffold619509_17.	1	p3	(TTG)5	15	1842	1856	GTTTCTGATGTTGTTGCCGA
scaffold619566_12.	1	p3	(AAT)6	18	272	289	CATCTCATGTCCTCGCCTCT
scaffold619655_15.	1	p3	(TGT)5	15	46	60	TGTAGCCGACCCCAATTTAT
scaffold619664_15.	1	p3	(TGA)5	15	93	107	TGTTTTTGAGAAGAAACAAGAAGC
scaffold619698_14.	1	p3	(ATT)5	15	405	419	TCCCCAAGAACAACCCATTA
scaffold619810_13.	1	p3	(ATT)5	15	626	640	GGCTATGGAAACTTGATGATGG
scaffold619919_10.	1	p3	(TTG)5	15	259	273	AATGTTGATGCTGTTTGGAGC
scaffold620058_11.	1	p3	(GAG)5	15	553	567	GATGTTGGAGCTGAAGAGCC
scaffold620484_11.	1	p3	(ATT)9	27	222	248	CCTCCATCAGTTCTGTCTAGGG
scaffold620678_14.	1	p3	(TGA)5	15	233	247	GTCCGGGTATTGTCTGCTGT
scaffold621022_11.	1	p3	(TAA)5	15	250	264	AAATGAAATCGTGCGAAAATG
scaffold621396_17.	1	p3	(TTA)5	15	1066	1080	GGTATTTTTGCATGCGGTTT
scaffold621669_17.	1	p3	(TTA)6	18	40	57	TCATTTTCATTTTCTTTTGTTTTTG
scaffold621918_12.	1	p3	(GCC)6	18	349	366	GGCACACTATTTTGGAGGGA
scaffold621921_10.	1	p3	(CGG)5	15	87	101	TTTTTCGAATATTCCGGTGG
scaffold622045_14.	1	p3	(TAT)5	15	334	348	AATAACATTAAACCCTAAACCCTAAA
scaffold622147_15.	1	p3	(TGA)5	15	1770	1784	TTTGATTGGGAATAATTGGG
scaffold622452_15.	1	p3	(TCC)6	18	555	572	ATCCTCCATTTCCCATTTCC
scaffold622493_18.	1	p3	(ATC)5	15	1284	1298	TAACTGGGCTGGCTAGGTGT
scaffold623095_14.	1	p3	(TGC)5	15	287	301	ATATGCGCAAGCTCACCTTT
scaffold623307_13.	1	p3	(CAG)5	15	868	882	GAAATCAGCCCGACTTGAAA
scaffold623833_13.	1	p3	(TGC)6	18	1435	1452	ACCTCATTCCTCCCAATTCC
scaffold624068_16.	1	p3	(TAA)5	15	115	129	TCTTGATGCTCACTGTTGCC
scaffold624072_10.	1	p3	(TTA)8	24	859	882	ATTTTTCGTCGGAGGGACTT
scaffold624105_15.	1	p3	(AAT)5	15	485	499	TAAAGAGATGCTTGGTCGCC
scaffold624217_12.	1	p3	(ATA)5	15	1302	1316	ATAGTGGGGCCTCGTCTTTC
scaffold624389_10.	1	p3	(ATA)5	15	354	368	AAATTATCAAATTTCGGGACGA
scaffold624545_15.	1	p3	(TTC)5	15	2587	2601	AATCAAATCCAATCCCACCA
scaffold624547_17.	1	p3	(AGG)5	15	683	697	GGATCTCGGGGAGCTAGAAC
scaffold624557_11.	1	p3	(TGG)5	15	301	315	CGGGCCAATAAAATCTCAAA
scaffold624793_20.	1	p3	(TTA)6	18	1593	1610	CGATCAAGGAACACATGCAC
scaffold625006_13.	1	p3	(CGG)5	15	1432	1446	CAATGAACAGTTCGTCGGTG
scaffold625317_16.	1	p3	(ATC)6	18	1627	1644	ACGAAAGCTGTCGGAAAGAA

scaffold625411_10.	1	p3	(CGG)5	15	141	155	GATTATTCTTGCCGTTGGGA
scaffold625752_15.	1	p3	(GGC)6	18	3602	3619	ATGATGGACTTGCTTTTGGG
scaffold625786_23.	1	p3	(TTG)5	15	68	82	TTTTGAATTGCTTTAATTTGTTGC
scaffold625942_15.	1	p3	(ATC)5	15	397	411	TTGAACGCCGTTAAGTTTGA
scaffold625965_15.	1	p3	(CCG)5	15	3722	3736	CAAAGGGGCTGAGTTGAGAG
scaffold626100_15.	1	p3	(ATT)5	15	6849	6863	TCAAATTTTGGCACTGTTGC
scaffold626167_12.	1	p3	(ATA)5	15	579	593	TAATTTGGTTCGGTTTTCGG
scaffold626207_14.	1	p3	(TAT)6	18	1624	1641	ATCCGTGCAGTAAAATGAAAA
scaffold626724_12.	1	p3	(CTC)5	15	283	297	ACGTTCGATCCAAAACCAAG
scaffold627157_14.	1	p3	(ACC)5	15	538	552	CTCTCATCTTCACCGCCACT
scaffold627181_15.	1	p3	(CAT)6	18	2818	2835	CTCTGGTGCAACTCCATCAA
scaffold627204_14.	1	p3	(ACA)5	15	608	622	ACTCAGCGAAGTGGCAATCT
scaffold627229_10.	1	p3	(GAG)5	15	306	320	ATGAAGAAGGAGGAGGGGAA
scaffold627828_15.	1	p3	(TGG)5	15	1968	1982	CACTTTTGGCGTTTGATTCC
scaffold627880_16.	1	p3	(TAT)5	15	949	963	TTAATGGGATGATAAGCGGC
scaffold627993_19.	1	p3	(TAT)6	18	260	277	GCTAAGTTGATTATGGTGGGC
scaffold628120_11.	1	p3	(AAT)6	18	48	65	CAGTTGCCCTTGGGATTAGA
scaffold628394_19.	1	p3	(CCG)5	15	965	979	CCCATCCGGAAATCTCTACA
scaffold628504_15.	1	p3	(TCA)5	15	689	703	GCATCTTCCCACAAGCAAAT
scaffold628603_15.	1	p3	(TCT)6	18	84	101	TTTGCTGAATTTTCTTGGCA
scaffold628604_17.	1	p3	(CGC)5	15	1477	1491	GCAGCCACAAATGACAGAGA
scaffold628769_11.	1	p3	(TAT)5	15	330	344	AACATGAAAAATCCTCAATCCC
scaffold628848_13.	1	p3	(ACA)5	15	91	105	GGCCAAACGTTTAGTCTACTTGA
scaffold628856_11.	1	p3	(ATG)5	15	29	43	TGTTTCCATCTACACCTTGAGAA
scaffold628888_15.	1	p3	(TTC)5	15	336	350	TGAGGTAATGGAACCCGGTA
scaffold628956_16.	1	p3	(AAT)5	15	254	268	TTTCTACATTGATGCCGACG
scaffold629305_14.	1	p3	(TCA)7	21	77	97	ATTGAGATCCATGGGGAATG
scaffold629403_17.	1	p3	(AAT)5	15	139	153	TTGATTTTGCTTTTGCATCG
scaffold629425_15.	1	p3	(TAT)5	15	510	524	TTGCAATAAACATTGGGGGT
scaffold629495_17.	1	p3	(TCT)5	15	137	151	CGTTTTCTTATCTCTGCGCC
scaffold629570_20.	1	p3	(CGG)5	15	1412	1426	GGAAAACGCATAATTCACCC
scaffold629585_15.	1	p3	(AGA)6	18	116	133	AAGGATGAGGAAGGCAAGGT
scaffold629724_15.	1	p3	(ATC)5	15	1579	1593	GCATTGCATCCTATCCCATT
scaffold629878_16.	1	p3	(GGA)5	15	316	330	AGTTGGACTCGGCTTTTGAA
scaffold629924_16.	1	p3	(TGA)6	18	3900	3917	AGGTTGCGTACATCTGACCC
scaffold630380_14.	1	p3	(GCC)6	18	309	326	TCGGTTGCGTTGTTATTTGA
scaffold630710_10.	1	p3	(AAG)5	15	379	393	GCCATTCTTAAAAGCCTCATTT
scaffold631006_16.	1	p3	(AAT)5	15	195	209	TGTCTCCCTCACACCCTCTT
scaffold631007_14.	1	p3	(CAA)6	18	137	154	AACAGGTTCAAACCAGTGGC
scaffold631260_16.	1	p3	(CAA)6	18	1159	1176	ATCTTGAACCCCACCATCAA
scaffold631334_10.	1	p3	(AAT)5	15	316	330	TGGAAAATCGTTGTTGACCA
scaffold631549_11.	1	p3	(AAG)5	15	59	73	TGAGAAGGTTTTCTGGGGAA
scaffold631652_10.	1	p3	(GCG)6	18	449	466	ATTACGGTGCCAATTTCAGC
scaffold631718_16.	1	p3	(TTA)5	15	305	319	GGTTCGGTCGGTTTAGGACT
scaffold631851_14.	1	p3	(AGA)5	15	80	94	CCCAAGATGACTAACCGCTC
scaffold631867_15.	1	p3	(TTG)5	15	2635	2649	CCTTAAAATCAGTCCCGCAA
scaffold632060_14.	1	p3	(TCT)5	15	1077	1091	CGGCCCAATATTTAGGCATT
scaffold632138_15.	1	p3	(TGT)8	24	40	63	TGTAGCCGACCCCAATTTAT
scaffold632186_10.	1	p3	(GCG)5	15	457	471	AATTCTTCATTCAGCGACGG
scaffold632199_10.	1	p3	(TTC)6	18	106	123	CCAAGAGACTGAAAGCTCCA
scaffold632312_10.	1	p3	(ATT)6	18	141	158	GGTTTTAAATTCGTTGAAACCCT
scaffold632435_10.	1	p3	(AAC)6	18	279	296	ATCAACCTACACCGTCCACC
scaffold632455_17.	1	p3	(GAA)5	15	544	558	AGAAATCCAAAAGGCAACGA
scaffold632556_12.	1	p3	(GAA)5	15	541	555	CCGCATCCTTTGATATGCTA
scaffold632565_12.	1	p3	(ACA)6	18	106	123	TAATCCTTGAACTCGGTGGC
scaffold632584_15.	1	p3	(AAT)6	18	331	348	AACAAGTCGGCAAAAATTGG
scaffold632602_14.	1	p3	(GAA)6	18	392	409	GAGTAATCGTCTCCGCTTGC
scaffold632911_14.	1	p3	(AAG)6	18	187	204	CTTGCCAGGTTGCAATTATG

scaffold632969_15.	1	p3	(AAT)5	15	1352	1366	GCATTTGAAACAATGCCAAA
scaffold633117_20.	1	p3	(CGC)5	15	651	665	GCGAAAGCCCAGAACTTGTA
scaffold633225_16.	1	p3	(CAT)6	18	1990	2007	TCTGTGGTTGTTGGCATAGC
scaffold633236_18.	1	p3	(CCG)5	15	431	445	TTCAGCCACTGACCTAACCC
scaffold633334_13.	1	p3	(ATT)8	24	45	68	CCATTGCACTCCGAATAGGT
scaffold633415_13.	1	p3	(CTT)5	15	408	422	GCCAATTCTGTGGACCTCAT
scaffold633538_19.	1	p3	(CCG)5	15	41	55	CACCAAAGGCAGGAAAGAAG
scaffold633765_14.	1	p3	(TAT)7	21	1297	1317	TTAACATGGAACCCGTAGCC
scaffold634138_12.	1	p3	(GCC)5	15	52	66	AGATGATGAATCCGCAGCAT
scaffold634290_14.	1	p3	(TAA)5	15	383	397	CGTGAGAAGATTGGGAGGAA
scaffold634484_16.	1	p3	(GAA)6	18	1946	1963	TCTGGCCTTCTTCGTGTTCT
scaffold634564_11.	1	p3	(TTA)5	15	579	593	GAATTCCCAACCAAAGCAAA
scaffold634749_10.	1	p3	(GAC)5	15	207	221	CGAATTTCAGAAGCGCTGTA
scaffold634787_18.	1	p3	(ACC)5	15	479	493	ACCCAGCCTCGATTATGTTG
scaffold634798_15.	1	p3	(TAT)5	15	262	276	AGGAATCCCAATCAGAGAAAA
scaffold635102_14.	1	p3	(GCA)5	15	386	400	CTTCAGCTTGGTTTTGGAGG
scaffold635208_15.	1	p3	(GAG)5	15	1619	1633	GTCGGATTTCTTCATCGGAA
scaffold635225_13.	1	p3	(TGA)5	15	221	235	GCAATGTATATTGGGTCGCA
scaffold635282_17.	1	p3	(CGG)5	15	32	46	ATCTACAACAGGCGGCGG
scaffold635292_16.	1	p3	(CCA)8	24	878	901	TCTTCTCTAGCCTGGTGGGA
scaffold635533_18.	1	p3	(CTC)6	18	189	206	AAAACCGCAAATTGAACGAG
scaffold635783_13.	1	p3	(TCA)5	15	171	185	TCAAACCCATCATGAAATCCT
scaffold635850_15.	1	p3	(ACA)6	18	361	378	CGACTAATGCTCAAACGCTG
scaffold635902_14.	1	p3	(GCC)5	15	191	205	GGGGTATTCCCGATTTCAGT
scaffold635926_14.	1	p3	(ATT)6	18	1973	1990	GTCACGCCTGTTTCTGTTGA
scaffold636079_11.	1	p3	(ATT)5	15	77	91	GTCTCAATGGGGACATCTGG
scaffold636104_16.	1	p3	(GAA)5	15	503	517	TGAAAGTCATGCGAGGAGTG
scaffold636166_16.	1	p3	(TAA)5	15	540	554	GAAATTTCCTCCCTCGAGATG
scaffold636416_10.	1	p3	(AAT)7	21	29	49	GGGTCCAACTACGGATAATGC
scaffold636556_15.	1	p3	(TTG)5	15	425	439	TTTCAAGCAACCTCGCTTTC
scaffold636586_17.	1	p3	(GAA)5	15	825	839	CGTGCCTGGAATTTCATTTT
scaffold636945_15.	1	p3	(CTC)8	24	580	603	AACTGAAACGACACCTTGGG
scaffold637444_15.	1	p3	(CAA)6	18	2480	2497	AAACGGACAACCACTTTTCG
scaffold637467_10.	1	p3	(ATA)6	18	514	531	TCGCCACTGAAAGAAAGAGG
scaffold637816_16.	1	p3	(CTC)6	18	879	896	AAGGGTCCCATCCCACTTAC
scaffold637823_11.	1	p3	(AAT)6	18	51	68	CATTCAAAATAAAATGATGATGATAA
scaffold637945_10.	1	p3	(ATT)5	15	400	414	ACTCGACCAAAAAGGTGTCG
scaffold637965_14.	1	p3	(TGA)5	15	1144	1158	AAGTGATGCAGGGAATCTGG
scaffold637984_13.	1	p3	(AGA)6	18	1718	1735	GCCAGGAGAAAGCAGTGTTC
scaffold638045_16.	1	p3	(ATT)5	15	276	290	TTGACTCGCGTAAAAGAATATAAAA
scaffold638060_10.	1	p3	(TTA)7	21	245	265	CGAAATTAATTAAGGAAAAGATTCC
scaffold638078_20.	1	p3	(GAT)5	15	416	430	CACCCTTTTTGTGGAAGCAT
scaffold638085_16.	1	p3	(ATA)5	15	3528	3542	CGTGAGAATCTTCGACCTCC
scaffold638190_15.	1	p3	(AAC)5	15	896	910	ACGACATGAAGCTTCTGCAA
scaffold638229_16.	1	p3	(ACA)6	18	1511	1528	TCACAATAAACCTCCAGTTCCC
scaffold638302_14.	1	p3	(ATT)5	15	545	559	ATTTTGCTCACCCTGCTCAT
scaffold638303_12.	1	p3	(AAT)5	15	646	660	ATGGGGACATCAAGTTGGAA
scaffold638358_14.	1	p3	(GCC)5	15	386	400	GTCTAATGTTTCCGCCTCCA
scaffold638386_16.	1	p3	(CGG)5	15	319	333	ATTTTTATGGATTGTGCCGC
scaffold638527_12.	1	p3	(ATA)5	15	142	156	TTTTTGTTTTTGACGGGTCC
scaffold638702_15.	1	p3	(ATC)5	15	561	575	CGCAGTTGATCTTCTGTCCA
scaffold638872_17.	1	p3	(TGT)5	15	44	58	TGTAGCCGACCCCAATTTAT
scaffold638901_15.	1	p3	(AAT)5	15	1716	1730	TCCAAAATAATTCGGCCAAC
scaffold639087_15.	1	p3	(AGA)5	15	911	925	AGCATTAACGATGCCTTGCT
scaffold639313_12.	1	p3	(ATA)5	15	924	938	CGCATCTTCCGAGCTATCAT
scaffold639585_10.	1	p3	(CAA)5	15	92	106	TGGGCTAGTAATCTGGGTCCT
scaffold639603_18.	1	p3	(GAA)5	15	828	842	CCTAAAAGGTTTTGGGGATCA
scaffold640294_11.	1	p3	(TTG)5	15	292	306	AATGTTGATGCTGTTTGGAGC

scaffold640334_12.	1	p3	(TAT)9	27	175	201	GCCACTTGTAACCTCCCAAA
scaffold640409_18.	1	p3	(ACA)6	18	358	375	AATCTCGATGCCATCTCCTG
scaffold640570_15.	1	p3	(ATT)8	24	99	122	TGCTAAAAACAAATGCCAAGG
scaffold640572_18.	1	p3	(ATT)5	15	311	325	AAACGTGAAGTCAATTTCAATGAT
scaffold640708_16.	1	p3	(TGA)6	18	704	721	GCATCATGCATGGTCTTACC
scaffold640727_21.	1	p3	(CTT)5	15	23	37	AAAAATTGGTGCGGGTGC
scaffold640769_14.	1	p3	(ATA)5	15	155	169	GGAAAATTGGGTCATATAGCTCC
scaffold640833_12.	1	p3	(TTA)6	18	565	582	TTGTTGCAGTAGCCATGCTC
scaffold640845_13.	1	p3	(TCT)6	18	182	199	CCCCCTACACCACTCTTTCA
scaffold640903_10.	1	p3	(GGC)5	15	56	70	TGTCAACGTAAAAGGAGGGC
scaffold641098_18.	1	p3	(GAA)6	18	208	225	CCATTCATCGTCGAAGACCT
scaffold641454_16.	1	p3	(TTG)5	15	917	931	TGTTATTTGCACAATCATTTCCTT
scaffold641545_11.	1	p3	(GAG)7	21	998	1018	ATGCTTTGCTTCTTATGCGG
scaffold641557_11.	1	p3	(TTC)7	21	54	74	GATCAGCAGTGGCGTTGTC
scaffold641720_19.	1	p3	(GCG)7	21	191	211	CATTCTTTCTCCGTCTTCCG
scaffold641800_12.	1	p3	(TTC)5	15	147	161	TGCTTTTCAGTTGGCATTTTT
scaffold641821_15.	1	p3	(AAT)5	15	271	285	AATTTCTCCCACTTGCCTTG
scaffold641897_15.	1	p3	(AAT)6	18	415	432	TTGGCAGCTAGTGCTCATTTT
scaffold642166_16.	1	p3	(TGA)6	18	43	60	CCCAAGACCCCAATTTGATT
scaffold642361_15.	1	p3	(GCC)5	15	492	506	CACCAATCAATAATGCACGC
scaffold642479_10.	1	p3	(ATT)5	15	91	105	GGATAGAATGAGGGTTTTCCC
scaffold642489_15.	1	p3	(ATC)7	21	1776	1796	CGTGCGTGTTGAATTCATGT
scaffold642561_21.	1	p3	(ACA)5	15	142	156	CGTGCCAATAATGACACAAAA
scaffold642568_10.	1	p3	(AAC)5	15	685	699	CGTTGTGCTCTTGAAACTGG
scaffold642595_14.	1	p3	(TGG)6	18	1568	1585	GTTTCCTCACTACACCCCGA
scaffold642917_18.	1	p3	(TTC)5	15	33	47	GGATCAGCAGTGGCTTTTTC
scaffold642956_11.	1	p3	(AAG)5	15	217	231	CCGGAATCTGAGAGAGATCG
scaffold643117_15.	1	p3	(CCG)5	15	942	956	CATCAAAAGCAGAGCAGCAC
scaffold643125_14.	1	p3	(AAT)6	18	179	196	CGCATACGATCTTGATTATGG
scaffold643174_16.	1	p3	(TTG)5	15	376	390	TTGGGATTAAGGCTTTGGTG
scaffold643178_10.	1	p3	(ATA)5	15	431	445	TGGTGAAAAATCAAATACTTGGAA
scaffold643179_12.	1	p3	(ATA)5	15	462	476	TGGTGAAAAATCAAATACTTGGAA
scaffold643326_14.	1	p3	(GTA)5	15	490	504	TGGAATAGCTTGATAAATGATTTGAA
scaffold643440_14.	1	p3	(CCA)5	15	616	630	AATCATCACAAGCCCCAAAG
scaffold643544_12.	1	p3	(TTG)7	21	63	83	TAGCCGACCCCAACTTATTG
scaffold643773_11.	1	p3	(AAG)5	15	67	81	GGGGGAGAAAAATAAAGAAAAA
scaffold643804_16.	1	p3	(CTT)5	15	968	982	TCGAGAACCAATAATGATGAGC
scaffold644040_17.	1	p3	(TTA)6	18	1197	1214	TTTGGTTTTGCTCCTCTGCT
scaffold644060_12.	1	p3	(ATA)6	18	1295	1312	TCTTCCTTGTTTCTTTCTTTGGA
scaffold644115_10.	1	p3	(AAG)5	15	198	212	CGAACAGAGGCAGCATAAAA
scaffold644287_15.	1	p3	(ACC)6	18	37	54	CCTCTCCTCCTTCTTCCCAC
scaffold644626_15.	1	p3	(TGT)5	15	210	224	AACCTTGGTTCATGTAGCCG
scaffold644647_10.	1	p3	(AGG)5	15	112	126	ATTGACAGCAGGGAGGTGAT
scaffold644724_12.	1	p3	(TGT)5	15	64	78	TTGGTTCATGTAGCCGACCT
scaffold645046_15.	1	p3	(GGA)5	15	962	976	TGGTAAAATTCCACTTCGGC
scaffold645069_15.	1	p3	(AAT)7	21	43	63	TGTTCGTATTAAATTACCGGGAG
scaffold645106_16.	1	p3	(TGT)5	15	721	735	AATGGCAAAGGTAAATGAGCA
scaffold645203_14.	1	p3	(ATA)6	18	803	820	AACCATTTAGAATTTTTCGGGA
scaffold645264_12.	1	p3	(AAT)5	15	724	738	GGTCAGTGAAGCCCACCTTA
scaffold645280_18.	1	p3	(TAT)5	15	463	477	AAGTCCAGCACTCCCAATTT
scaffold645295_11.	1	p3	(CAT)5	15	150	164	GCGAGACAACGAAATTCTCA
scaffold645321_10.	1	p3	(TGA)8	24	43	66	CCCAAGACCCCAATTTGATT
scaffold645365_16.	1	p3	(AAT)5	15	367	381	GGTTGATCGTGTTGAATTATGG
scaffold645433_16.	1	p3	(TTG)5	15	612	626	GTAGCAGCTCGGTGAGGTTC
scaffold645464_14.	1	p3	(CTT)5	15	165	179	GACGATGGTTGCCTTTGTTT
scaffold645504_16.	1	p3	(GAG)5	15	307	321	TGTTGGTGGTGGTGTCTTGT
scaffold645844_12.	1	p3	(TTA)5	15	349	363	GAGAGCAGTCCTTTTCCCG
scaffold645973_14.	1	p3	(CAT)7	21	855	875	CGTTCCTTGCAACAACAAGA

scaffold646043_16.	1	p3	(AAT)6	18	381	398	TCTTGCCTCGATTCCTTGAT
scaffold646215_18.	1	p3	(TGC)5	15	329	343	TGACCAGATAACATCGGCAA
scaffold646236_15.	1	p3	(AAT)5	15	2478	2492	TGTGGGGACGATTATTCCAT
scaffold646256_14.	1	p3	(ACA)7	21	2474	2494	CAGGAAAACCCAGAAGTGAGA
scaffold646375_16.	1	p3	(CAT)6	18	1184	1201	GAAGCAAAAACAAACCCACC
scaffold646382_15.	1	p3	(TTA)5	15	477	491	AAAACCTCATAAAACTGTCATGTCT
scaffold646448_14.	1	p3	(TTC)6	18	196	213	TCTTGCTGCTTTTTCCACCT
scaffold646570_18.	1	p3	(TGA)6	18	884	901	AATTGGGGTGCAAAACAAAG
scaffold646599_14.	1	p3	(ATA)5	15	2372	2386	GAACCCAAGAAGCAACATGTAA
scaffold646648_11.	1	p3	(AAT)5	15	625	639	TAGGGTTCATGTCCGGTTGT
scaffold646769_17.	1	p3	(ATA)9	27	185	211	CGTTCCAAACTTCGAAGAAAA
scaffold646867_13.	1	p3	(TTA)6	18	2075	2092	TTGACAACATTGCCACATACC
scaffold646919_16.	1	p3	(CAC)6	18	626	643	CAGCTGAGGGAGGAGTTTTG
scaffold647024_14.	1	p3	(TCT)7	21	365	385	TCCAGCTATCCCGTTTTGTC
scaffold647069_15.	1	p3	(GGT)6	18	730	747	GCAGTGGCGTTGAACTAACA
scaffold647092_16.	1	p3	(TAA)5	15	2370	2384	CCACCTCACGCAAAAAGAGT
scaffold647177_19.	1	p3	(TTC)5	15	784	798	AAATAAGGCATGGGTTGTGC
scaffold647326_10.	1	p3	(TTG)5	15	472	486	GAGCACGTGGAGAAGAGACC
scaffold647372_12.	1	p3	(ATA)5	15	545	559	CGAAGTCTCACGGTTGATTG
scaffold647492_10.	1	p3	(GGC)5	15	116	130	ATTCCGGTGACGGTTGAATA
scaffold647532_17.	1	p3	(GCT)5	15	978	992	AGGGGGAAAGCAAAGAACAT
scaffold647558_15.	1	p3	(ACC)5	15	643	657	ACTTCTCCTTCCACCGCTCT
scaffold647656_16.	1	p3	(TAA)6	18	849	866	GAACTGACTTCGGGGTGAAA
scaffold647758_14.	1	p3	(ATA)5	15	167	181	CAGTAAAATGCTGCCCAGGT
scaffold647817_15.	1	p3	(CTT)5	15	1608	1622	ACTCAGATCACTCAACCCGC
scaffold648009_14.	1	p3	(GAG)5	15	104	118	GAACGTGGGAGGTGAAGAGA
scaffold648136_20.	1	p3	(GAA)5	15	579	593	CACGTCGAGCTAGAACCTCC
scaffold648138_13.	1	p3	(TAA)7	21	1323	1343	CAATGAGGACATCCGAGGAG
scaffold648152_16.	1	p3	(GGA)5	15	3721	3735	TCCTCTGTTGTGTTGGATGC
scaffold648392_16.	1	p3	(GGT)5	15	3512	3526	ACAGACCCTCACACCATTCC
scaffold648520_17.	1	p3	(AAT)5	15	63	77	TGTGTGCGATTTAATCCTAACC
scaffold648567_11.	1	p3	(TTC)5	15	104	118	TCCATAAGCCATAGCTAAAAGAGG
scaffold648595_16.	1	p3	(TGT)6	18	2274	2291	GCTGACACAACCACAACACC
scaffold648864_12.	1	p3	(TAT)5	15	1109	1123	TCATTTTATCATGAATCCCAACA
scaffold649189_16.	1	p3	(TTG)8	24	1891	1914	AACCTTCTCTCTGGTGCCAA
scaffold649219_14.	1	p3	(TTG)5	15	50	64	TGTAGCCGACCCCAATTTAT
scaffold649257_13.	1	p3	(GCT)5	15	314	328	AAAGCATACGGGTGAAGTGG
scaffold649376_18.	1	p3	(GCC)6	18	3377	3394	TTCACCACCAGATCCTCCTC
scaffold649470_11.	1	p3	(TTA)7	21	115	135	CTTCGCCGCATATGAAACTT
scaffold649912_17.	1	p3	(TTA)8	24	1309	1332	TGAACTCGCTCCTTCCATCT
scaffold649917_17.	1	p3	(GGT)5	15	356	370	CAGAAATTATCCCACACCCG
scaffold650244_10.	1	p3	(AAT)5	15	46	60	GAACCCTTTCACCGTCCTCT
scaffold650477_16.	1	p3	(TAT)6	18	3505	3522	CAAGCAAAATGTGTTGATTGTT
scaffold650582_13.	1	p3	(ATA)7	21	670	690	CCATTTCCCGAAACGATAGA
scaffold650652_13.	1	p3	(GCT)5	15	514	528	AAATGCTGCTGTGTCGTGAG
scaffold650732_16.	1	p3	(ATC)5	15	160	174	TCAGAGGTGCACTCGAAGTT
scaffold651127_19.	1	p3	(CGG)5	15	1634	1648	GACCAGTTCACAAAAGTCCCA
scaffold651206_16.	1	p3	(ACA)5	15	334	348	CCACCGGACACATTCAATTA
scaffold651265_13.	1	p3	(AAT)5	15	499	513	ATATTTGGTTGGTTCAGCGG
scaffold651362_12.	1	p3	(TAT)5	15	259	273	AACTCGGCAAGATGAACTGC
scaffold651688_13.	1	p3	(CAT)6	18	157	174	AACATATTGACTCCCGTGCC
scaffold651713_10.	1	p3	(GAA)6	18	344	361	TTCAGGGATTCGATTTGGAG
scaffold652005_16.	1	p3	(GAA)5	15	527	541	TCAGAAAGGATCCTCCTCCA
scaffold652119_14.	1	p3	(TCT)5	15	203	217	GGGTTCTTGGGTGTCAGAGA
scaffold652207_15.	1	p3	(ATT)6	18	82	99	CGTGTAGGATGGGAAATTGAA
scaffold652222_15.	1	p3	(TTG)6	18	286	303	CGATCTCACTTCGTGGGAAA
scaffold652326_11.	1	p3	(CGG)6	18	72	89	ACATGAAGAGGACGAAGCGT
scaffold652402_16.	1	p3	(AAT)5	15	230	244	GTTAACCGCATGTCACTTCG

scaffold652415_16.	1	p3	(AAT)5	15	505	519	CCTATTTCCCAACCCAAACA
scaffold652416_13.	1	p3	(ACA)5	15	1030	1044	GCATGGATCTTTGGGAGAAA
scaffold652452_15.	1	p3	(ATC)5	15	943	957	ATCTCCACCACCACCATCAT
scaffold652622_16.	1	p3	(CTC)6	18	160	177	TTCCGTTGGCTTATTTTTGC
scaffold652819_13.	1	p3	(GGC)5	15	136	150	AGAGTTATTCAGGCCAGCCC
scaffold652827_19.	1	p3	(GCC)5	15	780	794	GTTGCTCAAATTCTTCCCCA
scaffold653011_17.	1	p3	(ATT)5	15	746	760	TTCTGATGCTCTACCAAAACG
scaffold653279_16.	1	p3	(TTG)5	15	238	252	CACTGATCGTACACGATGGC
scaffold653323_12.	1	p3	(TGG)5	15	351	365	GATAGGCGTTCGAAGGTGAC
scaffold653377_14.	1	p3	(TAT)5	15	772	786	ACGATGCTCGAGGTTCAGAG
scaffold653469_18.	1	p3	(TGG)5	15	1048	1062	TTCCATGTTCTGGAGAAGCC
scaffold653573_16.	1	p3	(TAA)5	15	821	835	CATTCCACCGGAAGGTCTTA
scaffold653577_11.	1	p3	(CCG)6	18	165	182	GAAAACCCCCACTCAACTCA
scaffold653804_10.	1	p3	(CAA)5	15	117	131	TGCAAAAACATCTTTCACAATCA
scaffold653817_15.	1	p3	(CAA)5	15	1106	1120	TTTGAATTTGGAAAAGTATGGAA
scaffold653978_10.	1	p3	(CTT)5	15	159	173	TCCGGTGCTGTCTTTTCTTT
scaffold654081_12.	1	p3	(AAT)5	15	287	301	AAAGTAGCGGTTGCGGATTA
scaffold654155_14.	1	p3	(TTA)6	18	1084	1101	AACGTCAACGCTCGTACCTT
scaffold654157_15.	1	p3	(GAC)5	15	1152	1166	TGATGAACTGCTGCCAGAAC
scaffold654174_11.	1	p3	(AAT)5	15	64	78	TGCATAATCAACGGTCAATCA
scaffold654317_14.	1	p3	(ATC)5	15	511	525	CACCTCTCATTCACATGCCA
scaffold654748_15.	1	p3	(ATA)5	15	759	773	CCAAAAAGGTGAAGGAAACAA
scaffold654864_14.	1	p3	(ATT)5	15	921	935	GTGAGCCACGCACTCTGTAG
scaffold654872_16.	1	p3	(GCC)5	15	436	450	TTCTTCTCCTCTGCCTCCCT
scaffold655196_15.	1	p3	(TTA)5	15	496	510	GGTGTTTTCGTTGGAGCTGT
scaffold655208_12.	1	p3	(GCC)5	15	894	908	CCCAACTTCCAACATCGAAT
scaffold655253_15.	1	p3	(CCT)5	15	1467	1481	AAATTCCCCACCATTTCCTC
scaffold655440_15.	1	p3	(ATC)7	21	162	182	CGCCTTGAGTTTGGGTAAAA
scaffold655761_14.	1	p3	(GAT)5	15	1541	1555	TTTGATTGTGCGATGTTTGG
scaffold655803_16.	1	p3	(TTG)5	15	3841	3855	AGTTCCCAATTTTTGGCTCC
scaffold655841_12.	1	p3	(TAT)8	24	644	667	TGTTCTGTTAAAACTTCACATCTCA
scaffold655903_10.	1	p3	(CCG)5	15	314	328	TCGATCCGGGACTTGAAATA
scaffold656025_18.	1	p3	(ATA)5	15	59	73	CTTCAAATGAATCTTCAACAGGA
scaffold656244_11.	1	p3	(TAA)6	18	204	221	TGAAGCCCAACAGATTGATTT
scaffold656330_12.	1	p3	(ATT)5	15	36	50	GAATTCTGAATGCATGGTTCTT
scaffold656543_10.	1	p3	(CGG)5	15	269	283	ATGGCGAGGGAGAGAGGTAG
scaffold656926_16.	1	p3	(GAG)5	15	670	684	CCATCTCTTTCCAGAGCGTC
scaffold657050_15.	1	p3	(TTG)6	18	336	353	CGACCTCACATAGTGGGACA
scaffold657177_19.	1	p3	(ACA)6	18	1293	1310	GTGCACATGTCAAGTTTGGG
scaffold657676_14.	1	p3	(ATA)5	15	894	908	TTGACCCCAATCTCGACTTC
scaffold657791_15.	1	p3	(CTT)5	15	448	462	CCGCTGATCTTTCTGCTCTT
scaffold657905_12.	1	p3	(CAC)5	15	322	336	GATTGCCTTGTTTACCCGTG
scaffold658273_18.	1	p3	(ATC)5	15	164	178	ATGGAATCTGGGGTTCAACA
scaffold658434_10.	1	p3	(TCA)5	15	638	652	CCCTGCCAATAGAAGATCCA
scaffold658636_12.	1	p3	(TCA)5	15	384	398	TGGGCGAAAATTCAACTAGG
scaffold658782_16.	1	p3	(TGA)6	18	45	62	CCCAAGACCCCAATTTGATT
scaffold658976_13.	1	p3	(ATA)5	15	462	476	TGAGCGAGGTGAAGAGTCAA
scaffold658992_11.	1	p3	(TGT)5	15	36	50	CCAATTTATTGGGATTAAGGCT
scaffold659030_15.	1	p3	(TTA)5	15	901	915	CACGCGGATCTGTGTCTATTT
scaffold659075_11.	1	p3	(TTA)7	21	1139	1159	TGCAATTTGGTTCCATTCAA
scaffold659115_12.	1	p3	(ATT)5	15	104	118	TTGCCTTTAATGCTGTGCTG
scaffold659221_13.	1	p3	(CGC)5	15	322	336	TGGTCGTAAGTTGGAAAGGG
scaffold659240_16.	1	p3	(TCA)1	30	2769	2798	TCCCAAAATGAAACTTGTAAATCA
scaffold659269_13.	1	p3	(ATT)5	15	123	137	AAAGGGCCTTAACACCAACA
scaffold659415_16.	1	p3	(GTG)5	15	638	652	TGATTCATCGCATTTACGGA
scaffold659462_12.	1	p3	(ACC)5	15	2243	2257	CGAGGCATAACCTCACCAGT
scaffold659934_10.	1	p3	(ACA)6	18	540	557	AAGCTAAGAGCTCCTTGGGG
scaffold659958_16.	1	p3	(TCC)5	15	545	559	GGTCCCACTCGAGTCTCATT

scaffold659977_18.	1	p3	(TCC)5	15	388	402	TTTGACATCTCTGCTGGTGG
scaffold660176_16.	1	p3	(TGT)6	18	47	64	TTGGTTCATGTAGCCGACCT
scaffold660204_16.	1	p3	(AGC)5	15	212	226	ATTCAGCTCTTGTTTCCCCA
scaffold660324_15.	1	p3	(TCT)5	15	1433	1447	AATCTCACGCAAGGTGCTTT
scaffold660419_13.	1	p3	(TTC)7	21	498	518	ACATTTCTTTGGCTTCCCCT
scaffold660463_16.	1	p3	(TCA)6	18	5085	5102	ATTTTCCTCAACTTCGGCCT
scaffold660578_16.	1	p3	(ATT)5	15	1291	1305	ATAATGCCGGTGCAGGTCT
scaffold660598_15.	1	p3	(AAG)5	15	979	993	ATGCATGCAAACCAGGATCT
scaffold660696_15.	1	p3	(ACA)6	18	404	421	CTACCGGAGGAAACCATGAA
scaffold660748_11.	1	p3	(TTA)5	15	617	631	CTTCCACCCTTGTTTTCCAA
scaffold660899_10.	1	p3	(CGC)5	15	289	303	ATGGTGGTAAGGTGTGGAGG
scaffold660949_17.	1	p3	(CTT)5	15	206	220	AGATCCCTCCCTCGCTACAT
scaffold661306_16.	1	p3	(ACA)6	18	4868	4885	GGGTGGTGAAGAATGAATGC
scaffold661352_13.	1	p3	(TCC)5	15	438	452	CAGTCACGGGATATGCAGAA
scaffold661391_16.	1	p3	(GGT)5	15	493	507	TTGGGGATTTCTGAATTTGG
scaffold661410_12.	1	p3	(GAA)5	15	1037	1051	TTCTCTTGCAATGCTTCACG
scaffold661463_17.	1	p3	(TAG)5	15	90	104	GAGGAGAGCAGCCACAAGAA
scaffold661529_13.	1	p3	(TAT)5	15	985	999	GGTGCGGGATAAAAATGTTG
scaffold661560_14.	1	p3	(GAT)5	15	404	418	ATATCAGCTCGCACAATCCC
scaffold661569_13.	1	p3	(TGT)6	18	44	61	TGTAGCCGACCCCAATTTAT
scaffold661701_15.	1	p3	(ATC)5	15	558	572	TCCATTAACTCATCGTTAAAATTCA
scaffold661753_12.	1	p3	(GAT)5	15	106	120	GGATGGGGATAGTGATAGGC
scaffold661841_14.	1	p3	(TTA)6	18	1447	1464	CATATTCAGAGTCGTTTGAGCTT
scaffold662014_15.	1	p3	(TAA)7	21	371	391	CTAATAGGGGGATTTTGCCC
scaffold662112_14.	1	p3	(TTC)5	15	1287	1301	TGAACTTTTTGTTCCTGCGA
scaffold662215_12.	1	p3	(TAT)6	18	201	218	CGAACAAGAAACGGGGATAA
scaffold662342_11.	1	p3	(TAA)7	21	493	513	TGAAGGCTTTTCTCCTGCAA
scaffold662671_10.	1	p3	(ATA)6	18	57	74	GGGGACATCTGAGTGTGTGA
scaffold663048_14.	1	p3	(ATC)6	18	1315	1332	CCAAGTGTTAGTGGCCAACC
scaffold663140_11.	1	p3	(AGA)5	15	547	561	ACAAGCAAATTTCTCCCCCT
scaffold663155_10.	1	p3	(TGT)6	18	42	59	TGTAGCCGACCCCAATTTAT
scaffold663292_13.	1	p3	(TTA)5	15	766	780	CCAATGTGATTGGCTAGTTGC
scaffold663347_15.	1	p3	(AAT)5	15	977	991	ATGACCGAGGAGCAAATTGT
scaffold663475_15.	1	p3	(GGT)5	15	2414	2428	CGGTTGACCCTGTTAGCATT
scaffold663798_11.	1	p3	(GAG)6	18	321	338	GACACAGAGGCTGACGATGA
scaffold663925_13.	1	p3	(AAT)5	15	334	348	CCGAGTAGCTGGGTCTGAAG
scaffold663931_19.	1	p3	(CAT)5	15	697	711	TGTCAGTCAGGGATTCTTTTGA
scaffold663942_18.	1	p3	(ATA)5	15	1443	1457	TGAGCATATTTTGTGTTGCTTG
scaffold664273_16.	1	p3	(ATA)5	15	1368	1382	TTTAGTGGGAATCACGGGAG
scaffold664419_11.	1	p3	(TTC)5	15	866	880	ATAATCGTCTCCGTCGCTGT
scaffold664531_13.	1	p3	(GAT)8	24	982	1005	AGCAGAGGATTGTTGACGCT
scaffold664554_15.	1	p3	(AAT)5	15	927	941	CACCCAACCCGAGTATCCTA
scaffold664565_16.	1	p3	(TGT)6	18	31	48	CCCAGTTTATTGGGATTAATGTTT
scaffold664957_15.	1	p3	(ATC)6	18	1133	1150	GTCCTTGCATTAGGCAGAGC
scaffold665059_16.	1	p3	(TTA)5	15	2522	2536	CCCAAAAGGGAGGAGTGAAT
scaffold665352_15.	1	p3	(AAT)5	15	2468	2482	GGGACAATGCTGATCTCCTC
scaffold665414_12.	1	p3	(AAT)6	18	881	898	TTTTGACAATTCTCAGCCCC
scaffold665430_15.	1	p3	(AAG)5	15	2517	2531	TAATCCCACTGAATTTGGGC
scaffold665432_12.	1	p3	(ATG)5	15	66	80	CGAGCTCGATCATGCAACTA
scaffold665472_12.	1	p3	(AAT)5	15	623	637	TGGTGAAAAGTAAGCATGCAA
scaffold665564_16.	1	p3	(CCG)5	15	496	510	TACTCCCACCGGAAATCAAG
scaffold665580_17.	1	p3	(CTT)5	15	1899	1913	TCGAATGCAACACTGGAGAA
scaffold665604_11.	1	p3	(ATT)7	21	382	402	TGACGAGCTTCCCTCTTGTT
scaffold665608_12.	1	p3	(GGC)7	21	1940	1960	GATCGGACAACCCATCAAAC
scaffold665663_14.	1	p3	(TAT)6	18	1190	1207	TTTTGCTCACCCCTAACCAC
scaffold665688_17.	1	p3	(CCT)6	18	499	516	CTTCTCCTCCATTTCCACCA
scaffold666123_19.	1	p3	(TGT)5	15	681	695	TCAAACGAAAACATGCATCC
scaffold666243_15.	1	p3	(ATT)5	15	1900	1914	CCAAGGTTGAAAGGGATCTG

scaffold666446_11.	1	p3	(CCA)6	18	372	389	CCCAAACTCATGCAAAACCT
scaffold666461_16.	1	p3	(AAT)6	18	1602	1619	TTACCTAGCAAGGGTTTGGG
scaffold666496_12.	1	p3	(AGA)5	15	1258	1272	AGAGAGACGGGGAAGAGGAG
scaffold666519_17.	1	p3	(ATT)5	15	730	744	GCCCATAAGCCCATCAAATA
scaffold666525_18.	1	p3	(CCT)5	15	217	231	AATGGAAAATAAGCAGGGGC
scaffold666536_14.	1	p3	(ATC)5	15	2922	2936	AGCACACTTCTCCTGCAACC
scaffold666537_17.	1	p3	(TAT)5	15	297	311	GGGAATCTTGTTTTAAGTATCCGA
scaffold666555_16.	1	p3	(CGC)5	15	218	232	AAGATCGAGAAAACGGAGGC
scaffold666612_13.	1	p3	(TAT)5	15	3045	3059	CAGCCGCTACTCTTCGAGTG
scaffold666635_13.	1	p3	(CTT)5	15	169	183	TGAGTGCATGCTCCAAAGAC
scaffold666641_15.	1	p3	(TGA)5	15	1000	1014	CATTGAAGAAGAAGGCGGAG
scaffold666643_16.	1	p3	(CCA)6	18	526	543	GAGAATTCCCGCAGATCAAA
scaffold666724_15.	1	p3	(CCA)5	15	1401	1415	GCAGCCAAGTTTGGTTTGTT
scaffold666901_10.	1	p3	(TAT)7	21	84	104	CCACCCCCTTCTTTTTCATT
scaffold666919_10.	1	p3	(GAG)6	18	530	547	GAGATCCCCGTAAACAGCAA
scaffold667001_16.	1	p3	(CGG)7	21	954	974	TGCATCTTGGCCCAACTATT
scaffold667145_11.	1	p3	(TAA)5	15	333	347	AGGGCATGCATAGGTGTAGG
scaffold667272_16.	1	p3	(AAT)5	15	4512	4526	TGAGCTCTGTTGGTCTTTGG
scaffold667488_14.	1	p3	(TTA)5	15	1212	1226	TGATTGAAAGCACCGTCTTG
scaffold667520_12.	1	p3	(TCA)5	15	173	187	TGGAAGAGTGCCCAAATACA
scaffold667604_16.	1	p3	(CAG)5	15	1900	1914	CTTCGGCTCTCCAACTTCAG
scaffold667637_15.	1	p3	(GAA)5	15	1265	1279	CAGCTCCAATGCAGTAGCAA
scaffold667908_15.	1	p3	(ACA)6	18	1381	1398	TTTCCAAATTTTCTCCTCCG
scaffold667921_14.	1	p3	(CCT)6	18	216	233	AGATGGATGTTCGAGTTGGG
scaffold667974_14.	1	p3	(ATT)5	15	557	571	CCATAGGCGAATTCTAAAGTGA
scaffold668086_10.	1	p3	(TTA)7	21	145	165	AAATTTTATGGGACGGAGGG
scaffold668175_16.	1	p3	(CTT)5	15	1079	1093	TCAGTTTGCACACTTTCCCA
scaffold668473_15.	1	p3	(GAC)5	15	2158	2172	TCTTAACGGATTCTCCAAAGATG
scaffold668550_11.	1	p3	(TTC)5	15	324	338	TCCATCGTACCGAGGCTAAC
scaffold668599_13.	1	p3	(GAA)7	21	279	299	AAGAGGTGTATGCCGGATTG
scaffold668617_18.	1	p3	(AGG)5	15	2817	2831	GCGTGGGAATTGTTTCAAGT
scaffold668669_15.	1	p3	(TTC)5	15	290	304	CATCATCCGTAAGCTCCCAC
scaffold668784_10.	1	p3	(GGC)5	15	51	65	GGGGTCCCTGTCTTATAGCG
scaffold668791_15.	1	p3	(CTC)5	15	2446	2460	CTTTCTAGTCCCCATTGCCA
scaffold668822_13.	1	p3	(AAT)8	24	1288	1311	CGTATAGTCCCGAGCAGAGG
scaffold668860_15.	1	p3	(AAT)5	15	1980	1994	TGCCTTGCGAATTGTGATTA
scaffold668868_15.	1	p3	(TCT)5	15	648	662	TCGGCGTTCCTGTATTTTTC
scaffold668869_15.	1	p3	(GCC)5	15	1191	1205	AGCCCATAAGCAACACGAAT
scaffold668932_17.	1	p3	(ATC)5	15	363	377	TGGGTGCGAACAACATTATTT
scaffold669042_10.	1	p3	(CGG)6	18	165	182	GCAGGCGATAAGCAGAAGTT
scaffold669360_13.	1	p3	(TGA)7	21	42	62	CCCAAGACCCCAATTTGATT
scaffold669370_15.	1	p3	(CCG)5	15	1540	1554	AGATCCAATCCAAATGCTGC
scaffold669488_11.	1	p3	(GAG)6	18	360	377	CCTTATCTGGGCCTTCACAA
scaffold669500_11.	1	p3	(ATT)7	21	82	102	CGTGTAGGATGGGAAATTGAA
scaffold669562_11.	1	p3	(ACA)6	18	460	477	ATAGGTTGTTCAAAGCCGGG
scaffold669594_18.	1	p3	(TGT)5	15	330	344	TTTGGGAGTGAATGGGAGAG
scaffold669672_14.	1	p3	(CTT)5	15	481	495	TGAATGTAATGGTCGTGCGT
scaffold670000_14.	1	p3	(TGA)6	18	1444	1461	GCTATGCCTGTGCCTGATTT
scaffold670038_17.	1	p3	(CCA)5	15	1220	1234	CATCGCCCCTCTACTTCTTG
scaffold670094_17.	1	p3	(TCA)5	15	3252	3266	CCAATCACAGTCGAAGACGA
scaffold670241_14.	1	p3	(CGC)5	15	1172	1186	GCGGCTACAACCAAATTCAT
scaffold670441_17.	1	p3	(ACC)6	18	329	346	CATGCCTCGAGTATGTGGTG
scaffold670833_13.	1	p3	(TGA)5	15	48	62	CCCAAGACCCCAATTTGATT
scaffold671043_15.	1	p3	(ATC)5	15	182	196	CAATCAAATTGGGGTCTTGG
scaffold671287_13.	1	p3	(TTA)5	15	197	211	AGCAGGCTCAGACCAAGAAG
scaffold671359_13.	1	p3	(ATT)5	15	80	94	TACTTCAACCCACGTGACCA
scaffold671402_16.	1	p3	(CAT)7	21	2467	2487	TGCAGGTTCTGAAACAGGAA
scaffold671471_17.	1	p3	(GTG)6	18	1531	1548	GGCCATTCGAGTTATGGAGA

scaffold671593_15.	1	p3	(AAT)8	24	37	60	AATTGTTGCATCTATTTTCTAAATCA
scaffold671644_17.	1	p3	(ACA)6	18	373	390	CAAGACCGTGACAGGCACTA
scaffold671731_15.	1	p3	(AAT)5	15	1352	1366	ATTGTCCCTCCACACCACTT
scaffold671739_10.	1	p3	(TGC)5	15	500	514	AATCGCATTTTCTCGACGAC
scaffold671883_18.	1	p3	(GGC)5	15	302	316	AGCCAAGAGCCCATAGTTCA
scaffold671894_16.	1	p3	(GAA)5	15	637	651	TTCCGATCAGAGCTTCTCGT
scaffold672194_14.	1	p3	(ATT)6	18	759	776	AAAATTTGTCCTTTCTACACGCA
scaffold672264_20.	1	p3	(TAT)5	15	856	870	AAAACCTGCCTCAACCCAG
scaffold672445_15.	1	p3	(TGA)5	15	48	62	CCCAAGACCCCAATTTGATT
scaffold672486_14.	1	p3	(ACA)5	15	8646	8660	TGCAGCAACAGTTGGAGTTC
scaffold672602_17.	1	p3	(TCA)7	21	1837	1857	AACGCAACCTAATGGTTTGG
scaffold672961_16.	1	p3	(TTC)5	15	986	1000	GGCAGAATTTGAATGGGAAA
scaffold673001_12.	1	p3	(TGA)5	15	77	91	TGATCCCACTCTCCTTCTCG
scaffold673009_13.	1	p3	(ACA)6	18	2182	2199	CATCACTTCTCCCAAAACCG
scaffold673018_15.	1	p3	(TCC)5	15	3955	3969	TACTGCCTCCAGATCCACCT
scaffold673047_13.	1	p3	(GGT)5	15	932	946	GGATCATTGTTATCGCGGTT
scaffold673250_12.	1	p3	(TGC)5	15	602	616	TGAACTGTCTTTGGCACGAG
scaffold673283_16.	1	p3	(ATT)6	18	1450	1467	TCAAAAACCAATTGATAGCACA
scaffold673352_19.	1	p3	(CGG)5	15	700	714	TGAATTCTTTCCTCCATGCC
scaffold673481_15.	1	p3	(GGT)5	15	425	439	TCAGCAAAAATGATCCCACA
scaffold673588_10.	1	p3	(GGC)5	15	307	321	GTCGAATTTTGCTGTGTGGA
scaffold673610_10.	1	p3	(AAG)6	18	66	83	GCAGGCCAAAGAGGAAGAGT
scaffold673614_16.	1	p3	(GGA)6	18	224	241	GCTTTGGACTCGGAGTTTGA
scaffold673783_15.	1	p3	(ATT)6	18	213	230	GACATTATCCATTTTATTGGGCA
scaffold673791_14.	1	p3	(GAA)5	15	1198	1212	GAACTCGAGCATTGCAACAA
scaffold673827_11.	1	p3	(ATT)8	24	1718	1741	CAAGAAAGCGAAATGCTTCA
scaffold673877_17.	1	p3	(GAT)5	15	180	194	GGAAGCACTCGCAAGAAAAC
scaffold673910_17.	1	p3	(TCA)6	18	178	195	TCACCCCCATACCCACATAC
scaffold673937_12.	1	p3	(TTG)5	15	174	188	ATGTAGCCGACCCCAATTTA
scaffold673943_10.	1	p3	(ATT)5	15	51	65	GGAGTGGGTGTCGGTTTTTA
scaffold673950_16.	1	p3	(GCA)5	15	228	242	AAAAATACGAGTGGCGATGG
scaffold674092_14.	1	p3	(ATT)7	21	175	195	TTTGGGTTTTAAATTCGTTGAA
scaffold674235_15.	1	p3	(AAT)5	15	208	222	AGAACCAGACCTGCTTGCAT
scaffold674289_16.	1	p3	(TTG)5	15	917	931	CGACCCACATAGTGGGAAAG
scaffold674441_16.	1	p3	(TTA)6	18	52	69	TTCGACGGTTTCAAAGAAAAA
scaffold674521_10.	1	p3	(TGA)6	18	408	425	TTTTGATTGGGAATAATTGGG
scaffold674534_17.	1	p3	(GCT)7	21	908	928	TGTTCGTCCAGAGACAGCAC
scaffold674546_14.	1	p3	(GAA)5	15	587	601	ATGTCTATCGTTTGGGCTGG
scaffold674630_16.	1	p3	(TTC)7	21	1590	1610	AAATTTGAGACCGTGGATCG
scaffold674732_14.	1	p3	(TGG)5	15	578	592	GGCTGACTCATGGAGAGGAG
scaffold674834_14.	1	p3	(CAG)5	15	645	659	ACTGCCTCATCCAAACTTGC
scaffold674841_11.	1	p3	(TAA)6	18	282	299	CCCCTATCCCCCACTGTTAG
scaffold674852_16.	1	p3	(ACA)6	18	546	563	TGACATTGTTTCGGTTGCAT
scaffold674914_14.	1	p3	(TCA)5	15	448	462	TCATGGTGGGGTGAGTTTTT
scaffold674941_13.	1	p3	(TGT)5	15	476	490	GATTCTGGTTCGGTGATGCT
scaffold674951_18.	1	p3	(AGC)5	15	228	242	GCTCGTACATCGAGTGATGC
scaffold675005_14.	1	p3	(TAA)6	18	368	385	GTGGAGCTGTGGTGGGTTAG
scaffold675080_15.	1	p3	(CAA)5	15	2057	2071	ATCCTATGTGCACCACGACA
scaffold675286_15.	1	p3	(TTA)5	15	3192	3206	AATGAGAAAATGAGGCGCAC
scaffold675311_17.	1	p3	(ACA)5	15	884	898	TTATGGCCAAAGACCAACCT
scaffold675378_15.	1	p3	(CGG)5	15	655	669	CGGATTGTTTTTGGAAAGGA
scaffold675537_19.	1	p3	(GAA)5	15	429	443	CAATGGAGGAGTGCAAGGTT
scaffold675836_14.	1	p3	(CGC)5	15	180	194	ACCTAAATCCTACCCCCACC
scaffold675890_15.	1	p3	(ACT)5	15	1064	1078	AAGGCCCTCTCAAAACCAAT
scaffold675935_14.	1	p3	(GGT)7	21	2756	2776	GAAGATGTATCAGGGCGAGG
scaffold676349_14.	1	p3	(CCG)5	15	39	53	GCATGAGGAAAAGGGATGAA
scaffold676398_17.	1	p3	(TTG)6	18	482	499	ACCGCAGAATTTAGGAGGCT
scaffold676541_13.	1	p3	(ATC)6	18	354	371	TCTTATTAGGGGCTTGTGCG

scaffold676817_14.	1	p3	(GTG)6	18	3813	3830	TTCAGTGTGAGGGGTGAACA
scaffold676849_15.	1	p3	(TTA)5	15	618	632	TTTTGTTGTGGCGTCTCTTG
scaffold676914_19.	1	p3	(TTC)5	15	573	587	GGAGATAGAGAGGGGCCAAC
scaffold677018_15.	1	p3	(AGA)5	15	1601	1615	GATTGGGGAGAGGATTGGAT
scaffold677109_10.	1	p3	(CCT)5	15	791	805	TGTCGGAGCAGAATTGTACG
scaffold677321_11.	1	p3	(TCT)5	15	348	362	AACGTATTCCTTCCCCCACT
scaffold677341_16.	1	p3	(TCT)6	18	6041	6058	TTCCCCACCATTTCATCATT
scaffold677483_13.	1	p3	(CGG)5	15	351	365	CCATCTCAAGGGTCTACCGA
scaffold677549_16.	1	p3	(ATC)5	15	186	200	TTGCTCCCCTCTATCAAAGTTC
scaffold677567_13.	1	p3	(CGG)5	15	834	848	GCCCTCGACTCCTTAGCTTT
scaffold677723_16.	1	p3	(TGA)5	15	101	115	CCCCAAGACCCCAATTTTAT
scaffold677848_11.	1	p3	(CCG)5	15	145	159	TACTCCATTACAGACCCCGC
scaffold677863_15.	1	p3	(TAT)5	15	1606	1620	GGCACCCTCTCATGGATACT
scaffold678042_14.	1	p3	(GCG)5	15	1342	1356	GTGTTTGTGATGGGCAACTG
scaffold678382_18.	1	p3	(CTT)5	15	899	913	AAGTCGTCGTCATCATCCTCT
scaffold678446_16.	1	p3	(AAT)6	18	46	63	GAGCATGCCTAGATGTTGCTT
scaffold678599_13.	1	p3	(AAT)6	18	100	117	AGTCTCAATGGGGACACCAG
scaffold678729_17.	1	p3	(TCA)6	18	2000	2017	ATCCTCCTCAGATCCTTGGC
scaffold678762_16.	1	p3	(CAA)6	18	1035	1052	TGTAGGCCAAATGTGTTGGA
scaffold678946_15.	1	p3	(TAT)6	18	408	425	CTCCAAATGCTCCTCTACCG
scaffold678957_17.	1	p3	(GCG)5	15	1240	1254	GGCTCGCAAAAATAACCAAA
scaffold679033_14.	1	p3	(GCT)5	15	234	248	GTAGTCGGAAAGTGGGGTGA
scaffold679249_16.	1	p3	(TTA)5	15	773	787	GTGCAAAAGCAGGCAGAAGT
scaffold679316_12.	1	p3	(ACA)6	18	1352	1369	CACTTACGAAATGTCAAGACGC
scaffold679404_15.	1	p3	(ATA)5	15	1070	1084	TTAGGACTACCGGTCCGATT
scaffold679449_16.	1	p3	(ACA)8	24	3071	3094	CCGAATGATGAGAAGTGGGT
scaffold679512_16.	1	p3	(ATC)5	15	794	808	TGAGGGAACTTTGTGAACCC
scaffold679688_11.	1	p3	(GAT)7	21	598	618	AGCTTAGGGCAACACGAGAA
scaffold679718_15.	1	p3	(TCG)5	15	494	508	CAATTCTTTTGTGCGTGAGC
scaffold679793_15.	1	p3	(TTG)5	15	397	411	CATTGATCGTACACGATGGC
scaffold679977_11.	1	p3	(TAT)5	15	236	250	TGGACCCAATATGTCATAACCA
scaffold680021_12.	1	p3	(TTG)5	15	235	249	GAAGGGGGAGACCGAAATTA
scaffold680090_18.	1	p3	(CTA)5	15	443	457	TTGCGTCTGATTTGTTGAGC
scaffold680154_15.	1	p3	(TAT)5	15	684	698	CATCATTTGATTGTGGTCCG
scaffold680165_14.	1	p3	(ATT)5	15	452	466	TCGAAATTGACACGATCCAA
scaffold680230_12.	1	p3	(GGA)6	18	317	334	TGGTTAAACTCCACCTTGGC
scaffold680274_10.	1	p3	(GAC)5	15	792	806	TTGTATCGAACGAGCATCCA
scaffold680332_21.	1	p3	(TAT)5	15	172	186	CAGAGAGGCGGTGGTAAAAA
scaffold680398_13.	1	p3	(CAC)5	15	235	249	GACCCGACTCCATTTTGATG
scaffold680628_13.	1	p3	(TGT)7	21	52	72	ATGTAGCCGACCCCAATTTA
scaffold680670_16.	1	p3	(TTC)6	18	476	493	GCATACCTGGGAGTGCATTT
scaffold680764_16.	1	p3	(TGA)5	15	3137	3151	TTTCCCTCTCAAAAACATCACA
scaffold680952_14.	1	p3	(AAG)6	18	1326	1343	AGTCGTCTCCTATCCCATCG
scaffold681155_13.	1	p3	(TTA)5	15	257	271	CCGGTCAAAACCAAATTACG
scaffold681172_16.	1	p3	(TAA)5	15	4535	4549	CATGAATGTGTGGTTTCATCA
scaffold681190_15.	1	p3	(TCT)6	18	504	521	TCGTAGCTCCCTTTGCATTT
scaffold681235_14.	1	p3	(AAT)7	21	436	456	AGGCGTTTCATTGTTCTGCT
scaffold681338_13.	1	p3	(AAT)6	18	558	575	ATTCGGCATCAACCAACTTC
scaffold681410_17.	1	p3	(GGC)6	18	610	627	TGCATGAACGCTTCTCACTC
scaffold681456_17.	1	p3	(GGC)5	15	237	251	AGGGGTAAAGTGCAAATCCC
scaffold681497_16.	1	p3	(TTA)5	15	1896	1910	GCAACCATGATCTCATCGAA
scaffold681582_17.	1	p3	(CAT)6	18	411	428	GTACCCTTGGCCAGAATCAA
scaffold681649_14.	1	p3	(AAT)5	15	1583	1597	TTCAGTTGGATGGTTGGACA
scaffold681659_16.	1	p3	(TGT)5	15	1125	1139	TTGGTTTGACGGGTGAAAGT
scaffold681748_13.	1	p3	(TTG)7	21	42	62	ATGTAGCCGACCCCAATTTA
scaffold681783_14.	1	p3	(CCT)5	15	143	157	GTCGCCTCACCTTCATCTTC
scaffold681896_16.	1	p3	(AAT)5	15	396	410	CCATTACCGATGCCTTACTTG
scaffold682032_13.	1	p3	(GAG)5	15	60	74	GACAGCGGTTGGTTCAGC

scaffold682128_14.5	1	p3	(AAT)6	18	228	245	CTCGTAGGTTTGGGTTTCCA
scaffold682169_17.2	1	p3	(TCA)6	18	621	638	GGTGAGCGATCAAAATCCAT
scaffold682196_17.8	1	p3	(ACA)7	21	875	895	CCGCCTGAAGTTCTTTTCTG
scaffold682371_17.8	1	p3	(GGC)7	21	680	700	AGAGGGGTGTTGAAGGTGTG
scaffold682474_15.8	1	p3	(TCA)5	15	4330	4344	TCCGGCGATTACTACAAACC
scaffold682577_17.5	1	p3	(TCA)6	18	600	617	TGGCTTCAGAAGAAACACCA
scaffold682681_16.9	1	p3	(TCA)5	15	2034	2048	GGATCAAATGTTTTGGGTGG
scaffold682707_14.7	1	p3	(TGT)6	18	46	63	TGTAGCCGACCCCAATTTAT
scaffold682813_14.2	1	p3	(CGG)5	15	866	880	TAGGGAGTGGAGCAGCAACT
scaffold682847_13.9	1	p3	(ACC)5	15	163	177	CTGCAGATGAGGGTCCTAGC
scaffold683020_17.3	1	p3	(CAC)6	18	1054	1071	GGTGTGCTGGAGATACCGAT
scaffold683164_12.1	1	p3	(ATA)5	15	218	232	ACTGCTCGCTATTTGGATGC
scaffold683206_19.2	1	p3	(TGG)6	18	1262	1279	GGAAATGGTGGTAACAACGG
scaffold683244_17.3	1	p3	(TCA)5	15	1020	1034	GTGCAGTTTCTCCTGCATCA
scaffold683403_16.8	1	p3	(TGT)7	21	41	61	TGTAGCCGACCCCAATTTAT
scaffold683406_15.2	1	p3	(GTA)5	15	673	687	GCAGACGATGCATTTTAGCA
scaffold683457_14.7	1	p3	(ATT)5	15	1962	1976	TTCTGTTGCTTGGTCATGGA
scaffold683590_15.4	1	p3	(ATT)5	15	513	527	TTGGCTCAAGTCTTTGCTGA
scaffold683664_15.5	1	p3	(AAT)6	18	575	592	TCTCCGTTGCTCCTACATCAT
scaffold684049_16.5	1	p3	(TGG)5	15	797	811	GGCATAGCCACGATTTCAAC
scaffold684240_14.0	1	p3	(GGC)5	15	159	173	GCGAGTTTCTTGAGGTCGTC
scaffold684335_17.1	1	p3	(TTG)5	15	1635	1649	CTGAAAGGTTGCATCAACGA
scaffold684340_13.5	1	p3	(TGT)6	18	43	60	ATGTAGCCGACCCCAATTTA
scaffold684364_18.1	1	p3	(TAT)5	15	479	493	CATTTTGTTACCCGAGCGAG
scaffold684382_16.3	1	p3	(ATA)6	18	288	305	AGATGGGATGAATCTGGCTG
scaffold684431_10.5	1	p3	(TAA)5	15	516	530	TCAAATACATAATTAGCACGGAGTG
scaffold684487_15.4	1	p3	(CAA)5	15	1510	1524	TCTGGATGCCTTGAAAAACC
scaffold684587_14.3	1	p3	(CTT)5	15	532	546	AGAGGAAGGAGGTGACCGTT
scaffold684640_14.2	1	p3	(TTG)5	15	783	797	TGGAGCATCCAACATGAGAG
scaffold684647_15.8	1	p3	(ATC)5	15	2390	2404	GATGCTTGGGGATGTCTGTT
scaffold684707_17.7	1	p3	(TCA)5	15	1073	1087	TGGGATTGTCATCCTCATCA
scaffold684774_14.4	1	p3	(TGA)7	21	50	70	CCCAAGACCCCAATTTGATT
scaffold684937_10.1	1	p3	(TAA)5	15	294	308	AAATGAAATCGTGCGAAAATG
scaffold684955_13.6	1	p3	(GGA)5	15	479	493	CGGTATCGGAGACGGTAGAA
scaffold684962_15.7	1	p3	(TGT)6	18	41	58	TGTAGCCGACCCCAATTTAT
scaffold685045_18.2	1	p3	(ATT)7	21	300	320	AGCGTAGAATCGCGAGAGAG
scaffold685072_15.5	1	p3	(ATA)5	15	642	656	AATCCCAAATTCATCCCTCC
scaffold685090_13.4	1	p3	(ATC)7	21	1256	1276	TGGCCAAAATTGCCTCTATC
scaffold685221_14.8	1	p3	(ATC)5	15	1183	1197	CAAAGCACCTGACAAGACCA
scaffold685365_16.1	1	p3	(GGC)5	15	638	652	GAGTTCTCCGGTGATCTTGG
scaffold685382_19.7	1	p3	(AGA)7	21	238	258	CCAAAGCTTGAAGAAATGTTTG
scaffold685440_11.6	1	p3	(GAT)8	24	54	77	GCAGACGAATTTAGTCGGGA
scaffold685448_15.4	1	p3	(TAT)5	15	1236	1250	AAGTGATGAAGGCTGCCACT
scaffold685554_16.9	1	p3	(TAA)6	18	604	621	ATCTCAAAAGACGCGAGGAA
scaffold685648_17.6	1	p3	(TGA)5	15	1490	1504	TCATTAGATTGGGAATAATTGGG
scaffold685675_17.9	1	p3	(GCT)5	15	547	561	ATGACGAAGGCTGAGATGCT
scaffold685691_14.9	1	p3	(CCG)5	15	476	490	AATATCCACCACCTCCTCCC
scaffold685756_15.6	1	p3	(GAA)6	18	2572	2589	ACTGGCAGCAACTCATTTCC
scaffold685903_19.2	1	p3	(GTT)5	15	89	103	TCCTTTTGCGTTTTATGTGC
scaffold685934_15.9	1	p3	(CAC)5	15	1036	1050	GGACTCGGGTGAGTCTCAAG
scaffold686097_13.4	1	p3	(TAA)6	18	227	244	ATAGGTCACGGGTCGAGTTG
scaffold686162_16.6	1	p3	(TTA)6	18	722	739	CAACTTTGGGATAAAATCTCCG
scaffold686166_13.9	1	p3	(ATT)5	15	183	197	TTTATCCCAAAATTGAGGCG
scaffold686201_17.4	1	p3	(CGT)5	15	347	361	AAAAACCGTTCCCACCCTT
scaffold686229_12.2	1	p3	(TCT)5	15	540	554	AGGCTTTCCAACACCAAGAA
scaffold686232_14.4	1	p3	(TTC)5	15	1141	1155	TCGGAGAACGGAAAATTGAG
scaffold686296_14.2	1	p3	(ATT)5	15	744	758	GTCCATGTCCTCGTCCTCAT
scaffold686345_16.3	1	p3	(ATC)5	15	1298	1312	CTTGGAAATGCCTGTTGGAT

scaffold686347_15.	1	p3	(GCG)6	18	1799	1816	CCTCCCCATTTTCGATTTTT
scaffold686489_12.	1	p3	(ATC)5	15	112	126	AGCAGGCTGAGAGAATGAGC
scaffold686608_14.	1	p3	(CTC)6	18	1798	1815	TGCACAGAAGATCCTGCAAC
scaffold686657_12.	1	p3	(ATT)6	18	1121	1138	TTTAAATCCAACTCACACATATACAG
scaffold686860_15.	1	p3	(CGC)5	15	2905	2919	ACGGTCTCGAACTCGCTTTA
scaffold686864_17.	1	p3	(AAT)6	18	237	254	CGAATAGTAGCTTCTGCGGG
scaffold686878_15.	1	p3	(GCT)5	15	1598	1612	ATCCATGGGAATTGGACAAA
scaffold686924_22.	1	p3	(AAC)5	15	777	791	GTAATCAGGGCCATTCCCTT
scaffold686941_19.	1	p3	(CCG)5	15	291	305	TCATGCACCATCAAATCCTC
scaffold687037_15.	1	p3	(TTA)5	15	2179	2193	TTGTATCCCCCAGTTTCGTC
scaffold687043_16.	1	p3	(CGC)5	15	571	585	ATTTCAACTACGACGGCCAC
scaffold687104_12.	1	p3	(AAT)7	21	43	63	CACTCGAAGAGTAGCGGCTG
scaffold687132_14.	1	p3	(ATC)5	15	246	260	TGTTTTTACCTGCGTATCTGTCA
scaffold687164_16.	1	p3	(ATT)5	15	1524	1538	AGTTGACGGTTGGAAGATGG
scaffold687182_15.	1	p3	(TTC)5	15	276	290	GTTTACCTGACTGGCGTGGT
scaffold687293_13.	1	p3	(ACA)5	15	576	590	CCCTGGAACAACACCAGTTT
scaffold687325_15.	1	p3	(CAC)6	18	361	378	GTGCTTCGGTCTGGATGACT
scaffold687505_18.	1	p3	(TCC)5	15	395	409	ACAGAAAGGTCGGCATCATC
scaffold687607_14.	1	p3	(TAA)7	21	58	78	ATCTCCACTTGTTGTCTCCAA
scaffold687632_15.	1	p3	(ATT)6	18	295	312	ATTCCTCGGGTTCTTGGAGT
scaffold687709_13.	1	p3	(CGC)5	15	335	349	TGATTTAGTAAAGTTGGAGGTGGA
scaffold687953_14.	1	p3	(AAT)5	15	498	512	GACCCTTTGTGGGATTTGAA
scaffold688085_14.	1	p3	(ATC)5	15	250	264	TTATGGTGCGTCGAGTCTTG
scaffold688211_15.	1	p3	(TTA)6	18	167	184	TCAAATGTTCGTCTTGCAGC
scaffold688282_13.	1	p3	(ACA)6	18	1204	1221	AATTGAATTCAGAGCACCCG
scaffold688443_18.	1	p3	(TGA)5	15	72	86	CCGACTACGACTATCCTCGC
scaffold688514_15.	1	p3	(ATG)5	15	66	80	AATCGTCGAATTCGGTTTCA
scaffold688556_10.	1	p3	(AAC)7	21	689	709	AACATACCATCGTGGCCAAT
scaffold688632_16.	1	p3	(TTG)5	15	49	63	TGTAGCCGACCCCAATTTAT
scaffold688801_15.	1	p3	(TGG)6	18	661	678	GATTTCATTTCAGCGCTTCC
scaffold688909_16.	1	p3	(TTG)9	27	39	65	ATGTAGCCGACCCCAATTTA
scaffold688975_12.	1	p3	(AAT)7	21	246	266	TCAGAATATGCAAGGGGGAG
scaffold689012_16.	1	p3	(TTA)5	15	790	804	ACGGATTCGAGTTTCAACGA
scaffold689169_12.	1	p3	(AAT)6	18	2042	2059	AGAGGGAGCATGTGACCTTG
scaffold689187_15.	1	p3	(CAT)6	18	554	571	TAGTCATCGAGCAAGCCAAA
scaffold689294_13.	1	p3	(CGC)5	15	140	154	TGACCAATCACCAATCAACAA
scaffold689352_12.	1	p3	(GCG)6	18	156	173	AGTGCAAATGTTGACGGGTT
scaffold689414_11.	1	p3	(CAA)5	15	509	523	ACGTCCTTGCCAAAGTTCAC
scaffold689422_14.	1	p3	(TGA)6	18	53	70	CCCAAGACCCCAATTTGATT
scaffold689592_13.	1	p3	(ACA)5	15	52	66	CACGCCAACTTACAAACTATCG
scaffold689790_18.	1	p3	(ATG)6	18	2076	2093	GTCTCAGGTTCGAATCCCAC
scaffold689962_16.	1	p3	(TTC)5	15	1905	1919	CCTTGAGCTCGTCAAAGTCC
scaffold690167_20.	1	p3	(GGA)5	15	378	392	ATTGTTGAGAGCCGAAATGG
scaffold690274_14.	1	p3	(TGT)6	18	46	63	TTGGTTCATGTAGCCGACC
scaffold690336_17.	1	p3	(GAT)5	15	2331	2345	GAACAAGGTGAAGGCTCCTG
scaffold690376_15.	1	p3	(ACA)5	15	889	903	GTTGCGAAATATGCCTCCAT
scaffold690492_16.	1	p3	(CTT)5	15	621	635	TCTGTTTTATTTCCCCGTGC
scaffold690559_17.	1	p3	(AAG)5	15	714	728	GCTGAACAATGCCTCGAAAC
scaffold690654_13.	1	p3	(ATT)5	15	481	495	TGCATTTCATCGCTTTATGC
scaffold690801_10.	1	p3	(TCA)5	15	294	308	GCCGTCTGATTGGAGGATTA
scaffold690813_11.	1	p3	(ATT)6	18	405	422	TGAAAATGAGTTGGGGGTGT
scaffold690951_15.	1	p3	(ATA)5	15	564	578	TGAGCATGATGTGTCTTGAATTA
scaffold690959_10.	1	p3	(TCA)5	15	294	308	GCCGTCTGATTGGAGGATTA
scaffold690980_12.	1	p3	(AAT)6	18	1180	1197	AAATATTTTAGAAAGAACAGATTTTC
scaffold691071_14.	1	p3	(CGG)5	15	112	126	AAGAGGGGGAGGAAAATTGA
scaffold691138_14.	1	p3	(TGT)6	18	69	86	CCGACCTTCCAAATTGTTGT
scaffold691161_13.	1	p3	(ATA)5	15	258	272	ATGGGTAGCCAGTTTCACCA
scaffold691204_17.	1	p3	(AAG)5	15	49	63	CAGTTCCATGTCACAAACGC

scaffold691215_13.	1	p3	(ATC)7	21	208	228	ACCAATCAAACCCAACGAAA
scaffold691235_15.	1	p3	(ATT)5	15	222	236	TCATTTCCGACAACTCGATG
scaffold691417_11.	1	p3	(CCG)5	15	174	188	CATTCCCTGCAATCCTCATC
scaffold691471_15.	1	p3	(AAT)5	15	227	241	CCATTGTAAACCCCTGCACT
scaffold691557_13.	1	p3	(ACA)5	15	427	441	CCAGAACCATGGACACACAG
scaffold691616_15.	1	p3	(TCT)5	15	1023	1037	ACTTATTGGCACGAAGTCGG
scaffold691653_14.	1	p3	(TCA)5	15	456	470	CTGCTAGACCCAGTGGTGGT
scaffold691756_14.	1	p3	(CCT)5	15	768	782	ATGTTTCTTCCGAGTGTGGG
scaffold691829_16.	1	p3	(ACG)5	15	350	364	GATGAGCAGCTCGACAATGA
scaffold691890_15.	1	p3	(TCC)5	15	55	69	GGCCACCAAGAATCTCAGAA
scaffold691961_14.	1	p3	(TTA)5	15	556	570	GGGTTGTTAAGATTTAATGATTATCC
scaffold692060_13.	1	p3	(ACA)6	18	1038	1055	CCTGGCCTTCAATTCATGTT
scaffold692111_17.	1	p3	(ATA)5	15	195	209	TCAAAGAAAGTGAGTAGAATCCAAA
scaffold692174_13.	1	p3	(TTG)7	21	422	442	TTTGGTTCATGTAGCCGACTC
scaffold692177_17.	1	p3	(ATC)5	15	54	68	TGTGTTTCATGTTTGTTGTGATAA
scaffold692229_15.	1	p3	(TAT)7	21	67	87	TGAAGTTTCGAAGACTGGAAGA
scaffold692292_18.	1	p3	(ATG)6	18	457	474	CCTCGATCCTGACCCAATTA
scaffold692325_14.	1	p3	(TTA)8	24	734	757	TGAATATTGGGGTGGGAAAA
scaffold692402_18.	1	p3	(ACA)5	15	166	180	AATCACGGGACCAAAATGAA
scaffold692833_16.	1	p3	(GCC)6	18	2385	2402	ACTTTTGTGACGGTTTTGCC
scaffold692860_13.	1	p3	(ATT)7	21	75	95	TGCACATGTTAGCCAGAACTTT
scaffold693109_11.	1	p3	(GTC)5	15	212	226	TCGATTGTATTTGTGCTGCAA
scaffold693228_17.	1	p3	(GCC)5	15	590	604	TCATTCTCTTCACCGGAAGC
scaffold693259_18.	1	p3	(TGG)7	21	210	230	AAGGTAACGGAAGGGTCTGG
scaffold693500_15.	1	p3	(TGT)7	21	38	58	TGTAGCCGACCCCAATTTAT
scaffold693522_13.	1	p3	(ATT)5	15	530	544	TATTGTCCTCCATTTCCCCA
scaffold693562_15.	1	p3	(ATC)5	15	409	423	ATTTCCTGTTCTCTTCCCCG
scaffold693671_13.	1	p3	(TGA)6	18	44	61	CCCAAGACCCCAATTTGATT
scaffold693981_15.	1	p3	(GAA)5	15	559	573	TCATGGATTCATGGTGCAGT
scaffold693999_12.	1	p3	(TTC)5	15	1517	1531	CCCGTTCAGACCACCTTTTA
scaffold694081_14.	1	p3	(CAC)5	15	148	162	TCAACCTGAGTCTCCATCCC
scaffold694082_12.	1	p3	(TGA)8	24	44	67	CCCAAGACCCCAATTTGATT
scaffold694368_11.	1	p3	(TAT)7	21	718	738	TGGGATGAGGAAAAACATGA
scaffold694444_14.	1	p3	(CCG)5	15	617	631	TCGACGCATCAGAAGACAAC
scaffold694475_18.	1	p3	(TGT)6	18	957	974	GAGCTTTTGGAGAGTGCTGC
scaffold694520_12.	1	p3	(TTG)5	15	1311	1325	GAAGGGGATCACCAAACTGA
scaffold694583_17.	1	p3	(TGA)5	15	1345	1359	TTCTATGAAGCCCTCAGCGT
scaffold694651_17.	1	p3	(TCC)5	15	800	814	TGCAGAAGGTCTCCTCCAGT
scaffold694740_10.	1	p3	(CTT)5	15	408	422	ATGGTTGCCTTTGTTTGGAG
scaffold694869_13.	1	p3	(AAT)5	15	932	946	CAACATTGCAAAATGGGACA
scaffold695150_17.	1	p3	(TGT)7	21	33	53	CCAATTTATTGGGATTAAGGC
scaffold695217_12.	1	p3	(TTA)6	18	997	1014	TGTTTACACGTGTGGGATATGG
scaffold695307_13.	1	p3	(TCC)5	15	266	280	TATCTGCAGCGCATCATCTT
scaffold695378_15.	1	p3	(GAG)6	18	262	279	GAGTCAAAGCCATCCACGAT
scaffold695394_16.	1	p3	(TTG)6	18	298	315	ATGGATGCACCGGTTAGAAG
scaffold695593_14.	1	p3	(TCC)6	18	3738	3755	GGCAATTGACCACCGTAAAC
scaffold695753_17.	1	p3	(AAT)5	15	335	349	TCGGGATTCAGTGATTAAAGC
scaffold696024_13.	1	p3	(ATG)5	15	1011	1025	CGTTTAGTGGTGCGAGGAAT
scaffold696088_17.	1	p3	(TCA)6	18	259	276	ACCAGTAGTTTCCGGTGGTG
scaffold696156_16.	1	p3	(AAT)5	15	454	468	TGAGGCGTAAGCAAATTTCA
scaffold696236_13.	1	p3	(TTA)5	15	159	173	TGTTGCACTATTTGCTTGGG
scaffold696391_12.	1	p3	(TAT)6	18	475	492	GACTATGGCCCAAAACCGTA
scaffold696396_16.	1	p3	(AAT)7	21	378	398	GAGGACATCGGTCTGAGAGG
scaffold696426_17.	1	p3	(TTG)5	15	151	165	TGATCCATATAGCCGACCCT
scaffold696529_13.	1	p3	(TTG)5	15	569	583	GGTTCATGTAGCCGACCCTA
scaffold696548_15.	1	p3	(CAC)5	15	500	514	CCCCAACCAAAATACCCTTT
scaffold696565_13.	1	p3	(ACA)8	24	1435	1458	CAAATCAAAATAATTGCAAAGTGA
scaffold696653_15.	1	p3	(TAT)6	18	226	243	TGCGAGCTAGCGTCATAAAA

scaffold696666_13.	1	p3	(ATT)6	18	555	572	TGCTTGATTAGCATTTTATGGG
scaffold696702_16.	1	p3	(TTG)5	15	532	546	TGAGGAAGCCGTTGAAGATT
scaffold696774_14.	1	p3	(TGA)5	15	1010	1024	CCGAAAAATTGGGAAATCCT
scaffold696783_11.	1	p3	(TCC)5	15	490	504	CTTTGCCTTTTCTGCCTCTG
scaffold696877_16.	1	p3	(TTG)6	18	2190	2207	ATACGATCCATTTTGCCGAC
scaffold696944_15.	1	p3	(GAG)5	15	517	531	GGAGGACGAGGAGCATCATA
scaffold696952_15.	1	p3	(TGC)5	15	1946	1960	CTTGCTGTGTCGATCCCTTT
scaffold697048_18.	1	p3	(AAC)5	15	271	285	GGCCGTGTACTACCGTGTTT
scaffold697212_16.	1	p3	(CAA)5	15	11072	11086	ATGGTCTCGCACAACACAGT
scaffold697382_11.	1	p3	(CGG)5	15	387	401	AGCAAATAAATCGGCAGAGG
scaffold697556_12.	1	p3	(GGA)5	15	538	552	GTCGAAGAACCTCGACAACC
scaffold697655_12.	1	p3	(TGA)6	18	96	113	TGCTATTTTCATCTACCCACCA
scaffold697775_11.	1	p3	(TAT)6	18	263	280	AAACGCCTAGCTCTCCACAA
scaffold697867_14.	1	p3	(AAT)5	15	676	690	GAGAATTGGGTAACCAGCCA
scaffold697883_17.	1	p3	(TCA)5	15	5875	5889	GGGGGAGAGGTTAGATTGGA
scaffold697891_15.	1	p3	(TAT)6	18	272	289	AGTGATTGATGGGCTAGGCA
scaffold698024_16.	1	p3	(ATA)7	21	719	739	TATTTTATCTCCTCCGCCCG
scaffold698055_15.	1	p3	(AAT)5	15	1197	1211	TGAAGGAAAGGGATGGGTAG
scaffold698313_17.	1	p3	(GCG)5	15	522	536	TGCAAGTTTGAGCGAGATTG
scaffold698454_17.	1	p3	(ATT)6	18	247	264	ATCTCGTGGGGGAAGACTTT
scaffold698486_12.	1	p3	(AAT)5	15	970	984	GCATTTCCACGTTCAGAGGT
scaffold698492_16.	1	p3	(TTC)5	15	62	76	TTCAACACTATTCAACACGACTGA
scaffold698641_14.	1	p3	(CAT)6	18	2477	2494	GCTGCATTGGGGAAAGTCTA
scaffold698716_16.	1	p3	(CCG)5	15	2435	2449	TCTCACTCAGCTCGAAAGCA
scaffold698771_18.	1	p3	(CAT)5	15	779	793	CGGCAGTTAAGGCTCAAAAG
scaffold698813_14.	1	p3	(AAT)5	15	628	642	TGAAGGCCTTAAATCACCAAA
scaffold698854_13.	1	p3	(GTT)5	15	1067	1081	ATCCATATACCGACCCCACA
scaffold698894_14.	1	p3	(TTC)5	15	854	868	TGTGCAATCCCCTAAGGTTC
scaffold698993_18.	1	p3	(CAT)6	18	230	247	AGCTTTTTCCTCTCCTTCCG
scaffold699014_16.	1	p3	(CAA)5	15	2271	2285	CCTTCCATTTGAGGATTGACA
scaffold699040_16.	1	p3	(TTA)5	15	73	87	CTGGGTAAACCCACGGACT
scaffold699182_14.	1	p3	(TTG)5	15	324	338	GACAGAGGCCTTGCAAGATT
scaffold699332_18.	1	p3	(TGA)5	15	2101	2115	ATTATCTCGCAGCATTGCCT
scaffold699400_14.	1	p3	(TTA)6	18	56	73	TCAGGTGTGATCAATGACAATTT
scaffold699585_14.	1	p3	(TTG)7	21	4487	4507	TTTCTGCAACATCTGAACGC
scaffold699642_16.	1	p3	(TAT)5	15	563	577	TGTACACAGTGAGGTCATACTTAGG
scaffold699764_12.	1	p3	(GAA)5	15	315	329	TGGTGACATCCACTACCTGC
scaffold700045_19.	1	p3	(CCG)5	15	533	547	GATAATTCCCAGCCCCACTT
scaffold700160_14.	1	p3	(TAA)5	15	832	846	GGCAATGCTATTGGGACAAG
scaffold700222_16.	1	p3	(AAT)5	15	1147	1161	TTAAGATGAGATTTGTCCTTCAAA
scaffold700235_14.	1	p3	(CCA)5	15	776	790	CAAATTCCTCAACCACCACC
scaffold700439_16.	1	p3	(GCA)6	18	522	539	ACAAGCATCATCCTCCCAAC
scaffold700478_14.	1	p3	(CTT)5	15	1816	1830	GTCTCCAGAAGACGATTCGC
scaffold700495_15.	1	p3	(TGG)6	18	109	126	GCCATATCACGGTGGAAAAG
scaffold700655_17.	1	p3	(TGT)5	15	45	59	ATGTAGCCGACCCCAATTTA
scaffold700700_15.	1	p3	(CTC)5	15	1350	1364	AGCTATAGGTGGGGATGGGT
scaffold700764_20.	1	p3	(TAA)5	15	99	113	TTTACCCGATCTTGCTTTGC
scaffold700869_18.	1	p3	(GGC)6	18	390	407	CACCGGAACCAAAACCTAGA
scaffold701073_13.	1	p3	(TTA)5	15	67	81	TGGTTCTCCAAATTCTTCCTC
scaffold701194_19.	1	p3	(ATC)5	15	166	180	AGGAATGGACGCAAGATCAC
scaffold701268_10.	1	p3	(ATG)5	15	439	453	GTACATCTCCCAAGACCCCA
scaffold701317_13.	1	p3	(TGT)5	15	49	63	GGTTCATGTAGCCGACCCTA
scaffold701334_16.	1	p3	(AGA)6	18	2139	2156	GAAAATGCTCAGGGGAGTCA
scaffold701366_17.	1	p3	(TTG)5	15	744	758	CAATTGCTAGGGCGGACTAC
scaffold701562_15.	1	p3	(CAA)5	15	999	1013	CCGTTTTGTTACCATTTTGC
scaffold701619_16.	1	p3	(CTT)5	15	2076	2090	AGGATACATGACACCCGTCC
scaffold701774_18.	1	p3	(TTC)5	15	378	392	ATCAAACCAACCCCAACAAA
scaffold701831_16.	1	p3	(TGA)5	15	3026	3040	TCCCAAGTCTGAGCTTTTCTG

scaffold702004_18.4	1	p3	(TAT)5	15	29	43	CATCAAACCCAAACCAACCT
scaffold702086_17.4	1	p3	(TCA)5	15	183	197	GCGAAAATTTAACTAGGCCG
scaffold702123_17.8	1	p3	(TGT)6	18	67	84	TTGGTTCATGTAGCCGACCT
scaffold702169_15.0	1	p3	(ACA)5	15	161	175	AATTGAGAGGTGGGACGATG
scaffold702205_15.9	1	p3	(GCA)5	15	1686	1700	CTTCAACTTGGCGCACTGTA
scaffold702294_15.6	1	p3	(CCA)6	18	1269	1286	CAATTTCTTTTTCCCCCTCC
scaffold702386_16.4	1	p3	(ATT)5	15	274	288	TTGGTGCGAGAATGATTTGA
scaffold702446_16.7	1	p3	(TCT)5	15	52	66	TCGTCACTTTCCTCTTCCTCA
scaffold702478_15.1	1	p3	(TTA)5	15	340	354	CACGATAAAACAATTTTGGAATGA
scaffold702510_17.2	1	p3	(TTG)5	15	1106	1120	CAAGATAGGGGGACAGCGTA
scaffold702525_10.9	1	p3	(TTC)6	18	1148	1165	ACAAGCCTCCAATTCACACC
scaffold702639_20.5	1	p3	(TTC)5	15	972	986	AGATATGGAAGATGCGGTGG
scaffold702734_12.8	1	p3	(TGT)7	21	45	65	ATGTAGCCGACCCCAATTTA
scaffold702758_14.1	1	p3	(GCG)6	18	250	267	TGAACCCAAATCTCTCCTCG
scaffold702789_13.3	1	p3	(ATT)7	21	185	205	CAATCCGCCAATCCTCTTTA
scaffold702801_10.6	1	p3	(TAT)5	15	773	787	TGCCTGAGGTCTTACCCTTG
scaffold702810_14.4	1	p3	(AAT)5	15	780	794	CGTAATTTTCAACCCCAACC
scaffold702818_15.1	1	p3	(GCA)5	15	2352	2366	ACAATCGATGAAGAAAGCGG
scaffold702917_16.7	1	p3	(CCG)5	15	1543	1557	AGAAAACCTTCCCCATTGCT
scaffold703016_16.4	1	p3	(AGC)5	15	2043	2057	ACCATGCGATGAACACGTTA
scaffold703049_17.6	1	p3	(ACC)5	15	985	999	CTCTTCGCCTTCAACCTCAC
scaffold703059_16.2	1	p3	(TTC)7	21	141	161	AAAAATTGGTGTGGATGTCTCT
scaffold703078_14.0	1	p3	(TGT)5	15	51	65	TGTAGCCGACCCCAATTTAT
scaffold703150_17.1	1	p3	(AAG)5	15	83	97	GTCATGCACCTCTTGAAGCA
scaffold703248_16.1	1	p3	(CTT)5	15	2318	2332	GGCGTTCAATCCTATGGAGA
scaffold703250_17.6	1	p3	(TAT)5	15	928	942	CCAATCAAATTGGGGTCAATA
scaffold703287_18.0	1	p3	(GCC)5	15	2277	2291	ATGAATATCCTTCGTCGCCA
scaffold703354_13.2	1	p3	(TTA)5	15	518	532	ACTTGGGTTGTGCCAAAGTC
scaffold703385_15.9	1	p3	(CCG)5	15	118	132	CCAGGTCGCTCAAATCTCTC
scaffold703429_14.1	1	p3	(AGC)6	18	2868	2885	ACTTCCTCCAGCAAGAGCAG
scaffold703438_16.8	1	p3	(ACA)6	18	2613	2630	CGAAAATAAGCCAACCGAAA
scaffold703693_17.1	1	p3	(GGA)5	15	1522	1536	CTGTTGCAGGGAAGGCTAAG
scaffold703871_14.2	1	p3	(AAT)5	15	56	70	GTCTCAATGGGGACATCTGG
scaffold703900_18.0	1	p3	(AAT)6	18	474	491	CCCATCCTTGTGATATGCAAC
scaffold703916_16.1	1	p3	(GCT)5	15	265	279	TGTCACCACTCCCAAACTCA
scaffold704036_11.2	1	p3	(GAT)5	15	1150	1164	TGCCCTTCCCGATTATAGTG
scaffold704150_13.0	1	p3	(TTA)5	15	588	602	AAGGGAATTAAGCCTGCCTC
scaffold704249_13.9	1	p3	(AAT)6	18	152	169	GCGATGGATTTTTCCTTTCA
scaffold704297_14.6	1	p3	(ATA)5	15	111	125	AGGAGCTAGCACACCATCCC
scaffold704328_18.8	1	p3	(TGA)6	18	3360	3377	AGGTGAAGCCCAGTCTGCTA
scaffold704366_13.7	1	p3	(AAT)7	21	568	588	CCACCATTCTTTTGACAGCA
scaffold704375_13.7	1	p3	(GGC)7	21	45	65	GTGAAGATTAGCTCCGCCTG
scaffold704448_15.0	1	p3	(ATA)5	15	296	310	ATTCCACTTCATTGCACACG
scaffold704592_15.9	1	p3	(AAG)5	15	176	190	CTCTTCGAGCGAGTTCAAGC
scaffold704597_12.9	1	p3	(AAT)7	21	169	189	TGGATGAGTATTGCCTGACG
scaffold704865_13.0	1	p3	(TAA)7	21	742	762	ATGCTTTGTGTTTTCCTGCC
scaffold704896_14.2	1	p3	(TTG)5	15	66	80	TGATTTATGTAGCCGACCCC
scaffold704983_14.6	1	p3	(CCA)7	21	879	899	GCAACTGAAAAACGGTTGGT
scaffold705000_16.1	1	p3	(TCC)5	15	1339	1353	CTGCACTGTATCGGGAACCT
scaffold705082_13.6	1	p3	(TCA)7	21	221	241	ACAGTAAAGCCCGGTTGATG
scaffold705129_17.0	1	p3	(AAT)5	15	499	513	TGAGCACCAAATTTATTATCGAA
scaffold705181_16.4	1	p3	(GGC)5	15	1090	1104	GAGCAGAAAGGAGGGGAAAC
scaffold705233_15.4	1	p3	(AAT)6	18	1010	1027	GCTCGGTATGCCATTTGATT
scaffold705522_16.3	1	p3	(GAT)5	15	147	161	GACATGGTTGTGGTTTGTGC
scaffold705537_18.2	1	p3	(ATC)5	15	754	768	AATTGCTTGTGTAGGGGTGG
scaffold705642_14.4	1	p3	(AAT)5	15	724	738	GGCTTGATCTTTGAGATGGG
scaffold705765_10.0	1	p3	(TCA)5	15	959	973	GGGCGGATTAGAAGAAGAGG
scaffold705778_10.5	1	p3	(AGT)5	15	86	100	GGAACCAACACAAACACACG

scaffold705836_14.	1	p3	(CCA)6	18	299	316	TCTTGGCGCCTCACTTTAAT
scaffold705910_10.	1	p3	(TAT)9	27	354	380	TCCTACCCAACCAACTAGCG
scaffold705936_14.	1	p3	(ATC)5	15	303	317	CCACAGCTTCCCAAACAAAT
scaffold706010_11.	1	p3	(CAT)5	15	404	418	TGCAGAACCCATGTACATCAA
scaffold706049_15.	1	p3	(TTG)7	21	861	881	TCCATTTCGCACAAAAGACA
scaffold706197_10.	1	p3	(TAT)6	18	300	317	CATACAGTCGGCATCCAATG
scaffold706293_16.	1	p3	(CAA)5	15	255	269	GACGCCATTTACGTCTTCGT
scaffold706297_17.	1	p3	(TAT)5	15	801	815	CAATTTCGGGTGGTAAGAGC
scaffold706370_13.	1	p3	(GAG)5	15	837	851	TTTGTTCATTCTCCCGAGTTG
scaffold706479_12.	1	p3	(TTC)5	15	837	851	TTGTCCCGTCAAGAAAAAGG
scaffold706480_15.	1	p3	(TTA)5	15	242	256	TGGATTTCGTCACCATCTCTC
scaffold706508_18.	1	p3	(ATC)6	18	572	589	AAACGCACTACACGAATCCC
scaffold706516_16.	1	p3	(GCG)6	18	175	192	CGTGATTTCTTTTTGGGCTC
scaffold706552_16.	1	p3	(CAG)5	15	1833	1847	GGTCTTTCTGCATCTCCAGC
scaffold706588_18.	1	p3	(CGG)7	21	2057	2077	TAGAATCGGATTTATCGCCG
scaffold706611_11.	1	p3	(GCT)5	15	626	640	ACTTCCAGCATACCTCCCCT
scaffold706617_13.	1	p3	(TGA)7	21	43	63	CCCAAGACCCCAATTTGATT
scaffold706646_17.	1	p3	(TGA)6	18	43	60	CCCAAGACCCCAATTTGATT
scaffold706649_14.	1	p3	(CGC)5	15	1729	1743	CCCCCACCCTACAAGTATGA
scaffold706718_13.	1	p3	(TTC)5	15	283	297	AAAACCGAGAGCAGAGTCCA
scaffold706748_17.	1	p3	(GGC)5	15	60	74	CTTGTTGCTCAGCACAGTGG
scaffold706817_15.	1	p3	(AAT)7	21	1258	1278	GGGACCCACATAACCATGTC
scaffold706915_14.	1	p3	(CAA)5	15	1397	1411	CAAGCCAACTTTGAGGAAACA
scaffold707025_17.	1	p3	(TTC)5	15	497	511	CCTTGCTAGGGCAGTACGAC
scaffold707062_16.	1	p3	(ATG)7	21	1094	1114	CTGGCATTGGAGGAGGACTA
scaffold707085_16.	1	p3	(TTG)5	15	498	512	GTCACCAAATACAAAGCCGC
scaffold707088_14.	1	p3	(GGC)5	15	307	321	ATCTTCAGCAAACCATTCCG
scaffold707089_12.	1	p3	(GCG)5	15	483	497	TAAGAATTGAATCGCAGGGC
scaffold707094_13.	1	p3	(TGG)5	15	88	102	CTAGGTGTATGGCGGAGGAG
scaffold707103_12.	1	p3	(GAG)5	15	1324	1338	CTTCTTCCCCTCCCAAACTT
scaffold707149_15.	1	p3	(TCC)5	15	498	512	ACCTCTAGCCCGGTGAACTT
scaffold707279_15.	1	p3	(TGA)6	18	46	63	CCCAAGACCCCAATTTGATT
scaffold707348_15.	1	p3	(TTA)7	21	499	519	TGATTTCCAAACATACGTTGTCA
scaffold707358_16.	1	p3	(TGA)5	15	49	63	CCCAAGACCCCAATTTGATT
scaffold707558_14.	1	p3	(ACA)5	15	462	476	AGCTCTCGACATCAAATCGG
scaffold707664_16.	1	p3	(ATG)5	15	254	268	TCCGGAGAAAGCTGATGTTC
scaffold707697_17.	1	p3	(GAG)6	18	1246	1263	CCGGTTATGAGGTCGGAGTA
scaffold707808_14.	1	p3	(ATC)5	15	82	96	AAGCCGGATAAGCGATTTCT
scaffold707965_14.	1	p3	(TAC)5	15	112	126	ACCCAACTTCCAAGGTTCAA
scaffold707969_11.	1	p3	(TGG)5	15	530	544	GGGTACTCGTAGTCAACGCC
scaffold707991_11.	1	p3	(ATT)5	15	361	375	GGGATGCATCAAAGTTGTCA
scaffold708142_12.	1	p3	(TTA)7	21	693	713	TCCTTAGTCAAGGGGAAATGAA
scaffold708309_15.	1	p3	(TCA)5	15	269	283	ATGTGGCCATTCTGGAAAAC
scaffold708336_14.	1	p3	(AAT)5	15	586	600	ACTTTGAACCCATCTCACCG
scaffold708437_15.	1	p3	(CCA)5	15	499	513	CTGGTTCGCAACACAGAAAA
scaffold708519_14.	1	p3	(ACA)5	15	620	634	GGATCCTAAAATTTGAAGGGG
scaffold708563_12.	1	p3	(AAT)6	18	664	681	CCCTAGCAAAAGAGAGAGGGA
scaffold708577_13.	1	p3	(TCA)6	18	146	163	CCACCCTTACTCCCCAATTT
scaffold708702_16.	1	p3	(AAC)8	24	3720	3743	GCTATTGAGCAATATCAGAAACCA
scaffold708760_12.	1	p3	(ATT)5	15	1563	1577	GCAACGAACCCCAAGTCTAA
scaffold708868_13.	1	p3	(TTC)6	18	947	964	AAGATTGCTCTCGCCTCAAC
scaffold708936_12.	1	p3	(TGT)6	18	42	59	TGTAGCCGACCCCAATTTAT
scaffold709004_15.	1	p3	(TTA)5	15	88	102	TGATTCTAAAATGAATCCAATCCA
scaffold709020_10.	1	p3	(GCC)5	15	215	229	GCCGACATGACCTTAGCAGT
scaffold709026_18.	1	p3	(CAG)5	15	316	330	TGCACATTTCAACAGCAACA
scaffold709092_15.	1	p3	(AGC)5	15	593	607	ACAAAATGGGCATGAACACA
scaffold709109_16.	1	p3	(ATT)8	24	698	721	TCGTTAATTGGTTCCATTTTGA
scaffold709187_15.	1	p3	(AAT)5	15	700	714	CCATGTCTTGAGAGTGGGGT

scaffold709254_12.	1	p3	(GCG)6	18	201	218	CGGTGGAGACTTAGGTGGG
scaffold709313_14.	1	p3	(AAT)5	15	262	276	TGCAGCTTGCTGCTGTTACT
scaffold709427_18.	1	p3	(CAA)5	15	913	927	TCATGCTTCTTGTTGGGAAA
scaffold709440_10.	1	p3	(AGA)5	15	369	383	GAAATCCGAAACGCCATTAT
scaffold709455_16.	1	p3	(TAA)6	18	315	332	TTTGTCAAAGAACACGTTCACAT
scaffold709458_15.	1	p3	(GTG)5	15	3069	3083	GTGGGATTTTACGGAGTGGA
scaffold709505_15.	1	p3	(AAC)6	18	555	572	CCTTATACGTTCACCCCAAGTT
scaffold709523_16.	1	p3	(AAT)5	15	563	577	CAACCGAAATTTTTGGAAGG
scaffold709585_17.	1	p3	(TCA)6	18	796	813	TGATCATATTCGGAGCCACA
scaffold709637_16.	1	p3	(TGA)5	15	655	669	GCCCAGGGATTCAAAGTACA
scaffold709750_15.	1	p3	(CGA)5	15	5053	5067	ACTCTGCCGCCAAAAGTCTA
scaffold709784_17.	1	p3	(TAT)6	18	195	212	TTGAGCCACTTATCATCTTTCAA
scaffold709819_17.	1	p3	(TGC)5	15	1231	1245	CGGAGGTAGTTGGCATTTGT
scaffold709851_15.	1	p3	(GGC)5	15	544	558	TATCGCCCGAGAAATGAATC
scaffold709927_15.	1	p3	(CAC)5	15	236	250	GACGTCTTGCAAGTGACGAA
scaffold709987_16.	1	p3	(GCG)6	18	442	459	TCGTCACCCTACAAGCATCC
scaffold710160_15.	1	p3	(TAA)6	18	105	122	TTGGGGTCGGCTACATTAAC
scaffold710179_14.	1	p3	(TGA)5	15	48	62	CCCAAGACCCCAATTTGATT
scaffold710207_16.	1	p3	(TCA)6	18	3889	3906	AATCTCAAACCCGACAATGC
scaffold710264_17.	1	p3	(CAA)5	15	769	783	TTCCCCTGCATGTTTAGAGG
scaffold710276_15.	1	p3	(ATA)5	15	3141	3155	ATAGTGCAGCAAGATTGGGG
scaffold710399_16.	1	p3	(GCT)6	18	677	694	TTCATACCTGTCCCGACCAT
scaffold710425_14.	1	p3	(GCC)5	15	394	408	TCCACATGCAGAATCGGATA
scaffold710454_14.	1	p3	(TCA)7	21	276	296	CCAAAGGAAGCAAACAAGGA
scaffold710461_14.	1	p3	(CGC)8	24	1618	1641	TCCACTACTCCAATGTCTGCC
scaffold710490_15.	1	p3	(AAT)5	15	1401	1415	ATTGTCTACCAATCGGGGTG
scaffold710546_16.	1	p3	(TAT)5	15	458	472	GTCAAGTTTGAGACGTTGCG
scaffold710625_11.	1	p3	(TAT)5	15	681	695	TAGCAACGCAATAACATCGG
scaffold710663_15.	1	p3	(TTG)5	15	44	58	GGTTGACTCACACGTGGAAA
scaffold710792_14.	1	p3	(ATT)5	15	406	420	TTCCAGTAAATCAACGAAACGA
scaffold710801_15.	1	p3	(TCA)5	15	3100	3114	CGTTGAAATCTGTTCCTCCC
scaffold710804_14.	1	p3	(TTG)5	15	76	90	ATGTAGCCGACCCCAATTTA
scaffold710909_14.	1	p3	(TCA)5	15	4995	5009	TATCAACCACCCATCAGCAA
scaffold710936_15.	1	p3	(TGT)6	18	45	62	TGTAGCCGACCCCAATTTAT
scaffold710962_14.	1	p3	(AAT)5	15	612	626	TGACAACCGCACGTAAATTG
scaffold710998_16.	1	p3	(TCA)7	21	2084	2104	AGTGCAAATCCCAGTGCTTC
scaffold711086_12.	1	p3	(TTA)5	15	738	752	GGGTTTGCGTTTGATTTGTT
scaffold711156_12.	1	p3	(AAC)5	15	461	475	CTTTGGAATTGGAAGGACGA
scaffold711215_10.	1	p3	(TAT)7	21	576	596	GGGAGAAGAGGGTATAGCGG
scaffold711225_13.	1	p3	(AAT)5	15	979	993	AAATCCAAAATGGCCTACCA
scaffold711260_17.	1	p3	(AAT)5	15	139	153	TGTATCTTCTCACGAGCATTGG
scaffold711304_14.	1	p3	(AAT)6	18	720	737	AGAACTGACGGGCAAATGAT
scaffold711472_12.	1	p3	(TAT)6	18	311	328	GTGCATTGACCGTGTTTGAC
scaffold711492_14.	1	p3	(AAT)5	15	744	758	ATTGTTTTAATGCATCGGCG
scaffold711502_17.	1	p3	(TGT)5	15	44	58	ATGTAGCCGACCCCAATTTA
scaffold711628_11.	1	p3	(ACA)5	15	1092	1106	TTCAACTTGCTCGGAACCTT
scaffold711687_17.	1	p3	(AAC)5	15	329	343	CGTTCCCAGACTTTCCAAAA
scaffold711743_15.	1	p3	(CAC)6	18	4840	4857	TTACACCCGCACCATCTGTA
scaffold711807_17.	1	p3	(CGG)5	15	85	99	AATCATGAAAACCGAAACCA
scaffold711853_12.	1	p3	(AAC)5	15	500	514	ACTACCACGCCAATTATGCC
scaffold711910_19.	1	p3	(ATC)5	15	164	178	AAAAGAAAGAACCGAACCCG
scaffold712078_20.	1	p3	(GGT)5	15	707	721	TCCGAGAAGATTTCGTCGAT
scaffold712140_15.	1	p3	(CCG)5	15	614	628	ATAACACTCGAACAAGCGGC
scaffold712171_14.	1	p3	(TTA)6	18	327	344	TCGTTCATGCTCCTCAGTTG
scaffold712207_14.	1	p3	(ATT)6	18	622	639	CACTCTGTGTACCACCAATCTCA
scaffold712261_13.	1	p3	(TTA)5	15	56	70	CCAGCAGTTGGCTCTATTTTT
scaffold712262_14.	1	p3	(ATA)5	15	145	159	CCGGAATTGAACACCCTTAAT
scaffold712318_17.	1	p3	(CCG)6	18	155	172	CATTCGGGAAAAAGGATCAA

scaffold712345_15.2	1	p3	(ATA)6	18	1200	1217	ACGCGTTAGAAACGTACGAA
scaffold712403_11.5	1	p3	(GAC)5	15	614	628	ATCCGAATGGATCAAAGCTG
scaffold712420_17.0	1	p3	(ATT)5	15	582	596	AACATGACACAATTCGTTCTGC
scaffold712430_12.6	1	p3	(AAT)5	15	1001	1015	CAATAAATTGGGGTCGGCTA
scaffold712535_15.7	1	p3	(TGA)5	15	47	61	CCCAAGACCCCAATTTGATT
scaffold712565_14.4	1	p3	(ATT)5	15	223	237	GTCCGGCAGAATACAAGGTG
scaffold712567_14.4	1	p3	(TCA)8	24	3543	3566	TCTTTTTCAGACGCAGCAGA
scaffold712598_11.4	1	p3	(ATC)8	24	325	348	GGGTGAGGATTACTTGGGCT
scaffold712613_13.6	1	p3	(ATA)8	24	3493	3516	GCAAGAGGCATGTTTTATTTGA
scaffold712707_17.1	1	p3	(ATG)5	15	1899	1913	GTTTTGAATTTTGCGACCGT
scaffold712790_14.8	1	p3	(CAA)7	21	3627	3647	ACTTTCTGCGGCAGTTCTGT
scaffold712820_16.3	1	p3	(TGT)6	18	41	58	ATGTAGCCGACCCCAATTTA
scaffold712835_15.0	1	p3	(AAT)5	15	883	897	GTCGAAAACTCAATGGGGAA
scaffold712855_13.9	1	p3	(TTG)8	24	1684	1707	TGGTGCTCCAAAAATTGTCA
scaffold712944_19.2	1	p3	(CAG)6	18	562	579	CCGGAGCCATAATTAGCAAC
scaffold712970_12.3	1	p3	(TTA)5	15	669	683	TGAGATCAAGAATTATGGCAAGA
scaffold713137_15.9	1	p3	(TTC)5	15	8313	8327	TCGAAAGCTTCACAACATGC
scaffold713205_15.8	1	p3	(ATC)5	15	860	874	GCAAGTCTCGTAGCTTTGGC
scaffold713483_14.4	1	p3	(TCA)6	18	292	309	AAAGCATATGGAAGAGCGGA
scaffold713552_17.9	1	p3	(CTT)5	15	571	585	CTGAGGCAGCAACTTCAGTG
scaffold713598_15.4	1	p3	(CGC)6	18	6331	6348	GTGTGGAAAAGGGAGTGCAT
scaffold713660_14.0	1	p3	(AAC)9	27	628	654	GAGTTGAAAGGCATGCAAGA
scaffold713746_15.8	1	p3	(TGT)7	21	41	61	ATGTAGCCGACCCCAATTTA
scaffold713777_15.6	1	p3	(ACA)6	18	2533	2550	TCCAAGCAAGCACATTTTTG
scaffold713807_15.8	1	p3	(CCT)5	15	875	889	CACCAACGAAGCCACCTATT
scaffold713897_16.4	1	p3	(CCG)7	21	399	419	GGTTCACGGTTTTGGGAATA
scaffold713947_14.9	1	p3	(ACA)6	18	1050	1067	TTTAGTGGGAGTCAAACGGG
scaffold713988_16.4	1	p3	(CCA)5	15	386	400	GGCTTAAAGACAACGGTGGA
scaffold714152_13.2	1	p3	(TCA)5	15	476	490	CAGTCTCAGGTGCGTCAAAA
scaffold714165_14.7	1	p3	(TCT)5	15	686	700	GAAACATATGCACCTGCCCT
scaffold714183_16.0	1	p3	(AGA)5	15	803	817	CGAATGACCAGCCAAGAATC
scaffold714211_15.4	1	p3	(TCA)6	18	1449	1466	TGTAGAACTCGGGTCAAGGG
scaffold714270_17.0	1	p3	(CAT)5	15	1735	1749	GGTGAGGTCTGGTCAGGTGT
scaffold714287_15.3	1	p3	(CAG)5	15	576	590	ACAGATGAGATGAGGCTGGC
scaffold714370_17.3	1	p3	(GAA)5	15	3749	3763	TTGTACCAGATCCCCCAGTC
scaffold714403_15.9	1	p3	(ATT)6	18	2882	2899	CACGTGTACGTGCGTTCATA
scaffold714448_15.3	1	p3	(GAG)5	15	344	358	TTAAACCTCCACCAGTTGGC
scaffold714449_13.0	1	p3	(CAA)5	15	180	194	GGAGCTTTCAACACAACTCCA
scaffold714464_13.2	1	p3	(TGT)6	18	44	61	TGTAGCCGACCCCAATTTAT
scaffold714475_14.1	1	p3	(AAC)5	15	637	651	AACGAATGTCACATCAACCG
scaffold714529_15.6	1	p3	(TGC)5	15	4445	4459	TGCACCTTGGCTTTCTTTCT
scaffold714592_13.3	1	p3	(ACC)7	21	720	740	CTTCCGAGCAAGGAGCTAGA
scaffold714629_18.4	1	p3	(CCG)6	18	592	609	GATCCTCTGGGCCAAATGTA
scaffold714730_16.3	1	p3	(ATT)5	15	345	359	GATCCGAAATGAAAACCCAA
scaffold714732_10.8	1	p3	(GTC)5	15	505	519	ATCCACCAAAATCATCCACC
scaffold714949_18.5	1	p3	(GAT)5	15	1030	1044	GGTCCTGGGTTTGGGACTAT
scaffold715074_16.5	1	p3	(TTA)5	15	1349	1363	GTTCGATGTGCAGATGAGGA
scaffold715220_15.3	1	p3	(CCA)5	15	1074	1088	TTTCTGAGTTGGGATACCCG
scaffold715229_12.9	1	p3	(TAA)5	15	179	193	CGCCGCCTAAATAGTCAAAA
scaffold715252_10.8	1	p3	(TGA)8	24	565	588	ATGCAGCAATTGGACATTGA
scaffold715260_10.7	1	p3	(GAT)5	15	433	447	CTCAACTTTCTTTCGAGCTGC
scaffold715391_14.6	1	p3	(TTG)6	18	1331	1348	ATGATTCATGTAGCCGACCC
scaffold715410_16.7	1	p3	(ATT)6	18	205	222	TCGAGTCCGCACATTAGTCA
scaffold715435_16.7	1	p3	(CGC)7	21	343	363	GAAACCACTCAGGCCAGTTC
scaffold715467_14.9	1	p3	(TGA)6	18	1118	1135	TTGTAAAACACCCCAATTTGA
scaffold715492_16.2	1	p3	(TTG)5	15	1060	1074	CTCCTTCTTTATCCGGGCTT
scaffold715518_13.1	1	p3	(ATA)5	15	130	144	CACCTTAGGTACCGCTCGTC
scaffold715519_16.1	1	p3	(TCA)5	15	1312	1326	TCCGAAATTTGTTCCACCAT

scaffold715564_15.	1	p3	(AAT)5	15	2247	2261	TCCAGGAGCCAAGAAAGATG
scaffold715732_13.	1	p3	(CTC)5	15	345	359	ATGAAATGAAGCTTCCACCG
scaffold715995_12.	1	p3	(AAT)7	21	187	207	TGGGGAGAGAGAGTGGAGTG
scaffold716061_15.	1	p3	(GAA)5	15	1448	1462	TGTCCTCATGGATTCTTGAAA
scaffold716147_17.	1	p3	(TCA)5	15	1961	1975	ATACCAGGGTCGAATCCACA
scaffold716170_15.	1	p3	(TCA)5	15	828	842	CTGTCACGTGTTGCAGTCCT
scaffold716216_14.	1	p3	(ATG)6	18	139	156	CTCTTGGAGAGGCCAACAAG
scaffold716233_15.	1	p3	(CGC)5	15	715	729	AAACCTTAGGCTTCCTTGGC
scaffold716235_16.	1	p3	(AAG)5	15	545	559	TCATGGAGAGAGGAGAGGGA
scaffold716300_19.	1	p3	(TAT)5	15	202	216	GGCTTAATACGTGTGTTGCG
scaffold716311_13.	1	p3	(TTG)5	15	482	496	GGTTCATTTAACCGACCCAA
scaffold716318_14.	1	p3	(TCA)5	15	355	369	GTGGGCAATCTTGTTGTGTG
scaffold716321_15.	1	p3	(TTA)5	15	422	436	GGTAGCACTGCATCTGTCCA
scaffold716407_13.	1	p3	(AAT)7	21	567	587	AACGGTGAAAAACATAATGCAG
scaffold716604_16.	1	p3	(TGA)6	18	45	62	CCCAAGACCCCAATTTGATT
scaffold716692_15.	1	p3	(TCC)6	18	97	114	CGTTTCTTCATCATCATCCG
scaffold716725_15.	1	p3	(TGA)5	15	3427	3441	ACACCAAAATGCATGAGACG
scaffold716750_11.	1	p3	(GAG)6	18	762	779	CACTGCTCTCACCACGATGT
scaffold716769_16.	1	p3	(CGC)7	21	80	100	CTTCTTTTCAAGCACTGGGC
scaffold716806_14.	1	p3	(TTA)5	15	70	84	TAGATTTGAACGACACCCCC
scaffold716825_16.	1	p3	(ATG)5	15	352	366	TTGGCTGGTTGATCTTAGCA
scaffold716826_16.	1	p3	(TTC)5	15	875	889	TGAGGCTGGGTTAGAATTGG
scaffold716987_16.	1	p3	(CGG)5	15	181	195	CTGGAAGGAGAGACGGCTTA
scaffold717225_16.	1	p3	(CTT)5	15	3849	3863	AAACGCCCTCCTTCTCTAGC
scaffold717331_20.	1	p3	(AAT)6	18	84	101	TTCGGTCCGATTAATCAAGAAT
scaffold717375_15.	1	p3	(CTC)5	15	2128	2142	CAGGAGTTCAAGTCGCACCT
scaffold717383_17.	1	p3	(AGA)6	18	1009	1026	CTCGCATCTTCTACGCCAAT
scaffold717481_17.	1	p3	(GAG)6	18	3713	3730	TTTTCCGAGCTTGTGTTGTG
scaffold717493_23.	1	p3	(AAC)5	15	257	271	TGCAAAATGGATTCAGGTCA
scaffold717538_15.	1	p3	(TGT)6	18	42	59	ATGTAGCCGACCCCAATTTA
scaffold717557_15.	1	p3	(AAG)7	21	696	716	CAAATGCGATTCAAGTGACC
scaffold717576_10.	1	p3	(ACA)6	18	467	484	TTTCGGACCATTGATATCTTTTT
scaffold717646_17.	1	p3	(ATG)5	15	211	225	GCCAAGGGAGTTGTTACGAA
scaffold717720_14.	1	p3	(TGA)7	21	2527	2547	TGAACGTATGGCCTTGGATT
scaffold717743_16.	1	p3	(AGG)6	18	2272	2289	AGAGGAGGAGGCTAAGCGAC
scaffold717769_15.	1	p3	(TGA)7	21	868	888	CCACTGAAATATTGAAGGCCA
scaffold717782_14.	1	p3	(GAG)6	18	185	202	TGTGGATGAAGATGAAGATTTTG
scaffold717812_13.	1	p3	(GAG)7	21	102	122	TGATGGTGTGACTGAAAGCC
scaffold717882_16.	1	p3	(AAT)5	15	1455	1469	GTTGGCCCTCCAAACCTAAT
scaffold717894_16.	1	p3	(ATC)6	18	453	470	CACAACAAAAACAATAAAAGGCA
scaffold717970_16.	1	p3	(AAG)5	15	309	323	ACTCAACACGGCCTGGATAC
scaffold717991_13.	1	p3	(CTC)5	15	848	862	TCTCCTTCCAACACCCAAAC
scaffold718036_14.	1	p3	(CCG)5	15	1267	1281	CGTCGTCCTTTTCTTCAACC
scaffold718041_15.	1	p3	(CCA)5	15	180	194	GATCACTGCAACAAGGGGAT
scaffold718061_14.	1	p3	(TAA)5	15	1344	1358	CCCATCTGACGGACAAAAGT
scaffold718078_14.	1	p3	(AAT)5	15	487	501	CATCGACAAAATCATAGTCCGA
scaffold718125_12.	1	p3	(GGC)5	15	560	574	TCAGTTACAGTGGGCAGCAG
scaffold718133_14.	1	p3	(ATC)7	21	115	135	ACCACCATCGACTGATAGCC
scaffold718203_14.	1	p3	(CTC)5	15	1826	1840	GCTCCTCCTCTTACGCCTCT
scaffold718233_14.	1	p3	(TCC)5	15	5104	5118	TCAACACACCAAAACACCAAA
scaffold718331_15.	1	p3	(TAT)5	15	272	286	CTTTATTAAAATTTCTTTCACCAAATG
scaffold718347_15.	1	p3	(TTG)5	15	48	62	TGTAGCCGACCCCAATTTAT
scaffold718539_13.	1	p3	(AAC)5	15	78	92	TATTGGGCCGTACCTCTCCT
scaffold718616_18.	1	p3	(ATT)5	15	468	482	ACCATGCCAGACTTTGGTTC
scaffold718668_14.	1	p3	(TAA)6	18	566	583	TGCAAATACCTAAAGGTTGGG
scaffold718672_13.	1	p3	(CCG)5	15	97	111	CCCTACCCTCCTCAGGGTTAC
scaffold718676_16.	1	p3	(ATT)5	15	326	340	TTTTGCATATCTCCATTCGGT
scaffold718686_13.	1	p3	(CGG)8	24	833	856	TGCTTTTCAGGGAGTTGGTC

scaffold718739_15.3	1	p3	(ACA)5	15	348	362	ACCCGCAAAAACACAAAAAG
scaffold718826_16.1	1	p3	(AAG)5	15	943	957	TTTCAATCACTTTTTCTCGACG
scaffold718869_16.2	1	p3	(ATA)7	21	2739	2759	GCTCGAATATGCAACGACAA
scaffold718926_14.9	1	p3	(ACA)5	15	482	496	GAAGGGAAGCATTCCAAACA
scaffold718950_15.0	1	p3	(TTG)5	15	48	62	TGTAGCCGACCCCAATTTAT
scaffold719004_15.4	1	p3	(GAA)5	15	1125	1139	TTATGGGGGACCCTATCTCC
scaffold719096_14.1	1	p3	(GAT)5	15	1494	1508	AACCGTTGATATTTGGCCTG
scaffold719124_15.0	1	p3	(GGT)5	15	466	480	AGTATGGGCATATGGCAAGG
scaffold719153_14.8	1	p3	(AAT)5	15	588	602	ATTGGGACATTTGGGTGTGT
scaffold719159_10.3	1	p3	(ATA)5	15	215	229	TCAAATAGCCGATTGCATCA
scaffold719225_15.2	1	p3	(AAT)5	15	675	689	GTGAAGTTGTCAATTCCCCG
scaffold719275_11.6	1	p3	(CCA)5	15	614	628	CGCTTCGTACGCTTTTAACC
scaffold719285_14.7	1	p3	(CTT)5	15	1233	1247	CGATGGATAAGGCCACTTGT
scaffold719494_17.3	1	p3	(TGG)6	18	1048	1065	GAGAGGTTGAAGGCGAACAC
scaffold719496_14.7	1	p3	(CCA)5	15	146	160	CACCAGCATTTCCATCTCCT
scaffold719547_15.5	1	p3	(AAT)5	15	922	936	CATGCGATCTAGAGTGTGGTG
scaffold719556_17.3	1	p3	(CGT)6	18	2085	2102	CGGAAGACCAGAGGTGAGAG
scaffold719562_13.4	1	p3	(ATA)6	18	241	258	CGAGAATTTCCTCGGATTCA
scaffold719770_16.0	1	p3	(TGA)6	18	189	206	TTAGCGTACATCTGACCCCC
scaffold719776_18.0	1	p3	(AGC)6	18	515	532	GACAGCATTGCTTTGCCTTT
scaffold719812_15.4	1	p3	(GAA)5	15	1803	1817	TCAACTCATGCAAATGCAGC
scaffold719843_15.9	1	p3	(CAT)6	18	1272	1289	GGTTAAGCATCGGATGAGGA
scaffold719917_16.0	1	p3	(TTG)6	18	128	145	ACCTCACATGGTGGGAAAAA
scaffold719937_16.6	1	p3	(TGA)8	24	2560	2583	AGGTTGCGTACATCTGACCC
scaffold720034_15.7	1	p3	(ATA)5	15	2107	2121	CACGGCAGAGCAATTCAATA
scaffold720364_13.3	1	p3	(TAT)6	18	540	557	AATAATTAGGCGTGCAACGG
scaffold720382_17.6	1	p3	(AAT)6	18	1046	1063	GAATCATCTCACACCACCCA
scaffold720424_16.8	1	p3	(CGG)8	24	226	249	GAAGTGGAGGTGACGGATGT
scaffold720451_18.3	1	p3	(AAT)7	21	627	647	TTGAATCCTCAGCGTGCATA
scaffold720464_19.0	1	p3	(CCG)5	15	2396	2410	GCCTCACAGCTGAAATCCTC
scaffold720547_14.6	1	p3	(CAA)5	15	87	101	CACAACTTGATCAAAATTGCAGA
scaffold720557_13.6	1	p3	(TGT)6	18	46	63	ATGTAGCCGACCCCAATTTA
scaffold720717_12.1	1	p3	(TCT)5	15	1579	1593	CTCGGTTTCTTGAGTCAGGG
scaffold720718_15.0	1	p3	(GAC)7	21	1509	1529	TCAAAACCTGAAGCTGTCCC
scaffold720780_15.2	1	p3	(CCT)5	15	1688	1702	ATCCAAAGGGCTTGCTTCTT
scaffold720801_15.4	1	p3	(AAT)6	18	909	926	TAGATGCCTGTTGGGGTCTT
scaffold720837_16.8	1	p3	(CCT)7	21	984	1004	ATCCTGAGTTGCACACCCTT
scaffold720863_19.3	1	p3	(AAT)7	21	1286	1306	CGCGTCGCCTAAATAAAAAT
scaffold720866_15.6	1	p3	(GTT)6	18	62	79	TGTAGCCGACCCCAATTTAT
scaffold720923_19.3	1	p3	(TCA)8	24	1132	1155	CCTCTGGAATGGGAGTTTCA
scaffold720936_16.7	1	p3	(GCA)6	18	852	869	TTAAACCGACCTCGCTGTTT
scaffold720949_15.4	1	p3	(ACT)6	18	390	407	ACATACGCGTGCTTCACAAG
scaffold721101_18.0	1	p3	(TGT)6	18	40	57	TGTAGCCGACCCCAATTTAT
scaffold721102_15.3	1	p3	(ATC)5	15	384	398	TGGAATCCTGTCCTCTGGTT
scaffold721128_14.7	1	p3	(TTA)8	24	496	519	GTTCCGGCCCTTCAATAATC
scaffold721162_17.1	1	p3	(CTT)5	15	2197	2211	TGATGTTGGTATTTTGGCTACC
scaffold721195_15.8	1	p3	(ATA)5	15	74	88	TGCAGCTCTTAACTCTATCGGA
scaffold721206_14.9	1	p3	(TTA)5	15	62	76	GCAATATCAATGTAAGATCATATTCA
scaffold721214_15.3	1	p3	(AAT)5	15	496	510	TGTTCCCGTGGTATGTTTTT
scaffold721273_14.1	1	p3	(TGA)5	15	166	180	TAAGGAGGCGAGAGAATGGA
scaffold721319_15.3	1	p3	(TAT)5	15	2014	2028	CTAAGCGAGATACCAAGCCG
scaffold721329_13.3	1	p3	(TAA)5	15	384	398	GGTTGGTTGTACAAAGAAACGAG
scaffold721398_17.1	1	p3	(TTG)5	15	2008	2022	GAATTTGCTTTGTCATTGGGA
scaffold721554_15.2	1	p3	(TAT)5	15	501	515	TCCATGCATTTCCAACACAC
scaffold721567_18.0	1	p3	(TCT)5	15	397	411	GAGAACCCTAAACCGAAGGG
scaffold721579_15.3	1	p3	(ATA)5	15	359	373	ACTCCAATGCTTCCCTTCTT
scaffold721591_17.2	1	p3	(TGA)6	18	5732	5749	GCACCCCTACAGCATTGTTT
scaffold721605_16.6	1	p3	(CGG)6	18	591	608	CCACTCCCTCCACTTTCTCA

scaffold721630_15.	1	p3	(ATG)7	21	1318	1338	GCATTGCTTGACTGAGTTGC
scaffold721722_13.	1	p3	(TTA)5	15	727	741	TTTGTTACGGGAATAACCCAA
scaffold721812_17.	1	p3	(TGA)6	18	43	60	CCCAAGACCCCAATTTGATT
scaffold721862_14.	1	p3	(ATT)5	15	511	525	TGTCTCGACGGACTGACACT
scaffold721868_14.	1	p3	(TTG)5	15	776	790	GGAGACCTAAGGATGCACCA
scaffold721905_18.	1	p3	(CGG)5	15	325	339	GTTCTGAGGTTGGTTGGTCG
scaffold721917_17.	1	p3	(AAT)5	15	519	533	TGGGTAGCTTACAAGTCCAGC
scaffold721922_10.	1	p3	(ATT)7	21	1066	1086	TCATCATCTGGCTTTGTGGA
scaffold721955_14.	1	p3	(CAT)5	15	6061	6075	CCGCTACAATCTTTGGTGCT
scaffold722006_16.	1	p3	(GAA)5	15	1844	1858	TCAGAAGAGAGTTTGCCATTGA
scaffold722013_18.	1	p3	(TGC)5	15	96	110	ATTCAAAGCATATGCCCTCC
scaffold722029_15.	1	p3	(TAA)5	15	143	157	CGTGTTTGAGTTTCTTGTTTGG
scaffold722068_16.	1	p3	(CGG)5	15	1972	1986	CCGTTTCTCCAGTTGACGTT
scaffold722076_10.	1	p3	(ACA)6	18	759	776	AACCTAATCCATCCCAACTTTT
scaffold722091_17.	1	p3	(TAA)5	15	701	715	TAGAAGGAGATGGGTCCTGC
scaffold722101_14.	1	p3	(AAT)5	15	200	214	CAAACAGCGATTTTGAGTCG
scaffold722123_12.	1	p3	(TGA)6	18	978	995	AGCTCATCGCAGGTTGGATA
scaffold722127_14.	1	p3	(GGT)5	15	2934	2948	GTTAGATTGGACCCCATCCC
scaffold722201_18.	1	p3	(CGC)6	18	655	672	TCAGCTCTAACCGGAGGAAA
scaffold722234_16.	1	p3	(AAT)7	21	125	145	TCACATCACTAGTCCGTGGG
scaffold722308_15.	1	p3	(AAG)5	15	618	632	ATAAACGCAACTCAAACCCG
scaffold722351_16.	1	p3	(CTA)7	21	399	419	CTACTTCTGCACTGCCTCCC
scaffold722352_13.	1	p3	(AAC)5	15	600	614	GCATTTCCGTGCAACAACTA
scaffold722465_14.	1	p3	(TGT)6	18	42	59	TGTAGCCGACCCCAATTTAT
scaffold722522_17.	1	p3	(ATC)5	15	274	288	CAAACCCACCAACAAACAAA
scaffold722539_15.	1	p3	(AAT)5	15	158	172	GCGTGTTTTCCAGAATCCAT
scaffold722747_14.	1	p3	(GAC)6	18	570	587	CTGATTCCATTTCCCCTTCA
scaffold722770_11.	1	p3	(CTT)7	21	886	906	ACATGAGAGCCTTGCATCCT
scaffold722809_15.	1	p3	(ATA)6	18	1032	1049	ACAAACGATTTCCCGTCTTG
scaffold722865_16.	1	p3	(ACA)6	18	3430	3447	CACGACGGAAACATGTAGTGA
scaffold722866_16.	1	p3	(CGC)5	15	1689	1703	AAGAGAAACTTGACGAGCGG
scaffold722871_15.	1	p3	(TGC)5	15	585	599	CTTGATTGATCTTGGTGCGA
scaffold722878_13.	1	p3	(ATT)8	24	63	86	GGGAGTGGGTTATCGGTTTT
scaffold722908_10.	1	p3	(GGC)5	15	297	311	ATTTGTAGGGTGGTGGTGGA
scaffold722934_15.	1	p3	(AAT)5	15	1062	1076	AGGGAAGTGGAAATAAGCCC
scaffold722953_13.	1	p3	(CGA)5	15	2574	2588	TGCGAACAATCTCTCCTCCT
scaffold722989_17.	1	p3	(TTG)7	21	71	91	TTGGTTCATGTAGCCAACCTC
scaffold723043_15.	1	p3	(ATT)5	15	955	969	AGCAAACAGCTCCCATCATC
scaffold723081_15.	1	p3	(ATA)5	15	985	999	GGGAAATGGCTTGCATAAAA
scaffold723112_17.	1	p3	(TCT)6	18	410	427	GGGTACAGGTGGATGGTAAGAA
scaffold723121_15.	1	p3	(TAA)5	15	363	377	TCTCCTGTGTGGTGTGTGGT
scaffold723125_17.	1	p3	(AAT)5	15	612	626	GCCCACACAAATTATCGAGG
scaffold723170_16.	1	p3	(GGC)6	18	44	61	GAATTGGAGGCGGAGGAG
scaffold723197_16.	1	p3	(GTT)5	15	153	167	CCATTTTCGCCTCAATCTGT
scaffold723238_19.	1	p3	(GCG)5	15	2014	2028	AGGTCCCCGGATTTGTTATC
scaffold723244_16.	1	p3	(ATA)5	15	321	335	GCCGAGGGTGATGTATCAAT
scaffold723287_13.	1	p3	(CCA)5	15	387	401	ACGCCTCATCGTCAAAACTC
scaffold723382_16.	1	p3	(TAT)5	15	5234	5248	GCCAGGTTTTCTGGGTACAG
scaffold723441_15.	1	p3	(AAG)7	21	635	655	TCGCGAGTAAAACAAAAACA
scaffold723709_16.	1	p3	(GGC)5	15	865	879	CCCAAACTGATTTCGCAACT
scaffold723713_13.	1	p3	(ATT)7	21	1186	1206	TGGAATCTTCCCTTCCCTCT
scaffold723742_12.	1	p3	(TGA)7	21	1548	1568	AAGAAGAGGGTTCGCTGTCA
scaffold723899_15.	1	p3	(ATC)5	15	981	995	TCGGCAAAACCCTTTTATCA
scaffold723925_16.	1	p3	(AAT)6	18	1568	1585	CGAAGGGACCACAAAAGGTA
scaffold723994_16.	1	p3	(GGA)5	15	647	661	ATTTTCTTGTGGGTGGAAGC
scaffold724039_17.	1	p3	(AAG)5	15	855	869	TGCCAAGCTTATATTATTGGTGC
scaffold724101_11.	1	p3	(TAT)6	18	216	233	GCTAACGACGTAAGGCAAATG
scaffold724217_14.	1	p3	(CTT)5	15	2990	3004	AACACCGAGTGCAACTTCCT

scaffold724260_12.	1	p3	(TGA)7	21	937	957	TTCTTCCACAGTTGGCTCCT
scaffold724274_16.	1	p3	(TGA)5	15	1583	1597	TTCGCTCTGTGTTTTCCTCA
scaffold724278_16.	1	p3	(CTC)5	15	1518	1532	CAATGAACTCCAAGGGGAGA
scaffold724281_13.	1	p3	(CGG)5	15	179	193	AGGATTTGAACCGGTGACAG
scaffold724467_16.	1	p3	(TGT)6	18	50	67	TGTAGCCGACCCCAATTTAT
scaffold724478_13.	1	p3	(TTA)6	18	1330	1347	CCCAGACTGAGTTATTATTTGATCC
scaffold724483_14.	1	p3	(AAG)5	15	361	375	ACTCTTTCAGCCCCTTGGAT
scaffold724487_14.	1	p3	(GGC)5	15	237	251	ATAGTAGCGGCTGCAGGTTC
scaffold724494_15.	1	p3	(ATA)7	21	684	704	TGATGTTCTTTGGGTGCTGA
scaffold724520_15.	1	p3	(CCG)5	15	574	588	AACAATAATATCGTCCGCCG
scaffold724534_16.	1	p3	(TGA)5	15	1252	1266	AGCCACTGCTTTTGTTGCTT
scaffold724536_17.	1	p3	(ACA)5	15	960	974	TGAATGTCCAACTCTTCCACC
scaffold724570_16.	1	p3	(TCT)5	15	1407	1421	TTGCTTCAGCACCTTGAAGA
scaffold724663_24.	1	p3	(ACA)7	21	924	944	GGTATTTTCATCCCGCTCAA
scaffold724670_15.	1	p3	(CAG)5	15	61	75	ATGGCCCTAAACACAGCAAG
scaffold724747_14.	1	p3	(TTA)7	21	1156	1176	GCCACAAATTCTGAAACCGA
scaffold724764_18.	1	p3	(CTC)5	15	433	447	AGTCTCTGCTGCTCAGCCTC
scaffold724777_15.	1	p3	(CCG)6	18	604	621	AATATGGCATGAGACGAGGC
scaffold724786_14.	1	p3	(ATT)5	15	326	340	GGATCGTGTGTGGGATCAAT
scaffold724850_16.	1	p3	(CAA)5	15	139	153	CTCAACCAGCATCGCTATCA
scaffold724896_14.	1	p3	(CTG)5	15	1021	1035	TCTGAATCCCTTTTCATCCG
scaffold724953_11.	1	p3	(AAT)6	18	773	790	CAGCCTTCCAGTTGGGATAA
scaffold724987_17.	1	p3	(GGC)7	21	466	486	GATCCACCTCTCCATCTCCA
scaffold725053_14.	1	p3	(TGA)5	15	48	62	CCCAAGACCCCAATTTGATT
scaffold725062_14.	1	p3	(GAA)5	15	909	923	CCAGGTGTTGTTTTTCAGCA
scaffold725080_13.	1	p3	(TTA)5	15	1827	1841	ATGTATATTTCGTTCTTTCTTGTTTTT
scaffold725108_19.	1	p3	(CTG)6	18	127	144	GATCTGTTGAAGGTAGCGGG
scaffold725127_17.	1	p3	(CGC)5	15	640	654	GATGCAGGGATACTGATTCCA
scaffold725135_17.	1	p3	(TTG)7	21	1313	1333	TGGCAAACAAAGGATGTCAG
scaffold725138_14.	1	p3	(AAT)5	15	800	814	TCACATGCTTTGCTGAAAGG
scaffold725219_14.	1	p3	(TGT)5	15	805	819	TGCTCACCCACATTCACATT
scaffold725227_15.	1	p3	(CCA)5	15	2413	2427	CCCCATATCTACCCCCTCAT
scaffold725252_15.	1	p3	(ACA)5	15	1181	1195	ATGTGGTCACCTGGGGAATA
scaffold725280_16.	1	p3	(AGT)5	15	1128	1142	CCTCGGATGAGTCGCATATT
scaffold725300_14.	1	p3	(CCG)5	15	810	824	TCTTGCCGCCTTGTTAATTT
scaffold725307_17.	1	p3	(AAT)5	15	221	235	TCCAAGTTACTGGCCAAACC
scaffold725363_15.	1	p3	(ATA)5	15	324	338	CTCCACGTTTTAACAACCGA
scaffold725377_16.	1	p3	(ATC)6	18	208	225	TGAACAAGGTTTCGATCTATGC
scaffold725384_17.	1	p3	(GGT)6	18	865	882	GAGGATTGGGGGTTTTCATT
scaffold725394_15.	1	p3	(AAT)5	15	879	893	GGCATTATCAGAATTTGGCG
scaffold725446_15.	1	p3	(ATG)5	15	702	716	GCTGCATTGCTTGAAATGTCT
scaffold725543_15.	1	p3	(TGA)5	15	45	59	CCCAAGACCCCAATTTGATT
scaffold725593_15.	1	p3	(AAT)5	15	2588	2602	TTCCTTGGAACTCTCAATCCA
scaffold725603_19.	1	p3	(TTC)6	18	440	457	CGTTGGTGGAATATCGTTGA
scaffold725607_14.	1	p3	(CTT)5	15	1076	1090	CACCTCATCTTGCTTCGTCA
scaffold725924_17.	1	p3	(ATC)7	21	404	424	GCAACGAAAAATACAAGCCAA
scaffold725951_18.	1	p3	(GGC)5	15	2039	2053	CACAACACCACTCATCCTCG
scaffold725954_16.	1	p3	(CAG)5	15	3479	3493	GATGCTTTGTGCAGTTGAGC
scaffold725965_16.	1	p3	(TGA)6	18	39	56	CCCAAGACCCCAATTTGATT
scaffold726097_16.	1	p3	(TCT)5	15	177	191	ATCTCGGGGTGCATTGTAAC
scaffold726100_17.	1	p3	(CCT)6	18	4726	4743	CGCCTCTTGAATAACCTCCA
scaffold726146_10.	1	p3	(AGG)7	21	328	348	AGTGGTGAAGTCCCACCTTG
scaffold726172_14.	1	p3	(GGA)5	15	1727	1741	ACTCTGGAAAACCGATGACG
scaffold726195_15.	1	p3	(TGT)7	21	45	65	TAGCCGACCCCAACTTATTG
scaffold726234_16.	1	p3	(TAA)6	18	1877	1894	TTTTAAAACGCCTGAAAAAGTAA
scaffold726362_16.	1	p3	(ATT)5	15	599	613	GCACTCGAAGAGTAGCGGTT
scaffold726404_14.	1	p3	(ATT)5	15	1032	1046	GGCAAATTTGAATCGGTGAT
scaffold726438_15.	1	p3	(TAT)5	15	770	784	ACCGTCATGGCCCTACATTA

scaffold726541_13.	1	p3	(TGT)7	21	113	133	GATTCATGTAGCTGACCCCAA
scaffold726553_15.	1	p3	(ATT)5	15	885	899	CGAAGGATCAACTTCATAGTCG
scaffold726670_14.	1	p3	(CTA)5	15	456	470	CCCCACAACGTTATTCATCC
scaffold726704_14.	1	p3	(TTA)6	18	393	410	TGGCAGCAACTACGACCATA
scaffold726717_18.	1	p3	(TTA)5	15	289	303	TTGCTGCTGGTATCAAAACG
scaffold726718_15.	1	p3	(CAT)5	15	1413	1427	GGTCATCAATTCAGGAAGCC
scaffold726723_17.	1	p3	(TCA)5	15	528	542	CGAACCGATAAAGCCAAAAC
scaffold726769_14.	1	p3	(CAT)5	15	1071	1085	GAACCATGATCTGCCTGGAT
scaffold726858_17.	1	p3	(TAT)5	15	267	281	GTTGAAGCCAAGCGTGCTAT
scaffold726926_13.	1	p3	(ATA)5	15	464	478	TGACAAATAAAAACCTACAAAATGG
scaffold726957_16.	1	p3	(GAG)5	15	770	784	AAGAGGAGGACGAGCATGAA
scaffold727127_14.	1	p3	(AAT)7	21	444	464	CATAGGGCAAGTACGGGAAA
scaffold727132_14.	1	p3	(TTA)5	15	662	676	CACCGGTTTTGGATTTGACT
scaffold727149_15.	1	p3	(ACA)8	24	896	919	CAAATTTAAGTGAGCTTTGCTTGA
scaffold727177_14.	1	p3	(TTA)7	21	1035	1055	ATGGCATCCATCTCTTCGTC
scaffold727182_16.	1	p3	(AAC)5	15	2194	2208	CTGCACACTTTGGTCCATTG
scaffold727192_13.	1	p3	(TGA)5	15	127	141	CCGGAACTCAATAACCAAAGA
scaffold727270_15.	1	p3	(TTA)5	15	2526	2540	ATGAGAGGGAGAGGGAGAGC
scaffold727297_13.	1	p3	(CAA)6	18	464	481	CATTCATTTCCAGGCCACTT
scaffold727315_14.	1	p3	(AAT)7	21	672	692	TGGAATCAAGAACCCCAAAG
scaffold727348_15.	1	p3	(TTG)5	15	129	143	CACATAGTGGGAAACGGCTT
scaffold727374_17.	1	p3	(GCG)6	18	812	829	AACAGCAAGGAGAGGCAAAA
scaffold727429_15.	1	p3	(CGC)5	15	4889	4903	GGTTTTGGATGAAGCGGTAA
scaffold727464_14.	1	p3	(ATT)5	15	298	312	AGTTCAGCGAGAACAAGGGA
scaffold727532_15.	1	p3	(CAT)5	15	573	587	CATCAACATTCCTGGGCTCT
scaffold727585_16.	1	p3	(CCG)5	15	1507	1521	TAAACTCCGGCATGGAGAAC
scaffold727637_16.	1	p3	(TGT)8	24	67	90	TTTGGTTCATGTAGTCGACCC
scaffold727698_16.	1	p3	(ATA)5	15	1959	1973	AACGAGCCAAGTGAAAGCAT
scaffold727816_15.	1	p3	(GCT)8	24	596	619	ACATCCTCAACCATGGCAGT
scaffold727891_15.	1	p3	(ACA)5	15	1509	1523	ATGTCCTGTTGATTCCGAGG
scaffold727900_15.	1	p3	(TCA)6	18	2059	2076	CGTACGTTGTACGGGTTCAT
scaffold727962_18.	1	p3	(CGG)5	15	2596	2610	AGAGTGGTAAAACTCCGCCA
scaffold728058_17.	1	p3	(GGC)5	15	329	343	TCATCGGGTCTAGGTGTTCC
scaffold728166_17.	1	p3	(AGG)5	15	1370	1384	GATTCCGACTCCAATCCTGA
scaffold728202_15.	1	p3	(ACA)5	15	127	141	TATTTCCGACAATTCGGTCC
scaffold728260_14.	1	p3	(TTG)5	15	34	48	CATTTCAGTTTACTGGGATTAAGG
scaffold728267_17.	1	p3	(AAG)5	15	2417	2431	AGTTGGAACCTCGAGCATTG
scaffold728315_14.	1	p3	(ATA)7	21	845	865	ATGTGGCGACATGAATTTCC
scaffold728354_15.	1	p3	(AAC)5	15	1053	1067	CCTGGCCTTAAGTAGCCACA
scaffold728364_17.	1	p3	(ACC)5	15	254	268	CAAACGACGAGCATCAAGAA
scaffold728386_10.	1	p3	(TAA)5	15	383	397	TCATACACGTGGACACCTCA
scaffold728538_18.	1	p3	(GCT)5	15	2579	2593	GAAGCAGAGGAGTTCCAACG
scaffold728563_15.	1	p3	(CTC)6	18	1587	1604	TTTAATTACCAACCTGCCGC
scaffold728618_13.	1	p3	(CTT)5	15	700	714	AGGCGATCAACTTCCACAAC
scaffold728710_16.	1	p3	(TAT)5	15	739	753	GATGAGGAATGTGATTGCGA
scaffold728755_17.	1	p3	(GGA)5	15	743	757	AATCATGGCATTGGCCTTAG
scaffold728756_16.	1	p3	(GAG)6	18	2306	2323	TGTCTGAATTTGGTGGAGGA
scaffold728840_15.	1	p3	(TTG)5	15	1092	1106	TGCCTCTCCTTCTTGTTGCT
scaffold728924_14.	1	p3	(TAT)6	18	2623	2640	CATCAAACCCAAACCAACCT
scaffold729016_16.	1	p3	(GCT)5	15	134	148	ATCTCGTTCGTCTCGCAGTT
scaffold729033_10.	1	p3	(ATT)5	15	158	172	TGCAAATTGAATCAACCAAAA
scaffold729107_15.	1	p3	(CAT)7	21	2248	2268	TCTGCCAGTAACTTTCGCCT
scaffold729119_14.	1	p3	(TTC)5	15	723	737	TTTCCTTTTCTTTTGCTACCCA
scaffold729153_13.	1	p3	(ATC)5	15	214	228	TATGGTTTGGTCCGATGGAT
scaffold729155_20.	1	p3	(TCA)6	18	1159	1176	TGGGTGATTGAGTTTCCTCC
scaffold729160_15.	1	p3	(TTA)5	15	2427	2441	TGGCCTAATCGTTCCTCAAC
scaffold729202_15.	1	p3	(TGG)7	21	1915	1935	TCTAAAGCCTCCCACGAAGA
scaffold729346_18.	1	p3	(AGA)5	15	1023	1037	TGAAACCCTAGCGAACCAAC

scaffold729349_15.	1	p3	(TGA)5	15	1180	1194	TTCGTTGTTCCACACTTCCA
scaffold729374_13.	1	p3	(CCT)5	15	176	190	CATCAACCTCCTTCTCCGAC
scaffold729407_15.	1	p3	(GCC)5	15	1530	1544	TCTTGGTGGTTCTGGTAGGG
scaffold729450_15.	1	p3	(ATA)6	18	7598	7615	TCAGCAACTACGTGCATCCT
scaffold729477_18.	1	p3	(TTA)6	18	277	294	CGGGCTCTTAAATTCATTCG
scaffold729534_15.	1	p3	(GCG)5	15	493	507	TAGGACTAGGGAAAACGGCA
scaffold729599_16.	1	p3	(ATT)6	18	52	69	CAACAACTCGTCACCCCTTT
scaffold729611_16.	1	p3	(AAG)5	15	143	157	TGGAGCAACTTCTTCGATCA
scaffold729643_14.	1	p3	(TTG)5	15	128	142	GCCAACCTCACATAGTGAGAAA
scaffold729668_16.	1	p3	(ATC)5	15	6189	6203	CAATCAAATTGGGGTCTTGG
scaffold729670_16.	1	p3	(TGT)5	15	38	52	TGTAGCCGACCCCAATTTAT
scaffold729673_14.	1	p3	(TGT)5	15	82	96	ATGTAGCCGACCCCAATTTA
scaffold729776_15.	1	p3	(ATC)6	18	1071	1088	TGCAAGAGATTGGGTTGAAA
scaffold729843_17.	1	p3	(ATA)8	24	46	69	GAAGCAGAAATCGGGATTGA
scaffold729874_19.	1	p3	(CAC)6	18	181	198	AACCCAAATCGCAAACAGAC
scaffold729926_15.	1	p3	(TGA)7	21	123	143	TTTTTGATTGGGAATAATTGGG
scaffold729957_14.	1	p3	(TAA)7	21	1571	1591	ATCCACCCCACACATCATTC
scaffold730055_15.	1	p3	(AAC)6	18	1402	1419	CGAAAAGATGTATGGCGAAAA
scaffold730086_18.	1	p3	(GGT)5	15	741	755	GGATTCGTGACTTTCAGGGA
scaffold730115_14.	1	p3	(TGT)5	15	46	60	TGTAGCCGACCCCAATTTAT
scaffold730173_14.	1	p3	(CCG)6	18	667	684	CCAAAGCAAAAACATCCCAC
scaffold730238_16.	1	p3	(AAC)5	15	120	134	AATCGACAATTTCGGTTTCG
scaffold730322_12.	1	p3	(ATA)5	15	286	300	GCCATGAAAAACAAGGAGGA
scaffold730399_18.	1	p3	(CGG)5	15	637	651	CACTGACCTTGGACTTCGCT
scaffold730429_15.	1	p3	(GCT)5	15	3063	3077	GTGAAAATCCTCCCTCGTGA
scaffold730463_16.	1	p3	(CTC)6	18	2158	2175	GCTGCCTCTGGACAACTCTC
scaffold730475_13.	1	p3	(TGG)7	21	2101	2121	GAGCCGATGAGGCTGTTTAG
scaffold730581_12.	1	p3	(GCT)5	15	600	614	TCAGAAAGAGGAGACGGAGG
scaffold730589_15.	1	p3	(TCT)6	18	201	218	TTCGATCACAAGAAACGACG
scaffold730624_15.	1	p3	(CCT)5	15	1793	1807	GGGAAGGGGGTACATGCTAT
scaffold730640_15.	1	p3	(CAG)5	15	434	448	TCAGCAGCAGCAAATACAGC
scaffold730730_14.	1	p3	(ATA)5	15	2699	2713	AGACAACGAGGGATGACGAC
scaffold730758_17.	1	p3	(AAT)5	15	2883	2897	TAACTTGAGCCGACATCCCT
scaffold730759_15.	1	p3	(CCA)6	18	250	267	TGGCAGCCCTAATTTACCAG
scaffold730779_15.	1	p3	(AAT)8	24	967	990	CGGGATGTAGTAGGAAAGCG
scaffold730784_18.	1	p3	(TGT)6	18	41	58	TGTAGCCGACCCCAATTTAT
scaffold730874_15.	1	p3	(CCG)5	15	185	199	ACCTCATGAGCACAATTCCC
scaffold730879_14.	1	p3	(TTG)6	18	154	171	GTTCGGAAAATTTTTGGCCT
scaffold730880_17.	1	p3	(TCA)7	21	485	505	GGGCTTAAAACTTGCCACAA
scaffold730902_11.	1	p3	(ATT)8	24	1576	1599	TCCCTTTTCAGAAGTCGCAT
scaffold730908_16.	1	p3	(AAT)5	15	483	497	TGAATGAATGGTTCGACTCAA
scaffold731027_17.	1	p3	(TTA)5	15	1687	1701	AACTGGACCATATTCGTCGC
scaffold731062_20.	1	p3	(TTG)5	15	507	521	GCATCGGCCTATTTACCAAA
scaffold731067_15.	1	p3	(TTA)5	15	907	921	ATTCTGGCAAATCATCGGAC
scaffold731099_13.	1	p3	(CCT)5	15	531	545	CACCACCCTCTCATGTCCTT
scaffold731128_14.	1	p3	(ATA)6	18	858	875	AGGAAATCACGACGGTGTTC
scaffold731151_14.	1	p3	(ATC)5	15	1542	1556	CCCACACGTTTTTCCTCATT
scaffold731165_14.	1	p3	(TCA)5	15	489	503	GCAACTTTCAAGGAAGCCAA
scaffold731171_15.	1	p3	(GAG)5	15	636	650	ACAGGAATATCCCGTTGCAG
scaffold731239_14.	1	p3	(AAT)5	15	48	62	GGTTCCCACGTCATCAAAAA
scaffold731259_17.	1	p3	(ATC)5	15	3394	3408	TTGGCATCATTATGGAAGCA
scaffold731335_13.	1	p3	(TTA)5	15	1025	1039	GGTGTTGATGCATGGAGTTG
scaffold731396_14.	1	p3	(CAC)5	15	1158	1172	ATGGAGCTATTGGATGCTGG
scaffold731510_17.	1	p3	(TTG)5	15	2152	2166	TTTTGGATTCGATATGGATTGA
scaffold731602_14.	1	p3	(ATT)6	18	111	128	CCTCCAAACAAATACCCCCT
scaffold731623_16.	1	p3	(ATT)5	15	1430	1444	CCATGAGATGGGGACAGTCT
scaffold731857_15.	1	p3	(GAA)5	15	680	694	CAAGCAAACGCAAAAATCAA
scaffold731873_16.	1	p3	(AAT)5	15	366	380	ATCCCACCAACACCTTCTTG

scaffold731918_16.	1	p3	(TGT)5	15	867	881	GATTGGATTTTTGGTGGTGG
scaffold731958_14.	1	p3	(TCC)5	15	557	571	AACTCCCACCTTCCATCACA
scaffold731967_14.	1	p3	(TCT)7	21	304	324	TTCTCTCCCAACAATGACATCT
scaffold731979_16.	1	p3	(TGT)7	21	32	52	CCAATTTATTGGGATTAAGGCT
scaffold731981_13.	1	p3	(TAT)6	18	1393	1410	CCTCCATGTAAAGAAAAAGAGTTCA
scaffold731989_15.	1	p3	(ATA)5	15	134	148	TGCCGAATAAAGCTAAATCCT
scaffold732030_16.	1	p3	(GGC)5	15	71	85	ACCAGCTTTGCTCTGCAACT
scaffold732053_14.	1	p3	(GAG)5	15	717	731	CGTCGAATTTCGCTGATCTT
scaffold732085_17.	1	p3	(ATG)5	15	546	560	AGTCAAGTGCCGCTCATTTT
scaffold732102_15.	1	p3	(TAT)5	15	164	178	TGACAATTCGAGCTTGATCCT
scaffold732116_16.	1	p3	(ATG)5	15	942	956	TAGGCGATGTACCTTGGGTC
scaffold732126_16.	1	p3	(GGA)5	15	930	944	TTGGAATGCGACAGAGACAG
scaffold732220_16.	1	p3	(CTG)5	15	308	322	GACACCATTGACTGTGCTGG
scaffold732278_16.	1	p3	(TGT)5	15	46	60	TGTAGCCGACCCCAATTTAT
scaffold732307_17.	1	p3	(TAT)5	15	53	67	AGCAACAGGCACACTGGAAT
scaffold732308_10.	1	p3	(TTA)5	15	811	825	ACCCAGAGCAAACTCGAAGA
scaffold732318_13.	1	p3	(GCC)6	18	564	581	CAGTTGCATGCAGAGCATTT
scaffold732387_15.	1	p3	(ATG)5	15	991	1005	CTCGAACGATGCAAACTTCA
scaffold732457_20.	1	p3	(GGC)5	15	1082	1096	TGGAGGAGGAGGAATGTTTG
scaffold732523_16.	1	p3	(AAT)5	15	348	362	GCCGGAAAACACAAATCAAT
scaffold732543_14.	1	p3	(CTT)5	15	1006	1020	CTACCCTCGCTCTTCCTTCC
scaffold732548_16.	1	p3	(GCC)5	15	151	165	AAAAATCTCCAGTCCGGCTT
scaffold732641_14.	1	p3	(AGT)5	15	1277	1291	CAGCAAGCAATTCAAGGACA
scaffold732657_16.	1	p3	(TGA)5	15	44	58	CCCAAGACCCCAATTTGATT
scaffold732659_12.	1	p3	(CCG)6	18	571	588	TCTAAAATAGCCACGCCTCG
scaffold732672_15.	1	p3	(GCT)5	15	902	916	GCAGGAGAAGAGGTGGTCTG
scaffold732679_14.	1	p3	(ATG)5	15	641	655	GGACTCTTCCGGATGTTTGA
scaffold732703_17.	1	p3	(ATT)5	15	115	129	AAGTGTGTCGAAATTGAGAAGAAA
scaffold732719_15.	1	p3	(CAG)5	15	1194	1208	TGATTTGTGGCACCCTGTTA
scaffold732722_16.	1	p3	(CTT)5	15	779	793	GACTGAGATGTCCCAGGTTCA
scaffold732727_15.	1	p3	(TGT)8	24	39	62	TGTAGCCGACCCCAATTTAT
scaffold732740_14.	1	p3	(ATC)5	15	1339	1353	CCCGACCCAACTCAGTAGAA
scaffold732789_16.	1	p3	(TGT)5	15	47	61	TGTAGCCGACCCCAATTTAT
scaffold732863_14.	1	p3	(ATT)6	18	4450	4467	GGAAACCCTAGTTTCGTGTTCTT
scaffold732871_15.	1	p3	(CAC)5	15	688	702	TTCATGACGTGGAAGCAAAA
scaffold732934_15.	1	p3	(GGA)5	15	177	191	CCATCTAGTTCCTCACCGGA
scaffold732952_16.	1	p3	(ATC)5	15	1254	1268	TAAAACCCCCTTCAAATCCC
scaffold732960_16.	1	p3	(AGA)5	15	1016	1030	TCATCTCAAGACCACCCTCC
scaffold732970_17.	1	p3	(TTC)8	24	575	598	TGAAATGGGAAGGACTTCAT
scaffold733036_12.	1	p3	(CGC)6	18	3869	3886	AAATCTCCCCCACCTCCATA
scaffold733040_14.	1	p3	(GAA)5	15	1973	1987	AAAAGTGTCATGGCGAAACC
scaffold733053_14.	1	p3	(AAG)6	18	659	676	CAAAGTGGTGGAGTGAGCAA
scaffold733085_16.	1	p3	(AAT)6	18	109	126	TGCATATACACACATGTTGACCA
scaffold733132_16.	1	p3	(ATT)5	15	580	594	GGCTGGGTAATAGCCTTTCC
scaffold733147_16.	1	p3	(CTC)5	15	269	283	AGCTTAGCACAGCAGCATCA
scaffold733162_16.	1	p3	(CCG)6	18	571	588	CCTCCTCGTCGTCTTCATCT
scaffold733222_14.	1	p3	(ATA)5	15	299	313	AGATGGGCCGGCTAAATATC
scaffold733241_13.	1	p3	(AAT)5	15	1139	1153	TCTTTGTGTAGCACCCCCTC
scaffold733292_16.	1	p3	(CTT)5	15	1085	1099	AAGGAGGGTCAGTGAGCAAA
scaffold733318_13.	1	p3	(GGT)6	18	383	400	AGGCATTGGATTCAGTGGTC
scaffold733322_17.	1	p3	(TCA)6	18	3073	3090	CACGTCCTCAGGCCACTATT
scaffold733324_15.	1	p3	(TTC)5	15	2030	2044	GAGGACTGGGCTGATCTTCA
scaffold733336_16.	1	p3	(ATC)6	18	2479	2496	TTCTTCAAACTCCCACCGTT
scaffold733420_14.	1	p3	(AAT)5	15	871	885	TGATGGAACTTGTGTGCATGT
scaffold733443_16.	1	p3	(GTG)6	18	3044	3061	GCTCTCAGTGCATCCCAGAT
scaffold733452_17.	1	p3	(ATC)5	15	596	610	TTCACACGCGAGAAGAGAGA
scaffold733476_16.	1	p3	(TCT)5	15	837	851	AAGATAAAGGACGGCCGAGT
scaffold733535_16.	1	p3	(ATG)5	15	598	612	GCTTCCAGCAGAAATCATCC

scaffold733551_15.	1	p3	(CTT)5	15	2098	2112	AATGCAGTCCGGGTTCATAG
scaffold733688_16.	1	p3	(TGT)5	15	46	60	ATGTAGCCGACCCCAATTTA
scaffold733737_15.	1	p3	(TGA)6	18	43	60	CCCAAGACCCCAATTTGATT
scaffold733753_13.	1	p3	(TGT)6	18	45	62	TGTAGCCGACCCCAATTTAT
scaffold733764_16.	1	p3	(TTG)5	15	2331	2345	ACAGCTCGAGCATTCATTCC
scaffold733825_16.	1	p3	(CGG)5	15	507	521	TTTCGTTGGGACTGGTTACG
scaffold733846_16.	1	p3	(ACA)5	15	709	723	CATTCAATTCGAAATTATGCATGT
scaffold733892_13.	1	p3	(ATT)7	21	817	837	TTGTGTGAACGAGGATTTGC
scaffold733993_16.	1	p3	(CAG)5	15	316	330	TGCAACCTGCAAGTCACATT
scaffold734003_18.	1	p3	(CGG)5	15	3663	3677	TAATGGGCCTTCACATCCTC
scaffold734029_18.	1	p3	(GAG)5	15	697	711	GTTTTTGGACTAGCCCATCG
scaffold734045_12.	1	p3	(ATA)7	21	415	435	TTCAAATCCGGGTCTCTCAC
scaffold734102_14.	1	p3	(ACA)5	15	2347	2361	TTGTCGTGATGGGTGAATGT
scaffold734109_14.	1	p3	(AAT)5	15	107	121	CGCATGACACTGATCTATCG
scaffold734128_16.	1	p3	(TGA)6	18	44	61	CCCAAGACCCCAATTTGATT
scaffold734287_13.	1	p3	(GAT)5	15	1606	1620	CCCCAACTCACATCAACACA
scaffold734312_17.	1	p3	(ATA)5	15	5900	5914	TTCTTGTTTTCCCTCACTGGA
scaffold734377_19.	1	p3	(AAC)5	15	1179	1193	TCCAGATTCAAGACCAAGCA
scaffold734421_15.	1	p3	(GTC)5	15	1264	1278	ATTACCGATGGCCGATGTAG
scaffold734449_15.	1	p3	(ATT)5	15	550	564	ACACCCCAGCATGAGGAATA
scaffold734496_16.	1	p3	(ATA)6	18	1213	1230	TTGTATCGTGTTCGCCACAT
scaffold734506_15.	1	p3	(ATC)7	21	3897	3917	TGGAACGATTGTGTGGAAAG
scaffold734522_12.	1	p3	(TCA)5	15	631	645	GCCAGGATGCAGAACAATTT
scaffold734523_16.	1	p3	(GGC)7	21	3258	3278	TTTTGGGTGGAGAAATGGAG
scaffold734552_15.	1	p3	(TGT)5	15	51	65	ATGTAGCCGACCCCAATTTA
scaffold734557_16.	1	p3	(ACA)5	15	583	597	CCCATGCCGAATGTTATTCT
scaffold734579_17.	1	p3	(ATA)5	15	704	718	CATTATACCACGGAGGAAGGA
scaffold734599_14.	1	p3	(CTC)5	15	354	368	CCCCACACACTCATCCTCTT
scaffold734607_16.	1	p3	(CAT)5	15	453	467	GTTGGGTTGGATTTGAGCAT
scaffold734615_19.	1	p3	(TTC)5	15	634	648	TGAAACATCCATTCTCCAAAGA
scaffold734647_15.	1	p3	(AAC)6	18	3486	3503	TAGATAACAGGCAATGCCGC
scaffold734701_15.	1	p3	(ACC)5	15	838	852	ACTCTTCAGCTCCCACTCCA
scaffold734715_12.	1	p3	(TTA)6	18	696	713	GTTCCTAGCTGTCGGCACTC
scaffold734770_15.	1	p3	(ATA)5	15	320	334	AAAAGAGGGGGAAAAAATTCG
scaffold734792_15.	1	p3	(TAC)5	15	1395	1409	CATATAAAGAGGGCAGCCGA
scaffold734798_12.	1	p3	(AGA)6	18	1890	1907	CCTGATGAGGCTAAGGATGG
scaffold734809_16.	1	p3	(ATA)5	15	906	920	CCGAAAATGTCCTTCATTGC
scaffold734812_14.	1	p3	(ATT)5	15	831	845	TTGAGGACCGGACTGACTTC
scaffold734994_18.	1	p3	(ATC)6	18	645	662	CAGCATGAGGCAGATTGATG
scaffold735098_16.	1	p3	(GCG)7	21	363	383	CATGACTCCGCATTAGCAGA
scaffold735107_15.	1	p3	(CAT)6	18	757	774	CCCCTTGGGATATGTGTTTG
scaffold735203_16.	1	p3	(GGA)6	18	378	395	GAGATTTCGGAGCTTGTTGG
scaffold735237_16.	1	p3	(TAA)5	15	3316	3330	TTGTCACTAAGCCAACACCAA
scaffold735266_18.	1	p3	(ATT)5	15	1220	1234	GGAAATGATTGTTCTCCTAGGTC
scaffold735352_14.	1	p3	(ATT)7	21	410	430	TGTTTGCTTTTCTTCATGCG
scaffold735359_17.	1	p3	(CAT)7	21	3352	3372	GGCCTAAAGCTGATGGACCT
scaffold735371_14.	1	p3	(GCG)8	24	2065	2088	CTTTGCTTCGTGCTTGAATG
scaffold735376_16.	1	p3	(CTG)5	15	1471	1485	AGGGGACTCGTCAGGAAACT
scaffold735412_12.	1	p3	(ATT)8	24	202	225	TCTTTTTCCATTGCTCACGA
scaffold735525_14.	1	p3	(ACA)5	15	3192	3206	ACTGCATCGGTGTCTCACAT
scaffold735556_14.	1	p3	(CGC)5	15	316	330	GAAGGCAGCTTGATCGTAGG
scaffold735591_19.	1	p3	(AAT)5	15	827	841	GGAGGAAGCATCTACGCAAC
scaffold735606_16.	1	p3	(TTC)5	15	670	684	ACGCTGTTTTTCCACTCCAG
scaffold735788_16.	1	p3	(CTA)5	15	167	181	CAATAACGGCAACACAAACG
scaffold735797_16.	1	p3	(CCG)5	15	1078	1092	TGCACGATCCATATCTGCTG
scaffold735864_16.	1	p3	(TCA)6	18	3425	3442	TGATGGAATCTCTGGGAAGG
scaffold735875_15.	1	p3	(AAG)5	15	1457	1471	AACAAAATCCCTCCCCATTC
scaffold735876_17.	1	p3	(ATA)5	15	1382	1396	TGCCTTAACACAAAGGGGAA

scaffold735908_17.	1	p3	(TTG)5	15	49	63	AGCTTTGGTTCATGTAGCCG
scaffold735952_16.	1	p3	(TCC)5	15	2417	2431	CCGATGAGTCGTTTCCACTT
scaffold735980_13.	1	p3	(CTT)7	21	427	447	TGAAACTGGACCTGGTATCAA
scaffold735983_16.	1	p3	(TTA)7	21	1049	1069	TGTAAAGAAACGGACGGAGG
scaffold735996_14.	1	p3	(TTC)5	15	623	637	TGGCACCCTTACATCTCCTT
scaffold736066_16.	1	p3	(ATA)6	18	5779	5796	TTCGGAGGACAATGCTCTCT
scaffold736077_14.	1	p3	(CAA)6	18	5519	5536	GGGACAAGCTATCACACAGGA
scaffold736097_18.	1	p3	(TGA)5	15	359	373	GTTGCGTACATATGACCCCC
scaffold736191_14.	1	p3	(CCT)6	18	1121	1138	GTTCCACCCCCTGAGGTATT
scaffold736194_17.	1	p3	(TCA)5	15	652	666	CTCAAGGAGCTCAACTCCAA
scaffold736219_14.	1	p3	(ATG)5	15	1855	1869	GGCTTATGTCCAACTGCTCC
scaffold736222_13.	1	p3	(AAG)8	24	86	109	GCACTCGAAGAGTAGCGGTT
scaffold736230_17.	1	p3	(TGG)5	15	1181	1195	TCTGGAAAAGAGAAGGCCAA
scaffold736335_15.	1	p3	(GGT)5	15	102	116	TGTGGGAAAAACATCGATCA
scaffold736366_17.	1	p3	(GAC)5	15	1467	1481	TCGGCAACTTTTGGAAGATT
scaffold736370_15.	1	p3	(TTA)5	15	777	791	TTTCTCGCCTAATGCCATGT
scaffold736407_15.	1	p3	(ATT)7	21	1446	1466	CGCGAACTAATCCGTCCTTA
scaffold736421_14.	1	p3	(AAT)5	15	3134	3148	CCCTCAATTTTGTACCCGAA
scaffold736446_17.	1	p3	(TGA)6	18	45	62	CCCAAGACCCCAATTTGATT
scaffold736448_14.	1	p3	(TAA)6	18	403	420	GCCAAAAGTAAAGGAAGGGG
scaffold736470_18.	1	p3	(AAC)6	18	2057	2074	TCAAAAGTCATCCCCTGGAG
scaffold736473_13.	1	p3	(GGT)6	18	1201	1218	CTGATCACCCAGTTTTGCCT
scaffold736519_16.	1	p3	(CCG)6	18	927	944	CTCCAATCTCTCTCCCACCA
scaffold736531_16.	1	p3	(CAG)5	15	2314	2328	AGCATTGGCTTCAGCTGTTT
scaffold736549_14.	1	p3	(TGA)5	15	41	55	CCCAAGACCCCAATTTGATT
scaffold736560_11.	1	p3	(GCT)5	15	1150	1164	ATCCTCAGATTTACCGTGCC
scaffold736582_16.	1	p3	(GGT)7	21	1219	1239	TCTGGAAAAGAGAAGGCCAA
scaffold736622_11.	1	p3	(ATG)6	18	1139	1156	TTGCTTGACTGAGTTGCTGC
scaffold736630_16.	1	p3	(CAC)5	15	1230	1244	TACATCACCCTCCCATCTGC
scaffold736676_13.	1	p3	(CCG)5	15	720	734	TACTTCATCGTGCTCAACGG
scaffold736742_15.	1	p3	(TCT)5	15	320	334	TCCTCCAGCTGTTCTTTCGT
scaffold736777_14.	1	p3	(CGG)5	15	125	139	TGAACAGCATGGTCTGGATG
scaffold736799_15.	1	p3	(TGA)5	15	2384	2398	GATAAGGGGATTGATTGGCA
scaffold736809_16.	1	p3	(CAA)5	15	1213	1227	GAAGCCACGAGAGAATTTGC
scaffold736831_13.	1	p3	(TAA)9	27	1231	1257	TGCCCTCACAAACAAATTCA
scaffold736875_16.	1	p3	(GTA)6	18	2097	2114	CGAGACCTAAATTGGTTGTGG
scaffold736905_15.	1	p3	(ACA)5	15	699	713	AAAAATCATTTATCCCCGGC
scaffold736926_16.	1	p3	(CAT)5	15	1909	1923	TGCTGATCCACCCTTTGAAT
scaffold736960_12.	1	p3	(ATA)7	21	590	610	GCAGCTGAGCTAGGTGCATT
scaffold736973_16.	1	p3	(TAT)6	18	629	646	GCAATTTTCAAGGTTAGGCAA
scaffold737052_14.	1	p3	(AGA)5	15	2620	2634	ATCTCACTCGGACATGGGAC
scaffold737068_14.	1	p3	(CTC)7	21	2835	2855	TTGGTTCAATCTCAAAGCCC
scaffold737079_14.	1	p3	(TCT)7	21	2378	2398	AAGGTAGTACCAGCCTGCCA
scaffold737111_15.	1	p3	(CAT)6	18	697	714	CCACGCCATAACAAAGGACT
scaffold737119_12.	1	p3	(TGT)5	15	45	59	TGTAGCCGACCCCAATTTAT
scaffold737133_14.	1	p3	(CAG)6	18	443	460	TCGGCATGTTGCTCTTTATG
scaffold737227_13.	1	p3	(AAT)5	15	1120	1134	GCGCTGAAAGAGGATGAGAT
scaffold737250_16.	1	p3	(CGG)7	21	2605	2625	GTCCTCCTCGTCATCGTCAT
scaffold737290_16.	1	p3	(TAT)5	15	637	651	CGACAGCACATGACTTTTCA
scaffold737303_17.	1	p3	(ATA)6	18	318	335	TGCAAGATGTGCCCCTATTT
scaffold737344_15.	1	p3	(CGA)7	21	513	533	GGACTATCCACCAACTCCGA
scaffold737357_14.	1	p3	(TGA)5	15	2030	2044	GTGCAGGCTTGCTTTTGTTA
scaffold737372_16.	1	p3	(AAT)5	15	256	270	AATAAGATTTGCACGCTGGG
scaffold737459_13.	1	p3	(AAT)5	15	1049	1063	CGTTGCTTGGCAATTCTACA
scaffold737468_16.	1	p3	(GGC)5	15	320	334	ACTCAGATCTGGCCTGGAGA
scaffold737477_15.	1	p3	(ATA)5	15	40	54	TGGTAGATCTGCTCCTTGTAGTGA
scaffold737518_18.	1	p3	(TTG)5	15	97	111	CTGAAAGGGAGTTGGAAGCA
scaffold737596_19.	1	p3	(TGA)7	21	40	60	CCCAAGACCCCAATTTGATT

scaffold737616_18.	1	p3	(GCG)5	15	1166	1180	ACGCCAATTTGGATTTTGAC
scaffold737617_16.	1	p3	(TTA)5	15	51	65	GGTCCTTCGTCGCATATGAA
scaffold737621_16.	1	p3	(ACA)5	15	5149	5163	AATGTCATATACCCGCCCAA
scaffold737755_14.	1	p3	(CTG)5	15	149	163	GGTGGTGAGAACCACGACTT
scaffold737764_17.	1	p3	(CTT)5	15	279	293	CCATCGGAAGTCTCAAGTCC
scaffold737782_15.	1	p3	(TGT)5	15	50	64	ATGTAGCCGACCCCAATTTA
scaffold737783_16.	1	p3	(GAA)5	15	1874	1888	GGGAGCCCTTGGATTTAGTT
scaffold737806_14.	1	p3	(ATT)5	15	96	110	TTGGGATTAAGGCTTTGGTG
scaffold737841_15.	1	p3	(TTG)5	15	533	547	GCACTTACAGCCAAGCAACA
scaffold737846_17.	1	p3	(ATC)6	18	742	759	TTGTGGGATAAAATCCCCTT
scaffold737861_10.	1	p3	(TCA)8	24	679	702	GAGTGTTCGCGCAGTTGATA
scaffold737876_16.	1	p3	(AGC)5	15	2261	2275	CAGTGCATGCAAGCTGATTT
scaffold737895_16.	1	p3	(TGA)5	15	1628	1642	GGATTCGAGCTCTTGTTTGC
scaffold737897_17.	1	p3	(TGT)5	15	50	64	TTGGTTTATGTAGCCGACCC
scaffold737930_19.	1	p3	(GAA)6	18	459	476	CCGATAAGCAGAGCTCCATC
scaffold738028_17.	1	p3	(ATA)5	15	497	511	TGGTGAAAAATCAAACACTTGG
scaffold738078_16.	1	p3	(GAA)5	15	1425	1439	GGGCTCCTCATGGTCTGATA
scaffold738083_15.	1	p3	(ATT)5	15	1706	1720	TGCCTTTCAAATAGCATTCGT
scaffold738098_16.	1	p3	(GCC)6	18	673	690	CTTCTTCCTCCGACGACAAC
scaffold738101_15.	1	p3	(AGT)5	15	473	487	ATGCTTCTCCCCCTTGAAAT
scaffold738147_15.	1	p3	(CTT)6	18	1784	1801	TCAGTTATAGCCGACCCCAC
scaffold738222_15.	1	p3	(CAT)5	15	1923	1937	AAGTCGTGCATTGACGTGAC
scaffold738228_15.	1	p3	(ATG)5	15	4927	4941	TCAACAGACATTGCAGCCTC
scaffold738278_13.	1	p3	(TTA)5	15	1536	1550	TGGAACAAACAAACAAGCACA
scaffold738313_18.	1	p3	(CAG)5	15	1130	1144	ATGCCGTTCTTTTGTTCTGG
scaffold738324_15.	1	p3	(CAC)5	15	4550	4564	CCCATTTTGACGCTCTGATT
scaffold738341_15.	1	p3	(TGG)5	15	615	629	GATTGATTCCGGTAGGCAAA
scaffold738352_15.	1	p3	(TGT)5	15	4739	4753	CACCTATTCGACCCTGCAAT
scaffold738386_17.	1	p3	(TCA)5	15	1658	1672	GCATAACCCGAACCCAATAA
scaffold738394_16.	1	p3	(AGA)5	15	822	836	GGGAAGATTCGTGTTTCAGG
scaffold738407_14.	1	p3	(TAA)6	18	5979	5996	TGACAGATGAATGGACCAACA
scaffold738410_13.	1	p3	(TGA)6	18	43	60	CCCAAGACCCCAATTTGATT
scaffold738416_15.	1	p3	(GCT)5	15	3801	3815	CATTAGCTCCGTGATGCAGA
scaffold738439_16.	1	p3	(GGC)6	18	1826	1843	GACCCGGAAAGGAAATTTTG
scaffold738452_16.	1	p3	(CGC)7	21	497	517	TATCCAATATAGGGCACGGC
scaffold738483_18.	1	p3	(TAA)6	18	1621	1638	CGTTGATTCTTCAAAATCCCA
scaffold738486_15.	1	p3	(CAC)5	15	4771	4785	GTATGTGGTAAGGCGAGGGA
scaffold738698_18.	1	p3	(AAT)5	15	594	608	GCCCGTTTCTGAAAGACTGA
scaffold738712_15.	1	p3	(GAT)6	18	844	861	ACGAAGATACAGTCCCACCG
scaffold738720_10.	1	p3	(AAG)5	15	433	447	ACATTTCAACCGCAGGTAGC
scaffold738721_17.	1	p3	(CGA)5	15	380	394	TACCTCCGAAGGAACGAGAA
scaffold738727_15.	1	p3	(TGA)6	18	44	61	CCCAAGACCCCAATTTGATT
scaffold738754_16.	1	p3	(CAA)5	15	1860	1874	CCATCACCATCACTTCCAGA
scaffold738837_17.	1	p3	(AAC)5	15	429	443	TGAATGCTTTATCCGAGCCT
scaffold738838_17.	1	p3	(TGA)5	15	48	62	CCCAAGACCCCAATTTGATT
scaffold738847_12.	1	p3	(TCC)5	15	1499	1513	TCCCTCCTCCTCCTCTTCTC
scaffold738933_14.	1	p3	(GAC)5	15	1337	1351	CCTCCCTCTAAAAACCCGAA
scaffold738943_15.	1	p3	(AAC)6	18	65	82	TCAGCTTCATGATACTTTGGGA
scaffold739014_15.	1	p3	(AAT)5	15	1764	1778	GCGTATTATTTTTCTCTCAATAGGG
scaffold739017_12.	1	p3	(CTC)5	15	123	137	TGATCATCCTCCTCATTCTCTG
scaffold739030_18.	1	p3	(TCT)6	18	963	980	CTCAGCTATGAAATCCGCGT
scaffold739057_15.	1	p3	(GAT)5	15	2006	2020	TCAACACTGCAGATGAACAGAA
scaffold739072_15.	1	p3	(CTT)5	15	1980	1994	GGAAGCTTCAAGTCCAATGC
scaffold739101_15.	1	p3	(TTC)5	15	1975	1989	TTTCCGCCATTTTTAGCATC
scaffold739138_16.	1	p3	(GGA)5	15	927	941	GCGGAGAGGAAGAGGAAGAA
scaffold739165_16.	1	p3	(ACA)6	18	2136	2153	TTAGATTGGAGATGCCGAGG
scaffold739181_16.	1	p3	(ATC)5	15	2712	2726	AAAGAAGCAACCATCAACCG
scaffold739190_15.	1	p3	(ATA)5	15	999	1013	CTGCAGAATCAACTGCTTGG

scaffold739223_16.8	1	p3	(TGT)6	18	47	64	TTGGTTCATGTAGCCGACCT
scaffold739249_15.8	1	p3	(TTA)5	15	5158	5172	TCGTCCATATCAAGGCTCAA
scaffold739259_14.3	1	p3	(TAT)5	15	431	445	AAAATGGATGGGGTGATTGA
scaffold739268_17.7	1	p3	(ACA)7	21	3113	3133	ACACCCGGACACAAGAATGT
scaffold739299_16.2	1	p3	(TGG)5	15	5372	5386	GAGTATTCTTGCCGTTGGGA
scaffold739307_15.2	1	p3	(TGT)5	15	48	62	TGTAGCCGACCCCAATTTAT
scaffold739332_14.4	1	p3	(CGC)5	15	1580	1594	TGGTGAACCCAAACTCTTCC
scaffold739367_18.8	1	p3	(GCG)5	15	1772	1786	GGAGGAAATTGGCATCAGAA
scaffold739457_14.7	1	p3	(AGG)7	21	30	50	AAACAGCTTCTCTCTCCGGG
scaffold739460_14.3	1	p3	(CTC)5	15	878	892	AAAATAATGATAACGGCGGC
scaffold739464_18.0	1	p3	(AAG)6	18	695	712	TGGTGAGCTTGAGGAGGTCT
scaffold739514_17.6	1	p3	(TGT)6	18	44	61	ATGTAGCCGACCCCAATTTA
scaffold739534_15.2	1	p3	(TGA)7	21	45	65	CCGAGACCCCAATTTGATT
scaffold739542_13.5	1	p3	(TGT)5	15	68	82	ATGTAGCCGACCCCAATAAA
scaffold739596_15.5	1	p3	(TGT)6	18	42	59	TGTAGCCGACCCCAATTTAT
scaffold739600_16.3	1	p3	(TGT)7	21	41	61	TGTAGCCGACCCCAATTTAT
scaffold739613_17.2	1	p3	(ATC)7	21	3054	3074	AAACCATCTTTCCCCAAACC
scaffold739631_14.1	1	p3	(TTG)6	18	3284	3301	CCCAGTTTTTGTTGCACTGA
scaffold739678_15.7	1	p3	(TTA)5	15	734	748	AGTGAGTTGATTCGGGTTCG
scaffold739704_16.3	1	p3	(ATA)5	15	146	160	CCCACATCCAGCTTTCGTAT
scaffold739713_15.6	1	p3	(CAA)5	15	872	886	CAGTTTCAAGGGGAATCGAA
scaffold739714_17.0	1	p3	(TGA)10	30	3779	3808	GTGAGGATGATGGTGGAGGT
scaffold739733_16.6	1	p3	(TCC)5	15	2006	2020	AATTACCTGTTGGCCTGCAT
scaffold739753_15.4	1	p3	(CAT)7	21	5898	5918	GAAATCGGAATCCCCGTACT
scaffold739861_15.5	1	p3	(GGA)6	18	642	659	GTTCTCCTTCGGAGTTGCAG
scaffold739881_15.6	1	p3	(TTG)5	15	2151	2165	AGCCGACTTCACATAGTGGG
scaffold739896_17.2	1	p3	(GCC)5	15	1253	1267	ACGTTGTTGTTGATTGGGGT
scaffold739916_18.2	1	p3	(GAA)5	15	960	974	AAATACAAAGCCAGCCAACG
scaffold739960_15.6	1	p3	(TGT)5	15	47	61	ATGTAGCCGACCCCAATTTA
scaffold739977_14.5	1	p3	(TAA)6	18	80	97	ACGTGTATTGGGTGGTCCAT
scaffold740019_13.8	1	p3	(ATA)5	15	2284	2298	GCAGAAGGCTCCACTCTTGT
scaffold740035_13.9	1	p3	(CAT)5	15	1620	1634	AACTTTTGCCTGAAACGCAT
scaffold740153_17.1	1	p3	(CGG)5	15	758	772	ACCATGAAGATGAAGCTGCC
scaffold740170_15.7	1	p3	(CAC)5	15	703	717	TCGTTTTCTTTCTCGGTGCT
scaffold740175_15.2	1	p3	(TTG)5	15	51	65	TTGGGATTAAGGCTTTGGTG
scaffold740177_13.6	1	p3	(TTA)5	15	2268	2282	ATTTCTCATACGTGCCTGCC
scaffold740198_15.7	1	p3	(CTG)6	18	1117	1134	ATGTTGATAGGGTTGGACGC
scaffold740213_15.4	1	p3	(CAT)6	18	2858	2875	GATGCGGGGGATTTAAAGTT
scaffold740254_16.7	1	p3	(CAT)5	15	332	346	ATCATCACCGTGGATCATCA
scaffold740330_15.7	1	p3	(AGC)6	18	3834	3851	ACTCTTACGAGGGACGGGTT
scaffold740341_15.8	1	p3	(ATT)7	21	150	170	AATAAAGTATGTGGGAAAGTCGAT
scaffold740428_15.0	1	p3	(ATG)6	18	265	282	GTGAAACACCATCTTTCCCG
scaffold740432_16.1	1	p3	(TGT)5	15	45	59	TGTAGCCGACCCCAATTTAT
scaffold740445_15.1	1	p3	(TGA)6	18	291	308	CGATTAGGGCTGTTATCGGA
scaffold740478_12.6	1	p3	(TAT)5	15	262	276	GATTCCCTATCTTGCTCCCC
scaffold740500_15.6	1	p3	(GAT)5	15	3629	3643	ATGCAACTTGCCAACCTACC
scaffold740505_15.8	1	p3	(CCG)6	18	1836	1853	CAAGCCACTCAAAATCAGCA
scaffold740509_15.6	1	p3	(CGG)5	15	3265	3279	AAATGCCGTTGGTGAGGTAG
scaffold740549_16.3	1	p3	(TGA)5	15	3839	3853	TTGCGTACATTTGATTGGGA
scaffold740562_16.2	1	p3	(GGC)5	15	2685	2699	TTTTGCATGTTCAGAGGCAG
scaffold740671_16.1	1	p3	(AAG)5	15	1795	1809	TTAGGCTCTCCAAAGGACGA
scaffold740673_14.5	1	p3	(TCC)6	18	608	625	CATTTCGACCTCCACATCCT
scaffold740687_14.5	1	p3	(GAA)5	15	3788	3802	AGAGAAGTTGTGGGGTGGTG
scaffold740688_16.3	1	p3	(TTG)7	21	2787	2807	AAATCTGTTCCAATTCCGGG
scaffold740704_14.6	1	p3	(GAT)5	15	736	750	TGTGATCAATGAAGGGGACA
scaffold740712_15.7	1	p3	(ACA)6	18	4039	4056	CGGCTGTTACTCCTTCCAAA
scaffold740714_16.1	1	p3	(CAT)6	18	598	615	AGGCTGAAAAGGATGCTCAA
scaffold740744_14.4	1	p3	(CTC)5	15	47	61	GTGTAAGTCGCGGTCTCGAT

scaffold740786_14.	1	p3	(CTT)5	15	1313	1327	TCCATCAACCTAACAGCAACA
scaffold740790_18.	1	p3	(AGA)5	15	263	277	AGGTGGCAACGAAAATGAAC
scaffold740802_14.	1	p3	(GGA)5	15	842	856	GACGGAGATCCCAATGAAGA
scaffold740811_15.	1	p3	(TGT)7	21	41	61	TGTAGCCGACCCCAATTTAT
scaffold740824_14.	1	p3	(AGA)5	15	2863	2877	CTCATTGACGACATCCAACG
scaffold740832_18.	1	p3	(AAC)5	15	3422	3436	AGCGGGATAATGGAACAGTG
scaffold740833_15.	1	p3	(TTA)5	15	753	767	CTGCCTGCAAAAATATCCGT
scaffold740873_16.	1	p3	(GAT)5	15	571	585	TGCAACTTGAGGCTGAGAAA
scaffold740884_15.	1	p3	(TTG)5	15	173	187	GTTTATGTAGCCGACCCCAA
scaffold740885_16.	1	p3	(ACA)5	15	1600	1614	GATGCTTAGTTGCCCATTCG
scaffold740977_14.	1	p3	(CTT)5	15	1365	1379	TCAGAGCTATTTGCTTCACCA
scaffold740985_11.	1	p3	(GCT)8	24	868	891	GAAGGAGGGGATGGAGAGAG
scaffold741038_14.	1	p3	(TGT)7	21	3070	3090	AGTGTTACGCACTCATTGCC
scaffold741071_16.	1	p3	(AAT)5	15	607	621	CGATAACGTGAGTCGTGACC
scaffold741078_16.	1	p3	(GCG)5	15	2381	2395	TACTTCGCCGTAGGTTTCGT
scaffold741092_13.	1	p3	(ATT)7	21	342	362	CGCCACTTGTTGGGTATTTT
scaffold741094_16.	1	p3	(TTA)6	18	1897	1914	CAACTGCACTTGGATCCTGA
scaffold741111_16.	1	p3	(CGG)5	15	536	550	TCTGGGGAATTTTCCTTGAA
scaffold741114_15.	1	p3	(CAT)6	18	1421	1438	TCTCCTACCCAAAACTCCCA
scaffold741117_17.	1	p3	(GCA)6	18	373	390	TCTGAAGCAGCTCCTGTGAA
scaffold741208_19.	1	p3	(ACA)5	15	2078	2092	ACAAATGCAGGGAGGTCAAC
scaffold741217_15.	1	p3	(ATC)6	18	1200	1217	GGGGCCCTGTCTAAAAATTG
scaffold741243_17.	1	p3	(ATG)6	18	1806	1823	TACATCTGACCCCCAAGACC
scaffold741246_15.	1	p3	(GCG)5	15	645	659	GCACGTAAAACCACCGAGAT
scaffold741304_16.	1	p3	(GAA)5	15	201	215	CTACCCACAACAGCATGACG
scaffold741311_16.	1	p3	(TGT)6	18	43	60	ATGTAGCCGACCCCAATTTA
scaffold741320_16.	1	p3	(TGA)5	15	49	63	CCCAAGACCCCAATTTGATT
scaffold741329_16.	1	p3	(TGT)6	18	45	62	TGTAGCCGACCCCAATTTAT
scaffold741335_14.	1	p3	(ATA)5	15	322	336	GAAAGGAAAGAGCCGTCCTC
scaffold741347_13.	1	p3	(ATC)5	15	726	740	TCACCATCATTTTCTTGCCA
scaffold741381_16.	1	p3	(CAC)6	18	1046	1063	CACCATTGTTGGCATCAGAC
scaffold741423_15.	1	p3	(AAT)5	15	425	439	ATTGGTATGCGCAACAATGA
scaffold741536_16.	1	p3	(CAT)5	15	5658	5672	TGTGGTCTCATAACAAACCTGA
scaffold741541_16.	1	p3	(ACA)5	15	2475	2489	TTGGTTGAGCGAGGAATACA
scaffold741588_14.	1	p3	(TTC)5	15	3267	3281	TTCATCTCCCGTGTCCTTTC
scaffold741594_16.	1	p3	(ATT)6	18	95	112	AAAAGTGGCATTTTGCCCTA
scaffold741610_15.	1	p3	(ATG)6	18	2685	2702	TGTGAATCCCAAATGCTTCA
scaffold741613_17.	1	p3	(GTA)5	15	59	73	TTTTGGCATGAGAAACTCCC
scaffold741639_19.	1	p3	(CAG)5	15	1022	1036	AAGGCGAATTCTTGGGAACT
scaffold741650_16.	1	p3	(TCA)6	18	1722	1739	TGTTGACGACGGAACTGAAG
scaffold741675_16.	1	p3	(CAA)5	15	3083	3097	GCAAGACAAACAAAGTGCCA
scaffold741677_14.	1	p3	(TTA)8	24	43	66	TTATAAAACCGACCCACCCC
scaffold741702_17.	1	p3	(GAG)5	15	847	861	TCTTCTTGCATGTCTCGTCG
scaffold741711_17.	1	p3	(TCT)5	15	138	152	CGTTTTCTTATCTCTGCGCC
scaffold741748_13.	1	p3	(TAA)6	18	542	559	GCATTTTCCTCAAAAAGGGA
scaffold741753_14.	1	p3	(AAT)6	18	69	86	GGACGGAGTTGTGAAGGAAT
scaffold741763_15.	1	p3	(CAT)5	15	49	63	CAATAGTCTAAGGGAGCACATGG
scaffold741790_16.	1	p3	(TGT)6	18	44	61	TGTAGCCGACCCCAATTTAT
scaffold741791_17.	1	p3	(TCT)6	18	195	212	TTCTTCCACCAATTACCCCA
scaffold741805_16.	1	p3	(ATC)5	15	600	614	ACCGCGTTATTATTTGCAGG
scaffold741806_15.	1	p3	(TGA)5	15	659	673	GCACACTCGAACAAAGCAAA
scaffold741820_12.	1	p3	(TCC)6	18	2578	2595	TTTTTCACGCACAACACACA
scaffold741824_19.	1	p3	(CTC)5	15	585	599	TTCCTCTCTCTCTCCCTCCC
scaffold741830_19.	1	p3	(CTC)5	15	737	751	TGCAGTAAATCTGTGACCCG
scaffold741933_16.	1	p3	(TGG)5	15	2678	2692	AATTCTCACCCCCGGTATTC
scaffold741955_18.	1	p3	(TTA)6	18	1369	1386	TCCGTAAGAGCATTTTGGCT
scaffold741960_15.	1	p3	(CCG)6	18	1825	1842	GAGGTGGTCGGTTGGTAAGA
scaffold741977_16.	1	p3	(CAT)5	15	3275	3289	AGGCTCAGTGGTCTCTTGGA

scaffold741985_18.	1	p3	(CCG)7	21	1270	1290	GTAAACGACGGTTAGCTGGC
scaffold742014_12.	1	p3	(TAT)6	18	1719	1736	TTTCGATGTCGAATTACAACAAA
scaffold742051_15.	1	p3	(TTA)5	15	1256	1270	TCGATTTTATCCCTCGCAAA
scaffold742055_16.	1	p3	(ATT)6	18	470	487	GACATCATCCACCGAGAACC
scaffold742067_17.	1	p3	(TGT)6	18	1476	1493	AAGGGAGGGAATGAAGTGGT
scaffold742069_16.	1	p3	(GAG)5	15	2125	2139	CAAACGAAGGAGGAGGATGA
scaffold742072_15.	1	p3	(AGA)5	15	1427	1441	CCCAAAATAACGGACCTGAA
scaffold742074_17.	1	p3	(AAC)5	15	2043	2057	AACCAAACAAGCCATTCCAG
scaffold742081_16.	1	p3	(AAC)6	18	2233	2250	GGGCATTACCTTTGCATCAC
scaffold742084_15.	1	p3	(TTG)5	15	48	62	TGTAGCCGACCCCAATTTAT
scaffold742106_18.	1	p3	(GGT)5	15	3533	3547	TGTAAGCTCACCAGCATTCG
scaffold742108_14.	1	p3	(TTC)5	15	278	292	CCAGCTTCAGGTTCTCTGTTG
scaffold742114_15.	1	p3	(GGA)5	15	2828	2842	ATTGACTCCCACCAGGAGTG
scaffold742125_17.	1	p3	(CCG)5	15	1550	1564	CCACTTATTTACTTCCGCCG
scaffold742167_14.	1	p3	(CTC)6	18	395	412	CCCGAAGCGAATTTATTTCA
scaffold742200_14.	1	p3	(GCC)5	15	3772	3786	AGTTGGGAAGGTAATTGGGG
scaffold742219_16.	1	p3	(TGC)5	15	2473	2487	TCGAACCCGTGACATGTTTA
scaffold742226_18.	1	p3	(TAA)6	18	426	443	TACATCGCACAAAATCACGG
scaffold742264_16.	1	p3	(ATA)5	15	2762	2776	TTATTTTGGGATTCACCCATT
scaffold742298_15.	1	p3	(TTA)6	18	2818	2835	CGTTAAATGCCACTGTGTTGA
scaffold742314_17.	1	p3	(TGA)5	15	49	63	CCCAAGACCCCAATTTGATT
scaffold742335_17.	1	p3	(TGT)5	15	49	63	TTGGGATTAAGGCTTTGGTG
scaffold742347_14.	1	p3	(ATT)5	15	267	281	AGCAAAAGAAGAGGTTGCCA
scaffold742362_15.	1	p3	(AAT)7	21	1453	1473	AAGAGGTGCATTTCAATCGG
scaffold742372_13.	1	p3	(ACA)5	15	4592	4606	GTTTACTTCCATTCCGCCAA
scaffold742403_16.	1	p3	(AGA)6	18	3195	3212	AGCCAAGATATCCGATGCAC
scaffold742408_15.	1	p3	(TGT)6	18	1252	1269	ATCAATGGGCATTGGATGAT
scaffold742430_15.	1	p3	(AAT)5	15	2675	2689	GCCGTTAAAGCGTGAAGACT
scaffold742440_17.	1	p3	(TAT)6	18	1246	1263	TGGATGACCGAACTCTGTTTC
scaffold742450_17.	1	p3	(GCT)6	18	617	634	TTTTCGTCACCTTTTGAGGC
scaffold742462_16.	1	p3	(TGT)5	15	45	59	TGTAGCCGACCCCAATTTAT
scaffold742463_14.	1	p3	(TAA)7	21	1119	1139	CTTGAAATTTTTGTGTGGCAA
scaffold742466_13.	1	p3	(CAA)7	21	3483	3503	TCACAGATCCACAGGTTCCA
scaffold742500_14.	1	p3	(TGT)8	24	2896	2919	AAAAAGTCGTGACCAAACAAAA
scaffold742506_14.	1	p3	(CAG)5	15	277	291	ACCAGCAATCTGGTGGATTC
scaffold742513_14.	1	p3	(TTC)5	15	358	372	TACCTTCTCCGGAATCATGC
scaffold742522_14.	1	p3	(ATT)5	15	918	932	TCAATGGTTGGGCTACACTTC
scaffold742525_15.	1	p3	(TAA)5	15	694	708	GGCCTTAATTGACCCAACCT
scaffold742528_15.	1	p3	(TGA)5	15	47	61	CCCAAGACCCCAATTTGATT
scaffold742563_16.	1	p3	(TTG)6	18	5273	5290	AACGTAAAGAGGGGTAGGGG
scaffold742607_15.	1	p3	(ATT)7	21	169	189	AGCCAGGTAAACACCAATGC
scaffold742609_14.	1	p3	(TAA)5	15	2848	2862	TCTCAGAGATAGTGCCAAGGTG
scaffold742618_17.	1	p3	(CAT)6	18	2600	2617	GAAAATGGGGTGGTTGATTG
scaffold742633_16.	1	p3	(CAA)5	15	1714	1728	ATTCAGGAGGCACGCATATT
scaffold742659_15.	1	p3	(ATT)5	15	255	269	TCCCTTTCAATTACATCGCA
scaffold742694_16.	1	p3	(AAT)6	18	762	779	AGGTCGGTTGAAAAGATGGA
scaffold742735_14.	1	p3	(AAT)6	18	979	996	ATGGGTTTTGCCATCAATTT
scaffold742746_15.	1	p3	(ACA)5	15	1880	1894	AAAGATCCAGTGTTGGCAGG
scaffold742770_14.	1	p3	(GAA)6	18	3794	3811	TAGTTCTCCGCCTGCTCAAT
scaffold742802_17.	1	p3	(TCC)5	15	6123	6137	GAGGCTTTCCACATCATCGT
scaffold742812_15.	1	p3	(TGA)6	18	31	48	TTTGATTGGGAATAATTGGG
scaffold742846_15.	1	p3	(ATT)5	15	1856	1870	GAGAAAAACAGAGGAGCAACAAA
scaffold742872_15.	1	p3	(TCA)5	15	2009	2023	AATGCTGCATCAACCAGTCA
scaffold742893_16.	1	p3	(ACA)5	15	2050	2064	TCAAGGTGTCCTCGATTTGA
scaffold742903_15.	1	p3	(TAA)5	15	1611	1625	TTCCAACATGCTGCCTAAAA
scaffold742913_16.	1	p3	(TAG)5	15	1130	1144	AGAGGCCAACAAAGAGACGA
scaffold742915_17.	1	p3	(CAG)5	15	3995	4009	GTGCTGTTAGCTCCTCTGGG
scaffold742916_16.	1	p3	(TGT)5	15	45	59	TGTAGCCGACCCCAATTTAT

scaffold742938_17.	1	p3	(TCT)5	15	492	506	GGATTAAGAAAGACATTGGACGA
scaffold742955_13.	1	p3	(TTC)5	15	271	285	TCCCATATTTGGAGTCCAGG
scaffold742965_15.	1	p3	(CAT)5	15	2169	2183	AGTTGGGATTTGCCAGTTTG
scaffold742969_16.	1	p3	(TGT)6	18	38	55	TGTAGCCGACCCCAATTTAT
scaffold742981_18.	1	p3	(GAG)6	18	4494	4511	ATTTGGTGTCGCCTAAATCG
scaffold743005_14.	1	p3	(TGT)5	15	51	65	ATGTAGCCGACCCCAATTTA
scaffold743014_17.	1	p3	(GGT)5	15	3468	3482	AAGCCTTTCATGTCACCAGG
scaffold743018_16.	1	p3	(GCT)5	15	5456	5470	CTACCTGATGGGCTATGGGA
scaffold743021_15.	1	p3	(GTT)5	15	1623	1637	GATCCATATAGCCAACCCCA
scaffold743022_16.	1	p3	(GCT)5	15	8663	8677	CGGAAAGAGTTTTGCTCAGG
scaffold743037_14.	1	p3	(TGT)6	18	45	62	ATGTAGCCGACCCCAATTTA
scaffold743045_15.	1	p3	(CCT)6	18	2085	2102	TCGAAAAAGTGCGTCATCAG
scaffold743048_15.	1	p3	(TTC)7	21	2817	2837	GTGCGCGTTTAATGTCTTGA
scaffold743057_16.	1	p3	(CCG)5	15	2221	2235	CACCGCCGTTCAGTAAAGAT
scaffold743093_15.	1	p3	(GAA)5	15	54	68	GGAAGATGCTCCAACTCCTG
scaffold743094_15.	1	p3	(GCG)9	27	1100	1126	TCTAACCCCACCATTTCTGC
scaffold743098_16.	1	p3	(TTA)5	15	243	257	TCCGTTGAAATAAGATCGGG
scaffold743126_16.	1	p3	(TTC)6	18	1118	1135	TGCTATGTGATGTTGGCTTG
scaffold743127_17.	1	p3	(ACC)7	21	2595	2615	AATCCGAAATGCAAAACTCG
scaffold743155_15.	1	p3	(TGT)5	15	47	61	TGTAGCCGACCCCAATTTAT
scaffold743156_18.	1	p3	(TAT)5	15	3209	3223	CACCCAGTTTGAATTTTAGCAA
scaffold743165_16.	1	p3	(CAT)6	18	2948	2965	GGTCCAAAAACTCAGGCAAG
scaffold743167_16.	1	p3	(CCA)5	15	4457	4471	ACTGGGCAACATAATCCAGC
scaffold743199_15.	1	p3	(TGT)8	24	39	62	TGTAGCCGACCCCAATTTAT
scaffold743213_14.	1	p3	(CGG)5	15	66	80	AAAATTATGTAATAGTTTGCCGACG
scaffold743219_15.	1	p3	(TTG)6	18	3327	3344	TTTGGTTCTTGTAGCCGACC
scaffold743231_16.	1	p3	(CAC)5	15	244	258	ATATGTTTCGCCTCTCCCCT
scaffold743239_16.	1	p3	(ATG)5	15	490	504	CAACGTGATGTCGATGGAAG
scaffold743249_16.	1	p3	(GCG)5	15	592	606	GCCGGTCAGTTAATCTGCAT
scaffold743250_15.	1	p3	(CCG)6	18	925	942	TAATCTACCAATGGCCCGAG
scaffold1350_16.1	1	p4	(AAGC)	20	675	694	TGAATTTGCCAAAAGCAGTG
scaffold1551_14.8	1	p4	(TCAA)	20	1304	1323	TCACATACCTGCAACCATGAA
scaffold4205_14.5	1	p4	(TAGG)	20	1651	1670	AATGCTCCAACTTCGACTGG
scaffold4332_15.2	1	p4	(ATCG)	20	825	844	GAGCACGGAAATCGAGAAAC
scaffold18302_15.4	1	p4	(GGGT)	20	1133	1152	GAGCCATCTTGTGACTGCAA
scaffold18303_15.4	1	p4	(CCCA)	20	314	333	GGCCTTCAAAAGCATAACCA
scaffold18349_15.3	1	p4	(CGAT)	20	104	123	TCGATCGATCTCTCCTGTGA
scaffold19199_11.2	1	p4	(AAAT)	24	1209	1232	TTGTGGTCTCACTCCTCCAA
scaffold24576_14.6	1	p4	(ATTT)	24	1325	1348	TGTGGTGTCTTGTGGTCTTGA
scaffold36007_12.4	1	p4	(GGGA)	20	45	64	GGTGTTTATTTCGGCTGGTG
scaffold37946_16.9	1	p4	(TCAT)	20	728	747	GCACTTTCACGGGAGTTGAT
scaffold39016_15.7	1	p4	(AAAT)	20	576	595	GAGGAAGAGTTTCGGATGGA
scaffold49950_16.0	1	p4	(TAAA)	20	2805	2824	CGGCAAATTAAAACAGACACG
scaffold57330_16.1	1	p4	(TTAT)	20	2378	2397	TGGTGCATAATGGCTCTGAC
scaffold58946_16.3	1	p4	(ATTT)	20	1534	1553	TCCACACACGTCTTCACATTT
scaffold60885_12.5	1	p4	(CATC)	24	1265	1288	TCAGCATTATGTGCTCTGCC
scaffold61097_16.7	1	p4	(AAAT)	20	1154	1173	CAGCAGAGATCATCCACCAA
scaffold65330_12.7	1	p4	(TAAT)	24	317	340	AGAAGCACAACCAACCAACC
scaffold66955_16.4	1	p4	(TTCT)	20	983	1002	CGGTTTCATAAGGTTGTCGG
scaffold107651_15.	1	p4	(CCAA)	20	1007	1026	TACATTGTGCCTCCTCCCTC
scaffold111948_14.	1	p4	(TTAT)	20	764	783	CCACTCATTTTTCCACACGA
scaffold120623_16.	1	p4	(AAAT)	20	3985	4004	GGCTCGAGTTGATGATCTTTG
scaffold124168_12.	1	p4	(TATT)	20	513	532	TTTCAGATCTGCCACAGACG
scaffold124671_15.	1	p4	(TACA)	20	276	295	CCTATCGTTCCACATGCCTT
scaffold124853_15.	1	p4	(CCAC)	20	422	441	CGAGATCCACGTGTCATTTG
scaffold125326_16.	1	p4	(ATTA)	20	1472	1491	TTGTAGTCCTTAAATTCCCGATT
scaffold126775_13.	1	p4	(AATA)	24	452	475	CATCTGCCATGCACCATTTA
scaffold137114_17.	1	p4	(AGTC)	20	931	950	TGTTCGGAGCTTGTGTTGAG

scaffold144284_14.	1	p4	(GAAA)	20	663	682	TCTCTCATTGGTGGCCCTTA
scaffold144356_13.	1	p4	(AAGA)	20	414	433	AAAGCAAACCAAACCAAACG
scaffold150875_13.	1	p4	(CCAT)	20	568	587	CCATGACACTGAATATCCCAGA
scaffold166093_15.	1	p4	(AAGA)	24	54	77	TCCCGTGCGAGAGTAAAAGT
scaffold167894_10.	1	p4	(GATT)	20	248	267	CAGTGACTGCGATCGGTCTA
scaffold170575_16.	1	p4	(ATTT)5	20	765	784	TTTCTGTTAGTCAAAATCGAGAGA
scaffold171052_12.	1	p4	(ATAA)	28	1459	1486	TGACAAAAATTGAGGCGTTG
scaffold180305_14.	1	p4	(ATTG)	20	636	655	GGATTGTGTGGCTACTGGCT
scaffold180742_17.	1	p4	(TTGG)	20	1030	1049	TGTCATGTCATCGTGTGCTTT
scaffold181162_10.	1	p4	(TTAA)5	20	245	264	TCTCAGATATGGGCGTCACA
scaffold212608_15.	1	p4	(AAAG)	20	904	923	GGTGAAGCAGAAAAACCAGC
scaffold224867_13.	1	p4	(AATA)	20	2194	2213	TGTGGTTTGCCTCACTCTTCT
scaffold228171_13.	1	p4	(TAAA)	20	201	220	TTATTTTTGGTACCCGGTGG
scaffold238727_15.	1	p4	(TCCC)	20	669	688	TTGATTTGCAACTCCCTTTT
scaffold241894_11.	1	p4	(TTTA)5	20	325	344	TCACTGCTCTTTTCAACCCTT
scaffold259208_13.	1	p4	(TATT)5	20	850	869	GACGTGGAATGTGGATGATG
scaffold262258_12.	1	p4	(ATAA)	20	59	78	TTTTCCGACTTTGGCAAATACT
scaffold268278_19.	1	p4	(ATTT)5	20	293	312	TGGAATTGACGACTCCATTG
scaffold280650_16.	1	p4	(AAAT)	20	91	110	CAAATTAAAATGCGCCACG
scaffold280939_15.	1	p4	(GAGG)	20	558	577	TGGCTTATGAGTAGGTCCGC
scaffold283553_12.	1	p4	(GATC)	20	280	299	TGGCGAGAAAACTCAGATCC
scaffold294280_13.	1	p4	(ATTT)5	20	417	436	ACACACGCAGGCAGAATATG
scaffold309554_16.	1	p4	(ATTT)5	20	39	58	TGAAGATTGCTTCCTTATGAATTG
scaffold314358_14.	1	p4	(TTGC)	28	1703	1730	TGCAGAGCAAATTCATGTCC
scaffold315660_13.	1	p4	(TATT)5	20	162	181	TGTTGGAAGAAACAAAACTGGA
scaffold322738_16.	1	p4	(TTGT)	24	4485	4508	GCTCCTCTTCACTGTCGGTC
scaffold357424_11.	1	p4	(ATTT)5	20	512	531	AGTCTTGGGAAGCGAAATGA
scaffold359091_10.	1	p4	(AAAG)	20	376	395	TTTTCCGTGGTATCAGAGCC
scaffold362989_10.	1	p4	(CTCC)	20	948	967	TCTTGTTTTCTCCCCAAACC
scaffold379093_12.	1	p4	(TATT)5	20	252	271	TGGGCTTCTTCAGCTTCTTT
scaffold401117_17.	1	p4	(AATA)	20	525	544	GGTGTGGTTTGCAGGCTATT
scaffold408858_16.	1	p4	(ATTT)5	20	2286	2305	TTGCAATAATCAAGTTCAAGCA
scaffold421065_16.	1	p4	(TAAA)	24	5969	5992	CTCTCGTTTGGACTCTTGGG
scaffold424451_15.	1	p4	(TAAA)	20	1408	1427	CCCCTATAACTCTCGGGGTG
scaffold424746_14.	1	p4	(TTTA)5	20	1082	1101	GTCTTGGTTGCCATCTCCAT
scaffold432935_14.	1	p4	(AAAT)	20	811	830	AATCGCAGAACATGAAACCC
scaffold433361_17.	1	p4	(AAAT)	20	3083	3102	TCCCCTCATCTCTGCCTCTA
scaffold434282_14.	1	p4	(TCTT)5	20	6551	6570	GAAGCAAGAGAGACGTTGGG
scaffold448298_14.	1	p4	(TGTA)	24	800	823	TTGTGTTGGCGGCAGTAATA
scaffold452632_15.	1	p4	(AATT)	20	1570	1589	AGGAGGGTAGGTGGTCTGGT
scaffold457263_16.	1	p4	(TCAC)	20	52	71	GCCTTCTTTTCACGCATTTC
scaffold469276_12.	1	p4	(AATA)	20	820	839	ATATATGGGGGAGAGGGACG
scaffold471287_15.	1	p4	(ATTT)5	20	428	447	TCATTACACCCGGAAATGGT
scaffold475041_13.	1	p4	(AAAT)	20	106	125	TACATGGCTGGCGTAGTTTG
scaffold475749_11.	1	p4	(ATTA)5	20	237	256	GGATTGGGAGCACAAACCTA
scaffold476383_11.	1	p4	(CGAT)	20	312	331	ATCCCAATGAAGATCGAACG
scaffold476605_14.	1	p4	(ATTT)5	20	61	80	ACTTGGGCCCGATCTATTTT
scaffold479255_12.	1	p4	(TTAA)	24	2004	2027	GGCATAAGAAAGGATGAATGTAA
scaffold492229_16.	1	p4	(CCGC)	24	745	768	TGGTATGGTGTGGAGAACCA
scaffold495441_16.	1	p4	(CCTT)5	20	427	446	TCGCTAACAACCAAACACCA
scaffold501321_16.	1	p4	(ACAT)	20	2245	2264	AAATAAAACCAAAACCGGGG
scaffold505269_13.	1	p4	(AAAT)	20	222	241	CAGGTTCAAATCCCACCAAC
scaffold512811_10.	1	p4	(AATA)	20	737	756	GCCCGATATTTATCAAGGCA
scaffold516141_15.	1	p4	(CCTC)	20	742	761	ACCCTAAGCAGAGGCTCACA
scaffold523703_12.	1	p4	(AATA)	24	2122	2145	CACATGTCCCAAGTGATTTCAA
scaffold523978_14.	1	p4	(TAAT)5	20	319	338	GCAACAAATGAATTGGGCTT
scaffold529630_12.	1	p4	(ATAG)	24	545	568	TTTGGGAGGGAAAACGACTA
scaffold530555_14.	1	p4	(ATAA)	20	2003	2022	TTGGGAAGAACAATGAAGGG

scaffold530624_13.	1	p4	(AAAG)	20	258	277	GGCTTGTCGTGGTTCAACTT
scaffold532563_13.	1	p4	(TCCA)	20	64	83	TTTGCCTATTTAAAGCCCCC
scaffold534298_14.	1	p4	(TCGA)	20	954	973	GGACGAAATTGATCGAAGGA
scaffold535680_16.	1	p4	(CATT)5	20	2589	2608	GCAAGGGTGGAGGAATGATA
scaffold536005_15.	1	p4	(AAAT)	24	230	253	TGCAGAGATTTCAGCCATTG
scaffold536011_16.	1	p4	(CTGA)	20	100	119	AAGAAAAGGCGTGAATGTGG
scaffold537975_15.	1	p4	(AAAT)	24	2736	2759	TTAGGAAAGCAGGCAACCTT
scaffold539125_13.	1	p4	(TTAT)6	24	654	677	CACTAGCACCTCATGGCTCA
scaffold552987_14.	1	p4	(TATT)5	20	1778	1797	GCCATTCACCATCTCTCGTT
scaffold554669_13.	1	p4	(ATTT)5	20	442	461	ATTTGGGGGAAACCATTAGG
scaffold555082_15.	1	p4	(AAAT)	24	1202	1225	CAAATAATTGCCGGACCAAA
scaffold559721_10.	1	p4	(TCAA)	20	242	261	CCCCCATGAAAAGTCAAAAA
scaffold559844_15.	1	p4	(TAAT)5	20	216	235	CAAGTCAAATACCCGTGTCCA
scaffold567931_15.	1	p4	(CACT)	20	289	308	ATAGCTCACCACCGACCAAC
scaffold569595_12.	1	p4	(AAAT)	20	349	368	CGTGTCATGTCGACTCGTG
scaffold571451_14.	1	p4	(AATA)	24	720	743	GTCCACCTTTCTCGCAGATG
scaffold574092_10.	1	p4	(CAAG)	20	109	128	GACGCAGGTACGGATATTTGA
scaffold580301_11.	1	p4	(GAGG)	20	318	337	TCTTTTGTTTCGGAAATCGG
scaffold588183_17.	1	p4	(AGTT)5	20	519	538	CCCTCGGATCTCATCAGAAA
scaffold588818_15.	1	p4	(AGTT)5	20	2823	2842	TGTCCAAGATGGGATTGGTT
scaffold590508_13.	1	p4	(TAAA)	20	1622	1641	GCATTTTCGGAATTAAAGCG
scaffold591015_16.	1	p4	(AATT)5	20	6907	6926	CAGATGAGGAGCACCAGTCA
scaffold591306_12.	1	p4	(GAGG)	20	501	520	TCCATTATCTGGCCCTTTTG
scaffold592220_10.	1	p4	(TACA)	20	275	294	AAAAAGCCAGGGCCTACCTA
scaffold597113_16.	1	p4	(ATAG)	20	558	577	GAGTTTCCTTGGCTGCACAT
scaffold597874_16.	1	p4	(TATT)5	20	1148	1167	AGCTAGTAGGGCAAAGTTGATTAG
scaffold598154_14.	1	p4	(ATTT)5	20	839	858	AAATTGATTGGAGCATTGCC
scaffold600096_16.	1	p4	(TTTA)5	20	1002	1021	TGCAATTCCACCAACTTTGA
scaffold600130_20.	1	p4	(TGTA)	20	298	317	CCGGAATCTGAGAGAGATCG
scaffold608297_15.	1	p4	(ATTT)5	20	1844	1863	CAAGCAATGGGGAATGAAAT
scaffold609679_10.	1	p4	(TTGG)	20	44	63	TTGTCCCTAAACCCCCTCTT
scaffold609955_12.	1	p4	(GCCT)	20	380	399	ACACATTTGGCTGGAAGGAC
scaffold618292_14.	1	p4	(TTAA)5	20	1634	1653	GGGAAAAGGACAATTCCTCG
scaffold621922_10.	1	p4	(TTGA)	20	43	62	GAAGCATTTCACATGTAGAGTATATG
scaffold627019_14.	1	p4	(CTTC)5	20	381	400	GCGAGGGTTTTCTTGGTACA
scaffold627354_16.	1	p4	(GGGA)	20	105	124	TAGCACTTGGGATGAAGCGT
scaffold630379_17.	1	p4	(AATA)	20	613	632	GCAATTTCATTTAACAATCACGA
scaffold633212_11.	1	p4	(TTTA)5	20	423	442	CTCTCCATGGACGTAGGTGT
scaffold637193_14.	1	p4	(TATT)6	24	279	302	ACGGCAAATTAAAATGCGAC
scaffold637968_12.	1	p4	(TATT)5	20	112	131	TGGGTTTGGTCCATCTTCAT
scaffold640410_12.	1	p4	(GGTT)	20	142	161	TGTTTCTGCAGGTTGCAAAG
scaffold642968_11.	1	p4	(TATT)5	20	493	512	GAAATATCCCCTGGAGCCAT
scaffold644448_16.	1	p4	(ATTA)5	20	1395	1414	TGAGTCGGACTTGCATTTGA
scaffold647194_11.	1	p4	(AATA)	20	685	704	CAATTCCTAAACCAGCCCAA
scaffold647811_14.	1	p4	(TATT)5	20	1516	1535	TCAATGTGCCATGATTTAGCA
scaffold653587_13.	1	p4	(AATA)	20	770	789	GTCAATCCGCACTTGGATTT
scaffold655002_17.	1	p4	(ACCT)	20	79	98	ACCCATTCCCAAGAGATGCT
scaffold655146_14.	1	p4	(GAAA)	20	698	717	TAATTTGTTGAGGGGAGGCA
scaffold655622_16.	1	p4	(TTTA)5	20	339	358	TCCTGTGCCAAGTTGAATAAGA
scaffold656850_18.	1	p4	(AAAT)	20	163	182	GTGGTATACCCAAAGCGCAC
scaffold657451_12.	1	p4	(TATT)5	20	1012	1031	CAACTCATGGTTGTCGGTTG
scaffold658766_19.	1	p4	(ACAA)	20	1414	1433	AAGAGCGTCCAAATCTCCAA
scaffold659505_13.	1	p4	(AATA)	20	505	524	TACATGGCAACCTCGTCGTA
scaffold659643_17.	1	p4	(AAAT)	24	1425	1448	TCTGTTTATAGTCCCCCGGA
scaffold661552_12.	1	p4	(TTTA)5	20	202	221	GAAGTTTTGGGGATCCGAC
scaffold661558_16.	1	p4	(AATA)	24	50	73	TGAAGAAATCAAATCCCACAAA
scaffold662814_16.	1	p4	(TTAA)5	20	1866	1885	CCTGATTAGCCACAAGGGAA
scaffold663928_16.	1	p4	(ACAT)	20	383	402	TGTGCTCGTACACTCGACAA

scaffold666666_15.	1	p4	(TTTC)5	20	2541	2560	TTCTCATCATCATCAGCTCCA
scaffold667242_17.	1	p4	(CAAA)	20	1398	1417	GCACAAGAGGAGGCAACTTC
scaffold670842_10.	1	p4	(TTCT)6	24	925	948	GTGAAGGAATCTCTGGCTCG
scaffold672696_17.	1	p4	(AAAT)	20	1141	1160	GCAGGCCATATGCTAGTGGT
scaffold675764_14.	1	p4	(ATTT)5	20	50	69	GAACGAGTTCGTTGACTAATTAAAA
scaffold676142_11.	1	p4	(AAAT)	24	47	70	CAGAGCGCACTCGAAGAGTA
scaffold677282_12.	1	p4	(TTAT)5	20	766	785	ACAATCCTGTAATTCGCGTC
scaffold677401_21.	1	p4	(AAAT)	20	227	246	TTTTGCACCCGAATGGTTAT
scaffold677644_16.	1	p4	(ATTT)5	20	376	395	TGGAATTTGTCCACCATAACA
scaffold677954_12.	1	p4	(TTTA)5	20	629	648	TGAGATATTTCCCGCTGTCC
scaffold678923_14.	1	p4	(CATG)	20	1259	1278	GCAATGCATATTTAGGAAGTGG
scaffold681418_11.	1	p4	(TAAA)	20	563	582	GCGAAACGAAATTTGGGAA
scaffold683701_14.	1	p4	(AATA)	20	749	768	AAGTGAGTTAAGTTTTGACCCAA
scaffold684812_15.	1	p4	(TTTA)5	20	296	315	GTCATTTCTCGTTTCGCGTT
scaffold687881_10.	1	p4	(AATA)	20	759	778	CCATTCATCATGATTCCTTCC
scaffold688114_14.	1	p4	(TTAA)	20	854	873	TGGTGTCCTGTGAAAAACCA
scaffold688827_14.	1	p4	(AATA)	20	597	616	ATGATGGCGTCATGTTTTCA
scaffold691984_12.	1	p4	(AAAT)	24	96	119	GCAAATTAAAATGTGCCACG
scaffold694377_14.	1	p4	(TTAT)5	20	261	280	ACTCGAACGAACACCCAATC
scaffold695096_15.	1	p4	(ATTA)5	20	694	713	CACCCCGTATGGAAATTCAG
scaffold695443_18.	1	p4	(AAAT)	20	165	184	CCAATTTTTCAATCACCGGA
scaffold695906_14.	1	p4	(GGCA)	20	261	280	GCCACGGATAAGTAACACCG
scaffold697713_15.	1	p4	(ATCC)	24	1945	1968	AAGCTGACTCGCACATTCCT
scaffold698805_15.	1	p4	(AAAC)	20	333	352	AACAAACGAGGGCAAGTGTC
scaffold699053_12.	1	p4	(CATA)	20	1330	1349	ACGCTCAAGCCATTCAAGTC
scaffold700333_14.	1	p4	(ATTT)6	24	43	66	TGACGTACGATCGAGTCCAG
scaffold700635_12.	1	p4	(GGGT)	20	25	44	TGGGAATTTAGGAATCGAGAGA
scaffold701183_13.	1	p4	(AAAG)	20	278	297	TGGAAAGCCCTTTTTCTTCA
scaffold704554_16.	1	p4	(AAAT)	20	1745	1764	TATTTGTTGGTGGGTCGGTT
scaffold705454_17.	1	p4	(AAAT)	20	531	550	TTGATGGGAGGCAACTCATT
scaffold707915_12.	1	p4	(GCAG)	20	539	558	AAGCACGTCAGCACAGACAC
scaffold708416_16.	1	p4	(TCTT)5	20	708	727	AACTGCCCCCTTTCAATTCT
scaffold708632_12.	1	p4	(TACA)	20	175	194	GACTATAATGGCCAGCACCG
scaffold709642_15.	1	p4	(GCCT)	20	762	781	GCCTGATTAATTGTGTGGGG
scaffold710333_15.	1	p4	(ATTT)5	20	672	691	AAGGCTCAAGAACAATGCAAA
scaffold710652_15.	1	p4	(CTAG)	20	1429	1448	CAGGCGGAACTAGAGAGGAA
scaffold711218_12.	1	p4	(AATA)	20	264	283	TGGTGGATTTTTATTTATGCAA
scaffold714710_14.	1	p4	(CTCC)	20	1062	1081	GCCCATTCATCGATTTGTTT
scaffold715985_14.	1	p4	(AAAT)	20	2199	2218	AAACGGATCTCTTGCGTTTG
scaffold716555_15.	1	p4	(TCAT)5	20	2539	2558	CGTTCTTCCTCAGCTTCTGG
scaffold716659_13.	1	p4	(ATGT)5	20	1249	1268	GGAAAGATGAAATGCTGGGA
scaffold717898_15.	1	p4	(CTGC)	20	850	869	GGCAGCTCCCACATACATTT
scaffold717962_15.	1	p4	(AAAT)	24	460	483	AATCAAGAAGCCTCTGCACG
scaffold718240_13.	1	p4	(CATC)	20	2512	2531	TATCTGCCTGCATATGCCCT
scaffold721219_16.	1	p4	(AAAT)	20	45	64	GGTCGGCTACATGAACCAAA
scaffold722963_14.	1	p4	(ATTT)7	28	368	395	TCCGTCCACCTCTCAATCTC
scaffold723761_16.	1	p4	(TATT)5	20	315	334	CCTGGAAAAATGTGGGTGAA
scaffold724599_19.	1	p4	(AAAT)	20	656	675	AGTTATTGGCCGAAAATCCA
scaffold725295_15.	1	p4	(CCTC)	20	1893	1912	ATTGGCTTTCCCGAGAACTT
scaffold726004_15.	1	p4	(TTTC)5	20	869	888	AGTCTTGTGGCCCAGAGAAA
scaffold726425_17.	1	p4	(TATT)5	20	771	790	AGCTAGTAGGGCAAAGTTGATTAG
scaffold727253_14.	1	p4	(TTTA)5	20	241	260	TTGTTTGCCACTTGCTTCAC
scaffold729308_14.	1	p4	(ATAA)	20	4621	4640	AGTGGGGAGTTTAGTTCCCG
scaffold729539_11.	1	p4	(TTAA)5	20	279	298	GCTGCAGATGGACTCACAAA
scaffold730205_13.	1	p4	(TAAA)	20	374	393	TTGTGTTATTTCATATCTTTGTGCTG
scaffold730642_15.	1	p4	(TTAA)5	20	849	868	GACTTCGTGGGCTTGGACT
scaffold731835_14.	1	p4	(AAAT)	20	222	241	AAGTTTCTTTGGACACCCC
scaffold732041_16.	1	p4	(TATT)5	20	93	112	CGTGTGCTGGGCTATTTTCT

scaffold732762_14.	1	p4	(TTCT)	24	2925	2948	TGGGTTTGAACTGAAACTGC
scaffold733823_15.	1	p4	(GAGT)	20	320	339	AACTGCGAGATTCAAAACGG
scaffold733994_16.	1	p4	(CATT)	20	296	315	GTATGCAAAGGGAAAAGCGA
scaffold734089_16.	1	p4	(GATC)	20	3325	3344	AGATTGAAGAAAAAGGGGGC
scaffold734118_14.	1	p4	(AAAT)	20	1167	1186	AGACCAGACATCCACTTGCC
scaffold734464_13.	1	p4	(AAAT)	24	3231	3254	GGGCTTCATGTATGCTTGGT
scaffold734483_13.	1	p4	(TTCA)	24	557	580	CAAAAAGCCCATCAGTCCAT
scaffold734892_16.	1	p4	(TATG)	20	1168	1187	CAATTTCCAGATGGAACGGT
scaffold734928_13.	1	p4	(TCTT)	20	272	291	TGGTTTGACATGTGATGGGA
scaffold735282_14.	1	p4	(AGTT)	20	190	209	GCTGCACCATCCATATTCAA
scaffold736148_16.	1	p4	(ATTT)	24	1740	1763	CAAAACCCCCACCTAAGACA
scaffold736332_16.	1	p4	(GATT)	20	181	200	GGGATGTGTGTACCTGAGGC
scaffold736671_15.	1	p4	(GTAT)	20	283	302	TGGATTTTCTTCCCATGTCC
scaffold737466_14.	1	p4	(TTAT)	20	850	869	TCCAAAATCTGGTTGCTTGA
scaffold737840_14.	1	p4	(ATTT)	20	770	789	TGCTTCCATTTGTGAAGATATGA
scaffold738175_13.	1	p4	(CTTT)	20	801	820	GGGGGAGATTGAAAGGGATA
scaffold738509_14.	1	p4	(ATAA)	20	137	156	GCAGAATTCCGAATGACGAT
scaffold739168_17.	1	p4	(TCTA)	20	1497	1516	AGTCTCCGGGGACAAATTCT
scaffold739390_14.	1	p4	(TTTC)	20	110	129	CGTGCTTGAACAAAAGCAAA
scaffold739734_15.	1	p4	(TGCC)	20	5458	5477	GGCAGGAAATATGGCGAGTA
scaffold740449_15.	1	p4	(TTAT)	20	941	960	TCCACCATGGAACACAGAAA
scaffold740496_16.	1	p4	(ATAA)	20	255	274	TCTTCCACGAGAATTGGACC
scaffold740667_16.	1	p4	(GCAT)	20	2213	2232	CGAGCTGAAAAAGACCAAGG
scaffold740879_14.	1	p4	(AAAT)	28	1280	1307	TTGAACGAAAATTGATGGTCC
scaffold741336_13.	1	p4	(TATT)	20	485	504	GCACAAAATGAAGCAGACGA
scaffold741447_15.	1	p4	(GTAT)	24	644	667	CAATTATTGGCCGCAAAAGT
scaffold741558_14.	1	p4	(ATTT)	20	1876	1895	CGGATTGCCAAGCCTATTT
scaffold741876_15.	1	p4	(TTTC)	20	3089	3108	ATGGTGTCAAAGTTCACGCA
scaffold742457_15.	1	p4	(TTTA)	20	1592	1611	GAAGGCAACAAGAGATGGGA
scaffold742712_16.	1	p4	(TATT)	20	1039	1058	AATCATGCAACCACAACAATTA
scaffold742933_15.	1	p4	(GATT)	20	1198	1217	AAACAAACCTGCAAAATGCC
scaffold743044_16.	1	p4	(ATAA)	24	6543	6566	GCATCGACCTTGGACAAAAT
scaffold743097_16.	1	p4	(TTAT)	20	3265	3284	AATGGCTCAGTAAACAATGGG
scaffold78862_14.0	1	p5	(GCGG	25	1209	1233	ACAAACCTCGATTCCTGTGG
scaffold129996_14.	1	p5	(ATAA	25	2190	2214	TTGCATCTTCATGTGCAATTC
scaffold209057_14.	1	p5	(ATTTT	25	28	52	TGCTCCCTCCAATTAAGACG
scaffold281552_10.	1	p5	(CAGG	25	240	264	GCGCCCATAAAAATGAAATG
scaffold346597_11.	1	p5	(CTTTT	25	41	65	CCGACTTTTATGGCTGCTGT
scaffold404725_15.	1	p5	(AATA	25	527	551	TGCGAATTGAATAAGGCAAA
scaffold419361_15.	1	p5	(AATA	25	767	791	GGCAACAAACAGAATCCCAA
scaffold436901_11.	1	p5	(CCAA	25	228	252	GCCGGGTCTAGTGAATGAAA
scaffold437080_10.	1	p5	(ACAC	25	85	109	ATTTGGTTCGGTTCGGTTTT
scaffold450612_11.	1	p5	(TTAG	25	74	98	GAGTATTCATTGTACACAATAAGGAG
scaffold498369_13.	1	p5	(AATC	30	470	499	TTTGTCATGACTTCGGCTTG
scaffold502759_17.	1	p5	(TAAA	25	49	73	TCTAAAAACATGGGTAAAAATGATA
scaffold549972_10.	1	p5	(GATG	25	81	105	TTTGAGGAGCTTTGCGTTTT
scaffold567385_10.	1	p5	(ACAA	25	64	88	AAAGAGCAATGTGGCATCAA
scaffold574523_12.	1	p5	(CCTA	25	186	210	TCAAACCAGGTTCTTCAATGG
scaffold588661_14.	1	p5	(AGAT	25	2021	2045	CAATGACAACCAAACATGCC
scaffold634405_15.	1	p5	(TCGG	35	1527	1561	TTGGCGGAAGCCATAATATC
scaffold637883_16.	1	p5	(GGGT	25	22	46	AAACGGGGTTGGGTTGTG
scaffold652062_16.	1	p5	(ATAA	25	407	431	AACGATAACGGTAACGATAACAA
scaffold679227_16.	1	p5	(AAAT	30	45	74	GGAAGGAAAGCTAAAAAGGATT
scaffold708599_14.	1	p5	(AAAA	25	254	278	TGCAAAAGCACTCTTCCTGA
scaffold720454_13.	1	p5	(ACCT	25	1226	1250	TGGCATGCGAGTGCTATTAC
scaffold732293_13.	1	p5	(TTTTG	25	1908	1932	GCAGACCATAATGCTTTTGTGA
scaffold733459_14.	1	p5	(TATC	30	1080	1109	GAAGAAGATGTCAAGCCGGA
scaffold733662_13.	1	p5	(TGCT	25	144	168	CCAAGAGAGAGAAAGGGGCT

scaffold737970_18.	1	p5	(ATCTA	25	227	251	TTCTCTTGGAATGGGATTGG
scaffold740060_14.	1	p5	(CTTTT	25	123	147	GTTCGAACCGAACCATGAAC
scaffold741982_15.	1	p5	(TTTAT	30	1285	1314	TGCAACAATTTTTGGTATATATCTTTC
scaffold741994_15.	1	p5	(ATATT	25	227	251	TTATTGCACAGCTTCATGCC
scaffold97925_17.0	1	p6	(TTGGA	30	420	449	AAAGCTTTGTCCCACATAGGAA
scaffold156626_11.	1	p6	(CCAA	30	252	281	CACTGCTGCTGAGGAGTTTG
scaffold339935_15.	1	p6	(TCCA	30	903	932	AAACATACCAACTCACCACTCC
scaffold502162_13.	1	p6	(TAGTA	30	215	244	GAGAAACTGCAGCAAAAGGC
scaffold540849_12.	1	p6	(ACAAT	36	367	402	AATTTCGTATCGAGTTGGCG
scaffold554235_20.	1	p6	(ATCG	30	204	233	GGATTTGGATGGGTTTTTCA
scaffold576716_13.	1	p6	(GATTT	30	908	937	TTGGTCAGATCAAACCGAATC
scaffold652042_14.	1	p6	(TTCTG	30	72	101	AGACAATCCATCTCCATCTGGT
scaffold722193_18.	1	p6	(GATT	30	1163	1192	TGCATCTGCTTCTGGTTTTG
scaffold736788_12.	1	p6	(CAAA	30	540	569	TCCGATCGAATGGACCTTAC
scaffold740076_14.	1	p6	(TGTG	30	1359	1388	CGCCTCGATTGAATCTTCTC

Tm(C°)	size	REVERSE PRIMER1 (5'-3')	Tm(C°)	size	PRODUCT 1 size (bp)	start (bp)	end (bp)
57.426	23	TACCCCTACCCTTTGGGAAC	60.046	20	207	1433	1639
59.728	21	TCTCACGATCCCCTTACCAC	59.927	20	178	21	198
59.955	20	AAACACGACCATTTTCAGGC	59.978	20	277	82	358
59.745	20	TTCTCATACTAAAAGGTCTTTCTCA	59.662	27	165	23	187
60.533	23	ATTTCCCGGCTTCTTGCTAT	60.061	20	132	599	730
59.844	20	GGCATTATGCTTCTGCCATT	60.067	20	148	362	509
60.397	20	CTATGCTTGCATTCACCCAA	59.688	20	279	14936	15214
60.217	25	CGTGCCAAAAACCGACTAAT	59.996	20	181	19	199
59.989	20	ATTTTGGACCACCCCTTTTC	60.032	20	158	667	824
60.119	20	CAAAACAATTCCTTCTACCTTTTTG	59.519	25	238	11	248
60.025	20	GCGTCTACGGTGCAGAAAAT	60.278	20	221	89	309
59.577	20	TGCGTGAAAAACAGATGGTG	60.699	20	173	20	192
60.073	20	ACCGTGTCTCCAAAAGATGG	59.966	20	179	162	340
59.842	20	CAATCTCGAAAATGGATGGC	60.414	20	193	272	464
58.973	20	CGTGAGAAGCAACCAAATGA	59.84	20	240	253	492
59.241	21	TTTATCCTTACGCAATCCCAA	59.442	21	197	414	610
60.626	20	CCCACACCCTCATTCTCTCA	61.071	20	232	369	600
60.299	20	CAACACAAGAACTCACCTCCC	59.607	21	242	383	624
60.232	20	AATTTCCACCGGTGTTCTTG	59.83	20	231	6	236
59.903	20	TTGGGAGGGAGAGATTGTTG	60.042	20	261	16	276
59.52	20	TGGGCTAAGTGGAGTGAGTG	58.879	20	150	13	162
59.756	20	CCGATTGTTAAAATTCCGGTT	60.062	21	210	16	225
60.198	20	TGTTGACTTGCTTTCTTGGC	59.05	20	113	661	773
58.254	21	GCTTAATCTTTCAACGCCGA	60.343	20	212	30	241
60.144	20	CAAATATGCTTTCTTGATCATCATT	58.646	25	240	622	861
60.066	20	CACCATTGTGTCCAGGTCAG	59.997	20	160	200	359
59.679	20	AATGATCTCATGGTGGAGGG	59.737	20	154	3	156
60.938	20	TCCACTCACCTAAACCCGAC	59.966	20	229	8	236
59.429	20	CCCCTTTTTCAGACGTTTTG	59.581	20	273	14	286
60.227	20	CGCGAACTTTACAGGGCTAC	59.904	20	239	85	323
60.13	20	TGGGCTCGAATCTCTTGTTT	59.813	20	183	121	303
59.772	21	TCAGGGGCATATGTGTCAAA	59.924	20	195	13	207
59.368	22	CCAGCCAATTTTATCCCAAG	59.406	20	208	1	208
59.927	20	GACTCGTAATGATCCCCCAA	59.75	20	209	252	460
59.694	20	GCCGTTTTAACGGTTTTGG	60.342	19	265	214	478
60.043	20	TAAGTACAGGAGCCATCGGG	60.088	20	116	66	181
59.99	21	ATTGGGATTTTTGGTTTGGA	59.111	20	115	132	246
59.989	20	CAAAACCAACAGCCGAGATT	60.11	20	277	219	495
59.182	20	CCGATATGCTATGCTTTTGC	58.421	20	163	76	238
60.005	20	CCATGTTGTAATTAATGTAGGGAA	57.155	24	125	2152	2276
59.997	20	GGTCACGAGAACACGCATAC	59.169	20	231	2250	2480
57.03	27	TAAGCATCCACTCGCATCAC	59.83	20	177	24	200
60.117	20	TGATGGATTGCATTTGAGGA	60.009	20	241	198	438
57.667	22	CGGAAACAAGCAACTACAGC	58.58	20	146	29	174
59.859	20	ATAATGCTTGTCGGTTTCGC	60.103	20	210	38	247
60.02	20	TCCCAAATTTTGTCCAAAGC	59.916	20	190	1023	1212
60.049	20	ACCCCACTAAACCCAAACTT	57.435	20	153	35	187
57.932	23	GCCATTTTCCAAGAGCTTAAA	58.508	21	273	28	300
60.052	20	ACACGAACGGTTTAGGATCG	59.993	20	161	132	292
59.95	20	CTTGACTTCAAACCCCAACG	60.52	20	196	336	531
59.985	20	GAGTCGCTGCAACAAATGAA	59.995	20	228	30	257
60.301	24	TCAGTGGTTGTAACATTGGCA	60.019	21	241	381	621
58.731	21	CACCCGAAAACCGAATAAGA	59.931	20	101	782	882
59.389	20	AATGCAGGGTTTGCAAGAGT	59.74	20	150	16	165
59.938	20	TGAGCGGCTACGCTAATTCT	60.138	20	229	16	244

60.153	20	CTCAACGGTATGCTCGGATT	60.096	20	231	406	636
58.76	22	AACAATCTGGATCGTTTGATACC	59.259	23	165	0	164
59.969	20	TCCAAAAATCAAAGCTTGAAGA	58.987	22	220	65	284
58.57	20	CGTCAGCATTTACCCCAACT	59.993	20	271	951	1221
60.065	20	CATTTTACGAACGAACCACG	59.083	20	268	143	410
59.67	20	TGGTTGCACATGAATCATCC	60.339	20	172	1333	1504
59.839	20	AACAACAACCCCACCCATTA	59.948	20	198	3118	3315
61.606	20	ATCCCTCGTGTTCTTCCTCC	60.456	20	172	8	179
59.64	20	ACCGTCCATCTTAATGCAGC	60.103	20	239	874	1112
60.103	20	CATCAGAGCCGTGATTGAGA	59.942	20	143	0	142
60.978	20	GGTTGTATGAAACCGTTAGTTGC	59.826	23	273	426	698
61.018	20	TCACTCCGCCAACTAACAAA	59.317	20	177	169	345
59.623	20	GTTTGTGGTGTTCATGTGGC	59.862	20	241	1849	2089
58.188	23	CGCTTCTTTTGTATCCCAGC	59.845	20	101	0	100
59.288	23	AGCATAAGACGATGCGAGGT	59.866	20	161	12	172
59.847	20	GCCCCCTTCTGAATCTCCTA	60.537	20	272	2564	2835
59.697	21	ATTCAAGCATGGAATCGCTC	60.185	20	202	12	213
59.081	23	CCCATTCCCAAATCCCTTAT	59.846	20	158	925	1082
59.399	20	GTCTTGCACGATTCTCCACA	59.837	20	158	654	811
60.162	20	TTATTGCCTACCAACCAGCC	59.96	20	183	4195	4377
59.442	21	CACATAAATGGGTTATCAATGGA	59.851	24	210	302	511
59.127	20	TCCAACAATCTCCCACTTGA	59.059	20	129	158	286
60.154	20	TGCGTTTGATGTTCGTCTTC	59.847	20	220	59	278
60.377	20	TTCGCTGGTTCTGAGTTCCT	59.989	20	278	61	338
59.808	23	TCCCTCTCTCTCTCTCTCGG	58.792	20	165	25	189
59.587	21	GCTAATTGCGCAACAAACTG	59.514	20	224	315	538
59.322	20	CGGTTTTGGTTTGTTCCTACA	59.884	21	255	1160	1414
59.773	20	CCCACTCTGGTGACACATTG	59.997	20	190	33	222
59.856	20	GTCGGTACTGGGGCAGATAA	59.955	20	228	422	649
59.315	21	TCTTGTCATCACCTTTCCCC	59.903	20	277	481	757
60.317	20	CCATACCTAACCTGTACCGTCG	60.652	22	177	504	680
59.795	20	TCTGCTATCGAAACAACCCC	60.074	20	267	189	455
59.907	20	CCTTTTTCTTGCAAGGATTGA	59.325	21	250	266	515
59.333	20	CGACCTGAAGGAGGCTAGAG	59.183	20	167	1217	1383
60.812	20	ACCGGCAAGAAGAAAACTGA	59.853	20	267	1525	1791
60.025	20	TCATTAGCCATGTGTTCCCA	59.924	20	125	981	1105
60.117	20	CATGAGCCGCTAGATTGACA	59.972	20	251	50	300
59.048	25	TGCGTGCCATTTATAAAACA	57.749	20	112	1	112
60.135	20	CCGAAAGAAGCAGGATAGCA	60.481	20	269	1394	1662
60.008	20	TACGGGATCTCTTTGGTTCG	60.066	20	243	884	1126
59.721	20	AAACTCCTCTCCCAGCCACT	60.252	20	226	2	227
60.19	20	ATTCCTCCTCAACCAAACCC	60.169	20	144	225	368
60.361	20	ATGTGCAAAGCTGCTGAAGA	59.746	20	260	293	552
59.166	20	TGGACGTAAATACCCTTTTACCA	59.667	23	125	236	360
59.9	20	GGGAAACCCACAATCATCAC	60.034	20	220	31	250
58.711	23	ATGCGCGCTGCTTTAATAAT	59.873	20	142	6	147
59.813	20	TGGGCAGTAGAATACCTCCG	60.088	20	118	84	201
59.034	20	TTTTGTTTGGGACAAAAATGA	58.032	21	280	90	369
59.691	20	TTCGAGTGACACAAGGCAAG	60.025	20	242	18	259
59.767	22	ATTAGGCGACAACCAACTCG	60.132	20	175	714	888
59.975	20	AGAGACGGCAGAAGGTGAGA	60.135	20	212	1263	1474
58.5	20	AATGGCCGAGAGGGTTTTAC	60.32	20	103	10	112
60.296	20	TCTCAGCCAACACATTTCCA	60.24	20	100	5017	5116
60.119	20	TGAAGTTAGGAAATAAGGAGGTG	58.743	25	137	315	451
59.194	24	GGCCCAAATCAATACGAAAA	59.773	20	152	26	177
60.656	20	TTGGCCTTGCCATGTATATC	58.457	20	278	249	526
59.894	20	GGGAAGCTATGATGGGGAAT	60.117	20	249	2139	2387
59.948	20	GCTTTCATTTTTCAGCCCAA	60.188	20	198	510	707

59.843	20	CAACAGTTTGGCATCAGAGC	59.445	20	163	70	232
60.021	20	GCTGGGACGATCACGTATTT	59.962	20	236	2098	2333
60.288	20	TTTGGTTATGGACATACGGTCA	60.11	22	171	650	820
60.218	20	ATGCATCTCGGATCACATCA	60.039	20	193	8	200
60.066	20	CTCTCTCAATGTGGCAACGA	59.984	20	188	581	768
59.925	20	TTCCACCGTTGAAAGATCAAT	59.42	21	151	48	198
58.212	23	ATTTATGCTGACCGGAGTGG	59.955	20	225	621	845
59.138	21	ATACGTGTGCGAAACAACCC	60.817	20	124	315	438
59.086	20	ATTCCCTCCTCAACACCCTT	59.795	20	216	101	316
60.111	20	CCCCACTCCCTACATTTCAC	59.259	20	218	902	1119
58.866	20	AAGGAGATGACACCTAAACCCA	59.864	22	156	12	167
59.883	21	TGGCTGTCATTATTTCTCATTTC	58.262	23	150	368	517
59.434	20	GGAAATAATAAACACAAACACCG	59.233	24	253	882	1134
59.564	20	TCCTTGAACCATTCCATCATT	59.234	21	116	149	264
59.929	20	GAGGGCCAAAATCTTTAGTGG	59.952	21	207	69	275
60.239	20	TCTACGTGGCATGTGGACTC	59.707	20	216	4	219
59.333	22	TTGAATTGAATTGGAGCAAAA	58.265	21	233	20	252
59.853	20	TATAACCGTCGGCTTGCTTC	60.23	20	254	17	270
60.074	20	TCATATCCACGAGAATGGCA	60.033	20	195	1264	1458
59.95	20	TGGTGGAGGTATGGTGTGAA	59.806	20	119	23	141
59.82	20	CCCAAGACCCCAATTTGATT	60.91	20	267	57	323
59.761	20	CATCGACACCACTCATCGTC	60.121	20	240	9	248
60.18	20	TGCTGCAGTCTGTCATGGAT	60.436	20	243	242	484
60.067	20	CGTTGCATGGTGTATTGGAC	59.847	20	200	29	228
60.124	20	GATGTTGGGTCTGCAGAGGT	60.12	20	237	566	802
61.023	20	TTCATCTCCCTAATCGACCG	60.029	20	269	411	679
59.706	20	TTAGCTTCACACCAGCAACG	60.05	20	276	18	293
60.037	20	TTGCCTAAAAAGTTGCTCCC	59.338	20	257	978	1234
59.93	22	TTTACCGACGTCTCACCATCT	59.607	21	155	18	172
59.17	20	GAAGGTGTCTTCAATGGAGGTT	59.484	22	151	163	313
59.244	20	TGTGAGCCATAACTCGACCA	60.263	20	251	6	256
59.831	20	AAAAATTTATCAGATTTACGAGCA	57.706	25	133	312	444
59.257	20	CTTAGCCCCCAAGTTTTCAA	59.198	20	280	303	582
60.162	20	AAAGGCGACAAAACCATCAC	59.978	20	195	572	766
60.129	20	GACAGCCTTTTTGTTTTGCC	59.73	20	171	8	178
59.801	20	CAGGATGTGGTCATCCTCACT	59.977	21	275	1875	2149
59.951	20	GTATGGGGGAGCTGAACAAA	59.933	20	231	1248	1478
59.867	20	GGACCGTTTTAACGGATTTG	59.315	20	271	166	436
60.492	20	GGATCAGTAAAATAATAGGCAGA	59.934	26	244	537	780
60.132	20	ATCCGTGCCCTATCAGGAAT	60.682	20	234	526	759
60.413	20	CCACATCCTCAGCTCAGACA	59.98	20	158	212	369
60.088	20	CGATCCTCCTCCTTCACATT	59.09	20	244	1542	1785
59.026	23	AAGGACTCAAGCCCCTCAAT	60.074	20	156	20	175
59.13	21	CAGACAGCAGAGGTGTGCAT	60.055	20	203	96	298
59.997	20	TGAAACGGAACAAGATTTGC	58.747	20	135	15	149
60.175	20	ACCCAGATTTGTTCCTACGC	59.056	20	214	796	1009
59.993	20	CGTGTCAACTGTGACGAGAAA	59.93	21	214	1837	2050
59.911	20	GAAACCCTAACCTGATGCCA	59.933	20	252	447	698
59.72	22	GCTATGCATCAACGCACAAT	59.724	20	253	409	661
60.301	20	TGCCTACTCCACCAACATGA	60.112	20	230	938	1167
59.988	20	ATGGCTAACCATCAATTGCC	59.791	20	268	501	768
59.676	20	TATTGTTGCGAAGGGCCTAA	60.58	20	249	221	469
60.257	20	CTACTCCAAGTCCGACCCAA	60.103	20	192	1185	1376
59.259	20	CACAATATCAAGAACCCCCAA	59.671	21	266	20	285
60.051	20	TTGCATCATCCAGGCATTTA	60.035	20	157	2174	2330
60.006	20	ATTTCAGCACCCCCAACA	59.893	18	130	1002	1131
59.505	20	TAGCCCACTAATCCCAAACC	58.903	20	113	17	129
59.859	21	GAACCTTCCATCTTCCACCA	59.903	20	156	2193	2348

60.001	20	ACCCCCAATTCTTGATAGCC	60.152	20	101	270	370
58.969	21	GAGCTCCACATCAACACCAA	59.682	20	169	12	180
59.981	20	TGCGTTTTGATGATATATAGGTGT	60.054	26	214	561	774
60.144	21	GGCCGTATTAGCAGCGTAAA	60.246	20	279	480	758
59.799	20	AGCCACGTGTGTTCATTGAG	59.751	20	241	515	755
59.761	20	ATCTGCCATAGCACCAAACC	59.962	20	269	362	630
60.047	20	CCTCGAAGTCGAAACCTGAG	59.982	20	192	604	795
59.483	21	TGAAAGCCTACCTTGCTTCC	59.452	20	246	3	248
59.152	20	CTCGGTTGAGCTCGGATAAG	59.971	20	161	81	241
59.379	23	CCTGACTTCGCTGTGGGTAT	60.134	20	169	2287	2455
59.865	23	AACCCACTCCTATTTCCTCTCA	59.101	22	145	175	319
59.933	20	TCAATGCTCTTTTCAACCCTTT	60.109	22	164	19	182
59.989	20	GGTGGTATGGTGTGGAGGAC	60.096	20	185	61	245
59.939	20	GGCATCAGAGCCAAGTTAGG	59.836	20	192	8	199
59.726	20	GGCACGATTCAAAAGTCACA	59.697	20	274	122	395
59.975	20	TGACAAAGGGTGTGTTGGAA	59.976	20	153	75	227
60.488	20	AACGAGGGGAGTGACACTTG	60.151	20	274	11	284
59.657	20	GTTGGCTTGTGAGCGTGTAG	59.515	20	155	52	206
60.047	19	CCATTGAGACTCGAACCCAT	59.927	20	183	75	257
59.272	20	GCCTCTCACATGCAACAAAA	59.847	20	253	308	560
58.774	26	CACGCAATCCACATCAAGTC	60.12	20	247	76	322
59.962	20	GAGAATGTTCGAGCGTGTGA	59.992	20	235	369	603
60.095	23	TACGACTCTTTCAAGGGGGA	59.665	20	233	1964	2196
59.815	21	GGGATGATGTTGAATTAGTGGG	60.431	22	280	20	299
59.23	20	ATATGTGGGATTCTGCCTGC	59.923	20	253	1421	1673
59.944	23	TCAAAACAAATACTAACATGCAC	57.428	24	192	1073	1264
59.576	20	TTGAGAGGATTTGAGTTGGCT	58.923	21	251	157	407
60.674	20	GCGACATGACACAATCAACC	59.975	20	165	430	594
59.926	20	TGATTTCCTAGATACGGGGC	58.998	20	131	46	176
60.08	19	GCGAGAACTTAGTCAACGGG	59.875	20	184	15	198
60.349	20	AGAAGACACTTGGGCCTGAA	59.844	20	203	222	424
60.903	20	CTCCTCTCTGCTGAGCCAGT	59.883	20	192	265	456
60.16	20	GCCTAGCCTATTTGAACCCA	59.182	20	163	233	395
60.052	20	TTTTTAAGGTGGGGAGAATGT	57.596	21	248	1093	1340
60.833	20	CAACCCAAGTTTACATGTGACG	60.318	22	280	47	326
58.144	25	GGGGCTGTATAATGCGAAAA	59.928	20	196	165	360
58.629	22	ACCATCCCGTTTCAAACTCA	60.353	20	178	7	184
60.262	20	TGAAATCCTTGAACCATTCCAT	60.542	22	200	15	214
59.056	20	AACAACCCTCCCCTCATTTC	60.169	20	121	92	212
59.89	20	GGACGGTTAATGATTGTCCC	59.105	20	264	909	1172
60.188	20	TATTCCGCCATAGAACCAGG	59.916	20	219	547	765
60.22	20	CCGAAAGCTGCAAGTCCTAC	60.015	20	176	256	431
59.369	20	AACCCTCCAATTCCAAGAGG	60.298	20	207	356	562
60.692	20	TCTTCGACGGAGGAGAATGT	59.803	20	194	1128	1321
60.21	20	TGGGCTACCAAACACAGCTT	60.689	20	189	765	953
60.031	20	TGGTTCAACCTAGCATTCCC	59.933	20	178	68	245
57.16	27	GAGAGGTTAAGGGGGCAGAC	60.074	20	258	561	818
60.018	21	TCCACCTAGTCTTTCAGCAGC	59.63	21	102	19	120
60.323	22	GAATGAAGAATGGTTTGTCCG	59.42	21	254	690	943
59.624	21	TTCCCTTTTCGTACGATTGC	60.074	20	234	1843	2076
59.756	20	TCAAACACCAATCGCTCAAA	60.234	20	131	3643	3773
59.778	20	CGGTTAAGATTCAGCAAGCG	60.895	20	221	73	293
59.988	20	TATACGCACTCACACACGCA	59.926	20	211	2608	2818
58.824	20	TCATTCACCATATCCACCCC	60.404	20	280	4	283
58.978	20	ATGGTTCCGATGAGATCCTG	59.886	20	212	10	221
59.894	20	GATAAAAATGGCACACGGCT	59.967	20	261	212	472
59.5	21	GAAATCCCACTGCCAACTTT	59.031	20	279	80	358
60.624	20	GGGAATGAAATGCACATTGA	59.33	20	272	438	709

59.685	20	TGTCCCGTTCTCTCTCTGCT	60.135	20	276	3	278
59.337	20	TGCCGGTCTTCTTCTGACTT	59.989	20	253	16	268
60.467	21	TGAAGTTAGGAAATAAGGAGGTG	58.743	25	279	828	1106
60.018	22	GGTTGAGCTCGGATAAGCTG	59.978	20	197	0	196
59.496	20	GCTTTTATTGACTCAAGATCCGA	59.75	23	268	6816	7083
60.199	20	AACCCCACACATTCAACACA	59.701	20	165	167	331
60.23	20	TCTGTTGTGCTGCTGCTTCT	59.929	20	183	389	571
60.517	19	ACAATGGTCCAAGACCGAAG	59.966	20	137	25	161
59.612	20	ACCACCGAGCACCATGTATT	60.263	20	207	2	208
60.268	20	TGGTTGAATTTTGTCCCACA	59.792	20	186	1433	1618
59.634	21	TCTCACGATATCCTGCATCG	59.781	20	187	26	212
61.271	20	CTCAAACCATACGCTTGGC	59.287	19	113	114	226
57.739	20	AGTGGATAAACCCTGCGAAA	59.569	20	147	0	146
59.184	21	TTGTCCTCATCATCGAACCA	60.048	20	211	15	225
59.747	21	CAAATTCCCACCCCTGTCTA	59.784	20	214	23	236
59.717	22	AGGAGATCGAGAGGGAGAGG	59.906	20	226	552	777
59.668	20	ATAATGGGGTTTCAGTCCGA	59.244	20	278	136	413
59.966	20	TGAATTCGGATATGCGATGA	59.997	20	261	3492	3752
60.24	20	CTTTCTCCATCCCATCTCCA	60.003	20	272	576	847
59.995	20	GAAGCCCGAGTAAGGAAACC	60.074	20	113	1574	1686
59.873	20	AGTGCCAGATAGGCCGTTTA	59.73	20	244	172	415
60.184	20	AGCCGTTTTGAGACGTTGTT	59.78	20	262	45	306
59.784	20	AAACCATTTGGGGACGATTT	60.411	20	168	28	195
59.839	20	CCCCGGTTTCATTTATAGCA	59.789	20	200	0	199
60.363	20	GGAGAGTACGAGAGTGAGGAGG	59.505	22	136	174	309
60.088	20	CTACCGTCAAATCCTGGCTC	59.694	20	271	678	948
58.78	20	CCGGGTTTAAAGCAATCAAA	59.937	20	143	24	166
57.573	20	TCCCCGTTTTTACTCGTCTG	60.103	20	168	25	192
60.074	20	CCTCCAGAAATTGGGAGTGA	60.042	20	224	3393	3616
59.759	21	AATTGAAACCCTGCAGCTTG	60.249	20	240	282	521
60.243	20	CACGTGTGTAAGTTTTGTGCG	60.26	21	262	90	351
59.943	20	TCTCCACTCTCTCCCACGAT	59.792	20	230	2993	3222
59.764	20	TAACCACCTCTTGGGTCCAC	59.82	20	170	1474	1643
57.265	20	TAGGCATTATTGGATTCCCG	59.751	20	159	30	188
59.902	19	TAATCCCGCTGAAAATGAGG	60.031	20	198	2	199
59.923	20	CCTTTGTCTTCGAACCCGTA	60.103	20	221	96	316
60.245	23	ACCTCTCAGGGTTCACCGTA	59.574	20	266	55	320
60.035	22	CTTTAGGGCCCTTGATTTCC	59.903	20	170	196	365
60.051	20	TCGACCTTAACCACCTCGAC	60.111	20	138	23	160
60.568	21	CGTCGGTTCAACTGGAGAAT	60.111	20	223	267	489
59.556	20	TCGAAAATGTCCGACTCTCC	60.195	20	224	26	249
60.039	20	GGGCTTTGAGTAACTGAGGTG	58.851	21	274	315	588
59.162	22	ACATAACTCTCCGGCCAATG	59.955	20	196	45	240
60.836	20	TCGAAATGCAGTGGTTGAAG	59.84	20	245	4	248
59.903	20	CGGAATATCGAGAAGGTTATTATT	59.689	26	266	69	334
59.885	24	CAACGGTGATGACGTCGTAG	60.175	20	230	151	380
59.693	21	ATCTTCCATCCATCGAGCTG	60.181	20	112	497	608
59.882	20	AGGGTATGTCCGGTATGCAG	59.836	20	264	2953	3216
59.247	20	CCACCACCTAATTCTCTGGC	59.55	20	163	1146	1308
60.249	20	TCAAGACTAAAATTGGTAAAGAA	58.241	27	133	415	547
58.743	22	CGAGTGTGTACATGGGCATT	59.445	20	278	6002	6279
59.615	20	GCAACGGAATACCACTCGTT	60	20	241	97	337
58.327	23	CCATTTTCAATCCTGTGCCT	59.933	20	100	7	106
59.934	20	CAAGTTGATGCTAGTCCTCCG	59.883	21	225	3216	3440
59.814	26	CCGGATTCTACTGTCGGAAA	60.066	20	279	429	707
60.488	20	AGGCTTGATCTTTGCTTCCC	60.713	20	212	186	397
60.766	20	TGGGAATGAAAAAGCCATGT	60.309	20	237	731	967
59.993	20	GAACTCGCTTAGTTGCTCCG	60.154	20	276	453	728

59.801	20	CATTTTTCAATCCCAGCCAT	59.762	20	274	616	889
60.005	20	CCGGGTCAACAGATTGAACT	59.966	20	200	409	608
59.831	21	TTACGCTTTCAAGGAATGGG	60.067	20	171	19	189
59.454	26	CCCACTTTTGGGTTATTACCTG	59.641	22	275	80	354
59.907	20	TTGTGTGATCGAACTACGTTAAA	57.469	23	107	277	383
59.813	20	AGTTACAAGCCAACCCAACG	60.03	20	269	252	520
59.515	20	CGCACTGCTGTTGGAATTT	59.856	19	236	203	438
59.989	20	CTTTGCCCCCTTTCTCTCTT	59.821	20	206	375	580
59.797	20	TGAATCAAAGCATGTCATTTCAA	60.482	23	195	919	1113
57.764	22	TAGCCCCAATTTTTGTACCC	58.807	20	237	239	475
59.325	20	TCGGGTACGACAAAACAACA	60.004	20	280	658	937
57.193	27	GGCTTCCATTACGAACCTCA	60.074	20	129	23	151
59.799	22	ACCTCCTCCTCTTCTCTCCG	59.945	20	188	12	199
59.259	20	CATGCAACCATCAAAACATCA	60.373	21	189	1	189
60.014	20	TGCGACGGAATTTAAAAAGG	60.068	20	172	165	336
60.008	20	TGACGGTGTAAATATGGGTTTTC	59.997	23	159	62	220
57.125	21	GAGTTTGTTCCATCATTCGGA	59.925	21	273	1	273
60.307	20	TTTTTATCCCATGTTTGTGCAT	59.234	22	255	232	486
57.208	27	TGCACACAAGACTTTGCCAT	60.31	20	196	938	1133
58.315	21	CAAACAAGAAAAGGAGTTAGTGG	60.529	24	225	56	280
57.85	22	GGATGATCACCATTCGAACC	60.143	20	143	1	143
60.027	20	ATCGAGTTCCCTTCCGTTTT	59.94	20	280	611	890
57.483	25	ACTGACAAAATTTCGGGACG	59.971	20	249	25	273
59.96	20	GCTAATTGGGCAGCTTCTTG	59.982	20	167	22	188
59.499	22	GGACACCAGGGTGAGAATTG	60.363	20	278	280	557
59.299	25	AACATGATACGGCCGAAAAC	59.829	20	167	0	166
59.247	20	CGCCGGTATTCGTGTAAGTT	60.018	20	180	426	605
59.726	20	GTCGACTTTTGATCGGGAAA	60.051	20	196	20	215
60.335	20	AAAAACATGCCCCACTTCAC	59.836	20	182	49	230
60.173	20	CCATGGTCGTCCAAATCTCT	59.927	20	126	228	353
59.379	20	GCGTGTATCCGCCAAAAATA	60.831	20	244	56	299
59.372	24	TACCCCAACCCACTAACACC	59.569	20	104	1	104
60.434	25	GCATGACACATGGCGTAATC	59.963	20	152	18	169
59.656	20	AACTCTCTCCCTCCTCTGCC	59.952	20	223	14	236
59.534	20	TGAGGAACCAATTATCCCGA	60.266	20	265	18	282
60.031	20	GGCCCAATACCGTGACATAC	60.081	20	239	130	368
60.071	25	AAACATGATTAACAATGATGGAA	59.553	25	201	1821	2021
60.732	20	GGAATGAAAGGCTTAATTCTTGTG	60.344	24	272	410	681
58.175	22	TCAGATAGCCCTCTCAGACCA	59.958	21	230	24	253
61.069	20	TTCCATCTTTCAACCTCATCG	60.059	21	136	538	673
59.973	20	GGGAATTCGAAGTGGGATTT	60.131	20	242	1365	1606
59.351	20	CCGAAATGAAGAAATGAGTTCC	59.945	22	230	1412	1641
60.096	20	GAGGTTTTGACGGGATTTAGG	59.822	21	103	307	409
60.149	20	TTGATGATGGAATGAAAATGAAA	59.291	23	276	45	320
59.832	20	CAAGCATAAGGATTTTCGGA	57.845	20	268	3388	3655
60.088	19	CCAGAAGGTGCAGTGGTATG	59.161	20	213	3539	3751
59.808	20	TTCGAATCGACGGTGTATGA	60.073	20	236	5779	6014
59.83	20	TCACAAATAAGGAGGTGCCC	59.933	20	275	42	316
59.635	20	AATTGTGTGAATTCTAAATTTTCCT	57.862	26	272	318	589
59.942	20	ATTTTTCCATGTGGCATCGT	60.199	20	275	1995	2269
59.943	20	TGAGGGGCCTCACTAACAAG	60.246	20	196	810	1005
59.576	27	TGATGCTCCTCAGAAAGCAC	59.116	20	124	18	141
60.135	20	TCCCACAAAATCAACCCATT	60.029	20	246	147	392
60.073	20	CTGCTGTTCTTGGTGCAAAA	60.027	20	194	32	225
59.871	23	TTATTTGTTGCGTAGGGGCT	59.609	20	277	176	452
59.962	20	GGAGGTATATGCCACCTGGA	59.773	20	198	395	592
60.225	19	ACGTTTACGGTCCTTACCGA	59.494	20	238	375	612
60.029	20	CTTGCAACTGGTCGAAATCA	59.84	20	225	1898	2122

60.755	20	GCCTTCTTGCCTGTTTCTTG	59.993	20	252	305	556
60.019	20	GATTACATGATGCAGTGCGG	60.104	20	194	432	625
60.074	20	GGGGATGGTTATGCATGG	59.534	18	124	409	532
57.761	20	AATGGCCACAAATGTTTCCT	59.292	20	109	740	848
59.697	21	TACTGTTCTTCAGCTCGGGG	60.388	20	136	23	158
60.045	20	TTTATATCGCCGAAAATGCC	59.898	20	229	22	250
59.002	20	AATGCACCCACAAATGGAAT	60.059	20	182	695	876
59.989	20	TGTGGATTAATATAGTGGTTCAAC	57.953	26	242	136	377
57.373	24	TGAGGAGCGTTGATCTTGTG	59.984	20	133	20	152
59.923	20	CCGCCCCAATAGAGACAATA	59.916	20	254	1598	1851
60.257	20	CTCGGATTCGTCACCTTTGT	60.111	20	272	72	343
59.88	20	TTTGTGGTGACCTTGAGGAA	59.109	20	131	41	171
59.948	20	TGTTTGATTCATTCCATTTCCA	60.167	22	262	1136	1397
59.16	22	CACGACTTGCAATCCGTTTA	59.729	20	238	0	237
60.929	20	CTCCCAATCCGGTTCTATCA	59.887	20	274	3165	3438
60.264	20	ACATGATTACCAACCGGCAT	60.081	20	226	2742	2967
59.67	20	TAATGCCCCGTTTTTCTTGT	59.451	20	280	47	326
57.425	21	TGAGGAGCGTTGATCTTGTG	59.984	20	126	24	149
57.298	21	TTTGGAAACCCATGGGATATAG	59.909	22	259	843	1101
60.49	20	GACCTTAGCTTGCGACTTGC	60.162	20	192	2	193
59.988	20	GCATCAGTAAATCCTGGCCT	59.154	20	196	92	287
58.935	20	TGAAATCCATCTCCCCTGAG	60.003	20	273	487	759
58.488	25	CAGCGTAAGAAAATAATTGATGG	59.557	24	232	10	241
60.134	20	CTCTTTCCGCACCTTCACTT	59.473	20	280	94	373
59.787	20	GTGGTGTGGTGTGAAGTTGG	59.89	20	181	96	276
60.257	20	CGTTTGGATCCGATTTGGTA	60.692	20	220	578	797
60.431	20	GACCGGGTACAGAGCAAAAA	60.11	20	179	19	197
59.899	19	CGATCATTGTGCGAATCAGT	59.679	20	176	8	183
58.743	25	TCGATTGGTTTGTGAATTGTG	59.43	21	273	2821	3093
60.269	20	TCCCTTTCGGTCTCCTAACA	59.665	20	278	59	336
59.72	20	CTCGCACCACTCCTCTTTCT	59.598	20	270	0	269
60.192	20	TCGGTTTTACCGGTTTTGAC	59.839	20	181	13	193
59.016	25	CTGTTCGGTTCGGAGAGAAG	59.982	20	166	18	183
59.992	20	GGATGAAGTTGAATTGTTGGG	59.278	21	253	62	314
59.948	20	TTTGGTGTTTGCTGTTGGAG	59.734	20	120	464	583
60.155	20	CGTGGTTCGATCGTAATTGA	59.542	20	260	0	259
60.08	20	CCCAACCCTTGAGAACTTGA	60.081	20	278	222	499
60.69	20	ATTCTAAACGCCGGTGATGT	59.457	20	104	44	147
59.992	20	GCAGGTGGATGGTGAGAAAT	59.934	20	212	245	456
59.934	20	GTGTAAAGTTGGTGGGGGTG	60.126	20	241	2644	2884
59.903	20	CCGGTGAAGTTGGATTATCG	60.323	20	247	3008	3254
58.255	20	GCAAATTTGTGGAAAAACCG	60.335	20	257	245	501
59.964	20	GTCAACTTTGGCAATGGGAT	59.797	20	223	61	283
59.572	24	GCTAAACTTTAAAGGTGATGCCA	59.692	23	201	106	306
58.81	24	ATGGGAAGGGCATTTTCAG	59.879	19	166	7	172
59.997	20	TCCTTCAAGGCCAGATTGAG	60.331	20	169	150	318
59.528	20	TTTCTCTCCAACCCACAACTC	59.173	21	278	190	467
59.562	20	TTCATCCTCTTGGCCCATTA	60.405	20	204	201	404
57.88	21	TCAAAAACCGGTGAAAAACC	59.817	20	276	1501	1776
59.942	20	TGTTTCTCTCGTGGAAGTCCT	58.929	21	231	379	609
60.167	20	AAGATTTGATCATGGGCGTC	59.9	20	207	527	733
59.489	23	TGGACATCCTATGCAATGTG	57.907	20	274	1205	1478
59.815	21	CAGACAAATCTTCGTTATCCCA	59.087	22	153	1048	1200
59.579	20	ACGCTCGAACTCGATGATCT	59.981	20	200	609	808
59.803	20	TCAAATGGTAACCAATCACTAAG	59.328	24	273	984	1256
59.853	20	CACCTGAATCCACTCACCCT	59.962	20	190	1424	1613
59.708	20	CAGCATACCAAGGGCATTTT	59.96	20	251	1684	1934
59.933	20	CTGAGTCATCTACAGGTCAATGG	58.732	23	229	483	711

58.149	22	CCTTTCTGAATGTGGCTGCT	60.397	20	231	17	247
59.96	20	GGTAGTGGGGAGTGGGATTT	60.052	20	157	451	607
59.756	20	TCATGTACGTTGCTTATGGCA	60.148	21	234	25	258
59.038	21	CATATGGGAAGGGCATTTTC	59.23	20	211	1135	1345
60.69	20	GTTTGGATATCGAGATCGGG	59.344	20	188	293	480
59.07	23	CCAACCCAAACTCACACACTT	59.915	21	269	36	304
59.938	20	TCTTTACCGCCTCCATCTTG	60.206	20	202	29	230
58.075	20	CAGATCTGATGGCCCAGATT	60.034	20	133	0	132
59.717	20	ACTGACATTCACAGGCATTG	57.067	20	151	21	171
59.725	20	AAAAAGTTGATGCCAAAATTAGA	59.605	25	147	251	397
58.858	20	TTTCTGCATTCCGAATTTCC	60.016	20	132	14	145
59.272	20	CCGCTGATTTCCGTTTTCTA	60.202	20	199	475	673
59.415	20	CCATCACCAGCTTTGTTGTG	60.152	20	160	34	193
60.103	20	CATGCATGAACCTGCAATCT	59.679	20	267	834	1100
58.884	20	CATTATCGCCACAAATCTGC	59.14	20	277	858	1134
58.532	22	GAGGGTCAACCAGGAAGTTG	59.549	20	136	25	160
60.481	20	GCATGCATGTGAAGTTGCTT	59.878	20	278	74	351
59.833	20	AGGTCACGCTCGAGAAAGAG	59.745	20	236	51	286
60.103	20	AATTTGGCCCCGTCTAAAAA	60.645	20	237	88	324
59.569	20	TGTTGCTTGCCAAAATTTCA	60.229	20	185	99	283
60.221	20	TCTAAGAGATGATTGCACCTGAA	58.986	23	243	374	616
59.556	20	GGAATGTCCACTCGGTCAAA	60.903	20	280	1553	1832
59.436	20	GGCCAAGAAATATTGCTCCA	60.038	20	262	248	509
59.188	21	CCCCCATAACTCCTTTCCTG	60.674	20	142	548	689
59.805	20	TTGAATCAACCCTTATCGCC	59.901	20	192	479	670
59.95	20	CTGAAAGCCATGTTTCAGCA	59.988	20	105	606	710
59.833	20	CATCGACAAGCACAAGCAAT	59.871	20	256	1842	2097
59.966	20	TGAATGATGAGTTTTGTGGGTC	59.836	22	223	7	229
59.363	25	CACTTGGCAAAAGCAGCATA	60.014	20	260	8	267
60.855	20	GGGTATATGCCACAGGATCG	60.177	20	260	99	358
58.242	26	CGTTCGATTTGCCGTTTTAT	59.964	20	278	27	304
58.612	24	CCAGCCCAATAACTCAACCT	59.052	20	159	12	170
59.886	20	CTGATCAGCGTGTGTAAACGA	59.92	21	240	5	244
60.384	20	CCCTCGTATGCTGTGGTTTT	59.993	20	268	649	916
60.142	20	GGGCCGAGATTTGTTAGAGG	60.949	20	180	751	930
59.871	19	GCACGCTCTCCTCTCACTTT	59.751	20	186	549	734
59.679	20	CCCCCTTTTGAGAAGAAAGC	60.18	20	250	14	263
59.245	22	ACCCAGTACCACCACCATTG	60.545	20	119	3	121
60.049	20	GCATCAGAGCCACGGTTAG	59.41	19	260	56	315
57.062	27	GAGGACGATGAGGGTGAAGA	60.199	20	232	28	259
59.677	22	CATGGACCCCACATGTCATA	60.048	20	174	20	193
60.155	20	CAGATCCAACGGCCATAAGT	59.955	20	257	877	1133
59.481	20	AAAATCAAAGGCCCACAATG	59.801	20	176	35	210
60.255	20	CTCAGCATATGGGAGGGGTA	59.91	20	253	311	563
59.786	20	ACATGGTTGGTTGCTTGGTT	60.277	20	163	285	447
59.592	20	CCAAGCTTTGTGAATTTTTGAA	59.272	22	267	1271	1537
59.752	20	TCAACTCTATCATATAAATTTTTGG	57.188	26	224	9	232
59.923	20	ACCTATGGTGGTATGGCGTG	60.657	20	193	716	908
60.116	20	CGAACCCTCACACTTCTGGT	60.151	20	206	11	216
60.081	20	TCCCGCTGATTTCTTCTCTC	59.508	20	277	3538	3814
60.449	20	TTGGGTATCCAAAAACCAAAA	59.195	21	269	1540	1808
59.789	20	CAAAACATACGTTGCGCTCT	58.992	20	147	173	319
60.029	20	GCGTGAAATTATTAAGCCGC	59.722	20	244	838	1081
60.532	20	TGTTTGGCGTAAGAGACGTG	59.904	20	240	973	1212
59.803	20	AGTCACACCCTCTCCCACAC	60.006	20	269	1349	1617
57.131	27	TTGAAGTCTGCTGTGCTGCT	59.929	20	228	20	247
60.144	21	ACTGTCACACACACCACCGT	59.96	20	204	12	215
59.82	20	ACACCAAATCAAGAACCCCC	60.979	20	277	10	286

59.315	20	TCACCTCCGTCTAAATTGCC	60.074	20	241	35	275
59.933	20	CGTAAAATTCCGGTGCAAAT	59.832	20	137	821	957
57.771	26	TAGAGGACACTTGGACCTGAAA	58.837	22	100	6	105
57.176	20	ACATGCCCTAAAAACCGATG	59.823	20	223	610	832
59.092	26	AGCGAGACCTTCTATCACGC	59.603	20	191	7	197
59.885	24	TTAATGAACGGTCCGGTTTC	59.801	20	220	21	240
59.697	20	GGTACCCCCACACAAACAAC	59.989	20	209	209	417
60.074	20	TGACTCTTCTAGCTCCATTTGC	58.745	22	125	2837	2961
60.149	20	CAAGGGGTCAAAGAAGGTTG	59.563	20	236	66	301
60.003	20	TTGGATGTAGCCCCATCATT	60.155	20	184	545	728
59.61	20	AGCCACTGAACCAAATGACC	59.973	20	265	2110	2374
60.005	20	GATGACGATGACGATGATGG	59.882	20	187	2049	2235
59.34	20	GCGATCGTTCACACACAATC	60.128	20	106	394	499
59.953	20	TCCGTCATCTATTAGCACCATC	59.07	22	137	106	242
59.598	20	CACTACTAGGGTTTGGGAGGG	59.866	21	215	97	311
58.909	20	CAACTGAGTTCCCTACCCGA	60.103	20	257	201	457
59.953	20	TCAATTCTTCATCGCTGCTG	60.096	20	280	1645	1924
60.258	20	TACAAGTGCAAGAAGCGGTG	60.05	20	209	909	1117
60.69	20	TGCTGGTACCTTCGGAACTC	60.255	20	188	68	255
60.02	20	CAAGCGAAAATGATCGGATT	60.038	20	200	2127	2326
59.165	23	AAAAGTTCACTAAAACTGCCTTCT	57.086	24	198	95	292
59.907	20	TTGTGTGATCGAACCACGTT	60.008	20	108	24	131
59.95	20	AATCGCCATAGCAAGAGAGC	59.579	20	127	1031	1157
58.816	23	CCACCGAGCTTCTACACGTT	60.312	20	188	6	193
57.467	22	ATGTTGGCTCCGATTGAAAC	59.939	20	276	29	304
60.249	20	ATATGTTGCCCAAGTGGGAG	59.813	20	214	149	362
59.189	23	TTGGCCTGTCTGCTATCATTT	59.722	21	192	23	214
60.039	20	TTGAAGCCTTGTTCCTTGCT	59.993	20	209	167	375
59.844	20	TAAGGTGGTGACGATAGGGC	59.955	20	201	398	598
60.053	20	GACAGCTGTGATGAAGGCAA	59.992	20	184	2712	2895
59.586	20	AGAGGAGAGGAGGTTGGAGC	59.952	20	210	48	257
60.104	20	GAAGATTGTGGGGCGAGTAA	60.074	20	225	1719	1943
59.934	20	CTCATGGATCAGGAATCTGGA	60.019	21	262	442	703
60.11	20	TTTGGTAAATACAACATAATTGGT	58.757	26	245	278	522
59.783	20	ATTGCATTGCATGTGTGGAC	60.409	20	278	396	673
60.054	20	AAGGAGGTGTTATGAAGGGATT	58.028	22	148	1416	1563
59.679	20	CGCGACCACGAAGTACATAA	59.752	20	244	69	312
60.331	20	TGAGCAAAAGTAATAAGAGCAAC	58.341	24	206	226	431
60.713	21	TGACTCTGCGTTTGTTGGAC	59.88	20	195	263	457
58.792	22	AATCCCAAAATCTATGGGGC	59.984	20	183	20	202
58.874	20	GCAGCCACTATCCTTTCACC	59.7	20	198	678	875
59.756	22	CAATTTCAAGAACCCCCAAA	59.772	20	240	5	244
59.455	22	TCATTATTCCGTCGATCGCT	60.574	20	181	2	182
59.875	20	CCAAAATCCCAGAACGAAAA	59.91	20	194	115	308
57.719	22	ATCCAATATGTGGGGCAAAA	60.016	20	263	2	264
59.872	20	AGAAGACGCTCACACAGGCT	60.205	20	185	33	217
60.003	20	TCCATTTTCCTCACCCCATA	60.126	20	219	334	552
59.435	21	TGGTAGGTGGGTTTAGGTGG	59.705	20	130	20	149
59.483	22	TGGTCAATTCACAATCCGAA	59.9	20	265	71	335
60.008	20	TTTTGAATCTTTGTCCCCAA	58.039	20	144	364	507
60.285	20	TCACCTAAACCACTTTTGAAGAA	57.979	23	238	68	305
59.42	22	CGTGGTTCGATCGTAATTGA	59.542	20	100	1	100
59.577	20	GGTTCGAGTCTCAATGGGAA	60.05	20	277	793	1069
59.978	20	TCAATTGTCACACGTGATTGAG	59.615	22	209	1028	1236
59.888	20	TCTGGACACATCCTTGTTTATCA	59.485	23	209	1076	1284
58.079	23	TCATCTTTTGGGAATGGTTTG	59.787	21	239	220	458
58.527	26	ACCTCATGGGGAAATTTTAGC	59.324	21	100	1	100
60.166	20	CTCTGTTCCACGCACACCT	59.881	19	224	19	242

60.495	20	GGTGGAGCATGGGAAAAATA	59.762	20	134	967	1100
60.203	20	CTTTCCTCAACCGAGCTCAC	59.989	20	252	16	267
59.966	20	GAGAAAGCCACAAATCTTTCC	57.916	21	262	3612	3873
59.948	20	AAATCAAAAGGCCCACAATG	59.801	20	153	281	433
59.973	20	TAGGGATCGCTCCAGAAAAA	59.778	20	146	2094	2239
58.221	25	AAATGCGCAATTTTAAACCC	58.982	20	246	150	395
59.984	20	CTTCCACTCCCACCAACCTA	59.959	20	245	257	501
58.045	24	TCTCATTTACACCGCCTCAA	59.272	20	274	699	972
60.303	22	AGTTTTGACATGAAAATTGAATGA	57.739	24	244	480	723
60.076	26	TTCCTTCATTCCTAAATGATTAATT	58.94	26	277	668	944
59.405	20	GCAGTACTTGCCGAATCCAT	60.103	20	277	43	319
59.894	20	GCCCCAATTATTTTAGTCCCA	60.029	21	253	318	570
59.978	20	CAGATCGACCGATCCACTTT	60.073	20	217	83	299
60.032	20	AAAGTGGAATTTGCTTCCCA	59.546	20	238	196	433
59.76	21	GCACATGCAACCTCAGAGAA	59.992	20	236	124	359
59.857	23	CCTGGGACACATAAGCCTCA	61.055	20	257	495	751
59.82	20	TGAAATGAAATCTTGGCCGT	60.448	20	275	171	445
60.181	20	ACATGTGATGTGATCCCCAA	59.611	20	116	1138	1253
60.008	20	TCGCATCATCAACCTTCTGA	60.353	20	223	594	816
60.132	20	GCTAGCTCGGGAGAGAGGAT	60.081	20	271	223	493
60.343	20	GACTAGCACGTGACCGGATT	60.142	20	262	252	513
60.393	20	CCAACCCAGAATTCGTCCTA	59.926	20	211	980	1190
59.918	19	TGTAGTTGATGGACGTGATTGTT	59.415	23	113	4	116
59.926	20	CACATCGACGACGCTACCTA	59.888	20	186	228	413
59.834	20	AAGGCCATTTCATCTTCAGC	59.273	20	200	813	1012
58.909	24	GGAAATAAGGAGGTGTTATGAAG	59.323	24	186	1222	1407
60.164	20	TGGACAAAATGAGTGGAGAGAA	59.711	22	203	1055	1257
59.993	20	AGCTCGAGGCTCAAAACGTA	60.154	20	271	870	1140
60.237	20	ATGGGTGTGGGTGTTAGTGG	60.545	20	127	271	397
60.497	20	TTTGTCGGGTCATTGCTACA	60.111	20	184	827	1010
59.903	20	TAATGGTGATGCCAGGGTTT	60.192	20	158	1220	1377
60.173	20	GGGAATGAGGGATGGAATTT	59.959	20	161	2290	2450
60.201	21	CCCGACTCGAGATTACCAAA	60.066	20	152	100	251
60.096	20	GTTGGTTGATGAGGTGGCTT	59.973	20	218	611	828
59.282	20	GGAGACGACCTTGCTCACTC	59.993	20	197	132	328
60.025	20	CCATCTCCAATTCGTCACCT	59.927	20	186	328	513
59.767	20	ATGGACAGGTGGCGTTAATC	59.82	20	254	592	845
59.2	20	CGTATACCCTCAAACATCCGA	59.831	21	176	790	965
60.073	20	TGCATGGTTTGAGTTTTGTGA	60.142	21	161	16	176
60.119	20	ACGGTACCACCCCAATACAA	59.971	20	112	2273	2384
59.801	20	CCCCCATCAATCATGAAAAC	59.991	20	219	535	753
59.806	20	CTCCTCTCCTATTCGCTCCC	60.306	20	261	150	410
59.641	22	AATCACAGCATTCAAAGGGC	60.081	20	184	18	201
59.572	20	TTCTCCATTTGTCTCCCTGC	60.195	20	193	2251	2443
60.149	20	GAACCACCACACCAAATTCC	60.073	20	221	397	617
60.234	20	CCATGCCCCAGTAATCATCT	59.773	20	219	118	336
59.849	21	TAAATAAGTTGCCAACCGCC	59.964	20	116	5	120
60.049	20	GCCAAGGATGAGAATGAGGA	60.158	20	202	60	261
59.532	20	CACAAACCATCATTGCAACC	59.823	20	270	971	1240
59.415	24	TGGACTGAACTGCAATGCTC	59.992	20	202	990	1191
60.223	20	CAGAGTGATGCGTGAAGGAA	59.984	20	195	334	528
59.805	20	GGTTACCGAACCGAACTGAA	59.971	20	264	154	417
59.048	23	AGTGGGCTTTGGCACAAGTA	60.689	20	114	1	114
59.072	20	TTACATCTGAAAATTTGACGCA	58.355	22	260	157	416
59.967	20	GGGGTTATCACTGGATCACG	60.195	20	187	509	695
60.991	20	AACCATCTTCGGAGAGAGCA	59.95	20	115	249	363
59.953	20	TCCATGACAGGAACCAAACA	59.935	20	212	1297	1508
59.95	20	AAGCTCATCCATTGGTTTGG	59.933	20	258	233	490

59.189	22	TGGCAGAAAGATTTTAGATATAGA	59.31	26	133	214	346
60.173	21	TTTCGAAGATCAACGAACGA	59.395	20	123	223	345
60.439	20	AGACCGAAACCGTTCAAAAA	59.587	20	258	633	890
59.792	20	CCACCAAGTCAGCACCTTTT	60.149	20	243	1073	1315
60.159	20	CGGCAAGGAGAAAGAGGATA	59.406	20	271	82	352
60.038	20	AACATGTAACCTGTAATCTGTAAA	57.047	27	226	182	407
60.02	20	CGGAAAACGACACCAGAAAT	59.971	20	164	49	212
59.96	20	CGGCCTAAATATCCCTTTCC	59.767	20	262	763	1024
59.574	20	ACGGGAGCATGAAATGAAAC	59.939	20	204	554	757
59.985	22	CCAATTTCGATTTCCTCCAC	59.363	20	272	0	271
59.575	20	TCAGCGTGAAATGTGGGTAA	60.111	20	224	1230	1453
59.931	20	GCGGCCACGTATTCTCTTTA	60.23	20	176	579	754
59.971	20	CATACATTCACACGGGGGAG	61.176	20	136	2377	2512
59.84	20	TCATCGACCCCATCTCTTTC	60.011	20	137	389	525
59.975	20	GACTTGAGCACCAAGAATCCA	60.248	21	143	82	224
59.7	20	GATTATGCAAGCCCAGCCTA	60.196	20	159	414	572
57.381	21	TCAAAATAGGCATAACCGATCC	60.168	22	150	46	195
60.009	20	ATGCAATCTAGTTGACGGGC	60.103	20	205	17	221
60.038	20	TGAATCGATTAGGCTTATCTTGA	58.055	23	146	87	232
57.658	22	GAAGTTGGGGGTGGAATACA	59.647	20	271	393	663
59.955	20	CGATGACCTTGAGGTTCGTT	60.111	20	227	3393	3619
60.096	20	GATGTGATACCCGGAGTCGT	59.81	20	167	31	197
58.86	26	AGGACACGTTGGACCTGAAG	60.151	20	105	24	128
59.88	20	TGGTTGTATGTCATTTAGCGG	58.57	21	247	303	549
59.829	20	GGCTTTCACATTAAGCCCTG	59.708	20	113	6530	6642
60.903	20	CAATGGTGGTATGGTGTGGG	61.898	20	105	18	122
60.02	22	ACCAAATAGGGTAAGCCGTG	58.973	20	241	1178	1418
59.823	20	ATCGGGCATTTCGACTACAG	60.096	20	160	830	989
59.536	20	GACAGCCCAAGATTGAGAGG	59.803	20	274	9	282
60.068	21	TCCAAGGCAAATTGAACTCC	60.051	20	258	229	486
60.24	20	AGCGACAAAGTGTGATGACG	59.905	20	169	120	288
59.569	20	GAATTGGTGGAAAGATTTGAGAA	59.472	23	244	15	258
59.487	22	CTATTTTGTGGCGCTGGAAT	60.096	20	256	22	277
59.982	20	CCCACCAACCCAGATCATAG	60.187	20	279	2448	2726
59.971	20	TGTGGTGTGAGGGCTGTAAA	60.152	20	220	2000	2219
59.248	20	CAGCACGCGCACTACATAAT	59.925	20	273	145	417
59.79	20	CCACACCTCTTGGACCAAAT	59.82	20	279	790	1068
59.835	22	TCTCCCTTTCCTCTCTCGTG	59.525	20	169	442	610
59.317	20	AACTCAGTTGGGTTGTTGCC	60.012	20	265	1110	1374
60.123	20	CCCACCAGTAGTCTGCCACT	60.174	20	230	3447	3676
60.545	20	TGCCATGATCATTGATTGGT	59.738	20	270	873	1142
59.992	20	CCCAACCAACAAGAACCCTA	59.824	20	117	455	571
59.775	20	CCCAGTTGCTCACAATGACA	60.722	20	200	374	573
58.792	22	AATCCCAAAATCTATGGGGC	59.984	20	199	20	218
59.993	20	TGGTAGGGTGGTAAACCAGG	59.705	20	102	210	311
59.942	20	CAATTCTCTCAACCAACCCC	59.381	20	191	30	220
59.226	20	CATCATGTAGTAGCGGGCTG	59.322	20	146	42	187
60.469	20	TCGTCGTCGTCAAACAAGAC	59.88	20	184	30	213
60.016	20	TGGGTTTGGTGTTGAATCCT	60.21	20	275	104	378
59.187	24	TGGACCGTTGAAATACAGAAAA	59.492	22	152	24	175
59.31	20	CGAAGTCGAAGCCTAACTCG	60.147	20	271	28	298
59.823	20	ATTGCCACAACTCCACCTTC	59.973	20	145	1832	1976
59.716	20	AGCCCACCTGATATGCTTCA	60.624	20	182	24	205
59.556	20	ATTCGAACCAAAATGCGATG	60.837	20	206	493	698
59.964	20	TGACAAAATATGGAACCACAAGA	59.37	23	156	23	178
60.134	20	AGAGCAGCAACAGTGCAGAA	59.929	20	164	204	367
60.014	20	GCGCGCAATCACTCTCTT	60.257	18	117	865	981
59.71	21	ATGCGGTTCAAAGGTAGGAA	59.569	20	214	36	249

59.627	20	CATCCTCCTTTTCCCAATCA	59.864	20	275	24	298
60.123	21	GGTTGACACACTCGAACCAA	59.571	20	225	5	229
59.445	20	GGTCCGAATGCTGGTATGTT	59.82	20	159	3143	3301
60.122	23	GGGGATTTGATTGATGATCG	60.096	20	280	97	376
58.074	21	TTAGACTGCGGATCACCACA	60.263	20	242	256	497
60.022	20	TTTGTCCCCACAAATGTCCT	60.21	20	244	2376	2619
59.904	20	GAAGCAGAGCATTGATGGGT	60.226	20	267	169	435
60.169	20	GACGCCACATCATTCTCTCA	59.794	20	280	4100	4379
59.933	20	TGACATGTCCTTTCACTCCAA	59.124	21	226	3126	3351
59.319	23	ATTTAGGCCACACAGGATCG	59.955	20	100	59	158
59.997	20	TCATTAAACCCGAATCCGTC	59.762	20	186	504	689
59.995	20	GGCACAGCTCCACTTTCTTC	59.997	20	198	117	314
59.67	21	CAGCCTTATCTCTGGCCGT	60.368	19	278	321	598
60.475	20	CAGAAAGTGCTTGTTCAGCG	59.781	20	163	1163	1325
59.745	20	CTCTGCGACGTAATTCCCAT	60.096	20	266	90	355
59.986	20	GACCAACTCTACTGGTGAAGGC	60.175	22	197	439	635
59.997	20	ACGCGATTATGGAAAAATGC	59.935	20	236	269	504
57.083	20	CGTGTTGTTTTGCTTGTTTCA	59.801	21	130	20	149
60.089	20	GGGTTCAATGTACGCAACCT	59.859	20	272	236	507
57.552	24	AGGAAGGATTAGGCGAAGGA	60.166	20	224	13	236
59.912	20	TGGCATTTCAGCTTTTGTAGC	60.391	21	145	96	240
60.038	20	TTGGTTCACACAACCACTCC	59.415	20	177	72	248
59.284	20	CGCTTTCGCCTCTTTATTTG	59.979	20	148	3	150
59.955	20	GGCTCACTCTCTGGCTCATC	60.104	20	242	1451	1692
60.051	20	CTTGGAGCTGTTTTCTTGGC	59.993	20	158	2641	2798
59.845	20	TGAAATACAAAAAGGGTGCG	58.674	20	253	687	939
60.587	20	CGGAGCAACCACCGTATAAT	59.845	20	279	67	345
60.209	20	GGGATTTGCTGCTGTTGTTC	60.646	20	233	3	235
60.257	20	CACATGTCATGAATCGGTGT	57.712	20	227	44	270
59.321	23	TGCGTCACACGTAATTCAGA	58.863	20	278	776	1053
59.604	20	GGGCCGAGATTTGTTAGAGG	60.949	20	279	926	1204
60.074	20	CGGTACGGTAAGTGCGGTAT	59.904	20	134	595	728
58.241	20	TCACACCATATTTTTCCCCC	59.481	20	219	755	973
60.08	20	TGCGTGTCTAAATGTGCCTC	59.871	20	142	379	520
59.569	20	AGCGTTGGATTTTTCAATGG	59.938	20	159	21	179
59.948	21	TGATCTTTTCGCCATTAGAGAG	58.605	22	107	209	315
59.829	20	TCCCAGTCTAAAAGTCCATGC	59.184	21	204	172	375
60.365	20	TCTCTCCCGACACACACGTA	60.309	20	116	100	215
60.11	20	TCAAGTCGCTACTCACCATCA	59.455	21	115	887	1001
59.945	20	ACAATGGAACGAGATCCAGG	59.927	20	198	323	520
60.073	20	TTTTTCTTGCTTTTGCTGTGAA	60.034	22	230	27	256
59.069	21	AAACAGGGGTAGCTGGGAAT	59.827	20	187	15	201
57.862	23	CAAGCTCAGTCTCAATGGGG	60.791	20	132	233	364
60.184	20	CTCTAGGGTTCAATTGGGCA	60.066	20	101	3000	3100
59.934	20	TTGCGATAGTTAACAGGCAGAA	59.911	22	162	359	520
59.978	20	ACGCTGCCTCAAAAGCTAAA	60.152	20	232	689	920
57.978	23	TTTTGGTGTCTAATCCATTTGTG	58.909	23	135	46	180
58.886	20	CCCAAGGTACATTGCGTCAT	60.776	20	233	575	807
58.374	21	TGAGAAACCGTAACCCAAGC	60.11	20	239	10	248
59.892	21	GCTGCAGCAATAAAATTCCC	59.688	20	229	2705	2933
60.067	20	TCGCTCTGAACCAAAAACCT	59.853	20	189	279	467
59.895	20	TGCACTCATCAGAGTTATCGG	58.888	21	161	3162	3322
59.992	20	ATTCAAACACGAGTCGCAAA	59.322	20	244	313	556
59.903	20	CAGGAGGGTTCACACAACCT	60.002	20	126	229	354
60.55	20	TTGGGGCTTGTAATAGCTGG	60.089	20	270	7154	7423
60.246	20	CATCTTCAACCCGTCACCTT	59.966	20	175	318	492
59.699	20	ATTGATATGGCACAGCAGCA	60.251	20	279	224	502
59.955	20	ATGCCAACACAAAAACACCA	59.864	20	213	189	401

59.562	21	TTGATTACGAATCCTCGCCT	59.668	20	270	83	352
59.943	20	TTAGTGTGGCCGGTTTAATTG	59.876	21	172	91	262
60.096	20	CCGATATAAGCGCCATCCTA	60.04	20	190	292	481
59.717	20	CCACGTACATCTTGTGTCCA	57.946	20	193	1050	1242
60.112	20	GCCAGCTTCCTCTCAATCAG	60.096	20	242	2204	2445
59.997	20	TGCAATTTGTTTCTCTCCCA	59.247	20	195	1739	1933
60.032	20	TGTGGATATGTAGATAATTTTTGG	57.748	26	240	60	299
58.973	20	TGGTAAAGGGACGGCATTAG	59.953	20	129	770	898
59.665	24	TCCTTCTTCACTTTTGCTCACA	60.03	22	148	10	157
60.136	20	ATCCTTCAACTGCAACAGCC	60.263	20	195	1498	1692
60.051	20	GGCCCGAGCTAAAAACATTG	61.816	20	267	38	304
58.93	20	CCTCCCAACTTGTGTGTGTG	60.039	20	196	0	195
60.328	20	CCATGTCTCTGGACTGGGAT	59.92	20	247	3446	3692
59.677	21	TCTTTTATGTGCACAATGCG	58.354	20	170	359	528
57.223	20	CCCCAGAATGCAGTCAACTA	58.722	20	128	77	204
58.743	25	TCCTCCTCTTCCACTTCCAC	59.228	20	189	62	250
60.31	20	CCAGTAGATGCCCCTCCTAA	59.146	20	278	450	727
60.021	20	TCTCGCAGATCAACGTCAAC	59.992	20	276	6	281
59.797	20	TTAACTTCCTCCAGCTCCGA	59.948	20	128	103	230
60.762	20	TTCGCATAATTTTTGTGAGAGG	59.253	22	242	56	297
59.923	20	TCGTTGCTCTCCATATTCCC	60.036	20	131	324	454
59.939	20	GATTTGGAACTCCGGTGAGA	60.05	20	204	1443	1646
60.103	20	TGTGACTGCTCTGGTTGAGG	60.022	20	106	15	120
60.008	20	CGATTTTGGGTTTGTTTGCT	59.975	20	265	539	803
60.218	20	CCCTCTCTTTTGGCCTCTCT	59.95	20	122	1525	1646
60.04	21	CTGTATGGGCCTTCGTCCTA	60.088	20	269	2810	3078
60.096	20	CATGCGCCTAGATAACGACA	59.856	20	228	700	927
60.039	20	CGCAGATATGCGTTTCTCAT	58.897	20	166	20	185
59.505	20	ATATACCGGTGCAAACGAGC	59.988	20	210	1162	1371
60.143	20	TGGTTGTGGTCAATGGAGAA	59.935	20	196	432	627
59.679	20	TCAGCAGAGCAGCCATATCA	60.675	20	108	155	262
59.312	20	CCTCAAATTGTTGAAAAACCG	59.478	21	224	413	636
59.83	20	CCGTCCATCTCAAAAATGAA	58.546	20	214	898	1111
59.775	25	CAGCACCAGATTTGCACCTA	59.864	20	227	278	504
58.652	22	TGAATTTCAGTCATGGATTCTCTT	59.136	24	166	24	189
59.939	20	GCATACACACTCCGCATTTG	60.142	20	239	5	243
59.878	20	GGCCATTCAAATTTCAAATCA	59.765	21	235	307	541
61.278	20	GTGGACGCTCCAGATTGTTT	60.119	20	169	1	169
59.694	20	CGAATATTCAGACGAAGCCC	59.668	20	274	92	365
59.789	20	AACGGGATTTACTGTTTTGACA	58.539	22	262	177	438
59.966	20	AGCCCGTACCCGGTCTATAA	60.702	20	205	76	280
59.563	20	ATTTGGTGCATTGATTTCGC	60.847	20	173	658	830
60.008	20	ATCCCCGACAAATTTTCACA	60.17	20	106	61	166
60.022	20	GACAAATCCAAGTGGGAGGA	59.903	20	142	1888	2029
59.934	20	CCATTTTCATTTCGGGCTAA	59.901	20	238	353	590
59.375	20	GGGAAGAGGGGGTATGAGAG	59.89	20	244	143	386
59.957	20	CAGTCGGGGGTAACACTCTT	59.062	20	108	2155	2262
60.118	20	CCCTAGCTTTGCCCTCTTTC	60.332	20	270	595	864
59.939	20	TAAACCCTAAAAACGCGTGC	60.13	20	243	19	261
59.697	20	ACAAGCCCTAGCTCTTTCCC	59.848	20	102	103	204
59.562	20	TTTCTGTTTTTGACAGCCGA	59.439	20	182	5	186
59.647	20	AGCACTCTGCGAGTCTCCTT	59.355	20	278	69	346
59.691	20	TTCGAGTGACACAAGGCAAG	60.025	20	262	9	270
60.003	20	AATCGCTGTATCTCCATCGC	60.207	20	180	1485	1664
59.551	20	AAGGTGTCGCAATCTCCGTA	60.657	20	115	349	463
59.69	21	CTTTTTGCCTTTTGCTGGAC	59.861	20	268	344	611
60.066	20	GTGCTGATGGTTTTGCATTG	60.119	20	156	72	227
60.049	20	CCCGACAGTGAATCGTACCT	59.989	20	137	30	166

59.933	20	GCCGAAAACAAAGTCCAGTT	59.218	20	274	28	301
60.125	20	CCTTATTTCCTATTCCCGCC	59.767	20	136	598	733
59.184	21	TTCATATACACGTGCGTCTTTT	57.425	22	158	586	743
59.79	20	GGCTGTGCTTTCTGGTTCAT	60.263	20	266	53	318
60	20	GTTAGGCCTTGGAATCGTGA	60.074	20	280	1428	1707
59.713	20	GCTTGTTACCGGTGGAGAAA	60.11	20	189	34	222
60.022	20	CCCCCAACACACTCAACA	58.839	18	108	988	1095
58.672	20	GGACGAGATTTAACCCCACA	59.79	20	199	31	229
60.112	20	CGCAGGAGGACAAAAGAAAG	59.986	20	231	2496	2726
59.758	22	TCAAAGGAGGATTGTGTTAAGGA	59.987	23	132	60	191
59.874	20	GACAGCCTTTTTGTTTTGCC	59.73	20	194	22	215
60.665	20	TGTTTGAGATTCAGTGGGGA	59.059	20	248	2666	2913
60.209	26	AATACGGCTGCGTAAACCAC	60.025	20	273	12	284
59.983	20	CCCACGTAGCAATTGACAAA	59.585	20	259	688	946
60.074	20	GGGTTGACATGGCTTCGTAT	59.82	20	155	151	305
59.032	26	ATGCTTTCCCTCTCCATCAA	59.629	20	112	80	191
60.015	20	ATATTCGAGTCATCCGCAGC	60.207	20	263	2703	2965
60.144	20	GTAACACCAACCACACAGCG	60.072	20	192	169	360
59.844	20	GAAACACGAACGGATTCTTGA	60.103	21	209	91	299
60.006	20	ATCATAGTTGACGCCCTTCG	60.096	20	171	94	264
59.027	20	TCAAAACTCACCGGAATCCT	59.526	20	259	1455	1713
59.933	20	GATGCGATCACTGCCCTATT	60.066	20	207	667	873
57.575	24	CATGTGTTGCTTAGGTGGCA	60.72	20	246	1745	1990
59.992	20	GTCAACTTGGGCAGTGGAAT	59.973	20	132	3056	3187
59.831	20	AGCGAATTTCTCTTGACGTG	58.104	20	242	1145	1386
59.982	20	CCAGAAGGATTCTTCGGCTA	59.406	20	269	136	404
60.011	20	CCGGTCCTGAGTTTGTGTTT	60.005	20	272	597	868
60.142	20	CGCGTAGAGTTACCAAACCC	59.632	20	127	98	224
60.046	20	GATTTTGCCTTGCATGTTGA	59.67	20	230	1919	2148
60.125	20	ACACGAGTGTGGAAAGGGAG	60.151	20	221	70	290
59.673	20	ATGGGTATGGATCTATGGCG	59.628	20	274	275	548
58.388	25	CGGGATTTGGTCTTTTCCTT	60.291	20	229	765	993
60.453	20	CTTCTCCACGTCATTTGGCT	60.255	20	251	136	386
60.058	20	ATGCCTCCACATCCTCAAAC	59.934	20	256	312	567
58.627	20	TTTTGAAGTGTTTCGGGGAA	60.452	20	274	1281	1554
58.852	22	GAGGCCTTGAGGCAGACTTA	59.574	20	279	845	1123
59.955	20	GGCTGGTATCACCATAACGC	60.361	20	119	90	208
60.109	25	AGGCTGTGAAAGCTCCATCT	59.043	20	147	41	187
59.844	20	TGTTATATGGCTGGGGCTAAA	59.464	21	160	177	336
59.945	20	TGCAACACCAAGTAACCATCA	60.019	21	148	210	357
59.673	20	TAGGCACAAGTTCGAAACCC	60.11	20	268	23	290
60.262	20	ATTTCATTTCATGGGTTTCG	57.399	20	159	34	192
59.925	20	CACGAGTGAGAAAGGGAGAGA	59.583	21	181	84	264
59.971	20	GGTTCGGTTTTTCGGTTTTC	60.683	20	203	179	381
59.505	20	ATGCAGCAGAGCCAATTTTT	59.851	20	206	4	209
57.4	22	AATTTCCCTGCTTTCCAGTTT	59.123	21	276	449	724
60.203	20	TGCAGGTTGGAATCAGATCA	60.201	20	115	74	188
59.834	20	TTTGGGTTTCTGGGTGTGTT	60.246	20	267	796	1062
60.483	20	TGCTGAATCTTAACCGTCCC	60.074	20	133	761	893
59.467	20	CGTTTTGCTTTAGGTTACAAGGA	59.722	23	261	222	482
60.301	20	TCAACCACCAACATTGTTTCTC	59.875	22	151	233	383
59.982	20	TTTTCCCTCTTCTGGGATCA	59.6	20	253	407	659
59.663	21	GTTGAGGAAGAAGAGCGGTG	59.989	20	176	142	317
60.894	20	CATCATCCTCCTCTTCTCGG	59.755	20	221	321	541
59.764	20	TATTCCCTCAGACCACTCGC	60.218	20	280	819	1098
60.082	23	AGCTGGTTACCTTCGAGCAA	60.015	20	196	26	221
59.492	22	TCTTGTTTCAGGTTATCGTCTAAA	57.253	24	218	43	260
60.088	20	AATTTTTCGCTAAAGGGGGA	59.909	20	203	578	780

59.518	20	CCAGGAAGGCTCTTCACAAG	59.982	20	171	3573	3743
59.933	20	TCTTGGGTTGTCTTGATCCC	59.903	20	188	592	779
59.561	22	CAGCTTGCATGTAAGGTCCA	59.864	20	195	470	664
59.711	20	GAAAACCCAAAACACATGCC	60.214	20	244	3	246
60.073	20	GATGATGATGGCTTATGGGG	60.118	20	143	88	230
59.175	22	TCAAGTCAACATAAACATAAAAA	58.978	26	136	93	228
57.552	24	GTTTTGGCTCCGTATGCTTG	60.637	20	144	18	161
60.067	20	TCGTGATTCGCAACTCTGAT	59.399	20	275	71	345
59.956	20	GTAATGTCAAATGCGCAACG	60.14	20	168	240	407
60.214	20	ATGGGTTAGCGTGTGATCGT	60.406	20	135	327	461
58.593	21	TTCAAAAATCAAAAGGTCGAA	57.419	21	272	3	274
60.068	21	GGGCCGAGATTTGTTAGAGG	60.949	20	169	1565	1733
59.836	20	CATATATTTCATTGGCCCCG	59.998	20	146	1452	1597
59.964	20	GCACTACATAAAATGAACATTCTC	58.234	25	269	1530	1798
59.91	20	CCACAAACCCTTCATCACCT	59.82	20	126	31	156
59.222	20	ATGTGGAGACGAGATGGGAC	59.928	20	174	1160	1333
60.153	20	TTTATCTTGCCCATGGAACG	60.827	20	239	5619	5857
60.298	21	TCCAGCTCTTCCAACCAAAC	60.232	20	168	306	473
60.234	20	GGGTTTTAAATTGGGGATTTTG	60.588	22	204	142	345
60.043	20	TTAGCCGATGAGAGGAGGAA	59.91	20	272	4676	4947
60.857	20	TCTTTTTCTTCGTCACGGGT	59.711	20	215	663	877
57.584	20	TACGAAGGAGGCTTGGAAAA	59.817	20	248	1020	1267
58.773	20	AAACAATCAACCAAGGATGACA	59.336	22	216	1765	1980
59.894	20	GATTCTCGCAGATCAACGGT	60.226	20	239	549	787
60.19	22	TGAATTCATCACCTCTACCGT	57.126	21	151	340	490
59.904	20	AGAGTGAAGCAAGGGAACCA	59.844	20	276	545	820
59.579	20	TGTGGCTATTTTAGCTCTTTGGA	60.257	23	156	8	163
59.847	20	CAATATTACAATGGGCAAGAGTC	57.725	23	253	1535	1787
60.194	26	CATGGCTGTCAGATCTCGTG	60.426	20	145	0	144
59.022	20	CACCTTGCTATGCAATACGG	59.206	20	280	96	375
60.27	20	CGAGAAGGAGAAACGTGGTC	59.844	20	250	194	443
60.264	20	TGCTTGTTGGCACCAGTAGA	60.449	20	139	262	400
60.343	20	CTGTGACGGTGCGTGTCTAT	59.776	20	157	138	294
60.126	20	AATTCTTTGAGGCGCAGAAA	59.96	20	264	2030	2293
60.17	20	CCATGCACTTCTTTCTTTGC	58.502	20	265	230	494
60.119	20	TTCCTGTTATCTGCCCAGAAG	59.322	21	179	719	897
60.051	20	GATCAGGAACCATTTGTGGG	60.173	20	183	1383	1565
58.161	20	GGCACCGACATCAAGTTGTA	59.572	20	258	93	350
60.065	20	GGGTGGGTTTGGAAAAGAGT	60.204	20	253	603	855
59.51	20	GCGTGTTCTTGGTGTTCTTG	59.339	20	218	89	306
59.359	20	ACAAATTCGAGATCGAACGG	60.074	20	269	563	831
58.799	20	AGCATCTGGAATGCAGGAAG	60.362	20	144	778	921
59.935	20	AAGGGCTTGGAACATGACAC	59.973	20	202	23	224
59.667	23	TGAAATAGGAGAATAGGGGCG	60.406	21	199	57	255
60.066	20	GAGAAAAGGGAAGCCTCAAGA	59.948	21	232	184	415
59.992	20	ATCCTCATCTTCACCATCGC	60.042	20	131	592	722
60.268	20	GCAAATCCGAGTAGCTTGGT	59.34	20	241	226	466
60.118	20	CGAAACAATAAGATGCTGTGTGA	60.18	23	159	111	269
59.458	21	ATGGAATTGGGTGTTGGATG	60.439	20	152	24	175
60.009	20	TTCACACAACCACTCCACAAA	60.033	21	121	274	394
60.102	22	CACCCGTATGGGACAAAATC	60.051	20	177	231	407
59.813	20	GGAGGATTTTCCTTTCCCAA	60.237	20	193	19	211
60.34	20	CGTGGACAGTTTCCCAAAGT	60.005	20	238	15	252
59.547	20	ATTACTCACACGCACACCCA	60.032	20	172	170	341
57.436	21	AAAGCCCCGATTTCGTATCT	59.93	20	184	0	183
60	20	TCTTGTGAGCCTGTGTTTGC	60.032	20	145	65	209
59.853	20	GCGGATAATCTGGAGATGGA	59.998	20	175	2658	2832
60.159	20	AACTTCTTGTCATCGCCACC	60.119	20	259	396	654

60.061	20	CACCAAATTTGAGGGTTATTATTT	59.905	25	229	147	375
59.967	20	GGGTATTTCTGGAAATCATTGAA	59.22	23	197	68	264
59.259	21	GTGGTAATTTTCGCACCCAC	60.235	20	276	150	425
60.112	20	CGAAAAAGAAGAGGTGAGCG	60.125	20	277	1088	1364
60.535	20	AAAGGGCATAATCTATGATCGG	59.339	22	175	44	218
60.768	20	TGTGTTTTTCAGTGTGTGGGA	60.033	21	132	74	205
60.202	20	AATTGCACGGTAGTTTGCAC	58.703	20	269	1589	1857
59.964	19	CAGATGTGGACGGGTCACTA	59.545	20	280	19	298
60.285	20	TGGCATTTTCGATCTCTGTG	59.799	20	179	73	251
59.741	21	AGGTTCAGACCCAGGCTTTT	60.11	20	222	158	379
58.926	20	GCAGGAAGTGATGAAGAGAACA	59.478	22	268	107	374
57.626	21	TGGTGGTTTTCAGATGCTCA	60.24	20	211	52	262
59.215	20	TCTAATTGGGATCTCCACGC	60.036	20	254	157	410
59.82	20	CGAAGCATTTTGATTTGCGT	61.131	20	242	127	368
60.228	25	GCCATTGTGAGGAAGGTTGT	59.973	20	177	3	179
60.904	20	GGGCAGCAGCTTTACTTCAG	60.154	20	266	3368	3633
59.96	20	ATCAGAGCATCAGAGCGGTT	59.981	20	172	492	663
60.331	20	AGGCAGACAGATAAGGGCTG	59.454	20	245	429	673
59.751	20	AAAAGATGCATGTGTTCCCC	59.797	20	206	314	519
59.83	20	ATAAAACGACGTCGCAATCC	59.967	20	180	226	405
60.058	20	CTATTACCCCTTCCCCGTTT	59.197	20	275	429	703
57.427	22	CGGATTTAAGGGTTATTACCTGAT	58.81	24	207	682	888
60.067	20	TAAATTGCACCCATCAACCA	59.786	20	176	931	1106
59.83	20	CCAAGTACACTCCTCCTCCTG	58.804	21	252	3981	4232
60.088	20	TGATTTGAGTGTAAACACGTCCT	58.688	23	160	96	255
59.691	20	TCGATCCTGTGGCCTAAATC	60.036	20	184	7	190
60.179	20	AAAAATGGCACATGGGTTGT	60.096	20	262	1647	1908
59.697	21	CCAATTTCGACCGTTGATCT	59.933	20	272	2272	2543
60.18	20	AGCCGACTCCATTTATTGCT	58.814	20	279	1041	1319
59.508	21	AAACACCTGTGGCTCAAACC	60.012	20	240	53	292
59.325	20	GGCTCAAACATGTCAGCCTT	60.263	20	264	32	295
58.686	23	AGGGAGTGCTCTCACCTGAA	59.986	20	213	170	382
59.859	20	TTGCACACCCTCTCTCACAC	59.872	20	184	442	625
59.966	20	TTTGCTTGATCCAATGGTGT	58.976	20	264	380	643
59.624	21	GCTGGATAGTTGGGAAACGA	60.074	20	216	20	235
60.11	20	GAGAGGAAGGTGTGGAGCAA	60.386	20	268	324	591
59.967	20	TGAAAATATCATCGGCCACA	59.891	20	279	300	578
59.647	20	AGCACTCTGCGAGTCTCCTT	59.355	20	280	70	349
59.555	20	GGAATAAAGCCGTTTGAATTTG	59.851	22	226	2	227
59.703	21	TGCGTTTTGACAATATATAGGTGT	60.083	26	179	62	240
59.712	20	GGCCTGAATTCACATCCATT	59.756	20	271	1348	1618
60.481	20	CAAAATTACAAATGGCCAAGA	57.705	21	132	51	182
59.955	20	CCACTACATTCAGGGCCATT	59.813	20	235	749	983
59.952	20	TGCTCACCACACTCTTTTCG	60.025	20	105	325	429
60.692	20	GAACGAATCAAGTTCCGCAT	60.081	20	248	98	345
59.301	20	TCTGGCCACTTGTTTCTCCT	59.844	20	275	573	847
59.867	20	CAACTCGCATACCCAAAAGA	58.771	20	236	22	257
59.861	21	CAAATTTCGCCGTTCTTTTT	59.231	20	248	2008	2255
59.993	22	TCCGTCTTATTGGTCCGTTT	59.429	20	280	402	681
59.522	20	CTGCAGGTTCATGTTGCTTC	59.445	20	258	553	810
59.665	20	GCTGAGCATTTTTAGCACCC	59.851	20	280	6	285
59.927	20	CGCTGTATAATGGGGATCTCA	59.93	21	159	2342	2500
59.878	20	GGACGATGGTTGTGATGATG	59.769	20	276	40	315
59.864	20	TTCGGACCATTCAAACTCGT	60.495	20	261	4089	4349
59.803	20	ATGGGTTCGAGTCTCAATGG	59.927	20	227	289	515
60.557	20	GTCCTCAACCTCTCAATCGC	59.81	20	168	75	242
60.111	20	CATTAAATCCTGTCCACATACAAA	59.241	25	170	579	748
59.959	20	TGATGGTTGCAAGAGAATGG	59.648	20	218	1780	1997

60.147	20	TGCAATGCATGGAGGAAATA	60.035	20	119	38	156
59.933	20	GGCAAATGGCATAACAAACC	60.196	20	220	309	528
60.564	20	TCGGTACCATCATCTGTTTCTTT	59.885	23	258	138	395
59.729	20	TTTTCTTTTCCTTTTATGCTCG	57.789	22	160	22	181
59.973	20	AGATTCTGGGGATTCTGCCT	60.037	20	213	1031	1243
60.001	22	TCATAGTTGACGCCCTTCGT	60.657	20	169	10	178
59.555	20	AAGGATGTGGGTTGAAGGTG	59.82	20	131	43	173
59.339	20	CAAGCAAATTGTGGCTCTGA	59.988	20	252	213	464
59.931	20	TCGTTGTGAATTACCCAAGAAA	59.492	22	124	165	288
60.142	20	CGCGTAGAGTTACCAAACCC	59.632	20	134	99	232
59.836	20	ATGGGAGCTCATGAACGAAC	60.081	20	277	869	1145
59.258	20	ATCGTGTTCCTCAAGGTTGC	60.119	20	165	2532	2696
60.199	20	CCTCTCACTTCTCTCCCCCT	59.801	20	216	19	234
60.133	21	TCAATGTCCCAACAAATCCA	59.75	20	270	33	302
59.993	20	TGAGTGCTCAGGCACAGAAG	60.333	20	188	83	270
60.447	20	TTAGGTCGATCCAACGGTCT	59.55	20	240	398	637
57.172	27	CAATTTCTGCTCTAATAAATCCAC	58.809	25	113	14	126
59.174	20	ACTTTGTTGGTGGAGCGAAC	60.156	20	264	3452	3715
59.072	21	CTTTATCCTTTGCGCGAGAC	59.982	20	190	2	191
59.61	20	ACCGACCGGAATTTTTATCC	60.02	20	249	882	1130
60.002	21	GATTCGATCCGAAAGGTCAA	60.014	20	243	1024	1266
60.02	25	GAAGCAGCCAATGGGAATAG	59.668	20	100	28	127
58.743	25	GTCCTCCGTTGGATTGTACG	60.375	20	199	3	201
59.93	20	TGCTCCCATTTAAACAACCC	59.801	20	259	722	980
58.255	24	TGGAAGAATCATAATCAAGAAGA	59.663	26	104	183	286
60.458	20	TTTTATTGGGCACCAAGGAC	59.801	20	264	2225	2488
59.964	20	AACCGTCCGCTTACTTCTGA	59.875	20	251	213	463
59.962	20	TTCTCAACCTCGGCTCTGAT	59.95	20	199	45	243
60.596	20	TATCATGCCAATCCACCACA	60.757	20	183	334	516
59.971	20	TTTCCCATGTTGTAATTAATGTAG	58.388	25	145	63	207
59.72	20	CTCGCACCACTCCTCTTTCT	59.598	20	278	5	282
57.108	26	TGGCCAAGTGTCAACAATTTA	59.073	21	274	109	382
60.318	20	CCCTAAGGAACCGGTCTAGC	60.089	20	186	155	340
59.956	21	TGAGTTGGTTGTTAGTCCGGT	59.506	21	166	35	200
59.772	20	GCCTTCTCGAATTTGTCTGC	59.962	20	215	180	394
60.777	20	CTCGTCTCCCTTCGCTTCTA	59.711	20	275	18	292
59.92	20	GAGCTGGAGTTGAGAAACGG	59.989	20	200	74	273
59.91	20	TTGCCCGGAATTCTTAACAG	60.067	20	160	268	427
59.989	20	GTGTTAATCGCTTCCGCATT	60.103	20	189	591	779
59.875	20	AACTCGCACCCCACAGTAAC	60.035	20	151	2350	2500
60.119	20	GCCTCAGAGGTCGAAATCAC	59.81	20	271	363	633
60.074	20	ACGTCATGTTTTCAATCGCA	60.119	20	254	18	271
58.901	20	ATCTTGGATCGACACTTGCC	60.081	20	179	16	194
59.807	20	ATGACTCAACGGCTGGTTTC	60.119	20	112	66	177
59.912	24	CGGACATGGTACATTTTCTGC	60.38	21	170	584	753
59.378	22	AAAGTTGATGGAAAAGGGGG	60.159	20	139	2043	2181
59.813	20	TTTTTCTGCATTGTCGAAGAGA	59.996	22	249	481	729
60.038	20	GGAAAAAGCCGATCAAATCA	60.016	20	268	105	372
60.24	20	GAGAGGGTTGTCAAAGAGCG	59.989	20	133	263	395
60.073	20	CGTTACCTTCATCCCCTTCA	59.926	20	183	15	197
60.053	20	TCTGTGTCAGCATGTGTGTGA	59.922	21	280	1848	2127
59.873	20	GAGAGAGAAAGGCTACGGGG	60.34	20	156	80	235
58.725	20	GCAACGGAATACCACTCGTT	60	20	100	8	107
59.285	20	TCAGGGATAAGTGAGCTCGG	60.353	20	226	433	658
60.278	20	CCGGGTTTGATACCTGAATG	60.184	20	248	1216	1463
59.297	20	AGACTTCAATGCCCCTCCTC	60.596	20	170	169	338
59.955	20	CTGTGCATGAAACATGGAGG	60.112	20	167	274	440
60.088	20	CTGAATGTCACGACCGACAC	60.162	20	238	606	843

59.937	20	CGAGGACATTTACTCATGGGA	59.94	21	251	447	697
60.603	20	CTCGTCGTGAACTCCCTGAT	60.261	20	276	400	675
59.468	23	CACCTCCTCCCTCACCAATA	59.92	20	248	114	361
60.046	20	TCAGAAACAACTTGCCCTCA	59.415	20	230	28	257
59.721	20	AATCGAGGAAGAGGGCAAAT	60.039	20	211	3087	3297
60.206	20	TTCTCTTTTGGTTGGTGAAGAAA	60.129	23	228	1723	1950
59.499	20	GTGGGTTGGGGAAAAAGAAT	60.032	20	219	227	445
59.682	20	GACAGGGGTTGGGGTTAAGT	60.088	20	233	62	294
57.122	26	AAAGCTTGCGAGTGCATTTT	60.025	20	148	27	174
59.332	23	TATCCCTTGCAGTCCCTTTG	60.066	20	254	0	253
59.693	20	AATGCATGCACCTGATTACAA	59.055	21	177	220	396
60.111	20	TGTACCATCCGGGATTTGTT	60.051	20	190	222	411
60.066	20	TTCGAAATTATGAGGCTCCAA	59.668	21	188	37	224
60.197	20	CTTCGGGTTAGCAGATCAGG	59.83	20	267	106	372
58.916	27	CCAAATAATTTTGTTTCCACCAA	59.974	23	124	97	220
59.701	20	TTTAACGGGCGGTTTTGTAG	59.993	20	190	105	294
59.644	20	CTTCCTTCCACCCAACAAAA	59.942	20	271	1205	1475
59.79	20	TACTGCATTGCGACCCTACA	60.28	20	237	333	569
60.246	18	CCCCTTTTGTAAGTCCCCAT	60.046	20	174	1	174
60.243	20	AAACATCGATCAGTCCCACC	59.786	20	115	196	310
60.656	20	AATGGCTGGATTTAGTCCCT	57.611	20	277	22	298
59.925	20	TTTGGCTACAAATTGCTAGGG	59.262	21	242	48	289
59.957	25	TTTTGGGAAATTCTTGCACC	59.916	20	101	0	100
60.131	20	ATTCCAAGATGGCAACTGCT	59.7	20	194	7	200
60.425	20	TATTCACAGCATTCAAGGGG	58.572	20	198	500	697
60.555	20	TGTCCATTTCCCCAAATTGT	60.029	20	280	3	282
59.749	26	ATACTGGTGTTGCCTGCTCA	59.318	20	178	26	203
60.226	20	ACCAACCAAGAAGTCGAACG	60.149	20	279	1840	2118
59.989	20	CATCCATCTCTCCCTCACTCA	60.207	21	117	170	286
60.307	20	AAAATCGGACTGGACCATTG	59.79	20	268	247	514
60.022	20	GGGGAATTTTGAGGTGGAAT	59.996	20	275	492	766
59.808	21	TGACTAGTGTGCATCGTGGC	60.907	20	208	89	296
59.924	20	TGTCTTGAGTTTGTATCTAAGAAG	59.365	27	139	221	359
59.877	20	CATCAACTCACCCTCACATTTC	59.454	22	183	390	572
59.927	20	AAATATTTCTAGCACATGAAATTG	57.859	25	246	45	290
60.088	20	TGAGAGCTTGAAGAAGAGCAAA	59.517	22	132	392	523
59.756	20	ATTAGGAACGGGGGTGAATC	60.017	20	210	662	871
59.973	20	TCCCGATCTTGGTTGTCTTC	60.05	20	216	17	232
59.724	20	GTCAACTTGGGCAGTGGAAT	59.973	20	274	763	1036
59.901	20	CCATTAACGCCCCTGATTTA	59.789	20	170	249	418
59.542	20	AGTCGGCATTCAAGTAGTCG	57.98	20	144	268	411
60.169	20	TGAAGTTGTAGCATGGGCTT	58.379	20	230	83	312
59.943	20	AATTGGAGCAAAATTGGCAG	60.074	20	253	335	587
60.096	20	AAGCAGAATGCAAGCAAGGT	60.022	20	168	526	693
59.79	20	CAGCCTGATAAATGGGACAAA	59.946	21	210	178	387
59.301	20	ATTTAAGCGCACGCCAATAC	60.123	20	216	207	422
58.035	22	CTGTCCTTCTCCCACTCCTCT	59.856	21	201	164	364
59.948	20	TCAAAACAACACCCAACCAA	59.834	20	261	84	344
59.381	20	CAACAGCCTTGTCTCTGCAC	59.622	20	240	338	577
58.379	20	TCATTGTACCGCAGCAAGAG	60.011	20	272	3744	4015
60.088	20	TGAAATTTCCCAACATTCGC	60.817	20	171	392	562
59.92	20	TGCAACTCGAGATGAGATGG	59.942	20	200	78	277
60.03	20	AATCACAATCTTGGGCTTGG	59.933	20	270	339	608
60.027	20	ATACCTTCGGTGCTCATCGT	59.579	20	280	512	791
59.43	20	TCCTCACCCTTTCCTTTCCT	60.045	20	101	50	150
59.623	20	TTGAAAAAGTCGGCTGAAAAA	59.855	21	234	953	1186
59.61	20	TGGATTTCTCACGAAAAGGG	60.044	20	252	646	897
58.646	22	CTTGACAAGGCAGTACCCGT	60.171	20	171	2	172

59.325	20	CAAAAGTCAAGGCTCGGAAG	59.986	20	163	3636	3798
59.713	19	TTGTCATAGCCAACCCAAAA	59.013	20	223	364	586
59.957	20	TCGTGCGACATAGTATGGGA	60.096	20	205	3	207
59.433	21	TCCTCCATTTCCAATCTGCT	59.629	20	258	87	344
59.585	20	TGGAAAGATTGAGATGGGATT	58.44	21	260	842	1101
58.882	22	TAGTGAACGTTGGGGACACA	60.001	20	182	104	285
59.267	20	GGCCCGAGTTGTTGAGATAG	59.694	20	140	521	660
60.039	20	TTTAAGCATTCTCTTGTAATCCCA	59.212	24	272	53	324
59.573	21	TCCAGAGACCTACATGGGCT	59.679	20	216	1291	1506
59.749	26	CCAGATATACCCCCACATGC	60.036	20	254	3	256
59.799	20	CTCAGGGCAAATAGGGACAG	59.688	20	279	4152	4430
60.208	20	AACAGGCGCCTTACCAGTTA	59.769	20	187	111	297
59.992	20	AATGAAATCCTTTGGGGTCC	59.996	20	186	2451	2636
60.873	20	CAATGGGGCTTGGTTTTCTA	59.931	20	271	1303	1573
59.934	20	TCGGTTCAGTTAGAGGCTGG	60.388	20	156	1628	1783
60.009	20	GTGGACGTCCCAGATTGTTT	59.827	20	250	1109	1358
60.031	20	CGAGTAGATCACAACGGCAA	59.864	20	159	377	535
60.112	20	AAGATCTTGGTTGTTGGGTTG	58.945	21	149	585	733
58.693	25	TCTCTTCGAAACTCGAATCGT	59.066	21	160	1	160
59.971	20	AGATCAAAGGGCCGAGATTT	60.039	20	209	52	260
60.016	20	TATATCAATGGCAGCCCACA	59.914	20	278	1790	2067
60.22	20	GTCCGATACGAGCTAAAGCG	60.003	20	190	14	203
60.005	20	TCGAAAGAGTTGACGAATGTT	57.468	21	249	87	335
59.325	20	CCAAAATGCCCTTGTATGCT	59.96	20	207	393	599
59.867	20	ACAAAACCCTAGACGGCAAC	59.101	20	238	145	382
59.971	20	ATAGGGATGGAAGGGTACGG	60.032	20	129	230	358
60.074	20	CGACGGGTGAAAATCCTAAA	59.931	20	257	95	351
59.871	20	CGTGTCCATGCCCTAATTCT	59.955	20	236	319	554
59.853	20	ATCGGGATTGGTGGAACATA	60.014	20	176	796	971
60.05	20	GTTCTCGCAAACAATGCTCA	59.995	20	275	149	423
59.702	20	CCCCGAAAATTAATCATTGC	59.259	20	230	2165	2394
60.17	20	TCAACATTGGGCATTTTCAA	59.907	20	247	983	1229
59.842	20	AATTCAAGCTTCAAACGGGA	59.685	20	236	418	653
60.008	20	AGTGAACCGAAGGTCCATTG	59.966	20	241	176	416
59.647	20	CGGGTTCGAATTTACCAGAA	59.931	20	257	1823	2079
59.758	20	TCGAGGTGTCGAACTTGTTG	59.873	20	262	1035	1296
60.065	20	AAAACATACTCAGCCACCGC	60.14	20	261	1266	1526
59.853	20	ATGTAGGGTTCCTGTGGCTG	59.989	20	253	340	592
60.242	22	AAAAGACCCTAAGCACTCACAA	58.061	22	227	4329	4555
60.517	21	TTCTTGTTGGTGTGTGGCAT	60.008	20	266	82	347
60.226	20	GCTTGTGGGCATGAATCTCT	60.226	20	266	625	890
59.986	20	ATTAAACGGGTAACTCGGGC	60.204	20	250	1903	2152
59.816	20	GACACGTGGTAGCACGAGAAT	60.194	21	188	235	422
59.725	21	CCTTCCTTCGTTTTTCTCCC	60.046	20	160	335	494
58.948	20	CCGAAGCAGCTATTCACTCC	59.978	20	111	1404	1514
59.212	20	GCTTTAAATGTGTTACAAAATCGA	58.332	25	277	247	523
60.352	20	GTAGTGGCTACGGTTTCCCA	59.993	20	134	3837	3970
60.197	20	CCCATTTTTCTAGGCACCTTT	59.489	21	259	201	459
59.878	20	TTACGGTTCCACTTTTTCGG	59.968	20	200	41	240
60.035	21	CGGAAGATCCGAGATCAGAA	60.295	20	189	35	223
59.668	20	TGTGGCATCAAATCTAGCCAT	60.484	21	236	333	568
59.968	20	CACGTCACACATTGGACTTTG	60.057	21	276	337	612
57.569	22	TTCACGCATTTCCACACATT	59.972	20	101	38	138
59.66	20	CACACAATACGCACACACCA	60.071	20	176	239	414
60.009	20	GTCGGACCAGCTCTCTATCG	59.973	20	266	249	514
59.499	23	AATCTGACGGCCGATATTTG	59.923	20	182	284	465
59.218	21	GCCATCTGAAACCCCATCTA	59.894	20	150	28	177
60.405	20	CAACCGATATCCCCTCCTCT	60.285	20	157	6	162

60.292	21	GGTGGGAATTGTGGAAGAAA	59.767	20	222	75	296
59.957	20	AAAAGCATTCCCCCATGATT	60.511	20	232	1544	1775
60.103	20	TGCTAAGAGAAAGCCCCTCA	60.088	20	213	534	746
60.118	20	GGGAGACAGCAAAAGCTCAC	59.997	20	189	409	597
59.95	20	CCCCTCGTATGCAATGAATC	60.296	20	279	105	383
59.311	20	GATGATAGAACTCTGGCGGG	59.653	20	180	232	411
60.578	20	TACCTTTTTGCCCTCGAATG	60.067	20	171	1	171
59.724	20	GCACAACCACTCCACAAAGA	59.726	20	264	83	346
58.994	20	CCGATTGGGCCTATCCTATC	60.623	20	194	101	294
59.688	20	CCAAATGTGAGACCCTTAACC	58.423	21	132	40	171
60.014	20	AGAGACTGACGCACGTTGTG	60.096	20	117	205	321
59.845	20	TCAATCTAAAACCCGTGCAA	59.157	20	139	237	375
59.601	21	GTTCAAGATTGTGCGAGCTG	59.596	20	211	18	228
59.5	21	ACCTGCACCAAAATGGAGAG	60.111	20	151	277	427
59.383	21	CGTGGTTCGATCGTAATTGA	59.542	20	105	102	206
59.241	20	AGGGTAGACATGGGTTTCCC	60.052	20	222	239	460
59.968	20	GAGGCGGTAGGAAACCCTAA	60.443	20	130	95	224
59.943	20	CAGTTGGTCAGAGATGGCAA	59.831	20	231	297	527
59.971	20	GGCGTTGGACCAGTGTAGAT	59.997	20	274	70	343
60.469	20	GATGACACGCATCAAAATGG	59.931	20	154	1298	1451
58.81	24	CTCTTCATATGGGAAGGGCA	60.029	20	197	10	206
59.783	20	GCATTTCATCCTCTTCCCAA	60.014	20	106	544	649
60.22	20	CACTGCGAACCAACATCACT	59.751	20	151	132	282
60.227	20	TTCTCAGCTCGGGTTCCTAA	59.948	20	243	147	389
59.518	20	ATTTGGCACATGAGATGTCG	59.527	20	246	615	860
59.911	20	CGGTCACATAAGCGTCCTCT	60.277	20	252	619	870
60.082	23	TGATGATGACAATGATATCGTGAA	60.217	24	175	71	245
59.836	20	TTAGGCCATGTTTGTCTGCTT	59.761	21	216	200	415
60.009	20	GGCCTTCATTCAAAAGCTCA	60.331	20	260	2897	3156
60.298	20	CAGCCGAAGTAACAAAGACG	58.579	20	213	2104	2316
59.526	20	ATTATCATACCTCGCCACGC	59.951	20	169	944	1112
59.894	20	CGTCCACTTCATTGAATTTCTTT	59.531	23	280	3919	4198
59.978	20	TTGCATTACATGCTCCCATT	58.994	20	247	225	471
59.9	20	GCACACCAAAGTGAAACCGT	60.996	20	234	103	336
57.864	20	CAACAAAGCATTGCAAAGTGA	59.903	21	224	0	223
58.048	21	TCAAATACTAGCATATCGATGAAG	59.623	27	174	88	261
59.83	20	ATGGACGTCGTGACTGCATA	60.144	20	168	25	192
60.971	20	CTTCACCTCCCAGATTTCCA	60.042	20	143	87	229
60.103	20	TGTGAGAACCATCTCGGTGA	60.246	20	134	6	139
60.262	20	CCCAGATAGCAATAAGGGCA	60.053	20	156	735	890
59.923	20	CATTGTCAGAAAGTGCCGAG	59.44	20	256	42	297
59.752	20	GGAAGCCAGGAAAAGAAACA	59.288	20	276	2118	2393
59.829	22	CGACAAAGACTTAACTACTTGTAA	60.049	27	278	853	1130
59.337	20	TCTTTTGAGACCCACCAACC	59.943	20	264	659	922
60.739	19	TTTGTTTGATATTCAACCACTTGT	57.681	24	102	268	369
59.982	21	TGTCGGCGGTTAAAAAGTTC	60.11	20	197	4467	4663
59.984	20	GCGTGGAAAGGCTGAATAAG	59.845	20	244	664	907
59.94	27	AGGGACACCTAACCCCAACT	59.717	20	115	1	115
60.173	20	AAAAACCTTTGTAGGCGCAA	59.758	20	265	365	629
59.172	21	CCAGCCCAATAACTTGACCT	59.052	20	235	70	304
60.461	20	TATACACGGCATACATGGGG	59.136	20	254	571	824
60.474	20	ATGGGTCCAAACAACCTTTT	58.266	20	168	257	424
60.162	20	CGTGTTAATTCCCCTTCCAA	59.795	20	191	1499	1689
60.081	20	CAAATTTGATAGCGGTCTAATGAA	59.557	24	170	1463	1632
58.161	22	CTCAGGGACTAGTTGAGCGG	60.005	20	188	65	252
59.682	20	CACTAATCATCACCGTGCCA	60.539	20	279	75	353
60.007	20	ATTTTCCCTCCAGTTGACCC	60.169	20	247	4485	4731
60.154	22	AGCGCAAGCACCTAGAAATG	60.543	20	209	722	930

59.146	20	TGCACAGAAAATGAAAAGCG	59.992	20	233	277	509
60.17	20	GCCATGTGAGAGGGAGAGAG	59.945	20	234	110	343
59.551	20	TCCAATGGATGTAATGAGTTATTA	57.297	26	167	374	540
59.844	20	AGCCGTCGTATTCTAAACGC	59.388	20	153	74	226
60.051	20	TGTTTGCTCTCTTACTCTCGGTC	60.068	23	195	66	260
60.765	20	AGTTGGGTGAAGATCATGGC	59.934	20	233	84	316
60.026	20	GGAGCAATAAAGGGCAATCA	60.038	20	156	2938	3093
59.93	20	GCTATGGTATGCTGTCTGCG	59.474	20	259	101	359
58.201	20	TGCAGGACAATATCCATCACA	59.94	21	174	12	185
57.769	27	ATCTCGTTTCAAGCCCAAAA	59.685	20	150	35	184
59.95	20	TGATGACGATCTTTTGAAACCA	60.481	22	234	17	250
60.195	20	CCTAAGCCTACTCCCCACCT	59.593	20	162	109	270
59.722	20	ATGCGCGTTTTTAGGGTTTA	59.624	20	198	2366	2563
59.711	20	CAGAGTCCTGGGAGCTCATT	59.405	20	230	1072	1301
59.992	20	TGTGCACAAGCTTGGAAAAAT	60.663	21	209	1575	1783
59.454	20	ACTTGTGCTCGCCTTTCATT	59.882	20	272	2202	2473
59.988	20	TGAAGACCATGAGCACAGGA	60.402	20	249	265	513
60.59	20	GGGACGGATCACTCTTTTGA	60.05	20	270	74	343
60.184	20	ATGGAGGTATGGTGTATGGG	57.047	20	247	2478	2724
59.402	20	AGTCCCCACGAGGAAGAACT	60.111	20	275	690	964
60.475	21	TTGACGATATATAGTGTTTTGACA	58.972	27	187	286	472
59.773	20	CATGGGTGGTATGGTGTGG	60.517	19	144	17	160
59.955	20	AGCTGTTAGGGTTGTATAGTGAGT	57.436	27	165	338	502
60	20	GCCTTTGCCCTTTTTCTCTC	60.32	20	129	298	426
59.91	20	TTCAAAAACGAATTTGGCGT	60.468	20	178	231	408
59.837	20	CTTGCCATGCATGTAAGGTG	60.134	20	164	1059	1222
60.074	20	TCCTCTCGTGTTCATCCTCA	59.34	20	156	59	214
59.712	20	CGTCGATCTCAGTATCTTCGC	59.992	21	239	80	318
60.536	20	GGTAAATGGTTACCGGTTTGG	60.33	21	214	49	262
60.227	20	TCACGTTGCAAAAATAGCGT	59.373	20	272	46	317
59.859	20	TGGAATCTTGTTGGGGAAAG	59.903	20	251	599	849
60.309	20	CATATACGCGAACCCGAGAT	59.945	20	258	215	472
60.053	20	AGCCACCTCCTAGCCATCTC	60.756	20	108	344	451
60.038	20	CCCATGTTTGTAATTATTGTAGGG	60.228	25	168	1909	2076
59.803	20	TGCCCATGATTCTGTAGTTTTG	59.996	22	255	180	434
59.679	20	TTTTGTGATTTCCCATGTTTG	58.374	21	136	94	229
59.645	20	AAGTGGTGTGTTCGAGGCTT	59.769	20	264	203	466
59.919	20	TTTGAAGGCCGGAATATGAG	60.031	20	225	0	224
59.76	21	GGGTGTGGTTATTCCAATCC	58.959	20	253	3	255
58.686	25	CACTCAGTGGACACATTGCC	60.162	20	251	145	395
60.555	20	ACTGACATTCACAGGCATTG	57.067	20	223	72	294
60.096	20	GGGACTTTCTCTCTCCTGGG	60.186	20	205	187	391
59.622	20	CATGCATGATCAATGTTGTAAGA	58.571	23	158	7	164
60.864	20	TCATGATAATGCATGTCTCTGAAA	59.614	24	100	430	529
59.161	22	AACAGTGGGTTTCGCGTATT	59.499	20	126	29	154
60.057	20	GACTAGTTTTCTGCGACGGC	60.022	20	200	866	1065
60.008	19	TTCTGCTCTCCCCTCCAAC	60.333	19	260	108	367
59.903	20	TCAACGCATCTACAGGTTGC	59.871	20	119	290	408
60.298	22	TCCAATTGTTGTCTTCCATCTG	59.971	22	157	284	440
58.57	21	GGTTTTGATGGTTGTGATTTGTT	60.014	23	185	98	282
60.163	19	TGTGGTTGATGAGTTGGCAT	59.967	20	279	4092	4370
60.16	20	GCCTGAACAGTCGAGGTGAT	60.269	20	149	24	172
59.931	20	AGACGCTTGACGTTTGTCGT	60.896	20	216	33	248
60.269	25	TGGTCGTGAGATAGAGTGCG	60.008	20	206	1	206
59.844	20	TGGCATCTTCTCTCAAATTCAA	59.823	22	222	329	550
59.733	20	TGTTTCGATGTGCATGGAGT	60.12	20	122	259	380
60.008	20	ACCTGTGAAAGCGATCGTG	59.846	19	126	2521	2646
60.143	20	AAAATCAAAGGCCCACAATG	59.801	20	106	1700	1805

59.837	20	TAAAAAGATGAGCCCACCCA	60.439	20	186	160	345
59.685	20	TGAGGAAGAAGTGGGATGATG	60.058	21	157	42	198
60.065	20	GAGCTCTGGTTCCCACAGAC	59.841	20	235	835	1069
59.988	20	CGAAAATGCCCTTTTATGCT	59.212	20	246	1179	1424
59.903	20	CATCAAGAGTCGGCTGTCAA	59.984	20	182	54	235
60.053	20	AGAGGAAGAAGGGGGTGAAA	60.045	20	217	467	683
58.809	23	TCATCCCGTTTCAAACTCAA	59.097	20	154	43	196
59.546	20	TGATGTGCAGCTCAAACTCC	59.992	20	267	831	1097
58.994	20	CCACCAAGTATCGGTCCAGT	59.844	20	266	107	372
60.103	21	TGATGAAAAACAATTGACCAAAA	59.372	23	223	1	223
58.869	20	CCTCAAAATCTTTGAAGGCTC	58.059	21	176	95	270
60.232	20	CAACTGAGTCCCCTATCCGA	60.065	20	260	100	359
59.569	20	TGTTGCGATTTTCATTTTCC	58.601	20	202	34	235
59.864	20	CCCTCATAACTCCTGACTGCTC	60.268	22	191	592	782
59.815	21	TTCAACCATCAACTCCACCA	59.935	20	258	236	493
59.859	20	ACCATCGATGCATTCACAAA	59.931	20	277	1570	1846
60.089	20	AAAATCATGTTCCGTCCCAA	60.17	20	244	45	288
60.375	20	TCAGTTTCGAGTTATGAAGTTAGG	59.749	26	100	163	262
59.813	20	TTAATCTTGACCGCCGATTT	59.547	20	280	39	318
58.94	21	TTAAATGGCCTCGGTATTCG	59.922	20	240	26	265
60.406	20	AAGCTCGGAGTTGCCAGATA	59.978	20	191	30	220
59.82	20	GGTGAGGGGGAAAAATAGGA	60.124	20	104	73	176
59.823	20	CATATGCATCCGCAATTCTG	60.058	20	280	4547	4826
59.937	20	TGTTGTGTTCGTGTCCGATT	60.008	20	241	189	429
59.592	20	GTTATCGTTGTTGGGGATGG	60.051	20	197	3585	3781
59.903	20	CGTCACGGTTATCCTTCGTT	59.993	20	259	77	335
59.862	20	TTTAGCAGAGTTGGTGAAATCAT	57.952	23	220	572	791
59.849	21	CACCCTAACACGCACAAATG	60.027	20	134	314	447
60.029	20	GAGATTGGGGACTTGGTGAA	59.903	20	120	548	667
59.682	20	AACACCCCTCCTCAATTTCC	60.169	20	105	20	124
60.063	23	ATGCACCAAAAATTGACACG	59.444	20	197	724	920
60.074	20	GGTGATTGTATCGCCACCTC	60.348	20	255	2320	2574
59.993	20	GACCGCTAAAAACCGTGAAA	60.11	20	261	459	719
59.928	20	TGATTGGGCTTTGTCTTTTTG	60.096	21	180	48	227
59.671	20	GCCGTACATGAAAGACAAAACA	60.039	22	217	142	358
59.873	21	GGGAGATTTGAAATGTGGGA	59.727	20	270	124	393
59.853	26	AGAACACGAGGAACTTGGGA	59.697	20	154	6	159
60.169	20	CTCAACTCAGAGCTCCATGCT	59.76	21	167	610	776
59.78	20	GCGAATGAAACCCAAGAAAT	59.022	20	178	214	391
59.968	20	TTAGGCCAAGGCAATCAATC	60.038	20	172	103	274
61.042	20	CCCCTCCCCACATTCTTTAT	60.011	20	105	9	113
59.45	21	GGGTGTTTTGACAATATCACGA	59.73	22	230	1943	2172
59.87	20	AAAGATCTCTGCAAGTCCGC	59.579	20	216	285	500
59.74	20	GCTCTCAACCATACCTGGTCA	60.126	21	263	275	537
60.088	20	AATTTTCGTTCATGCCCAAG	59.938	20	218	218	435
59.826	20	TTGAGCTGTTATGCGTTTTGA	59.5	21	148	83	230
59.664	20	CGTGCTCAAACTACATCCGA	59.864	20	268	215	482
58.25	22	TGGTGGGTTGAATGCTATGA	59.924	20	203	442	644
59.989	20	ATCCAAACGAACTTCCAACG	59.971	20	207	41	247
60.069	24	TAACCCAAACCCACCCAATA	59.91	20	106	17	122
59.074	24	ATATGCCCGGTAAAAGAGCA	59.569	20	245	14	258
60.151	20	ACCGACCCATCTCTTGTGAC	59.969	20	210	461	670
57.462	27	CCTGCCCACTTTGAAGAAGA	60.366	20	247	1	247
60.011	20	ATCAACATGCAAGCATCCAA	60.08	20	200	46	245
60.14	20	TTGCTCTCATTGTAATCTCTCCC	59.739	23	120	0	119
57.479	20	CAGCTCCAATCCATCTCCAT	60.034	20	227	309	535
59.96	20	TCTAGCACGGTTGCAATCAA	60.401	20	245	90	334
59.96	20	GCTAATTCGGCAGCTTCTTG	60.117	20	144	441	584

60.263	20	GTTCGACTGATGGGTGCTTT	60.119	20	212	1227	1438
60.14	20	TTCAAAAATGAGTGGACCAGA	58.187	21	128	1214	1341
59.95	21	CATGGCCTTCTTCTTCCAAC	59.67	20	191	999	1189
59.882	20	CCTAAATGTGGGAAGTGGGA	59.784	20	172	1488	1659
60.074	20	TGTGGAAGCAAATGGTTAGC	58.773	20	157	505	661
57.538	22	TGGGACCACAGGATAGGAGT	59.38	20	244	6	249
59.29	22	CACCTTTTCTCCCTCTTCCC	60.045	20	218	78	295
59.989	20	GATGATCCGTTCGCACTTCT	60.226	20	223	136	358
59.567	20	ACGAAATTGATGTGTTGGCA	59.972	20	226	228	453
60.323	22	GTTCGAACCCTGGTCTTCAC	59.555	20	247	968	1214
60.046	20	ATGACCTTGCCACCATCTTC	59.934	20	227	442	668
60.349	20	CCTCGATTCACTCATCGCTT	60.362	20	233	225	457
59.097	22	ATCAATCTTACGGACTGGCG	60.096	20	222	295	516
59.973	20	AAGATCGTGCAAAATTTGAAAAG	59.672	23	249	28	276
61.448	23	GGATAGGCGGTTGAGATTTG	59.528	20	115	12	126
59.674	20	TCAGTTTGGTTTATGAGTAGGACA	59.15	25	136	1073	1208
59.946	20	CGTGGCAGGCTAATATCCAT	59.945	20	152	97	248
59.95	20	TGACATCGGACCATTTTCTG	59.496	20	203	31	233
59.989	20	GCGCTTTTTGCCTGATATTT	59.349	20	210	561	770
60.035	20	GAATGTGTACTGTGCAGGGC	59.169	20	254	3928	4181
59.336	20	TAACTCCGTATTCTTGCGGG	60.089	20	224	140	363
57.128	26	AGGAGGAGCAAGAGAGGACC	59.952	20	257	37	293
58.783	23	TATGGGTCAGAAAAGCCCAC	59.933	20	241	189	429
60.28	20	GCGTTGCGTATGGAAGAATC	60.615	20	279	682	960
59.651	20	ATTTGGGGTGAGCTTCACAA	60.495	20	240	239	478
60.017	20	GATGTTGATTGCTGCGAAGA	59.955	20	251	2236	2486
59.48	20	CGTTAAATCTCTGTGTTGAATCTG	58.016	24	180	249	428
60.11	20	CTTGTCACTTTCTCCCTCGC	59.989	20	193	1	193
60.074	20	TTTCAGAGGGGATGAAATGC	60.014	20	229	51	279
59.972	20	ATGGACCACCCACCAAAATA	59.91	20	247	77	323
60.399	20	CAACCCACCATGATTTCACA	60.216	20	229	752	980
58.406	27	GGCCGAAACAAGAACATCAT	59.939	20	239	314	552
59.973	20	CCCGATTCCCTCTCTTTTTC	60.011	20	131	515	645
58.876	24	TTTGCTGCTGATGTTTGTCC	59.847	20	212	43	254
58.46	21	TTGACTAAAACATGGAAATAATG	60.054	27	160	19	178
59.939	20	GCAGTTTTGCTCCCACTCTC	59.997	20	230	1238	1467
60.073	20	TTGTTCCAGAAAGGAGGTTGA	59.697	21	117	713	829
60.016	20	GGTCGATACATCAGGCAACA	59.527	20	196	1006	1201
60.029	20	TGCATGATGAGGTCTTCGAG	59.942	20	233	6018	6250
58.2	23	TTCGACTTAATCAATAAAGATAAC	57	27	264	94	357
59.931	20	CTCCAATCTCCAATCCATGC	60.426	20	243	500	742
60.206	20	CAATACAACTGCCGAGCTGA	60.011	20	119	88	206
60.495	20	CCGAAGGGATAGGATTGTTG	59.382	20	163	26	188
60.073	20	GAACTTGCTGTTTTGGATGGA	60.103	21	154	103	256
61.008	20	CACGAAATTGATGGAAGAGGA	60.059	21	198	344	541
57.914	21	TGAATAAGAGTTCAATGAATTTCA	59.912	26	223	48	270
59.924	20	AAGGAGGTGTTATGAAGGGATT	58.028	22	121	222	342
58.644	21	ACACGCTTGTCAAACATTTCT	57.402	21	242	656	897
60.029	20	TGTGCAGAGGGACTTTAATGC	60.264	21	112	385	496
60.008	20	TAAGTTGATGTGTGCAGGGG	59.566	20	254	764	1017
59.464	20	ACAAACTAATCAAGTTCCGCA	57.439	21	117	222	338
58.785	20	TCAATTATTATCTCGATCCAACCA	59.713	24	275	551	825
59.934	21	GACATGATTACTCGTCCCCC	59.218	20	279	1338	1616
59.927	20	TTGAACAATGGTACCTCCTCC	58.898	21	144	497	640
60.035	20	GAAACTCCCAATTTGGCTGA	60.051	20	263	701	963
59.874	21	TAGTTCACCAACTCCGGGAC	59.966	20	183	5647	5829
59.924	20	TTCTCTCTTCTATTTCTTTCCTTTTT	58.425	27	234	79	312
59.588	22	CGGACCGGGTGGTCTAAATA	61.972	20	100	2078	2177

60.178	20	CATTTGGATCCTCAAGTGGG	60.309	20	127	2618	2744
60.074	20	GGGCCTGGTAATCCATTCTT	60.152	20	259	219	477
58.348	21	CTGTTGCCGTCAGTTCATGT	59.751	20	161	0	160
57.987	21	TTGGGATATCCGTTTCTTGG	59.756	20	256	320	575
60.011	20	AAACTTCTTTCCAACCGGAAT	58.991	21	200	63	262
57.844	20	TTTGGATCATGATTTGAGTTTGA	59.442	23	280	491	770
57.192	20	AATGACCGATCTCTCTATCCCA	59.925	22	100	344	443
60.014	20	ATGAGAGCCGCACTTTGTCT	60.02	20	195	318	512
59.955	20	CAAAAGCTCGGTTTAATCTGC	59.023	21	248	149	396
60.198	20	ATTGGGGATGGAAAATTGGT	60.245	20	143	46	188
59.916	20	AGGCTGCTCTACCACAAGGA	60.012	20	260	104	363
59.522	20	GCATGATCAGGGTAAAATCCA	59.776	21	190	558	747
60.149	20	TCAGGGTTTTAGCCACAAGG	60.103	20	201	304	504
58.288	23	GGAATGAGAAACTTTGGAGCC	60.067	21	268	0	267
58.743	25	GGGACAACGACTACGGAGAA	60.111	20	266	1	266
59.311	20	CATTTCCCTTCCTTTCTCCC	59.875	20	228	2112	2339
59.982	20	ATCGAACCCACGAGAGCTAA	59.836	20	267	2096	2362
59.166	20	AAAATGCTGACATTGGAGGC	60.081	20	208	2464	2671
60.376	20	TGAAGCAAAAGAACCAGAATCA	59.861	22	190	230	419
60.096	20	TGTTATCATTCCACCCACGA	59.774	20	184	166	349
59.953	20	CTTGTAGGCAACGGGAAGAG	59.869	20	190	45	234
60.042	20	TTGCCTCAACTACCCAAACC	59.971	20	109	10	118
60.149	20	CCGAACCACGTACATCCTCT	59.989	20	215	475	689
59.401	20	ACAGGGTCGGCTCATTTTTA	59.569	20	254	5	258
60.251	20	AGGGGAGGAGGAAGAGGATA	59.091	20	244	390	633
59.623	20	TCCCATTTCGCTTTCCTTTA	59.655	20	279	5594	5872
60.019	20	GCGGGTCTAACCCAGATGTA	59.955	20	264	579	842
59.701	20	GTCTTCTCTCCAATGGCAGC	59.957	20	247	429	675
59.522	20	TCAGTTTTCGAGTTATGAAGTTAG	59.749	26	102	384	485
59.44	20	ATACGAGCCCGAAGGCTTAT	60.082	20	172	657	828
59.619	21	TCCTAAGAGATTTGATTGAAAAG	59.651	25	168	39	206
59.971	20	AATGCGCCTCCCACTTTAAT	60.821	20	163	177	339
57.142	21	CCGAGCCCTCTCTCTTCTCT	60.23	20	259	455	713
57.459	27	GAATGCTTAATGGGAAGCCA	60.038	20	121	2	122
57.235	25	ATGAACCTATTTCGTTGCCG	59.96	20	242	1	242
59.967	20	CGGGGTGTAACTTGCTTGAT	59.993	20	272	1020	1291
61.066	20	TTTTGAGGTGAGAATTGCCC	60.051	20	246	107	352
59.993	20	GTTATGCGTTTTGACGGGAT	59.829	20	278	997	1274
59.67	20	ACACTGAAACCGAACCGAGA	60.69	20	254	35	288
60.059	20	GCGTGACTATCCACCGTTTT	60	20	113	43	155
59.823	20	CACATGTACGCGCTCTTGAT	59.895	20	172	6	177
59.853	22	CCCAATTAATTTCGCCATTG	60.144	20	104	456	559
59.797	20	CACCCTCAATCACTCACACG	60.154	20	171	361	531
60.27	24	GCCTAGTTGGCACAAACTCC	59.74	20	152	598	749
59.705	20	GGATGGTGTTTGTGGCTTGT	60.823	20	148	171	318
59.565	20	CAGCTGCCTGCTGTAACTGA	60.347	20	218	12	229
58.775	20	GACCCAGCAATGGGTATATGA	59.659	21	279	767	1045
59.905	20	TGTTCCCTGGCAGCTACTCT	60.012	20	243	397	639
57.794	22	GCCAGATGCATTTCAATGTG	60.08	20	243	104	346
60.119	20	CAAAGGCCCACAATGGTTAT	59.685	20	145	332	476
59.533	20	GGCAAGTGGGTTACCGATTA	59.823	20	172	13	184
59.96	20	GGGATTTGTGGCAAGAAAAA	59.916	20	149	343	491
57.631	27	TCCATTTATGGAATCCTTCCC	59.971	21	243	9	251
59.989	20	AGGAGTTTCATGCCCCTTTT	59.94	20	211	435	645
60.088	20	TACCTTTTTGCCCTCGAATG	60.067	20	202	688	889
58.407	20	CAATTTCTTGCTGGGTCCTT	59.17	20	280	184	463
60.639	20	AACAAGAGAGACAAGGCCGA	59.989	20	136	0	135
60.082	20	CGGAAATTATTTTTAACACCCG	59.633	22	255	588	842

57.369	24	CGTGCAATTAAATTCAAATCTTGT	59.476	24	250	217	466
59.763	20	TGCGTTTTGATGATATATAGGTGT	60.054	26	121	520	640
59.75	20	GAATAAACAACAATGAAGTGGAA	58.585	25	165	148	312
60.103	20	GAAAGCCAGCATTGAAACCT	59.316	20	259	79	337
59.667	22	TAACTTATTAATCGGGTTAAACAA	58.599	27	100	958	1057
59.966	20	CATCCATGCAATGGAGATGA	60.444	20	216	240	455
59.566	20	TGAAATTTGGCCTTGGAAAC	59.916	20	269	172	440
59.851	20	ATCATTTATTTCGGCAACGC	59.935	20	135	169	303
58.308	20	CGGAACCGGACCATATTAGA	59.778	20	251	86	336
59.964	20	GAAGAACAATTACAATGTTTATCC	57.771	26	204	75	278
58.821	20	GTACGTTGGAACACGTGGC	60.024	19	223	845	1067
59.996	20	TTTTTGCGAGGATTTTGGAC	60.053	20	203	102	304
60.212	20	CGTAAGATTTTTAAAAGAATTGAT	60.128	27	115	135	249
59.989	20	TTAAACCGAATGGCGGTTAC	59.832	20	215	13	227
59.997	20	TTAGCACTTCTGCCTGGGTT	59.875	20	226	613	838
60.118	20	ATGGTGGCTGCATGTCATTA	59.955	20	190	6250	6439
59.971	20	ATTAAATGCGCCTCCCTCTT	60.061	20	179	162	340
59.812	20	GAATTGAGTTTTTCAACTCTATGG	59.17	26	252	1546	1797
59.976	20	CCCAAAAAGGGATAACATGC	59.273	20	240	1003	1242
58.861	22	CCCGCATCACTTGAACTCTT	60.255	20	238	9	246
60.008	20	GTCCACGGGAGAGAATGAGA	60.199	20	279	160	438
59.685	20	CAATTTGACGTGATTTAACGTGT	58.978	23	240	369	608
58.2	21	TTCTGCGACCCTTCACTCTT	59.989	20	280	148	427
58.995	20	GGAGGAATTGGGATTTTTGG	60.482	20	101	192	292
59.607	21	GGTTGTGGCTCAGAGGGATA	60.073	20	232	45	276
59.276	23	TTTTCACCTTCAAATGTCGC	58.747	20	219	453	671
60.112	20	CCTCCATGTTCCTCATCGTC	60.475	20	161	548	708
60.096	20	CCGCCATGTTTCGATGATTA	61.747	20	271	2174	2444
59.95	20	TCCCCATTTTTGATCACCTC	59.727	20	207	73	279
60.223	20	AGGCCGAGTGAAAACCATTA	59.569	20	138	203	340
57.536	20	GGGGTTGTACTCGTGGGATA	59.67	20	262	88	349
59.691	20	TTTTCCGGAGTTCACCTCAC	60.088	20	273	156	428
59.694	20	CGATGTCAAGATGCACAAGG	60.263	20	277	2284	2560
59.987	18	TACCACACGTGTTGGCTAGG	59.634	20	280	1312	1591
60.219	21	AAACCAATATTTTGCGGTCG	59.832	20	270	32	301
59.899	21	ATCTTGCTGCTCCAAGGTGT	59.874	20	130	161	290
59.744	20	TGGGTAGGGGTGTTCAAAAA	60.198	20	232	210	441
60.103	21	AATCATGCTGCATATATAAATGTC	57.471	26	103	107	209
60.118	21	ATAGATTGTCCCTCGAACGC	59.154	20	218	37	254
60.285	20	TCGGAGCGATAAGGAATCTG	60.309	20	276	7	282
59.392	23	GGCGTCGCTGTAATAGTCCT	59.364	20	180	329	508
60.197	20	AAAGAAACAATCCCAACCCC	60.032	20	216	341	556
59.916	20	GACTCCCTTCCTCAACTCCC	60.05	20	236	92	327
59.875	20	CACTCACTTCCTCCGTCACC	60.713	20	166	584	749
58.297	20	AGGGCATCACTAGAAAGCCA	59.836	20	224	32	255
59.872	20	AATCATTTTCCGCACCCATA	60.153	20	171	92	262
58.397	23	CAAATTGATTATGAAGAAATTGG	58.222	25	269	578	846
59.931	20	GCGGTTCCATACAGTGACCT	59.997	20	219	460	678
59.801	20	AGGGTTTTTCTGGGGAGAGA	60.045	20	262	3	264
60.127	23	CACACACACTCTATAAAATGCAC	60.501	26	114	420	533
59.728	20	ATTTGTGGGTGGTTCGTGAT	60.096	20	252	840	1091
59.955	20	GAACGAGGAGAAGGACATGC	59.81	20	172	42	213
60.159	20	GTCCACTTTGTTTCTGCTGCT	59.534	21	100	311	410
60.07	20	ACCTCTCATCACCGTTCCAG	60.112	20	182	7	188
60.444	20	TGCATATCTTGGTGAGTGTATGG	59.897	23	148	333	480
60.088	20	TCACTGGCTTGAGTTTGACG	60.025	20	186	263	448
59.006	21	TCATCGAATCACATGCTTGC	60.79	20	199	1469	1667
59.864	20	GACGGTCAGCCACTCAATCT	60.269	20	196	103	298

60.034	20	TTGGGAGAATTTTCAACTCTTG	58.352	22	191	77	267
59.089	24	CACAAAGGCAGCACTTGTTC	59.49	20	246	7	252
59.894	20	AAATCAAATGGGAATGTCGG	59.622	20	134	18	151
59.992	20	TTCCTTTCCCTCCAAAACAA	59.518	20	218	846	1063
60.111	20	TTTCTCTCTTGGTTGGTGAAGA	58.955	22	105	158	262
57.424	20	CCACGGTTCCTTGGTAATTG	60.22	20	206	491	696
60.025	20	ACACGAGTGTGGAAAGGGAG	60.151	20	161	59	219
59.556	20	AAGGCCAAACGAGAGCTACA	60.015	20	160	187	346
59.924	20	TTCCGGTCCAAACCAAATTA	60.16	20	221	142	362
60.009	20	TCTCGTCCTCCTTCGACACT	59.986	20	225	1	225
59.741	20	CGATACCATCATCCCAATCC	59.975	20	203	545	747
60.266	20	AATTTACACCTGTCCCTGCG	59.993	20	130	247	376
60.309	20	TTGAGTCGAGGAAGATCGGT	59.803	20	112	705	816
60.252	20	ATTGGCAAATATGCGAGGAC	59.929	20	132	29	160
58.554	22	ATCGGTTATCACCGGATCG	60.697	19	160	310	469
59.799	21	CTCGAGTGAGACCGAAGTGA	59.125	20	239	76	314
58.994	20	ATTCAAAGGGCATTTTCGTC	59.022	20	158	340	497
59.96	24	TTTTTATACAAGGGGCGGAA	59.429	20	150	71	220
60.049	20	CTCTGCTGTGAGCATTCGAT	59.143	20	143	64	206
59.635	20	ATGTAAGGCCCATAATCGCA	60.31	20	131	699	829
59.802	24	TGATAACCTTGAGGAAACTTGC	58.378	22	278	9	286
61.391	20	GGGTGGGTTTGGAAAAGAGT	60.204	20	272	78	349
59.989	20	AAATGCCAAATAAAGCTAAATCC	57.912	23	252	2781	3032
60.096	20	CTATGCATGGGTTCCGTTCT	59.955	20	165	25	189
59.984	20	GGCAAATTCCCACAAAAGAA	59.916	20	262	80	341
59.656	20	TTTCGCCCCTTCTAGAGTCA	59.948	20	217	1	217
57.555	23	TCAAGGAGGGTGTATGAGGC	60.073	20	267	5	271
60.147	20	CCATGTTTGTAATTATTGTAGGGA	58.388	25	108	87	194
59.933	20	CCTAGAACTGGCCTCACGAC	59.867	20	156	74	229
60.081	20	GAGAGAGAGGCAGACATCGG	60.096	20	202	82	283
60.074	20	GGCCCTATGCATGTGAAGTT	59.962	20	268	432	699
58.674	20	TCACTCTCGAGCCTAACCGT	60.012	20	211	441	651
58.199	26	ATGTTGGAAACCCTTCCCAT	60.422	20	280	2976	3255
59.019	20	GGATTCCTCCTCCTTCCTTG	60.008	20	202	116	317
59.987	20	TGAGAACCCGGTTTGATTTC	59.91	20	263	6511	6773
58.093	27	AATCGAACCTGGGTCTCTCA	59.655	20	172	10	181
60.081	20	GAATCACACCAACGCCTTTT	59.978	20	158	4067	4224
58.124	25	GGTTTTGACATAACTTAGGTGTTT	59.358	26	119	0	118
59.834	20	TCTTTCGTCGTTCATTGCAG	59.988	20	165	233	397
60.029	20	TGCACCACGTCATCTTCTTC	59.837	20	230	1114	1343
59.933	20	CTTTCCTTTCCTTCCAACCC	59.912	20	256	10	265
60.162	20	AAATTGGCATTTGTGAAGCC	59.945	20	182	748	929
59.777	19	TGGGTGGAACCCTAGATGAC	59.779	20	164	64	227
60.103	20	TTCTCACCAGTCTGTCAACCA	59.294	21	252	1000	1251
59.902	20	GGGTATGATTCGAACTGCGT	59.962	20	246	0	245
60.538	20	ATGAAAAATGAGGGCTGCAA	60.585	20	273	972	1244
59.04	20	AACTGAGTCCCCTACCCGAT	59.817	20	275	134	408
59.724	22	TGGCTACAATACAACGCCAA	60.133	20	190	96	285
61.606	20	AAAATCGTCCCAAATCCCTC	60.131	20	174	0	173
58.844	21	CTGAGCAATCTGTTCGTCCA	59.984	20	224	85	308
59.541	20	TGGGTTTTGCTGTCTTTTCC	60.088	20	178	6	183
60.218	20	GGGGTTAAGATTTGGGGAAC	59.51	20	255	70	324
59.845	20	ATAGGCTTGGGAAAGCAGGT	60.096	20	276	408	683
59.811	20	CGATAAATGGTTGACGGCTT	59.96	20	162	300	461
60.081	20	CCGACCTAGCATAGTGGGAA	60.088	20	263	1403	1665
60.12	20	CCTCTGCAGCTTCCAAAGAC	60.134	20	136	1061	1196
60.969	20	CGCATCATGTTGTTGGAAGT	59.572	20	238	983	1220
59.967	20	TCGGAGTGTTACCGTCTTCC	60.111	20	262	668	929

60.431	18	GTCACTTGCGGGTATTGGAC	60.384	20	149	43	191
59.284	20	GCATAGTTCATTCAAAAATGTCG	58.689	23	211	689	899
57.497	27	TTTAAACTGACGGCCGAGAT	59.708	20	161	68	228
60.61	20	TCCTCTCCAGCCAAAAAGAA	59.926	20	203	278	480
60.12	20	CCCAAAAATTGAACATATCGAA	58.848	22	194	546	739
60.039	20	TCGAGATGGGGTGCTTTTAC	60.074	20	234	97	330
59.871	20	GCCTTCTAGCATCTCTTGCTCA	61.155	22	234	176	409
59.923	20	GATGATGATTGCCCCATTTT	59.587	20	132	300	431
59.228	21	GCAAACGATCAATCCCTGTT	59.939	20	270	741	1010
59.647	20	GGTTAAAGATCAAACCAAACACG	59.801	23	276	99	374
60.096	20	CACATGGATAGAAGGGGTGG	60.187	20	192	898	1089
60.051	20	TTTTGGATCCGAACATCCAT	60.133	20	278	1571	1848
59.951	20	ATGTAATTCATTCACGCGCA	60.103	20	112	42	153
59.813	20	ACGTTGATAAGCCATCCCAG	59.955	20	229	12	240
59.946	20	AACCTCATTGCTCTCCGCTA	59.978	20	144	323	466
60.853	20	CGCCTTTATGTGACGTGGTA	59.609	20	258	2450	2707
60.019	20	TAAGACTGGTGGGAGTTGGG	59.959	20	187	275	461
59.731	26	ACGGCGGAAACATTAGACAG	60.132	20	208	86	293
60.103	20	TAACCCCCAAAGCTATGCAC	59.96	20	274	496	769
60.249	20	TCCCAAAAGCAATAATGCAA	59.146	20	268	285	552
59.769	20	GTTGGACTTTTGGCCTTTGT	59.077	20	176	332	507
59.988	20	TCTCACGTCTCACACCCTTG	59.864	20	255	15	269
60.386	20	TCGTGTTCTATATTCCCGTATCG	60.226	23	102	957	1058
60.006	20	TTGACCACAGCAGTACGACC	59.751	20	217	324	540
59.156	23	ACCACGCCAGTCAGGTAAAC	60.035	20	220	318	537
59.405	20	AGACACATGCACTCGCTACG	60.08	20	154	211	364
59.996	20	GGCGAGCCATATGTCATTTT	59.929	20	114	3603	3716
59.805	20	TGTGGATCTTGGTTTGGTGT	58.827	20	254	205	458
58.903	20	GTGTTGGTGGACGAGGAACT	60.009	20	186	45	230
59.967	20	CCCAACTGTTTCAGCCATTT	59.971	20	121	545	665
59.596	20	ATCGTATTTTCATCGACGCC	59.929	20	151	475	625
60.733	20	TGGAGAGGGTTGTTGGTGAT	60.363	20	101	107	207
60.041	20	GGGTATTTATGATATTTCCAACAC	57.935	26	228	11	238
60.532	20	CCACTAGGGGTGGCAATCTA	59.948	20	229	1235	1463
58.743	20	GGGCGAGTTAAGCTCGAATA	59.456	20	239	27	265
60.015	20	GAACTCAAACTGGTTGGGGA	59.943	20	244	333	576
59.293	20	GCTGGATTGGCATCATTTTT	59.907	20	246	107	352
60.626	20	GCTTGATTTTCCTTCCTCCC	60.017	20	156	33	188
57.53	21	CGGTCCAGTCTAAACCCAAA	59.964	20	260	32	291
59.926	21	ATGGCGAAGAAAGCTACCAA	59.845	20	267	41	307
60.488	20	TGTTTTCTAAAAATAGGACACACC	59.056	25	224	155	378
57.837	20	GCCTATCAGGTCGTTGTGGT	59.997	20	148	34	181
59.978	20	CCCTTTTCGATCCTTTGTGA	60.044	20	157	73	229
58.941	21	AAGTTGGTTTCCCACAGACG	60.005	20	162	114	275
60.519	20	TCCACTTGCAGCATTTAACAA	59.359	21	216	446	661
59.316	20	TTGGACAAAAGTACCAGGGC	59.971	20	272	1493	1764
59.261	22	ATTTCGGTGAATGCAAGACC	59.939	20	280	1467	1746
58.558	27	GCACCACACCGAACTCAATA	59.572	20	206	39	244
59.288	20	TCATATGTCACGTTAAGACATGGA	59.406	24	223	382	604
59.944	20	GACGACAACGTTGGTGTTTG	60.049	20	162	980	1141
59.734	20	TCCATGTGTATGCTGCTGGT	60.144	20	213	299	511
60.088	20	GGTGTGAAGAACTCCCTTGG	59.549	20	158	28	185
59.769	20	ACGCAAATCCTAACAGTGGG	59.993	20	254	1082	1335
59.872	20	GATGATGGGGAGGGTAGGTT	60.015	20	182	20	201
59.803	20	CCGAGGTGGAGTAGTATCCG	59.569	20	176	339	514
57.301	23	GGAATACGATTCGGAGCATC	59.491	20	270	1	270
59.861	24	TCCGGAATTAGGTGAAAGCA	60.576	20	160	213	372
60.441	23	CACGTTTCTTTAACCGCCTC	59.747	20	220	21	240

60.605	20	CTCTGTCACCCCAGAAAACC	59.549	20	127	1551	1677
60.042	20	GCCCTCATGACTCTCAGCAT	60.381	20	280	824	1103
59.691	20	AACACCTTAAAATGTCGCCG	59.996	20	221	78	298
58.93	20	CATGTGTCTTATGTTCGCAGG	59.209	21	236	2510	2745
58.079	23	GCTACCCTTTTTGACCTACGG	60.008	21	254	26	279
59.578	21	TGTTGTTCGGGTTGATTTGA	59.941	20	101	51	151
60.713	20	GAGTTTGGGAGTTGAGCTGG	59.844	20	228	570	797
59.826	20	AATTGCGGAGTTGCTGTTTC	60.257	20	278	5190	5467
60.001	20	TCCTGAAAGCAAGCAAAGGT	59.993	20	170	1102	1271
61.031	20	CAAAGGCCCACAATGGTTAT	59.685	20	110	17	126
58.51	27	TTCCCCAGTGTCACACAGAC	59.55	20	122	3	124
57.083	25	AGTGACCACCCAACCACAAT	60.135	20	216	66	281
60.626	20	CCCACAAAATAGGGGGAAAA	60.873	20	175	233	407
60.184	20	TCACTCTCATCTCTCTCACCTCA	59.19	23	258	142	399
59.916	20	TCTTATGCCAACAAGACGAAAA	59.758	22	178	25	202
58.264	25	TATATGCTCGCGTTTCATGC	59.832	20	146	272	417
59.062	20	AGCAATGTTGTTGGGTGGTT	60.277	20	135	1118	1252
58.273	23	AGATCTGCTCACCAATCGCT	59.981	20	272	15	286
59.864	20	AAATCGTGTTTCGTGCATCA	60.119	20	209	213	421
60.366	20	CTTGCCTAACTCCTCCTCCC	60.204	20	208	81	288
59.943	20	GATTTCTTTGGGCAGAACCA	60.051	20	107	757	863
57.552	24	CGAGAAAGGTTTCTTCGCAC	59.993	20	220	6	225
59.894	20	GGTCTTTTGTGTTAACATCATGC	58.553	23	223	292	514
59.072	20	ATCAGCTGTCCCTTTTCCCT	60.074	20	260	155	414
59.956	21	GACGGAGGTGATTCTTTGGA	60.05	20	190	256	445
57.734	23	AAAATGAAATTGATCATTTGAGGA	58.904	24	254	56	309
59.962	20	GAGGCAACTTGGGAATTGAA	60.051	20	273	2324	2596
60.615	20	GACTCTGCATTTGAGTCGCC	60.956	20	265	387	651
60.061	23	CCTTCCTTTTGCTTGTTGGA	60.22	20	133	142	274
57.606	22	TCACCATAGGATTCTCTCAATCTG	59.615	24	275	12	286
57.588	23	GGGTTCCCACGTCATAAAAA	59.662	20	104	1412	1515
59.518	20	TCTGCATTCTTGCATATCGG	59.792	20	163	1285	1447
58.842	22	TCAGCCTTATCTCTTGCCGT	59.978	20	196	16	211
59.996	20	AATGGCTGTGGAGAATCCAG	60.073	20	189	201	389
60.017	20	CGGTTCCAAATTGCTCCTAC	59.569	20	244	357	600
58.885	22	AAGCCTCCAGATTTAAGCCC	59.688	20	267	76	342
60.334	21	ACGCCAGCCTCACTCAAA	60.557	18	131	3	133
59.803	20	TGTTCTTGTGTGTGTGCGTG	60.412	20	272	627	898
59.664	20	ACGGAAAAAGGACTCCGACT	60.11	20	277	246	522
60.006	20	CGTTCCCATGGCCAGATA	60.435	18	174	36	209
60.039	21	AAACCCGGAATGGGTAAAAA	60.393	20	279	8	286
59.485	21	TCGACCTCGTGCTAATGATG	59.823	20	217	192	408
58.909	20	ACGGATCGGAAATCCATAAA	59.23	20	193	994	1186
60.292	20	GAGATCGGAGTGACTCTGGC	59.952	20	151	60	210
60.177	20	ACATACGTTCCTCGGACAGC	60.142	20	158	328	485
60.134	20	GCACAATTAAATGCGCGATA	59.705	20	171	131	301
60.088	20	GCAGCAGCTGAATCACAACT	59.195	20	145	1595	1739
59.691	20	ATCAGAGCCGAGGTTGAGAA	59.95	20	144	7	150
60.255	20	CTACAAAATGCGCGAGATCA	59.976	20	210	3425	3634
59.293	20	GGGGAACTTTAATTTTGTGCC	59.708	21	246	448	693
60.539	20	CCGTTGAGCCGAATGTTTTA	60.989	20	280	44	323
60.214	23	CCTGTGTGTGCTCCAATCTG	60.309	20	214	790	1003
60.408	21	ACGAAATTGCCCTTGTATGC	59.967	20	203	84	286
60.088	20	ATCACATCATCCTCCCCTTG	59.737	20	266	1	266
59.883	20	TTTCGTGTGTGTTCCTCTCG	59.873	20	229	108	336
61.021	20	AGAATTCTGCCTCCTGCAAA	59.955	20	196	1857	2052
60.593	20	ATCGATGTGTTGGCATTCAA	59.931	20	193	246	438
60.155	20	ACGTTCCGGTCTGTATTTCG	59.993	20	259	2347	2605

60.096	20	TCTCAACCATCACGAAATGC	59.654	20	269	1280	1548
59.107	21	TGAAATTTGGAAATAAGGAGGTG	59.382	23	102	686	787
60.04	20	TCTTTCAGCACAAATGCGAG	60.134	20	246	3328	3573
59.64	26	CTGAAGGCCGATATTTGCTC	59.807	20	264	907	1170
59.923	20	CATGTGGACCATCGATCTTG	59.918	20	173	13	185
60.096	20	GTCAGACCAGCTCCCCTTC	59.783	19	192	1002	1193
59.995	20	TTGACCAAGGTGAGAATTTGAA	59.587	22	216	27	242
61.066	20	TGGATTTCATCATCAAGTCTCC	58.984	22	208	51	258
60.229	20	ACGGCAGCTTCTCTCATGTT	60.02	20	213	816	1028
59.998	20	ATTGATTGTTAGCGGATGGC	59.929	20	224	830	1053
59.212	20	TTGTGAATGTGGTTTATTTGGC	59.742	22	136	12	147
59.801	20	TCTCAAACCGTGAGATGAGATT	58.792	22	183	962	1144
59.931	23	TTCCGTTTGAACTTTTCATTTTT	59.098	23	277	194	470
59.395	20	CGGATTTAAAGGTTATTACCTGAT	58.157	25	223	889	1111
60.151	20	GCCTTTGCCCCTTTCTCTAT	59.688	20	263	85	347
60.723	20	TTTCCGAATATGAAAACCGC	59.907	20	257	104	360
60.102	23	TGGATATGGTTTTTGCAGGG	60.692	20	168	89	256
59.273	20	TCGTCCAACCAAATTGTTGAT	60.22	21	268	607	874
60.656	18	TGACAATGTTATCGATGGCG	60.488	20	169	5	173
59.973	20	CGTACGCATGTTCAATTTGG	59.992	20	168	2171	2338
59.789	20	TGTCGAGACAATCGTGGAGA	60.402	20	244	467	710
58.991	21	GGGTTTAAAATAGCGCGTTG	59.624	20	156	326	481
59.823	20	AATTAAGATTTCGGGAAATTAGTC	57.21	25	243	167	409
57.308	27	ATCAAAATTCCAATTGGCCC	60.865	20	179	11	189
59.61	18	TGCAACTCCAATAAAGAATTTGG	60.342	23	254	26	279
60.227	20	CGAACAAGGGAAAACAATGG	60.336	20	264	276	539
59.705	20	CAATCAACATGCAAGCATCA	59.232	20	194	4	197
60.012	20	AAACAGCCGTTATCAGCCAC	60.14	20	254	80	333
60.029	20	CCTTGGCTATAAAAAGGGGC	59.93	20	161	532	692
60.188	20	GCGGGTAAATATCAGTTTTTGA	58.2	22	237	191	427
59.901	20	TTTGTGATGCTCCATGCTTC	59.805	20	168	378	545
59.846	20	TCAAGGGTTAGGGCTTGCTA	59.839	20	186	195	380
59.653	20	AATTGAATGGCAAGGATTGG	59.762	20	184	2116	2299
59.717	20	CGCCATTTTAGTGGTGGAAC	60.365	20	222	104	325
59.989	21	GTCCTCCGAACTCATGGTGT	59.969	20	256	54	309
60.134	20	AACCTCAGTGTTGCAGCAGA	59.622	20	275	179	453
59.903	20	TGCGATTCTGGAAGTGAATG	59.799	20	175	583	757
59.91	20	GTACGGTTGCTCATCAGCCT	60.285	20	264	1891	2154
59.957	20	TTTCCCACCGAAAGCTACAG	60.241	20	255	2060	2314
60.786	20	CTCTGAGCTTGGGAAACCAG	59.982	20	100	373	472
60.659	20	CCCAAGACCCCAATTTGATT	60.91	20	260	381	640
60.22	20	GGAGTGTAATCAAATGAGAGCAA	59.672	24	178	67	244
60.361	20	GTGCTTTGTGTTGGTGGATG	60.008	20	243	487	729
59.953	20	TGTTTCATGTGTCCATGTTTCA	59.864	22	235	2567	2801
59.803	20	ATGAAACTGCGTTCCCACTC	60.119	20	246	530	775
60.32	20	GGTTCTCACAGGAGGGTTCA	60.088	20	177	53	229
59.157	20	TGCATAGGTTGTTTCATCATCTT	58.642	23	265	243	507
59.894	20	ATGTTTTTCGGATCCCTTCC	60.131	20	228	10	237
60.035	20	AGTGGGGAGCCTTACCTTGT	59.994	20	265	180	444
59.928	20	GCGAAGAAACATTCAGGGAA	60.192	20	171	9	179
60.088	20	AGGCCTAAAATGCAAGCTCA	59.982	20	252	2030	2281
59.982	20	CCCCAACAAAAACACCAAAC	60.103	20	262	2634	2895
59.52	20	ACCTTCACCAATCACTGCCT	59.579	20	222	632	853
58.923	20	ACCTGGACTCATGTGGCTTC	60.12	20	264	1366	1629
60.277	20	TTTGTCTCCCACATTCATGG	59.343	20	180	632	811
58.544	21	AAAGCCTACCTTGCTTCCGT	60.262	20	233	35	267
59.778	20	TGCCATTAATGACGGTGAAA	59.93	20	176	15	190
59.047	23	CCGGAAAATGTGGATGAAA	59.31	19	280	10	289

60.168	20	TCACCAAAATCTATAGTTATCACA	59.412	27	170	342	511
59.917	20	AGCAGCAAGAACAAGGTGGT	59.914	20	252	770	1021
59.731	23	AGAACATCAGCGGGCATATC	60.066	20	173	236	408
59.919	20	ATTTCTCACTGACTTGGGCG	60.255	20	126	172	297
61.003	20	TGTGTGTGTCCAGTAGGGCA	61.223	20	280	784	1063
59.811	20	TTAAACCCTAAAAACGCGCA	60.593	20	279	323	601
59.36	24	GCAGTGGATTTTTGGTGATG	58.976	20	212	1637	1848
59.784	20	CGTGTGGATTGTAGCAGGTG	60.175	20	170	24	193
60.195	20	AAACCCAGTAATCTCAGCCG	59.195	20	119	7	125
60.016	20	TATTGACGCGTTTTGGCATA	60.096	20	223	134	356
58.943	20	TGACGTGGCATTTTCAGAGA	60.39	20	263	18	280
59.872	20	TTCGTTTGGCATGTTTGTGT	60.011	20	267	296	562
60.315	23	CATTGTACTACATGGATGAATGAT	60.03	26	223	388	610
58.995	25	TTGACGTTTCACCTAACCCA	59.021	20	208	258	465
59.779	20	GCAAGACCTCCACACACAAA	59.726	20	274	234	507
60.448	20	CAAAAGGCCCTCAATGGTTA	59.931	20	135	3020	3154
60.017	20	TTGCCCAACTCATGTAGCAG	59.864	20	276	466	741
60.186	20	TATTTCGAGAAATGGCACCC	59.901	20	273	143	415
60.038	20	TGCGTTTTGACAATATATAGGTGT	60.083	26	194	2885	3078
59.91	20	CACCCTCTCCGAACAACATT	59.966	20	224	775	998
59.866	20	TCGGAGTAGATCTCAACACGC	60.412	21	239	43	281
59.844	20	TAAACGCCGGTGAGGTAATC	59.96	20	138	314	451
59.969	20	ATACCGGCCTAACCTATCCC	59.182	20	257	0	256
59.655	20	ATCGAAACACATCCCCAAAA	60.17	20	222	352	573
60.096	20	TCAACCTCGCAGATTGATTC	58.799	20	175	1148	1322
58.792	20	AAAACCAATGGTGGAGCAAG	59.971	20	236	896	1131
60.168	20	AATGCTCGAGGGCTAAAACA	59.845	20	208	138	345
59.071	21	TTGATCGATTGTTTTCTTGGC	60.067	21	147	668	814
60.209	26	GCAATAAGTGAGTGACTTCCCC	60.004	22	222	14	235
59.911	20	TGAAGTGTTATGCGTTTTGACA	59.274	22	169	94	262
59.476	20	TGAGTTATGAAGTGTTATGAAGG	59.11	25	165	176	340
60.173	20	AGTCGCTGCAATTTCCAGTT	59.882	20	112	29	140
60.036	20	CACTCTCCTGCTCCAGCTCT	59.883	20	183	27	209
60.269	20	CGGTTAGTCCAGCCATCTCT	59.308	20	186	173	358
59.374	24	ACCAATGGTGGTATGGTGTG	58.984	20	102	17	118
60.262	20	ATTTCATTTCATGGGTTTCG	57.399	20	180	42	221
60.025	20	TGCGCTAACAAGGTCCCTAT	59.73	20	144	221	364
59.835	20	TTGAAGATCAACGGTCCACA	60.088	20	183	41	223
60.299	20	TTGGGTTGAAATGTTTACATGG	59.603	22	195	152	346
59.901	20	AAACGCCACTTCAAACCATC	59.978	20	120	307	426
60.104	20	CACCAAATTTGAGGGTTATTATTT	59.905	25	260	187	446
60.202	20	CGGATTTAAGGGTTATTACGTG	57.682	22	212	36	247
58.956	21	TGAAATTAGATTCGAAATTGCAT	57.856	23	184	151	334
59.871	20	CAGTTGCACCCAACACAAAC	60.049	20	274	535	808
59.827	20	AGCCACTCCCTCCAAAAGAT	60.074	20	141	116	256
59.72	21	CCGGTTTCGTGAGCTTTCTA	60.378	20	240	30	269
59.534	21	CATCCAATTTTGAGGGTTGG	60.162	20	233	680	912
59.971	20	ACGGGAGAGGCATACAAATG	59.955	20	170	2183	2352
59.95	20	CGATCACACTCCAAATGCAC	60.12	20	237	773	1009
60.11	20	TCGAGGAGCGTGGTTTTAAG	60.378	20	181	37	217
60.423	20	TGGAACCATGGGTAAAACAA	58.719	20	246	123	368
59.532	21	CCACACGACATACGATACACG	59.92	21	128	244	371
59.921	23	TAATGCAAACGGGATGTCAA	59.93	20	249	2095	2343
59.972	24	TGTTACTTTTCATCGCACTCAA	58.489	22	243	1255	1497
59.883	20	TGCGTGATTTACACCCGATA	59.953	20	122	173	294
59.989	20	GGTTTTCTCCGGTGATCGTA	59.933	20	217	36	252
59.96	22	AGCAATTCTGATGGAATGGG	59.894	20	235	48	282
60.036	20	ACTTGTCCACCCACATGACA	59.846	20	232	1132	1363

60.081	22	CAATCCCCTCAAACAAAATCA	59.787	21	279	1097	1375
59.898	20	TTTGCAGTTGCACCAGTTTC	59.888	20	239	53	291
60.051	20	TCACTCGCGCTAGATTCTCA	59.847	20	125	276	400
58.189	27	TTGATTCTGGAATATCCCGC	59.862	20	242	2	243
59.81	20	TCGTTGTAAACCCGTAAGGC	59.996	20	220	81	300
60.008	20	CATCACACAAAACCAGTGGG	59.848	20	197	289	485
60.036	20	CCGGTATGCTGACGATAACA	59.566	20	241	1013	1253
59.465	20	ACAAATAGATCGGGGGAAGG	60.145	20	272	89	360
60.293	20	CACAACATGACAGCAACCCT	59.597	20	240	7	246
60.34	20	CATGCCTTAAAATCCACGGT	59.823	20	228	9	236
60.278	20	GAGATGGTTGCACCATAACG	59.002	20	212	31	242
59.685	20	GACGAGATCATGGCTCGATT	60.189	20	164	99	262
57.898	26	AAATATTTCTAGCACATGAAATTG	57.859	25	114	1	114
59.226	20	GGTTTTGACCATATTTACTGTTTTG	59.631	26	267	199	465
59.91	20	TCAACAACCAGTCCACTCCA	60.129	20	208	100	307
59.927	20	GCAACGGAATACCACTCGTT	60	20	163	87	249
59.621	22	TGAAAAGCTTTGAGTGTGCC	59.05	20	158	657	814
60.445	21	AGGGTTTAAAATCGCGCA	59.257	18	280	693	972
59.801	20	CAGCATATTCTTTGGACGGAA	60.081	21	247	124	370
59.668	20	ATCGCTCCACATGACACGTA	60.144	20	244	131	374
59.694	20	GTTGGTCCATTTGCCATTGT	60.624	20	216	48	263
59.549	20	TGAAATTGTCATCTCCCCCT	59.336	20	211	69	279
59.937	20	TTCTTTTACTTTGCATGCTACTTTT	59.476	26	280	275	554
59.727	20	CTGGAAAGATGGTGGCAAAA	61.001	20	278	248	525
60.547	20	ACGGAGCAAATTCAATCCAC	59.939	20	278	244	521
60.034	20	GAGACCCGGGTTTACCTCTC	59.935	20	132	88	219
58.842	22	ACCATCGTTACCGATTTCCA	60.192	20	193	32	224
59.773	20	AAATTTAACATGGTCCGCCA	60.188	20	227	82	308
60.004	21	AAAAACCCTGATGTGGATGC	59.797	20	273	28	300
58.976	20	TTGGACCAAAATAGCCTCCA	60.439	20	166	10	175
59.259	20	CATTGATCATCACCCTGTGC	59.925	20	209	3	211
59.96	20	CCAAGTCTTGCATTTGGTTG	59.17	20	217	1568	1784
60.282	20	TCCCCAACTCAAGGACACTC	60.088	20	258	356	613
59.847	20	GAATCATGCTACTACACGTCGC	59.803	22	260	495	754
58.028	22	CCCATTAATAGCGATATATGTAAG	58.562	27	140	151	290
60.074	20	CACCTAACCCATTAACCCCA	59.541	20	243	49	291
59.787	20	TTACCGCTGGGATCATTTTC	59.901	20	181	98	278
59.783	20	GGATGGGTTATCACTTGAATAGG	58.769	23	102	153	254
59.989	22	TGAAGTTAGGAAATAAGGAGGTG	58.743	25	254	213	466
60.027	20	CCCTCCAAGGAATCTGATGA	60.003	20	239	14	252
60.333	20	CAAGAAGTCCTGCGTCAACA	60.025	20	173	1	173
59.635	24	GGGATAATTAATGCGATTGTGA	58.83	22	274	540	813
57.221	24	TCTGTTTTGAGCTGGCAATG	59.988	20	190	47	236
60.416	20	GCTCCTTGTGCATCACTCAA	59.992	20	268	226	493
59.61	20	GAAGTCTCAAGTCAATGTATGAT	57.445	25	115	570	684
59.706	20	GAACGGAGAAAATATCACGAAAA	59.512	23	237	576	812
60.088	20	TTTCTCAACCGAGCTCACCT	59.989	20	121	833	953
59.486	20	TTCCAGATGCCTCTCAGCTT	60.096	20	279	1775	2053
59.996	20	CACCCCGGATAGTAATCCCT	60.032	20	271	480	750
58.276	27	TTTCTCAAGGGTATGGGTGG	59.784	20	246	29	274
60.02	20	GCCTTGAGGGGGAGAATTAG	60.032	20	167	77	243
58.82	27	TGAAATAGGAAATGCAGGGG	59.894	20	272	2	273
60.111	20	TTTCACCACCTCCATTCCTC	59.903	20	273	65	337
60.029	20	CACTGTTGTCATCGGTCCAC	60.005	20	245	103	347
60.232	20	TGTGGAAGGGTGTGTGATGT	59.846	20	274	1388	1661
59.547	20	TGATCTTCACCTTAAATCTGCAT	57.9	23	259	70	328
59.123	23	AGTTTGGGGGAGGAGAAAAA	59.912	20	279	65	343
60.02	20	AAGGAGGTGTTATGAAGGGATT	58.028	22	268	40	307

59.81	20	AAGGTTGGAGAGGGGACAAC	60.349	20	224	10	233
59.967	20	GCTCGACGGAGGTTTGATAG	59.836	20	165	389	553
58.651	20	ACCTCAACAAACCACCCAAA	60.246	20	204	26	229
59.833	20	AAAATCACTAACCCACCCCA	59.146	20	191	34	224
60.199	20	ATGGCCATCTCTTTCCCTTT	59.903	20	196	402	597
58.745	20	CCCATTTTCTTCTGCTCCAA	60.184	20	183	1144	1326
59.923	20	TTGTCCCACATAGGAAAAATAAA	57.644	23	243	447	689
60.257	20	TTGTGAGTGAAAGTGGTGGG	59.565	20	118	716	833
59.476	20	GCCTCGGTGGAATTTATTGA	59.901	20	264	2392	2655
59.859	20	CATGAGAAATGGGGTTGCTT	59.933	20	180	32	211
59.751	20	TGCACAATACAAGCACCCAT	59.995	20	123	880	1002
59.726	20	CTCGTGTTTTATCCTCCCCC	60.683	20	107	4	110
59.919	20	ATGGTGGTTTGGTGGAAGAA	60.21	20	189	600	788
59.971	20	ATTATGGCGCCGCTATTGTA	60.452	20	152	253	404
59.844	20	AATTGTCTGGAGCCAAGGTG	60.111	20	235	243	477
60.065	20	TCCACGGTGATGCTAGAGTG	59.855	20	212	452	663
57.201	27	TGGGCTGAGTATGTGTTTGTG	59.624	21	145	3	147
60.049	20	TTCTGAAACATGATGGCGTC	59.654	20	239	1371	1609
59.485	20	CCAAGTCAATTGTCGATGGTAA	59.861	22	269	815	1083
59.928	20	AGCTTCCATGGAGGTTGATG	60.073	20	165	237	401
59.181	21	GGAAGCACTTTTTGAACGGT	59.218	20	254	395	648
60.582	20	TCAGCCGACTTTTTAATGGC	60.209	20	192	37	228
57.73	23	TTTTTAAATGGACGGTGATGA	58.005	21	117	14	130
59.962	20	GGTGTTTGTTGCTTCGCTTT	60.292	20	231	566	796
59.831	20	TCAGCAGAGCAAAAGGGTCT	60.134	20	265	1757	2021
58.909	21	GCCTAAGGAATAAACACCTAGCA	58.895	23	235	24	258
60.051	20	GGGATGAGTTATCACTTGAATAG	59.765	25	215	291	505
59.904	20	CCTATGGTGGTATGGTGTGG	58.569	20	248	214	461
59.951	20	TACGTGATAGGATACGGCCC	59.807	20	276	44	319
59.973	20	TTCCGTTGGCAAGCTAACTC	60.386	20	268	751	1018
60.195	20	CATGAAAATCATGTTCCGCA	60.466	20	159	312	470
59.975	20	CTCCAAAATGGTGCAGTCCT	60.111	20	204	423	626
57.414	24	ACACGAATCAAATCAATGGC	58.424	20	277	27	303
59.894	20	CAAACAAGACCAAGTGGGGT	59.861	20	131	283	413
59.923	20	GACTTGTGTGGGGAATGGAT	59.636	20	272	364	635
60.172	20	ACCGACGTGGCCTAACATAG	60.015	20	261	240	500
59.656	20	CAAATGTTGCACAATCATTGAC	58.945	22	211	77	287
60.238	20	GTTTGGATATCGAGATCGGG	59.344	20	117	96	212
59.072	21	ATCATAGTTGACGCCCTTCG	60.096	20	103	19	121
59.993	20	TATTCCAAAACCATCGCACA	59.93	20	277	79	355
59.505	20	TGCTTTGGCTTGGTCTTTTT	59.861	20	224	1103	1326
58.516	21	TCGGAGTTCATCATGACACAA	60.104	21	186	346	531
60.053	20	TGTGGTTCGATATTTTGTTTGG	59.736	22	118	222	339
60.111	20	AGCCTGCAATTGATACCGAG	60.235	20	239	679	917
60.397	20	TCCTAACTTCATAACTCGAAGACT	59.858	26	279	0	278
59.991	20	ATTAACCGTGAAAATGGCGA	60.323	20	154	331	484
59.75	20	GCAAACCATACACGAACACG	60.035	20	204	108	311
59.53	26	CAGGATGGACTCGAACGAAC	60.656	20	144	9	152
59.573	21	TTTGTCACAGTATTTCATCATTCG	59.055	24	192	4755	4946
59.923	20	CGTCTGCGCTGTAGATTCAA	60.157	20	134	259	392
59.901	20	GCCGGAGATTATCCATCATT	58.812	20	270	85	354
60.356	20	AAGGCCGAGATTTGTTAGAGG	59.733	21	174	1789	1962
60.701	20	ATGGCTTGGAAAAGATGGTG	59.933	20	266	930	1195
60.339	27	AAAATCCTGTCAATGAAAAAGCA	59.997	23	273	89	361
59.303	21	TGATGGGCCATAATCAAAGG	60.66	20	149	368	516
60.088	20	TTGCAATGGACCTAAGCATTC	60.089	21	119	947	1065
60.074	20	AGGTTGATCATTTCCATCGC	59.9	20	164	1034	1197
59.679	20	GAGAATCCATGGCGGAAGTA	60.036	20	124	636	759

60.309	20	CCACCCATTCATTCCCTCAT	61.882	20	100	147	246
57.643	26	GCTACTCCCGTCGAAGATTG	59.836	20	234	13	246
59.83	20	GCCCAACAAATGAACCGATA	60.701	20	278	2118	2395
59.927	20	TCTTCCCCAAATTGGTTTCC	61.023	20	187	199	385
59.939	20	TTCTCTCATTTCCCCAAACG	60.044	20	228	484	711
58.756	24	CATGGAATGGCTGTCAGATG	60.072	20	106	20	125
60.278	20	TCATGAGGACGAATATGCCC	60.833	20	195	2	196
60.917	20	CAACGTTTGTTCGTGTTTGTG	60.096	21	212	18	229
60.153	20	GGCTACGAGAAATGGATGGA	60.036	20	144	705	848
59.522	20	CACACACACGTGGCATGATA	60.029	20	147	69	215
60.096	20	CCTCCCGTCTAATCTCCACA	60.065	20	239	20	258
60.562	20	CGGAAATGACCCCATAATGA	60.523	20	256	253	508
60.353	20	GCAGCTACGTTTGTGTGCAT	59.942	20	129	1229	1357
58.672	20	AGATCCATGTTCATCTCCCC	58.741	20	130	87	216
57.587	27	GATGATCACGATGAAGCCAA	59.61	20	172	77	248
60.134	20	ATTTAGCAAGCCCGATGATG	60.06	20	145	727	871
60.423	20	CCTCCAATGATTGCCAGAAT	59.894	20	166	364	529
60.202	20	TTCAATCTCAACCATCAATTTTT	57.674	23	204	478	681
60.216	20	CATATGGTGAATGCCCCTTT	59.645	20	163	254	416
60.103	20	CTGGTTTGCGTGGTTCTTTT	60.147	20	224	660	883
59.648	20	CTGTTGGCCGTTGTTTTACA	59.627	20	201	1138	1338
58.857	21	CTCTTCATTGACACGCGAAA	59.988	20	275	155	429
61.027	20	CCCTATTTAGCTTTCTTTGCGA	59.885	22	259	29	287
60.21	20	TATGGAATTCCGACGAGCAT	60.435	20	276	478	753
60.029	20	TGTGCAACTTGTCTGGTCTCA	60.494	21	275	566	840
60.031	20	CAGTTCTGGCCGTGCATT	60.84	18	209	656	864
59.402	22	TGGAATCCGAGAAAATCAGG	60.006	20	190	895	1084
59.761	21	CCTCCGTATTTTGGGTAGCA	59.953	20	200	1004	1203
60.035	20	ATGTGCGCGTGTACTTATCG	59.782	20	188	669	856
59.95	20	TATTGGGGGAAGAAGCACTG	60.066	20	231	2020	2250
59.664	20	TTGAATCCATTGGTGAAGCA	60.049	20	202	220	421
59.688	20	GAGAGAAACATTAATTCCTTCACC	59.9	25	179	49	227
59.888	21	TGGTGGAAAGACCAGACAGA	59.23	20	272	0	271
59.756	20	AAATCAAAATAGGGCAGGGG	60.143	20	215	31	245
58.914	20	CTTTTGCTGTGGCTTGTGAA	60.027	20	254	204	457
60.66	20	TGCAGGTTAGGTACCTTCGG	60.125	20	244	2796	3039
60.06	20	TACAGCCGCTCTTGGAACTC	60.538	20	124	75	198
59.364	20	ACGATTGAAACCCTCCCTCT	59.935	20	241	261	501
60.096	20	ATCCGCTTTCCCAAGTTTCT	60.074	20	264	3289	3552
60.565	20	ACCATATTTAAGGGTTATCACCTG	57.552	24	278	254	531
60.081	20	GTTTTGCAGGTGGTGGATCT	59.973	20	171	1179	1349
59.071	21	GCGGATGTAATTTGGGTGAA	60.701	20	231	249	479
60.055	20	AAACCGAGAAAGAAACATTTCAA	59.194	23	201	1102	1302
59.82	20	TTGTTAGTGCGTGTTTTGGG	59.627	20	179	29	207
59.928	20	CGAACTTAGAAGGGCCACTG	59.869	20	235	20	254
59.596	20	TCTCTTTTGGTTGGTGAAGGA	59.697	21	166	290	455
59.126	20	CCTTGTGTGATCAAGGGTCC	60.363	20	176	1771	1946
60.118	21	GCTAATGGTGCCACAGTTGA	59.722	20	264	37	300
59.702	20	ATCAAAGGCCACAAATGGTT	59.292	20	232	97	328
60.406	21	AACTTCTTGCTGGTTGAGGC	59.478	20	263	48	310
60.255	20	GGTTATCACCGGATCACGA	59.311	19	123	687	809
59.032	20	TCCCTTCCCCATCTCAATAA	59.315	20	274	1194	1467
59.934	20	TTATATCCCCAAAAAGCCCC	59.982	20	263	400	662
60.033	20	AGCTCACTAGGATGGCAAGC	59.603	20	201	218	418
59.577	24	AAAAATCATGCCACCGTACC	59.691	20	212	10	221
58.831	25	TTTTAACGAATAAACATGTTCCAA	57.778	24	107	103	209
59.021	26	TGTTTTCACGAATAAACATGTTAC	59.448	26	276	131	406
60.576	20	ATCCATCATCTTCCGTGAGC	60.042	20	199	706	904

59.894	21	GGTTTTCAACCCATGTTTTTG	59.211	21	273	1565	1837
60.263	20	CAAATTTTCCGCTTTGTCGT	60.11	20	199	1032	1230
59.964	20	GGTTATTAGTTATTACGGATTTAAT	57.055	27	164	278	441
60.192	20	CGGACTTCCTTTCTGCAAAC	59.853	20	278	91	368
60.204	20	CTTCGAACATGCACACTCGT	59.905	20	139	449	587
60.096	20	TTGACCGAGTGAAGTAAACCC	59.087	21	241	3285	3525
59.691	20	TTGACATGAGCGCATAAACC	59.694	20	161	941	1101
60.324	19	GCCCTCAACTCTCCCTCTCT	59.952	20	104	9	112
58.522	23	CCGGATCAGCTCTCTTTCTC	59.116	20	180	1608	1787
60.384	20	TGTCGTCTATCACCTTCCGTC	60.126	21	191	63	253
59.927	20	TTGATTCCTTTTGTTCCCTATTT	58.142	23	269	226	494
58.272	27	GGGAGCTTCAGTCTTTCATCTC	59.466	22	118	14	131
60.051	20	TAGAGTTCCAAGAGGGGGCT	60.204	20	202	5	206
60.147	20	TCTCTCAACCTCACTCGCAA	59.701	20	264	418	681
59.104	22	TCTACGACCGAAATTCACTCC	59.184	21	104	23	126
58.811	21	CGAACAAGGGAAAAACAATG	58.121	20	126	90	215
59.848	20	CAAGGGGAGAGAGGTCAATG	59.649	20	266	425	690
57.955	21	TCAACTTTTGACGGTCCGA	60.224	19	280	140	419
59.89	20	AGGATCGGCATATCGAGAAA	59.628	20	276	146	421
59.13	25	TTCTGACTTTGTTTTTGTGCAG	58.135	22	184	39	222
59.991	23	TGACTTTGATCAAGTGATAACATC	60.287	26	174	386	559
60.192	20	TCGGATAATCTGAAAGCGAA	58.455	20	263	1083	1345
59.955	20	ATCCTCCCCTTCCTTGCTTA	60.032	20	150	478	627
59.549	20	CATGTCAAAAATGCCCCTTC	60.309	20	268	483	750
59.499	21	CCCTCCTCACCTCCTCTCTT	59.801	20	263	933	1195
57.551	24	ACCTGCACCAAAATGGAGAG	60.111	20	257	60	316
59.792	20	CCGAATCCATTCCCTACTCA	59.887	20	263	2825	3087
59.484	19	CGGAGTGTTTGGGTAGTCGT	60.028	20	241	150	390
60.214	20	CCACTCCACAAAGATCTCACA	58.71	21	104	212	315
58.826	22	ATGTCCGTCGTTGGTTCTTC	59.973	20	173	24	196
58.45	20	TGCAATGCTTCAATTCATCC	59.628	20	230	0	229
61.027	20	TCGATCACGATAATCACCCA	59.883	20	199	16	214
60.096	20	AGGAGGGGAGTTGTTGGGTA	60.736	20	278	620	897
60.142	20	AAGGTGTTGTTGGGTTTTGC	59.875	20	256	242	497
60.103	20	AAATCCCTTTTCCTCTCCCA	59.875	20	147	245	391
59.777	20	TTGAATGGTTATCACCTGATCG	59.823	22	129	106	234
60.659	21	GCGGAAATTACTTACAGCCATC	59.996	22	178	295	472
59.989	20	GAATCCATGCAAACAGCAAA	59.67	20	161	2331	2491
59.411	20	ATGCGCGTTTTTAGGGTTTA	59.624	20	151	394	544
59.855	20	CATGTTTGGTGACTTGGTCG	60.001	20	244	16	259
59.904	20	CATCCAGGAACCACTTTCGT	59.966	20	265	225	489
59.975	20	AGCCCCCATTTTTCATTTTC	60.13	20	146	253	398
59.751	20	TCTGCAGTCTCCGTTTTTCA	59.566	20	137	407	543
61.532	20	CATGCCAAAACTCCACTCCT	60.111	20	262	298	559
59.88	20	GGACCGGACCGTTAGGTAAT	60.074	20	277	219	495
59.945	20	CCCACATTGGTTGGAGATTA	58.27	20	218	148	365
59.94	20	GAGGTTTTGACGAGATTTAGGTG	59.187	23	142	391	532
60.323	20	ATGGTGGTATGGTGTGGAGG	60.51	20	139	218	356
59.967	20	GAGCGAGTGGTTGTGAGGTT	60.307	20	280	27	306
60.263	20	CGAAAATGAGCTTCCACACC	60.636	20	162	241	402
57.496	21	TTTGATTCTTGAGTACACCATCG	59.144	23	171	57	227
59.148	21	CCATTGACTTGGCATCAAAA	59.518	20	279	109	387
59.992	20	CCATTTCATCTTCGGCATTT	59.901	20	231	74	304
59.941	20	TGATTTTTCATGTTTTGGAGCA	60.468	22	215	302	516
60.578	20	CGTTCCTCTCTCTCTCGGTG	60.127	20	167	60	226
59.962	23	GGCTTGAAGAATGATGAAGATG	58.789	22	113	132	244
59.781	20	CATCATTGTTTCGCAAGCAG	60.401	20	209	1007	1215
60.096	20	TCAACCATCTTGTTCTGTGGA	59.124	21	198	698	895

57.104	23	TGGTACTTAAAATGAGAGAGATG	59.913	25	243	303	545
59.797	20	TGTATCGTCCGCGATGTAGA	60.243	20	152	209	360
59.474	20	CGGCCGGTTTGTAACCTT	60.883	18	256	2169	2424
59.884	23	TGCACCCTTTGACATCAGTT	59.139	20	180	50	229
59.685	20	TTTTTGTTTGTTCCCAGGTTG	59.862	21	105	21	125
58.456	21	TCGTGTTCCGATCCTAGCTT	59.836	20	217	17	233
60.255	20	TAAAACAGAAGCAGACGCGA	59.752	20	154	41	194
59.917	20	TGGTGTGTACTTTTGTAGCAATCA	59.618	24	259	106	364
60.34	20	CAAAAGAGCTGTGGGAGAGC	60.134	20	215	87	301
59.874	24	GATGATGCATGTATACTATCAAAA	57.305	26	245	1336	1580
60.305	20	GGGAGGGTGGTTTGGTTAGT	60.088	20	266	17	282
57.333	24	TCACACTCACGCACTCACAA	60.07	20	121	3	123
59.805	20	TTCGTAGCATGATTTAAATGGTTT	59.021	24	242	575	816
59.827	20	TCCCAAGTGCACAAGTGTTT	59.187	20	276	295	570
59.823	20	ATGATTGGGACACGTGTTTG	59.267	20	196	1618	1813
59.726	20	GTGCAGTAGGGGTTGTCGTT	60.035	20	243	92	334
59.988	22	GGAAATAAGGAGGTGTTATGAAG	59.323	24	137	809	945
60.333	20	TTACAAACACCGATTCGCAC	59.59	20	146	62	207
60.148	20	ACGAAGGGTATTTTGGGAAA	58.417	20	179	208	386
58.974	20	GTAAACCGTCACCCCAAAAC	59.195	20	125	53	177
59.624	22	CCGTCGACAAGCTCAGAGTA	59.187	20	190	4	193
59.992	20	TGTATCACACAACGGTTCATCA	59.888	22	241	246	486
59.94	21	CACCAACCCAACCCATTAAC	59.948	20	105	54	158
59.916	20	GGGTGGTTATGGTTTGTAGGTG	60.385	22	171	1337	1507
60.187	20	CTCCGCCTTGACTCCTTCTA	59.569	20	109	308	416
59.823	20	TCGACCAAAATTTAAAAGTCCT	57.036	22	273	834	1106
58.874	22	TGTGGATATGTAGATGATTTTTGG	59.637	25	184	11	194
60.139	21	GGAGGTCAGGATCTGGTCAA	60.048	20	162	797	958
60.265	20	CCATCACACTAACCTCCCTCA	59.974	21	259	150	408
58.436	26	AAATATCGGCCGTCAGATTG	59.923	20	189	1	189
59.03	22	CAAACCTTGGCACTTGCATA	59.729	20	100	94	193
60.36	21	TGCATAGGCTGTCTCTTGGA	59.547	20	227	108	334
60.362	20	TGGTGCATGAGACGAGAATTA	59.287	21	163	177	339
59.425	21	TTGGAATTGGAACCAGCTTT	59.546	20	272	88	359
59.96	20	GAGAAGGTAGGGGGCTAAGG	59.191	20	180	29	208
60.554	20	TACCATGTGCTTGGAGTTGG	59.566	20	277	1015	1291
59.024	20	CCATGAATCTTTCACATTTTTCA	58.976	23	207	219	425
60.382	20	TGGTATTGGTCCACCTGTGA	59.806	20	207	360	566
59.95	20	AAAGTCAGCCGAGAAATTCAA	58.962	21	143	752	894
59.894	20	TTGACAATATTTAGTGTTTTGACA	58.99	27	187	63	249
60.131	20	TTGTCAAAATCTCATTCATTTGC	59.114	23	126	50	175
60.257	20	CACACGAGCCTTCTTCTTCC	59.989	20	274	70	343
59.875	20	CCTTGAGGACTTCTTGGGGT	60.48	20	118	67	184
58.695	20	AGTCCTGGCACTTTGCTTGA	60.975	20	274	540	813
59.797	20	GTCCTCCGAACTCATGGTGT	59.969	20	179	73	251
60.073	20	CGCATCAACACACCAATGAT	60.399	20	216	52	267
60.195	20	TGGGACTCAAGCTGTTGTTG	59.873	20	240	1078	1317
60.21	20	GTTTGACAGCCCGACAAGAT	60.119	20	247	200	446
60.14	20	GTCGTGCTTAAACGTGGGTT	60.037	20	233	534	766
60.924	20	GAAAGCCTACCTCGCTTCCT	59.983	20	178	642	819
59.801	20	AACCGGTTAAAAACCGAACC	60.089	20	121	391	511
57.845	21	GGAGATCTTGCAGGATAGGCT	59.825	21	255	6	260
59.971	20	TTCACCGGATGAAAAAGGAG	60.044	20	268	67	334
60.157	20	GACGACCGATATTTGCTCCT	59.154	20	155	922	1076
60.088	20	TTCATGAAATCAAGCAAACCA	59.147	21	101	13	113
59.934	20	GCAAGAGTGAGTGAGGAGGG	59.986	20	123	339	461
60.012	20	TCAAGACAACCGAGCAAGTG	60.025	20	187	163	349
59.875	20	CCAACCCATTCTTCACCAAC	60.21	20	212	184	395

59.929	20	ATGGGAATCGGGTAAAAACC	59.888	20	255	225	479
60.081	20	GGGTTCGTTGTTAGCTTTCG	59.747	20	268	284	551
57.001	22	TGTTACGCCCGTGATAATGA	59.953	20	205	1143	1347
60.288	19	TGGATCCCAATGAAAATGAAA	60.117	21	276	390	665
59.986	20	TGAAGAATGAAGGGAATGGG	59.864	20	174	760	933
60.029	20	AGAGCGAGAGATGGACGATT	58.995	20	211	75	285
59.457	20	CAGAACTTGTCGTGGTGGTG	60.194	20	250	109	358
60.196	22	CTCCGGCCATAGTTTCTCAC	59.694	20	126	95	220
58.466	23	CTGTTCTTGCGCAAAATTATC	57.614	21	168	706	873
60.168	20	AAAGAGGTGTTATGAAGGGACAA	59.056	23	220	18	237
60.269	20	AAGCACACAATAACCAAAGTATT	59.08	25	153	64	216
60.073	20	TCCCACTTGCTTGTTGACAT	59.139	20	186	39	224
59.989	20	CCAGCTTCGAACGTTGTATGT	60.183	21	213	1919	2131
59.276	20	TCAAGGAGTTGTACCTGATAGCC	59.666	23	253	1478	1730
59.502	23	TTAGCAGCAGATGCAAAGGA	59.712	20	125	538	662
59.966	20	TGAAATCAGGCCATCTCCTC	60.158	20	221	7	227
59.971	20	CTGTGCTGCTGGAAAATTGA	59.988	20	235	340	574
59.68	23	CACCAGCACCATCGTACATC	59.992	20	211	23	233
59.547	20	GAGGGGGAAAAGAGAGGATG	60.008	20	185	183	367
59.553	22	TCAGCTGACATTGGGTTGAG	59.831	20	268	1372	1639
60.371	19	TCGTAACTGAAAATCATCGGC	60.089	21	246	355	600
60.008	20	TTGGGAAAGCACTATGGACC	59.933	20	241	53	293
60.053	20	TCACTCATTCAAGAACATAGCCA	59.761	23	177	375	551
59.933	20	TGACATGCTCTTAAGGATGGG	60.081	21	100	217	316
59.94	20	CTCATAGTCAAACACGATTGCTT	58.464	23	177	77	253
59.5	20	GGACATGAAGTAACTGCACATGA	60.052	23	272	200	471
59.583	21	GAAGTGGGTGTGTGCTGAAA	59.726	20	173	274	446
59.742	22	TTCCAGGAAATCGGGAGAT	59.425	19	259	401	659
59.801	20	TAGTACGAACACGCGCAGAG	60.217	20	280	512	791
60.595	24	CATTGCACGTACTTAACCAAAA	57.851	22	269	17	285
59.827	20	GGGGTGAATGATCAAGATGG	60.135	20	177	11	187
60.044	20	AGAAGGCGGATAAGGTTGGT	59.962	20	272	3617	3888
59.999	21	CTTCATCACCTTCCCCATTC	59.336	20	249	171	419
60.059	21	GAGGGAGTTGTTTAATTGTCGG	59.871	22	276	97	372
59.415	20	ATTTCCAAATCGGTACATGC	57.424	20	273	881	1153
60.08	20	AAACCCATTTATAACGGCGA	59.323	20	211	258	468
60.134	20	GACTTACGTTCCGCCAACTC	59.74	20	215	1963	2177
59.526	20	CTCGTCAACAGCTCGGTACA	60.049	20	259	135	393
60.119	20	TCCATCTTCGTCCACCTCTT	59.655	20	107	15	121
59.694	20	CTAGGGTTAGCATGCTTGGG	59.724	20	220	2	221
60.008	20	GTCCTCGCGAAACAGAGATT	59.434	20	135	317	451
59.325	20	GCTGGGTAAAACTGAATAATACC	58.575	24	109	129	237
59.458	20	TTTGCCTCTCCATCTCCATC	60.158	20	277	5	281
60.048	20	GCAAAACTTAGGAACGAAGCA	59.527	21	218	24	241
59.923	20	TTGAAATCCTTGAACCGTGTC	59.963	21	153	150	302
60.466	20	ACCATCTCGGGTTGTAGTGC	59.997	20	163	630	792
60.066	20	GCTTTATGTTGTTGATCCGTCA	60.003	22	152	30	181
60.088	20	CAGCAGATGCTTTCATCCAA	59.948	20	132	922	1053
59.978	20	CCGTCGTCGTTATGAAGAAAA	60.117	21	149	106	254
57.815	24	GTGAAATTATTCGTTGATAAACTC	57.681	27	233	305	537
60.012	20	TGGTGGGTTGAATGCTATGA	59.924	20	240	1448	1687
57.051	25	ACATGGACGTCCCAGATTGT	60.246	20	131	2	132
60.636	20	GGTAGGGTGGGGATGAGATT	60.015	20	259	123	381
59.986	20	ATGGAAGAAAAACCCAACCC	60.032	20	245	210	454
57.433	26	CCCTGCACCTCTTTCAAATC	59.67	20	194	16	209
59.564	20	CGTTTTCCCTATTTTGTGCAT	59	21	251	81	331
60.214	20	TAAAACAATAAGGTCGCCCG	59.958	20	241	871	1111
60.075	21	AGGTGGAATAGGCAGTGACG	60.134	20	274	99	372

60.365	20	GCGAGCGAGTAGGTTGTGAG	61.136	20	110	2	111
60.162	20	TATCATTCTATGGTGGGGCG	60.681	20	202	830	1031
60.166	20	ATGGTTCGCCATAAAAATGC	59.801	20	162	37	198
60	20	CTTCACCCCCTACTCCATCA	59.92	20	266	393	658
59.895	20	TCGCTATGCACACTTTCTGG	60.011	20	127	646	772
60.224	20	GGATGAAGGTGTTCGTTCACA	60.95	21	115	355	469
59.968	20	CGCGCCTCTACTTTTTAATTACC	60.473	23	190	797	986
60.903	20	CTCGACATTGTTTGAGTGCAA	59.896	21	175	211	385
58.411	20	TATGCCATTTTCATCTGGGG	60.66	20	246	1885	2130
58.931	21	GCCATTTAAAAAGTCGGCTG	59.72	20	226	1109	1334
59.75	20	TTAGGAATGGGATGGTGGTG	60.572	20	267	82	348
59.916	20	TAAACGGGCCAATTTAAACG	59.835	20	240	118	357
58.155	20	GCTTGCACCCCAAATTAAAA	59.943	20	167	0	166
60.117	20	TACAACACTGACCATCCCCC	60.634	20	127	3919	4045
59.939	20	CTTCGCCACTGTTACCCTTC	59.734	20	250	791	1040
60.234	20	ACGTGTCCGAGTGTGTTGAA	60.203	20	119	79	197
60.249	20	ATGCAAGCTTTGTTTGGGAG	60.249	20	244	698	941
60.103	20	GTGTGTTGTTCTGCACTGGG	60.203	20	257	27	283
59.049	20	CTGGGTATACCTTGCCTCCA	59.948	20	180	111	290
60.205	20	TCTATCGGATTAAATGGAATAAGC	60.184	25	102	9	110
60.214	20	TCGGTGTATGCTGTAAACGAA	59.24	21	134	112	245
59.859	20	CAGTCACGACTTGCCAAAAA	59.881	20	221	852	1072
59.975	20	TCGTATGAATTTTTGTATGGACG	58.927	23	194	605	798
59.894	20	GGTTTACCCATAGCGCACTC	59.597	20	156	809	964
59.086	20	CCAACACTATTCGGTTTGGG	60.22	20	271	434	704
59.17	20	TGAATCCTCACAATATAACCTATT	59.283	27	232	86	317
59.982	20	AGCCAAATTTGCAACCTCAG	60.249	20	279	1215	1493
59.43	20	TCAATTATGTCATGAATGTTCAAA	57.148	24	224	76	299
60.245	20	TTGTCGTGGTTCGGTATTCA	59.964	20	272	53	324
59.861	20	ACTGACATCCACAGGCATTG	59.551	20	122	76	197
60.221	20	TTTAACGACCGAGTTTTGGC	60.11	20	265	521	785
58.22	27	TGCAAATCCAAAGGTCAACA	60.088	20	135	0	134
60.134	20	GTCGAGGGTTTGGAGCTGTA	60.255	20	245	8	252
60.002	20	TTGGTGAGTAGGATGAGGGC	60.073	20	270	1336	1605
59.547	20	TCATGAATGAAGCAGAAGAGGA	59.955	22	267	260	526
59.96	20	ACCCCAGGCTGAGTGAGTTA	59.721	20	252	320	571
60.21	20	TTCAAAACCACCTTCGAACC	59.948	20	214	483	696
60.073	20	TTATCATAGGATCACCCTCCC	57.807	21	154	59	212
60.472	20	TGTATGCAGTCCATTTCCGA	60.073	20	274	637	910
58.82	21	TCCAAATTACAATCGTCGCC	60.837	20	274	147	420
59.823	20	ACGTTCGGCTCGAGAGTAAA	60.015	20	169	79	247
59.969	20	GTGTCGACCTCGATGCATTT	61.078	20	275	818	1092
60.074	20	CCCAAAATTGCGAATGCTAT	59.928	20	222	608	829
59.934	20	TCATTATCCTAACTCGGATGTGG	60.21	23	200	398	597
58.568	20	CAACCTCTGCAAACCCAAAT	59.971	20	275	373	647
60.061	20	ATCTGGTATCAGAGCCACGG	60.096	20	275	71	345
59.957	20	GGCTTCCATGGTGGTTTAGA	59.933	20	105	14	118
60.038	20	CAACCATCCCAAACTTCACA	59.389	20	157	333	489
59.923	20	TTGTATGCTGAGGCTTGTGC	60.019	20	228	30	257
59.929	20	AGCCACTAAGCCACCTTCAA	59.875	20	275	592	866
57.635	20	CCAAATTTAAGGGTTATCACCTG	58.849	23	151	98	248
59.375	20	ACATAGAGAAGGGTTATCACTTGA	57.537	25	154	70	223
59.476	20	TCAAAGCCCAAAAGTATGGC	60.074	20	214	81	294
59.923	20	GCGGAATACGAAGAGTCACC	59.7	20	244	14	257
60.192	20	CGAAGTAATGCTCACACGGA	59.864	20	263	55	317
59.645	20	CAAACACCGATTCACATTGG	59.816	20	167	269	435
60.471	20	TTGCTGGTGGAAACTCCTTT	59.711	20	279	1698	1976
59.982	22	TTGGCATCCATCGTAACAGA	60.073	20	169	11	179

59.977	23	GGGCATACGCTTCGATACAT	59.951	20	209	23	231
60.7	20	CTTGTTCCTATTGCCAACGA	58.771	20	177	87	263
59.745	20	TTCACTCACCCTTTCGATCC	60.05	20	267	1409	1675
60.204	20	CTGAGATTTGTACTGCGCCA	60.011	20	208	18	225
60.195	20	GGAGTTGGGCTAAGTGGGAT	60.328	20	220	158	377
60.255	20	CGCTTTGTTTTCGTGTTTGA	59.888	20	255	394	648
59.88	20	CGTTCATTTTCTGTCCGGTT	59.971	20	155	441	595
60.096	22	ATGCGCGATTTTAAACCCTA	59.586	20	175	5005	5179
59.937	20	GTCGAGGTGGTCTCAACGAT	60.12	20	269	47	315
58.984	20	CAACACAAGGACATCCATCG	59.96	20	141	888	1028
60.399	20	AAAGGGCGATGACACAAAAC	59.978	20	124	144	267
59.973	20	ATCACGAGATGGGGACTCAG	60.072	20	278	1190	1467
57.536	27	CTGTGTTAAATTTTGGAAGAGAAA	57.213	25	280	96	375
59.996	20	GGATACCATGGGCAACCTAA	59.645	20	280	904	1183
59.673	20	CGCTCCGTAATTCTCACTCC	59.836	20	219	58	276
58.703	20	GAACGAGCATCCATGTCAAA	59.654	20	267	184	450
58.008	26	AATTGAGAAGGGGGAGAGGA	60.008	20	132	59	190
59.96	20	AATCCTTTCCTCTTTCCCCA	59.875	20	219	150	368
60.073	20	CACCTCTCCGATTAAACCCA	59.926	20	154	340	493
60.012	20	TTTCTTTGAGTGGGATGCAA	59.247	20	266	114	379
59.925	20	TTGCTTCTCAAACTTGATTAGGTA	58.301	25	204	5	208
60.081	20	AAACGAAAAATTGGGGTTCA	59.292	20	230	26	255
59.425	20	AAAACCGTAGTGGGTTAAAATTC	60.041	24	182	96	277
59.676	20	TTGGGTGATGTGCTTGAAGA	60.24	20	127	162	288
60.12	20	TTGAATTCTATGGCTTCCGC	60.175	20	208	352	559
60.031	20	TCTTCGTGTTCTTCGTCGTG	60.025	20	232	3483	3714
59.948	20	TGGAGGAATGAAGGTGAAGG	60.042	20	105	108	212
59.989	20	GAAGAAATTCCAATAGAGTTGAT	57.932	25	254	18	271
59.763	20	TGCCTAATTTATAGATAATGGACC	59.68	25	274	1070	1343
60.144	21	AAAATATGATCTTACTCCCACTGA	60.035	26	205	611	815
60.096	20	GGGGTAACTTGTCATCCCCT	60.052	20	138	12	149
59.801	20	CTGAAATCCTGGGCGTAGAT	59.15	20	275	91	365
59.831	20	TTTGTCCAAACAAATGAAAACA	58.097	22	257	253	509
60.243	20	CTGTAATCCCGATTGCTGCT	60.235	20	118	805	922
59.813	20	ATTGTGACATGGCCGAAATC	60.733	20	183	149	331
59.823	20	AAAGAAGACCGAGAGACACACA	58.991	22	159	0	158
60.228	20	GAGAAAAGACAATTCGGCCA	60.192	20	180	67	246
59.581	20	GCACACGAGCTCTCACTCAC	59.771	20	247	400	646
59.96	20	TAGCCGATAAAAATGGCACC	59.928	20	224	107	330
59.759	20	GACTCTCGCACCATCCATTT	60.081	20	220	270	489
59.889	20	AATTTGTACACACGTCCACCA	58.813	21	250	81	330
59.304	20	GCGTTGATCCAACGGTCTAT	59.962	20	208	149	356
60.578	20	CATGATCCAACCTTATTCCTCC	59.666	22	241	30	270
60.08	20	AGTCATGCGATCTGAACGTG	59.862	20	223	48	270
60.376	23	GCATGCTCTGTTTTCTGCAA	60.142	20	278	3	280
60.873	20	TGCGAAAATTTCTGGAATCA	59.232	20	123	318	440
60.007	20	CAATTTTGTCTGCTGCATGG	60.257	20	138	467	604
59.94	20	TTTGCAATATTCAACTACGAGCA	59.802	23	188	56	243
59.406	20	TGCAGATCCTCGGTACCTTT	59.694	20	232	384	615
59.337	20	TTACGAAAATACACGTTCGGG	59.876	21	214	20	233
61.235	20	TCCCCAGTGTCACACAGACT	59.113	20	258	259	516
59.659	21	TCTGCACGCTGCAATAACTC	60.165	20	262	1149	1410
59.685	20	TTTAGGATCGGAATATCGAGAAA	59.122	23	280	5	284
60.035	20	ACTTTGGCAAATCACACAGAT	57.186	21	276	164	439
60.206	20	ATGTTTTGTGAAAGTCCCGC	59.978	20	117	523	639
60.299	20	GGTAAAGAAACGGTGGAAAGG	59.858	21	158	122	279
59.933	20	GATAATTAGTGGAGGCGGCA	60.06	20	128	1530	1657
60.004	21	TGAAGAGAAGAGGTCGGGAA	59.92	20	213	30	242

59.756	20	CGTTATGGATGTGCCATTTG	59.809	20	236	762	997
60.255	20	TACCGACGAATGGTTGTTCA	59.964	20	274	507	780
60.298	20	AGCTTCAGGCCTTCAGTTTG	59.615	20	223	1363	1585
60.903	20	TGTTCAATCTGCCACCAAAA	60.088	20	255	1079	1333
60.323	20	GTGTGGGGGATTGTTGAAAT	59.508	20	280	87	366
59.839	20	CACAATCCCAACAAAAAGAAAA	59.007	22	238	2	239
59.566	20	TGCAAGTAAAACCATGCTCG	59.872	20	251	153	403
59.933	20	AGTTGCTTAGCGACCCCATA	59.73	20	257	4027	4283
59.239	20	GGTTCGGGTATTCACGTTGT	59.717	20	259	685	943
59.68	23	GGAGTTGCAGTTTTGGATGAA	60.103	21	193	207	399
59.143	20	TGTTCTGTCCTTTGCACGAG	60.025	20	268	23	290
60.405	20	AGACACCTAAGCCCATTCCC	60.328	20	153	27	179
59.089	24	CAAATTTCGGTTTGTTGGCT	59.975	20	133	32	164
59.943	20	CAAAAACCGAAAAACCGAAA	59.951	20	266	425	690
59.803	20	TACCCAACCCACTAACCCAA	60.081	20	140	63	202
60.439	20	CCTAACCCCACTAATGACCC	58.24	20	112	688	799
60.015	20	TTCGTGATTATTGCTGCTGG	59.833	20	140	514	653
60.11	20	CACATGTTGAGGTACACGGC	60.032	20	216	138	353
60.103	20	TATTACAGGGGCCAGTCGTT	59.452	20	231	2912	3142
59.916	20	ACCACCATCTTCTACGACCG	59.989	20	217	307	523
59.729	20	GAAGCCTCAAATCACAACCC	59.532	20	218	352	569
59.962	20	CAGTTGAAAAATTGCCAAAACA	60.014	22	187	610	796
59.476	20	AGCCATTTAAAAGTCGGCTG	59.361	20	154	30	183
60.015	20	CTGCTCTCTTGATTCATGGCT	59.588	21	252	1121	1372
59.928	20	ACCTTGAGGCATTTGAGGAG	59.284	20	257	216	472
60.06	20	TCGATTTGGAAAACAGAGCA	59.395	20	242	360	601
59.95	20	TGATGCCTCAAATCACAAGC	59.805	20	198	1073	1270
60.504	19	CCACTCTAGACCCTAGCCCC	60.088	20	194	162	355
60.028	23	GCATTATAACCACCGCAACA	59.448	20	250	74	323
59.717	20	GAGTAGGAGTCCGGAGCAAA	59.43	20	240	240	479
60.19	20	TGACCGGACGAAAATACTCC	59.933	20	182	202	383
59.585	20	TTGGCCTGTTACGACTCAAG	58.923	20	147	159	305
59.928	20	TACAGTCGACCTCAGCTCCC	60.408	20	208	21	228
59.773	20	TAAAACCGACATCCCCACTC	59.79	20	110	2	111
59.847	20	CATTTGGAAAATCAATGGATGA	59.638	22	206	751	956
59.827	20	TTCAATACTTTGAGGATAGATTGA	59.474	27	267	20	286
60	20	GTGTGTCACTCCCCGATCTT	59.969	20	203	18	220
57.31	27	TTTATCAAAAGCCGAAACCG	60.068	20	169	10	178
60.291	20	TGTTGTCCGGTTCTCTCTCC	60.238	20	256	274	529
59.993	20	ATACCGCTTCCAAAATGTGC	59.967	20	143	2858	3000
60.357	20	AGCGGTTATTACCGGATCG	59.93	19	230	46	275
59.927	20	TCACGCACTCACGATCTCTC	60.146	20	151	999	1149
59.943	20	TTTTACGGGTTGGGCCAT	61.09	18	280	708	987
60.111	20	TGAGGGAGGGAAAGAGAATTAAG	60.076	23	129	176	304
59.303	21	TTGACGCAGCTTGAAGATTG	60.134	20	232	4	235
60.074	20	GGAGAAACTGACCGGATTGA	60.05	20	148	1091	1238
60.001	22	AGGCAATTAAGATTCGCCCT	60.061	20	185	6	190
58.462	21	CCGATCCCATCCCTTAATTT	59.978	20	256	249	504
58.78	20	ACGCTCCACCAAAAGGAGTA	59.734	20	227	26	252
59.809	20	GGAAATGTGATTTGATGGGC	60.141	20	162	31	192
59.083	20	CATTCCTTTTTATGTGTTTGTTTCA	59.38	25	242	1125	1366
59.315	20	TGTGGGTTAGCATTTGATCG	59.542	20	242	622	863
59.943	20	TGCTCTGAGAGGCCTGATTT	60.096	20	254	494	747
59.81	21	GTTAAAAACCGGACTGCACC	59.476	20	138	52	189
58.38	20	CCACAATTTTAGGCAGTTTCG	59.634	21	163	483	645
59.688	20	CCCATTTTCTCCATCCCTTT	60.124	20	141	224	364
60.54	19	CAAAATCTTACACCTGGAGCC	58.707	21	277	232	508
60.11	20	ATTTTTCGCCGAAGAGGATT	60.041	20	270	553	822

59.429	20	TCCGAGTTGAAGTAGTGGCTT	58.994	21	216	251	466
59.366	24	GCGTTTTGATGATATATAGATGTTT	59.327	27	189	306	494
60.066	20	ACCGTCCATCTTAATGCAGC	60.103	20	258	2789	3046
60.323	20	AGGAAAATGTGTCGAGAGGG	59.137	20	280	129	408
59.797	20	TTTCCTCCCAACATTCGTGT	60.353	20	224	88	311
60.096	20	TGAGGAGCGTTGATCTTGTG	59.984	20	200	271	470
60.507	20	CAGACGGTATTGCCCTTCAG	60.647	20	244	1175	1418
59.509	23	CCCGGTGTAAAGAAATCGAA	59.931	20	205	26	230
59.697	20	TCTGCAAAAATGAACAAACTATA	59.639	25	178	12	189
60.038	20	CACGAGTGAAGAAAGGGAGAG	59.072	21	143	41	183
59.312	20	GCCGCGAAACAGACATAAAT	60.103	20	151	175	325
60.173	20	CGGTAACACAAAATTGCAGAA	58.736	21	240	2179	2418
60.142	20	AACATGCTTCACCATATCCAAG	58.976	22	280	928	1207
60.061	21	ATATGGAAGGCAGTGGTTCG	59.955	20	270	405	674
59.46	24	ATATGTTCACCAAGCCGCTC	60.103	20	226	6	231
60.059	20	GCAAGCAAAATGCTACGAGA	59.21	20	244	99	342
60.151	20	CGCGAAGACAATGTTGAAAA	59.849	20	265	25	289
60.217	20	TGTTTTGTAAAGGGGTCGAGA	59.595	21	246	845	1090
59.934	20	TGCAAGAAAGTGGACTGCAA	60.574	20	199	517	715
58.847	20	CTCTCAATGGACCAGCACCT	60.261	20	264	1466	1729
59.262	23	GACACAATTAACCAAAAACATTG	59.705	24	242	332	573
60.155	20	TTTGTCTGCGTGGACAAGTT	59.339	20	240	217	456
60.044	20	TAATGCATTCGCCAACTGAG	59.833	20	213	125	337
59.861	20	TCGTCGTCGCTTTCATCATA	60.366	20	126	2473	2598
59.953	20	ATTTTTGTTGGCCGAAAATG	59.81	20	170	261	430
58.687	21	AGGTGCCCCTACTTCTTTGG	60.488	20	245	1	245
59.528	20	TGCTCTTGTATGCTGCGTTT	59.638	20	275	659	933
60.111	20	CGACGGATATTTGTTCTTGTG	58.161	21	196	157	352
60.352	20	TTCCCATCTAATCTCGTCCG	60.029	20	183	746	928
59.597	20	TTTGGGAGACAAACACACTCTC	59.232	22	233	92	324
59.588	20	CCACCCACACCTAAGGAAGA	59.959	20	118	3	120
59.175	20	CCCTAATACCCACTAACCCCC	60.643	21	110	1	110
59.941	20	TCATTGTGATGTGTGGGAAAA	59.808	21	219	874	1092
59.82	20	CGACTTGTCGTTGTTCGGTA	59.758	20	265	221	485
60.34	20	GAGGGACAGCCTAGAACTTTGA	59.886	22	134	294	427
59.986	22	GAAGTGCATCTCGATGACGA	59.95	20	165	38	202
59.82	20	CCACCTGAAAAAGGGTTGAA	59.942	20	265	218	482
59.612	21	CCCACACATTTGAGGGAAGA	60.892	20	234	253	486
59.622	23	GGCAACTTGGGAGTTGAAAA	60.088	20	275	353	627
59.434	20	AATGACACGCAAAAAGGGAC	59.978	20	101	173	273
59.75	20	AATCTGACGGCCGATATTTG	59.923	20	171	962	1132
59.966	20	TTGTCACACATTTACACACACG	58.016	22	220	137	356
59.667	23	TGGACTTAACTGGTAGCCCG	60.125	20	180	186	365
59.49	20	TGGATGTGTAGATGATTTTTGGA	59.329	23	169	43	211
59.627	20	AAGCGATCCTTACAGGCAGA	59.978	20	230	61	290
59.883	20	ACACACACGATGGATCGAAA	59.967	20	234	97	330
59.269	20	AGCATCTCTTGCTCTCTCATTG	58.842	22	161	1	161
59.973	20	CCATTTTTACATGCCGCAAT	60.7	20	203	805	1007
59.563	20	CCTCACCAACTCAACCCACT	60.002	20	212	26	237
59.101	20	TTCCTCCTTGCAACAAATCC	60.051	20	204	169	372
60.032	20	GGTGCTGTGTGATGTTGGAG	60.162	20	190	57	246
59.96	20	TTTCACCGTCCAAAACACAA	59.981	20	213	380	592
59.873	21	GCATGCAGAAGATGTGGAGA	59.95	20	215	1570	1784
59.967	20	ATGCAAGCTAACCGCTAGAA	57.835	20	266	52	317
60.157	20	CGTGTCAAAATTTGCTTGTCA	59.761	21	244	91	334
60.02	22	GGATGGGAGTACATTGGTGG	60.05	20	247	67	313
59.433	22	TTTGGGGGTGAGGTGTAAAG	59.824	20	215	522	736
59.595	21	GCGTTTTGATGATATATAGGTGTT	58.907	26	156	384	539

59.946	21	AGGAGCCTCACTGACCTTCA	59.986	20	136	342	477
60.23	20	CACTTAGCTCATTGATTTTCATCAC	59.24	25	153	602	754
59.888	20	AGAACTAGGGCACTCCATCG	59.308	20	278	78	355
59.926	20	CGAACCACCACACCAAATTC	61.196	20	154	487	640
60.059	26	CTCAACAGTCAACAAGCACACA	59.986	22	212	313	524
60.469	20	TTTAAGGGTTATCACCTGATTTTC	57.757	24	278	55	332
60.133	20	GAGGAAACCAGCTGTCCAAG	59.844	20	250	2029	2278
59.997	20	CATGCCTCAAACAACCTCAA	59.691	20	122	578	699
59.734	20	CCATTCACACACACACTCAGA	58.078	21	258	183	440
59.882	20	AATGGGGACACACACTCACA	59.846	20	126	355	480
59.931	20	GCCTCATCGTCGGATTTTAG	59.668	20	273	87	359
59.837	20	GTGGCTGCTGTGTGAGGTAA	59.905	20	222	171	392
59.224	23	ATTTCATTTCATGGGTTTCG	57.399	20	108	11	118
60.034	20	GACACAATGCACACCTCACC	60.013	20	272	1060	1331
59.614	20	TCGGTCGTCAGATTGAGAAA	59.369	20	222	2067	2288
59.67	20	CATCCAAATCAGGATCAGGTC	59.351	21	221	2405	2625
59.322	20	TGCATGTATTTGGGCTAAAGTG	60.02	22	150	18	167
60.241	20	TTTACCCGTTGCATGTGTGT	59.888	20	248	1416	1663
60.013	23	GAAGGAGACGATCGAACAGC	59.957	20	280	157	436
59.709	27	CAAATCCCATCAACCCAAAC	60.029	20	109	18	126
60.024	20	GGAGAAGAGATCGGAGACGA	59.486	20	190	36	225
59.982	20	CATTGCTGCTATGCCTGAAA	59.976	20	247	846	1092
59.916	20	GTGGCCTGAGATAGCCGTTA	60.235	20	202	9	210
60.019	20	CCCGTCTCTATCCCTCCTCT	59.653	20	246	2240	2485
60.049	20	GAGTGAGGAGCAGAGGGATG	59.945	20	205	476	680
59.523	21	TGCATTCAAAAGCCACATCT	59.276	20	228	418	645
60.142	20	GACCGCGAAGTTTACATGGT	60	20	238	53	290
59.973	20	TGTTTAGCAGTCCACCTCCC	60.111	20	253	3498	3750
60.386	20	TCCAATTAACGTTCCATTCACA	60.223	22	226	2381	2606
60.088	20	TTTCTACTCCCTTCCCCTGC	60.569	20	259	988	1246
60.096	20	GGTGGCTTCTCTCTTCGTTTT	59.878	21	221	10	230
59.93	22	TCTTCGACCCAACACCATATT	59.302	21	100	31	130
57.239	26	AAGGCGTTTTGTAAATTGGC	59.124	20	273	5	277
59.708	20	TCATCTTGTCAATTTCGCCA	60.197	20	188	204	391
59.761	21	AGCGGTTATTACCGGATCG	59.93	19	225	72	296
60.34	20	ACGGCTGGCATTTGTTAGAG	60.27	20	168	71	238
59.957	20	TGTTGTTGTTGTTGCTGCTG	59.504	20	222	99	320
60.081	20	TATGGGTTATCACCGGATCG	60.544	20	267	651	917
59.547	20	ATTAGGGTTCCTCCTTCCCC	60.497	20	112	3	114
58.302	27	CAGGATCTTTTGTTATCTTTGACG	59.224	24	174	4	177
59.962	20	AGCTTCAGTCACGCACACAC	60.104	20	250	96	345
60.016	20	TATGGGTTATCACCGGATCG	60.544	20	129	297	425
59.737	20	TTTCTTCCCATCATCACCGT	60.317	20	280	778	1057
60.166	20	AACACACACGCACTCACACA	59.818	20	147	262	408
60.015	20	TTGTCCAGTGTGTGTTTTTGG	59.495	21	224	59	282
60.128	20	GCCACATACTTTGGAGACGC	60.667	20	268	1242	1509
59.98	20	GATGGTTTCCGAAAGTGGAA	59.91	20	257	1689	1945
59.581	20	GGGCTCAGTAAACTGCTCTCA	59.63	21	243	95	337
60.886	20	CCCAAACATTTGAGGGTTGT	59.688	20	205	558	762
59.911	20	TTTTATGTAAATTGTCGTGCGT	57.373	22	130	190	319
59.755	20	GCTTGGTGAAGGAAGTGAGG	59.844	20	122	24	145
59.632	23	TCCTTTATTTTGATGTAGCAACCA	59.904	24	272	698	969
59.587	20	TGACCCTTTGATGTTATACACGA	59.393	23	209	534	742
59.993	20	CGAGAAATGAGAGCGTAGGG	59.971	20	260	86	345
59.853	20	TGGTGACTTGAAGAAATTTGGA	59.587	22	159	50	208
58.88	21	GTGGGTTTAAGTGGGGTGTG	60.126	20	104	77	180
60.317	20	CGACCCAGATTCAAACCCTA	59.926	20	275	73	347
60.434	20	AATGATTCCTTGGCACTTGG	59.933	20	160	490	649

59.962	20	GGATGCTGATGGAGGGAATA	59.854	20	246	446	691
60.008	20	GGACCAACTTGGAAGTACCG	59.449	20	103	23	125
59.74	20	ATAATGGTGGCAGCTGTGCT	60.688	20	201	484	684
57.155	20	TCCTTTTGGCGTAGTGAGGT	59.734	20	166	11	176
59.867	21	ATTGAATCTACGTCCACGGG	59.813	20	255	70	324
58.5	20	CGCTCGGGCTCATATCTATC	59.791	20	231	37	267
60.183	20	CGCTCCACAAAGATCTCACA	59.984	20	114	181	294
59.67	20	TGCATGCAAAACTGAGCTTC	60.142	20	174	375	548
59.758	22	AAGTGTTTTCCCACAGACGG	60.005	20	177	40	216
59.847	20	CTCTGCATGTACGCTACCTACC	58.954	22	219	42	260
60.285	20	TCGTGTAAGTTAGCCGGGAC	60.132	20	267	0	266
59.997	20	AATTTCTGTCCCGTTTTCCC	60.166	20	280	48	327
60.029	20	AAGGAATGGTTTGATGGGTG	59.647	20	216	145	360
60.088	20	TAAGTTGCTCGTTGGCATTG	59.872	20	189	3313	3501
59.95	20	AAATTGACAGCGATGGAAGC	60.221	20	171	109	279
58.161	20	AGGGGTTATCACCTGAATGC	58.864	20	156	484	639
59.73	20	CTGGAAAAACTTCCCACCAA	59.942	20	177	5835	6011
59.73	20	CGAGCGAGTGGTTGTGTAAG	59.51	20	100	12	111
59.823	20	GCTCATGGTTCAGGGTTCAT	59.934	20	242	223	464
60.033	20	ATCCGCCTACATTGGATGAC	59.78	20	188	1448	1635
60.118	20	GCCGGAATCGAGAATATGAG	59.628	20	202	390	591
60.066	20	GCGAGGTAGGCTTTCGAACT	60.894	20	249	71	319
59.809	20	CCTCTGCCTCGTCTGGTTAG	60.005	20	230	29	258
58.809	25	CTCCTAAGTTGCCCCATTGA	60.066	20	112	24	135
59.822	20	TGCATTCACCTTCTCTTTGC	59.002	20	200	157	356
60.456	20	TGGTGTAATAATTTGGTTTCATCG	60.006	24	254	245	498
59.296	25	GTCTTCCGCGTGCGTATAAT	60.124	20	222	23	244
59.997	20	GTTTACAACTCACAACGCGG	59.245	20	145	170	314
59.933	20	CCATATTTAAGGGTTATCACATGA	59.713	27	124	960	1083
59.988	20	TTCCTCCCTCGTTTTTCGAT	60.929	20	256	3303	3558
60.006	20	TTTGTCTTCCCGTTTGTTCC	59.948	20	278	146	423
59.751	20	ATAACCCGGTCAACAAGCTG	59.993	20	249	25	273
59.844	20	ACCAAAGACGGGCTAAAATG	59.087	20	214	399	612
59.988	20	TGTTGCAGTTGTGGGTGATT	60.008	20	168	366	533
57.299	25	CATCAACTCCATCCCCATTC	60.135	20	276	14	289
59.52	20	CGTAGGACAACGACGGTTTT	60.03	20	109	21	129
60.025	20	TGCGTAAGTTTTGGTGCAAG	59.911	20	260	168	427
60.011	20	CTTGATTGGTTGACGTCCCT	59.966	20	232	242	473
60.706	19	GAGCTGCGGTTTTGATCTGT	60.406	20	265	198	462
60.009	20	TGCTGTGGGGAGTAAACACA	60.152	20	276	2	277
60.612	20	TGCCTCACCACCAATGTAAA	59.964	20	217	537	753
57.229	25	CAGGCCCAATACCTTGACAT	59.813	20	134	21	154
59.734	20	CCTCCGAACTCATGGTGTTA	58.569	20	245	206	450
60.7	20	GATCATCCCGTGGTTTGTTT	59.653	20	268	29	296
59.982	20	GTCAACTTGGGCAGTGGAAT	59.973	20	249	102	350
59.454	22	TGCAAGCATCAAACAACACA	59.877	20	179	3	181
59.317	20	CGGGAAGCCTTTATCTATGC	58.809	20	222	613	834
58.899	22	TGACTAAGGTCCCATCACGA	59.086	20	234	51	284
57.557	25	TCTTATCACATCAACCGCCA	60.073	20	127	20	146
59.881	20	AAATCTACCTCTGCCACCCC	60.328	20	254	181	434
60.04	20	GTCACGAGGTTGAATTGTGC	59.143	20	177	1551	1727
59.882	20	CTTTTGGATGACGGAAGGAA	60.044	20	150	121	270
59.429	20	TTGGATGTTTCTGGAGCGAT	60.603	20	280	153	432
59.658	24	CATCGTGAATGTTGGGAGTG	59.96	20	172	3	174
59.799	20	TGCTGCTTCTCTTGCTGAAA	60.011	20	158	416	573
60.125	20	TACATGGGACGATTCCGATT	60.155	20	154	2864	3017
59.853	20	CCAGCTCAGTGGTGGAAAAT	60.111	20	204	100	303
59.304	20	GTGGAGAGGAGGGATGATGA	60.008	20	116	171	286

59.537	19	ACCTGGATCACGGGTTTAAT	58.24	20	280	2129	2408
59.779	20	GGGTGAAAAATGATTCAGAGGA	60.299	22	131	68	198
60.027	20	CATGATGCGAGGATCCTTTT	60.036	20	182	164	345
60.173	20	TGCGTTTTGACAATATATAGGTGT	60.083	26	251	50	300
58.93	20	CACCACTCTTCGATGGAACC	60.51	20	247	83	329
59.564	20	AGCGGTTATTACCGGATCGT	60.711	20	231	146	376
59.465	25	ATTTCTTACCCGTCCGTCG	59.94	19	214	21	234
59.505	23	TTGCAATATTCAACTACGAGCA	58.52	22	104	27	130
59.784	20	GTGGCGTTATTGGGTTCATT	59.691	20	268	4	271
61.21	20	TCAGCCTAGTCGCGATTTTT	59.982	20	276	195	470
60.074	20	GGGATGGGAGAAGATGTTGA	59.862	20	166	507	672
59.569	20	AGCCACTCCCTCCAAAAGAT	60.074	20	203	12	214
60.011	19	TATGCACGAAGCCAATTCAC	59.694	20	257	1987	2243
60.181	20	TCGTCCCATCTTTTACCCTC	58.981	20	256	337	592
58.608	20	TTTGAACTCTCGGCCTCTTG	60.508	20	249	79	327
60.184	20	CGGGCGTTTTTGTAGGTAAA	59.993	20	247	2252	2498
58.121	21	AATAAAATGTACGGGCGCTG	59.985	20	158	23	180
60.014	20	CGAGTGTGAGGCTGTGAGAG	59.757	20	127	64	190
60.065	20	AGTCACCACCGAACCAGAAC	60.009	20	249	21	269
59.934	20	TCTTACGGAATTCCACTGGG	59.926	20	129	177	305
59.572	22	AATCCTCAAAACCTTGCGTT	58.695	20	249	70	318
60.045	22	ATAAGGGCCTGGTCATTCCT	59.789	20	266	1982	2247
60.435	20	ACAAATTTGCCCTCGTATGC	59.967	20	125	126	250
59.053	25	CACTTGAGGAAGGATGATGAAG	58.789	22	100	425	524
59.984	20	CTTTTTCGACTTTGATCCGC	59.823	20	242	9	250
58.079	23	TAGGTGAGGTCGGGTCACTC	60.112	20	195	31	225
60.261	20	TCGTCCGAAAATCCTTTCAC	60.051	20	246	272	517
60.088	21	ATCGGTTATTACCGGATCGC	61.031	20	259	291	549
59.358	26	AAATGTTTGAAATATCGGGGC	60.035	21	100	10	109
59.997	20	TGGCACAATAGGAAAGCAAG	58.917	20	105	480	584
59.67	20	ACAAACTTATGGACCGCTGG	59.993	20	103	587	689
60.141	21	ACGTCACCCCACTTGGTAAA	60.269	20	199	1708	1906
59.083	20	AGTTGAGGTTACGCCAAACA	58.283	20	238	64	301
58.861	22	TATAACCGATCCCACCCCTT	60.391	20	126	94	219
60.11	20	AGTAATTGTCCAGGGGGAGG	60.183	20	139	386	524
57.85	20	ATATGAAGTGGGGATGGACG	59.629	20	258	1135	1392
59.556	20	CATCCACTTAAAGCAAGGCA	58.917	20	280	733	1012
60.128	19	CGACATTGCCCTATGAGAAAA	60.081	21	115	35	149
60.155	21	AAATTAAAATTATGGCAACTTTCC	57.89	25	258	3636	3893
60	20	CCATGGATGTCAGTCATTGC	59.925	20	264	1513	1776
59.907	22	CCGTCGATTTCTAGTGTTTGG	59.618	21	190	393	582
59.438	21	AGTTTTTCCGACTCAAGGCA	59.853	20	251	186	436
59.762	20	TCTTGCACATCTTGGTGAGTG	59.889	21	229	18	246
57.767	25	ACCTGTAGAATCTCTTACTCTATC	57.215	27	223	593	815
60.987	20	GATGGAGACACCTAAGCCCA	60.073	20	172	5	176
60.08	20	ATACGAGTAGCGATCGGCAT	59.719	20	263	24	286
60.052	20	GGCATCACAAAAAGCAGACA	59.847	20	271	64	334
60.081	20	TGAACCTTGAATCGAGTTTACAT	57.814	23	187	8	194
60.103	20	TTGTAGGCAACGAGCCTTCT	60.015	20	232	3460	3691
60.423	20	TTATGCATGCACTCCACCAC	60.549	20	170	320	489
60.155	20	CCACTGTTGGAATCACATGC	59.967	20	263	371	633
58.933	20	TTCATCAGGTCGTGGATTGA	60.048	20	122	445	566
57.617	23	GCCTCGGTTGCTTATTTGTT	59.229	20	279	378	656
59.988	20	GGTGGTTTGAGGGTGAATGT	59.679	20	172	44	215
59.903	20	TTGTCTCACTCACCGTGCTC	60.03	20	277	4176	4452
59.799	20	TCCCGTTTTACCCTTGAATG	59.795	20	196	89	284
60.791	21	CCTCACTCTTTTACGCCTTCC	60.248	21	102	16	117
59.708	20	CCTGTTCTCCGCTGTATTCC	59.694	20	149	2772	2920

59.978	20	CATGCAAACATGGAACATTG	58.389	20	268	297	564
60.015	20	TTGATCAAGACCTTTTGGGG	59.903	20	226	82	307
60.379	23	GCTGCTCCTTTGACTCCAAC	59.997	20	146	73	218
60.143	20	GATGTTCCACAAAACCACCC	60.073	20	175	538	712
60.153	20	GACCGCGAACTTAGAGGAGTT	59.899	21	266	110	375
59.939	20	ACCCTCCTTCAGCCAAAAAT	59.94	20	252	588	839
60.439	20	GATGATTGCACCATAACGCA	60.498	20	148	479	626
60.006	20	TGTTGTCATAACAAAAATGACACC	59.837	24	100	352	451
59.645	20	TCGCCATATTCGATCACAAA	60.035	20	235	180	414
59.238	22	GTTGTGCGCATGATTGAAAG	60.265	20	130	1	130
60.284	20	GGTGTTGGCCGAAAGTTTTA	59.975	20	103	71	173
58.178	25	TCGCATGTTGATTTTCCAAC	59.523	20	278	853	1130
59.848	20	TCGGCATGACGTAGTTTGAA	60.257	20	222	1767	1988
60.066	20	GGCCAAATATTTCCCTACCG	60.508	20	212	92	303
59.978	20	ACCATATTTAAGGGTTATCACCTG	57.552	24	274	304	577
59.954	20	CCCGTGACACAACAGATCAC	60.005	20	258	578	835
58.4	21	AAGTCCCCATTAAAGATGTAAGTT	58.935	26	280	229	508
60.807	20	TCATAAGTTAACATAAACCAAACT	59.079	27	109	79	187
59.969	20	GGATTGCTGAAAACTGGCTC	59.82	20	276	32	307
58.932	20	AATACGACGGCGAAGAAAGA	59.845	20	239	25	263
59.682	25	TCGGGTTCCAAATCTCGTAG	60.066	20	228	38	265
59.95	20	AAGGCCACACTCCAAGAAAA	59.711	20	176	673	848
59.639	20	CATCCCAGTTGTCTTGGGAG	60.501	20	181	18	198
59.677	20	ATGTCACACCCTCCCCAATA	60.05	20	171	233	403
60.483	20	ATCATGTAGTCGCGTGCTGA	60.445	20	161	829	989
59.195	20	TTTTCGAGTTTCTTGTTCTCCA	58.994	22	246	321	566
59.925	20	CGAGAGCTGAGAGACAAAGAGA	59.112	22	277	535	811
60.053	20	ACCCTCCTTCAGCCAAAAAT	59.94	20	244	1284	1527
59.956	21	CACTTTTAACTCCAAACCAGGA	58.288	22	220	105	324
59.799	20	CTTTCGTTGGCGATTTTCAT	60.074	20	236	40	275
60.255	20	GGGGAAGGAAAGAGAACGAG	60.183	20	221	37	257
60.089	20	AACGGTTATCACTGGATCGC	59.962	20	204	424	627
59.734	20	TCTCCCTTTCCTCACTCCTG	59.375	20	258	2	259
60.733	20	ATTTGCTTAAAATGAATCAATGG	57.325	23	191	275	465
60.908	21	TTTGTTTTCATTAACAAGACCATCA	60.047	26	217	1070	1286
60.066	20	TCCGTCATCGACCACTATCA	60.072	20	278	477	754
60.045	20	CGGCCGGTTTTTAATGTTTA	59.835	20	210	2187	2396
60.101	24	TGAGTGGAACGATCCATATAAATT	60.427	25	258	680	937
59.55	20	CCCACACTCACACGATTTCA	60.57	20	174	1163	1336
59.966	20	GCAGACATGTTTCGCTACCA	59.871	20	183	202	384
59.267	22	AATGCGCCTCCCACTTTAAT	60.821	20	120	4	123
60.263	20	TGCATTCGTCAGTAGTCCGA	60.413	20	178	480	657
59.033	21	CTACAAGATCAACCGCCTGC	60.796	20	201	104	304
59.346	20	CCCGTACCTCAATTAAAAGGG	59.719	21	263	716	978
59.801	20	CCGAATTCCTCTACCGTCAA	60.066	20	192	393	584
59.934	20	TGCACACTGTCACACTCCAA	59.905	20	201	2043	2243
59.75	20	CCAGGCTAGCCAGAACAATC	59.836	20	177	202	378
60.032	20	CACCCTCACATCTCTTGCATT	60.126	21	115	228	342
60.797	18	ATAAGAGGTATTTTGACAGTATCG	57.206	25	122	91	212
59.836	20	ATCGATGTGTTGGCATTCAA	59.931	20	250	225	474
59.816	20	CCACCCGTGTATGTCATGTG	60.722	20	226	397	622
59.778	20	CGAAATTGACGGAAGAGGAA	60.184	20	242	103	344
60.328	20	GCCGGATTTAGAGCAATCAA	60.175	20	212	184	395
59.339	20	GAACTTCGCCATCGTCTCTC	59.957	20	188	13	200
59.308	20	TGGATGAAAATCATTGTTCGC	60.832	21	275	583	857
60.111	20	TGGACTTCTCCAATCCATGC	61.016	20	239	234	472
60.452	20	TGCAATTCCTTCTGAACCCT	59.67	20	232	108	339
59.882	20	CTCGTTCTCTTCTTCATCTAAACA	57.05	24	123	281	403

61.225	20	CAGGCTAAAGATCGTCCGAG	59.971	20	249	213	461
60.39	20	TCATGGCTGGGTCTACATGA	60.072	20	177	3247	3423
57.497	26	CAACACTCAATTATAGGAAAATC	59.318	27	250	210	459
58.133	20	GGGTAGTTGAAATGCAAGCC	59.574	20	168	416	583
59.523	20	GGGGAAGAGAATCAAGAGGG	60.008	20	103	369	471
60.508	20	AACACTGATTCGCACAAGGA	59.293	20	229	61	289
60.038	20	CATATTCCATGGTCCCCAAC	59.871	20	109	4452	4560
59.12	20	TCTTCACCTCAGTCTGCACG	60.178	20	215	1120	1334
60.038	20	TGCATCACATTTGTTCATATCG	59.448	22	195	88	282
60.309	20	ATCTCCATCTCCTTCCTCCG	60.553	20	276	947	1222
60.142	20	TGCCCTTGTATGCTCCCTAT	59.551	20	280	3139	3418
58.616	21	TGGGTTTTTACGAAAGGCAG	60.103	20	207	25	231
59.938	20	CGTTCATTTCGTACCTTTAGAAGT	60.307	26	131	103	233
59.505	20	TGCTCGTTTCATATGTTGCC	59.694	20	139	147	285
60.331	20	GGAAGGCGTTGACATTTGAT	59.939	20	259	93	351
61.799	20	AATGTTGTCCCGGACTCCTC	61.291	20	100	59	158
61.248	20	TGGTAGTGAAATAAACATAAACT	59.645	26	237	0	236
58.165	23	GGTTTTACGAACCACAATCCA	59.716	21	130	151	280
59.989	20	TACATTTCCCCAACCACTCC	59.647	20	173	12	184
60.423	20	CGTAAAAATGGTTATTATTGGATC	59.202	26	143	98	240
59.955	20	AATGGAGGCGATTTTGTGTC	59.939	20	246	1247	1492
60.549	20	TGCTTTGATTAATCCCTCCG	60.031	20	277	166	442
60.048	20	ATGGCATATGAGGCTTGGTC	59.923	20	175	181	355
61.11	20	GCCTATGCAGTCACAAATGC	59.306	20	266	734	999
60.648	20	ATCGCAATTCGATTAGGCAC	60.067	20	274	103	376
59.985	22	TGTTGCGTAATAGGCGAGAA	59.467	20	209	330	538
59.998	20	ACGATTACAACGCAACATCG	59.614	20	137	346	482
59.317	23	CCATTCAATTTAACTTCGGCA	59.95	21	217	97	313
60.028	20	GTTGGCAACCAGATATGCCT	59.962	20	127	304	430
60.14	20	TCCAATGGATGGAAATGGTT	59.991	20	279	288	566
59.439	20	GGCTAAAAGTTGTTGTCTGGCT	59.825	22	184	9	192
59.894	20	ATGTTGCAGCATAGGCATGA	60.251	20	279	608	886
60.037	20	CAATGCCGCTGAACATATTG	60.096	20	171	684	854
60.376	23	TTCTGTCCCGTCTTCTTCGT	59.844	20	170	13	182
60.723	20	GGACCCTAATACCACTAACCCC	59.847	22	102	513	614
59.955	20	CCTTCAACAAATGGTTCATGC	60.359	21	187	1721	1907
60.042	20	TTTCCAGGATCGAATTGAGAA	59.631	21	262	235	496
60.03	20	TTCAAACCTGGTTCTCGTCC	60.088	20	243	70	312
60.807	21	CAACATCACCAAACACTCCG	60.001	20	225	8	232
60.894	20	TTCATCATTTCATTTTATAAGCTT	59.91	26	189	107	295
59.943	20	TGGTTGGTGGAAGAAATCAA	58.947	20	215	59	273
59.182	20	CAATGTTTCCATGTTCCGTG	59.816	20	262	1324	1585
59.979	20	ACAGAAATTGCCTTGGTTGC	60.118	20	134	249	382
59.049	20	GTCCGATTTGCCGTTCTATC	59.533	20	215	1028	1242
59.993	20	TCCAGCATTTGTATGTCCCA	59.924	20	213	1442	1654
60.294	20	CATGAACCTGAAACAGCGTG	60.301	20	229	2155	2383
59.983	20	ACAAGAGCTGAAATGCCCTT	58.936	20	215	30	244
60.005	20	TTGAATCATTTGCGTTGCAT	60.081	20	268	4312	4579
59.743	22	GCCAAAAAGTCAAGGCGTTA	60.244	20	262	3	264
61.061	20	GATGTCGAGATCCAACCCAT	59.744	20	230	364	593
59.762	20	TTAGGTGTTTTGACATGTTCACTC	58.225	24	165	236	400
59.534	20	CCCACTTCCTCCAACCAGTA	59.959	20	244	536	779
57.509	23	TGTTGTAATGAGGCTTTTGGAA	59.625	22	237	15	251
59.271	22	AAATATCAGGCCAAAAACGC	59.081	20	191	242	432
59.95	20	TTCCCCATCACCATCACTTT	60.173	20	166	111	276
60.074	20	CCGCCTGATTTGTTTCTCAT	60.074	20	127	159	285
59.665	20	TCCGATGACTAAATGGAAGACA	59.569	22	141	5522	5662
59.864	20	TTTCGTTTGCCTAAAATGCC	60.075	20	233	218	450

59.706	20	TACACAATGCCAAACATGGG	60.234	20	265	5399	5663
59.989	20	CAGTGGTCCTGGGAACCTAA	59.959	20	152	6	157
59.578	21	GTAATGGCGGTGAAGATGGT	59.82	20	276	100	375
59.926	20	CCTTGGCGGTTCATATCAGT	59.955	20	171	65	235
60.123	21	GAGAAGTTGTCGGTTTGGGA	60.088	20	213	639	851
60.147	20	GGACCTTGTCCAGAAACCAA	59.943	20	148	87	234
59.747	20	CATACTCTCACCAATCCCCG	60.331	20	141	4	144
59.978	20	TCCCAGCATTCTTGAACACA	60.24	20	138	71	208
60.162	20	TCATGTTGCTACACGTTGCT	57.926	20	149	175	323
59.274	21	TCGGGTAGTCAAGTTTGCTTT	58.893	21	255	20	274
59.864	20	TGTACAAAAGCTTGTGGTGAAGA	59.836	23	240	36	275
59.853	20	GCAACGGAATACCACTCGTT	60	20	167	1466	1632
59.481	20	GCACACTCGAAGAGTAGCGA	59.344	20	216	776	991
59.267	22	AAAATACCAAAGTCGATTATCCAA	59.264	25	162	39	200
58.161	21	TATGGGTTATCACCGGATCG	60.544	20	119	104	222
60.152	20	AAAAAGCATTTCACACGTTCTG	59.312	22	179	294	472
59.727	21	CGCCACAATTACCAAAATGA	59.42	20	280	844	1123
59.844	20	CACACGTTATATTTATAGTTTTGTG	59.19	27	124	223	346
59.955	20	GCGAATTCAGCTAGAACAACAA	59.541	22	180	1836	2015
60.211	21	AGCTTATCACTATCACCCTCTTCC	59.22	24	100	28	127
60.192	20	ACGGTTCACATACTCCTGCC	59.997	20	235	150	384
59.208	22	TGCAACCAACAAAAACAACA	58.626	20	190	25	214
59.969	20	TCCTTGGAACCTAGAAATGGTT	59.001	22	256	9	264
59.938	20	GGGAGAATGCCTTGTTTCAA	60.051	20	145	309	453
60.183	20	ATCCTTTTCGCCATCTTGAA	59.645	20	190	127	316
58.423	21	ATGGAATTGGGTGTTGGATG	60.439	20	115	132	246
57.315	21	AAGGAGCTCAACCTACGTGAA	58.994	21	271	201	471
59.824	20	AGGTTGCAAGGACAAGCCTA	59.875	20	274	700	973
60.175	21	TTGATTTCCCACCCTTCTTC	58.956	20	213	53	265
58.695	20	TGCCTCTAATGCACACAAGAA	59.478	21	279	67	345
60.344	20	GAGCCAGGATTTCACGGTAG	59.694	20	267	1022	1288
61.196	20	CAAGGGTGATTGTAGCCAGC	60.657	20	158	890	1047
59.206	24	CTCGCTAACGGCACTAAACC	59.904	20	106	148	253
59.967	20	GGTATTGTCGGAACTTCGCT	59.198	20	163	101	263
60.326	20	TGCAGAAAGCAGGCAGTAGA	59.888	20	190	4388	4577
60.255	20	AGACGATTGAGAGAAAGCGG	59.574	20	106	503	608
59.938	20	AAATTTATTGTAATCTTCCCTCCAA	59.594	26	233	559	791
60.189	23	CACCAACCCAACCCACTAAC	60.126	20	120	11	130
58.984	20	ATCAATGGTCCACATCGGTT	60.057	20	217	25	241
59.708	20	TTCCTCTTGTCGCCATTTTT	59.685	20	280	319	598
59.964	20	GAACAATTACAATGTTTATGAAAT	59.51	27	105	25	129
60.286	20	TGGTTGTGTGAACCAACTCTG	59.626	21	141	272	412
60.044	20	GGCCATTAAAGCTTCACCAA	60.074	20	220	49	268
59.917	20	GTTTGAGGTCGGAGATTGGA	60.05	20	137	248	384
60.144	20	CAAGCTCATTTTGTGTCCCA	59.691	20	243	1056	1298
59.923	20	ATCGATGTGTTGGCATTCAA	59.931	20	145	79	223
59.945	20	AATGAAAGCGATCGTATGCC	60.067	20	190	887	1076
57.436	27	AAGGAGCAGGTGTGGTTGTC	60.159	20	240	18	257
59.784	20	TATTCACACAGCCCTTTCCC	59.933	20	211	107	317
60.081	20	AATTTGGAGAGGGAGGGAGA	60.008	20	102	27	128
60.195	20	AAGGGATTCACCTGCCTTCT	60.074	20	161	1158	1318
59.42	20	TTGATCCTGCAATCTCTCGTT	59.828	21	187	9	195
60.185	25	GACTCTTCACAACTTCTACACAAT	57.679	26	275	822	1096
59.933	20	GACACCCAATCCCATGAAAC	60.034	20	203	5	207
59.651	20	ATTTGCGTCGCCTAATGAAC	60.103	20	132	182	313
59.921	21	TGCTGAGAGTGTGTTGGCAT	60.473	20	108	1218	1325
59.964	20	CCCTCAATCGATCCATGTCT	59.886	20	177	498	674
60.312	20	GATCCCGTGTGTGAACTGTG	60.005	20	141	56	196

57.251	27	TTTGGTTCAATGGGTTATTCG	59.685	21	190	87	276
59.097	21	GCATGATCAGGGTAAAATCCA	59.776	21	191	46	236
60.188	20	ACAGCCACCATAATCGAAGG	59.955	20	262	285	546
60.218	20	GAACGGGCAGCAGTCTAAAG	60.015	20	157	58	214
59.6	21	CCTTCAGCATTTGAGATCGG	60.734	20	102	6	107
60.235	20	TGCTCACCTTCGATCTCTGA	59.656	20	214	47	260
59.888	20	GGTGGGAGGGAATTTGAGAT	60.133	20	235	1961	2195
59.971	20	TGTGTTTTATCCCTCGCACA	60.111	20	210	37	246
59.948	20	AGAACATGGTTTCCGAGCTG	60.255	20	101	163	263
59.988	20	TCTCCCCCTCTTCCCTCTTA	60.139	20	260	4096	4355
59.865	23	CACCTCACCTTCTCTCCACTCT	59.91	22	149	92	240
59.951	20	AGGCTAAACAAGGCCCAAAC	60.483	20	276	91	366
60.218	20	CAGAAATTGCCTCTGTTGTTC	57.468	21	170	111	280
60.008	20	TAATTTCGGCCAACACCTTC	59.938	20	180	1380	1559
59.027	21	TGCCTCAAGGCTAAACAAGG	60.378	20	259	87	345
60.088	20	CCTCTCGTGTTTCTTCGTCC	59.844	20	122	38	159
60.144	20	TACACCGAAGGATATCCCCA	60.148	20	266	285	550
59.697	20	AACAAGTGTGTTTGTGAGTGGG	59.969	22	146	385	530
60.068	20	CCCTCACCCCTTATGGTTTT	60.046	20	255	112	366
60.263	23	AACTCTGCCGGAGAATGTGT	59.727	20	232	1259	1490
59.472	25	TTCTGGATTATCCTGCGGTC	60.036	20	219	200	418
57.335	20	GGTTAAATTTTGTCCCTAGTTAGC	59.109	25	103	141	243
60.074	20	TTTCTTGGCGTGGTGTTGTA	60.149	20	190	442	631
59.988	20	GAAGACACGGTTGGACAAAAA	60.001	21	264	233	496
59.78	20	TGTAGTGGTTCGTGGACTGC	59.751	20	219	32	250
59.928	20	AGCTTCCATGGAGGTTGATG	60.073	20	184	5	188
60.155	20	ATGGGCTCAAATATCGGACA	60.296	20	258	18	275
60.119	20	TATGAAGGCTAGGGGTGTGC	60.096	20	231	276	506
60.038	20	TCGTGGAGAAACTATCCAAGG	59.181	21	244	762	1005
58.987	22	CCCCTACGTTGAAATTGTCG	60.357	20	232	368	599
59.938	20	TTCGTTGATTTGAAACTCTAAAGC	59.028	24	159	341	499
59.864	20	TATGTCGCATTTGACATCGG	60.488	20	232	78	309
59.446	20	TACCTCATCACCATCCCCAT	60.011	20	150	40	189
60.073	20	TCCCGTTGTTGCTTTCTCTC	60.375	20	271	137	407
60.044	20	TAGGAAAATCATGCACGTCG	59.688	20	148	1360	1507
60.656	20	AGGGGTTATCACCTGAATGC	58.864	20	248	268	515
58.371	20	GTGGGCATAAGAGACGGAGA	60.218	20	153	2138	2290
59.945	20	GCGGAGATAGAGACAAGGCA	60.504	20	178	203	380
60.068	20	GAGCTGCTGTTGGAGGAAAC	59.997	20	279	69	347
58.697	20	GAGTTCTTATCGCCTCCGGT	60.599	20	255	9	263
59.91	20	TGGATTTGGGATTCTTCTGC	60.014	20	271	1807	2077
59.569	20	CATTTCCCCCAACTTCACAT	59.647	20	207	21	227
59.839	20	ACTTTCTCGCCTGGATTTTG	59.312	20	136	143	278
59.993	20	TAGAACATTAGCGGGATGGG	59.916	20	137	187	323
60.212	20	GGATGAATTGATGGTTTTTGG	59.125	21	169	145	313
59.671	21	TGGAATTTGAAAGTTTGGAACA	59.469	22	272	713	984
58.576	23	GGAGATTGAGCATCAGGAGC	59.917	20	226	32	257
60.059	20	GAGAGGGAAAAGTTGGGAGG	60.045	20	237	272	508
59.747	20	ATGATTATTTGCCTCGTCCG	59.923	20	259	1669	1927
59.945	20	GTGGAAGAGAAGATGCTCGG	59.95	20	164	47	210
60.067	20	CAGAGCGCTAGAGGTTTTCC	59.218	20	233	447	679
60.015	20	GTAAAACCCGACACCTGCAA	60.924	20	240	92	331
59.961	27	GGGAAAGATTATTGGAACCTTG	58.864	22	215	1	215
59.996	20	ATCGAAAATGCCAAAAATCG	59.907	20	241	3140	3380
60.027	20	TCTTGCAATGAAGAACGTCG	59.988	20	150	63	212
58.866	20	GCAAGGCCAATGGAAATATG	60.289	20	160	1711	1870
59.95	20	TCATCTTCAACCCCCAACTC	59.903	20	248	1539	1786
60.214	20	TGCTGGTGTTGAATGGAAAA	60.088	20	211	287	497

60.206	20	AAACGCTCGTAGTGTCCCAG	60.312	20	124	208	331
58.017	20	TGCGTGGTTCAGATTGAGTT	59.293	20	280	1131	1410
59.844	20	TCCTCATGTACGTTGTTTATGGA	59.393	23	221	7	227
60.187	20	TGATTGAGGGTGATTGGTTAGA	59.429	22	100	29	128
60.212	20	CCGCCAGCTTTTATTCAAAC	59.72	20	271	1	271
60.655	23	GATGCACTGCACAATCAACC	60.128	20	219	216	434
60.134	20	AACTCCCCCACGAACTCC	59.896	18	101	41	141
60.111	20	TTTTGATGATATATAGGTGTTTTGA	58.782	27	136	2035	2170
59.983	20	CGACTTGTCGTGGTTCGATA	59.716	20	242	233	474
59.844	20	TCCTCTCTCTTTCACCACCG	60.377	20	201	1	201
59.922	20	ATAGTGGTGGGAGGAGGCTT	59.957	20	229	34	262
60.138	21	GATGAGGGATGCCATAAGGA	59.854	20	240	667	906
60.833	20	GGGATGGCTTGTTCACTCTC	59.661	20	215	18	232
59.997	20	TTTCAGCCGTTTGGTTTTGT	60.514	20	274	312	585
58.922	24	CGTTTCCGACTACCCTTGAA	60.103	20	259	4	262
60.081	20	AGCACTGCAGTCTCTGGCTT	60.352	20	174	393	566
59.993	20	TTATCCCAGCTCCGCTAAAA	59.81	20	161	1887	2047
59.992	20	TTTGCGTGAACAATGGTGTA	58.601	20	272	178	449
60.025	20	AATGCATGTCTCCGAGAAAAA	59.699	21	225	1122	1346
59.891	25	TCTGTTGGCAAACACAGGTC	59.726	20	108	63	170
59.565	21	CACCCACACACTCACACACA	60.088	20	126	17	142
59.993	20	CGGTACGAGCACAAACACAC	60.222	20	183	419	601
60	20	CGTGTTTATCCTCACCCGTT	59.853	20	166	70	235
60.096	20	TGGCAGAAGTGGGAGTCTTT	59.844	20	137	74	210
60.142	20	TGTGAAAATTTGGTTGCAGAA	59.192	21	194	191	384
59.801	20	AAAATCAAAGGCCCACAATG	59.801	20	216	106	321
60.192	20	GGGATGGGAGAATTGGAAAT	59.959	20	201	375	575
59.973	21	CCAACTATCCATGAGAAATGAGG	59.843	23	100	3	102
59.91	20	GGAATCATCACCATGCAACA	60.339	20	224	53	276
59.982	20	AAACCTTCGGCTTGAAAACA	59.724	20	277	60	336
60.35	23	CCAATCTCAACAACACACGC	60.16	20	170	55	224
60.029	20	GGACGCCACAAATTGTTTCT	59.978	20	192	103	294
59.009	20	CCATTCAAATAAAAATCAAGGGA	59.243	23	279	309	587
60.499	20	ATAACCCACCTCCCCAAAAG	60.046	20	125	43	167
59.623	21	AGTCGCTGCAATTTCCAGTT	59.882	20	215	3	217
57.862	23	GCAGGCAGCTGATATGTTCA	59.979	20	200	13	212
59.43	20	CCCTAGCCTTTGCCTCTTTC	60.332	20	234	35	268
60.054	20	TGATATAGTTTTTCGTGGCATCA	59.507	23	215	53	267
59.819	22	ATGATCGACCAACCCTGTTC	59.786	20	155	25	179
59.788	24	CCATTGAGACTCGAACCCAT	59.927	20	143	839	981
60.617	20	GCGACGTTACCCACTTTCAC	60.559	20	129	82	210
59.805	20	TGGCAACAAGATACCCACAA	59.964	20	124	571	694
59.989	20	TTTCAATGGGAATCGGAAAC	59.739	20	203	1191	1393
60.014	20	CAGTTGAACCAAACACCCCT	59.861	20	280	278	557
59.853	20	TGCGGGGATATATGTGGTTT	60.038	20	275	403	677
61.072	20	CAACGCCATGCATTTATCCT	60.857	20	153	16	168
59.942	20	TCTGTTGCTCCAAATCATTCA	59.262	21	221	1496	1716
60.096	20	CTAACCTTGGGCTCTGATGC	59.836	20	136	76	211
58.944	24	TGTCGCGTTGCAGATCTAGT	59.621	20	209	43	251
60.134	20	GGGATGGGAAGAGCATTTAAG	59.917	21	274	1052	1325
59.797	20	GCTTGGGCGAAACATGTAGT	60.14	20	280	132	411
59.097	20	GCTCGCATAACACCCCTTTA	60.096	20	225	684	908
60.012	20	CTGGTTTGGAGAAAGCGAAG	59.986	20	269	340	608
59.434	20	CGGTATCACCCTCCTTTTCA	59.926	20	127	88	214
59.569	20	CTCTATTTGGAGTTGGGGCA	60.066	20	229	3663	3891
60.067	20	TCTCTTTCTCACACCCTTTTCA	58.955	22	212	355	566
59.691	20	CCGACATGGGGAAATTGTAG	60.184	20	246	339	584
60.088	20	GGTTCGTTTTCGTCGTGATT	59.978	20	114	483	596

60.277	20	CAGCAATTTCGATTTCAACG	59.301	20	180	77	256
60.444	20	TAAAGGAGCCCAGAAAAGCA	59.953	20	186	2075	2260
59.664	20	CTGGTCCCCCTTTCTCTCTC	60.186	20	217	59	275
59.859	20	CATGAATCCAACGTACGCAT	59.425	20	228	1428	1655
60.545	20	CCTTATGCGGTTCTTGGAAA	60.067	20	258	0	257
59.721	20	TCGGAGTGTCTCTGTGCATC	59.988	20	256	795	1050
60.067	20	TGAAGTTAGGAAATAAGGAGGTG	58.743	25	105	659	763
60.212	20	ATATTAGCCCGCTCTGATGC	59.305	20	265	2938	3202
60.929	20	CAAGCAAAGGCCAATATCGT	60.096	20	114	63	176
58.956	21	TCAATGCATGATACGCCCTA	60.058	20	237	2147	2383
59.934	20	TCAAATGCTCGACTTATGCG	59.976	20	279	414	692
59.961	21	ACAAACCAAAGTTGCGATCC	59.978	20	193	694	886
59.536	20	GATCGCTCATGCATCAAGAA	59.914	20	123	368	490
60.315	20	ACCATATTTAAGGGTTATCACCTG	57.552	24	236	262	497
60.169	20	TGAAACATGAGGCCTTGCTA	59.42	20	158	562	719
59.945	20	TAGTGGTATGGAGTGGGGGA	60.187	20	140	45	184
59.996	20	CGTGGATGCCCTAGATTGTT	59.955	20	250	379	628
59.702	23	GGACCGGTTAGACCGAATTT	60.187	20	123	268	390
58.982	20	CTGTCCTAACCCGCTGTCAT	60.134	20	277	4	280
59.945	20	CGACACGGATTGAATCACAC	59.967	20	140	366	505
60.068	21	CAAGGCATGCAATCAAATGT	59.548	20	255	504	758
59.605	20	TGAAAAGGCCGGCATAAATA	60.405	20	189	224	412
59.661	20	CCACAAATCATGATGAGCAAA	59.533	21	191	2674	2864
59.878	20	TTCATCCCTAGCCATCGAAC	60.036	20	196	10	205
59.682	20	CCGTACGGTCCCAACATATC	60.074	20	253	1393	1645
60.365	20	CGAAAATCAATGGATGGGAT	59.581	20	227	1370	1596
60.142	20	CACGAGAGAGGAAAGGGAGA	59.525	20	103	28	130
59.558	20	GCAGTTGGGAGAGGAAAACA	60.232	20	178	189	366
60.142	20	GAAAAGCTTGGCCATTCAAC	59.691	20	114	189	302
59.089	24	AGGGGCAAATGTTGATGAAA	60.309	20	221	26	246
59.807	20	CTTCCCCCTTTTCTCTCGTC	60.183	20	258	779	1036
59.822	19	AGTTGAAGGTGACGCTCAAAA	59.906	21	279	27	305
59.935	20	CGTAAAATTCCGGTGCAAAT	59.832	20	161	67	227
59.844	20	ACTGTGGAAAGGGAGCTGAA	59.844	20	115	657	771
60.066	20	AAAGCAAGTTCGATATATTAAAAC	59.345	26	205	31	235
59.021	24	GCGATTCTCATTCCAATTCAA	60.031	21	117	697	813
60.195	20	CCCTAAGATAATGCCACCCA	59.778	20	150	88	237
60.088	20	AGGTCTTGACAGGTTGTGGG	60.002	20	206	903	1108
59.14	20	AGGATACAAGGCAAAAGGCA	59.708	20	213	180	392
58.926	24	GCGTTCACACCCTCATTTTT	59.978	20	191	27	217
60.399	20	CCAAGAACACTCTCCACTCTCC	60.288	22	187	1	187
59.823	20	ACAAACTAATCAAGTTCCGCA	57.439	21	219	344	562
59.838	21	GTTATATCTATAGGGAGGGTTATC	57.293	26	227	1193	1419
60.008	21	TTCGATGATAACTATGGGTTTGT	57.589	23	276	375	650
60.111	20	TGGAAAGAAGGGAAAGTCAA	57.367	20	257	1356	1612
59.813	20	CCTTCCTAGGACATTTGCCA	60.066	20	228	26	253
59.415	20	GCTATGACCCAAGAACCGAA	60.074	20	209	5	213
58.467	25	TTCAAACCGAGCTTGAGATG	58.999	20	255	42	296
60.027	20	CACTTACACACGCACACACG	59.848	20	263	212	474
59.123	20	AGCCCAACGGCTGATTATAC	59.07	20	137	50	186
60.307	20	TCAGGATCTCACCTTCACCC	60.048	20	275	19	293
59.542	20	CCTCCTCCTCACACTGCTTC	59.986	20	201	696	896
59.872	20	CTCTGACCTTGAGGGCTTTG	59.982	20	276	142	417
59.978	20	ATTTGCGATTTATGATGGCG	60.802	20	164	1133	1296
59.864	20	CGTGAGGAAAAACCGTGATT	59.971	20	255	370	624
58.78	20	GCTCAGCCCAACTTCCTAAA	59.452	20	242	30	271
59.809	20	GCACGCGAGACAACTATCTG	59.621	20	123	239	361
59.224	23	CTGTCCCGTCTTCTTCGTTC	59.844	20	173	19	191

59.978	20	GGCCGATTGGAGTATAACGA	59.923	20	279	789	1067
58.83	21	AAGCTTTCTGAATTTGTTTGCAG	59.946	23	235	66	300
59.933	20	TTTGCATGTGTTGCAAATGA	59.691	20	252	35	286
59.899	21	TGGCTCCAACATCACAAAAA	60.088	20	194	261	454
59.707	21	AAGGAGGTGTTATGAAGGGATT	58.028	22	143	70	212
59.88	20	CTCCGATTTCTTGGTGTGGT	59.966	20	225	74	298
59.766	20	TCCAGTCTCAACAAACGTGG	59.72	20	251	1919	2169
60.102	23	TACAGCTCCTACCCGCAACT	59.898	20	229	296	524
59.794	20	CGAAAAATTTAAAATCAAACGAT	60.521	25	219	4	222
59.915	20	GGGAATGAAGAAGTTTCGCA	60.192	20	253	332	584
60.034	20	TTGGTGAGGTGGCATCATAA	59.924	20	185	232	416
59.762	20	TGCAGATTGACGAAGGAAGA	59.522	20	139	970	1108
59.009	26	TGGGAGGAGGCTTAGGATCT	60.169	20	113	2	114
59.901	20	CCAGCAACTACAGGACAGCA	60.049	20	157	836	992
60.067	20	CACTTATAGATGGGTTAGCGTGT	59.972	24	164	238	401
60.016	20	TTTCTGAGCCTAACCTTGGGT	60.116	21	252	150	401
57.717	22	AATTTTCGACTTTGCCGTGT	59.615	20	238	17	254
58.236	23	TCCTGACCCTTTTTGAGATTG	59.157	21	221	23	243
59.712	23	GGGTACATGTTACGTGCCCT	59.74	20	280	37	316
59.52	20	ACAGGTATCCGAAGGGATGA	59.361	20	108	7	114
60.018	20	CAATTAACGGTAGCCATCACAA	59.89	22	271	436	706
59.439	20	GGTTCATCGGAAGAGTTCCA	60.05	20	237	193	429
60.075	20	GCCGATCATGTCCTCAAAGA	61.159	20	255	101	355
58.984	20	ACCACGCCAGTCAGGTAAAC	60.035	20	144	67	210
59.245	20	CCAATGACACGACACAAACA	58.974	20	186	569	754
59.694	20	AAAATAAGTGGGGTGCTGGA	59.429	20	130	713	842
59.999	20	GAAATGGTGTAAAAGGGGGTT	59.101	21	230	145	374
61.128	20	TGGACACCCCAGATTGTTTT	60.21	20	177	261	437
60.124	21	TGCTTACTGTTGTATGGGGTG	58.566	21	238	166	403
59.823	20	TCTAACGGCCCAGATTTGTT	59.569	20	275	664	938
60.352	20	GAGTTCGTCAAACCTCCCAA	60.088	20	265	838	1102
60.096	20	TACGAGACCGAAAGGAAAAA	57.49	20	208	2	209
60.014	20	GCGCAGCAGCATGTTAAATA	60.009	20	147	3078	3224
60.053	20	ATCCACTGCATGAACAACCA	59.967	20	175	75	249
60.045	20	GTGGCCTTTGTGGGCTACTA	60.132	20	194	2564	2757
59.464	20	AGATTCAGACGCATTTTGGC	60.221	20	251	2112	2362
60.214	20	TGAATTGGTGACACACACGA	59.541	20	209	1113	1321
59.864	20	TCCATCTGCTGTCTAACCCA	59.241	20	225	23	247
59.716	20	TTGAGGACATTTATTCGTCGG	59.946	21	153	413	565
59.935	20	TCACTCATACCCTCCCTCCA	60.465	20	273	304	576
59.933	20	TGCAACGCCAACTACAAAAG	59.911	20	145	9052	9196
60.372	21	TGCCTAACGTTAAATGGGCT	59.609	20	249	0	248
60.152	20	ATTTGGCTTCCAAAGCTTCC	60.562	20	209	335	543
59.697	21	CCACTAACCCAAACCCATCA	60.605	20	119	12	130
59.96	20	TGCTGTGAATTGTCCAGCTC	59.992	20	246	917	1162
60.14	20	AACATGGTTGGGCTAAGTGG	59.853	20	175	5	179
59.569	20	TCATTTAGAATTGGTGGAAAGATT	58.153	24	273	7	279
59.952	20	TTCCTTCAATCCATGCAACA	60.049	20	207	511	717
60.12	20	TGCCAGCGTATTGTGAAGAG	60.011	20	187	150	336
59.705	20	ACAACAAAAGGCAAAGGCTG	60.284	20	252	781	1032
59.923	20	GGCTTGCCCTTAACCCTATC	59.93	20	222	408	629
59.75	20	CCCCAAGAACACTCAAGAACA	60.133	21	233	358	590
60.149	20	CCACCTTGTAGCTTTTCCCA	60.103	20	221	1128	1348
59.637	20	CACTTTTCCAGTCTGCTCCC	59.844	20	130	415	544
60.055	25	AATCGGACCGGATCGTTAAT	60.531	20	210	134	343
60.081	20	TTAAACAAAGCGTGCAGACG	60.052	20	169	2611	2779
60.089	20	TATCAAACGAAGATGTGGCG	59.688	20	200	112	311
59.799	20	AGATTTCGATTTCCCCGAAC	60.265	20	189	213	401

59.923	20	CCCAGTAACCAACGCATACC	60.249	20	162	399	560
60.073	20	GGGGTACCCAATATTCTCCG	60.391	20	264	43	306
59.931	20	CCATATCAGAGAAGGGCAGC	59.797	20	242	42	283
59.96	20	GGAGTGCTCATGATCCGTAGA	60.233	21	207	154	360
60.044	20	ACGAACAGAATCCTCATCCG	60.073	20	268	87	354
59.026	20	TTTGACCGAACCGTTGTGTA	60.004	20	189	2312	2500
59.887	21	TGATGCAAATCACCTTCGTAA	59.172	21	271	105	375
60.125	20	GTGGACGGCCATAAGAAGTC	59.556	20	262	191	452
59.803	20	TCGGGGTATCAGAAATCGAG	60.029	20	167	79	245
60.745	20	GAAAAAGTGCTGGGTTGAGG	59.711	20	225	48	272
59.867	20	TGTAGGCGCCATCTTTTTCT	59.845	20	162	625	786
59.916	20	AATTTTTCGATCATGTGGGC	59.768	20	156	13	168
60.045	20	TCGTGTGTGTGAATTAAAATGAA	58.136	23	261	101	361
60.448	20	TATATATGGGTTATCACCTGATCG	57.071	24	149	463	611
59.997	20	CATTCTGTGTTCTCTGTTTTCGAT	59.696	24	260	916	1175
59.598	20	CATGGCGTTGTATTTGTGCT	59.614	20	199	1999	2197
59.216	21	TGGAAGGCTGTTCCGATAAC	60.074	20	188	1323	1510
60.776	20	CACCCTCTCTTCTGGTCAGC	59.986	20	230	537	766
60.01	22	ACCTGCACCAAAATGGAGAG	60.111	20	135	51	185
58.718	26	CTCCCAGCTCACGTTCTACC	59.867	20	270	4	273
60.011	20	TTTCTTCCATTCCATGGTCC	59.727	20	220	74	293
59.586	20	TGCCGTATATGGTGCTCATT	59.019	20	280	202	481
60.251	20	ACATGGAACTGCACCAGATG	59.551	20	231	100	330
59.343	21	CCGGTCGAATATTTCCTTCA	59.894	20	271	252	522
60.218	20	CATCAGAGCCACGGTTAGGT	60.134	20	240	87	326
60.169	20	TGTGTGTGAGTGTGTGGGTG	60.088	20	196	57	252
60.01	20	TCACGTCAGGTTCACCATGT	60.005	20	205	238	442
61.021	20	GAGAAGGGGAGAGGGACTGT	59.661	20	190	53	242
60.116	21	TCAACAGAGAATGCAAGCAAA	59.6	21	162	82	243
59.072	20	CGGATTAGCCACGGTCATAG	60.481	20	257	174	430
60.324	20	CTCCACTCCAAACCACCATT	59.82	20	225	356	580
59.791	20	TGTCCGTATTCATTCCGTGA	59.924	20	262	511	772
61.204	20	CGGGTAACGGGTAGGGTATT	59.96	20	280	84	363
60.357	20	CCTTAACATGTCGGGTTCGT	59.853	20	199	7	205
59.916	20	TCCATTCCGAAAATCAAAGG	59.872	20	153	184	336
59.15	20	GACTTCCGCCTTGTTCTTTG	59.853	20	219	225	443
59.342	20	GATTAACCTCGCATCCCTCA	60.036	20	160	439	598
59.225	22	CCAACCAATACGGGACACTT	59.711	20	262	717	978
59.528	20	AAAATCAAAGGCCCACAATG	59.801	20	226	975	1200
60.035	20	GACATCTCCCTCTCCGACC	59.583	19	194	328	521
60.301	20	CTGTCTCTCGCTCTCGCTCT	60.182	20	274	428	701
59.942	20	GACTGTGAGGAAACGTGCAA	59.88	20	223	500	722
59.111	23	GGGGAGAATGTAATATCCCGA	59.992	21	222	24	245
60.182	20	CCCTAACTCGACCCAGATCA	60.065	20	221	41	261
60.578	20	GATGCAGAATGTCGGTGAGA	59.794	20	237	1109	1345
57.268	23	TGGAGGTGAAGAGAGGGAGA	59.913	20	253	167	419
60.103	20	ACTATCAGCCGCCAAATGAT	59.556	20	140	210	349
59.648	20	TCAAGGATTCAAGCCCACAT	60.461	20	100	19	118
59.757	20	GCCCAAAAAGAACACTCACC	59.574	20	277	50	326
60.179	20	CATGATAATGCACGTCTCCG	60.096	20	104	91	194
60.008	20	TGAAAGTGATTCCCCTTGATTT	59.814	22	177	6	182
60.036	20	GGAAATAAGGAGGCGTTATGA	58.213	21	127	184	310
59.813	20	GTTGGACTCAAGTCATGCGA	59.837	20	156	298	453
57.33	26	CATCCCCTTCATTCAACACC	60.173	20	105	9	113
59.75	20	ATGTCTCAGCCGATCGATTT	59.658	20	162	1965	2126
60.088	20	CGTTGCATGGTGTATTGGAC	59.847	20	253	2217	2469
59.787	20	TTGCCTTTAATCGATCCTGG	60.031	20	176	4	179
59.948	20	TTCCACCTTTCACCCTGTTC	59.943	20	200	513	712

60.103	21	GAAGGAATTGCAAGGGACAA	60.051	20	181	285	465
59.878	24	TGGTTTTGGATGATGGATGA	59.707	20	159	22	180
60.699	20	CACCTAAAGCCCATGCATTT	59.96	20	279	47	325
59.822	19	CCCCTTGAACTCCAGCAATA	60.066	20	203	201	403
60.251	20	CAGTGGCTACCGAGCATTTT	60.27	20	120	2922	3041
60.035	20	TCCCCAAATGAAAGAATGGA	60.244	20	190	243	432
59.872	20	GAAAACGCCAAAAATCGTGT	59.982	20	114	20	133
59.903	20	CGAATTCTCTCTCTGCAAACC	59.066	21	103	289	391
60.074	20	GGCATGAGCGTGTAAGATGA	59.83	20	193	162	354
60.042	20	TGTCCGAAAAGGCAAAAATC	60.053	20	169	29	197
60.074	20	AGTAGTCGTCGAGGTGGTCG	60.321	20	228	298	525
59.052	20	CCCCGAACAGAGTCAAATGT	59.966	20	275	599	873
59.668	20	CTGGAGGAAAGAGCTTGAATC	58.134	21	168	1563	1730
59.943	20	GGGCACTCTTGTGTTTAGCC	59.74	20	260	1211	1470
59.953	20	GTTAGCCACCAATGAGGCAT	59.962	20	274	440	713
59.051	25	GTCTAGTGATGACGGGGAGG	59.53	20	198	1	198
60.22	20	TTGTTTTCCAAGCCCCATAA	60.294	20	134	320	453
60.022	20	TGGGAACTTGAACTTGGAAGA	59.697	21	247	351	597
60.291	20	ACGTCTTTGTGTCGAAACCC	60.012	20	173	178	350
60.02	20	TCGATAAAACTTTACCAACACCAA	59.817	24	250	15	264
59.82	20	TAAGTTCTCCACAGCGAGCA	59.74	20	177	143	319
59.318	27	GGACGTCTTTCTTGAGCAGC	60.142	20	203	4	206
58.286	21	GAAAACAAAATGGGGAGCAA	59.916	20	241	19	259
57.416	20	AATGCAGCGGAAGAACAAAT	59.713	20	201	4	204
59.966	20	GGTAGCGAGAGAGGGGAAAG	60.34	20	255	555	809
59.836	20	CTTTGTGAAGTAGTCGCCCC	59.734	20	177	10	186
59.836	20	GGCAACGGAATACCATTTGT	59.691	20	147	42	188
59.215	20	TTGACAATATTTAGTGTTTTGACAT	58.99	27	269	189	457
60.034	20	ATTTGGCCGGTTCTCTTTTT	59.945	20	198	4527	4724
60.173	20	GAGGACGTTGTGGTGGTCTT	60.009	20	188	199	386
60.542	20	CTGCACTAACGCCATTCCTT	60.27	20	271	223	493
57.318	22	AAGGAGGTGTTATGAAGGGATT	58.028	22	129	95	223
60.048	20	GGGAGGGATAAATGGGAAGA	60.089	20	244	1358	1601
57.885	21	ATATGTGGCTTGAGATCGTGT	57.152	21	248	136	383
59.933	20	TCGACCGAAGAGCTATCCAT	59.797	20	228	159	386
59.911	20	TTTTATGTAAATTGTCGTGCGT	57.373	22	253	182	434
60.401	20	ATCTGGGTTACACTGAGCGG	60.134	20	216	1	216
59.616	20	AGACTGCGGTGCAAGACTTT	60.058	20	263	1453	1715
60.24	20	TTCAACCAGGCAAAGACCAC	61.075	20	189	136	324
59.923	20	ACCGGAATAGCATCAGTTGG	59.955	20	221	7	227
60.665	20	TGGCTGTCAGATGATGTAAGTTC	59.256	23	175	354	528
59.744	20	GCATTCGGTTGATTATGCAG	59.14	20	243	953	1195
59.988	20	GATTGGCTCCATCCTCTTCA	60.158	20	254	385	638
60.045	20	GAACTCCCCTCTCTCTCGGT	59.807	20	120	89	208
60.149	20	CTTTCTTCTTCATTTCGCCG	59.953	20	128	3	130
60.036	20	TAGGTGTAGGTAGCCAGGGG	59.073	20	171	466	636
60.013	20	GCACTATCTCTCCCTCACCG	59.827	20	123	319	441
60.048	20	TATGCAGTGGATTTGGTGGA	59.924	20	195	179	373
60.463	20	GAAGCCTCAAATCACAAGCC	59.82	20	142	106	247
59.232	22	TACCGTTGGTTAATCCTGCC	59.823	20	117	0	116
59.992	20	GTCAACTTTGGCAACGGAAT	59.978	20	176	42	217
59.989	20	CAAGAGCTGAAGATGTGATTGC	60.022	22	198	259	456
60.619	20	TTCGAATGGATTTGTTGGGT	60.17	20	156	394	549
60.03	20	GTTGTCTGAAACCCTTCCCA	59.943	20	122	238	359
59.312	20	CGACCCTGTAAGGTTCTTTGA	59.225	21	272	130	401
59.929	20	GCGAAGAAGAGGGGAAGAAT	59.789	20	232	61	292
59.982	20	TTCTACAGCGAATGATGCCC	61.141	20	229	844	1072
58.982	20	AATCATTCCATTCCCCGATT	60.345	20	246	37	282

59.145	22	AAGGAGGTGTTATGAAGGGATT	58.028	22	238	34	271
57.077	21	TGGCAAACACAGGTCACAAT	60.008	20	163	5	167
59.4	20	GGTCGTCGGATTTCATTTTG	60.309	20	261	2756	3016
60.322	19	GGATACGGTGTCGGAAACTC	59.41	20	269	1391	1659
59.972	20	TTGAAATTTCGGCTTCAACC	60.053	20	221	4	224
59.203	20	CGACAACAATGCAAGGAAGA	59.84	20	183	14	196
60.074	20	TGTAAATACGGTCTGTGCATGTT	59.46	23	149	323	471
59.276	21	TGCTTTGATTTGATGGTTATGG	59.832	22	173	4291	4463
60.073	20	GATGATGGGGAAGAGACCAA	59.862	20	142	254	395
59.801	20	TCTCAAAATAACCAAAATCAGCA	58.796	23	220	109	328
59.846	20	ATAACCCGTGTGTGGGTTTA	57.729	20	230	102	331
60.257	20	TGTCGAGAGGCAAGTGTTTG	60.025	20	177	32	208
59.267	20	TCGCAGTCCATCACTCCATA	60.225	20	139	268	406
57.589	23	TGGAACTTGTGTTTGTACCCA	58.934	21	199	18	216
60.608	20	CGCAAGTACAACAACATGCC	60.18	20	270	235	504
60.111	20	AACTTGTATCACTGGAAGAATTCA	58.329	25	275	102	376
60.001	20	CAATTTTCATTGCCCCTCAC	60.309	20	176	46	221
59.83	20	GACGAGAATGCCCCTGTATG	60.483	20	200	331	530
60.151	20	TGAGTGGAAGAGAGGGAGGA	59.913	20	128	80	207
59.931	20	AGAGCCACGTTAGGCTCAAG	59.639	20	279	79	357
60.074	20	TCAACAGAGAATGCAAGCAAA	59.6	21	186	11	196
59.915	20	GGTTCTGAGACCGGGATAGG	60.842	20	273	0	272
59.858	20	AGGAAGCGAGGTAGGCTTTC	59.983	20	190	199	388
59.836	20	TCTTAGTGATTTTTCTTCGTCCA	58.064	23	247	666	912
59.708	22	GACAACAGTCACGTGGCATC	60.171	20	278	590	867
59.934	20	CGTGTGTCAGCGTGTCTCTC	60.685	20	177	1617	1793
59.984	20	TGGTTCATGCCATTGTGAAT	59.781	20	124	39	162
59.591	20	GAAATTTCACGAAACAACGAATC	59.877	23	258	299	556
59.09	20	TCTTCCAAGATGGGAATGGA	60.395	20	187	112	298
59.827	20	CCGTCTGGTCATCCCTTTTA	59.926	20	260	558	817
59.867	20	TCTCTCTTGGTTGGTGAAGAAA	58.955	22	169	53	221
60.47	24	ACCTTGAAATGCAACCGAAG	60.11	20	264	1627	1890
58.381	25	GCTCGAGCTCAGACATCAAGA	60.839	21	276	454	729
60.633	20	TCCAAGCTTTAATTGCGGAC	60.209	20	133	441	573
59.992	20	TATCCCGTGGGTCAAATACG	60.576	20	234	962	1195
59.96	20	TGGATGCGAAACATGAAAAA	60.051	20	271	513	783
59.795	21	TTTCACCACCGCCTTAATTC	59.938	20	249	28	276
59.971	20	CTGCTCTCCCAAGCAGAATC	60.096	20	244	3682	3925
59.742	20	CCTTTCAGGCATTTAAGTGGA	59.211	21	275	1747	2021
59.836	20	GTACACGCACCAATCGTCAC	60.04	20	276	886	1161
59.472	22	TCAGTTTCTGAGTTTTGAGGTTTG	59.835	24	108	747	854
60.057	21	TCTAAGCTTGTTAACCCCCG	59.221	20	232	9	240
60.265	20	TTTTCGACCAATAGGAACGG	59.931	20	132	1333	1464
59.978	20	GAGATGTGGTGGTGGTGATG	59.801	20	136	388	523
59.751	20	AAAGTCCAAATGTTGGCGAG	60.11	20	121	1552	1672
59.827	20	TAAATCACAAAACCCACGCA	59.969	20	135	343	477
59.67	20	CCCAGCAACTGTTGGCTACT	60.312	20	239	305	543
60.11	20	TTTTTAGTAGGGTTTTCAAGTTCAC	59.564	26	265	356	620
59.966	20	CATGCTTGAATGAAAACCACA	59.576	21	122	272	393
59.841	20	TGTAGGGGCAATGATGTAAAAA	59.363	22	232	25	256
60.088	20	CAGCCCAATAACTCAACCTACC	59.892	22	101	44	144
60.501	20	GGAGCCTCCGAACTTTGAA	60.324	19	188	56	243
60.002	20	TCCACTGTCTTGTGCCTCAG	60.022	20	127	891	1017
59.764	19	GCCAAGAGGTGAGTTTCTGG	59.844	20	168	9	176
59.54	20	ACAGTTGAAAAAGGAGGGCA	59.711	20	280	765	1044
60.05	20	CTTTGAATTGCAGCTCGACA	60.134	20	267	1127	1393
58.06	20	TTTCTTGTGTGTGTGCATGTG	59.203	21	170	181	350
58.826	22	TACGAATCTCAAGGGGCAAC	60.074	20	212	99	310

59.855	26	ACGTAGTTTGTGGGGGAAAT	58.293	20	280	916	1195
60.49	20	TATGCAGATTGGTGTGTGGC	60.549	20	262	141	402
59.667	24	CGTGCTGAGCTTATTCACCA	60.011	20	191	2	192
59.26	20	TGCGCAACCAATGTAATAGC	59.731	20	234	785	1018
59.521	20	GATCGTGTCCGGTTTGTGTA	59.42	20	251	104	354
60.067	20	GGAACCTGTTTTCCCAGTCA	59.943	20	215	215	429
59.624	20	TCGAAGGTGACTATCCCGAC	60.073	20	241	108	348
59.872	20	GCAGCATCCTTCACCATTTT	60.081	20	162	72	233
57.874	25	GCAGTAGGGTTGGAGATGCT	59.313	20	263	7	269
59.928	20	GTGGACGTCCCAGATTGTTT	59.827	20	182	665	846
60.178	20	GCATAGAGGGCAAGAAGACG	59.978	20	192	427	618
59.248	20	CGTTTTGATGATATATAGGTGTTTT	59.637	27	237	378	614
60.264	20	CCCTTAATCTTTGTGGTTGTGA	58.994	22	273	1896	2168
59.985	21	TTTGAGTTTGCATCTAAGAAGGTG	59.828	24	117	835	951
59.609	20	TTTGGTTTTATCGAAGAGGCA	59.707	21	260	845	1104
60.111	20	GACTCTCCAACTAAGGGGGC	60.074	20	276	243	518
60.557	20	CAGGAGCACTACAGTTCACGA	59.097	21	264	2128	2391
60.068	20	CGGCCAAGATTTGTTAGAGG	59.702	20	195	380	574
60.024	21	CATTCGGTTGAACCCTCAGT	59.966	20	109	189	297
59.82	20	GGATTGATGAATTTCCATTCG	59.221	21	194	1757	1950
60.376	20	CCATCATTCCAATTCAAGGAA	59.748	21	264	1869	2132
59.443	21	TTGACCAAGATACACCTTGCAT	59.499	22	185	17	201
60.289	20	GCTCTTTTATTTACCTTTTATGCTC	60.067	26	212	338	549
59.93	19	GAGGGTTGTTGTTGTGGGAC	60.261	20	200	0	199
58.753	20	CCGAGATCTTTTCATGAGTGC	59.828	21	249	834	1082
60.307	20	TATGTTTCGGCCCGGTATTA	60.165	20	154	45	198
59.964	20	GTTCAATTTGGACGTTTGGG	60.206	20	267	530	796
58.388	25	TGAATCTCATGTTATTGAGTGATG	57.699	25	206	671	876
59.937	20	TTTTTCAACGTTTGCCATCC	60.846	20	183	189	371
60.088	20	GCCGGAATCCATTACTTCCT	60.286	20	220	17	236
60.21	20	CTTGTGAACTCCGATGGACA	59.676	20	156	448	603
59.935	20	TCTCGAGCAACAGAGCTCAA	60.008	20	219	155	373
60.152	20	GAAATCCCGCTCAATCTCAA	60.155	20	218	396	613
58.792	20	TCGGCAGAAAAGAAGAAGGA	60.066	20	114	428	541
59.621	20	GATGGCCCAGATTTGTTTTG	60.309	20	102	106	207
59.238	23	GGCGAACATGATGAATGAACT	59.954	21	280	23	302
57.557	25	GAGAGAAGTAGCAAGCGCGA	60.955	20	181	10	190
59.939	20	AAATGCTCATGCATGCTGTC	59.836	20	182	44	225
58.707	23	ACACACAAGCCTCGCTCTTT	60.058	20	223	658	880
60.435	20	TCAATGACGAAACATATCCCA	58.832	21	192	1779	1970
59.673	20	CTATCGAGCGTGTGGCAATA	59.856	20	146	24	169
58.004	25	CTTGTGGCTTGCAAACATCT	58.926	20	162	73	234
59.981	20	GCAGTGGGTTTTGAATGGTT	59.836	20	225	210	434
59.993	20	GCATTTGAAAGGTTTTATATGATC	60.438	27	160	491	650
59.64	20	CTTACGGAATTCCACTGGGT	58.909	20	247	14	260
59.976	20	CGTAACCTTGGTGTAGCCGT	60.052	20	252	563	814
59.993	20	ATGTATGGCAGGTGACCCAT	60.081	20	274	123	396
59.146	20	AGTTGTCAATGGAGGTTGGG	59.82	20	252	267	518
59.787	20	AGAGCGAAGAAAGCAGATGG	59.717	20	143	1357	1499
59.849	20	ATGAATGTGGAGCAACGTGA	60.12	20	268	2148	2415
60.132	20	TTTGAACGCGTGACTTCTTG	60.027	20	259	4833	5091
59.267	22	GCATTAAATGAGCCTCCCAC	59.533	20	125	5	129
60.042	20	AAATGCTGGTAGAGGCAACG	60.27	20	257	322	578
60.142	20	TGATACAGGTGTTCCAAACAATG	59.777	23	247	6310	6556
59.964	20	AGGGAGAGGCTTTGGATGAC	60.596	20	232	39	270
60.214	21	TGCATGTGTGGGGCTATTTA	59.953	20	218	1005	1222
60.255	20	AAATTCCGTTTTTGCCTTCC	60.292	20	183	193	375
60.564	20	AGAAAGAAGTCGGCAACCCT	60.247	20	163	1170	1332

59.173	21	TCGGGCAACTGGAGCTAATA	60.732	20	212	2	213
59.962	20	TGCCACCCTAGATCCGTTAC	59.955	20	175	517	691
59.052	20	TGAAACAAAAATATAGCTAATGCC	59.293	25	273	385	657
57.436	27	TGACGAGTCCATTGTGCATT	60.12	20	159	14	172
59.236	22	GGGAGAGGATCAAGAGAGGAA	59.763	21	201	37	237
59.844	20	GATGTATCGCCCAAAGGAGA	60.036	20	225	2484	2708
60.111	20	CTGCCTTCCAACCATACACA	59.566	20	267	453	719
59.688	20	AATGGGACTGGCGATTGTAG	59.955	20	267	95	361
60.012	20	GGTCACCGTTCCCTGAAATA	59.79	20	257	1395	1651
60.162	20	TGTGAATGGAGGACAAACCA	59.935	20	156	201	356
60.081	20	TGGCAACAAATATGACTGCAT	59.055	21	116	341	456
59.905	20	TCTCCGAGGAGACAACTTTCA	59.974	21	170	4000	4169
59.33	25	TCTTTGAATTCAGCACGCTA	57.257	20	140	35	174
60	25	TTTTGATGATATATAGGTGTTTTGA	58.782	27	150	616	765
57.548	22	GATGGTGGGTCTGAACGAAT	59.786	20	212	554	765
59.911	20	CTCCGAGATCAGAGCTCACC	60.096	20	227	1756	1982
59.516	20	CCCATTTCTAACTACCCAAATCC	59.962	23	212	231	442
57.926	20	GGTTTGATGACGTGGCTTCT	60.119	20	194	1107	1300
60.073	20	AATGCCTCTGCAAAAAGCTG	60.523	20	189	2874	3062
59.469	23	CCCACCCCACTACTCAAGAA	59.959	20	116	8	123
57.236	26	GCTTTCCCATTTTGCTTTTT	58.361	20	280	646	925
59.247	20	TTGTGATTTGGTGTGTGTATGG	59.22	22	249	247	495
59.817	20	AACGGCTTGGATTCTTTCCT	60.074	20	147	397	543
59.823	20	ATATCCCTTGCACGACGAAC	59.962	20	274	523	796
60.096	20	TAGCCCATTATCTCCCACCA	60.288	20	162	1575	1736
59.938	20	TGCCTCTGCTATTACATGCC	58.897	20	211	967	1177
59.271	24	TGGAGAAACGAACTGGAACC	60.088	20	252	205	456
60.173	20	TTGTGGCAGGTTATTCATGC	59.548	20	201	432	632
59.964	20	CACCATGACGGCAGATGTAT	59.399	20	251	636	886
60.119	20	CGGCTTCACCAGTTTCTTTT	59.355	20	138	246	383
60.203	20	ATTGTATGGCGAGAGGTTGC	60.103	20	278	27	304
60.483	20	CACACGTTCTTCCCCAGATT	59.966	20	143	45	187
59.646	20	TTTTGAGGAGTTTGCGCTCT	60.132	20	239	756	994
60.011	19	GATGATTGCACCATAATGCG	59.921	20	126	2678	2803
60.073	20	CCTGCTTTTGGATGTTGGAT	59.933	20	172	1036	1207
59.703	19	GTGCATCCATCTGAGCATTG	60.233	20	246	186	431
59.884	19	GTCGTTCTGAGCTGCCTTTC	60.142	20	237	2257	2493
59.96	20	GGGTCCCACCACCTAACATA	59.526	20	232	567	798
59.911	20	TCCCTTAGACCTTACATAATGAAT	60.001	26	221	45	265
59.957	20	AGATGCTGGAATCTTCGTGG	60.218	20	138	151	288
59.82	20	TCCAAAACTGGGAACCATTC	59.767	20	140	325	464
59.746	20	TCCATTAAGAATTTCCCATGC	58.888	21	178	1623	1800
60.062	23	CAGTGCGGACGGTTAAGATT	60.132	20	208	19	226
60.136	20	GAAGCTGGTGCAATTGTTTG	59.322	20	247	96	342
59.518	20	TTCTTGGTGGCGGTAGGTAG	60.125	20	198	1	198
60.119	20	TGACGATGAGACGTGTAGGG	59.701	20	279	303	581
59.293	20	CTTTCTTCACTACTGGAACTTTCAT	57.353	25	222	54	275
60.035	20	GATAAGAACTCTGGCTCCAAGG	59.371	22	255	354	608
60.096	20	TCATGCACGTGTTTCACAAA	59.721	20	276	184	459
60.032	20	AAAAATCTCAGGGACGGGAC	60.306	20	173	3450	3622
60.021	20	GTTTGCTTCCACGGCTAAAC	59.752	20	268	1205	1472
60.02	20	GTGTCGATTGTGTTCATGCC	59.975	20	188	96	283
59.883	20	ATACTTTGGCCCAGTTCGTG	59.993	20	261	2980	3240
59.969	20	TCGAGTGTTCGTTAGTTAGTGAGG	59.876	24	106	141	246
59.717	20	GGTGGTTGCTGGGTTAGAGA	60.111	20	200	7	206
59.225	20	ATTTCGAAGATCAACGGACG	60.074	20	206	195	400
59.394	20	GTTGTTTGGTTCACGGGTTT	59.734	20	249	109	357
60.053	21	CGTTCTTAATTAGCGCCGAA	60.347	20	114	1020	1133

59.988	20	GAGCGTCGATCTGGTGAAAT	60.226	20	253	385	637
59.573	21	GCGATCGAGAGAGAGAGGTG	60.246	20	176	1068	1243
60.362	20	CAAACAACGATCGACAATGG	59.964	20	207	35	241
60.642	20	TGACGTTAAGAGAGTTTTCACTGG	59.855	24	179	1004	1182
59.948	20	TTTGGCAAGGGTTTGAAAAG	60.081	20	243	167	409
60.014	20	ATTGGAACGTTTGAAACCGA	60.344	20	251	221	471
59.15	20	GGGGATTTGTCAACTGGAAA	59.767	20	236	58	293
59.763	20	CCTCACACATTCAGCCCTCT	60.261	20	276	144	419
60.042	20	ACCAACGTCCCTCATCTACG	59.989	20	247	191	437
59.485	21	GCAAACGGTATAGGATCGGA	59.923	20	192	247	438
60.11	20	TGGCTCTCACACTCACTCTCA	59.747	21	187	106	292
59.632	20	TTCGGCTTAATGGTCGAATC	60.038	20	208	61	268
60.05	20	TGATCCATTTGCAGAAGTCG	59.799	20	264	415	678
60.133	20	AACACGTGGAGATGACACCA	60.005	20	181	551	731
60.173	20	GCTCCATTTGTAAATCACCCA	59.815	21	222	158	379
60.034	20	TCACACAGATTAAACACTGAAAC	60.128	26	253	567	819
60.051	20	TGGAAATTTCGACACGCTTT	60.617	20	252	566	817
60.218	20	CGCGAAGTACCTGCGTTAT	58.956	19	274	35	308
58.353	22	AACTGCTGGACCTCCACAAC	60.159	20	194	308	501
60.034	20	GGGGGAAAAAGAAAGGTTGA	60.271	20	196	15	210
60.073	20	TGAATCAATCACGTTTCGCA	61.204	20	218	14	231
59.202	20	TTTGGAGATGGTGATGGTGA	59.893	20	276	65	340
59.274	25	TAGTCTTTCTCCCGTGCGTT	59.875	20	274	19	292
60.11	20	CAGCAAGAAAAATACACCAGCA	60.298	22	134	95	228
60.43	20	CCTTGGCCTTCTGACATCAT	60.073	20	190	135	324
60.683	20	TGACACTCACGCACACACAC	60.437	20	265	599	863
59.493	20	TGTAGCGTGGTGAGACAAGG	59.897	20	276	84	359
60.241	20	AGCCCGAGCCTAAGCATATT	60.211	20	265	285	549
60.472	20	CCCCCTTAACTACCACTTATGAAA	59.692	24	213	368	580
59.716	22	AAATCCCGTTCTGGGAAACT	59.805	20	275	1633	1907
59.401	20	GGGATTTGGGACGATTTTCT	60.131	20	147	199	345
59.803	20	TTAGAAACGGAGGTTGGGTG	59.964	20	139	15	153
59.607	21	TGAGCCTATCTTGGAGCACA	59.547	20	190	410	599
59.587	22	TCCCTCTCATCTCTCTCGATTC	59.919	22	118	87	204
58.003	23	TATTGTTCGCGCATCATTGT	60.103	20	126	51	176
59.96	20	GTTTCATCCCTCGCACATTT	59.939	20	260	200	459
59.664	20	ACGTTAAGGAGGGGATCCAT	59.651	20	258	19	276
59.871	20	CGTCCACGGAGAGGTTAGAG	59.861	20	169	264	432
59.84	20	TACGAGCGCATAGCCTTTTT	60.006	20	120	1375	1494
60.066	20	ACCTTAGTTGCGAAGACGGA	59.875	20	164	47	210
59.682	20	GGTTTCTTACTCGGGCTCCT	59.713	20	215	213	427
59.948	20	GAAAAATCAAAGGCCCACAA	59.916	20	246	93	338
60.11	20	GAGTTTATCAGCGGTCTCGC	59.985	20	157	3475	3631
60.088	20	GGCTTTCTTAACTTGTTGGAACC	60.376	23	205	3	207
60.02	20	GTGATCAACATCCGTGATCG	59.925	20	148	638	785
61.266	20	ATTCGGGAGATGTTCCAGTG	59.927	20	170	190	359
59.871	22	ACATTGGGGACAATGTTGGT	59.95	20	139	71	209
60.08	20	ATCCATAATGTCCCCGTTGA	60.014	20	277	269	545
59.966	20	TTTTCCTGGAACGTGAAAATC	59.054	21	279	162	440
59.359	20	TGTACCTAAAAAGTTGTTCCCAC	57.314	23	280	442	721
59.998	20	CCACTCCCACCCATACAAAC	60.088	20	145	3416	3560
59.989	20	CGTCACAGCCTCTTCAACAA	60.025	20	123	644	766
59.845	20	TCCGGTAGGTAGCCATTGTC	59.955	20	265	428	692
60.07	20	TGAGCCCGTAAATCACACAA	60.111	20	183	293	475
59.962	20	TTCTTCCACGTCCTCTAGGTG	59.338	21	160	226	385
60.832	20	TCTCTCACGCACTCTCACAAA	59.76	21	166	66	231
61.136	20	TTCGTCGTTCATTGCAGTTT	59.322	20	123	7	129
60.292	20	AAGGAGGTGTTATGAAGGGATT	58.028	22	180	267	446

60.272	20	CTCGAAAATTGAATGACAAGGA	59.202	22	181	255	435
60.159	20	TTTGTCACATGCATTCCAGC	60.675	20	211	96	306
59.931	20	TTTCTCATTGGCAGTCACCA	60.24	20	171	45	215
60.06	21	TTGATTCCTCCTCACTTGCC	60.195	20	162	14	175
59.758	20	CATGAGCAATTGAGCAGCAT	59.979	20	266	67	332
59.931	20	TTTTCTTCCCCACACACACA	59.976	20	183	287	469
60.081	20	TGGAGCTTTGATCCTTGCTT	59.955	20	151	26	176
59.706	20	GGGGGCATTTTGCACTATTA	59.795	20	260	238	497
59.934	20	TGCCATCTCCTCATCACTTG	59.787	20	189	420	608
59.971	20	AATTCAAGAATGCTGCCCAC	60.081	20	267	247	513
59.078	22	TCACTGGAATGCTATGGTGC	59.679	20	208	2	209
59.648	20	CGGATTTAAGGGTTATTACCTGAT	58.81	24	116	136	251
59.499	21	TTTGCGCATAAATATTGGTTTC	59.039	22	264	0	263
59.571	23	CGAACATAGTGCACCCACAC	60.032	20	235	29	263
60.074	20	TTAGTTATATGTATGGGGATGGTT	57.868	27	122	107	228
59.72	20	TCTTTTTCCTGAACGATGAGC	59.443	21	267	1480	1746
59.807	20	TTCTTTCCTTTGAGCATACGATT	59.302	23	187	11	197
59.903	20	ACACAAACGAACCGGAAGAG	60.149	20	216	379	594
59.95	20	CAGGCAAATAGCTACCGAGG	59.861	20	227	106	332
60.111	20	ATCAATCTTGGGCTCCTCCT	60.037	20	211	2968	3178
60.066	20	GACTCGGAGGTGAAGGTGAG	59.835	20	192	77	268
60.306	20	GGATCTTAATTGGTTCGATTTTG	58.914	23	169	650	818
59.653	25	TATTTATGGTGGCTGCGGTT	60.343	20	265	509	773
60.404	20	GCACATTGATATCGTGTCCAA	59.415	21	253	193	445
59.904	20	CCTATGGTTGTATGGTTTGGAG	58.377	22	171	38	208
57.272	25	CCATCCATTTGCAACCATAA	59.232	20	225	34	258
59.96	20	AACTGGACCGAAAAATGCAC	59.978	20	118	554	671
59.934	20	TTGTTCAAAATTCGTCCAAAA	58.175	21	277	140	416
59.055	21	CGGGGCGTGACATTAGTTAT	59.845	20	147	39	185
60.056	20	AAGAGGTTATCCCTCGTCCA	58.594	20	278	425	702
60.119	20	ATTGTCAGCCCACTTTGACC	59.973	20	259	429	687
59.274	22	CCGCCTGCATTGTTTCTAAT	60.096	20	138	5	142
60.088	20	CATTCGAACATCATCATCCG	59.883	20	275	338	612
59.449	20	TTCCTTGGACCAAAATAGCC	59.019	20	183	42	224
60.05	20	ATTGATCGCATTCAGGGAAA	60.414	20	260	380	639
60.232	20	AAACAATTTTCTGGCCATGC	59.945	20	249	146	394
59.903	20	ACCATCCCACCAGCATTTAG	59.813	20	127	154	280
60.164	20	GGCCATCAGGGATTCAAGTA	59.894	20	120	166	285
60.133	20	CGCTGATGTGATCTCAATGG	60.225	20	252	88	339
59.049	20	ACTGGTGAAGATGCCTGGAG	60.261	20	264	602	865
58.881	23	GGGTCAATCGGCAAAAATAA	59.773	20	218	492	709
60.067	20	TAAATTGCTCCGTCTCCAGC	60.352	20	161	83	243
59.966	20	ATGGTGTTCTTCCATCAGGC	59.934	20	216	1	216
60.342	21	GGGTTGCCAGGTTGAATAAA	59.801	20	210	262	471
59.813	20	TGTAAGCAGGTATCATCATAAGC	58.854	24	126	94	219
60.689	20	TTTCTCCCAACGTAGCCAAC	60.11	20	253	10	262
59.803	20	TTACACTCCCACTCCCGTTC	59.966	20	275	279	553
59.903	20	GTGTAAAGCATGGGGAAGGA	59.933	20	250	298	547
59.541	20	GAAACATTTCCACTGAATCAACT	59.913	24	138	149	286
60.51	20	ATGTTGGTCCAAGTCCAAGC	59.973	20	184	280	463
60.523	20	CCATTTTGTGCCCTTGATTT	59.801	20	190	91	280
60.359	21	GAGATGCGAGCTGATGTTGA	60.104	20	212	55	266
60.134	20	TTCCGAACTTCATCCTTTGC	60.192	20	249	581	829
59.13	23	TGACTCACTATGGGCACAGC	59.862	20	108	375	482
59.682	20	TGTATGGTGCTTGGTGGTTG	60.427	20	188	35	222
60.111	20	CGGTTTGTTTTCGTGTTTGA	59.603	20	216	451	666
59.194	23	TGCCTACGCATCAAGACAAC	59.871	20	204	1	204
59.834	20	CGAGGAGAGGAGAGACATCG	60.088	20	241	42	282

59.154	20	AACCGGAAAAGTGGAAGAAAA	59.967	21	192	348	539
59.973	20	AGGTGGGCTTAGTTGAGGTG	59.208	20	213	19	231
59.745	20	TCAATCAAACCAACGAAACAA	59.048	21	212	645	856
60.198	20	TCAATGTAAATGCCAATCTCTTTC	59.525	24	197	298	494
59.937	20	TTCTCAGCATATGGGAAGGG	60.029	20	239	759	997
59.499	20	TTCTGAGGATGGAAATCAACA	58.131	21	277	2117	2393
59.955	20	TGGCAGTAGATTCATTCTATCTTTT	58.871	26	250	7	256
59.971	20	AGTCACCACCACTTTCCTGG	60.002	20	274	56	329
60.096	20	AATCTCTGCCACCTTTCCCT	60.074	20	164	650	813
57.101	25	CACAACTCCACCTGACATAATCA	59.906	23	172	547	718
60.578	20	GATTATGGCATACGTGTGGG	58.723	20	151	389	539
58.71	25	CCATTATGTCGATATCCATCCA	59.507	22	233	105	337
59.756	20	CCTATGGTTGTATGGTGTGGAG	59.238	22	113	98	210
59.904	20	ATTCTGAACCAACTGGCACC	59.973	20	274	1695	1968
60.032	22	GAAAAGCAAGGAAAAAGCCA	59.451	20	260	2819	3078
60.177	21	AAGACAACAGGCCAACTTGC	60.299	20	252	5328	5579
60.263	20	ATTTGTGTGGCCATTTGGTT	60.096	20	183	96	278
60.037	20	AAGCAAATTCCAAGATGACGA	59.699	21	274	4639	4912
60.249	20	CAACCCTACCTCCTTCTCCC	59.928	20	117	953	1069
60.844	20	ACGTGGCCTTTGATGGTAAA	60.365	20	279	69	347
58.925	20	AACACTATCACAAGGTTCCGAGA	60.047	23	236	70	305
59.834	20	TTTACTTTTGAGGTGGCGCT	59.883	20	140	4182	4321
60.125	20	CCTTCTTGGGATGTAGGGGT	60.183	20	171	446	616
59.494	22	ATGTTGTGAAGCACATGGGA	59.967	20	220	1008	1227
58.891	20	CAAATCCCTCTTTTCTTATTCTCAA	59.236	25	250	174	423
59.975	20	CCACGGATTACTCTGGGAAA	59.926	20	277	599	875
59.989	20	TGCATTTATCAGCTTTATCAGCA	59.895	23	223	549	771
60.538	20	GCCAAATTAAAGACCATATTTTCA	59.68	25	215	2643	2857
59.41	20	TGCATCCATGATATGGCG	59.988	18	216	384	599
60.073	20	TGTAAACCGACCTCCCACTC	59.966	20	167	1832	1998
59.691	19	ATAGGCTCCCCCGATCATAA	60.623	20	231	1306	1536
59.45	20	GGGAGAAAAGGGGAAATAAGTG	60.173	22	220	50	269
60.02	20	GATGAACTCTCTTGGGTGGG	59.505	20	113	262	374
59.853	20	CTCTCATTCCGGTGTGGATT	59.927	20	246	107	352
59.397	27	TTCTCATTTCCCAAATGTCG	58.546	20	277	488	764
60.17	26	AAGGGTGTTTTCTCTGCATCA	59.726	21	251	31	281
60.502	20	ACGAGAGAGCGAGTTGGGTA	60.012	20	179	321	499
57.922	21	TCTTCGCATGCTTATTTGGA	59.401	20	196	41	236
59.867	20	ATAAAAAATGGCAGACGGCAG	60.096	20	254	528	781
60.004	21	ACCGGGATAAAATAGGGCAA	60.508	20	235	1630	1864
60.359	21	ATTATCATATTTAAGGGTTATCACC	57.31	27	135	330	464
57.94	23	TTTCACTCTTCACGTTTGCAC	58.963	21	182	10	191
60.059	20	AAAACCCTAAACAACCAGTGAA	57.717	22	252	49	300
59.856	20	TCAAAAATTGCGTCATTGCAT	60.081	20	200	247	446
60.193	25	AACAATACAATCCCGTGCAA	58.895	20	246	3	248
58.114	23	TTGCAAAAGTCACACTCTGTCA	59.534	22	248	52	299
59.73	20	TCTCCTACAACAACCCTCGG	60.103	20	233	192	424
59.821	20	TAGTTTTGCATGCATTTGGG	59.562	20	148	8	155
60.935	20	TAAAGGATCACGTTGGGAGC	60.074	20	265	168	432
58.82	20	CCGTTTATTTTTCACACGTTCA	59.904	22	177	1118	1294
57.051	25	GCAACGGATCTGATTTGGTT	59.939	20	241	31	271
60.169	20	GAATCGCAGAACCGATGATT	60.043	20	270	1247	1516
60.348	20	TCCTTATTGTTGGGTGTGGG	60.605	20	150	987	1136
59.709	21	GATCTAAGGGCCGAGATTTG	58.74	20	101	171	271
59.938	20	ATTCGAATTCCTAAGCGCAA	59.816	20	109	251	359
60.088	20	GTGGTACTTGCACGCACATT	59.646	20	261	62	322
60.374	20	TAGTCATGCGGGCTACATCA	60.243	20	220	312	531
60.21	20	TGAGGTGAAGTGTGGAGTGTG	59.766	21	180	28	207

60.237	20	GAGCCACAGCTACAGGCAAG	61.136	20	267	29	295
59.691	20	TCTCGGTGAGCGAGTAGGTT	60.012	20	117	5	121
60.223	20	TCCATTTATCGGAGTTACGGTT	59.737	22	207	249	455
59.009	23	CCTCACGCACTCCACTAACA	59.897	20	233	8	240
59.824	21	AATTGATGGAACGGGGATTT	60.378	20	263	83	345
59.875	20	TTGTCACATTTTTGGTGTTTCA	58.964	22	249	1609	1857
59.923	20	GGGATTCTTGATGAATGGGA	59.685	20	133	40	172
59.966	20	CAACGCACGGGTAAAAGACT	60.168	20	144	1422	1565
59.806	27	AGGCCTATAAATGCGTTTGG	59.101	20	228	34	261
59.91	20	ACAGACATCGGGAGAAGGTG	60.112	20	198	2602	2799
60.111	20	CATGCAAGCAGCACTTCAAT	60.019	20	278	109	386
58.616	23	AGGTAGCTGGGAGGAGGAGA	60.349	20	186	16	201
60.21	20	ATTGGCCGTGAATTTTTCTG	59.938	20	261	137	397
59.364	20	TCATGAAATTGTTGGGGGTT	60.029	20	192	195	386
59.873	20	TCTTCACCTATTATTTCAACAAGA	57.674	26	156	38	193
60.473	20	TCTTCGAGTACGCTCTGGGT	60.012	20	178	48	225
59.83	20	GTGCGTGACGGTTGGTATAA	59.469	20	280	64	343
59.959	23	GTTTTTCTCCCCAGTGACCA	59.943	20	234	15	248
59.79	20	ATAAAAATGGCACCTGGCTG	59.96	20	238	19	256
61.021	20	ATTTAGGGCAAGAGCCCATT	59.93	20	186	343	528
59.308	20	CCGATGTTTTCGAGGATGAG	60.594	20	266	204	469
59.78	20	TCGGCTACTTTGAAGGGAAA	59.817	20	237	228	464
60.319	20	TCTCGTGTTTGACCGTAATCAT	59.499	22	144	1015	1158
59.823	20	CAGAAATGCCACAGCAGAAA	59.988	20	186	861	1046
59.458	22	GAGTTGGAGTTCGGGATCG	60.606	19	278	2987	3264
59.019	20	GCTTTCACGGGAGAAAGTTG	59.853	20	252	2642	2893
60.758	20	TGTGTGGATCAATAACTGTCAGAA	59.54	24	209	37	245
59.89	20	TTAAGGTTGGCTTGGGTTTG	59.968	20	185	2254	2438
59.249	25	TGTAGTGGCTTCAGCTCGTG	60.199	20	194	41	234
60.021	22	TTTAAGAGATAGTACCGGATCGC	58.853	23	215	42	256
59.232	20	GAGGTCGGGTTCGTGTAGAG	59.721	20	128	16	143
59.966	20	CCACTCTTTTGGGGCAATAC	59.429	20	232	31	262
60.11	22	CCACGCATGTTTCTGTCATC	60.12	20	128	920	1047
59.476	20	GGAAACCACTCACCGTGTCT	60.009	20	228	383	610
60.103	20	CGATAAAATGGCACACATCG	59.953	20	248	1046	1293
60.011	20	AGCTTTTCACGCATTTCCAC	60.257	20	101	25	125
60.331	20	TGCACTGCATAACAAGCGTA	59.086	20	216	50	265
59.633	20	CGTATGAGCTCTGAGAGTGAGTG	59.315	23	233	1002	1234
59.989	20	CGTGTGTGAGTCCCCATGTA	60.44	20	166	231	396
60.074	20	TCCAACATCCAACCTCCATT	60.173	20	220	624	843
59.533	20	TGGTGGGGCTTAATTAGGTG	59.817	20	277	1318	1594
60	20	CACATTGGTAGAAGGCCGAT	59.955	20	202	434	635
59.007	23	GCAGGATAAGGGGTGTTGTT	58.912	20	116	2	117
59.971	20	CTGAACCGAACCGAAATTGT	59.971	20	205	724	928
59.795	20	TCTTTGAGGTAGGGCTGGAA	59.807	20	248	466	713
60	20	GGAGCTCCCTAAAGCATTCC	60.173	20	241	448	688
60.46	20	GCCATGACCAACTTTCTTTTC	58.684	21	106	26	131
59.986	20	TCTTTGGGAAGGAGGTTGTG	60.081	20	137	928	1064
59.331	20	TGCTTCTTGAAAACTTTCTTCATTT	59.84	25	213	866	1078
59.637	22	GGTGACATGGCTGGATTTCT	59.934	20	146	294	439
60.05	23	AATTGCTTCAATGTCACCCC	59.797	20	272	117	388
60.009	20	TGGAATGTACTGCTGATGTGG	59.581	21	201	0	200
59.973	20	TGGAAAAGAATTCGTCCTCG	60.184	20	223	77	299
60.309	20	TGCATACACGAGTGGAAAGAG	58.937	21	215	449	663
59.996	20	ATGACGAGAAAATGGTTCGG	59.933	20	136	425	560
57.866	21	CCTTGTAGCCCCTTTGAGC	59.822	19	280	111	390
60.049	20	CTTGTTTAGGGAGAGCACGC	60.015	20	250	1868	2117
57.436	27	GCAAGTCGCTCTTCTCGTCT	59.898	20	196	18	213

60.152	20	CTTTCTCTCTCCCGCGTATG	59.971	20	278	203	480
59.734	20	CCGAATTTCTTTGCACAGGT	60.11	20	275	11	285
59.816	20	TGAAATGAAGAAAAAGAAATTGG	57.512	23	150	96	245
60.145	20	TGGAGAAGGGACAAATGGAG	60.042	20	182	191	372
60.326	20	ACCAATATCCAACGGCAAGA	60.331	20	183	1278	1460
60.096	20	TTTCAAAATTCCCCACAAGC	59.916	20	219	2716	2934
60.736	20	TGAAGGTTGGAGGAATGGAG	60.042	20	276	146	421
58.275	22	CAGCTTGAAGGGGAGTCTTG	59.982	20	250	0	249
60.282	22	ATGTAGTGTGTCACGGGCAA	60.032	20	258	590	847
59.901	20	TATGGGTTATCACCGGATCG	60.544	20	259	641	899
59.939	20	TGAAGTTAGGAAATAAGGAGGTG	58.743	25	169	352	520
59.955	20	AATTGTATTCTCCCGAGCCC	60.286	20	177	636	812
59.924	20	TTGTAGCCGTTATAGTGTGGGA	59.536	22	265	12	276
59.88	20	CCTGTTCAGCTATCTTTTGCG	60.025	21	278	55	332
60.382	20	ATGGGTTAGCGTGTTATCGC	59.988	20	120	177	296
58.892	20	ACACTACCCTCCTCGTCCCT	59.991	20	211	72	282
58.097	22	CAGGTAATGCTAGCCGGAAA	60.223	20	197	380	576
59.792	20	AATCTTGCGAACCAAACACC	59.978	20	118	20	137
59.899	21	TGCGAACAACAAGAAACAGG	59.881	20	207	2457	2663
60.074	20	GGAAATAAGGAGGTGTTATGATA	57.235	25	225	94	318
59.951	20	TGGGTTATTTTGGCCCATTA	60.012	20	262	17	278
59.934	20	CTGCAAAATTGGCTGAGTTG	59.464	20	101	709	809
60.34	20	ACGTGTTGGATGGAATGCTA	59.002	20	153	79	231
60.011	20	AGCTCTCGTCAGCAGTTGGT	60.205	20	218	770	987
58.293	22	AGATGAATGAAGTACGGCGA	58.326	20	162	0	161
60.307	20	GGTTATCCTGTGGAGCGTGT	59.997	20	226	429	654
59.763	20	TTGTTTTCTATTCTTTATAATTGCC	57.667	26	275	6	280
60.713	20	TTGCAGTTGCAGTTGGTGAT	60.31	20	185	821	1005
60.175	20	AAGGGCACCGCTAATGTAGA	59.73	20	145	80	224
59.787	20	GCTTTGTCGGTTTCTCCATC	59.676	20	186	52	237
58.116	24	CCAAGTTACTCCCAGCGAGA	60.388	20	116	1	116
59.967	20	GCAAGAAATGGCTCCCTACA	60.214	20	260	794	1053
59.626	22	TGAAGGCCCAACCTTAAGAA	59.679	20	224	4	227
59.638	20	TGAAGTCACAGCGAGGTTTG	60.025	20	110	2	111
59.586	25	TGACGGTCAAGATTTGCTCA	60.39	20	130	1	130
59.836	20	TCCATCCTTCTTTGCTGCTT	59.955	20	179	631	809
59.697	20	TTAACCTCCCGTGGACGTAG	59.986	20	181	372	552
60.467	20	TTTTTGGCAATTTGTGACGA	60.088	20	202	39	240
59.157	20	TCCAATGGATGTGAATGGTT	58.617	20	274	67	340
58.527	21	CCTGCTTTTGTGCATAGGTT	57.906	20	175	253	427
59.672	25	AAATGATAGGGCACACAGCC	59.962	20	182	83	264
60.111	20	AAGTCGCGCAAACTTGAGAT	60.022	20	178	3813	3990
60.173	20	AAACCTGGCTGGACTGATGT	59.579	20	213	1763	1975
60.169	20	AAGTGAAACTGCTGTATGCTGAG	58.737	23	248	472	719
60.011	20	ATTTGGGGATGAATCTGACG	59.75	20	212	11	222
59.152	20	CTCGGTTGAGCTCGGATAAG	59.971	20	183	71	253
59.982	20	TAGCCTGGTCGTTTTGGAAG	60.241	20	266	1002	1267
58.268	24	TCAACGGTTTTGATTTGTTCC	59.831	21	182	73	254
60.126	20	GTGCATGGTAGGGCAAACTT	60	20	270	1540	1809
60.059	19	TGCGTTTTGACAATATATAGGTGT	60.083	26	103	292	394
59.763	20	ATGGCTGGGCTCTGAAATTA	59.668	20	241	351	591
59.931	20	GCGAATTCAAACCCCTTGTA	59.938	20	227	8	234
60.177	20	TAACACCACCACCCACACAC	60.178	20	115	1762	1876
59.948	26	TTACAAATGGCCAAGAGAGTTT	57.94	22	102	8	109
60.066	20	TTTTTGACAGCGAAAGTCCC	60.227	20	242	4197	4438
59.959	20	TTTCCCCTTTGCTCTCTATTTC	58.887	22	272	138	409
60.035	21	CCGAAGATCCGAGATCAGAA	60.295	20	209	35	243
60.119	20	CCAACTGAAGAACACGAGTTTG	59.813	22	269	1208	1476

59.542	20	GGCAATCCATTCCGTACAAG	60.331	20	249	21	269
59.157	20	GATCGACGCCTCAGATTTGT	60.226	20	169	948	1116
59.95	20	CCTCTAGCATCTCTTGCTCTCA	58.983	22	270	255	524
59.01	21	AGCAAGATTGATCCTCCTCG	59.386	20	277	21	297
59.759	20	ACAGGGTACTCAGTGGACGC	60.182	20	209	17	225
59.411	22	ATTTCCACGAAGCATCATCA	59.079	20	269	239	507
60.236	20	TTTCCAACTATCCAAACGGC	59.938	20	250	634	883
57.771	26	CACACTATTAGGGTTTGGGAGG	59.757	22	116	4	119
60.294	20	CCCCGAAAAACCCTCTATCT	59.415	20	254	2290	2543
59.6	21	CGAGCTCGGACCTTCAGTAT	59.454	20	112	21	132
59.811	21	AGGGCAAAAATAACCAACCC	60.055	20	272	83	354
60.083	26	GACCAAAAAGAGACGACCGA	60.232	20	121	1	121
60.006	20	ATCACATGGTGATGCCTTCT	57.939	20	215	28	242
59.928	20	TGGTGGCTTCATTTCCTGTT	60.495	20	210	549	758
59.478	21	TCTCGTGTACAAAAGCCGTG	59.904	20	109	0	108
60.104	21	TAAAACCATGCACGTAGGCA	60.133	20	268	0	267
57.425	21	GGGGTCTTGGCGTACTAACA	59.993	20	106	17	122
59.621	20	AAGGGATGTTTGCACCTGAA	60.495	20	161	50	210
60.199	20	TGAAGTTAGGAAATAAGGAGGTG	58.743	25	156	953	1108
59.476	20	GAGTTTTCATCTTACCTTGAGGG	58.333	23	210	46	255
58.388	25	TTGTGGGGTTGTGGTGAATA	59.667	20	187	35	221
59.034	20	TGGCCGGAGTTTTAGGTATG	59.953	20	266	43	308
60.118	21	GTTTTTAAAGAGCTGGGGGC	60.075	20	186	981	1166
59.617	23	GCAAAACAGCCAGAGGATTC	59.82	20	203	0	202
60.012	20	TAATTGAATTCCTGGGTCCG	59.756	20	265	899	1163
59.395	21	TGGCTATTTTGGTTTCTACAACA	58.731	23	236	64	299
58.976	21	TATCAGGCTTGATGATGGCA	60.182	20	266	228	493
60.377	22	CGCAGCAGGTCAAGATTACA	60.011	20	267	535	801
58.4	21	TTGAAGCATCGTTTGTGTTTTC	60.152	22	272	6	277
59.608	22	TGGTTTATATTTCGTTGATTTGC	58.141	23	258	31	288
59.229	24	GGGTGTTCATGGTTCGATTC	60.181	20	274	31	304
59.763	20	TCGAGTCCAATGTTGAAAGAAA	59.724	22	279	439	717
59.962	20	TCGATGAAGGTGACGAAGTG	59.831	20	232	22	253
59.667	23	TCCTTTTTGTCATTCACCTTTG	59.108	22	232	488	719
59.532	20	TCTTGGACTGCGTTAGGGAC	60.255	20	199	188	386
59.368	20	AATGGACCGGTGAAAACAAG	59.83	20	264	565	828
59.822	19	ATTTGGAGGAGGATGGGTTT	59.629	20	187	2432	2618
60.033	20	CTTCCTTGGGCACAACATTT	59.971	20	232	716	947
60.192	20	ACGTGAAAAACGGGAATGAA	60.344	20	189	113	301
60.299	20	TCACACAATTTCACTCTTCACTCT	58.044	24	169	97	265
59.786	20	TGGACTTCGTCACAACCAAA	60.128	20	124	269	392
60.073	20	CCATGAGCCCCAGTAAAGAA	60.066	20	257	3075	3331
61.296	20	CCCCCTCGTGTTTCTTGTAA	59.964	20	197	23	219
60.032	20	AAAAACCGCCACATCAGAAG	60.11	20	268	1879	2146
58.624	27	ATTTGACCATGGTTTTGGGA	60.029	20	223	18	240
59.821	21	TCAAACACGAGTAGAAAGGATTT	57.147	23	161	66	226
59.956	21	TCTCCTTCACCCATTTGGAG	60.042	20	126	815	940
57.426	20	AAATTTGGGCCCTTAGATCG	60.272	20	191	56	246
59.951	20	TGAAGTTAGGAAATAAGGAGGTG	58.743	25	188	136	323
60.096	20	TCTGATTCTGGGATTTTGGC	60.014	20	266	573	838
58.677	20	GAACTCTCATGCCCTGGAAA	60.195	20	160	113	272
60.08	20	CATTATTTAAAGCACGCGCA	59.872	20	216	452	667
58.028	22	CAAAAATGGATGCAAATACGG	60.192	21	106	14	119
59.813	20	GCTGGAACGTGCCATTTACT	60.14	20	140	19	158
60.088	20	TGCTCTTCACCTTTGTGTGC	60.032	20	132	529	660
59.485	21	TTAATCGTCCATTTCGTCGG	60.827	20	270	241	510
60.831	21	AGGGCCTCTTTTTGTCTGAA	58.909	20	206	10	215
59.976	20	GTAGCTGCACATTGTCCGTC	59.323	20	270	75	344

60.111	20	GATCACCATCACCATCCTCA	59.269	20	153	1389	1541
60.537	21	CCCTTCAATGGTGTTTCCTG	60.345	20	209	357	565
59.555	20	TAGGGGTCAGTGTGGGTTGT	60.275	20	173	299	471
60.096	20	CAATGTACCCCGATGTGAGA	59.369	20	278	764	1041
59.239	20	TGAACACGTTGCCAAAACAT	60.011	20	120	76	195
60.039	20	TTAAAAACTCGACCCGATGC	60.074	20	146	143	288
58.815	22	TCAAATCAGGAAAACCCCTT	58.477	20	201	55	255
58.687	21	TGTTTTTGGAGGGAAAATGG	59.772	20	122	38	159
60.495	20	GGAAGGGCTCAACAACACAA	61.075	20	224	0	223
59.799	20	CATGTTTTGTTTGGCTGTGG	60.004	20	277	194	470
59.72	20	TCGGTTAGAAAATGGACCGT	59.429	20	280	11	290
59.24	21	GGGGTGGGAATGATGTGATA	60.404	20	214	69	282
60.088	20	TTTGATTTGTGTTGGCAAGG	59.561	20	107	360	466
60.203	23	ACCACGAGATGGAGACCAAC	59.969	20	219	410	628
60.11	20	GCTGAATCTTAACCGTTCGC	59.851	20	221	80	300
59.587	22	TTGATACAGATGGTACGCCG	59.566	20	275	47	321
59.964	20	TCAACAGAGAATGCAAGCAAA	59.6	21	217	89	305
60.046	20	ACGGATATGCCCTTGTATGC	59.813	20	227	43	269
60.206	20	AGATGGCGGTAAACATGGAG	59.955	20	232	116	347
57.615	23	CCCTAATTGAGTAGAAAACCACA	57.399	23	263	1341	1603
59.072	22	TGCTGACTTGATTTTCGAGC	59.152	20	187	0	186
58.703	20	TGATACGACCTTGGGGGTTA	60.184	20	224	2	225
60.144	20	CACCCAAAAAGGTTATTATTTGA	57.25	23	279	308	586
60.235	20	GACCGAGTTGGTGGAGTAGG	59.574	20	233	2591	2823
57.804	20	GGTCTTTCTTTTTCCACGCA	60.227	20	185	485	669
60.127	20	TTGGTTATCGCTTGAACGAG	58.917	20	247	6	252
59.154	22	GCGTTTTGACAGGATTTGCT	60.257	20	103	4	106
59.2	20	TCTCAAAAGTCTCATTTTCACAGG	59.799	24	257	2269	2525
60.309	20	ACACCTTGTCTCCCAAATGC	59.973	20	218	2314	2531
59.962	20	CTCGATCTCCATCACCACCT	60.072	20	235	1654	1888
59.969	20	CCCTCGGATGCTATGCTAAA	60.188	20	182	2434	2615
58.787	25	CTTACAAAATCCGCCGTGTT	59.996	20	257	14	270
60.082	20	GACCGAAGCCACCATATCAC	60.348	20	145	316	460
58.121	22	TCTCTCCAACTCATTTCGCA	59.522	20	188	165	352
60.088	20	CCCCTTAAGTGTGAACGCAT	59.993	20	253	499	751
59.341	21	GCTGGAATACAACTACCCCAA	58.962	21	272	1439	1710
60.263	20	CAAATTTGAGAGGCTTTCGAC	58.962	21	191	2077	2267
58.188	20	TTAAGTTTGGGGGTGCAGAG	60.103	20	104	212	315
59.438	21	TCAAACTTACCGTCTTTGTCCA	59.649	22	239	13	251
59.882	20	CGAGTAGAGAAGGGGTGGGT	60.502	20	181	3	183
61.031	20	TGGCGGACACTCATGTTTTA	60.111	20	116	18	133
59.823	20	TTTGTCACCCTCTCCCAGTT	59.549	20	264	711	974
60.111	20	TTTTCTGACAAGGGTGGGAC	59.943	20	274	1156	1429
59.853	20	CTCGTGCTTGTCTTCCACAA	60.025	20	216	1135	1350
58.447	26	AATTCGAACCTGGGACCTCT	59.935	20	137	622	758
59.992	20	TCCACAGACAGATGGAGCAG	59.98	20	248	335	582
60.154	20	GCAATGGAGTGGAGGAGAAG	59.803	20	140	156	295
59.676	20	CACACAGAAGTTGTGGGAGG	59.148	20	161	13	173
60.199	20	TCCTTTGAGGATGGATTGATG	59.879	21	204	91	294
60.192	20	AATTGGTTTGCTTGGTTTGC	59.982	20	271	101	371
59.805	20	TTTTTCCGAGCAAATGAAAA	58.394	20	239	1103	1341
59.184	21	ACCACCTAGCAATGGTTTCC	58.912	20	264	5	268
59.493	20	AATCCGTATTTTTGTCCCCC	59.888	20	176	690	865
60.142	20	TCGAAGTTTGGTGTTGGTGA	60.128	20	199	78	276
59.813	20	GCAATGTGCTTCCATCTTGA	59.805	20	187	954	1140
60.038	21	ACCTTGACGAGGTGGTTGAC	60.009	20	258	24	281
60.192	20	TCTCTCTTGGTTGGTGAAGAAA	58.955	22	195	153	347
60.003	20	CCATAAGAAAGTGAGCCCCA	60.066	20	260	554	813

60.614	20	CGTTAGGTCCGTCTCGATTT	59.195	20	126	44	169
58.278	20	ACCATGAAGCACATCACAGG	59.551	20	236	1825	2060
59.979	20	TGACAAGCAGGTAGACCACG	59.897	20	214	18	231
59.049	20	TTCCGTCTACCCCTTTTCCT	59.934	20	176	839	1014
57.628	22	TCACCTCCTCTATCGGAACG	60.21	20	219	0	218
60.177	20	AAAAATAGAGTTATCACAGGATC	58.199	26	134	217	350
60.224	20	CACCCCGGGCTAGATATTTT	60.164	20	261	4162	4422
60.298	20	ACCCCTTAGGGCAAGGTAGA	59.955	20	268	28	295
59.997	20	TATGGGTTATCACCGGATCG	60.544	20	246	768	1013
60.362	20	CTAATGCCCTCCAAAACCAA	59.931	20	243	361	603
59.972	20	CGCTGTAGATCTAACGGCTGA	60.549	21	259	321	579
59.866	20	CCTTCCATGGCTTTGAAAAA	60.046	20	222	585	806
60.448	20	GAGGCAAATTATTCGGATTTTC	58.99	22	230	1196	1425
59.972	20	CCCCATCAACCTCCATACTG	60.187	20	241	1211	1451
60.422	24	CCTAGCCAGGAACATACCCA	59.948	20	146	41	186
57.858	27	GATGATGATGATGCAGGTGG	59.882	20	271	3	273
60.063	20	CAGCTGCTTTGTTTCCATCA	59.988	20	240	149	388
60.255	20	TCAGGTCCACGTATTTTCCC	59.79	20	117	441	557
57.73	23	GCTTCTTTGCCGATGAAGAG	60.096	20	269	18	286
60.096	20	GGGTTATTACCTGATTACCTCCC	59.052	23	154	338	491
58.78	20	CTTCTAACGAAGCCCAAACG	59.876	20	267	82	348
59.73	20	GCTTCCACTGCCTACTTTGC	60.022	20	245	176	420
59.967	20	AATTTGGCAGCTTCTTGTGC	60.395	20	112	77	188
60.665	20	CCAGATGCAGCATGAGAGAA	60.096	20	209	693	901
58.982	20	TCCACCGTGGTTAGTTGACA	60.001	20	238	109	346
59.42	20	CTCAGCTCAGGGTGGAGAAA	60.523	20	230	167	396
58.486	22	CATCTGAGGAAGGCACATGA	59.787	20	153	59	211
59.264	20	ATAGTTGGTGTGAGACGGGC	59.997	20	200	159	358
59.155	20	CACAATATTTGAGGGTTATCATTT	58.787	25	195	466	660
59.886	20	TGTGCGTAGAACAGAGAGCG	60.347	20	268	9	276
59.92	20	TAGAGGACATCGCGGAGAGT	59.973	20	172	44	215
59.84	20	GGTAGGATTTCAACGGCGTA	59.96	20	219	1168	1386
59.853	20	TGAAAAGAAAAGAGGCACTCG	59.618	21	212	63	274
60.277	20	GGTGAAGACGGCTTGTTGAT	60.119	20	161	742	902
59.81	20	ATTTCGAAGATCAACGGACG	60.074	20	137	97	233
60.235	20	TTCAAAGGCCGAGATTTGTT	59.685	20	262	23	284
59.415	20	CAACAACCTAATCATCCAACCA	59.724	22	224	230	453
58.97	23	CCACCAACTTGTCCACTCCT	60.002	20	248	1982	2229
59.946	21	GGCTTCACATTTCCCATCAC	60.326	20	228	52	279
59.109	26	TTTTTGCGAGGGAGAATGTC	60.192	20	125	0	124
58.896	24	CGGACGATATCGGTTATTGG	60.167	20	123	0	122
59.946	20	ACTCCTGGTGAATGGCAAAG	60.111	20	199	22	220
59.545	20	TTCGGATCTTCACATGGTCA	60.048	20	236	488	723
59.997	20	TATGGTGGTATGGTGTGGGG	61.296	20	221	179	399
59.803	20	CTGGTGTCACAACGGATGTC	60.005	20	194	40	233
59.875	20	TGCAAGAGCAGCAGGATATG	60.119	20	216	275	490
60.029	20	CCGCCTACTCTCCCTCTTTT	59.842	20	240	37	276
59.107	24	GCGAGCATCATACACGAGAA	59.979	20	254	2436	2689
60.05	20	TTCTCAGTGCATCCATTTCG	59.799	20	205	750	954
58.279	21	GGAGTTTGCTGTTGAGACCC	59.703	20	229	332	560
60.173	20	AGTCGCTGCAATTTCCAGTT	59.882	20	112	3	114
59.222	20	AGCCTAAACACACACACCTCA	58.285	21	103	105	207
59.85	22	GCAAGGGGCAAGTGTTATTT	59.091	20	223	513	735
60.34	20	ATCACATGCCATTCAGTCCA	59.925	20	234	1794	2027
60.431	20	AGCCGTTGTGGGATATCTTG	59.955	20	125	1117	1241
60.559	20	GGCTAATATAATTTATCTCCATGC	58.976	26	215	235	449
59.967	20	TGGCACTACTGTGAATTGGG	59.566	20	257	5728	5984
60.016	20	TTGAGAAGTCAGAAGCGGGT	59.989	20	109	778	886

60.111	20	GAAAGCCTACTTGGCGATCTT	59.87	21	142	413	554
60.154	21	GTTCGAAAGCCTACCTCGCT	60.894	20	186	5	190
58.992	20	ATGGGAAGAGGGGGTATGAG	60.147	20	110	2109	2218
59.912	20	GCAATTAAAACCCCCTCGAT	60.15	20	248	285	532
60.156	20	TCTCTCTATCTTTTTGGTTGGTGA	59.304	24	232	4	235
59.404	23	CTCAGCATACGGACGCATTA	59.856	20	192	12	203
59.679	19	ACTGTTGGACGGTTATCGCT	59.621	20	151	87	237
59.938	20	ATGCGCGATTTTAAACCCTA	59.586	20	214	31	244
59.566	20	CCGAAAATCTCCGTCAAGAA	60.184	20	192	258	449
60.215	22	GGTTTGGGTTTAATTTGGGC	60.4	20	229	8	236
60.137	21	TCACTTCGAACCTTCTGCAA	59.566	20	185	7	191
59.746	20	AATTCATTCAAGCAGCAGCA	59.572	20	269	98	366
59.823	20	CCAAAATTTATGGTTATCACAGGA	59.191	24	172	79	250
57.388	23	CCCATGTGGGGAGATATGAT	59.44	20	191	801	991
59.839	20	TTTTGTGGAAGATGCAGGTG	59.691	20	173	2903	3075
57.222	23	TCGCATGCCACTAAAAATGA	60.215	20	213	20	232
59.971	20	CTCAACGGTGAAGTCGGATT	60.111	20	194	204	397
59.934	20	AATAGAAAAACCACGCAGGG	59.087	20	179	159	337
60	20	GGCGTCTGGTTTTTGTTTGT	60.015	20	259	15	273
59.716	21	AAAATTTCACATATTTGATCGGAA	58.838	24	192	34	225
60.69	20	ACAATCTGGGGCGTACACAT	60.263	20	229	82	310
60.142	20	CGGGGGTAAGAAAGTCAACA	59.964	20	264	938	1201
60.537	20	GGCTGCCAGAATAAAAAGGA	59.297	20	278	497	774
60.103	20	TGGTGATGCCAGAACAGAAG	59.831	20	231	279	509
60.081	20	ATTTAGGGGCTTTTGAGCGT	60.095	20	268	772	1039
59.586	20	CAACGGTTTTGGTTTGTTCC	60.241	20	152	76	227
60.126	20	GTTTGGCTGGTGCAGAGATT	60.263	20	220	370	589
60.119	20	GACTCACGGTTTTTCGGAAG	59.711	20	262	475	736
59.701	20	TGTTCGGAAGATTGAACGTG	59.691	20	212	94	305
60.275	21	TCGGACCAAATTACCCTTCA	60.301	20	254	396	649
60.025	20	TGAACAATTGAACACCGGAA	59.941	20	237	7	243
58.903	20	CGCGACAGAGTGGTATCAGA	60.008	20	253	369	621
59.113	23	GGTGAATCTGTAAAAGGTCATCG	59.885	23	235	337	571
60.247	20	TTGTTTTGGTTGGCAATTCA	59.946	20	264	67	330
60.171	20	TTGTGGAGAACGAACTCGAA	59.415	20	207	262	468
59.637	25	ACATGTGCTGTGAGAGTGGG	59.738	20	263	500	762
60.061	20	AAAAACCGTTCCACATTCAAA	59.348	21	166	1271	1436
60.142	20	TCAAACAGAACACACCTTCCC	59.997	21	105	177	281
59.22	25	CAACCGCATAGGCACAGTAG	59.366	20	121	15	135
60.053	20	GCAAATTTCTTCGAGACCCA	60.192	20	111	174	284
60	20	CAGTTTGACATCAGAGCCGA	59.984	20	150	41	190
60.055	23	TCAATTTGAATGGTTATCACCTG	58.865	23	116	230	345
59.429	22	TTAACGACTTGAACCCATTTTT	57.74	22	279	305	583
58.444	20	CTAGCTCCTTCCCCTTCACC	60.204	20	111	21	131
59.966	20	CCAACATGAAAGGCCATGAT	60.723	20	202	408	609
59.939	20	TGTGATTTCTACCATTTATTCTTTG	59.708	26	243	5	247
60.066	20	AACATGTTCTTGACGCACCA	60.16	20	153	50	202
59.172	21	TTGTTTGCATCCCACACAAC	60.413	20	158	264	421
59.816	20	GAGAATGTGAGACATCATCATCA	59.059	24	152	228	379
59.601	23	TTTCACAGAACACAACGATCA	57.72	21	260	10	269
60.298	20	TGATGATGAAATGACATGGAAA	58.82	22	131	81	211
59.606	21	AATAGGAGAACCAAACCGCA	59.569	20	220	1781	2000
60.408	20	ACCACTCCCCACTGCAATAA	60.375	20	164	297	460
60.111	20	CAACATAAATGGGGCGTAGG	60.202	20	103	1099	1201
60.695	20	GTGTTCTCGTGAGAGTGCGT	59.051	20	204	6	209
59.083	20	TTCCAAACCTTTGTTCCGAG	60.081	20	230	821	1050
58.935	25	GGGCCATTGGTTCTGTATGT	59.676	20	115	4	118
59.964	20	TGATTAATATCAGGGGGCGA	60.247	20	207	10614	10820

59.971	20	CAACGACTCCGATCACTTCA	59.831	20	276	883	1158
61.84	20	GAGACGATCGAACAGCATGA	59.95	20	278	0	277
59.862	20	AGGCCTTGATGTCCCTTCTT	60.074	20	205	110	314
59.873	20	AGAGGAGTGACCTTTCCGGT	60.111	20	248	249	496
58.955	20	GATAGGGGCACACCAAGAGA	60.073	20	257	17	273
59.971	20	TGATACACGAGCGTGGAAAG	59.864	20	126	217	342
59.779	20	ACGACAGTGGACAAGGGAAT	59.43	20	231	88	318
59.162	22	TGGGCTGAAGTATGTGTGGA	60.112	20	273	526	798
59.315	20	TCTGTTTGCCTTTCGAATCC	60.192	20	271	418	688
59.82	20	GCAGACTTTAAGGCAGCCAA	60.523	20	268	5296	5563
59.168	21	CGTGGTTCGATCGTAATTGA	59.542	20	208	373	580
59.996	20	TGCTTCCTTTTGCTGCTACA	59.752	20	275	215	489
60.05	20	GGTTTTCTCGCAATCCACTT	59.174	20	244	2270	2513
59.962	20	TGCAGGTACCTTCGGAACTT	59.734	20	272	49	320
59.624	20	TAGGGGAAAAGGGGAAAGTG	60.284	20	152	242	393
57.694	20	ACGCAGTCTAGAGATATATGTTGA	57.442	26	122	420	541
57.088	20	GGTGCCCACCAAATTTATGA	60.564	20	203	659	861
60.859	20	CTGAGCTCACTCGCCTTTCT	59.891	20	199	1499	1697
59.872	22	TTGTCATTGGGCATCGATTA	59.891	20	241	47	287
59.17	24	TTGTGGGAAGCATTTTCTCC	60.051	20	267	87	353
59.903	20	ATTTAGCCGTTCCTCGGTTT	59.966	20	180	2865	3044
58.78	20	TCCTTCAACCAGTTGTTCCC	59.943	20	179	69	247
59.984	20	AACTGGCTAACCCATCACCA	60.375	20	246	81	326
59.974	20	TTCACAATTAACAAGAACAATTTC	59.077	26	145	591	735
59.883	20	CAAGAGCAACAACACCATTCA	59.749	21	122	724	845
60.049	20	TGCTAACTCAAATTTCGGTGC	60.258	21	207	541	747
60.292	21	GACACGAGATTTACATGGTTCG	59.499	22	109	1	109
59.154	20	GATTCCTCGTGGGATTGAAA	59.871	20	270	48	317
58.961	23	GATTGTAACGTTATTTGGCCG	59.376	21	153	1259	1411
60.154	21	TGAGGGAGAACTGCGGTATT	59.694	20	194	16	209
60.232	20	AACTGAGTCCCCTACCCGAT	59.817	20	205	321	525
59.929	20	TTTGAGGCGAATCGAAATCT	59.784	20	225	1023	1247
58.842	22	TAAAAGGTTCCCCACAGACG	59.964	20	129	74	202
59.942	20	TTGTTAGTTTCCATTCCGCC	59.938	20	100	212	311
59.962	20	ATGCACATGCTACTTCCACG	59.746	20	238	572	809
60.915	20	CGGAAATTTTACCCGGATGT	60.902	20	221	42	262
59.737	24	ATATCTCCCTTTTCGGCCAT	59.761	20	187	13	199
59.955	20	TCAAGTCAAACTTGCCAAACT	57.528	21	252	960	1211
59.823	20	GATCGCATCAGAGAGTCGGT	60.381	20	229	1112	1340
58.409	20	TCTTCCCCAACTACTTTCCAG	58.305	21	280	264	543
59.607	21	ACCCATTGGTGCTCAAACTC	59.973	20	242	450	691
59.133	20	TTGCTTCAGAGGTGAAATCACTA	59.031	23	280	130	409
60.011	20	CCGCCATTCTCCGTTAACTA	60.089	20	269	1105	1373
60.08	20	CCCGGATTTACGAGACAAAA	59.931	20	265	73	337
59.843	25	TCATCAGCCGTCAATCATTT	59.079	20	148	6	153
59.786	20	CCATCTCCACCTCCATACTCA	59.935	21	110	1902	2011
60.134	20	ACGCCCCAAGTTGTTTCTTA	59.609	20	265	147	411
59.917	20	CATTTTGGACGGTCCTGTTC	60.353	20	271	181	451
60.701	20	GCATATACGAAGGGTATTTTGGA	59.289	23	204	477	680
59.959	20	CTGAGTCCCCTAACCGACAA	60.103	20	172	178	349
59.989	20	AATTAATGTGGCATGGGGAA	60.016	20	246	54	299
60.103	20	TCACCCACGTAGAAGCTTGA	59.44	20	277	387	663
60.103	20	GAATCCGACAACGAAAGATGA	60.066	21	210	511	720
59.945	20	AGCAGTAGTGCCCCTGAAGA	60.012	20	275	995	1269
59.935	20	AACACTCTGTGTTGTTGGGAAA	59.538	22	270	72	341
59.864	21	CGGGGCTTCACCTAGTCTAA	59.331	20	251	113	363
57.69	24	TTTTGATTCCCCATTAAAAAGTT	58.076	23	223	257	479
60.096	20	CAAGAATCGCCTGCAAAGAT	60.352	20	251	1152	1402

60.036	20	AAGATTTGATCATGGGCGTT	59.391	20	158	35	192
57.546	20	AGCCGTGCCTTCAACATAAC	60.14	20	216	694	909
59.901	20	GCTCCCTTAAACACGAATGTG	59.623	21	239	106	344
59.934	20	GCCCCTTAAAACTCTCCTTGA	59.712	21	264	382	645
60.055	20	TCGAACTCATGCATTCATTTTT	59.592	22	277	2039	2315
60.067	20	CACCCGAAAACCGAATAAGA	59.931	20	125	160	284
59.966	20	TGCAAGCTCAGCCTAATGAA	59.712	20	163	26	188
60.112	20	CACCCGTGAAGCACAAAATA	59.585	20	252	140	391
60.023	20	ACCGAATTCCTTCCAAGGTT	59.805	20	226	2045	2270
59.75	20	CATGGAACAACATGAGCCAC	59.967	20	256	377	632
60.004	20	GTGATGTGCAACGCTATTGG	60.142	20	158	1163	1320
60.083	26	CCGAAAATCGGAGGATGATA	59.856	20	153	5	157
59.547	20	ACTTTCCCCGTGGACGTAG	59.974	19	259	219	477
59.928	20	ATCGGTTATTACCGGATCGC	61.031	20	109	276	384
60.237	20	CTGGAACTGCAATGCTTCAA	59.988	20	235	414	648
59.903	20	GCTTTCAATCCTCCAGCATC	59.78	20	213	16	228
60.119	20	CATTACACCACCCTTCCCAC	60.088	20	201	332	532
59.162	20	GAGGTTTCCAACTTGCTTCG	59.853	20	213	169	381
59.989	20	TTGTGAGAACCAACTCGGTG	59.72	20	274	232	505
59.091	22	GGTTGTTGCCGCTTCTACTT	59.383	20	264	0	263
60.031	20	GAGATGGTTCGAGAACGAGG	59.803	20	150	438	587
60.397	20	ATTCAATTGCTGGTGGAAGG	59.933	20	265	28	292
59.708	20	TTGGAGATAGAATGAGATAGAAT	58.905	27	168	218	385
59.73	20	CAACCCTACCTCCTTCTCCC	59.928	20	211	163	373
60.214	20	CAAGAGCTCTCATTCTCTCCCT	59.23	22	251	618	868
60.162	20	GCATCAAAATTCAAAAGCGA	58.89	20	269	382	650
59.004	20	ATCCGGCCATGTTGCTATTA	60.31	20	243	1550	1792
59.984	20	AAACCTAGCATTGGGGAAGG	60.312	20	211	88	298
59.573	25	AATTGATGGAACGGGGATTT	60.378	20	157	8	164
59.387	20	GGACAAAACTTCATGGGAGC	59.532	20	277	316	592
59.28	23	TTCATGATTCAAAAGCATCAAAA	59.595	23	136	66	201
57.665	23	TTTTCACATGCCATACACCAA	59.841	21	183	25	207
60.074	20	TCTCACCTTCGGTCAGAACC	60.238	20	263	289	551
59.849	20	GGAAGAGAGAGAAGGGGTGG	60.186	20	270	195	464
59.72	20	AATGGAAGGGACGAGTTTGA	59.526	20	135	292	426
59.938	20	TTAAAAACCGAACTGGACCG	59.968	20	193	2813	3005
59.935	23	CCACTCTCCCTCTCAGTACTTTTC	59.823	24	280	93	372
59.82	20	GGAGATCGAAGGAGCTGATG	59.91	20	221	313	533
59.265	20	TGATTACATCGATCCAACGG	59.35	20	270	54	323
61.146	20	GGGTGGGTCGATTCAATATG	60.014	20	243	9	251
60.058	20	TGGAGCTCTTGTTCCTCACA	59.545	20	133	75	207
60.016	20	GAATACCCCCTACTTTGCCC	59.666	20	233	5	237
59.144	26	AACAACTTTGAACCTGCGCT	59.92	20	226	9	234
60.658	23	TCTGCCTCGTCTGGCTAGTT	60.156	20	241	1	241
59.953	20	CGAAAGCTGGAGCTGAGAAC	60.277	20	123	10	132
59.01	20	AAAACATGCCTTTCGACCAC	59.978	20	246	96	341
59.76	21	ACGGTGTACCTTCCCCTCTT	59.856	20	227	49	275
59.624	20	ATGCATGGCCATAACTCACA	59.955	20	270	166	435
60.045	21	GAGGCAATTAATCAGGGCAA	60.038	20	186	1861	2046
59.861	21	ATATTACCTGCACAAGGCCG	59.982	20	253	86	338
59.666	22	TGCAACCAAGTTCCAAATCA	60.088	20	258	189	446
59.778	22	TCCCAACTGAGATCGGAATC	60.011	20	277	5	281
60.162	20	GTTCGCATACAAACACGCAC	60.188	20	231	106	336
60.242	21	GGCCCACGTACATGACTACC	60.263	20	231	2263	2493
59.726	21	AAGATGGGCGAATAAGACCC	60.286	20	122	77	198
59.917	20	TGTTGGGGTTGTTGTAGGGT	60.126	20	202	1792	1993
60.102	23	ACAAAATTGTGCCCAAGGAG	59.971	20	194	13	206
59.955	20	CTGATTCGCACAAATGATCG	60.22	20	231	36	266

59.694	20	TGCAATGCATGGAGGAATTA	60.035	20	179	84	262
59.997	20	TTGTTGTTGTTGGGCATTGT	59.864	20	222	1884	2105
60.251	20	AAGTTATCTGTGGCCGATGC	60.103	20	259	2368	2626
59.542	20	CTGAACCACATGTTCCCCTT	59.82	20	134	2	135
60.133	20	AACGGACGAACAACGAAAAC	60.015	20	235	320	554
59.89	21	AAACGACATCCTGACGCAAC	61.107	20	274	225	498
59.957	20	TATCATTGCTCGTTTTGGGG	60.827	20	254	190	443
57.589	21	GAACAAGGTTCCATTTCACACA	59.875	22	173	39	211
60.24	20	CCCCACTTGGCTTGAGATAA	60.066	20	267	54	320
58.694	22	GGATTGCATCATCAAGTCTCC	59.503	21	203	0	202
59.141	22	AGTTGTCGAATCCGCAAGAG	60.397	20	198	552	749
57.197	25	TATCCTTGCACTCTTGCCCT	59.836	20	252	13	264
59.72	20	TGTTTGAATCCGAGTTTCCC	59.91	20	235	47	281
57.636	25	GAAGTTGAGCCATATTCATTTGC	59.989	23	181	440	620
59.96	20	TCTTGGGAGGGAAAATGACA	60.43	20	185	448	632
59.941	20	GGGTCAAGTCATGTTCCCAC	60.223	20	237	615	851
59.809	21	GAGAGAGAGGCAGACATCGG	60.096	20	116	55	170
60.155	20	TGAGGATGCAAGCCTCAATA	59.375	20	232	3038	3269
59.435	20	GGACCGCTGGATAATCCTCT	60.431	20	210	98	307
59.075	20	AAGCTGGTGGATTGAATGCT	59.7	20	172	175	346
59.233	20	CATACAATTCCCCACCCTTG	60.044	20	213	90	302
60.162	20	GGGTAGGGGTCCCTGTATGT	59.935	20	192	434	625
60.011	20	GAGCACGAGGGTGAAAGTGT	60.307	20	252	59	310
59.938	19	CCCAGCTGAATGCGAGTTA	59.956	19	280	265	544
61.191	20	TCTCGTGGTGCAGTGGTAGA	60.463	20	255	28	282
58.379	20	TTTGCATGAGCTAACATGCC	59.839	20	206	650	855
60.134	20	CATTCCCATCATTTCGGCTA	60.797	20	109	1929	2037
59.807	20	AACGAATGTAACAATACGTACAC	57.736	25	233	382	614
60.132	20	AGCACTCGTGGATTCTGGAC	60.269	20	152	962	1113
60.375	20	TTACAAAAATGCCCTTTCGC	60.075	20	249	427	675
59.64	20	GGTACAGCCGAGTAGCGAAG	60.037	20	269	215	483
60.667	20	AAGAACACAACGAGGATGGC	60.119	20	260	254	513
60.529	20	TTATCCTCACCCGTTTTTCG	59.931	20	148	293	440
59.574	20	AACCCTTTGTCCCGATCTTT	59.805	20	245	3835	4079
58.52	25	CGATTTGGAATCGATAAGCA	58.721	20	269	560	828
60.177	22	ACCTCTTCCACGGCCTCTAT	60.096	20	130	85	214
59.725	20	TCTTATTGGCCCGTTTATTTT	57.725	21	276	251	526
58.741	20	ATCTCACCAAGATGCCCAAG	60.073	20	100	7	106
60.081	20	TGTAATGGAGGGGGAATCTG	59.744	20	212	186	397
59.839	20	ACAAACTTATGGACCGCTGG	59.993	20	159	502	660
60.149	20	GTGCACGAAATTGGAGGAAG	60.636	20	179	2074	2252
59.853	20	CCTATGGTGGTATGGTGTGG	58.569	20	238	231	468
60.117	20	GCGAAGGAACTGTGGAGAAC	59.851	20	156	328	483
60.082	20	AAAAATCGACAAATTATCAGTACC	58.166	25	275	433	707
59.957	20	CACCTTTGCAAAAGGGAGAA	60.22	20	254	10	263
59.963	21	AACACAGCTGAGTAACCGGG	60.171	20	102	1291	1392
59.882	20	TAACCAGGCCCTTTCTCCTT	60.068	20	265	1437	1701
60.134	20	GCGTGTTAAATTTGGATTCCC	60.541	21	280	2247	2526
59.964	20	TGGCGAATATTTTGTTTTTGA	58.213	21	145	281	425
58.278	20	CTACAAATGTTTTGGCCCCT	58.949	20	183	1275	1457
59.685	20	AATTCAATCCCCAAAAACCC	59.867	20	269	363	631
59.774	22	AAGCCACTTTTGTCAAGGTGA	59.766	21	234	1097	1330
59.651	20	GGCTCTTCGGCAGTGAATAG	59.978	20	253	252	504
59.917	26	GAAAACGTCGAGTTTCAGGC	59.859	20	193	28	220
59.813	20	ATTGCCTTGTTGTTTGGGAC	59.836	20	201	46	246
59.67	20	GGTCTATGGTCGATTGGGTG	60.195	20	203	4617	4819
60.042	20	AAACAGAAAAATTCCCCTTCATC	59.725	23	264	4454	4717
60.149	20	TCCGTTGTAAAAAGACCGTTG	60.018	21	201	38	238

59.722	20	GTAGAAAACCACGAGGGGGT	60.225	20	256	2162	2417
61.009	20	TCACGCTAAAGAGGTGTTTTGA	59.92	22	252	212	463
58.876	24	TCGTGCTCATTTGTGTTGGT	60.16	20	183	7	189
58.745	20	GCCAGCCAGGAAAACACTAA	60.249	20	127	346	472
60.586	20	AAATTCACGTGTTAGAGTTGATTC	59.424	26	231	911	1141
59.962	20	CCGTGCTTACATCAAGCAGA	60.011	20	227	15	241
60.228	20	ATCCCCTTCATTCAGCACAC	59.934	20	122	10	131
59.91	20	TCAAGAGTTGCATGTGAGCC	59.992	20	251	1470	1720
60.074	20	ACTGACATTCACAGGCATTG	57.067	20	204	57	260
60.011	20	TTAAACCCTAAAAACGCGCA	60.593	20	239	106	344
60.124	20	GGGATGGAGGAGGAAAGAAG	60.008	20	251	339	589
59.948	20	CCGAAAAGCTGAAAGAAACC	58.949	20	115	819	933
60.326	20	CCTGTTGTGCCCATCAATTA	59.395	20	183	9128	9310
60.058	19	TAGGATGATTGGCAACACGA	60.073	20	196	0	195
60.156	20	TCCAATCAAGGCAAAGATCA	59.2	20	205	5464	5668
59.74	20	GGTGATGTGTGACGTTGGAG	60.005	20	214	105	318
60.112	20	AGATCAAGGTGGCTGCAAAT	59.7	20	251	700	950
59.839	20	TGTGGTTGATGAGTTGGCAT	59.967	20	112	1229	1340
58.804	22	TTCCAAGTCTTCCCCTTCCT	60.045	20	176	3	178
59.717	20	TTTGTTTTCCATCGTATTCCA	58.005	21	143	4091	4233
60.104	20	TTTGAGTCGTTCACCACGAG	59.873	20	230	98	327
59.691	20	TTCAAAATTGAAACCGGACC	59.778	20	234	24	257
57.59	21	CTAGGCATGGAATCCGAGAA	60.17	20	269	59	327
59.432	24	TGTTTGATATGGCAGGGGTT	60.192	20	216	634	849
60.022	20	TGCAAGTGCATATCAATGAACA	60.14	22	135	1314	1448
60.468	20	TGCTGAGACATAGCGGACTG	60.16	20	169	228	396
60.133	20	GGTGGGTTCGACGACAATAG	60.375	20	131	541	671
60.005	20	TCAACTTCTTCAACAGGCCA	59.415	20	244	2186	2429
59.853	20	CAACCTAGAATGAGCATTGGC	59.722	21	207	703	909
57.234	21	CACGGGTCTTTCTTCTTCCA	60.224	20	201	9	209
60.228	20	AAGCCAGTGCTGGTTGACTT	59.914	20	239	1156	1394
59.714	20	AATGTGGATGCCCCCTATTT	60.399	20	252	233	484
59.934	20	CAGACGCCGACATTTATCCT	60.096	20	144	176	319
60.167	20	GCGTGATCTTGGTGTTCTTG	59.293	20	168	1948	2115
58.972	21	AAAATTCGATGATTGGCTCG	60.038	20	212	333	544
60.014	20	CCTTCAAGCTGTCGAACTCC	59.989	20	278	444	721
59.801	20	CCAAATTAAGCGAACCGAAA	60.068	20	222	334	555
60.056	19	TGTTGGAGTCTTGAACAAGGG	60.133	21	261	309	569
59.832	22	CATTGACTGTCACAATCCCG	59.96	20	251	1013	1263
60.161	20	TTAGGGTTTAAAATCGCGCA	60.564	20	280	7557	7836
59.56	20	TATGGGTTAGCGTGTGATCG	59.566	20	244	119	362
60.026	24	GAGATTGGTGGTTGTGGGAT	59.636	20	195	0	194
59.769	20	TGGAATAGGAAAGGTGCAGG	60.066	20	216	650	865
60.073	20	TCTTAATCCTTTGGCATTCAA	57.388	21	212	1124	1335
59.838	20	GGAGGGTGCACATCTCTTTC	59.661	20	268	2	269
60.032	20	CGCGGATGGTTAAGATTCAG	60.597	20	191	1435	1625
59.978	20	CAAAATCAGGCACCAGCTAA	58.917	20	232	909	1140
59.833	20	TTGTCCCCAAACAACGAAAT	60.206	20	185	54	238
59.28	23	CAGCATACCAAGGGCATTTT	59.96	20	215	24	238
58.96	22	GCCTCAAATCCTATTCTATTTTGC	59.549	24	246	77	322
60.195	20	CAACCCTTCCAGTTCTGGTC	59.549	20	258	1280	1537
59.937	20	CTACCACCGATCCCTCTGAA	60.065	20	228	1073	1300
59.405	20	AGCAAAACGGTCATCTGCTT	59.882	20	273	21	293
59.933	20	CACCCCTGAGCTCACTTTTC	59.844	20	218	644	861
59.805	20	TGTCCACTGATGTGGCATTT	59.967	20	189	297	485
59.52	20	CAGCCCACAAATCCTTGACT	60.111	20	214	710	923
60.272	20	ACTTGTTGAAATTCACCGGC	59.978	20	278	528	805
59.933	20	TTGAGGCTCCCAACTTTCAC	60.232	20	260	987	1246

59.473	20	AAAAATGTCCCCGAAGATACA	58.43	21	245	485	729
60.012	20	CACTAAAGTGTGCTGTCATCG	57.006	21	184	19	202
59.835	20	ACTCCCCCTCGAAGTTTTGT	59.972	20	261	219	479
59.694	20	TCATCAATTCTTTCTGCGCTT	59.974	21	279	1240	1518
59.858	20	CATGCCGAAAGAGTTTACGA	58.917	20	248	44	291
60.029	20	GTTATGCGTTTTGACGGGAT	59.829	20	200	514	713
60.04	20	TCTCATCATCTCCCCTCACC	60.008	20	227	324	550
60.192	20	AGTAGAGAAGGGGAAGGGGG	60.797	20	168	469	636
60.529	20	AATATCCATGCCATTCCCAA	59.979	20	272	166	437
60.245	21	TGGTGTTGCAATGCTACTGA	58.863	20	276	676	951
58.81	24	TTGGATTGAGAAAGCGATCC	60.155	20	278	15	292
60.029	20	GGGTTATCAGCAGCTTTTGC	59.851	20	259	1081	1339
60.221	20	TCGCACTTGGACTTTCCTTT	59.853	20	272	11	282
57.757	20	TTCAAATGTTTTTGTAATTTCCCA	59.653	24	100	30	129
59.993	20	GGCCGCTGATCATTTAGTTG	60.606	20	276	1217	1492
60.457	23	GAATGTAGGTATAAGACTGTGAA	57.394	26	280	5	284
60.118	20	GGTTTGCCCCTGTATCTCAA	59.933	20	230	219	448
57.978	23	GCGACATACATTGATCTGCG	60.251	20	249	32	280
59.95	20	TTCCTCTCGTGTTTCATCCC	60.05	20	198	3	200
59.955	20	TTAGCCCATCAAAGTCCAGG	60.066	20	185	196	380
60.038	20	GTTGCGTTCCACATAAGCCT	60.14	20	170	2736	2905
58.941	19	ACCTACCATAACCGTCGCAT	59.34	20	223	21	243
59.931	20	AACCTTATAGGATGTCCGGC	58.019	20	265	776	1040
60.058	20	CCGAGTGCCTATTTTGCCTA	60.223	20	224	6804	7027
59.663	21	CGCGTCTATCGATACTGATCC	59.705	21	256	3227	3482
59.505	20	AAAAGGTCTGCCCTTGCTTA	58.973	20	268	228	495
60.024	20	GGCTTCCGAGTTTTTCCTGT	60.61	20	225	900	1124
59.971	20	ACAGTCCACACATGAAGCCA	60.162	20	176	1078	1253
59.682	20	GGGGTTATCATGGGATCAAG	59.055	20	211	6	216
59.507	23	CGGTTAAAAACCGAATCGAA	59.937	20	226	380	605
60.564	20	CGAAGTTAGAAAATAAGGAGGTG	58.471	25	152	115	266
59.931	20	GAGGCCGTCGGAATTTATTT	60.28	20	250	1336	1585
57.795	21	TCGCGTCTGACTCCTCACTA	59.726	20	164	34	197
58.78	20	GTCCACGGTGGTGCTAGAGT	60.182	20	104	32	135
60.255	20	TTTGTGTCGTCGGTGTGATT	60.008	20	217	937	1153
60.005	20	AAAAGGGGAGAAAAGAACGG	59.566	20	241	32	272
59.988	20	TTACCGAGCTTGATGGGAAC	60.074	20	178	488	665
59.66	20	TTTCTCTCGTGCCATTCTCA	59.522	20	265	312	576
57.591	23	TGGTAAAACTCGAAGGATGGA	59.555	21	191	33	223
60.05	20	TGTTGCACTTTTGAACAATGG	59.618	21	176	69	244
59.945	22	TTACATGTGTGGGGATGGAA	59.623	20	139	224	362
60.096	20	CGTGTTTATCCTCACCCGTT	59.853	20	200	235	434
59.42	20	AAACATAAAAGCCACCTGCC	59.091	20	204	16	219
60.624	20	TAGCATCGTGAGTAGCGTCG	60.18	20	167	0	166
59.273	20	TGTGGCATCACATGGTCTCT	60.121	20	237	35	271
59.29	22	GCCGATCGAGTTTTGGATAA	60.038	20	152	215	366
60.005	20	GGTGTGTGAGGGAAGGAGAG	59.682	20	242	853	1094
59.962	20	GAACACTATTCCCATCCCCC	60.388	20	146	28	173
59.945	20	ATAGACCCAGACACGGGCTT	60.903	20	197	27	223
58.877	20	TGCTCAATGAACTCCTTTGG	58.847	20	138	11	148
60.37	20	ATCTTACTGGCATTGTCGGC	60.103	20	217	1213	1429
57.576	24	GGGTGGGCTCCATTTTTAGT	60.187	20	200	11	210
60.135	20	AAAGAAAAGGACGGGAGGAA	60.046	20	114	80	193
59.962	20	AACGGCCGAGATTTGTTATG	59.96	20	229	883	1111
59.668	20	TGTGCGTGTAAAGCTGGTTC	59.911	20	237	741	977
59.926	20	TACTTTTGGGCAATCCTTGG	59.931	20	167	3147	3313
59.565	20	TTGCCAAACACACATTTTCAA	59.999	21	268	1298	1565
59.801	20	GAAAGGTGCTTTGCCACTTC	59.859	20	204	12	215

60.194	20	AGTAGGATTCCGGTTCGCTT	60.096	20	247	221	467
59.302	21	TGCCTATTTTGAATTTTGGTG	57.705	21	145	368	512
60.243	20	TATGGGTTATCACCGGATCG	60.544	20	217	1096	1312
60.048	20	TCGATCATAAGAGCATCCCC	59.998	20	138	490	627
60.145	20	CGTCCCACAAAATATGTCCT	57.393	20	212	45	256
60.617	20	CAGTTGGGTCAGTGACATGG	59.997	20	223	111	333
60.336	20	CGCTTAAAAACCGGACCATA	59.958	20	147	894	1040
57.538	25	GCCGAGATTTGTCAGAGGTT	59.288	20	103	23	125
59.782	19	GGGGTGACCTTATCACTCCA	59.779	20	189	0	188
60.189	20	CAAAAAGGAGCTCAACGGAG	59.986	20	143	105	247
59.735	20	CAAAATTCCCACCCAATCAG	60.162	20	271	107	377
59.853	20	AAAATGCACCATTTCTTGCC	59.945	20	276	1243	1518
59.925	20	GCTTCATTATTTTTGCCCCA	59.907	20	141	24	164
59.901	20	ACGCTATGAGAGCGAGGGT	59.989	19	274	38	311
60.196	27	TTCCGGCTACTTCGAACTTT	58.973	20	262	565	826
59.903	20	AACATGGGCAAGAAACAACC	59.836	20	257	869	1125
59.2	20	CCGGATCCTATTCACCTCAA	59.887	20	276	1044	1319
59.789	20	TTCATTGGAAAGTTAGGGCG	60.067	20	133	365	497
59.697	20	GAACAACCAAGGCAATTTCAG	59.601	21	235	25	259
59.923	20	CTGAATCGCGAAACATGAAA	59.809	20	178	498	675
59.089	24	ACCATGATGAATGTGAGGCA	59.925	20	267	31	297
59.955	20	ATTGGAACAATACTATACAACCAC	57.118	26	135	87	221
58.968	20	TTCTTGATGTGTTGGCAAGC	59.847	20	138	170	307
59.209	20	GGTCCATGGCCTGTTATGTC	60.203	20	258	248	505
59.779	20	TTAGTGGGCTAAGTGGGGTG	59.986	20	172	205	376
58.585	22	TTGCATCAAGTTTTAGAGCAGC	59.674	22	227	35	261
59.938	20	ACTGAATCAGCGCTCCAGAT	59.981	20	243	115	357
59.935	20	CTTCCCTGCACAAAAGTCGT	60.291	20	278	57	334
60.03	20	AAGGTCAGGAAAACCCAAGG	60.332	20	255	2782	3036
59.943	20	TACAGGTTCACCCTTCTGGG	59.959	20	158	178	335
59.997	21	ATTTTCCCGGTGAAAGAAGG	60.291	20	123	252	374
59.657	20	TTTCTTTTCTTTTCTTTCCATTTCA	59.678	25	276	101	376
59.127	20	GCCATCCTCTCCAAGCTACA	60.362	20	233	2214	2446
58.188	24	CGGCTATTTGAGACGACATTT	59.238	21	279	2	280
59.094	20	CGACCCAGATTCAAACCCTA	59.926	20	204	184	387
59.402	23	TGGTGGTGGGAGAAGAGAAG	60.229	20	207	84	290
60.241	20	GCCACACACGAAATGAATTG	59.972	20	127	351	477
60.292	20	CGAACGGTATAGGATCGGAA	59.916	20	227	79	305
59.843	20	GCCTTCCATTCCAAAAATCA	59.878	20	151	113	263
59.178	20	GTTGGGGGATGAAGAAGGAT	60.133	20	265	449	713
60.255	20	TGAGGCAAACTGAAAAACCA	59.293	20	246	323	568
59.92	20	TCGATCCCACAGAGATTGGT	60.475	20	255	324	578
59.997	20	CTGTGCATTTGCAGACCACT	59.905	20	206	397	602
59.585	20	ACAAGTTTGGGATTGCTCCA	60.495	20	272	206	477
60.03	20	CACCCCTTATCTTCCACAGC	59.55	20	231	173	403
59.896	21	GTACCTGCACGTTGCGTAGA	59.935	20	253	4225	4477
60.035	20	AGGGGCAAGTTGGCTATTTT	59.966	20	183	2577	2759
60.111	20	ATCGTCGAACATCCTTTTGG	59.933	20	255	2315	2569
59.909	19	TGATTGCATTATCAAGAACCAAA	59.485	23	135	107	241
60.564	20	GACACGTGGCAGCACTAGAA	60.056	20	219	445	663
59.917	20	AAAACTTCCTAAGCCCCCAA	59.939	20	206	665	870
60.32	20	CCCAATTGTCGTGTGTGTTC	59.855	20	213	2	214
59.682	20	CCACCTATCTGCATCCACCT	59.95	20	108	1497	1604
59.973	20	GGCGGTGAAACGATAAACAT	59.829	20	230	227	456
59.729	25	TTGACCCCAATGGATCGTAG	60.713	20	278	166	443
57.236	20	TTGGTGTTGGTGTTGTTGCT	60.049	20	225	45	269
59.708	20	ATTCGTTTTTCCTTCCCAGG	60.291	20	140	51	190
59.654	21	AGGTTGAGTCGGACGAGTTG	60.298	20	256	590	845

59.972	20	AGCATCAATGGAGTATTGAAAAA	57.835	23	252	345	596
59.823	20	AATGTCGTGACACCTAGCCC	59.997	20	173	84	256
59.601	21	TCGGGAGTCTGTATTGAGCC	60.218	20	190	27	216
59.997	20	TGGTAAATCACTAGACCCAAGGA	59.879	23	277	10	286
59.213	22	TTGCGGATTCTAAGATTGGG	60.031	20	151	60	210
60.278	20	ATTGAGAGAATGCGAATGGC	60.185	20	268	19	286
59.518	20	ATGCCCATTCAAACTTCAGC	60.081	20	113	86	198
60.535	20	TGATGGATGGATGGTCTTGA	59.85	20	104	92	195
60.134	20	TATGTATCGTCCGCGCTGTA	60.259	20	255	633	887
60.042	20	TAGTGCCGTATTGTTTCCCC	59.823	20	257	77	333
59.978	20	TTGGACAAGCATCGGTTACA	60.111	20	215	575	789
59.971	20	TGAAGTAGGAAATAAGGAGGTGT	57.525	24	263	215	477
60.088	20	AGCGTAAACACGTCCCCATA	60.386	20	231	155	385
58.512	26	GCTTGCAGCCTTCTGTGTTA	59.224	20	227	1	227
59.243	21	ATAACCCCACCAACCTAGCC	60.074	20	102	29	130
59.94	19	GGAGTATCACTTGAATGCACCA	60	22	280	15	294
59.064	20	AGGGGAGAGATGGAGGTGAT	59.889	20	236	111	346
60.422	20	AGCTGATCCTGCGACATTG	59.959	19	256	366	621
60.207	19	CACTCCCCCGTAAAACAAGA	59.964	20	272	370	641
59.955	20	CCTCCGTGGACGTAGATCAT	59.95	20	191	21	211
60.323	20	CGGTTCATTCCCATCCTAAA	59.756	20	210	227	436
60.166	20	GCCGTGTTAGCCAACGTAAT	60.025	20	246	57	302
60.183	20	CGTAGTGGAAGTGACAGCGA	60.049	20	171	284	454
59.801	20	ACCTTTTGCATTGTCAGCAA	59.322	20	225	393	617
59.109	20	CTAAGCACCACAAGCAAGCA	60.195	20	209	179	387
59.55	22	GAGCTTCCGCATCGTTCTTA	60.49	20	239	3	241
59.648	20	TGCATACGGAATTTCAGCAA	60.215	20	239	512	750
59.797	20	ATTCGAAAATGCTCGTGAAA	58.361	20	237	1908	2144
60.038	20	TGATCATTATTGGAACGCGA	60.035	20	209	82	290
58.923	21	ATCTCCAAAACCCGACAACA	60.353	20	271	110	380
59.756	20	TGTTATGCATTTTGACGGGA	59.93	20	180	89	268
59.862	20	CACTTAAGGGGGTTATCATTGG	59.604	22	209	99	307
59.95	20	CATGAACGGTTTAGGATCGG	60.323	20	255	159	413
59.929	20	TGCTGTTAATGAAGGCATCG	59.833	20	129	297	425
59.955	20	TGGAGAGGACCTTGGAACAC	60.088	20	229	2570	2798
60.195	20	CGTCCATTTCTGCAAATCCT	60.074	20	171	393	563
59.853	20	AAAATTGAAGCGCCAGAAAG	59.474	20	269	101	369
59.904	22	TGTCCGTTAAGCAGTAAAGACG	59.464	22	196	435	630
59.867	20	CCTACTCCACCCCTTCATCA	59.92	20	140	2762	2901
59.875	20	CGCGTGTGAAACTCTAGCAA	60.195	20	137	194	330
59.182	20	TGAATGAATCACAAAAGGGGA	60.294	21	228	24	251
60.195	20	GTTTTGCCCATTTTACCCCT	60.055	20	198	23	220
59.996	20	AGCTCTTTCTCCACAGACGG	59.598	20	255	2154	2408
59.92	20	TGAATCCTCCCGTTTTCTTG	60.044	20	227	176	402
59.691	20	TCCTTGTGGTTCTACAAAATAGCA	60.056	24	131	168	298
59.786	20	CACACCCACACGCACTTTAC	60.072	20	187	386	572
59.878	20	AGGATATTGGCGATGTACGC	59.951	20	263	445	707
59.116	20	CCGATCTTAATCTTCGCTGC	59.945	20	201	165	365
59.996	20	GGAAATTGATGGATTTGGGA	59.558	20	187	674	860
59.971	21	TCTCAGATCCAAACGCCTAGA	59.963	21	169	199	367
60.011	20	TTCGGGGCATACATGTGTTA	59.809	20	222	3066	3287
59.851	20	GAGTTGGGGGATGAACTGTG	60.363	20	215	70	284
60.016	20	GCTCCTAAAATATTGGTTTCTATTT	59.441	27	146	406	551
59.205	24	CAGCATTGCTTGCACTTCTAA	59.264	21	193	1104	1296
58.212	23	TGTTTTGTAATTTCCCATGTTTG	58.816	23	102	23	124
59.373	21	CGAGTATTGGTTCAATAGAATTGA	60.143	26	275	310	584
59.978	20	TGTGTACCGCAGTTCAGAGG	59.897	20	244	94	337
60.12	20	TTTGATCTACCTCGGCCATC	60.036	20	125	2321	2445

59.542	20	ACCACCTCGGCGTAAATATG	59.845	20	205	158	362
59.62	21	TGAAAAGTCACACGAAAACGA	59.352	21	181	239	419
60.131	20	TGGTTGTTGTGAGGGTTTCA	59.976	20	245	21	265
59.989	20	AGAAACACCATTGCAGTCCC	59.973	20	142	2263	2404
60.103	20	GGGGTTATCATGGGATCAAG	59.055	20	262	275	536
60.048	20	GAACCAGAACTACCCCACCC	60.607	20	245	1282	1526
60.215	20	ACCGGAACCGGAATTAGAAC	60.187	20	221	322	542
58.382	21	TGTGTTTTGACAATATTTAGTGTTT	58.633	27	101	151	251
57.68	21	GATCAGCCATCAACCCCTTA	59.894	20	179	0	178
59.402	20	CAATCCGCACACCATATTCA	60.343	20	258	555	812
60.074	20	GCAAATATTGGCCGTCAGAT	59.929	20	226	399	624
59.948	20	ATGGTGGTATGGTGTGGAGG	60.51	20	170	93	262
59.293	20	TGATGGAACGGGGATTGTAT	60.014	20	188	619	806
60.501	20	TGCTTGGGTCTACCCTTTTG	60.103	20	202	3383	3584
59.903	20	GTCTGGAGTCCATGAGGCTG	60.829	20	121	77	197
59.928	20	TGACGGGATTTAGGTGTTTTG	59.847	21	104	367	470
59.962	20	AGAACGAGAGAAATCGACGG	59.43	20	184	93	276
59.995	20	CAGCCCCTTTTTCATTTTCA	60.046	20	213	228	440
59.439	20	GTGGACGTCCCAGATTGTTT	59.827	20	164	3	166
60.894	20	ACAAATAAGCCCACAGCCAC	60	20	174	74	247
59.873	20	CCCTAAGTTCCCCCACTGAT	60.183	20	192	1053	1244
60.03	20	TCGACCTACGAGAGTGAGGG	60.399	20	279	363	641
59.972	20	CAACTTTTCCGGTCCGTTTA	59.968	20	276	714	989
59.969	20	GGGATGAAATGAAGTGGGTG	60.173	20	267	397	663
59.547	20	TCTTCGATGAACTCTGAAATGC	59.457	22	191	279	469
60.425	21	CGAACCCTTTCATTCTCCAA	60.044	20	278	293	570
58.974	20	TTTTCTTCAAAATGCACAATAATTT	58.319	25	237	97	333
59.536	23	CCATCGTCGCTATCACATTG	60.096	20	165	79	243
60.872	21	TGCAACAAATGGATGGTTGT	59.823	20	118	18	135
59.245	22	GGCATCAAAGTTGTCGATCAT	59.954	21	111	3	113
59.945	20	TCCCACATTGGTTGGAGATT	60.173	20	247	26	272
60.212	20	AATTAACGAAGGTCCCCACC	60.053	20	127	3669	3795
59.791	20	TTCGGTCACATTCAATAAGGC	59.952	21	244	1047	1290
59.779	20	TGCAAACCCATGATTGACAC	60.376	20	151	695	845
59.542	20	CAGGCTTGCAGCAACTAACA	60.195	20	236	689	924
59.84	20	GGATAATTTGGACAGCCCAC	59.249	20	176	826	1001
57.062	26	AAGAGGGGTGAGGGAGATGT	59.929	20	197	0	196
60.461	20	CAACGAAATCCTGCCAATCT	60.074	20	179	65	243
59.985	20	AACCGATCATTTCATCAGCC	59.9	20	271	2715	2985
60.176	24	GAGGCCTCGATCTTCTGTCA	60.497	20	104	11	114
58.943	20	TACGGTTCGGTTTACGGTTT	59.379	20	257	150	406
58.94	26	TGGGCTAATCACTCTCAGCA	59.547	20	178	11	188
60.222	20	CAATTTGAGAATGGGATGGG	60.126	20	236	776	1011
60.636	20	GTTGACAAAACGCACGTGAA	60.742	20	228	583	810
60.953	20	AACATTGCGGACTTGGTACA	59.05	20	265	774	1038
60.053	20	TGAGATGATATTATGAACTGCATC	59.394	25	264	208	471
60.397	20	CGTGATGCAACGCATTCTTA	60.807	20	248	227	474
59.964	20	TCCGAGAATCTGTTAGAGGAGAA	59.491	23	255	103	357
59.603	20	CCTTTTGCAAGCACTGATGA	59.988	20	196	533	728
59.36	20	TGAAAAGGGGTGAGAGGATG	60.042	20	252	124	375
60.003	20	TTTTTATGCACAAGCCTCCC	60.074	20	275	51	325
59.843	20	AACCACAGCCCTACATCTCG	60.134	20	263	344	606
60.249	20	TCATTTGTTCCACTTCATTTGG	59.839	22	250	4339	4588
59.794	20	GCGTGGCCTAAGTTGTCCTA	60.27	20	257	645	901
60.124	20	TAGTGAAGCAGCTGACGTGG	60.199	20	144	65	208
59.982	20	GGTTGATGGATCTGCGTTTT	59.939	20	224	68	291
59.927	20	TCAAAAATATCCTCGCTGCAT	59.696	21	128	4	131
59.773	20	AGAGTTGGGGATCTGCAAAA	59.67	20	211	103	313

59.917	20	ACCGTCTCGACGAAAGCTAA	60.015	20	224	343	566
60.257	20	TGAGGCATGCAAAGATGAAG	59.948	20	234	199	432
60.088	20	TTGCGTATGATAGGGTTAGCA	58.342	21	240	26	265
60.081	20	CATGCTACATTCCGTGATGG	59.948	20	201	592	792
60.081	20	TTTCTTATTTCCCGGCTCCT	60.034	20	137	553	689
59.776	20	AAAGAGGAAGAGGGAGGCAG	59.95	20	238	644	881
59.767	20	AATCCTTGCTCTGGCTGCTA	60.118	20	259	3	261
59.902	20	GGGATGTTTGTACCTGAATGC	59.307	21	121	3	123
59.96	20	ATAAAAATGGCACCTGGCTG	59.96	20	220	158	377
59.577	20	CAAGAGGCAATCACGTTGAA	59.84	20	232	281	512
60.472	20	GTTCCTTGCGTGGCATTATT	59.967	20	185	1027	1211
59.318	27	TCAAGAGCAAGCAAAGATCTAAA	59.7	24	164	6	169
59.938	20	TACTGACTTGTTGTGCGGGA	60.301	20	271	381	651
60.165	23	ACGGTCTGGTTTCAGTTTCG	60.149	20	146	769	914
59.028	20	GGAACCGGCTAAGATGATGA	60.036	20	227	244	470
57.369	25	CCCGCATGTCATAACCACTA	59.42	20	274	268	541
60.096	20	CCAATGGCGATATTTCCTGT	59.784	20	213	168	380
60.049	20	TGGTGTCTATGTATGGGTGGA	58.709	21	210	651	860
60.668	20	TGGACATAAATTGTAGTGCCAAA	59.415	23	176	667	842
60	20	ATAAATGCCTACGTCCACGG	59.845	20	231	151	381
59.935	20	CACCCTCCTTCCTCAAACAA	60.081	20	277	404	680
59.576	21	AACAAAGGGGGTTGGAGAAT	59.668	20	232	3177	3408
60.183	22	CGCGTGCTCCTAACTCTTTC	60.154	20	118	29	146
60.386	20	AAATGGTTGTTTGTCCCCAA	60.066	20	203	146	348
59.923	20	TAGTCAGAACTTGCATGCCG	60.011	20	171	46	216
59.989	20	TCTCTCTCTTTTTGGTAGGTCAATG	60.165	25	262	144	405
57.139	20	TAGAATGTTCCGAAATGGGC	59.901	20	176	23	198
60.051	20	TGTGAAGTGTTGCTGATGTGA	58.855	21	220	1168	1387
59.95	20	GCGGATCCCCCTTAATTTT	60.102	19	280	302	581
59.666	20	TGAAAATTAGAAACAGCACATTTG	60.051	25	272	767	1038
60.088	20	TTTATCAGGGAAGGACGTGG	59.926	20	165	3064	3228
59.78	20	TCCGGACGGAAAGATTACAC	59.933	20	251	9	259
60.045	20	CTGTTATGTCGTGTCCGGTG	60.025	20	244	1066	1309
59.989	20	CGATTTGGCAAGGAAGAAAG	59.817	20	183	430	612
60.088	20	TGGCGCCTTCTATTCTCCTA	59.938	20	151	342	492
59.23	20	CCCGTACAATATCAACCACAA	58.28	21	180	61	240
61.072	20	GAAGTGTTATGCGTTTTGACAAT	58.249	23	235	1789	2023
60.103	20	ATCTCACGATATCCCGCATC	59.884	20	235	101	335
60.12	20	GAGGAATCTTCCCAATTCACA	58.97	21	277	14	290
59.766	20	TGAGACGAAACTCATGCGAC	59.992	20	246	48	293
60.029	21	TCCACATATGCAAGATTTCAGC	60.103	22	125	50	174
60.11	20	ATGAGCACCAAATCTTTGCC	60.081	20	153	203	355
59.829	20	ACGGATATGCCCTTGTATGC	59.813	20	249	23	271
60.812	20	AATCCACACCCGAAATATGC	59.651	20	157	375	531
60.008	19	CAAATGGTTTGGGGTTTTTG	60.06	20	271	116	386
59.245	20	TCGGCATAGATGACTTAAAAGC	58.544	22	205	1454	1658
60.134	20	CAACCGAAGCAATAAGAGGG	59.702	20	266	6	271
58.421	21	GCAACCAACATCAACGTGAC	60.016	20	251	553	803
59.576	27	AGAAAACTCACCCTGCCTCC	60.628	20	272	112	383
60.375	20	TTTAAGGGTTATCACCTGATTTTC	57.757	24	211	830	1040
59.972	20	GTTCGGTGAAGATTGGAGGA	60.05	20	225	31	255
59.964	20	AACCAAGATCAGGCTGCAAT	59.7	20	171	669	839
60.43	20	CTTAGGGGACACCCAAGTGA	59.959	20	276	382	657
60.46	20	GACTCGCAAAGACTTGAGGG	59.989	20	153	34	186
59.762	20	GTGACGTGCTGGTTGTCCTA	59.751	20	225	1027	1251
57.559	23	TGACAATTGCAAATATGGCG	60.474	20	217	3	219
59.96	20	GCTGCATCGATGTATTGTGG	60.104	20	130	1998	2127
59.813	20	GAATCTCTTGCCGGATCAAA	60.155	20	259	692	950

60.159	20	TCATTCTCGGGCAAAAATTC	60.016	20	271	52	322
59.749	26	GTCGCTACAAGCAGTCACCA	60.056	20	264	3	266
60.117	20	GCGACTTTTCAGTTTCCAGC	60	20	208	749	956
59.837	20	CATTTGCAGATGCTGATGCT	59.979	20	268	1014	1281
58.863	20	GCGTGTGTCTGAGGATGTTT	58.727	20	181	17	197
59.948	20	GCAAAATACCCTGAGTGGGA	59.933	20	153	307	459
59.429	20	TGGAGGTCGAACTCAATTATGA	59.569	22	157	209	365
60.246	20	ATTCATCAAACCCAGTTCGC	59.939	20	229	20	248
59.975	20	ATAGCCAAGGCAGCTCTCAA	60.118	20	231	1867	2097
59.82	20	ATGTGAACGAAGTACCCCGA	60.375	20	187	263	449
60.582	20	GAAAAACGCTAGGCGGATCT	60.711	20	214	23	236
58.931	20	TCACACTAGTGGCATCGCTC	60.016	20	203	212	414
59.269	21	AAAGCGCGATTTTAAACCCT	60.095	20	235	2183	2417
57.192	22	TGGGACATTTTTAATTTTGCCT	59.728	22	232	1480	1711
61.489	19	TTTTTCGTGGATATAATTGGGC	60.044	22	175	64	238
59.528	20	CACCTCGAGCTTCGCTTCTA	60.807	20	263	4779	5041
60.088	20	GAAGGGAAAGAACCTTTGGG	59.912	20	252	1288	1539
59.996	19	TGTTGAATCACATGTCCCGT	59.812	20	200	271	470
60.059	20	GCATGCATCTGTCGGATCTA	59.788	20	173	334	506
59.569	20	GGAAATAAGGAGTTGTTATGAAG	60.434	25	134	2768	2901
59.031	20	CATGTTCTAGGCGTTTCGGT	60.132	20	268	81	348
59.847	20	TTTTACTTTGGCCGAATTGTC	59.111	21	118	290	407
59.915	27	TTAAATTTTCGAACGCCTGC	60.205	20	129	212	340
60.118	20	GAAAGTTCGGATTTTTGGCA	60.053	20	244	98	341
57.756	24	AGCTCCAATAGTTGCTTCGG	59.476	20	192	0	191
60.132	20	ACTGCGCACACTTTGTTTTG	59.951	20	191	2168	2358
60.035	20	AGCCGATTTCTTTCACTCCC	60.578	20	226	35	260
59.03	20	AAAATCAAAGGCCCACAATG	59.801	20	142	2168	2309
59.948	20	TGGCGTCTGGTAAATCAACA	60.111	20	247	1343	1589
59.688	20	GATTATGAATCGGGCGAGAA	60.001	20	242	1702	1943
59.844	20	TGCATTGCCATGTTACTTTCA	60.126	21	167	146	312
60.103	20	ATCTCATACGTTGCCAACCC	59.82	20	238	456	693
59.799	20	CAGCAACCAAGAAGGGATGT	60.111	20	277	2010	2286
60.388	20	AAAAGGGAGAAAGAGGCCAA	60.18	20	227	4090	4316
60.22	20	GGCCGGTTAAAGGAGAAAAG	60.068	20	195	21	215
59.9	25	GCGGAAATTAACCACAACCA	60.732	20	147	8	154
60.042	20	CGCGTTACGAATCCAAGTTT	60.131	20	160	639	798
59.74	20	CCTTCTCGAGCACTGATTCC	59.95	20	221	81	301
60.003	20	GGCGGAATCACATTAGCATT	59.929	20	230	268	497
59.982	20	TCTCTCTTTTGGTTGGTGAAGA	58.955	22	183	210	392
60.034	20	GGACGCATCAGGTATAAAAGGA	60.332	22	240	6	245
59.968	20	CGCATCTGATTTTTGCAATC	59.261	20	258	1598	1855
59.896	21	GAAGAAACCCCTTTTTCTTCTCTT	59.682	24	247	593	839
59.615	20	ATCATCACCACAACTCACCG	59.393	20	104	333	436
59.813	20	TCGGATGGTTTATGGATGGT	60.014	20	274	295	568
60.005	20	TGTTCATACGCATTGGAAAAA	59.063	21	156	188	343
59.752	20	GAACTCCCCTCTCTCTCGGT	59.807	20	203	76	278
59.449	20	ACGCCCCGTATTTTGAATTT	60.547	20	278	1431	1708
59.31	22	GTTTGGCCTTGCATTTGATT	59.945	20	161	1952	2112
59.476	20	CTCCACCAAGCTTACACAACA	58.837	21	177	608	784
59.978	20	GCGTTGTCGTTTCTTTGGAT	60.118	20	222	267	488
58.987	22	ATAGCCATTGGCCTAGCCTT	60.082	20	278	1638	1915
60.177	20	TTGCTTTTCCGAATCTGTGA	59.395	20	210	581	790
59.238	21	GCGTAGTCTTGTCTTTCGCC	60.022	20	191	249	439
60.683	20	CCCCTAAACCGTAAATCAAGC	59.851	21	207	2	208
60.088	20	TGAAGTTGATCAAGCAAGGG	58.847	20	201	1187	1387
59.853	20	AACATTAATGGCGTCGAAGG	59.96	20	264	4526	4789
58.941	21	CGATCGTAATTGATCTACGTCCA	61.213	23	266	91	356

59.847	21	GTTGGTGCCAAAATTGCTCT	60.118	20	226	2	227
59.647	20	ATTACGAGCCACGGCTACAG	60.292	20	228	72	299
59.984	20	ATTCACATTTTCCCAGTCGC	59.939	20	235	1081	1315
59.933	20	GAAAAGCCGAATGCAGAAAG	59.96	20	170	1118	1287
60.291	20	CGGTTATCACCGAATCGC	60.033	18	280	97	376
60.03	20	GGCAGTACGTGTGCGATAGA	59.895	20	105	80	184
59.305	20	TTTCCACAAGTGAAGCAACG	59.881	20	260	3659	3918
60	20	AAGGCTATCGTTGCTTTCCC	60.582	20	149	378	526
60.147	20	TACAAGGCCCGACTTGAGTT	59.734	20	246	10	255
60.005	20	CTTTTGCACCTTTTTGCCTC	59.861	20	230	474	703
59.789	20	ACCCTCACCTCCCCTCAC	59.888	18	248	13	260
59.875	20	GGAACTCCCCATAACTGCAA	59.933	20	181	388	568
60.492	20	TTACGTAAAAATGGGTTATTATTT	57.411	26	164	491	654
60.791	20	AACGTGACATGTTGCTGAGG	59.751	20	200	838	1037
58.759	21	TCCGATGTGGGATCATAACA	59.732	20	119	358	476
59.669	27	ATTTCGAAGATCAACGGACG	60.074	20	140	9	148
60.163	20	AAGGAGGTGTTATGAAGGGATT	58.028	22	249	120	368
60.134	20	CCCCATGTAAATAGCCGTTG	60.202	20	254	24	277
59.903	22	TGATTTGTTGGGGCTTTAGG	59.931	20	251	471	721
59.948	20	AAAACAAGAATTCGGCATCG	60.074	20	182	283	464
60.009	20	CCACCATCTTGTAGGTCGCT	60.134	20	123	1808	1930
59.335	22	TGAGTTTGCATCTAAGGAGGTG	59.378	22	269	503	771
60.156	20	TGAGGATACTCGATTTCACGG	60.081	21	135	362	496
59.83	20	GAGAAGGGTTATCACTTGAATAG	57.473	24	267	87	353
59.898	20	ATTTCAAGGTTGGGCATCTG	59.933	20	243	2703	2945
60.817	20	CGTTTAAGCCAATATCATTGTTCA	60.247	24	279	477	755
59.767	20	TTTCAACCTCGCTATCGCTT	59.982	20	182	269	450
60.005	20	CATGCGCATTTATGAGTCCA	60.632	20	212	120	331
59.405	20	GAGGAAAACAGAGGCTGTTCA	59.463	21	138	84	221
59.96	20	TCGAAGTTTGGTGTTGGTGA	60.128	20	197	49	245
60.255	20	CCACGTTAGGCTCAGGAGTG	60.843	20	103	4	106
57.853	21	TCGTATCGCTTCCATGTTGA	60.22	20	227	5	231
60.278	20	TTCAACATTTCTTGCCCAAA	59.133	20	201	339	539
59.837	20	TTCTTTTGGGGCAGTGAATC	60.051	20	195	577	771
59.685	20	TTGTTTAACTCCCACTAATGCAAA	59.937	24	208	25	232
60.257	20	TGTTTCCATTTCCATGGTACG	60.602	21	261	2248	2508
60.025	20	GATGATAGAAGGGGGCATGA	59.854	20	279	1905	2183
60.049	20	AATCCAGCAATTTGCCTTGTA	59.6	21	277	2502	2778
60.246	20	CAAAGTCCGGCGTAGAATGT	60.132	20	220	344	563
60.02	20	TTGAGTCCCAAAACATGCAA	60.088	20	278	773	1050
59.017	22	CATGGCATGCACATTTTAGC	60.103	20	224	1266	1489
58.547	20	GAACTCGGATCTTTCACCCA	60.05	20	198	754	951
58.277	20	TGGTGGGAGCCTATAGCAAC	60.096	20	254	18	271
59.813	20	GCATTGGGACACCTAAGCAT	59.962	20	225	529	753
60.006	20	CAATATTACAATGGCCAAGAGTC	57.725	23	185	62	246
59.401	20	TGAGAAACTCCCTTGGGTGA	60.624	20	128	314	441
59.566	20	TGGTAGGTTTGTTTTAGGCCC	60.223	21	202	4	205
58.497	21	CCATGTTAAAACGGGCACAT	60.617	20	106	37	142
59.871	20	TGAAACGGACAAACGATGAA	60.088	20	146	159	304
59.866	20	AAAAGGGAAAAACCCTCAGC	59.571	20	150	410	559
59.982	20	AAAATACCCTTCCCCGAATG	60.013	20	177	83	259
59.817	20	AAGGGTGATGTCGCACTTCT	59.727	20	279	43	321
59.971	20	GGATGATGCCTTCAAGGGTA	59.894	20	236	460	695
60.578	20	ACACCCAACTCAGTCAAGGC	60.159	20	237	587	823
59.956	24	CATGCTAGAGGTGACGTTTTG	58.445	21	231	1631	1861
59.55	20	TTTTGTCTTTTGGGATTCGG	59.91	20	207	2087	2293
59.81	20	ATCCAACCCATTTGTGGAAA	60.029	20	279	332	610
60.002	20	CTAACATCGGAACTTGCCGT	60.132	20	259	592	850

60.103	21	TGGTGTACAGAGTGCATGTGA	58.719	21	279	174	452
59.246	27	GCGAATATAACCCGCTCTGA	60.196	20	219	44	262
60.134	20	CCTTGGGCGTTGATCTTAAA	60.067	20	119	99	217
60.457	23	CAGGAGAGATAGGGGGAAGG	60.023	20	263	18	280
59.962	22	CATCATCACCTGATTGACGC	60.08	20	261	42	302
60.024	21	GCGCAGATCTAATGGTCCAG	60.765	20	179	204	382
58.81	24	AGGTGGCAACATAATCAGCC	59.962	20	149	9	157
59.962	20	TTTCGCACGCATTAAATCAG	59.842	20	167	335	501
60	20	TGTGTGATGTTGGAGTTGGG	60.416	20	229	52	280
59.813	20	TTCCACGTTCGTGTTCGATA	60.111	20	232	239	470
60.081	20	TTATATTTCAGGGGGAGGGG	59.971	20	180	250	429
59.874	20	TTCCTTCACTCCCCCTCTCT	60.186	20	221	1849	2069
59.619	27	TTCTTATTTCTCACTTTAAGACCAT	58.093	27	216	451	666
60.119	20	AAAAACCCTTCTGAAACCCG	60.324	20	171	414	584
59.83	20	AGGCGATTTTGGGTGTTATG	59.823	20	251	71	321
59.486	20	ATGGGATTCACCTGCCTTCT	60.853	20	138	8	145
60.088	20	TAATTGTTTCGGGCTAACGG	59.958	20	208	200	407
60.517	20	ACCCACCAACATCACCAAAT	59.95	20	219	57	275
59.559	20	GGGCGTTTTATTTCCCATCT	60.15	20	243	157	399
60.081	20	TCATTATACGGGCCCAAGAC	59.784	20	231	44	274
59.756	20	TCGCCTAACTTATGCAATGAAA	59.753	22	157	230	386
58.03	20	TACATCGTCCACCCCATTTT	60.051	20	273	147	419
59.55	20	TCGTGTGGTTTTGAAGCAAG	59.881	20	238	264	501
58.402	23	ACCACCGGCTAAACCAGTC	59.981	19	208	17	224
59.864	20	GATATGATTTTGCGCGGAGT	60.067	20	230	28	257
59.783	20	CAATTTTCGGCAGCATTACA	59.702	20	237	351	587
60.152	20	TTTTTCCCAAAACACCCCTA	59.288	20	202	1262	1463
60.212	20	TAGAGTTCCAAGAGGGGGCT	60.204	20	209	4	212
60.286	20	GGCAACAAGAAGAAAATCGC	59.829	20	253	390	642
59.837	20	CACTACTCATCATCCTCTCTTTCTC	57.758	25	144	904	1047
60.448	20	CTGCAGACGTTTCAAGGTGA	60.025	20	211	736	946
59.126	23	TCATTTATGAAGCAAGGGGG	59.894	20	105	33	137
60.386	20	AAGCTTGGGCTTTCTTCTCC	59.962	20	235	3881	4115
59.871	20	CAGCGAGATCTTCGTCCATT	60.362	20	131	126	256
59.963	21	TGGCGTCTGTTCCCTTAATC	60.074	20	198	23	220
59.923	20	CATGCCAACCCGTCTTATTT	59.823	20	238	2420	2657
59.079	20	GGGTGGAGCAAAATCTGAAA	60.051	20	217	40	256
59.845	20	CAAGCAAATTGTGGCTCTGA	59.988	20	227	500	726
59.682	20	GATCGGTGAAGATTGGAGGA	60.011	20	210	11	220
60.195	20	GCGAAAGACATACGGGGTTA	59.96	20	250	44	293
60.448	20	CAGAGCGCACTCGAAGAGTA	59.49	20	276	63	338
60.603	20	ATCACGTGCACCGTCATCTA	60.144	20	185	320	504
59.807	20	CCACGAGATCAAGAATGGAA	58.643	20	250	1	250
60.195	20	CCCGTTTCGGAGTTTGTCTA	60.103	20	233	1097	1329
59.174	20	TTCAGCCCACATATGTTCCA	59.924	20	104	36	139
61.031	20	ACCCAACCCACGCAATAAT	60.066	19	272	20	291
58.038	20	ACAATTCCACGGAGAACCTG	59.966	20	248	773	1020
59.411	23	TCCATGGATCTGGATCATCA	59.806	20	249	117	365
57.929	20	TTGGGTTGCTGAAAATAGGC	60.074	20	237	27	263
59.696	20	AGGCCCGAGCTAAAAACATT	60.095	20	146	62	207
59.848	23	TGCCTAGGTGGCTACTATGTGA	59.791	22	169	30	198
60.173	20	TTGTGATTCTGAAAAATAGATCGT	58.337	25	204	321	524
60.134	20	ATCGAAAGACGAACACGCTT	59.882	20	220	585	804
59.823	20	GAAGATACTTCATGCTTGTAAAAC	58.527	25	185	358	542
60.237	20	TGTGGGACAAGCAAATGAAA	60.088	20	280	466	745
59.9	20	AACATGCACTTTCATTCGTGTT	59.545	22	219	59	277
60.336	20	AAAGGTAGCGGGGTCTTTGT	59.998	20	117	334	450
60.162	20	GCAAGGTTCATGGAGTGGTT	59.973	20	233	202	434

59.64	23	CCTAACCCCACTAATGACCC	58.24	20	143	3	145
57.833	20	GGTTGACGTTGGATCTGCTT	60.119	20	214	146	359
59.933	20	ATTTGGTCTCTTCCCCTCGT	59.935	20	269	680	948
59.797	20	CATGTTCCGAATCTTCGTCC	60.461	20	171	4	174
59.938	20	TGTGGCCCGTTTCTTATTTC	59.938	20	177	28	204
60.015	20	CGCATATAGCTCGACTGCAA	60.14	20	136	269	404
60.117	20	AAACCCTTGAAACAAATAAAATC	58.132	24	259	45	303
59.539	22	TGAGTTGGTGGAGGGTTTTC	59.943	20	218	102	319
59.671	21	TCGAATTGAAGTTAAAGCTTAGTT	58.353	25	132	275	406
59.161	20	GAAACGAGTTCCGAAATGGA	60.051	20	220	47	266
60.081	20	TGAAGCCTTTAAATGGGCAC	60.074	20	204	377	580
60.591	20	CACCCATTCATTCCCTCATT	59.605	20	136	198	333
59.803	20	GGACACAACAGAGGGGAGAA	60.088	20	237	352	588
59.962	20	GGCGAATGCTATGCATTTTT	60.068	20	260	683	942
59.934	20	TTCTTGGTGGCGGTAGGTAG	60.125	20	178	223	400
60.284	20	GGTGTTGGCCGAAAGTTTTA	59.975	20	107	0	106
59.91	20	TGCTCTCTCATTGTAATCTCTCTC	59.688	25	153	836	988
60.017	20	ATTGTTGTGGTGCGTTTTCA	60.011	20	236	415	650
59.927	20	TCCGATTGACACCTACACCA	59.96	20	167	1163	1329
59.967	20	GAGGGGGTGACCACAATCTA	59.779	20	229	211	439
60.045	20	TTCACGCAACACAAACCCTA	60.149	20	240	131	370
58.359	20	TTGGGGGAGGGTTTAGGTAG	60.172	20	121	12	132
60.065	20	AAAGAGAGCTGCAAATGGGA	59.955	20	152	44	195
59.894	20	ATTGGGGAGGATAAAGGACG	60.145	20	140	37	176
60.032	20	CCTGGAAACAAAGAAGCACC	59.711	20	275	706	980
59.982	20	CAGAGCCCTATTCATGCGAT	60.199	20	158	12	169
60.163	20	CTCCAGCAATTTCAGCTTCC	59.955	20	174	73	246
59.668	20	CACTTAAGGGGGTTATTAGTGGA	59.692	24	150	1203	1352
59.816	20	GCTGCTGTATTAAACCGAACG	59.793	21	258	510	767
60.13	21	TAAGGGTTATCACCGGATCG	59.778	20	231	8	238
59.78	23	TGCTTTAATCCATACAAAGACCC	59.407	23	128	14	141
60.454	25	ACGCCTGCTTGAGAGATTTT	59.08	20	220	8	227
59.947	20	TGAGGGCAGTCAAAAATTCG	61.137	20	131	86	216
60.062	22	TGGTTGAAACCAGATCGAAA	59.097	20	275	1348	1622
57.122	24	GTCCACGGGAGAGAATGAGA	60.199	20	178	5	182
59.267	21	CCCCAAACAACGAAATGAAT	59.662	20	193	221	413
59.738	21	CGAGGAAGAAAATGGAAGCA	60.323	20	178	194	371
59.154	23	TTGTGGCATTCTTGACCAAA	60.088	20	177	231	407
59.992	20	ACGGTTCCCATCAGCAATAC	59.82	20	262	732	993
60.05	20	TTCCCCTCCACCCTCTATTT	59.761	20	269	334	602
59.83	20	TTGTAATCGGACCGGTTTTC	59.801	20	217	380	596
57.782	25	CACCTTCTGGACTCAGACGA	58.964	20	267	250	516
57.515	20	GAGCGCATTCGAAGAGTAGC	60.265	20	256	69	324
58.404	20	ATATCGGCCGTCAGATTGAG	60.059	20	216	325	540
59.726	20	ATAGGGTCATGCGTGTGTGA	59.992	20	169	98	266
60.301	20	TGCGTTTTGACGATATATAGTGTT	59.092	25	169	1279	1447
59.013	20	CCCAACTTTTCTCCCCAAAT	60.159	20	256	1027	1282
59.05	20	CAAACCAAAGCATGCGTAAA	59.742	20	183	69	251
59.563	23	AAGTAGTCCTTTCCTCGGGC	59.713	20	241	125	365
60.184	20	TAGCCGAGAAGAACCTTGGA	59.948	20	183	79	261
60.003	20	TCCTGCCACATGTAATGGAA	59.924	20	147	6040	6186
60.03	21	AGATTTCACTTTGCAACCGC	60.257	20	243	2850	3092
60.051	20	AACAAACAAGCCCCCTCTTC	60.476	20	177	554	730
60.074	20	GCCTACCTGGGCCATTTTTA	61.155	20	230	12	241
59.445	20	TTTGCATCTTAGCGAGTTGG	59.062	20	253	936	1188
59.279	20	CGTATTGAATGAGGGAGGGA	59.887	20	214	406	619
58.268	20	TGGAATTTGGTTTTTGTAACTTGA	59.797	24	250	267	516
57.687	25	TTAGTAGCTTCGGGGTGCAT	59.73	20	235	200	434

59.457	20	AATCTCCATCCAAGCACCAC	59.934	20	198	470	667
60.448	20	CGAGGAATACGAAGAGTCGC	59.978	20	200	42	241
59.365	22	CATCGAGCCCACTTAGTGCT	60.419	20	248	991	1238
60.278	20	ATTGAGAGAATGCGAATGGC	60.185	20	274	19	292
59.473	21	GGGACGAAAATAACCCTCGT	60.187	20	215	706	920
57.647	21	GGAAATAAGGAGGTGTTATGATA	57.235	25	129	1309	1437
60.119	20	GGTTTTCTTGCCAAAAATGG	59.429	20	205	433	637
60.812	20	CGATCCATATGGCAAGAGAAA	60.045	21	226	12	237
60.478	26	GCGGAAGAATTTGCTCTCAG	60.096	20	232	20	251
57.608	20	ATTTCATTAAAATTGATCAACGG	57.193	23	122	22	143
60.048	20	ATCGGCGCTAGACGACATAC	60.265	20	145	1335	1479
57.024	26	GGTGTGTTGGCATTGCTAGA	59.722	20	193	1015	1207
60.773	20	AAGGAGGTGTTATGAAGGGATT	58.028	22	198	236	433
59.83	20	TTTTCCTCTCCCCTCTTGGT	60.045	20	274	319	592
59.934	20	CGCTGGTCTTGGAGATCAAT	60.218	20	251	1140	1390
59.101	21	TCAATTACATTCCCGTGGGT	60.051	20	235	1252	1486
59.006	20	TCAACAGCAATGAATTTGTGG	59.576	21	244	133	376
60.04	20	TCAGCTGCGATGTCAATTTC	59.955	20	110	94	203
60.493	20	CGGTGACGGTTGAGAATGAC	61.527	20	152	51	202
60.61	20	AATTGTGTGGGCGATTGATT	60.199	20	278	3737	4014
59.95	20	AGCGTATTTCTTGATTGCCG	60.23	20	250	575	824
60.058	20	TCCCTATTCCCACTCCTTCC	60.264	20	191	657	847
59.887	20	GCGTCTCTCGACGTTACACA	60.056	20	225	64	288
58.866	20	TGGAGGAAGATATTGTGACGTG	59.993	22	269	2123	2391
60.096	20	TCAGTGTTATCGAGCCTCTCAA	60.015	22	278	17	294
60.366	20	TCGGGATATTAAATCCATCAGG	60.002	22	128	220	347
59.823	20	CGCTTTCACCACGAACACTA	59.904	20	246	64	309
59.481	20	AACACACACGGATGTGGAGA	60.005	20	231	5852	6082
60.032	20	AAAAGAGAAGCCCTCCAAGC	59.962	20	230	551	780
59.83	20	CGAAAAAGCAAATTCCATCA	58.744	20	273	9	281
58.658	23	CGAGTGGTTTGGGAAGAAGA	60.224	20	262	0	261
60.042	20	AGGGCCAGAAAAACCAAGAT	59.94	20	268	349	616
59.577	20	TGCTGGGATACACAGGGTTT	60.375	20	172	96	267
57.73	23	ATGCCCTCATGACTCTCAGC	60.381	20	232	16	247
58.988	26	TTTCATGATCAAATCTTATGAACC	59.741	25	156	30	185
60.047	24	TTGAAACGAAATAGGGGTGG	59.795	20	267	532	798
59.933	20	TGTTGGTGGATTGTGCATTT	59.823	20	176	123	298
59.797	20	TTTAAGGGTTATCACCTGATTTTC	57.757	24	212	569	780
60.134	20	CACCTCCCAAACACAAAGGT	59.861	20	142	3943	4084
59.622	20	AGGTCTTGACAGGTTGTGGG	60.002	20	262	27	288
59.691	20	AGATGAGATCAATGCCCCAG	60.034	20	138	3188	3325
59.975	20	CCAGTTCAAAAGCATCACCA	59.691	20	234	1253	1486
59.962	20	ACATCCAGCCCACAAAGAAC	59.973	20	161	3047	3207
59.94	20	TTGCCATGTTCTGCTTCTCTT	60.008	21	240	1053	1292
59.907	20	AAAGAAAAGAGACAATCCGGC	59.717	21	252	504	755
59.871	20	GAACGAATGCATGGGTGTAA	59.4	20	261	886	1146
59.879	20	CAGAACCCTCAAATCCCTCA	60.042	20	215	8166	8380
57.268	20	AGAAATGGGGTCGACATGAA	60.317	20	232	43	274
59.716	21	CAACGAAGGATTTGGTGTTG	59.021	20	274	3247	3520
59.989	20	GATTGGACTTGTTTCTCGGC	59.676	20	228	30	257
60.032	20	TCTTCCAAGAATGGAGCAGC	60.483	20	183	962	1144
61.706	20	TCATTTGCCCCCGTATTTTA	60.144	20	177	0	176
57.785	25	CCACGAATCATGATCGAAAA	59.474	20	229	2331	2559
59.982	22	AAGATATATAATTCATTGAGCTTT	57.982	27	105	175	279
57.749	22	TGATTTCGAGAAGCAGTAGGTG	59.517	22	114	237	350
60.103	20	ACCAGAACCGAAGTGATTGG	59.966	20	238	627	864
60.11	20	TGGAAGGATTGAAGGAGGTG	60.042	20	224	1929	2152
59.282	20	CACCTTAAGATCTGCTCCGC	59.978	20	240	125	364

60.461	20	GGCAGTCACTGGAAGGAAGA	60.386	20	275	1161	1435
60.008	20	CACCCGAAAATGAGTTATTATTTG	60.438	25	166	242	407
59.598	20	GGCATTGCAGAGTTGAGAAA	59.002	20	144	4778	4921
59.967	20	TGCGTTTTGACGATATATAGTGTTT	59.092	25	253	266	518
59.967	21	AAAATAGCTTATTGAATTTGATTTC	59.723	27	195	108	302
60.183	25	GCCAGATGTGAATGGGTCAC	61.369	20	184	130	313
59.942	20	TCCCATTTCCATTTCCAAAC	59.599	20	156	494	649
59.933	20	CACCACGGAAGAGAGGTAGG	59.715	20	168	65	232
58.148	20	TCCGATTAATGGGCTCTGAC	60.036	20	117	1744	1860
60.089	21	TTTTTGCCTGATATTTGTATAACGA	59.061	25	273	891	1163
59.605	21	AAAGTTGAAGGTTGGGGAGG	60.332	20	257	13	269
57.486	27	TTCTGTCGAGCTTAGCCTCA	58.9	20	173	9	181
60.11	20	TCTCTCCCTCTCTCTCTTCGG	60.215	21	150	122	271
59.31	26	GGACGCATAACCCGTAAAAA	59.832	20	109	2	110
59.874	20	TGGAAGATCCGAGAACCACT	59.655	20	265	1121	1385
59.919	20	TTGTTGAACCGTGTGCAAAT	60.011	20	225	23	247
59.937	20	GCTGACATGGCTTCGTATCA	59.83	20	269	1702	1970
59.711	20	CAAAACAACTGCACCACACC	60.049	20	219	837	1055
60.05	20	GTCAACTTGGGCAGTGGAAT	59.973	20	176	51	226
59.592	20	TGTGTGCTTTATTGGAGCGA	60.401	20	277	10	286
60.067	20	GGATTTGCACACCCCTAAGA	59.933	20	277	217	493
59.717	24	GAACCGCCGGAAAAGAAT	60.014	18	268	5	272
59.967	20	CGGGAGGAATATCGCACTTA	60.053	20	202	954	1155
59.968	20	AGCCTAAGTAATGGCGCAGA	60.003	20	145	228	372
59.131	24	GAAGCCGGGTGTCAAATAAA	59.938	20	263	521	783
60.008	20	CAATGCCTAGTTTACCCCCA	59.817	20	252	644	895
60.365	20	TCCGGCCAAATTAAAAGAAA	59.538	20	105	778	882
60.111	20	ACCAACCTCCATTGAAGAGC	59.141	20	199	91	289
58.652	22	TATGCTCGCTGGATTACGTG	59.856	20	251	506	756
59.247	20	TTCCGTCTTTAGGCATGAGC	60.352	20	266	6	271
60.133	20	GACCCACGACCGTGTACTTT	59.891	20	263	66	328
59.434	20	TGTTGCCGTAAACAATGGTC	59.444	20	194	203	396
60.066	20	CAGATGTGGACGGGTCACTA	59.545	20	220	29	248
59.21	20	TATCCATTTGCCCTTTTTGC	59.907	20	249	226	474
58.145	20	TGGTTCGATCGTAATTGATCT	57.168	21	129	20	148
60.073	20	TCTTGGTGGGATTTGGAGAG	60.042	20	179	162	340
59.711	20	TCACTTCTTGGAGTTTGGCA	59.415	20	133	73	205
59.92	20	CAACCTCAGCTTCTTCCCAG	59.982	20	192	147	338
60.012	20	TGCAACCATTTTGTTGGAAA	59.946	20	247	37	283
60.172	20	ACGGATCGGAAATCCATAAA	59.23	20	212	270	481
57.239	26	CTTCGATGGAGTTCCCTCCT	60.586	20	187	7	193
59.903	20	ATGGGGTGAGACAAAGCAAG	60.111	20	272	121	392
59.926	20	AAAAGAGCTTGGGCCTCTTC	59.962	20	248	772	1019
60.096	21	CCGACACAAGCTGAAGTGAG	59.616	20	152	42	193
59.991	20	ACCCACTTTTCAAATCAGCG	60.11	20	125	2854	2978
60.081	21	GTTTTGGCATGCTAGTGGGT	60	20	146	70	215
59.894	20	CCCAATCTTTTCCACCCTTT	60.159	20	145	86	230
59.774	23	AAATTCCCGAAGAGCCATCT	60.039	20	258	49	306
60.265	20	TTCTCTGTTCTGGCAGTGGA	59.545	20	204	109	312
59.779	20	GGGCATGCCAAAAATATCAC	60.161	20	275	967	1241
60.118	20	CTGTGAAATTGCACGGCTTA	59.872	20	116	102	217
60.014	20	AGTTCAAGTTTGGGGGTGTG	59.861	20	189	343	531
59.831	21	TCAAGATTTAGGGGTTATCATTTG	58.508	24	113	170	282
60.05	20	CTTTCCTTGGGGACTGTGAA	60.081	20	195	5224	5418
59.978	20	TTTTGGCGGGAAAAATAGC	60.026	19	159	322	480
60.331	20	CTGAATTTGGAAGGAACGGA	60.044	20	248	523	770
59.756	20	CCTATGGTGGTATGGTGTGG	58.569	20	207	93	299
59.173	22	GTGGACGCTCCAAATTGTTT	59.978	20	143	63	205

60.288	19	GGCAACAGCTCTTACCGTTG	60.827	20	279	131	409
59.724	20	CACATCCTCACACACTCACACA	60.697	22	241	2630	2870
60.954	20	CCAACACAAATGAACCTGGA	59.389	20	215	19	233
60.011	20	ATTGAAACCGTGAAAACCGA	60.344	20	232	865	1096
60.439	20	CACGAACGGTATAACATCGG	58.917	20	272	706	977
60.119	20	CCCTCGTATGCAATGAATCTG	60.475	21	266	357	622
60.255	20	GTGAGGGGGTGACAGAAATG	60.363	20	268	39	306
58.851	20	CTGATTCGCTAGCTTCCCAC	59.978	20	119	20	138
60.721	20	GGAACCAAGTCTTCAGATGC	57.288	20	260	44	303
58.884	22	ACCGACAAAAGGTAGGCTCA	59.734	20	229	267	495
59.682	20	GCATCGTGTGAAGCATTGAT	59.685	20	138	219	356
59.273	20	TTGAAGGGAACGAGACCAAG	60.224	20	252	51	302
60.517	20	GGATTCCATCAACACCAACC	60.034	20	160	60	219
58.057	21	CTCATTGGAATTTTCCGGGT	61.042	20	269	914	1182
60.017	25	GAGCATTTGATGGAGGATCG	60.57	20	239	30	268
59.84	20	CTGCCCATTTTACCCTTTTT	58.113	20	111	866	976
59.931	20	CATTTCCTTCAAGCACACCA	59.691	20	247	102	348
60.885	18	CCATTTCAGTATTTGCCGGT	59.823	20	278	357	634
60.327	20	ATTTTCTGGCGACGGTACAC	60	20	158	1833	1990
59.706	20	ATGTTATCGTGTGGATGGGC	60.613	20	234	358	591
59.013	20	TCCCAATGATTGTTTGGTCA	59.75	20	213	750	962
60.14	20	CACTCACAGCCAACAGGGTA	59.745	20	148	1268	1415
59.801	20	TTCCAATTGCGAAAAGATTTG	60.061	21	180	62	241
59.779	20	ACTCCCAATGGATCGCTATG	59.917	20	245	2	246
60.134	20	TGAAAGCAGCATAAGCATGG	59.976	20	143	1304	1446
59.993	20	ATCTGGAAAACACGCCACAC	60.966	20	209	168	376
59.96	20	ATCCAAACGGCGAAGTGATA	60.469	20	187	60	246
59.976	20	TCCGGCAATCTCCTTAATTG	60.031	20	160	290	449
59.23	20	CGACACGAATCCAAAACTGA	59.691	20	276	1444	1719
60.058	20	TTGCAAACATTTTGAAGGACA	59.192	21	190	275	464
59.752	20	ACTGGACGGAAATCGGAAG	60.058	19	256	275	530
59.95	20	ACCACTGCATTCACTTTCCC	59.973	20	264	949	1212
58.676	24	TTGCTCGCGAGATTTCTTTT	60.096	20	269	649	917
60.11	20	CATGCCAAGTGGTGTGATCT	59.551	20	216	390	605
57.197	24	GGATGAGGTTGTATTGAAACTGC	59.891	23	142	59	200
59.917	20	CCCTAGCCTTTGCCTCTTTC	60.332	20	164	190	353
58.9	20	AGCGTTATTTTGCAAGGTCG	60.264	20	117	6	122
58.37	22	GGTGAGGAGGAACACGAAAA	60.088	20	253	14	266
57.719	22	GGGTGGCCCTCAATTTTATT	60.02	20	270	32	301
60.021	20	AACGGGGAAACATACGTCAC	59.717	20	209	896	1104
60.029	20	GAGCCTGACTTGCTTTCACC	59.997	20	256	299	554
60.36	20	TTTCTCTCTTGGTTGGTGAAGA	58.955	22	211	22	232
60.05	20	GCACCTATATACGCACGCAC	59.238	20	258	11	268
59.536	23	TTGACCGATCTCATTTGAAAAA	59.564	22	253	61	313
59.923	20	CCAAAATCACAATCTATCAATCCA	60.076	24	222	6193	6414
59.883	20	CGTATACTTGCGGGGTTGTT	59.883	20	223	657	879
60.603	20	TGAAATAGTAACCGCCGACC	59.96	20	244	174	417
57.238	25	CAAAGGCTCGGAATATGCAC	60.606	20	149	0	148
58.978	21	GATCAATGTTTGACGTCTCGAA	60.118	22	226	94	319
59.348	21	AACCCACTACCCATTCCCTC	60.052	20	142	0	141
59.877	20	TATTTGCCACCCAGAACACA	59.964	20	243	548	790
60.125	20	TTGAGCGAAAAGCCAAAGAT	59.96	20	152	3441	3592
57.439	21	TCAACTTTCGGAAGCGTACA	59.464	20	113	8	120
59.873	20	TGTCCCGTTTTCCTTGTTTC	59.948	20	242	117	358
59.787	20	CGAACATCGTTGCTGCTCTA	60.157	20	216	450	665
59.653	22	GAGGACGCCCAATGATAAAA	59.901	20	219	925	1143
57.054	25	CCAAACATGCTTCTCATGCT	58.877	20	210	21	230
58.412	23	ACTGGAAGAATTGGAGGGCT	60.074	20	207	105	311

58.963	22	CTTAAGCATGCACGACTCCC	60.796	20	262	745	1006
60.066	20	CTTCTTCCCCGTTTTGTTCA	60.081	20	259	1002	1260
59.871	20	ATTCCTCCTTTTCAGCACCC	60.443	20	275	10	284
59.9	20	TCCGTCTGCTTGGAGAACTT	59.989	20	232	866	1097
59.999	20	CCACTCTCTCTCCTCTTTCTCTC	57.98	23	151	641	791
60.268	20	GCCTCTTGAAACTCTGCCAC	59.997	20	274	269	542
60.074	20	TTCGCACGCTATAAAACAAGAA	59.916	22	130	668	797
60.388	20	CCTCCAGACGTGAAGAAACC	59.697	20	266	1520	1785
59.957	20	TGCCTCATTTGTGTTAATTTGG	59.868	22	231	41	271
59.931	20	CCTTTCCAGGAAGATTGTGG	59.521	20	189	73	261
60.386	20	TTTAACCTGTAGGGCACCCA	60.357	20	200	1611	1810
60.895	20	TTGCGCCTAAGGAGGAGTTA	59.975	20	247	1938	2184
59.52	20	GGATAGGCTAGATGACGTAGATG	57.085	23	216	112	327
60.036	20	TGCATTGGAAAAAGTTGTGG	59.561	20	240	309	548
59.934	20	TGGAGTTTTTGCTTTCTGGG	60.22	20	274	1719	1992
59.88	20	GGGAGTCTTTCATGCCACAT	59.934	20	157	230	386
59.88	20	TGGAGTTGGTGGTGTCTTCA	60.129	20	145	1030	1174
59.319	22	TTGGAACGCCACTAGTTTCC	60.11	20	276	116	391
59.791	20	GGTGTGTTAAATGCGTGAGG	59.05	20	272	3166	3437
57.063	27	CACCGTGCATTACAAGATGA	58.129	20	182	8	189
59.835	20	CAACCCTACCTCCTTCTCCC	59.928	20	199	18	216
58.749	20	GAAATCTGAAGTTGTTCCCGA	59.16	21	268	57	324
60.156	20	GAGGCGCGATACACTACACA	59.895	20	194	100	293
59.873	20	TCTGAAAATCAAAGGCCCAC	60.051	20	190	2038	2227
59.239	20	AGTGGGACCAAAATGCAAGT	59.454	20	231	368	598
61.136	20	AAGCTGTTGACTTCAGCGGT	60.058	20	269	10	278
60.214	20	AAAGGGAAAAGACAGCAGCC	60.743	20	272	94	365
59.871	20	CCACATATTCATTTCCCCCA	60.384	20	110	2405	2514
59.829	22	TGGCATTTCAGCTCTTGTAGC	60.537	21	203	26	228
59.966	20	GGCTGCAGAAGTGTTGATGA	59.992	20	201	4485	4685
60.066	20	TGTTCAGCTATGTTTGCCGA	60.401	20	144	88	231
59.773	20	GTTGGGGGTTGGGTTATCTC	60.422	20	235	0	234
59.547	22	CCCAAACTTGGGGAAGAAAT	60.159	20	180	741	920
58.775	21	CGATCGTGAGAGGGAGAGAG	60.088	20	261	108	368
59.67	20	GGTGGGTGCCTAGGTTTTCT	60.361	20	185	83	267
60.051	20	ATACGAACACTGCACCACCA	60.032	20	119	529	647
60.114	24	CAAAATTAGTGTCAGCACCGAA	60.166	22	148	1493	1640
59.803	20	GCAATATCCTCTTCAACGCC	59.674	20	267	149	415
60.035	20	CCATTCCATGTCACAAACGA	60.367	20	149	789	937
60.155	20	CAATCTTAATTCCGTCCCCA	59.756	20	127	492	618
59.923	20	CTCGGGTCATTGGATTGAGT	59.927	20	232	43	274
59.859	20	AAGGGAAGGGGAAGTGAAGA	60.045	20	217	98	314
60.005	20	GAAAGGAAGAATGCGAGTGG	59.813	20	109	383	491
58.955	22	TAAGTTGGAGTGGAGTCGCC	60.255	20	224	21	244
59.006	20	GGTTCAAAAATCCGGGAAAT	59.999	20	217	467	683
59.774	20	AAAATGCAGCAAAGGGTCAC	60.118	20	278	231	508
59.34	23	CTTTGTGACAGGGTTCCGTT	60.005	20	146	43	188
59.946	20	CCTCCTTCTCCCAAAACCTC	60.045	20	105	5	109
59.985	20	TCCCTAGTTAGCTCCTAGATATTG	59.225	26	204	192	395
59.966	20	ACAAAGTGGGAGGGCTTTCT	60.11	20	173	2759	2931
59.533	20	CAAGGATGAGATGAGGGCAT	60.034	20	161	70	230
60.323	20	ACCTATGGTGGTATGGTGTAGAG	57.076	23	256	22	277
59.433	24	CACATTTCCCTCTCCCTTCA	60.042	20	219	42	260
60.46	20	GGGAAAATAGCTACTCCCATTT	57.766	22	267	588	854
59.668	21	TCTTGAAAACTCCAAGCCCA	60.745	20	135	1	135
60.153	20	GGATTTCACCTTTGGATGGA	59.727	20	147	33	179
59.881	20	TTATTTGCACGCGCAGTAAT	59.379	20	264	25	288
58.816	23	CGGCTTTCTCTATCAGCCAG	60.11	20	240	8	247

58.068	23 CCTCACCACCTCAAGCTTTC	59.844	20	199	119	317
60.323	20 GAGTCCAATTGAACCTCCGA	60.05	20	224	1094	1317
58.992	21 CACCAACTGCTTTATTGCCA	59.729	20	235	469	703
59.577	24 TGATGAACTCGTCAATTGGAA	59.112	21	241	430	670
59.369	20 TGTTGGGTTGGTTTGACAGA	59.976	20	239	22	260
60.096	20 CACGTGTGGACATCCATATCA	60.256	21	271	87	357
57.092	21 ATGCCGTGTAAATCCATCAA	58.846	20	280	445	724
59.916	20 TCGGACCAAATTACCCTTCA	60.301	20	277	22	298
59.901	20 GCCAAGAACAGACCGAATGT	60.119	20	113	84	196
60.032	20 TTTGCAAACCCTACTTCACTCA	59.785	22	249	52	300
60.203	20 TCTCGAGATATTACTGGCGTGA	59.867	22	187	2	188
59.939	20 GCCCTATCACAACTCCGAAA	60.074	20	276	360	635
59.743	21 CGATATAAGCAGTCGCCACA	59.856	20	269	0	268
60.17	20 TCGAAATCAGCATATCAAAACAA	59.616	23	268	42	309
59.215	23 ATTGTGCCCCTATTCAACCA	60.192	20	209	1	209
57.643	26 TTTGTGTGCATGGAATTTTTG	59.453	21	244	3	246
58.961	23 CACAAATTTGGGTTGCCAG	59.949	19	161	135	295
60.203	20 GAATAAATGCAATCACGCCC	60.297	20	262	398	659
59.411	20 CAAAATTTGGACGGGAGAAA	59.91	20	267	14	280
59.494	22 AGGCTTGAGTTTCCTCACGA	59.989	20	125	5	129
59.702	22 GCAAGATAAGGGAGTTGGCA	60.214	20	145	597	741
60.375	20 TTACATCAACCCGTCAACCC	60.615	20	277	796	1072
59.593	20 CCAGCGCAGACAGAATACAA	60.011	20	279	41	319
59.715	20 TTATGATCGTCGTCGTCCAA	60.073	20	269	90	358
59.002	23 TTCGTGTATTAAGGTCACGGC	60.011	21	187	654	840
60.319	20 AGCCAGAGACTCGGATTCAA	59.95	20	190	905	1094
60.14	20 TATGCCACAGTCCCAATACG	59.42	20	253	1099	1351
59.962	20 CCAACCTCCATTAACAACCC	59.146	20	218	17	234
60.042	20 GACCGATCGTGAGGCTTTTA	60.214	20	255	397	651
60.06	20 GGAGCTGCTCTTTGAGATCG	60.24	20	274	1006	1279
59.609	20 CCCGTATATTCACGACTCGTTT	60.257	22	241	304	544
59.888	20 GCAAATTATTCACACCCGCT	59.967	20	144	5421	5564
59.182	20 TCGACACATTCAGGCAAATC	59.654	20	166	3	168
60.206	20 GCCGTCAGTAGCTTAATCGG	59.867	20	248	1948	2195
59.677	20 ATTTTGTTGAGGGGTCGATG	59.79	20	274	2458	2731
60.02	22 TTTGCTTAAAATGGATCAATGG	58.98	22	264	85	348
60.142	20 AACATCAAAACTGCCGAAGC	60.257	20	246	219	464
59.495	21 ATTTCAGTTTGGAATCGGCA	60.448	20	278	402	679
60.32	22 CCAAGCCACACATCTCTCAA	59.831	20	262	245	506
59.938	20 TTCCGCACCAAGATTTAACC	59.938	20	276	40	315
60.042	20 TGCGTTTTGACGATATATAGTGTTT	59.092	25	151	608	758
59.654	23 CACCCCACCTTAACCTTTGA	59.824	20	219	12	230
58.974	23 TTGCAGTAGCTTGTGAACGG	60.05	20	222	34	255
60.261	20 AAGCTTGTCCGTCGATTTTG	60.249	20	201	115	315
58.311	23 AGAGGCAGCATACCCATCAC	60.104	20	143	1983	2125
60.11	20 CCATCTTTCTCAAATTCGCC	59.645	20	136	96	231
59.996	27 TTCTACCCATGCAAATCAAGTG	59.996	22	121	65	185
60.226	20 GATGGCTCATTTGTTCCGTT	59.939	20	225	85	309
58.697	20 TGGATATTGTTGCCGTTTGA	59.93	20	265	0	264
59.993	20 TCGCCTTCACTCTCACACAC	60.03	20	125	828	952
60.68	20 ATGCCAACTTTTCCTCATGC	60.081	20	279	1771	2049
59.767	20 CAGCATACAGCAGTTTCGTTT	58.121	21	136	1059	1194
58.741	20 AATTTCACCAAGATGTCCAAGA	58.554	22	102	20	121
60.11	20 AGTTTTGGTGAAGACCGCAC	60.156	20	192	52	243
60.044	20 GAATTGCGTAGCCTCCAAGA	60.352	20	137	185	321
60.081	20 CGTTGCCGGTTAAAGCTAGT	59.424	20	267	4	270
59.859	20 GTGAGCACCCCAGATTGTTT	59.973	20	240	1492	1731
59.92	22 AAATTTTATGGGACGGAGGG	60.013	20	251	368	618

59.866	21	GAATCCAGAAGGGCAGTTGA	60.195	20	182	3235	3416
60.015	20	ACGCGCGTTTTTAGGGTTTA	61.796	20	124	300	423
58.847	20	CCTCGACTTGACAACTTTGCT	59.529	21	280	105	384
57.397	22	AGGTTTTTCAAACGATTGCC	59.067	20	196	702	897
60.02	20	AGTGGTAGCACGACATTCCC	59.997	20	219	2194	2412
59.595	21	ACAGCAATCATCCAACCACA	59.967	20	211	523	733
59.12	20	TTTAAGGGTTATCACCTGATTTTC	57.757	24	144	72	215
59.886	21	CCAATCTTGTTCGGGTTCTT	59.028	20	200	11	210
59.756	20	TGAAAGCGATTGTAAGCGTG	60.014	20	220	102	321
60.177	20	TGCGTTTTGACGATATATAGTGTTT	59.092	25	274	1010	1283
60.015	20	TTCCCTATCTCTCCCAGCAA	59.767	20	100	3204	3303
60.412	21	AAACTCCAAAGTCCAAACTCCA	60.012	22	128	0	127
60.202	20	TTTCCCTCTCCATCTCTAGCA	59.017	21	263	1095	1357
59.66	23	AGAATCTGCTTTGCCCAGAA	59.955	20	257	449	705
60.578	20	ACCATCACCATCGTCACCTT	60.246	20	160	48	207
60.033	21	CCCTGCACCCTTTTAAATCA	59.931	20	206	78	283
60.21	20	AGGTGGTGGAGTGGTGTGAC	60.915	20	227	111	337
60.243	20	GTCTGCAAGAGAGAGGCCAG	60.284	20	233	539	771
59.916	20	TTTTGATGATATATAGGTGTTTTGA	58.782	27	238	396	633
60.053	20	AACGGACGAACGATGAAAAC	59.978	20	175	3243	3417
59.706	20	GACATGTCGCTCATGTCACC	60.13	20	145	4254	4398
59.964	20	CCTTTCTCACCTAATTACAACCC	58.153	23	203	3329	3531
59.982	20	TGCACGATTTGACTTGCCTA	60.401	20	203	685	887
60.104	20	TCTACGACCACAATTTGTCCC	59.845	21	165	521	685
60.074	20	TCAGCCACCACCCTAGTAGC	60.277	20	265	343	607
59.816	20	CAAATATTAGGCCAAAAACGC	58.687	21	202	2456	2657
58.643	20	TGAATTTCCATCGTTGATTTGA	60.302	22	141	133	273
59.996	20	GGAGGTGGAGGAGAGAGAGG	60.336	20	111	469	579
60.263	20	TCATCATAATATTGATTTTTGCACT	59.703	27	116	896	1011
60.157	20	CAAACTAATAGCAATGGCCGA	60.102	21	134	3808	3941
60.12	20	CCAGGTTTTGGAACTTGGAA	59.942	20	261	1439	1699
60.088	20	GGCTCAAAAGACAAGTCCCA	60.232	20	238	136	373
59.967	20	GTGGGGATGGGAGGTTTATT	59.881	20	200	1076	1275
60.027	20	TAGAGGGGCCTAGTGGGTTT	59.955	20	254	17	270
60.006	20	GTTATTTCGGGGTCTGGGAT	60.017	20	262	2433	2694
58.861	22	ATTTTGTGAATTTGGCCGTT	59.32	20	140	356	495
60.243	20	GGGCCATAGATCTTGTGGAA	59.894	20	220	539	758
60.401	20	CCTTGAATCCAGGTTGAGGA	60.042	20	185	30	214
59.101	20	CCCAATTTCACCATCCTTCA	60.692	20	178	168	345
60.074	20	GAGTTGAGGGGTGGTTGAAA	59.943	20	178	70	247
60.137	20	CCAACGGGTAGATACCCAAG	59.308	20	280	685	964
59.803	20	GGATTAGGTGTTGGCTGGAA	59.933	20	206	501	706
59.955	20	CCAATTCCATCAAATCCAGG	60.126	20	184	86	269
60.545	20	GGTTCGGAAAAGGTTAGGCT	59.593	20	262	42	303
60.173	20	CGACTTGTCGTGGTTCGATA	59.716	20	239	87	325
59.933	20	CGAGAAAAACAAAATTATACGAG	59.565	26	229	610	838
58.019	20	CTTTTCGTTTTTGCGTCGAG	60.904	20	169	80	248
60.013	20	GCATGTGAGGATGTTTGTGG	59.967	20	139	1804	1942
58.874	20	CAAGAGACGCATTAAGACGC	58.677	20	217	1327	1543
59.856	20	TCACACCAAGAAGGGGACAT	60.363	20	204	108	311
60.027	20	ATTCCCCATCATCAAACCAA	59.991	20	188	83	270
60.291	20	TGCGTGAAATCGAAAGTGAG	59.988	20	185	466	650
59.504	25	GCTCGAGTTTTAGTGTGGGG	59.734	20	272	150	421
58.856	21	TTGCTCACCCCTACCTATCG	60.088	20	199	26	224
59.859	20	CACAAGAAAATTATTGTCGCTCA	59.307	23	270	584	853
60.008	21	GATCCTGGTATCCATCTCGC	59.469	20	190	630	819
60.003	20	AAGACCCCATTTCCCCTAAA	59.639	20	265	1382	1646
59.597	20	GGTCTCACGGGTGGTTTTTA	59.83	20	242	1560	1801

59.931	20	CACCGCGTCTTTTCACTACA	59.904	20	217	2311	2527
59.601	21	AATCATGGTGCACGAAATTG	59.4	20	183	411	593
59.962	20	GGTTGTGGTGGAGCAAAGTT	60.012	20	160	4427	4586
59.969	20	CTCTTGACTTCTGATCCGGC	59.95	20	161	88	248
60.074	20	CGAGATTCTCTCTCGCTCTCA	59.981	21	238	253	490
58.77	23	GGCAAGCTTGGGTATGTGTT	60	20	256	2	257
59.711	20	TATGTGTTGCAGGGGATTGA	59.924	20	159	585	743
58.823	20	GTTGGTGCTTGATGGTTGTG	60.008	20	133	2022	2154
60.298	21	CCAAACGACATTATGACGCA	60.523	20	268	173	440
59.938	20	TTCAATATCCGCCAGAGTCC	60.036	20	196	2273	2468
58.072	21	TGTGTCGCGAATTTTGAACA	61.233	20	212	8	219
59.839	20	GCTCTTCTCAACCCTTTTATGC	59.398	22	244	95	338
59.111	21	TTGTGCCGCTTGTAATATGC	59.731	20	236	43	278
59.859	20	GTCACCTGCTCATGTTGCAT	59.714	20	214	257	470
58.462	20	TTGGTAGGAATGGTTCGAGG	59.926	20	264	0	263
59.922	21	AATTCTTGGGGTTGATGACG	59.79	20	222	556	777
60.067	21	GAAACACATCGTTTCCTGGG	60.353	20	251	76	326
59.881	20	TTTCCATCGGACCAAGTCTC	60.05	20	238	954	1191
60.194	20	GTTCAAATACACGTCGCCCT	60	20	212	19	230
59.827	20	CAAAAGCACAAATTGGGAAA	58.649	20	242	45	286
60.064	21	TTAACCTGCAACGGTCAAAA	59.202	20	217	1470	1686
60.038	20	CTCTAGAGTGTTTGCGGTGC	58.677	20	230	69	298
59.647	23	ACGTGGAGTTCCAAATGCTC	60.119	20	270	3	272
59.459	22	AGTATGCCGTTTTTCCTCCA	59.569	20	280	1319	1598
60.556	20	ACCTCCTCTCCGTCGCTAGT	60.414	20	252	2	253
59.243	20	TCTCTCCCTTTTCTCACGGA	59.92	20	136	832	967
59.997	20	TGGTTATTACTGGAACGCGA	59.182	20	110	784	893
59.928	20	TCTTCAAAGGAACCGACTGG	60.224	20	280	75	354
59.343	20	CCCGGGTTTTCTTTTTGTTT	60.19	20	199	1399	1597
60.051	20	CCCCAAATGGAGACGATAAA	59.756	20	180	4639	4818
59.953	18	AGGTGACAATTGTGATAGCCA	58.09	21	280	123	402
59.859	20	ATTTGTACGGCGTTTCCTCA	60.502	20	154	661	814
60.734	20	GGTCAACTTTCTGCACACCA	59.726	20	212	606	817
59.615	20	GTGGTGGTATTTGGTCCGAT	59.532	20	260	31	290
59.883	20	AACGCTCCAGATTTCATGCT	59.843	20	270	435	704
60.031	20	CAAGCAGACTAAGCATGGCA	60.157	20	239	79	317
60.177	20	TAATGGCGAAAACAGGAAGG	60.067	20	197	149	345
57.557	25	CTTTAGAGCGCCTGCAAGAC	60.292	20	267	19	285
59.859	20	ATTTTCCCAAATGCAAGCTG	60.074	20	250	252	501
57.379	21	CGCTTATATCGTGTCGGGTT	59.982	20	100	36	135
59.948	20	CCACAGCTATGCCTAAGTGC	58.555	20	188	3269	3456
60.411	20	GGCATTCAAATCAACCATTG	58.82	20	233	81	313
60.096	20	GGTCGGCTACATGAACCAAA	60.894	20	116	32	147
60.112	20	GTAGGAGGAGTGATCGGGGT	60.336	20	278	737	1014
57.111	27	ACTTCAACAGCCGCAAAAAT	59.752	20	175	278	452
60.132	20	GAGCAGTTATCACCGGATCA	58.672	20	237	29	265
59.707	20	AAAACGGGGCTAAGGATTGT	59.835	20	246	277	522
58.743	25	GAACTCACAAAGTATGGGGCA	59.985	21	127	3	129
59.215	21	AGGGATTCGAGTTGCTTTGA	59.813	20	263	5193	5455
59.033	21	CCCCATGAAGCAGAGATGAT	60.034	20	117	757	873
59.871	20	ATGCACGTGAATGCTTTATTT	57.351	21	190	34	223
59.187	21	ACATTCTGGAATGGTTCCCA	60.173	20	185	1247	1431
59.905	20	TGGTGATGTGTACTTTTGGCA	60.019	21	188	1936	2123
60.324	20	AGGACTCACTGAAGGAGGCA	59.986	20	279	662	940
59.903	21	TCTTGCGTTTGATTCGTTGA	60.379	20	225	369	593
58.732	21	GGAGCAAGAACTTGAGGCAT	59.434	20	240	170	409
60.634	20	CCGATTTTGTTCCTTTTCAA	57.728	20	230	642	871
60.345	20	TGTCTTGAGGGGAGTGTTGA	59.23	20	278	352	629

60.201	20	GTGACATTTTTAGGCGGGAA	59.938	20	195	1183	1377
60.332	20	AATCTTGAAGTTGTTCGCGG	60.249	20	221	17	237
60.191	26	AAGCCTAACAAGTGGATATTAAG	58.116	26	166	1299	1464
57.905	27	GTCGGGCAATGATTCTGTTT	59.939	20	260	9	268
60.089	20	CAGGTAAAACCTAAAATAGCGCC	60.36	23	258	4905	5162
60.324	20	TGGTTATTACTGGAACGCGA	59.182	20	188	1106	1293
59.502	24	AGGCATACTTGGTTGATCCG	59.955	20	258	10	267
59.989	20	CACTAGGGCTTTGCTGCTGT	60.592	20	161	2868	3028
59.366	20	AGCACTCCCTTTTACCACCA	59.592	20	246	68	313
60.395	20	TCTTCGATTGGAGTTCAGGC	60.34	20	241	552	792
59.803	20	AAAGTTAAGTAGGACTGGATCCA	59.856	26	100	26	125
58.521	26	CAGATCTGATGGCCCAGATT	60.034	20	105	18	122
59.679	20	CCTTCTCTGGCTGTTGTTCA	59.007	20	236	1349	1584
59.919	20	TGAACTAATCAAGTTCCGCGT	59.761	21	170	53	222
61.129	20	AATTTCACCCTGATTCCAATG	58.751	21	279	43	321
59.175	20	TCTTCGCTGTCTCTCAGCAA	60.008	20	228	1226	1453
59.993	20	AAAGGGAACTTCCTGTTTTAGC	58.034	22	174	93	266
59.957	20	TGGCTTCAGTTGCAGAGAGA	59.855	20	162	84	245
59.916	20	ATCGGTTATTACCGGATCGC	61.031	20	206	24	229
59.931	20	CTGGGCCCACACCTAATAAA	59.817	20	145	159	303
60.84	20	CCTCTCTGCAACACCATTCA	59.831	20	197	505	701
58.695	20	ACCATCGAACCCCACAAATA	60.051	20	217	13	229
60.048	21	GGGGTGGGGGTATGTTAGTT	59.805	20	219	9	227
60.052	20	ATTTCTCCTCCATCATCCCC	60.096	20	127	261	387
60.257	20	CGAATCAGAAAGAACGTAGCG	60.025	21	180	31	210
59.837	20	GCAAATCAAACCCTTGTCAAA	59.967	21	213	717	929
59.707	20	ACTTCCTCTGGCATCGCTTA	59.978	20	152	1045	1196
59.924	21	GCAGTTGGAGAGGGTGAGAG	59.986	20	206	119	324
59.723	20	TGCACCTTGTGCAGATTTGT	60.31	20	175	598	772
59.878	20	CACGGTTTGGGCTTAATTTTT	60.219	21	279	467	745
60.051	20	AAATCAAAAGCCCACAATGG	59.801	20	128	64	191
59.968	20	CATGCACAGATTCCGTCACT	59.707	20	215	303	517
59.607	21	CATGGTGCATGAAATTGGAG	59.924	20	130	134	263
60.183	20	AATCATCCTTTCGCAACTGG	60.074	20	220	471	690
59.897	20	ATGTGCGTGTGAGTGTTCGT	60.236	20	199	105	303
57.252	22	TCACATGAGATGATTAATTGGACA	59.343	24	181	64	244
60.452	20	TGGAATAACCCAAGCCAAAG	59.931	20	179	2622	2800
59.986	20	TGATTCGGAGGAATACGAGG	60.029	20	199	421	619
59.05	20	AACAGCAAATCCGAGACACA	59.293	20	150	552	701
59.078	22	CCATTTTCAGGTCCTCACCA	60.892	20	125	31	155
59.679	20	GGAGATCAGCTACGGTCTGC	59.981	20	238	43	280
60.221	20	TGAAACTGCTGTATGCTGAGTTAT	59.424	25	170	312	481
59.231	23	TTGGCAAGAAAACAACAGCA	60.415	20	227	37	263
60.067	21	TTCACAAAGAAATCAGCACGA	59.454	21	186	70	255
60.249	20	TCAACGGTTTAAAATTGTTCCT	57.74	22	171	129	299
58.359	20	TCCATCCACAGCAATGAAAA	60.049	20	149	342	490
59.887	20	TTTCACTTCGATCCCACCTC	60.05	20	128	65	192
59.53	20	ACGACAACAGCAACACAAGC	59.953	20	240	216	455
60.104	21	GGAGACAGAGCCTGTTGGAG	59.986	20	196	15	210
60.315	20	CATTGGGTGGAAGTGTAAAGAA	58.994	22	172	540	711
57.989	27	GCAGCCTTATGTGGAGGATG	60.624	20	225	29	253
59.539	22	GGTCAGTTTGTCCGAATCTTG	59.583	21	105	256	360
59.162	20	CGCTGAAATTAGTTGAGGCA	59.062	20	272	133	404
60.24	20	TCATGTACCCCCACATGTCA	60.665	20	275	283	557
59.542	20	TTGGGTGTAAGACATAGAAGGAA	57.815	23	153	898	1050
59.202	21	GCGAAAAACTCGAAAAACCA	60.223	20	256	1554	1809
58.81	24	TGGATGATGTGATGTTTTTAGAGG	60.237	24	176	11	186
59.685	20	AAACTCAAATCCGAGATCTAATG	59.874	24	280	32	311

60.074	20	CTCAACGGTATGCTCGGATT	60.096	20	235	490	724
60.136	20	GAAAACCTGGAGTCAGCTCG	59.989	20	265	427	691
59.803	20	GAGAGGAGAACTGCGTGAGG	60.135	20	161	74	234
60.31	20	CGCTTCTTCGCTATGGCTAC	60.138	20	218	393	610
58.9	20	GGAAGAAGAAGCTCGCAAGA	59.836	20	200	3301	3500
60.05	20	AAGCCGATCGAGTTTTTCCT	60.208	20	181	120	300
59.726	23	AGAAGACGGAGAGCCACAAA	59.989	20	165	1310	1474
60.164	23	CAATAGCGTGTGTTTTGCGT	59.799	20	273	587	859
59.976	20	CCCGGTTTTGACTCTTTGAC	59.569	20	151	450	600
59.891	20	ACCCTCGAATGATATGCTGC	60.066	20	169	26	194
59.732	22	AACCGGTTAAAAATCGGACC	60.055	20	248	208	455
59.803	20	GCATGGCATGAAATTGTTGA	60.476	20	273	118	390
60.129	20	TTTTCCGGTGATGGATGAGT	60.317	20	174	449	622
59.729	20	TTGTCTAGCAATCTTCGAGTTTT	57.422	23	280	135	414
59.272	20	TCGACAATGTTAAAAATCAAATAA	60.026	27	171	65	235
60.162	20	TCAAGGAGTCACAACGTGAAA	59.324	21	179	132	310
60.439	20	CTGATGAACAAGCCGAACAA	59.84	20	278	532	809
60.246	23	ACGATCGTAAGGCGAAATTG	60.096	20	104	4	107
59.955	20	TACCCAACCCACTAACCCAA	60.081	20	171	136	306
57.599	24	ACTTTCAGCATGGAAGAGGG	59.284	20	120	0	119
59.544	23	CAAATGCAATGACTGTTGGG	59.964	20	208	30	237
59.545	20	AGCGGTTATTACCGGATCG	59.93	19	249	2231	2479
59.926	20	GGATACCCGAGCAGTTGAAA	60.074	20	248	2251	2498
59.847	20	CCAAGATCAATGGTTCCTAAGTG	59.879	23	128	1272	1399
58.941	21	ACAATGCGAGTGCATTTTTG	59.735	20	186	111	296
59.571	22	TGTTGATGTCCGCAAAACAT	59.972	20	174	79	252
59.178	20	GACGAGATCATGGCTCGATT	60.189	20	265	14	278
61.434	20	CAGCTGAAAGGAGCCATCTC	60.096	20	275	44	318
59.883	20	TATATTTGCTCTGGCAGGGG	60.053	20	217	681	897
59.662	20	GGATGACATAACGTTCCGCT	59.962	20	186	28	213
60.11	20	CTGGAAGGAGTGGCTAGCTG	60.149	20	159	1248	1406
60.636	20	TCATAGGTAAAGCCGCAACC	60.096	20	211	23	233
59.792	20	CAATGCTTCCATTTGCACAC	60.119	20	264	91	354
60.288	20	GGCTCAACAACACAATTCCA	59.547	20	262	16	277
59.868	20	GCTTCATGAATGGCATGACT	58.674	20	247	44	290
59.989	20	TGCAGTTCATCTTTGCCTCA	60.539	20	122	1134	1255
59.955	20	AAGAAACAAACAGGGTACGAGG	59.56	22	262	264	525
59.972	20	TTGGTAGGGGTCAGCACAAT	60.375	20	225	115	339
60.096	20	TTCGTTATTTGATTGGGGGA	60.124	20	235	1199	1433
59.992	20	AGGTATCGTTCGCGCTGTAG	60.428	20	170	105	274
59.752	20	AAGCAAGAAGGTTGCAACTGA	60.045	21	150	353	502
59.496	20	TCATGTCAACTGTCGAAGGG	59.676	20	120	7	126
59.933	20	ACCTGTCTCAATCCGCTCAC	60.269	20	188	1434	1621
58.947	20	GTCCGGAACAAGGGAAAGTT	60.34	20	236	2	237
59.96	20	TAGCCTAAGTCGGGACAGGA	59.83	20	256	600	855
59.946	20	GCATGATGCAGCCCTAGATT	60.207	20	224	1919	2142
58.864	20	GGAGGGTGAGATCAATCGTG	60.475	20	184	61	244
59.933	20	CCTCCCCGATATTTTCAACA	59.756	20	222	8	229
59.997	20	TCGACTTGTGCAATCAGTCC	59.837	20	246	753	998
59.984	20	ACAAAAATGCCCTCGTATGC	59.967	20	241	22	262
57.857	24	TTTTTACCCTTTCCGCTTCA	59.693	20	210	48	257
59.526	20	ACGACACTCGAATGGAGGAA	60.656	20	244	241	484
59.763	20	GTGTGTGTGCGTGAGTGAAA	59.321	20	184	426	609
60.049	20	CTAGCCGTTGGTGGGAGTAA	60.125	20	148	463	610
59.442	23	CCACAACTATGTGGGAAAAA	59.71	21	208	405	612
60.323	20	CACTCGAAAAAGGCATCCAT	60.074	20	193	2588	2780
58.826	23	TCGTTTTAGTTGGCCATAATCT	57.848	22	202	286	487
59.91	20	TTTTTCAGCACCACTTCACA	57.867	20	181	114	294

59.592	20	GCAGACCAGCTTTTACTGGG	59.875	20	192	454	645
60.249	20	GGGATGACAGAATGAATGTGAA	59.797	22	203	507	709
59.881	20	AAAGAGAGCCACGTGTGTGA	59.467	20	202	134	335
60.089	22	ATCGTTTTCAAAATCAGGCG	60.074	20	238	207	444
58.694	22	ACAGCGCGGAAGTTACAGAT	59.904	20	240	26	265
59.369	21	AAATGCCCTGCTGTAGGAAT	58.672	20	209	372	580
59.964	20	GACATCGTCGTCCCTGCTAT	60.104	20	235	1109	1343
59.978	20	ATGCTTAATGTGCATGTGCG	60.697	20	280	1932	2211
59.988	20	CGCTCACAATGATGGATACG	60.096	20	121	5036	5156
59.245	20	GGGTCAGGGGGTTAATAAGG	59.527	20	129	468	596
59.845	20	TGAACAAATTACACAAACAAAAC	60.54	25	129	521	649
59.335	21	GCAAACAACCAGCACAATCA	60.709	20	174	1587	1760
61.184	20	TCGTGGAGTGAGTGGAAGTG	59.864	20	273	112	384
60.194	20	ATACACGTTGCCCCTCAATC	59.82	20	196	847	1042
59.78	20	ACGCCTGAATATCGGTCATC	59.923	20	243	221	463
59.923	20	TCCATTCCGAAAATCAAAGG	59.872	20	116	24	139
60.378	20	GCCGACCCATTTAAATAACG	59.323	20	122	28	149
60.096	20	GTGGTGACAGTTCGATGTGG	60.005	20	163	2967	3129
59.78	20	GGGAAGATAAGACAGCCACG	59.694	20	217	20	236
59.735	20	TGAGCCAACTGAAAACACACA	60.331	21	119	2849	2967
60.238	20	CCATGGCCTAGCTTTGGATA	60.053	20	167	199	365
59.706	20	GCATCTTGGCTCATGTGATG	60.233	20	162	302	463
59.91	20	TCCCTGTCCTTTTTCCCTTT	59.912	20	144	584	727
58.294	22	TGCAAGCATCTTTTGTCTCG	60.134	20	215	11	225
57.487	25	GTTTGTTCACCGGAATCACC	60.218	20	249	19	267
59.767	25	ACGTGAGGTGAGGGATGAAG	60.112	20	271	46	316
57.085	26	TGGTTGTGGTTTGGTTTCTTC	59.861	21	222	1	222
60.073	20	ATCATCTCGGGGTGCAATAG	59.917	20	214	18	231
59.96	20	CGGGGTATTACATAAATGATGC	58.285	22	206	27	232
59.727	20	TGAAGGTGTTTGTGGGTTGA	59.976	20	136	5	140
59.862	20	GAGTCTGCCACGTGTACCAA	59.751	20	204	368	571
58.999	20	TTTTTGATGAGCTGGAGCCT	59.955	20	258	3989	4246
60.266	20	GGGCCGAGATTTGTAGAGGT	60.464	20	240	96	335
60.011	20	GGTCGATTCTTTCCCCTTTC	59.881	20	150	994	1143
59.926	20	GTGGGGGCTTAACAAAGTCA	59.971	20	187	397	583
60.24	20	CCAAAATCTAATGCGCGTCT	60.23	20	245	970	1214
59.072	22	AATGTGGGGTGCGATTTTTA	60.188	20	256	1949	2204
60.331	20	TCGAGGCGTTTTCTTGATTT	59.823	20	203	778	980
59.829	20	GCCAGCTTGTTTTGGGATAA	60.074	20	202	252	453
60.481	20	TGGTGTCTGAACAGCAGAGG	60.022	20	272	164	435
58.774	20	ATGACTTCGCCATTTTCCAC	59.939	20	280	216	495
60.051	20	TGTCCCAAAATCGTGTCTCA	60.088	20	264	15	278
60.281	23	GGATAGGTTGAAACTGCCCA	59.933	20	278	49	326
59.691	20	TGCGCATCTAGCTTGAGAGA	59.995	20	280	523	802
59.37	21	CCCCGATTCTTTTAGCCTTC	60.034	20	147	121	267
60.11	20	GTGACCGTTGGTGATGAGAA	59.525	20	189	1758	1946
58.451	21	CGACCTGGTGGGTTGTTCTA	60.943	20	268	1	268
59.971	22	GTGTGATTGGAGGGTTTGCT	59.973	20	122	14	135
59.059	20	CATCAATGGCCTGATTTGTTT	59.815	21	166	97	262
61.019	20	CCTAAAACACGACAGGGGAA	59.964	20	261	60	320
59.716	20	ATGACACGCATAAAGGGACC	59.82	20	240	249	488
59.517	22	AGCGGAAGAACAAAAACGAA	59.861	20	223	6	228
60.601	20	AACTGTGGCAAGATCCATCC	59.934	20	122	33	154
59.967	21	TTACAGATAACCGTTCCCGC	59.96	20	225	44	268
59.801	20	CATAAAATGGACACGCACCT	58.502	20	132	79	210
60.437	20	CACACACGCGCATATACAAA	59.211	20	107	1637	1743
60.187	20	AAGTTAAGCGTGTTTGCGCT	60.082	20	173	1313	1485
59.203	20	TCGGATTTTTATAGGCTTCTTCA	59.285	23	278	1344	1621

59.847	21	TCAATCATGAGCGTCCGTAA	60.22	20	138	14	151
59.766	24	CGAAAATAGCCAAGTCGGAA	60.202	20	268	1	268
59.801	20	GCTTTCAGGGTTTAAAATCGC	60.089	21	277	222	498
59.851	20	TCATGATAGGATGGGGCTTC	59.854	20	224	2507	2730
60.037	20	TGGAAGGAGAAACGATGACC	60.05	20	194	55	248
58.444	21	CCACCTTTTCATTCCGACTC	59.526	20	148	44	191
59.989	20	GCTCCCTCCATTTTTGTGTG	60.495	20	180	417	596
58.631	24	AACACAGCAGGTTTCGATCC	60.119	20	244	12	255
59.978	20	ACTTCCCTTCATCAGCCCTT	60.074	20	188	1267	1454
59.813	20	GGCCGGTTAAAGGAGAAAAG	60.068	20	280	233	512
59.569	20	TCAAAACAGAGAAGCCCACC	60.232	20	202	414	615
59.959	20	TCGATGTGGTGGAGAACGTA	60.112	20	123	82	204
60.048	20	AGGGTTTGAATGAGGTGTCG	59.966	20	146	334	479
59.571	20	AATTTGTCGTTTGACCAGCC	59.978	20	269	1004	1272
59.917	20	CTCCTTCGACACTTTTTCGG	59.846	20	259	808	1066
59.986	20	TGTTGGAAATCCTCGTTTGA	59.097	20	203	9	211
60.173	20	CAAGCTTACCCGAGCTGAAC	60.015	20	249	10	258
59.428	21	GACCGATCATTGCTATCCTCA	60.051	21	185	542	726
60.074	20	TTTTCTCGAGTTTCACGCCT	59.993	20	259	4678	4936
59.844	20	TTTTGGTTCAGGGGTGGATA	60.162	20	119	170	288
59.963	21	CTTGTCGTATCCCTCCTCCA	60.065	20	165	1271	1435
58.308	20	GAAAACAAGTGTTGCGGGAT	59.978	20	280	84	363
60.142	20	TAACTGCCTCTTTGCACCTG	59.072	20	227	7	233
60.134	20	AATACCAGGCAAAAGAAGCG	59.361	20	240	961	1200
61.031	20	AAACGGACGAACAATGAAGG	59.971	20	152	23	174
59.55	20	AGAACATTCTCATCCCGGTG	59.927	20	269	67	335
59.315	20	ACGCAAAAGCCCCTTCTTAT	60.095	20	233	127	359
59.284	20	ATGGAGGATCACACCACGA	59.901	19	240	558	797
60.21	20	TCTCGCTTCTCTCTTACCGC	59.859	20	140	977	1116
59.981	20	CTCTCGTACGCTGCCTCTCT	59.914	20	183	331	513
60.159	20	CAAAACCACAGCCGACAATA	59.585	20	264	1488	1751
59.74	22	CAACATGTGAGATTCCACGC	60.12	20	262	304	565
60.124	20	AAAAATGACGAATGGGAGGG	61.042	20	267	92	358
60.801	20	AAACTTGAGCAATGTTGGGC	60.118	20	267	429	695
58.876	20	TTCGTATCTTGCCCATGGAT	60.296	20	249	241	489
59.845	20	GGACAGTTTGTCCGAATCTTG	59.583	21	279	130	408
60.13	20	AAGGAGGTGTTATGAAGGGATT	58.028	22	262	1156	1417
59.875	20	CCAAACGGCCGATAAGAATA	59.922	20	196	4	199
60.558	20	TGGGTGAAAACCCATAGACG	60.745	20	280	504	783
59.82	20	AAATTTTGTTTCCCACCAAATAA	58.744	23	252	135	386
60.074	20	TTCCCACAGTTTGATCACCA	59.935	20	263	876	1138
59.056	22	GTTGGCAGAATTTGTCCGAT	59.939	20	144	0	143
59.952	25	GATCACAGGCCATCTTTTCC	59.488	20	279	4	282
58.355	22	CCGCATTTATGTGTGCAAAA	60.508	20	278	40	317
60.214	20	CAGCGAAGATGTGAGGATCA	59.942	20	127	513	639
59.968	21	CGACGTGCTTTTGGTAATTG	59.226	20	139	1307	1445
59.182	20	AGCAAAGTTGCTACCGAGGA	60.015	20	196	1200	1395
59.264	20	TCAGTTGATGCCTGATGAAGA	59.384	21	184	1471	1654
59.823	20	CTTCCAGAAACCTGAGCAGC	60.134	20	272	1883	2154
60.017	23	TGCCGTCTCACACATTAGAAA	59.332	21	164	2303	2466
60.045	24	CCCACCAATTTTGAGACGTT	59.83	20	265	67	331
60.353	20	TTTAACGAATGCTCCAGCG	59.961	19	280	111	390
61.096	20	CGCACTTGGCTCCTTTTTAG	60.011	20	275	1009	1283
60.243	20	AGTGTTTTGACATGATTACTCGTC	57.373	24	101	2147	2247
57.681	24	TCGATTTGGATTCGAATTTTG	59.893	21	170	58	227
59.942	20	GGTTTGCGAGCATAAAAATGA	60.089	21	272	512	783
60.081	22	AAGAGAAACCTTGGCCCCTA	60.068	20	121	11	131
59.787	21	AGCGCACTCAAACAATAGCC	60.416	20	279	686	964

60.483	20	CAATGCCTAGTTTACCCCCA	59.817	20	242	0	241
59.647	20	GACCGAAAATGGAGGTTCAA	59.91	20	174	247	420
59.597	20	CACACACTCACGCACACATT	59.183	20	160	408	567
60.457	23	ATTGTTGCCGGAAAATATCG	59.795	20	256	19	274
60.154	20	CCCTCGTATGCAGTCAAACC	60.517	20	274	693	966
59.929	20	CTAGGCATGGAATCCGAGAA	60.17	20	254	12	265
59.482	20	CAACCTTGGCCACATAACCT	59.853	20	233	3	235
60.003	20	CCCACAATTAGGTCCCCTTT	60.046	20	163	259	421
58.287	20	CGGTTATTACCGGATCGCT	59.93	19	266	1528	1793
59.93	21	GTGGCGACATCCGAATAACT	59.962	20	216	178	393
60	20	CATAGCCGATAAAAATGGCG	60.424	20	199	80	278
59.457	20	CGAAATCCCCTTTTTCAACA	59.91	20	224	1029	1252
59.758	20	CGGCTCAAGATACCGATGAT	60.059	20	234	572	805
60.02	20	AGAATATTCATGGGGTCCGA	59.2	20	269	1128	1396
59.83	20	AACCCGGATCGGAAAAATAC	60.02	20	274	835	1108
59.803	20	TGAGTTGCACGTGTGTGAGA	60.07	20	200	323	522
59.894	20	TGGGCACATTGCTCATTAAA	60.073	20	266	2805	3070
60.288	20	AATGTTTGTCGGGCCTAAAT	58.443	20	266	547	812
60.439	20	TGATGTGTGATGCCTCCCTA	60.072	20	260	710	969
60.154	20	GTGAAGGGCCAATTTCTTGA	60.051	20	245	1468	1712
58.583	26	ATAAGTTGGGTCACGGGTTG	59.711	20	264	210	473
59.966	20	CTACGTAGCCCCCAAATCAA	59.953	20	201	221	421
57.869	22	AGGGCAGTCAAGACCATCAT	59.535	20	250	0	249
59.679	20	ATCACCAGTGGCAAACACAA	60.008	20	174	69	242
59.885	20	CGAATATCCCCCAATTCAAA	59.593	20	276	2278	2553
60.074	20	GCCTGCCTATTAAACTCCCC	59.93	20	178	33	210
60.37	20	TTTTGTTATGATAGGATAAAACCT	58.996	26	259	466	724
60.002	20	CACCATGCTCAGGAATGCTA	59.823	20	234	2201	2434
60.149	20	AACCCTAACCCGACTCGTTT	59.864	20	257	41	297
60.732	20	GCAGCTGTCCATTGTGAGAA	59.992	20	261	218	478
57.528	21	TCAATGATGAAACGGGGATT	60.133	20	134	80	213
60.088	20	AACTCACCCACACACACACG	60.541	20	274	4	277
59.01	20	ATGGAGAAAAGGTACGCACG	60.132	20	158	8	165
59.264	20	TGAATCGAGTGTTTCTTGCG	59.988	20	205	1332	1536
58.925	20	CATGAAAGGAAACAAAATCGAA	59.098	22	119	762	880
59.638	20	TTTGTTATGCGTTTTGACGA	57.846	20	277	95	371
60	20	CCTTCTTCCACCGTTCTTCA	60.224	20	114	4327	4440
59.123	20	ACAAGCCCGTAGGGAAAAAT	59.835	20	273	44	316
60.045	20	GTTGGTGGGATTTGAACCTG	60.21	20	237	873	1109
60.842	20	GGGCTGCACACGAATGATTA	61.98	20	150	673	822
59.986	20	GGGAGGATAAACCGAGGAAG	59.897	20	161	2263	2423
59.831	20	TTCTCATCCACAGACCCCTC	60.048	20	120	1927	2046
59.316	20	TCGATTCAGCAACCAAACAC	59.697	20	190	27	216
60.594	20	TTTTTGGTTGAATAGGGGTGA	59.302	21	280	98	377
60.361	20	TGCAGGGCTGAGTATAGGGT	59.717	20	271	83	353
60.034	20	CAGCAAGGAACTGATGGACA	59.831	20	176	1327	1502
59.67	20	CCCTAGGATGTGGGGGTAAA	60.919	20	252	1737	1988
59.996	20	GTGGGTTTACCCAGAGCGTA	59.993	20	116	524	639
57.118	26	TTTTCAATCATACTTCCGGTTTT	58.955	23	220	57	276
59.726	20	TTTTGACCAATCCTTTTGGG	59.772	20	273	259	531
60.074	20	CGGCCAAATCAAAAGAAAAA	60.047	20	100	486	585
59.962	20	CCTCCATTCAAGCAGAAAGC	59.955	20	189	926	1114
59.953	20	TTGCAATAGCATGCCAACAT	60.103	20	224	191	414
60.149	20	TTCGGCATTATAGGAGGACG	60.053	20	278	35	312
59.79	20	GCCGTAGATCTAACGACCGA	60.235	20	127	1314	1440
59.406	20	TTCTTGATGTGTTGGCAAGC	59.847	20	134	206	339
60.792	20	GACCCAAAAGACTAGGTGCG	59.734	20	197	278	474
59.979	20	CAATATGAGAATGGCCGAAA	58.576	20	159	428	586

59.901	20	GTGGACGTCCCAGATTGTTT	59.827	20	144	777	920
59.637	20	CACGTGGCATTTAACTGGTG	60.027	20	258	1217	1474
60.175	20	AAGGGGAAGTTATTATTTGATCAC	59.882	25	194	278	471
60.051	20	AACAGTGAGGGAACACCAGG	60.002	20	233	186	418
59.95	20	CGTTGATGAAGCACCGTATG	60.134	20	160	671	830
60.074	20	TTCCTACGCACTCACATTAAGA	57.601	22	184	229	412
61.091	20	TTGGAAGGGGCTTGAGTATG	60.066	20	102	1325	1426
60.07	20	CGATGACATTAACAATAACAACA	60.095	26	169	381	549
59.129	20	CACCCTTCGATACTCCGAAA	60.066	20	259	54	312
59.967	20	CAGATCAATGGCCCAGATTT	59.894	20	230	504	733
59.907	20	TGTGTGGCTTTTCTGCAAAC	59.888	20	277	565	841
60.356	20	GCGGACACAGGATTTCAACT	60.119	20	280	80	359
60.201	20	ACGGTGATAGTTTGCGTTGA	59.199	20	279	6155	6433
60.053	20	TCTGTGGTTCCATTCCATCA	59.893	20	214	506	719
60.852	20	ATCACAGGAGATTGGCATTT	57.043	20	223	496	718
59.938	20	GCCTGAACCACCAACCTTGT	62.297	20	191	207	397
58.145	20	AGCAACTCCTCAAACGCAGT	60.058	20	176	67	242
60.088	20	GCCGCAGTTGAGATCTAAGG	59.978	20	219	1040	1258
59.883	20	AAGTGGAGGTTCCATGTTGG	59.82	20	160	59	218
60	20	TTGCCTTTAGCTTTAGCCCT	58.299	20	224	2706	2929
59.916	20	GATTGCGAGAGACCAAAGGA	60.34	20	205	258	462
59.903	20	CATGCAGTTTTTGCATGGTT	59.59	20	272	1428	1699
58.556	22	ATTTCGAAGATCAACGGACG	60.074	20	124	34	157
59.267	22	AGAGAGACGACGGATCGAAA	59.95	20	237	16	252
59.774	20	GCAACGGAATACCACTCGTT	60	20	176	84	259
59.93	19	AAACAAAAGGCAACTGATTCG	59.257	21	273	19	291
59.429	20	AATTTCACATCCTCCCTCCC	60.133	20	268	42	309
60.088	20	TTGGAGGGAGAAAATTGTGC	60.051	20	275	1075	1349
60.12	20	ATTCTCAACAAGGGGCTGAA	59.67	20	219	230	448
57.069	26	AATTGCCACGTTGAGGAATC	59.939	20	270	2	271
60.008	20	GCGTTGGGATCGTGTTAAGT	60	20	196	3369	3564
60.892	20	TGAGCTTCCAACGTAAGTTTCAT	60.176	23	147	3181	3327
57.542	20	GCATGATACCAATGCTGCAC	60.112	20	241	48	288
59.948	20	GGATTGGAACTCCAAAACGA	59.91	20	227	400	626
59.95	20	GTTGACGGCTGGAACCTTAG	59.734	20	162	1396	1557
58.381	25	ACATTCCCGTTGTGTGTTCA	59.855	20	246	57	302
60.088	20	TGCAAGTGGGAGGGAAGTAG	60.246	20	218	583	800
59.781	20	TAATTTGGCAAACTCTGGGC	60.074	20	128	785	912
58.829	23	CGGACCAACCCGTTTATATG	60.067	20	163	67	229
60.088	20	TCCACGTCTTGTTTTCCATCT	59.583	21	280	4276	4555
60.192	20	AACATTGTTTGGGAAAAACCTT	58.822	22	162	828	989
59.801	20	TCGAAGGTCAATGGTTCACA	60.088	20	211	122	332
59.964	20	GCGCGGAGTTTAAGAAATGT	59.365	20	239	290	528
59.995	20	GCCATCAGATCTGCACTGAA	59.95	20	203	1237	1439
60.096	20	CTCGTTTCTTGCTAGCTCGG	60.284	20	235	660	894
60.081	21	GGCAATATTACCATGACGGG	60.038	20	276	2013	2288
60.447	21	GCCGGCAACTCACTTAACTC	59.882	20	114	38	151
60.12	20	GTGTGTGTATGCGCATGTGT	59.038	20	238	92	329
59.935	20	TGAGTCTGATGGACTGCCAC	59.827	20	274	101	374
60.096	20	GATCTAACTAGGCCCGTCCC	59.925	20	162	242	403
59.973	20	GAAAAACCCTAATCCGCCTC	59.909	20	141	80	220
59.56	24	AACCCGTGTTCTTCAGTTGG	60.005	20	242	213	454
59.663	21	TCCATGAAAGATTGGGGTGT	60.173	20	240	1734	1973
59.942	20	GATCGCCGAAGGTTTTTGTA	60.074	20	271	815	1085
60.238	20	CACCCCGAGATAACTTTCCA	59.926	20	224	16	239
59.783	20	TGTTCACCAAGTTCGCAAGA	60.427	20	162	115	276
59.697	20	GATGCTCCACTTCCTACTCCA	59.298	21	233	104	336
60.001	20	CTACCATCTCGGGATGCAGT	60.096	20	253	1328	1580

60.074	20	TGTGTAATTGTGTTGTGTCATGTTT	59.278	25	210	309	518
60.014	20	AGGTTCGGACAAACAACAGC	60.156	20	212	1223	1434
58.575	24	GCTATGAGCATGTCATCAACA	57.291	21	125	0	124
57.312	24	CCAAAAACCATCTGCCCTTA	59.931	20	182	1	182
59.661	20	CATGGGATCTCAACGATTCA	59.451	20	259	661	919
59.526	20	CAGCACTAACACACACACGCT	60.026	21	260	59	318
60.199	20	TGCATAACACGGGTGGAGTA	59.988	20	252	1364	1615
59.907	20	GAGGTCACCCTTTGTCCGTA	59.966	20	257	222	478
60.44	20	AACCCGCGAGTTGCTACTAA	59.904	20	137	283	419
60.038	20	GTGTAGATCTGGCGGGTAGG	59.574	20	279	373	651
58.823	21	TTGACTTAACAAACCCCAAGG	58.98	21	247	98	344
60.119	20	AATTGAGTTCGGGATTGTGC	59.939	20	271	18	288
59.864	20	TTACAATGACGTCAGCACGC	60.876	20	208	3	210
59.901	20	TTCTACGAATGTTGACGGAAAA	59.625	22	113	536	648
60.118	20	GATACGTGATGCGTTGATCG	60.104	20	183	140	322
60.218	20	TTAAATCTCCCCACAAACGG	59.795	20	241	11	251
60.032	22	GTACAGAGCGAAAACGAGGC	60.022	20	243	193	435
60.495	24	AAGCATGAGTTGTGTGCTGG	59.905	20	244	0	243
59.72	20	CTCCCGAATTGGGTTTTCTT	60.291	20	213	11	223
59.864	20	GTGGATCATGAGCGACCTTC	60.633	20	232	629	860
60.11	20	AGTGGTTATTACCGGATCGC	58.93	20	210	2692	2901
59.264	20	GATGGTGAATACGATTGGCA	59.355	20	268	118	385
59.043	20	TAGGCCCGAATGAAATGAAG	60.031	20	202	203	404
58.949	22	CTTCCCAGCAGAGAATCGAG	60.088	20	149	5	153
60.299	20	CCGGGGTAATCTCAAAACCT	60.18	20	247	540	786
60.103	20	ATCGGCCATTCCTATTTCCT	59.761	20	148	409	556
59.173	22	AGCCCATTCGTGATTTATGG	59.784	20	260	16	275
60.133	20	GCGTCCATTCATCAAGATCC	60.435	20	233	23	255
60.34	20	TTGATGCAGCCCAATGTATG	60.488	20	237	205	441
60.157	20	GAGCGGGATTATCAGACGTG	60.624	20	210	3	212
59.971	20	GGGAGAAACAACCACCATTG	60.21	20	252	600	851
59.997	20	CATGAGCCTCCAAACCCTAA	60.066	20	151	1056	1206
59.797	20	AGCACGAGAAAAAGACCAGC	59.621	20	176	1618	1793
60.058	20	AGCAAGAACTCACGCCTTTC	59.621	20	265	108	372
59.614	20	TTTTGCTGTGGTCCCCTTAC	59.971	20	151	444	594
59.745	20	TTTGGGTAGGCCTGAGTCTG	60.246	20	276	3281	3556
59.693	20	AGCTTCAAACATTGATGGCA	59.276	20	247	243	489
60.457	20	GCTTCGCAACGAAGGAATAC	59.851	20	270	17	286
59.566	20	CTCCAACCTGCCACAAAAAT	59.971	20	135	2515	2649
59.905	20	GGGATGTGTGGGATTGATTC	59.995	20	245	930	1174
59.836	20	TCACGCAATCACACAGATCA	59.823	20	271	1049	1319
59.257	20	GGTGAACGTAGGGGTGAAAA	59.83	20	198	109	306
59.111	21	TCGCGTAGAAATCCTTATGC	58.017	20	191	16	206
59.988	20	TGAAAGAAAACAAGAAAGAATCA	60.499	26	240	4238	4477
59.48	19	AGCGAGGGAATTAGGAGGAG	59.805	20	257	2	258
60.138	20	TCCAAAGAAATTGAGGTGCC	60.051	20	255	250	504
59.996	20	AACGAAGCAGCCGTAGAAAA	60.018	20	264	974	1237
59.946	20	TTATCTGTCCTCTGGCCTTGA	59.822	21	237	6	242
58.165	25	TGCGTTTTGATGATATATAGGTGT	60.054	26	244	1913	2156
59.685	20	ATCCAATGGCCATGATTTGT	60.021	20	145	3	147
60.349	20	TGCACAAAATCCCACAAAGA	60.088	20	243	11	253
60.667	20	TTGCCTATTTTGGAGGATCG	60.031	20	224	47	270
60.074	20	GGTTGTGAGAACCAACTCTGTG	59.664	22	187	118	304
59.651	20	TTCACTGCTTATCGCCACTG	60.011	20	236	41	276
58.619	21	CAACCACGTACAACCTGCAC	60.072	20	236	739	974
59.742	20	AGAGGAGGAACCCATGGAGA	60.991	20	215	355	569
59.748	22	GGTTGAATGGATATGGCTCAA	59.776	21	269	140	408
59.364	21	GGGGCGTGACAAGGATACTA	59.955	20	267	62	328

59.939	20	TAGGGAGCTGTCAATTTCGG	60.206	20	210	1109	1318
59.16	21	CAGATGGGAGGAGAGAACGA	60.34	20	236	1	236
59.95	20	AGGCAATATCAATCTCGGTGA	59.542	21	158	120	277
60.042	20	GGGGAAGCACAGTCTAGGGT	60.511	20	277	77	353
60	20	GGTGTTGTGTGATGTCGGAG	60.005	20	203	75	277
59.967	22	GTTTAGTGATGGAACGGGGA	59.79	20	144	47	190
59.903	20	CACGTGGCGCTAATTGAGTA	59.895	20	198	112	309
59.673	20	CTCGTCGTGTTCAAGGCTC	59.561	19	233	1618	1850
60.119	20	CCTCCCAAATTGTCGAGTGT	59.966	20	232	31	262
60.162	20	AGCAAAAATGCCACGTATCC	59.967	20	213	6	218
60.067	20	ATCTCCAATCACGTTCCACC	59.786	20	170	871	1040
60.434	25	CAACTTGCAGGTGCTAACCA	59.904	20	128	19	146
59.996	22	ACCCTCCTTCAGCCAAAAAT	59.94	20	256	76	331
60.049	20	AGTGTCTCCAGTCTCCACCG	60.306	20	225	2950	3174
60.885	24	GGGCTGAAAAGCCAATTAAA	59.189	20	280	9	288
58.439	22	GGCATTGGACATCAACATGA	60.339	20	187	72	258
60.246	20	TCGGCTCCTCAGACACTTTT	59.989	20	223	105	327
59.95	20	TCGCCTTAACCACTTTGAGG	60.241	20	275	363	637
57.171	23	GTAGAGGCGGAGTGCTTTTT	58.604	20	233	0	232
60.547	20	ATGCTGCTCTAAGGCGTGTT	60.044	20	250	2776	3025
59.696	20	CAAACCGGACTGGACCATTA	60.745	20	271	9	279
59.696	20	CAAACCGGACTGGACCATTA	60.745	20	267	9	275
59.967	20	AATCTTTGAGGACCCCCTTT	58.896	20	120	18	137
60.227	20	CCTATGGTGGTATGGTGTGG	58.569	20	259	53	311
60.052	20	CTCTGCATGTTTGTTGGGTG	60.152	20	216	1864	2079
59.381	20	TGGCGTATGCTGAGAGAATG	59.972	20	136	222	357
58.888	23	AAAATCAAAGGCCCACAATG	59.801	20	221	212	432
60.244	20	GGGAGTTATCATTGGATCAAGC	59.805	22	179	537	715
59.945	20	GGTCGACATTAAATCTTGGCA	59.952	21	264	581	844
59.926	21	CCAAAGAACTGATATCCTCACCTT	59.901	24	145	525	669
60.229	20	TTATCAAGGGCCCTACCTCC	60.278	20	204	605	808
59.772	20	CGCCTACCCTCCTCTCTTCT	59.972	20	107	89	195
59.326	23	CTTTTTAATCCACCTGGCGA	60.067	20	203	15	217
59.971	21	TCATGTGCCTGGATTGGATA	59.883	20	237	34	270
59.463	22	GCTGAACGAGTAATTCTTGGTG	58.906	22	278	561	838
58.955	22	AAGATGCACGTAGGGAGGTG	60.134	20	207	6	212
59.434	21	AGAAAACCCGGCTCGTATCT	60.096	20	238	184	421
59.823	20	TCAAAACTGCATTTCTGGGTT	59.601	21	214	675	888
59.809	20	CATGATTGCCATCCTCCTCT	60.034	20	141	659	799
58.161	20	AGAGCAAAACCCATCAGTGG	60.111	20	100	1726	1825
59.842	25	CAAATTCAAATGCCTCAGCA	59.809	20	243	0	242
59.955	20	TGAGTGACAAGACCCTGCTG	60.022	20	202	635	836
60.287	19	CCCGATCCAAGGTTCAACTA	59.926	20	279	38	316
59.592	22	CGTGGTTCGATCGTAATTGA	59.542	20	128	18	145
59.579	20	TGCTAACAATGATGGGCAAA	60.073	20	111	2757	2867
60.214	20	GTGGGCTGTGGCTTTTGTAT	60	20	188	353	540
59.943	20	CCGAGACAGCACTCACGATA	60.008	20	239	4147	4385
59.707	25	AGCATTTGATCTGATGCACG	59.83	20	151	3	153
58.381	21	ATGGCCCCCAAGAAAATAAT	59.512	20	268	123	390
59.08	21	ATGCCTTCTCTTTCCTGCAA	59.955	20	246	4215	4460
60.011	20	ATTGACGCCTACATTGCCTC	60.103	20	232	107	338
60.149	20	CCTCTCATGTTTTCCCCAAA	59.903	20	201	267	467
59.997	20	ATCCTCATCTTTCCCCAACC	60.133	20	170	1400	1569
59.028	20	TTGTCCTCACCCTCTCCATC	60.048	20	119	1	119
57.458	27	ATGCACTACCGGATAGGCTC	59.178	20	197	49	245
60.306	20	ACACCCACCACACCTCATCT	60.291	20	197	118	314
60	22	GCCAAATTAAGGGCATGAAA	59.907	20	139	258	396
59.978	20	TCTCCTCCCCTTTTAATTCCT	58.212	21	218	51	268

59.583	21	CACTTGGACCTGAAAAGGGA	60.081	20	141	0	140
59.799	20	TGCTATCCCATTGCCCTAAG	60.053	20	198	263	460
59.823	20	CGTTAGGCTCGAGAGTGAAGA	59.766	21	161	3	163
60.051	20	TTGAATTTTTGGGGTTGGAA	60.138	20	251	125	375
60.363	20	CCCACCAGTGCCATACTTCT	59.989	20	116	657	772
59.933	20	TCTTCAATCCTTCTTCCCCA	59.6	20	159	32	190
59.923	20	TTCGAAAATGGAGGGATGAG	60.006	20	211	99	309
59.96	20	TGGGTGGATCTTGAAAGAGG	60.042	20	227	753	979
59.927	20	GCCCTCCCAAAAGTAACTCC	59.94	20	211	40	250
59.861	20	CAGTCCACTTTTGAATGGCA	59.691	20	207	25	231
59.934	20	CAGGCACATGCAAAAAGAAA	59.849	20	177	102	278
59.121	25	TCTTCATCCCATTGACCCAT	60.135	20	264	112	375
60.274	22	TTCCGATTGCAAGAAAAACA	59.277	20	269	288	556
59.972	20	TTCATCATCTTCCCTTTCTGC	59.259	21	176	64	239
59.959	25	AATCCATACTGCCAAAACGG	59.823	20	251	228	478
59.914	22	GTCTCTTCCTGGGAGGGTTC	60.05	20	153	2	154
57.01	23	GGTCATTTTAGCTTGATCAACAG	57.952	23	174	524	697
60.082	23	TGTTTCTCGATAGCCCGTTT	59.708	20	243	1913	2155
59.545	20	TTTGAGAAAGCAGTGGCAGA	59.716	20	252	9710	9961
60.314	20	GGCAATCAGTAGCCCAAAAA	60.074	20	273	2516	2788
59.091	20	GGTCGGCTACATGAACCAAA	60.894	20	159	0	158
60.258	20	AAGCGAAGGTGTTGATGAGC	60.406	20	233	84	316
59.957	20	GCGTGGTCTTGCCAATTTAT	59.967	20	272	2773	3044
59.744	23	CTCAAGCTCGTCACCCTTTT	59.473	20	147	7	153
59.993	20	AAGGAGGTGTTATGAAGGGATT	58.028	22	268	973	1240
59.96	22	TTGATTCTGGAATATCCCGC	59.862	20	151	92	242
59.75	20	GACCTAAGCCACTCGCTACG	60.037	20	240	294	533
60.147	20	GAGCCCCACTATCTTCACCA	60.073	20	221	48	268
59.349	20	TTCTTTCTCATTCTCTCGGCTC	60.096	22	146	1149	1294
59.941	20	TCCTCATTGTTTGTGTGGAAA	59.01	21	206	56	261
60.012	20	ATGCCTCAAACAACCTCACC	59.973	20	161	986	1146
60.083	26	TGGATGAGCTCCAATGTGTC	59.637	20	147	1	147
59.995	20	GACGCTCCACATGATGACAC	60.13	20	265	118	382
60.036	20	AAAACTGCGAAATGAGGAAGA	58.962	21	154	253	406
60.11	21	TTGCTACAAAACCAGTGGCA	60.293	20	205	1060	1264
59.966	20	CGATGTTTATTTGAGGCGCT	60.23	20	108	190	297
60.584	20	TTTGTGAACGTCGTCATTGT	57.571	20	200	243	442
60.019	20	TCCACGTGGCACTTCATCTA	60.263	20	219	2319	2537
59.92	20	CCAGCAGACAAAAAGCATCA	59.988	20	131	467	597
59.75	20	TTCCATTGGGTTTTGGGTTA	60.024	20	142	4045	4186
59.206	20	TGCCCCTTCTGACTCTGTCT	59.986	20	230	193	422
60.703	22	ACTGCCCAACAATGGCTTAC	60	20	189	6	194
60.201	20	CCATGATTTCCTTTAATTCGATG	59.7	23	115	217	331
59.93	22	TGTTTTGCCCGTACGTTGTA	60.029	20	245	194	438
60.713	20	TGAGCTGGCAGAGACCTTTT	60.134	20	134	209	342
60.03	20	TTAGGCCCCTCCCTACATCT	59.919	20	147	335	481
59.9	20	CTCACCAGGCCAGGGTAGTA	60.126	20	212	1216	1427
59.971	20	TCCCAACAAAACGAAAAAGT	57.25	20	201	1235	1435
60.011	20	CGCTCTCTCATTGTAATCTCTCTC	58.83	24	136	345	480
60.096	20	TTAATGCACTTCGACGATGG	59.688	20	248	736	983
59.907	20	GCCCAGCTTATTTGGTGAAA	60.074	20	238	1678	1915
60.081	20	GTCAAGCCTGGGACTGAGAG	59.986	20	261	1176	1436
59.83	20	GACTGGAGGAGAGCGAGCTT	61.212	20	213	118	330
59.052	20	TTCAAACATGGCAACAATGG	60.357	20	139	409	547
60.131	20	AAATCCTTTGCACAACCCAC	59.836	20	111	48	158
60.058	20	TTCTTGGCAATCATGTCCCT	60.461	20	183	66	248
57.333	24	TCACACTCACGCACTCACAA	60.07	20	121	15	135
60.22	20	TTTGTACCAAAAAGTATATAAATG	57.58	27	260	597	856

59.455	23	TCGTTCAAGTCGGTCACATT	59.139	20	195	46	240
60.118	20	CAGATCTGATGGCCCAGATT	60.034	20	143	276	418
59.697	20	GCCCGGCATACAAATAGAGA	60.06	20	270	22	291
60.199	20	AGTCACCGACAACTCCAACC	60.009	20	250	20	269
60.523	20	TAACCACCCAATCTTCGCTC	60.074	20	181	96	276
59.966	22	TCGTGAGAGATAGATATGGAGAG	57.233	24	261	88	348
59.41	21	GGGTCTGACATTGTAATAAAGGG	58.812	23	272	31	302
60.817	20	CACGTTCGGGTTTGATAAGG	60.357	20	250	446	695
57.154	22	GGGTGTATGTGAACCAACCA	59.112	20	203	628	830
60.011	20	AATTTGGCTTGTTACAGCGG	60.131	20	253	563	815
58.4	21	CCTCCATTATCCACTCTCGC	59.653	20	258	739	996
59.556	24	AAGAGCAGAAAGGGGGAAAA	60.18	20	248	32	279
58.013	23	TTTTCCGGTTAACAAATCGC	59.943	20	279	792	1070
60.088	20	TGTCGAAATGGGAGTCACAA	60.088	20	105	1226	1330
59.847	20	TCAGAACATGGGCAAATTCA	60.049	20	169	491	659
60.375	20	GGGACATCTTGGTGGGAATA	59.605	20	279	35	313
59.697	20	GGGAACATTCGAGCCATAAC	59.391	20	163	41	203
59.768	24	GAGAGAGGCAGACATCAGGC	60.104	20	280	21	300
60.011	20	CAGATGATGTCCCAGCAAAA	59.648	20	259	36	294
59.583	22	ATCGTCCCCTCTCTTGCAG	60.356	19	204	375	578
60.683	20	TTGTGTGATCGAACCACGTT	60.008	20	123	48	170
60.116	21	CTCGTCATCAACTTTTCCCC	59.526	20	209	411	619
60.472	20	GGATAGGAATCTCAAGAGTATGC	60.007	25	185	1013	1197
60.844	20	TCTCTCTTTCTTGGTTGGTGAA	58.955	22	190	142	331
59.89	21	ATTCGGACATCGAGATTTGG	59.894	20	238	69	306
59.778	20	CGAATACTCCAAATGACACCAA	59.861	22	238	53	290
59.322	21	TTGAATATGCAATCACCAAAGAA	59.485	23	219	26	244
57.122	26	GGTGCACCACCCCTATCTT	59.794	19	251	590	840
60.298	20	AAGAAAACAGAGGTAGTGAATTG	59.658	26	231	287	517
59.273	20	TTAACAACGTTTCGGAATTTTT	57.813	22	280	122	401
60.117	20	TTCACCATGATTTCGATACACA	58.895	22	230	656	885
59.791	21	TTTCTCCTCGTATGCGTATTCA	59.742	22	277	644	920
59.145	21	AGAGGGAAAACAGGGGTAGC	59.576	20	124	7	130
60.031	20	ATAAGCAACGAAGGGAGTGC	59.34	20	212	279	490
59.939	20	AATCTTCGCCCTTTTGTCCT	60.074	20	274	1615	1888
59.955	20	ATTTTATCCGACTGGCGTTG	59.96	20	272	457	728
59.933	20	AACAAAATCACCCCCTCACA	60.21	20	108	4	111
57.727	24	TTTCACTTTTTGCACTCCCC	60.088	20	151	0	150
59.263	20	TATCACCATAACGCACCCCT	60.214	20	247	127	373
60.255	20	CCAGGTGGAGTTACACCCAT	59.697	20	208	732	939
59.357	20	ATGGCCATGTTTTTGGATGT	60.059	20	202	651	852
59.566	24	GAATCACTTTGCAAGCACCA	59.847	20	183	221	403
60.081	20	GTGGAATCAGTGAGGAGGGA	60.048	20	182	66	247
59.903	20	ATTGAATCGCAAGCACATGA	60.228	20	124	194	317
59.84	21	GATTTTGAGCCTTTTGCTGC	59.967	20	212	5	216
60.214	20	GGGACTGTGAAACAGGGAAA	59.943	20	251	271	521
59.84	20	TGCAAAGAAAGAATCTGGGG	60.184	20	259	805	1063
59.839	20	TGAGATTTTCCTGCCAAACC	60.051	20	187	1596	1782
60.578	20	CTCTTCAGCTGCTCTCCGTT	59.891	20	244	304	547
59.396	21	CATGTGTGAATATCCGCTCG	60.096	20	190	39	228
59.989	20	ACGGCATTGAAGAAATGAGG	60.074	20	268	56	323
59.897	21	TCGAATCCGAATCTTTCACC	60.014	20	276	836	1111
59.792	20	GCTTTTACCAAGGTGAGGCA	60.249	20	249	686	934
61.165	20	GCCTTTGGTGGACTTTTCAA	60.088	20	240	1	240
60.119	20	TCCCGTTTCACTCTTCTGCT	59.989	20	264	917	1180
60.135	20	ATGCCAACTCACCCATAAGC	59.962	20	276	3	278
59.773	20	GAACCGTTTAAACAACCCGA	59.839	20	271	107	377
60.41	20	ACATCTCTTTGTCTCCCCCA	59.505	20	256	199	454

60.012	20	CAAGTTTCATCTTCCTCGCC	59.813	20	199	229	427
60.263	20	TTACCGTGTGTGTGCATGTG	60.071	20	104	1210	1313
58.388	25	TCAAGTAAATCAGCCGTCCC	60.074	20	270	0	269
59.973	20	GTCGGGAGAGAGGGGTAAAT	59.397	20	279	20	298
60.484	20	GGGGTGGAAAGGGTTTAGAA	60.159	20	245	485	729
60.475	20	TGGCAATGTGGTGGTAAAGA	59.964	20	187	164	350
60.011	20	CCATCGTTGTCGAAATCCTT	59.933	20	207	274	480
59.001	20	ATGAATGGATTCCGGTCAAA	60.133	20	276	6	281
59.928	20	TGGAGCATACGCAACATCAT	60.104	20	248	28	275
60.096	20	TGGGGCCTACGAGAAATATG	59.916	20	170	311	480
59.971	20	GGATTTCCGTTGTTATTGCC	59.277	20	276	83	358
59.971	20	TGGTTAGCACCAAATAGCCA	59.182	20	194	50	243
60.607	20	GAAAGTTGGCTCAAGCTCGT	59.621	20	274	12	285
59.797	20	GAGAGCTATACCGACGGCAG	60	20	256	386	641
59.984	20	AACACACAGAAGGGAGTGGG	60.002	20	240	635	874
59.935	20	CGTCGGTCAGAACCTTGATT	60.111	20	166	26	191
60.074	20	ATTTCCTTGGCCTTCTTCGT	60.074	20	189	1432	1620
59.939	20	GTCTTGGGGGAGTAACCCAT	60.052	20	217	2444	2660
60.111	20	GAAGTGCAGTTTCCCCTTCA	60.232	20	204	816	1019
58.188	22	AAATGGAGCAAACATTACCGA	59.465	21	244	551	794
59.615	20	CCATGTCAAGGGTTCGAAGT	59.966	20	235	118	352
59.564	20	TCCTTTGCACCTATTCGTCC	60.074	20	102	1846	1947
58.427	27	TTGTTGGTGGGTTTGAGTGA	59.976	20	218	6	223
59.942	20	GGTTCGAGTCTCAATGGGAA	60.05	20	224	399	622
59.933	20	CTTAAACCCTTGAGCCATGC	59.708	20	202	137	338
60.096	20	GAAGAAATTCCCCCAAGACC	59.744	20	278	1814	2091
59.744	21	ATGTGTTTGGTTTTGGCTGC	60.934	20	220	94	313
59.231	22	TGTGGTTGAAATCTAGCCCTTT	60.001	22	149	10	158
59.981	20	GCACTGCTTTTTGGTGATGA	59.847	20	200	270	469
60.008	20	TGACACAGATTTGGTGCTTG	58.246	20	238	385	622
60.191	20	AGAGGTTAGGGTGTTGGGCT	59.994	20	255	690	944
59.933	20	ATGCCACCTCCAATTTTCAC	59.797	20	121	134	254
59.847	20	GTCATCATCGTCTTCCCCAC	60.335	20	123	28	150
57.781	24	TGTGTTTTGACAATATTTAGTGTTT	58.633	27	101	756	856
60.523	20	GTTAGGGATACCGCTAGGCA	59.205	20	273	72	344
57.034	27	GAAATTTCTTGCCCGAATCA	60.016	20	202	52	253
60.332	20	AAAAGAAGCAGCAGTCGGAA	60.132	20	116	5	120
59.402	21	CTCAAAAGAGCACCTCCTGC	60.134	20	200	9	208
60.103	20	CCTCCCGAATTTCTGTGTGT	59.966	20	211	819	1029
57.729	24	TAGTCAATGGAGGGTGGGAG	59.92	20	241	544	784
60.112	20	GTTGGATGTTAAGGATGCCG	60.331	20	275	137	411
59.95	20	CGTGAACACACCGGTTCAAT	61.814	20	270	336	605
58.405	20	GGGTTGTGGTGAAGGAGAGA	60.088	20	195	22	216
59.761	20	TGCTTAAAATGGGTTTTCCG	59.937	20	220	169	388
58.897	20	TCAATGACCACACAACCACA	59.376	20	260	135	394
60.156	20	CACTAAATAAATATTTTGGCATAT	57.149	27	247	19	265
60.331	20	TCAGATGAAAAGCCTACAGGAA	58.973	22	126	224	349
59.722	20	AGCCGAGGACATTCTTCTGA	59.95	20	248	370	617
59.827	20	CAAGTGCAGCAACTTTTGGA	60.027	20	241	65	305
59.882	20	TCCTCCCAACATATTGTGCAT	60.207	21	225	57	281
58.028	20	AATCTCGCATCCCAATTCTG	60.036	20	121	72	192
60.54	20	GCGACTGGCACCTTATCTTC	59.843	20	179	2076	2254
59.955	20	TGGAACCCATCAACACAAAA	59.792	20	263	379	641
59.75	20	CGGGTTTCGCTATTCATCAT	59.923	20	153	12	164
57.416	21	AGTTTTTAATCGTGGCCGCT	60.976	20	156	135	290
60.46	20	ACCTTTTACGGGGAAGGAAA	59.808	20	191	81	271
59.799	22	GGAGTGTTGGAGGAGGAGTG	59.682	20	276	6	281
58.649	22	CGTGGTTCGATCGTAAATGA	59.542	20	217	114	330

57.6	26	AGTCAAGGAGGGCAGAGTGA	59.986	20	274	4	277
60.006	20	TGCATTTATCCGATTTATCAAAA	58.561	23	207	814	1020
59.836	20	GTCGTGGATATGGGCTGACT	59.957	20	196	1105	1300
60.134	20	TCATGTTAATTGGTGGTATCATTTC	59.898	25	188	3400	3587
59.955	20	TGAAACTGAAGATTTGGGGC	60.051	20	176	1234	1409
59.162	22	ACAGGGCTTGGGACAAACTA	59.592	20	245	1892	2136
60.073	20	CCAGTTTTACCACCGCCTTA	59.99	20	172	803	974
59.937	21	GGGTATGTGGACAGAGTGGG	60.238	20	125	81	205
58.572	20	ATTTGTGCGAGTCTCGTGTG	59.905	20	248	698	945
59.824	20	TATTATCACGGTTTTCCGGG	59.655	20	150	510	659
58.858	22	TCATGTGTCTTCCACCATGAA	59.951	21	188	5026	5213
57.063	22	TCTTTCTTTCCCTTGCTCCA	59.926	20	221	123	343
59.976	20	CCAATGCATTACGAGTTGGT	58.502	20	224	418	641
59.992	21	TCCTAGCCCTCAATCTCGAA	59.91	20	252	608	859
60.11	20	GCACTCTCCAGCTCGATTTC	60.104	20	181	977	1157
59.325	20	GTACTAGCAACGGAGATGCG	58.555	20	215	41	255
59.976	20	CACCCGACGTATTCGAGTTT	59.993	20	249	176	424
60.081	20	TCACTTCTTGCCGATGAAGA	59.522	20	274	477	750
59.801	20	TTCATCATCAGCTGCTGTCC	59.95	20	216	1039	1254
60	20	TGCCACAGTTTCATCTTCCA	60.24	20	190	4610	4799
60.456	20	CGGAGTTGAGGACTTAACGG	59.728	20	249	109	357
59.434	20	AGGTTTGGAGCCATTTTGTG	59.971	20	142	324	465
59.933	20	CAACACAATACTAATGCAATCCG	59.437	23	223	14	236
59.169	20	TTGGGGGAGAATTGTTTGAG	59.903	20	248	84	331
60.044	20	CTTGACGACTTCGAACCTGA	59.007	20	249	113	361
59.072	21	ATCATAATTGACGCCCTTCG	59.923	20	105	11	115
60.192	20	ATGGACCCTTGTTGGTTTGA	60.21	20	146	299	444
60.11	21	GATGGAAAATGGTGATTGGG	59.991	20	187	84	270
59.01	21	CCGCACACCCCTATCTTTTA	59.953	20	229	356	584
59.135	20	ATTGCTTTGACACCACCACA	60.008	20	279	47	325
59.933	20	GACGAAAATTGCCCGTAAAA	59.943	20	247	103	349
59.693	21	ATTTCAAATCCTTCCCACCC	59.996	20	217	25	241
59.929	20	GAACATCGACTCACTGTATTGTTT	57.373	24	166	233	398
59.988	20	AGCTTCTGCTTCACACAGCA	59.929	20	232	107	338
57.321	26	TCCCTCAAAACAGATTCCCA	60.43	20	207	663	869
60.119	20	TGTCCGAAATTCTCTCACCC	60.05	20	210	38	247
60.131	20	ACTGCAACCCATCCTTTGAG	60.111	20	213	24	236
59.328	26	AAATCCTTGCACCTCCTCCT	60.074	20	132	2	133
59.848	20	AAGTTGGAACGAGCGAAAAA	59.861	20	239	87	325
59.82	20	CTCCATGCCTCTGCTCTTTT	59.574	20	186	594	779
58.158	20	GGCCCAGTAGCATGAATATGA	59.937	21	267	108	374
59.216	21	CGTAGTTGCTACATGTTAAAGAAA	57.052	25	280	21	300
59.881	20	AAAATCAAAGGCCCACAATG	59.801	20	277	2	278
60.095	20	CCCCCAGCAAAATAAAAAGG	60.637	20	162	4425	4586
59.789	20	CCCCAAGAGAGGATTTCACA	60.042	20	262	15	276
59.64	20	TCGTTTCTTCACTCCAACCC	60.088	20	162	241	402
60.363	20	ATGAAAATGGGCGAGAGTTT	58.647	20	225	231	455
59.85	20	AATACTCACGGGAAGCATCG	60.096	20	147	13	159
58.864	25	CCAATGACACGTTATGCTCAA	59.6	21	198	92	289
60.199	20	GTTGTTTTTGTCGCGGATTT	59.982	20	280	1	280
60.126	20	CAGCAATTTCGATTTCAGTGAG	59.883	22	193	262	454
59.52	20	CGGGATTTAGGTGTTTTGACC	60.579	21	280	1935	2214
59.848	20	ATCGATAATTCGCACCCAAG	59.923	20	234	960	1193
60.149	20	TCTGGGCTCCCAAATTTTTA	59.52	20	277	824	1100
59.91	20	GGGAGATGAGGGGAAAAGAG	60.008	20	171	279	449
60.088	20	TGGCTTAAGGCAATTTGTTAAT	57.918	22	241	222	462
58.573	21	CTTTGAATTGCAGCTCGACA	60.134	20	271	652	922
60.206	20	TCGTCCGAAAATCCTTTCAC	60.051	20	272	77	348

59.931	20	CCAAATGATTTCCCTTTGATG	59.26	21	229	60	288
59.805	20	CACTTTCTGCACCCCAAAAT	59.971	20	261	888	1148
58.2	22	ATACCGCTGACGACAACCAT	60.406	20	134	4	137
59.813	20	ATGTAGGGAAAGATGGCACG	59.955	20	275	412	686
59.772	20	TCTGGTTTGCAAAACTTTCTGT	58.927	22	167	896	1062
59.343	20	ATTGCTCTCCAACCCACAAC	59.973	20	257	130	386
60.13	20	ATTTCGAAAATCAACGGACG	59.938	20	162	221	382
59.6	20	GCTGGTGTTGGGAGAGAGAT	59.258	20	212	507	718
59.109	25	ATTACGTCGATCCAACGGTC	59.82	20	135	2	136
61.031	20	CCCAGTCGTATCACTTTGGC	60.517	20	201	22	222
60.184	20	CACAGGAACAAGAGCGAATG	59.44	20	273	132	404
58.895	21	ACATTGAAAACCAGCCGTTC	59.978	20	145	114	258
60.352	20	ACGGATTTGTCGATCGGTTA	60.331	20	224	1336	1559
59.182	20	GTTCGTCCCACCCTACTTGA	59.966	20	196	53	248
60.149	20	CTTCGGCAACGAAATACCAT	59.96	20	147	92	238
59.746	20	TGTAGGGAGTGGGATGTGTG	59.388	20	206	186	391
59.079	20	GGGAAATTTCAGTTGCAAACA	59.967	21	249	3	251
58.984	20	ATGTGCAGGAATCTCAAGGG	60.073	20	224	17	240
60.22	20	ACGTAGTGGGAAAAAGGGCT	59.998	20	273	127	399
60	20	CTTATTGCCTCCATCGTCGT	60.096	20	223	83	305
59.847	20	TGGGAATCTTTGCATCTTCC	60.014	20	127	333	459
60.066	20	AATTGGGGTGCAGTTCAAAG	59.971	20	180	110	289
59.813	20	CACTTAGGGGGTTATTAGTGGAA	58.515	23	279	7706	7984
60.096	20	CATCCACGTGTGCTAACTCG	60.324	20	184	2394	2577
59.952	21	AAACAAATATGGCCTCCCAA	59.273	20	196	584	779
58.83	21	ATGACAACCCACCAGAAAGC	59.973	20	172	950	1121
59.945	20	AGACCGAGCGCAATGAATTA	60.742	20	225	265	489
59.916	20	GTTGTGTAGCCAAACATGCG	60.18	20	151	0	150
60.207	20	ATTAAATGCCGGTCAAAGCA	60.456	20	267	150	416
60.448	20	TAAGATCGAACGATCCAGCC	60.177	20	208	97	304
59.882	20	GAAACTGACCACCACGGAAT	59.827	20	193	462	654
59.281	20	ACAAAACCACGGCTGTCAAT	60.419	20	183	16	198
59.833	20	AAAAACACGAAACTTGATTGTGA	59.952	24	270	102	371
59.055	20	CGGAATGAGCCACAGAATTT	60.074	20	240	27	266
59.925	20	TGTTTGGTTGCTTGCTTGTT	59.366	20	204	1152	1355
59.074	21	GGGGTCTTCTTTTGGGACTC	59.912	20	180	462	641
59.332	26	CCGGGACCGAAACATAGAT	59.759	19	232	2015	2246
59.967	20	CCAATTTGAATGGTTATTACCTGA	59.191	24	141	581	721
60.06	20	TGGATGACGAGGTCGAGATT	60.622	20	253	91	343
59.691	20	TCGGAAATAGGTGGTTTTCG	59.931	20	267	18	284
59.898	25	AGGAGCAATACTGCTTGTGGA	59.89	21	146	10	155
60.081	20	CAACTTGGGCTAAGGATTTTG	58.751	21	152	59	210
59.887	20	GCGGTATACTGCCTTTCCAA	60.096	20	197	19	215
57.806	25	CAATGGTAAAACAACGCTCG	59.226	20	265	1	265
60.088	20	AACATGGCCGGAGAATACAG	59.955	20	258	144	401
59.955	20	TCGAGACTTCGGTTGGTTTC	60.232	20	165	3	167
60.001	20	TTTGTCTCCTGGGAGAATGG	60.042	20	253	396	648
60.118	20	GAGATGTGTGTGTGCGTGTG	59.772	20	264	983	1246
59.847	21	ATCATTCCCAGCCACACATT	60.203	20	152	9	160
59.989	20	AACCGTCAGATTTCAAACCG	59.971	20	230	384	613
60.111	20	ATTCACTCACCACCGTCCAT	60.246	20	253	22	274
59.966	20	GGGAGAGAGAGCAGCAGAGA	59.969	20	247	235	481
60.668	20	CGGATGAACACCCCTACTTG	60.366	20	256	1263	1518
60.274	20	TCAGCCTACTTTCGGCCTTA	59.975	20	132	130	261
60.493	20	GAACGATGCTGCCATGATTT	61.014	20	215	456	670
59.797	20	AGGCACCAAAGAGATAGGCA	59.836	20	260	6	265
59.993	20	TTAACCGCCAAACTCAAACC	59.975	20	109	507	615
59.502	20	TTAGATCATACACGTGGCCG	59.566	20	152	416	567

59.73	21	CAAGTTGAAGTTATGCCCCC	59.429	20	275	0	274
62.397	18	TCATGGAAACATGACGTGCT	60.12	20	228	39	266
60.011	20	CTGGGTAAAAATTGTGCGCT	60.131	20	243	1087	1329
59.901	22	TATTTTGGGCCTGAATGGAC	59.762	20	141	18	158
59.391	21	GTCCACGGTGGTGCTAGAGT	60.182	20	105	62	166
59.799	20	CAGTTTTCGTTGCACCCTTT	60.147	20	263	1664	1926
59.424	23	TTTGTGGTGGTGAAGATGGA	59.935	20	263	0	262
60.125	20	GTGGGGGACTTATCTGTTAGAA	57.236	22	278	53	330
59.597	20	TGACCGAATTCAGACATCCA	60.048	20	174	1005	1178
59.93	20	GGTGGTATGGTGTAGAGGACC	58.242	21	264	42	305
60.683	20	CCATTGGTATTGACAGCGTG	59.988	20	115	487	601
59.875	20	GCACTCTCACGAGCTCACAC	59.771	20	140	882	1021
59.272	20	TCATGCCTAAATGTTTTGATGC	59.971	22	180	282	461
59.75	20	AGAGCTTGCCGAGAGAAAGA	59.454	20	159	180	338
60.361	20	TGTGCTTCTCCAAGGCTTTT	59.993	20	245	132	376
60.86	20	TGTGGCTTATGGAGGTTCAA	59.123	20	132	172	303
60.725	20	TTCAATTCTCTGCGTTGTGC	59.995	20	205	375	579
60.22	20	AAATTACGGCCACAACAAGC	60.003	20	175	2203	2377
60.035	20	ATCTCACTTCACCTCCCCCT	59.929	20	202	78	279
59.262	20	TGTCTGTGAGAATGGCCAAG	59.831	20	201	107	307
59.973	20	CAAGTCCAAGTCCGAAGACC	59.697	20	223	19	241
59.939	20	GCTAAAAATGTGGTTGGCGT	60.003	20	279	1310	1588
59.897	20	ACGCCACAAATTTTCTCACC	59.978	20	211	429	639
59.801	20	GACCGAAAACCGTTCAAAAA	59.953	20	224	221	444
60.237	20	TCGCCCTTTGGATTTATTTG	59.901	20	278	48	325
59.329	20	GGAATAAAGGGTGGTTGGGT	59.919	20	203	53	255
59.9	20	GTCAGAATGGATTGAGTGCG	59.245	20	156	71	226
59.973	20	TCCCTAACAAATCACACCGA	58.973	20	111	142	252
58.644	23	TGTCCAAACAAATAAAAACATTC	60.139	24	187	15	201
60.156	20	GCATGAGAAAATCCTCCCAA	60.014	20	110	18	127
59.97	25	TGGGTGGTGGAAAAGAAGTT	59.425	20	199	38	236
57.416	26	CACACACAATGTTGGGAGGA	60.416	20	130	28	157
59.498	23	ATATTGGTTTCGGATCGTGC	59.791	20	221	4327	4547
59.231	22	TGTGGTTGAAATCTAGCCCTTT	60.001	22	153	10	162
59.485	21	CGCATCACTCTTTTTAGCCA	59.062	20	263	466	728
60.183	20	GTTATGCGTTTTGACGGGAT	59.829	20	210	250	459
59.008	25	GATTCGGAAGGTCGACAACT	59.141	20	142	8	149
59.583	21	CAAATGTCGCGGATTTTGAT	60.837	20	251	150	400
59.948	20	CTTTTATCCCCAAAATGCCC	60.489	20	208	412	619
59.447	21	GCCATGATAAATCCACCACA	59.205	20	268	40	307
60.053	20	AAAGCAATAATATTTGTGCCATGA	59.783	24	201	74	274
60.27	20	CGCGGACACATCATGTAAAC	59.995	20	185	102	286
59.943	20	TCACACATAATTGAGTTATCATTG	59.685	26	228	90	317
60.112	20	AGGTGAGGGAGACAATGTGG	59.962	20	239	457	695
59.811	20	ACCGTGTCGGATACACATGA	59.837	20	213	31	243
59.997	20	AGAGAGCATTCCCACAAACA	58.287	20	107	643	749
60.016	20	GCAAGGACGAATTCCAAGAG	59.813	20	269	1423	1691
59.915	20	TCCCCTATCGGTATTTTCCC	59.978	20	207	90	296
59.933	20	TGGGCTAGCAGACCATCTCT	59.973	20	259	68	326
60.24	20	TTGCCACCCCTAGAGAGAGA	59.943	20	247	76	322
59.628	20	ACTTCACCCGTACGTTGCAC	61.016	20	169	526	694
58.849	23	ACGATTTTGCCCTTGTATGC	59.967	20	213	7	219
60.822	20	ATTAGGGGAGAGAGGGCTCA	60.169	20	240	218	457
59.543	20	ACCCGAAGCTAGGAAGAAGC	59.983	20	142	87	228
60.025	20	GTGCACATTTCCCTTTCACC	60.362	20	247	225	471
59.5	21	AACGTGCCCTATTCACATTTTT	59.778	22	141	12	152
59.569	20	GACCAACGTGGCCTAACCTA	59.993	20	254	439	692
59.572	20	CATTGCAGATTTTGATGAGCA	59.824	21	253	2067	2319

59.823	20	TAAAAAGGAAACAGCCGTCG	60.236	20	126	145	270
59.546	20	AACCTTTGATCACACACGCA	60.16	20	171	13	183
59.989	20	TCCAACTCATCTTTCGGACC	60.05	20	277	586	862
60.932	20	CCCTAATTTATGAAAGAGTGGGA	58.576	23	195	313	507
60.088	20	TTGTGTGGGTCGATTCTTGA	60.088	20	257	1169	1425
60.11	20	CAACACCAACCACGAACAAC	59.897	20	263	58	320
59.104	22	TCCATCCTCCATAATCCTGC	59.854	20	221	95	315
60.375	20	TGCCTGCATGATCAAATAGC	59.799	20	247	2644	2890
57.516	24	ATTGACCACCATCATTGCG	60.346	19	158	98	255
59.352	23	GGACGCACCAGACTGTTTCT	60.307	20	199	867	1065
60.285	20	GTGTGTTTAGCAGGGACCGT	60.035	20	198	1696	1893
59.972	20	GTGTGGATGTGCGTGTTTTC	60.016	20	223	620	842
61.041	19	GCTAGACCATTGTAAGGGGG	58.528	20	194	70	263
60.288	20	TCCACGGATGTAAATTGTTCC	59.677	21	124	1727	1850
57.605	22	GCCATGCGCAGTATAATTGA	59.691	20	138	91	228
60.032	20	ACATTTTTCCACACTCAGCG	58.775	20	280	261	540
60.089	20	ATGGGAAGGGGAGTTAGCAT	59.789	20	108	43	150
60.015	21	TGACTCATACCATGGAGCACA	60.128	21	237	399	635
59.945	20	ACCATAGAACCACACGGCTC	59.997	20	267	146	412
59.982	20	ACCATAGAACCACACGGCTC	59.997	20	183	232	414
59.72	20	TCGTCCGAAAGAAACCTTTG	60.22	20	264	28	291
59.962	20	TCACAACCAAGGTTTGGACA	59.976	20	215	909	1123
58.869	20	ACAAGAGGATGAAGGCCAGA	59.803	20	258	78	335
59.347	20	CCTTCGGATTGCATTACCAC	60.331	20	222	51	272
58.566	20	TTACAGATAACCGTTCCCGC	59.96	20	158	0	157
60.103	20	CGGGAGTATTTGGTCACACC	60.232	20	190	549	738
59.598	20	GGCAGGCACAGAAGAGAAGA	60.678	20	270	2186	2455
59.098	23	TCATTGACCAAGTCTTGACGA	59.278	21	252	228	479
60.111	20	TGCAACCTACTCAAAGACTTCGT	60.341	23	266	571	836
60.132	20	TGATGCCCCAAATCTGAAAT	60.274	20	245	33	277
60.209	20	GCTTACTGATGCAGAAGCCC	59.985	20	249	105	353
59.844	20	ACCCCTCACATGCTCTTCAC	60.12	20	275	630	904
59.592	20	TTCGTTGACCCCATATGTCA	59.774	20	208	444	651
59.82	20	CAGCACCAGAATTGCTCCTA	59.024	20	144	184	327
59.488	20	GATTGCCGACTGAACCTCAT	60.081	20	273	152	424
57.837	27	TCCACACCATCTCAATCCAA	59.893	20	234	543	776
58.64	21	CCCAACACTCCATTCTTCGT	59.966	20	117	9	125
59.703	21	AACCAGAACGGCTTGAAAAA	59.724	20	280	1057	1336
59.933	20	CGATCGGTCAATCGAATTTT	59.901	20	177	434	610
58.801	20	AACCCTAGTTTCTGCTGCGA	60.015	20	175	20	194
60.177	20	TGTCGTAGATCACACGGTGG	60.593	20	269	2654	2922
62.397	18	TCATGGAAACATGACGTGCT	60.12	20	230	39	268
60.081	21	AACTCGATAACGGATGCTCG	60.235	20	223	12	234
59.903	20	CCTTCAGAGGCATGGTTTGT	60.111	20	176	44	219
60.418	20	ACGGGAGGGAGAGAGGGTAT	61.214	20	255	212	466
59.465	20	CCATTCTTTTAGGGCCAACA	59.931	20	276	388	663
59.993	20	CGATCCCTCTCTCTCACGTC	59.945	20	170	101	270
60.362	20	AATGGATCGGAAGCAATGAG	60.036	20	179	789	967
60.104	20	AAATCCTTTCCCCAATAAACG	59.216	21	280	3265	3544
59.916	20	GACACCGTTACGCAGACTCA	59.905	20	128	1480	1607
59.874	20	TCCCCTAATTCACGTGTTGA	58.973	20	263	612	874
59.976	20	GCCGATTCCTCCTTTCTCTC	60.293	20	128	4302	4429
61.006	20	TCGTCGATGATCGTATAGCAA	59.295	21	279	33	311
59.903	20	AACACGCGTTTTTAGGGTTT	58.676	20	217	72	288
59.109	20	GAGTGGGAGATTGTTGGGAA	59.903	20	241	70	310
59.232	20	TGGGTTCTCTCTCCCCTTTT	60.045	20	210	136	345
59.752	27	ACGTGTGAGACTTCGTGTCG	59.94	20	276	1098	1373
60.161	20	AACTGCTGGACCTCCACAAC	60.159	20	143	101	243

59.973	20	CCCCACCCAAGTATTTTTGA	59.657	20	101	140	240
60.068	20	CATGACTCTCAGCATATGGGC	60.64	21	262	32	293
58.947	20	CCACCTTACTCACGCCTCTC	59.867	20	251	40	290
59.993	20	ATGGTGGATTTTCCTTTCCC	59.996	20	172	45	216
59.767	20	CACACAAGCAACTTCCCTCA	59.873	20	239	640	878
59.73	20	TATTTTGGGCTTTTGCTTGC	60.205	20	219	2416	2634
59.988	20	CAACGAGCCTTCCTTTTGTC	59.853	20	257	356	612
60.496	21	TGAAGAAGGAAGCTAAAATGCAG	60.03	23	155	17	171
59.41	20	GCATTTGTTAGAGGTTTTGACCA	60.389	23	280	2196	2475
59.288	20	GGAGATCGACCAATTTGGAA	59.871	20	232	80	311
59.813	20	CGTGGTTCGATCGTAAGTGA	59.716	20	210	307	516
60.048	20	CATCTCTCCTTCTCTTTCTCGG	59.593	22	252	16	267
59.975	20	AAAAATGAAAACGTTACTTCTGCC	59.949	24	178	129	306
59.55	20	GTGGACTCTTGGGGTTGAGA	60.088	20	227	20	246
59.797	20	CCCTTTTCTCCTTCTCGCTT	59.955	20	221	255	475
58.446	20	GTCTCGATGGTGTGATCGG	60.063	19	158	15	172
60.269	26	CATATATGGGGAGCGTACCG	60.188	20	273	5	277
60	22	GCCGAAAATACCCCCAACTA	61.029	20	172	94	265
59.954	21	GCTTGCCCAGACTTTCAATTT	60.607	21	280	54	333
60.031	20	GGTGGTGGGCGAGTAATAAA	59.823	20	123	289	411
59.579	20	AAGTCCACACAGGTGACTCG	58.725	20	148	214	361
59.989	20	ATTGGCGAGGGGAGAGTG	61.188	18	228	1405	1632
60.043	20	TCAGCTCCAGCTCCTTGATT	60.096	20	219	1082	1300
57.439	21	TCAACTTTCGGAAGCGTACA	59.464	20	117	37	153
59.32	20	CACGCATTCCCAGAAAATCT	60.074	20	118	10	127
59.966	20	CCCTACGGGATTCTCCCTAC	59.783	20	226	356	581
60.125	20	AACCGAAATCACCGCTACAC	60	20	160	144	303
59.933	20	AGAGCAAACTCCGATGGCTA	59.978	20	256	1308	1563
59.758	20	AAGACACCTAGTTGCCCCCT	59.994	20	183	68	250
60.035	20	GCCACTGATCCCCAGAGTAA	60.073	20	267	1065	1331
59.724	24	TGCAGGGTTCGATTCACATA	60.073	20	238	269	506
60.688	20	CTTGGCGGATCATATCACAC	58.953	20	228	4	231
59.31	20	TTCACGAACACACCCACCTA	60.001	20	140	205	344
60.08	20	AAAAAGTGCGCCAAAAACC	60.103	19	269	130	398
60.147	20	GTGCCAGTGAGGACAAAACA	59.726	20	234	25	258
59.839	20	CGGTTATTAGTTATCACCCGAAA	59.322	23	191	785	975
59.518	20	GCGTTTTAACTCGTCGTGGT	60.176	20	233	1096	1328
59.917	20	GAGCTGAAGCACTTTGACCC	59.997	20	148	1628	1775
60.042	20	AAAATATGCAGTGGCTTGGG	59.96	20	173	1812	1984
59.586	20	GAACCTGAAATGCAAGGAGC	59.82	20	129	1258	1386
59.473	20	GAACTAGGCGAGAACGATGC	59.985	20	178	390	567
59.896	21	GCTTAGGAGGGTTTCCTTGG	60.068	20	239	227	465
60.155	27	CGTAAAAGGAAATGCATGAAAA	59.151	22	187	264	450
59.813	20	CCTTGTTCTCCTGCCTTGAC	59.844	20	218	99	316
60.56	20	ATCGGTAATTCACACGCACA	59.995	20	181	66	246
60.175	20	GTTGGCCCTTGATTGTTGTT	59.836	20	183	142	324
59.415	20	AACTAAAGGGGAAGCTCTGC	57.695	20	219	567	785
60.146	20	CTGGGTACGGCTAGAAGGAA	59.331	20	152	238	389
58.999	20	AGGGTCGTTCATGGATTACA	57.864	20	174	347	520
59.973	22	GAAGTGGGAGGATTTGGACA	59.903	20	112	482	593
59.933	20	AGAAGTGTAGAGCGGTCGGA	60.012	20	135	1792	1926
60.157	27	GCCTGCAATTACTTGGGGTA	59.96	20	156	68	223
60.148	21	CGTCGAAACGGATATTTTGG	60.315	20	232	48	279
60.397	20	GATGCCTTTTTGCTTTGCTC	59.967	20	187	1919	2105
59.67	20	TGTAACTTGATTGCTAAGAAATTG	58.849	25	251	90	340
59.694	20	GCATATCCAGCACGCTAACA	59.862	20	263	146	408
60.142	20	TGTAGTGAACTCGACGCTGG	60.049	20	206	209	414
60.188	20	TTTGCATGGGTCAAAGTGAG	59.691	20	264	8	271

60.042	20	GTCCACATTTTGCAGCCTTT	60.118	20	117	65	181
58.819	20	TGGTATCAGAGCGGGATTTC	60.036	20	142	629	770
60.029	20	AAATGGACAGTTACGGGCTG	59.993	20	217	127	343
59.175	22	TTGGGATATGAAAATGACACCT	58.303	22	117	295	411
59.973	24	CTCAGCATACGGGAAGGGTA	60.088	20	248	8	255
59.864	20	ATCTGGCCCATCTGAAACAC	59.934	20	152	394	545
59.872	20	CCCCTCACCAATGTCTCACT	59.962	20	230	69	298
58.895	20	AAGAATTGATCATGCGCGTT	60.615	20	221	1572	1792
59.174	20	TATGGGAACTGCAACATGGA	59.924	20	143	600	742
60.118	20	ATTCCCACAACAAAATGCAA	58.869	20	271	376	646
59.846	20	CAAGCTGTCAACCCAAAACA	59.734	20	269	42	310
59.409	20	GGAAGAAACTCAGCTGAACCA	59.463	21	187	179	365
60.135	20	TGGAAACAAGGGAAAGTCAA	58.173	20	218	0	217
60.232	20	TTAAGAGGGAGGGAAAAGGC	59.661	20	176	851	1026
57.86	20	TCGACGTGTAATCACCCTCA	60.112	20	263	9	271
60.157	20	TTCGGGTCCAGAAAGTTGTC	60.088	20	279	273	551
60.067	20	GCCATAACCGTGTAAAAATGC	59.38	21	272	16	287
59.694	20	TGTGAATGCACCTGAATACG	58.129	20	244	128	371
60.159	24	CCTAGGCCTCTTCTTCCACA	59.425	20	166	6	171
59.621	24	TGATTCACGCTAAAGCACAA	58.075	20	226	8	233
59.942	20	TTCGTCGACTACTCATGCAA	57.997	20	189	2401	2589
59.371	20	CAAATCCCACCATTTAGCACT	58.962	21	280	38	317
60.68	20	AAAGACCCGCAACGTACAAC	60.037	20	252	12	263
60.003	20	TCAACAGAAACGCACACACA	59.912	20	154	115	268
59.017	21	ACGGTGGTGCAAGAGTGATT	60.577	20	146	1	146
60.905	20	GGGATCCCTCGTATCTTTCC	59.728	20	150	4533	4682
59.839	20	GAGGGTGAGTTGGCATCATT	59.934	20	212	118	329
59.434	21	TCGACTTTCAGTATTGCGATTG	60.264	22	264	357	620
60.11	20	ATTCGAACACCACCGACTTC	59.973	20	276	118	393
59.866	21	TGGCACATATTTCAACGAGTG	59.6	21	266	8	273
59.261	20	TTGCATGCATTGCTTAAGTCT	58.597	21	250	209	458
59.82	20	CATGGGGAGAGGAGTTAGCA	60.21	20	161	253	413
59.127	20	CCAATATGGCGAACCACTCT	59.955	20	251	190	440
60.573	20	TTGATGGGGTGAAAATTCTTG	59.787	21	280	79	358
59.854	20	CTTTGTTTGGGAGTCGAAGC	59.853	20	243	1167	1409
59.596	20	AAGCATTGATGTCTGAATTTGAA	58.755	23	240	273	512
60.056	20	CAACAGTTTGGCATCAGAGC	59.445	20	270	117	386
60.216	21	TGTTGCCAGAAAAAATTGTCG	59.706	20	250	20	269
59.734	20	CGTGTATGCTGCATGTTTGA	59.307	20	238	347	584
59.845	20	CCTATGATGGTATGGTGTGGAG	59.195	22	253	73	325
59.998	21	GGGTTTCTCTGTCACCCCTT	60.349	20	229	53	281
59.988	20	GAATGAGCAGACGCGTTTTT	60.395	20	277	24	300
60.068	20	AGCTGCCTGCTTCATGTCTT	60.164	20	230	115	344
60.112	20	CGATAAATCATGCTGATATCGTAC	60.247	25	174	134	307
60.21	20	ATCGGCTACTTACCGCAGAA	59.867	20	120	26	145
59.791	23	CTTCAAATCCCTCCCCAAGT	60.298	20	154	347	500
60.008	20	GCAAGAGTAACCGGAAACCA	60.11	20	190	3211	3400
60.188	20	CGTTTTGACAATATTTAGTGTTTTG	58.7	26	134	996	1129
60.291	20	CTCATATGACCACAACCCGA	59.369	20	257	24	280
60.201	20	GACCAAACCCCAAAGTGAAA	59.807	20	270	113	382
59.722	21	TGTGTGGCTTCTTACACCCA	60.152	20	271	2103	2373
60.044	20	GAGTTTTGACGTCCGAGTCC	59.703	20	181	1207	1387
59.439	20	TTTTTACCATTTTGCCCTCG	59.937	20	208	1044	1251
59.989	20	CCCATCTCCACGACGTTATC	60.34	20	271	1506	1776
59.968	20	ACTTACACACGCACGCACTC	59.977	20	118	27	144
58.413	20	CGATCCATATTGGGTCAAAC	57.735	20	211	9	219
60.003	20	TACCAAAGAGCAGGGAGGAA	59.807	20	160	1877	2036
60.004	20	GGATCAGTATGGCAGTTGGG	60.34	20	128	65	192

59.092	25	CTGATCTGGGTTGGGAATTG	60.309	20	115	3	117
59.711	20	ATATGTGCTGGAGCCTTGCT	59.866	20	260	2116	2375
59.999	20	GACCCACTGACCTCCGTAAA	59.966	20	229	376	604
59.993	22	ACGCAAGTGTACGTGGTCAA	60.222	20	222	251	472
59.933	20	TCCCAGCCTGTTTCAATAATTC	60.312	22	241	2912	3152
60.045	20	TTTTTCGAGGTCCATTTTCG	60.046	20	249	6	254
62.397	18	AAGTATTGGTCGATCGGTTTTT	58.931	22	136	39	174
59.992	20	TTCACAGAGGGTGGTTTTCC	59.943	20	224	394	617
59.636	21	TCGCGGATTTTTGGATAAAC	59.907	20	226	0	225
58.655	20	GCAGCAAATCGATCCATACC	60.444	20	209	970	1178
59.907	20	CGGATTTATTGGTTATTACCTGA	57.222	23	182	469	650
59.355	20	TGGGGAAGTGTTTATCAGGC	59.933	20	192	156	347
57.842	20	GGTAGTTGATGAAAGCCGGA	60.074	20	179	31	209
59.95	20	CACACTTTACACACACTGAAAATG	59.163	25	182	359	540
60.142	20	CAGAGCCCACGGTTAGTCTC	59.867	20	245	139	383
59.989	20	GGGTTGTGTGCCCTATCATT	59.676	20	254	8	261
59.918	21	GTTTCTTTGTGGGTTTGGGA	59.807	20	191	4815	5005
58.976	23	TCGCTCAACCAAGTAAGTCG	59.072	20	201	362	562
58.955	22	TTGGGAGGAGAGATTGTTGG	60.042	20	277	17	293
59.586	22	GGTTCCCACGTTACCAAAAA	59.702	20	254	2114	2367
59.985	20	GCTAACACCACGCCACTACA	59.788	20	215	1241	1455
60.149	20	AGCAGTTATTGTGATGTGGGTG	59.92	22	251	20	270
60.615	20	GTCGTTGCCTCATCTTGGTT	60.119	20	260	270	529
60.162	20	TGGGAGGGAGATAATAGGGC	60.245	20	274	160	433
59.938	20	TTTGTGCTTAATTTTGTTTCTAATC	59.969	26	177	148	324
60.096	20	GAGAGGATTTTGGGACGACA	60.05	20	197	941	1137
60.008	20	ATCCCCAATTTACCAAACCC	59.756	20	199	3	201
59.769	22	CGATCTGGTATCAGCGGTTT	60.096	20	200	343	542
59.066	21	ATTTTTGGATGAGGCAGTGG	59.933	20	279	1229	1507
59.833	20	TTTTCTGACCAACACCACCA	59.976	20	279	1212	1490
58.32	21	AAGGAGGAAGTGAGGGGAGA	60.186	20	232	15	246
59.504	20	TTGACAATATTTAGTGTTTTGACAT	58.99	27	145	344	488
60.008	20	CCTTTCTCTTGGCCTCCTCT	59.95	20	191	338	528
60.103	20	CGGGAGTATTTGGTCACACC	60.232	20	189	137	325
58.966	20	ATGCAACTCCCAAACGAACT	59.598	20	267	2413	2679
59.527	20	AGATTTACGTGGTTCGGTCG	59.993	20	153	1137	1289
59.148	21	CCACATTTAAGGGTTATCACCTG	59.654	23	102	231	332
60.051	20	GTTTGGGGTGTTTGGAGTTG	60.246	20	151	217	367
59.645	23	GGTGGGCTTGGTGTACTAACAT	60.172	22	112	917	1028
59.971	23	TAATAGGCCCACACCACCTC	59.813	20	244	61	304
57.235	25	TGGGAAGACAATTGGTGTGA	59.935	20	159	5	163
60.032	20	TGTGAGGCCCATCATACTTG	59.522	20	257	1265	1521
60.074	20	CCGATTCTGCCTCACTCATT	60.218	20	190	205	394
59.137	21	TACGAGGAGAGACCGCAAGT	60.012	20	272	77	348
59.929	20	TGTTTTGACAATATCACGACCC	59.73	22	175	241	415
59.788	20	GCAGATGCCACAAAAGGATT	60.081	20	187	843	1029
59.587	20	GGCCGTGAGTCCATTGTAGT	59.997	20	277	19	295
59.893	20	CGGTGATCATGCAACTACCA	60.539	20	279	989	1267
59.127	20	TACTACATCAACCGCCAGCA	60.28	20	278	370	647
60.026	24	CCGTGAATTTACCCATAGCG	60.335	20	117	7	123
60.081	20	GGAGGGATCGGATAGAAAGG	59.859	20	254	1355	1608
60.755	20	CCAATACTGGTCGGGCATAC	60.214	20	114	1	114
59.415	20	AACAACGTTATCTGCGACAAGA	59.813	22	194	528	721
60.095	20	GGATCATTAGGGTTGCCAGA	59.894	20	124	303	426
60.969	20	TTTCTTGGCCTACACCGAAC	60.11	20	277	55	331
60.366	20	GTAGCATTTGCCGCATTTCT	60.238	20	242	963	1204
59.916	20	GAAAAGAGCTGCAAAGGGTG	59.993	20	201	552	752
58.967	24	CGATCCATCCCGTTAGTACG	60.344	20	270	466	735

59.916	20	AAACCCATTTCCACCTGTCA	60.21	20	184	281	464
60.009	20	CCATGAAAGCTTGGTTTGCT	60.249	20	115	845	959
59.962	20	TGATTCCGGAAAGAAGATGG	60.006	20	145	980	1124
59.969	20	GGCGCACTGAATTGTTGTTA	59.735	20	216	3	218
60.425	23	AGGGTCACGAATCCTTCCTT	59.935	20	265	74	338
60.554	19	AAAATGCCCTTGTATGCTGC	60.103	20	146	21	166
59.916	20	TAGGATTTGAACCTGCGACC	60.074	20	227	76	302
60.47	20	TCTGCTGCAAATTTGGAAGTTA	59.89	22	179	851	1029
59.292	20	CCGTCGATTTTCAGGTTTTG	60.472	20	186	105	290
59.844	20	CGGAGAGGACTTACCGGATT	60.455	20	242	29	270
59.756	20	TTCATTCAAGCTACCCACTCTTT	59.317	23	163	105	267
59.924	20	TGGCCATGTTGGTAGATTCA	59.924	20	150	27	176
59.924	20	TGCTTCACCACTCAATCTGC	59.992	20	189	1080	1268
60.287	20	CGAAACGTAAATCAGCAGTGA	58.978	21	228	829	1056
60.096	20	TGTCCACTTGTGTCACGGAT	60.005	20	221	67	287
59.688	20	CCCACTGCAGAAATGGAGAT	60.073	20	125	695	819
60.362	20	TCATCATTTCGATCCTGTGG	59.451	20	148	1	148
60.117	20	TGGGTTTTTCTCATCTTCGG	60.044	20	197	612	808
59.72	22	TGGCAATTTGTCTTTCAATCC	59.93	21	198	21	218
59.88	20	AGCATCTCCAATGCCAGGTA	60.624	20	201	14	214
59.658	20	CGAGTGGATCCTCTTCAAGC	59.95	20	224	1270	1493
60.074	20	CAGCACTTTTCATGTTGTTGC	59.381	21	187	854	1040
59.864	20	GATATGATTTTGCGCGGAGT	60.067	20	230	215	444
60.025	20	AACGATTGGAGCATTATGGG	59.784	20	193	142	334
59.903	20	TTTTGTCGATGATATGGTTGTG	58.413	22	192	38	229
60.173	20	TGTAACAAATAAATTAACGTACTG	57.577	27	200	1055	1254
60.074	20	GCGTGTTCTAGGTGTTCTTGG	59.788	21	225	126	350
60.378	20	CTCATTGTAATCTCTCCCAAAGTT	57.927	24	158	399	556
60.416	20	CATGCATGATGTGATGTCAGTC	59.999	22	166	41	206
59.912	23	CCATTTACTAAGAACGACATGCA	60.404	24	277	1645	1921
60.203	20	TTTTCGGATCGAAATTAGGTT	57.759	21	205	466	670
58.754	23	TTTTTCTTTTGCACGACTGC	59.087	20	156	13	168
61.016	19	TCGTCTTCCCCAATCATCTC	60.011	20	273	4	276
60.504	20	GAGCACAACCATGGTGAGAA	59.682	20	266	115	380
59.281	20	TTTTTGAAATCCAACGACCC	59.778	20	145	115	259
57.357	20	CCATTGGCTCGTTTATTTTAGA	58.331	22	280	171	450
60.074	20	TACAGATCGGGTCTTGAGGG	60.065	20	268	443	710
60.149	20	AGTATGCTTCTCCGAGTCCG	59.454	20	219	507	725
60.064	19	GCATACAAAGGTAAGGAGGCA	59.238	21	141	636	776
60.126	20	GGGAGAAAGACACGTGGAAC	59.555	20	271	133	403
60.255	20	GCAACATAGTTTATGCATCCCA	59.859	22	232	62	293
59.901	20	ATTGTGAACCGGTGGTTCTT	59.308	20	252	120	371
59.75	20	GCATGATCAGGGTAAAATCCA	59.776	21	200	266	465
59.918	21	CCTTACACCTCACACCCCAC	60.275	20	168	456	623
59.85	20	TTTTCCTTCATTCCCATTATGTC	59.22	23	257	398	654
58.12	20	AACGGCCAAATCTAACGAAA	59.586	20	265	285	549
58.917	20	ATTTCAAAAAGTGGGGTCCA	59.264	20	265	0	264
59.787	20	GAAAGAAGAAGAGAGATAGATA	58.05	27	130	607	736
60.073	20	CCATCGTCCTTATGGGCTAA	59.916	20	249	222	470
59.703	21	CCCTCCATCTCTCTTCTCCC	60.149	20	246	9	254
60.553	20	TCCCTGCTGCTCTCTCTCTC	59.969	20	150	3	152
59.976	20	CCAAGCCCATAAGCATCCTA	60.053	20	195	28	222
59.803	20	TTCTCCTTGTTTCCGTGGAC	60.088	20	280	65	344
59.839	20	TGATTTGATTCTTCGCGTTG	59.809	20	108	2489	2596
57.318	27	TTGGTCCTCGATTGTTATGAA	58.079	21	280	316	595
57.593	21	GGATGGACCTTCCCAAACTT	60.169	20	242	50	291
59.874	20	CGCTTCAACTTTTCCACCAT	60.11	20	161	611	771
60.318	21	TCCCAGTACGCAGACTTTTCT	58.994	21	280	34	313

59.968	20	TTAGGAATTTGTTCCCGTGC	59.938	20	267	64	330
58.62	21	CGGCTTCTCCCTATCAAATG	59.662	20	105	500	604
59.889	20	AAAAACCCCGACTCAAACTT	57.697	20	224	309	532
60.765	20	GTGGACACCTTGTCAAAGCA	59.726	20	116	29	144
59.94	20	TTGACAATATTTAGTGTTTTGACAT	58.99	27	258	602	859
58.388	20	TAAATTTGAACTTTGCCCCG	59.937	20	134	796	929
59.086	20	GTTGCCCACAAGTTCGAGTT	60.156	20	216	314	529
59.873	20	TGCAAAATGGGGATTTGATT	60.132	20	227	1055	1281
57.771	26	CACTTGGACCAGAAAAGGGA	60.081	20	109	14	122
60.11	20	AGACGTTGCATGTGCTTCTG	60.056	20	250	1697	1946
59.775	20	TGCTGAGTTTTGAGTCACGA	58.112	20	178	131	308
60.195	20	GGATCCGAACCAGAAAACCT	60.306	20	267	1851	2117
60.264	21	GAACCAAGGGATTGAGTGGA	59.903	20	275	1256	1530
60.207	21	GTTTGTTGAAGCAACTCGCA	60.035	20	230	99	328
60.39	21	GCTGATTCTGAAGGCATGGT	60.226	20	280	100	379
59.993	20	AACCAGAACCGTGAAATTCG	59.971	20	217	416	632
59.83	20	CCAACCATAATTGTTTCGGG	60.046	20	246	298	543
60.103	20	CGTCATAAACAGCCGGAAAT	59.96	20	224	1049	1272
59.833	20	CCCATAACCATGACAAACAATG	59.975	22	231	429	659
57.73	23	TGCTACAATGACGATGCCAC	60.697	20	130	20	149
59.123	20	GGTTGGGATGGAATGAAAAA	59.599	20	246	301	546
59.324	21	AAAATCACTAGCATGCACGG	58.799	20	193	14	206
60.032	20	TTCATAGTCGGCTCAATCCC	60.036	20	232	309	540
59.962	20	CCTTGCTAGATGGCCAAAAA	60.202	20	280	318	597
60.038	20	TTCCACCTCATATCATTCCCA	60.14	21	210	145	354
60.096	20	ATCCTTGTCCTCCTGTCCCT	59.929	20	179	706	884
59.931	20	CCATTGCATGCGTCAGTATC	60.104	20	225	3525	3749
59.318	20	TGCAGAGATGGTGATGGTGT	60.121	20	248	7	254
57.878	20	CGTCGCCTCTTATTGGACAT	60.096	20	252	13	264
60.027	20	ATGAGCTTTGTATGCCCCAC	59.962	20	270	89	358
57.543	18	ACAAACGCCATCAACATCAA	59.972	20	118	0	117
59.89	20	AATGATTGAAGCTTCCCCCT	59.903	20	146	319	464
60.134	20	GCTTGTTGGATGCCTTTGAT	60.081	20	153	10	162
59.844	20	CGAGTTGCTTCTATCGTCACC	59.89	21	223	676	898
59.381	20	TTGGCATGTAATGCGAGTTT	59.186	20	277	976	1252
60.096	20	CAAGACGGACAAGTTGGGTT	60.005	20	263	240	502
59.286	22	TTGGAAGCAATTGCATGATT	59.115	20	196	31	226
58.994	20	CACGTCAGCTTCATCTCCAA	59.984	20	238	325	562
59.805	20	CAATGCGCTGTGTTCTTCAT	59.871	20	146	415	560
58.123	23	AGCACCGACTGAAAATGAGG	60.255	20	178	1	178
59.713	20	TGTGCTGCTTCAATTCGTTT	59.469	20	279	49	327
60.249	20	AACCCATCCTCTCATCGAAA	59.483	20	131	108	238
59.075	20	CCATTTTGCCCTGATATGCT	59.923	20	193	104	296
59.795	20	AGCGATTTCATGGAGATTGG	60.036	20	253	662	914
59.762	20	GCACACAAATAATGGTTTCTTCC	59.771	23	215	145	359
58.867	20	TCCTCTCGCTGTATTTGCAC	59.028	20	258	711	968
59.51	20	TTTTTAAATGGATCGGCCTC	59.011	20	270	2	271
59.935	20	AAACGGGTGAGCAAGACAAC	60.156	20	256	1558	1813
58.941	19	TCCAGTTTGGGTGGTTTAGC	59.971	20	244	49	292
59.973	20	CATGTTTTTGGATTTTGGGG	60.024	20	127	948	1074
60.5	20	TCTCGAACCACTTTCAAGCC	60.375	20	275	130	404
60.712	20	GGCTTGGTTGTTGTAGATTCTG	58.767	22	280	989	1268
59.791	21	TGGGAAGATCTCTCCATTCTG	59.224	21	228	240	467
60.112	20	AGGGGTTATCACCTGAATGC	58.864	20	117	159	275
59.886	23	CGAATTAATCCGTCCAATGAA	59.781	21	247	764	1010
58.509	20	GAATCACTTTGCAAGCACCA	59.847	20	242	157	398
60.195	20	TGCAACCGAAAATTAGGGAA	60.427	20	179	140	318
59.348	24	TCAAATTTTTCTCATGCATATTTGT	59.012	25	230	516	745

60.006	20	TTTGTTATGCGTTTTGACGA	57.846	20	252	290	541
59.385	22	CACGTGCAACCAGATTCAAA	60.699	20	142	82	223
58.994	21	GCTTCCTCTGAATGCCAAAG	59.955	20	142	115	256
60.096	20	TCACGTTAAAGGGCGGTATC	59.96	20	131	21	151
59.722	20	GAAGCGAATCGTCGAGAAAC	59.962	20	198	311	508
60.082	23	TAGCCATGATCTCCCGATTC	59.998	20	228	299	526
59.642	20	GAGGGCTATGCTGATTTGTTC	58.803	21	259	47	305
59.275	22	CCTCCTTGTGTTGCCAAGTT	60.149	20	160	120	279
60.423	20	TCAAGGGACCAGAGGAATTG	60.042	20	261	67	327
59.901	20	TCGGGGTATCAGAAATCGAG	60.029	20	260	54	313
60.081	20	CCATATAACGATGCCATCCC	60.001	20	264	26	289
60.032	20	ATGGTGCAGAGGATAGACGG	60.096	20	253	1264	1516
57.152	22	ATAACCCCCACCAAAACTCC	59.919	20	250	15	264
60.255	20	CCATCCCCCTCTCTTTCTCT	59.63	20	255	144	398
59.225	22	TTCGCTTCCAGTTTTGTCCT	59.853	20	265	8	272
60.083	26	CAACAACAACGTCGTCCATC	60.008	20	198	4	201
60.818	18	CCGACAATTCATCTTTTTCTCA	59.202	22	278	11	288
60.156	20	GGCCGGATTGCTGATATAGA	60.023	20	140	935	1074
59.962	20	AAGAGCAATCTCTCTCCCCC	59.778	20	166	579	744
58.707	21	CTGCCACCATTGATGCTAGA	59.823	20	166	61	226
58.21	27	TCGCTTCAGTCAGTTATCCG	59.024	20	158	11	168
58.294	22	TACATTCATTGGGGTGTGGA	59.623	20	102	15	116
58.686	21	TGGCAGATTTAATATTTACGTTCA	59.061	25	212	167	378
59.719	20	TGGAAGGGAAAAGAACCTCA	59.641	20	189	434	622
60.361	20	GACCTGACACAACCCTCCAT	59.817	20	266	52	317
59.315	20	GTGGACGCTCCAGATTGTTT	60.119	20	268	496	763
59.134	22	GGATCATGCTGGAAGCAGTT	60.226	20	125	7	131
59.182	20	TGATACAAGTGTTGAAGCCAAA	58.346	22	203	444	646
59.871	20	GGCATGTTGACACCCCTACT	59.851	20	223	312	534
59.746	20	CGGTGATAACTAGGAACAAATCC	58.941	23	190	576	765
57.821	25	CCCGGTATGCTGACGATAAT	59.807	20	202	0	201
59.579	20	ATGGTTGCTTGATGGAGAGG	60.073	20	148	6837	6984
59.844	20	AGCAACTTGGTCTGCGATCT	60.02	20	146	1	146
59.123	20	TGGGTCCAAGAAAACCAAAG	59.942	20	118	275	392
59.89	20	ACACGGAGGTGATGCCTATC	59.957	20	218	543	760
60.025	21	TGCGTTTTGACGATATATAGTGTT	59.092	25	100	509	608
60.606	20	AAATGGTTGTTTGTCCCCAA	60.066	20	221	17	237
59.141	20	GAGGGAATCGGAGTTCATCA	60.011	20	272	320	591
60.103	20	CGTCTTCCTCCTTGGACTTG	59.837	20	267	4574	4840
60.032	20	TCCGTTGAGATTTTGCATCA	60.197	20	257	38	294
59.988	20	TCATGGATGGGGACTTGATT	60.135	20	137	664	800
59.773	20	TTGTTGGGAAAGAAGAATGGA	59.532	21	271	31	301
59.962	20	GCGAAATGAATGTACCGGAT	59.791	20	263	672	934
59.934	24	CCTGGTGGATTGTTCTGTCC	60.363	20	259	40	298
59.933	20	CCTTGACAACGACGACCAAT	60.954	20	270	570	839
60.162	20	TCACTCACACGCACTCACAA	60.07	20	103	22	124
60.058	19	TGAAGCAAGAAAAGGGGCT	59.94	19	168	591	758
58.109	22	AACATGAGACGCAAACACCA	60.16	20	256	67	322
60.081	20	CGCGTTACGAATCCAAGTTT	60.131	20	248	206	453
60.667	24	AACCGAAAAATTAATCATCACC	57.085	22	203	157	359
59.626	21	TACAAAGCTGCTCGGTCCTT	60.015	20	233	30	262
60.211	21	GAGATTGGTGGTTGCAGGAT	59.934	20	263	254	516
59.955	20	CGTGTATGTGTGTGAGTGTATATG	59.332	26	182	151	332
59.682	20	GAAAAAGTAGCGATGTCGGC	59.851	20	236	4300	4535
59.744	20	GCTTGCGATTAGGAATGGAG	59.807	20	234	314	547
59.271	22	CTCAAGAAAGTTGTGGGGTTG	59.619	21	279	11	289
60.029	20	GCAACATCTAATGGTTGTGGG	60.242	21	215	125	339
57.929	23	CCTTAGGATTCTCACAGCCG	59.83	20	263	4	266

59.926	20	TTGAGACATGGGTATTTGATGA	57.944	22	224	204	427
59.297	20	GCAAGACCAAATCACTCTTTCC	60.117	22	198	613	810
59.666	22	CATGTTTCGGAGCATGATTTT	59.952	21	268	130	397
59.566	27	ACTCACGTGAAGTATGCCCC	59.997	20	148	106	253
59.989	20	CGCAAGCATGTTAATTTTATTCA	59.213	23	175	238	412
59.78	20	GAATGCATTTCCGGTGACTT	59.939	20	280	1214	1493
60.384	21	AGTGAGAGAGAGGGCTGCTG	59.883	20	275	54	328
59.988	20	TCTTCATCGTTGTAACCCTCG	60.118	21	236	92	327
60.197	20	CCATTTCTGCCACAAAACCT	59.971	20	189	481	669
60.039	20	CCCTCCACCGCCTAACTATT	60.332	20	106	52	157
59.862	20	CAACACTTCACAGCTTCTCCC	59.899	21	221	425	645
60.088	20	ATGGATGGGGGTTAAGGAAG	60.011	20	220	69	288
60.053	20	AACAAAGGGGCAATATGCTG	59.96	20	152	112	263
59.7	20	AAGGAGGTGTTATGAAGGGATT	58.028	22	280	318	597
58.787	21	ATGTCGCAGGTTCAACGTC	59.698	19	263	12	274
60.535	20	AAAAGAGACAAAAGGCAGCAA	59.144	21	257	31	287
60.081	21	TTGGGATTGGTCGTTTCAAT	60.17	20	217	701	917
60.235	20	TGGCTTCTGTACGATCCCAT	60.483	20	218	119	336
59.41	20	TCATGAGGTGGCACAATGAT	59.925	20	215	766	980
59.855	20	CAATTCCTTCCAACACCGAA	60.863	20	171	111	281
59.834	20	CGTGTGTGTAACGTGTGTGTG	59.591	21	148	1185	1332
60.159	20	AAGAAAATAACCACGTGCCC	58.952	20	190	96	285
60.157	20	TTCTTCCTCATTGGTAGGCG	60.206	20	105	57	161
60.025	20	ATCGGAGTTGATTTGATGCC	59.9	20	230	324	553
60.032	20	TGCTTTTTATAACTCGCCCG	60.218	20	208	1323	1530
60.011	20	AGGTTGGCTCGACTTTGTTG	60.291	20	186	49	234
59.572	20	TTTCCATGGCTATGCTTCTCT	58.941	21	184	111	294
57.528	21	TCATGGGTTCTTTCCTCACA	59.059	20	279	534	812
59.951	20	TAGCAGCTGATATTCCCGGT	59.691	20	165	72	236
59.708	20	TGGATGTTGGTTTTGAGCTG	59.691	20	245	669	913
60.008	22	TGCCTAAAGAACGTTACACGG	60.172	21	266	2	267
59.939	20	GGAGAGACTCGAGATGCAATG	59.965	21	142	84	225
59.943	20	AACGAGGTAGCAAGTTGGACA	59.788	21	101	481	581
59.199	20	ATCTGCCAATGAATTCACGA	59.079	20	253	66	318
60.046	20	GGCCGGATCTCACTAAATCA	60.036	20	236	2052	2287
58.574	20	TTGATTTGTTTAATCTAATGGATG	57.304	26	273	779	1051
59.983	21	GCGTTTTGATGATATATAGGTGTT	58.907	26	183	126	308
59.96	20	ATCGAAGTGACGATGGAAGC	60.226	20	262	3376	3637
60.144	20	GCTTGCTGAGTTGGCATGTA	60.019	20	207	248	454
59.799	20	AAGGTGACAACCGATCAAAA	58.048	20	266	248	513
59.989	20	CCCGAACAGAGTCTCCTTGT	59.3	20	254	488	741
59.978	20	ACTGTTATGAGGCGGGATTG	59.955	20	275	2	276
60.288	21	TTCAGTCTTGAAAAGGAGCCA	59.978	21	278	54	331
59.314	20	TGTTCTTCACGGTTCAATGC	59.697	20	261	33	293
57.925	24	GGAGAGAGAGGGAGGGAGAG	59.489	20	229	251	479
60.081	21	TAACCCCAAGTCTGGGACTG	59.959	20	172	36	207
59.621	20	AGGATCGAGAGAGACGTGAGA	59.142	21	265	82	346
59.898	20	AGAAGAAGCAGAGACCGACG	59.745	20	192	86	277
60.27	20	AATCACTTCCCACACGTTCC	59.827	20	153	12	164
59.901	20	GGCCTCATGAACTCTTGAATG	59.685	21	208	881	1088
59.997	24	CCGTACCGGAAATTAACGAA	59.826	20	241	672	912
59.569	20	CACTTCCACACGAACACACA	59.15	20	236	527	762
59.986	20	CCAACTGAGTCCACTACCCG	60.557	20	167	41	207
60.074	20	GGTTATCACCGGATCGCT	58.462	18	191	1935	2125
58.035	25	CCCAAACATCCAACCAATTC	60.029	20	263	217	479
59.784	20	ACTCTATCTCTCTCACACAATCTT	57.487	27	246	188	433
60.016	20	AAATAAGGAGGTGTTATGAAGGG	59.323	24	184	352	535
60.309	20	AGCTCATGGATGTTTGACCC	59.934	20	242	306	547

59.939	20	TCCAGCCTTCCAATCTCAAC	60.195	20	280	24	303
60.103	20	TTCCTAAGTCGTGTTGCGTG	59.904	20	245	796	1040
59.897	20	GTAGGAGCCCACAGTCCTTG	59.721	20	157	351	507
59.91	20	CGCCGTTTTAAGACCCATTA	59.958	20	254	767	1020
59.569	20	GATATGCGAGATGGATGCCT	60.028	20	155	3547	3701
60.949	20	TTCTCAGCATATGGGAAGGG	60.029	20	235	8	242
60.049	20	TTTTTGTTATGATAGGATCAAACC	58.947	26	178	1786	1963
60.053	20	CGTGTGGGAAAGATATGCCT	59.955	20	183	995	1177
59.762	20	TCATCGATTACGTTGAGATGAA	58.241	22	280	756	1035
60.212	20	TCACCCACTCTCGTCACTTG	59.864	20	105	2	106
60.278	20	CATTCCTGTCGCCTTCAAAT	60.074	20	278	37	314
59.971	20	GATCAACCTCCTCCACCTGA	60.048	20	277	507	783
60.008	20	CCTTATTTTTAACCCTAAAAACGC	58.713	24	258	210	467
59.56	20	TGCAACGCTTGTTTCAAGAC	60.035	20	275	1067	1341
60.012	20	TTACGAGCTTGCGAGATTGA	59.712	20	276	118	393
59.917	20	TATCAGTGACCACCCAACCA	59.806	20	260	22	281
57.616	21	ACTGAAAGAGAAGCAGCCGA	60.277	20	253	66	318
60.096	22	GGTCTTGCAGGCTATTACGC	59.873	20	263	61	323
60.423	20	ATGGGATATTCGGGGAAAAG	59.978	20	206	421	626
60.531	20	TCTTTCATGCAATCGCTTTG	59.953	20	229	504	732
59.833	20	CATCCATATTTGGGAGGTGG	60.006	20	217	138	354
60.065	20	TCCTCAATCTGGTGCTTGTG	59.831	20	137	1860	1996
59.962	20	TGGTTTCCGTTTATATGACGA	58.031	21	126	81	206
60.14	20	TTTCGTGGAAGGATACCGAC	59.933	20	266	25	290
60.263	20	AATAGGGGCATCACGATGAG	59.917	20	218	2455	2672
60.029	20	AGCAGGATAAGGGAGTTAGCA	58.111	21	200	405	604
59.024	20	AGCTGTAGGCAGCGAACAAT	60.044	20	103	14	116
59.955	20	CTTGTGGGAGGAAGAAACCA	60.081	20	149	343	491
58.02	20	CAAAACACCTAAATCCCGTCA	59.847	21	255	113	367
57.235	25	ATCGAGAGGAAAGTGGAGCA	59.95	20	263	11	273
60.218	20	CGTATTTAATTCCAACTTTGGGG	60.752	23	247	45	291
60.074	20	TGCGACGATGATGATACGAT	60.065	20	139	251	389
60.096	21	TTTGGACTGTATCGGTCTACCA	59.494	22	244	23	266
60.192	20	TCATGAACTAATCAAGTTCCACA	57.291	23	256	93	348
59.853	20	ATCTTGGTGGGACTACGTGC	59.997	20	275	155	429
59.701	20	TCTCCCTAACGTGCTAACTTCA	59.041	22	244	284	527
59.452	20	CTTGGACCAGAGAGCCATTC	59.803	20	279	1259	1537
60.032	20	GGAGCCCATTGTTTTTCTGA	60.051	20	177	60	236
59.933	20	AAGCTGTGCATGAAGCAGTG	60.207	20	207	671	877
59.223	20	TTGGAATTTCTGGGAGTGGT	59.381	20	271	2038	2308
60.066	20	ATTTTGATGGGCTCCAGTTG	59.933	20	169	1968	2136
59.694	20	CCGAATGTAGTGGATACGGC	60.352	20	106	331	436
59.939	20	CATGAACAAATGATGGCTGG	59.924	20	234	282	515
59.969	21	ATAGGGCACACAACCCTTCA	60.375	20	278	135	412
60.183	20	GACGGCACCAGCTTCTTTAG	60.015	20	257	41	297
59.205	20	TCAATGTGGCGCAATTAAAA	60.074	20	278	289	566
59.962	20	CCTCTTCAAACAGAGAGCCG	60.126	20	161	849	1009
60.256	21	ATTTTATGGTCTTCCAACATTTTT	57.249	24	271	108	378
57.983	20	AGATTCATGGTGCTGCAGTT	58.316	20	189	349	537
59.694	20	GCCTTGCCTTGTCCATATTC	59.533	20	274	134	407
60.734	20	GTAAAGGGTGAGTGGTGGGA	59.82	20	273	259	531
60.073	20	GAGCGCGAAAATAAGACGAC	59.988	20	258	3632	3889
59.184	21	TGATGGTCCGGTTAATACTCG	59.831	21	190	101	290
60.149	20	GGACTTGAGCTTGTTCGGAG	59.989	20	163	245	407
60.045	20	AGCATTTGGAGATGGTTTCG	60.074	20	257	322	578
59.861	20	TTCCAAACAGTGCACGAGAG	60.025	20	193	5557	5749
60.012	20	GGGACGACAAAAAGTTCCAA	59.948	20	280	750	1029
60.008	20	TCGTCCATTGTAAACAGTTCCA	60.399	22	175	132	306

60.18	20	CTCAGCCGTACAGAAAAGGG	59.869	20	275	63	337
60.104	20	AAACTGGTGAGACTGTGGGG	60.002	20	185	1618	1802
60.156	20	GATGGATAAATGATTGCGGC	60.262	20	246	86	331
58.95	20	CTCTCAAACTCACGGCCTTC	59.989	20	130	30	159
59.555	21	TTTCTCTTAGACCGAGCCCA	59.948	20	263	3	265
60.773	19	ATGAGTTTGATGGAGCGAGG	60.218	20	270	308	577
60.074	20	TGTTTCATGTGGCATCAAGG	60.517	20	218	0	217
60.41	23	AGGCGATTCAGTCGAACAAT	59.7	20	100	36	135
60.132	20	TGGCAGCTCATAATCAGTGG	59.823	20	172	304	475
60.073	20	GCAGCAGTGCAACTGAAAAG	59.788	20	277	5001	5277
57.444	22	AAATTCATGGGGATGGACAA	59.991	20	157	2	158
58.777	23	TGCATTGAATGGACTTAGCC	58.723	20	244	24	267
59.907	20	ATGCACCCTCACCCTTTATG	59.813	20	221	28	248
60.11	20	GGCTTGGAGGGTTCTTCTTT	59.691	20	249	219	467
59.933	20	TGACCCACTCCAACTCTTCC	60.088	20	227	673	899
59.837	22	TTTGCACCTGAGGAGGTGTT	60.69	20	126	51	176
60.111	20	AATTGCCCTTTCATGCATTT	59.415	20	205	1251	1455
59.716	20	GAAACAGAGGGAGGGAAAGG	60.045	20	248	47	294
57.52	20	CCTCATTCAACAACTCATCCAC	59.454	22	280	1083	1362
58.161	22	AAGGTCGGCAGAAAAGGTTC	60.61	20	274	289	562
59.055	21	AAGAAAAAGTCGCTGCCAAA	59.996	20	274	57	330
59.942	20	TCCTGACAACGCAAGATCAG	59.984	20	240	194	433
59.316	20	GAGCAATTGTTGGACCGAGT	60.119	20	155	532	686
59.259	21	AAAAACATTGCACCCCAGAC	59.836	20	146	24	169
60.012	20	ACCGACCAAAAATCAAACCA	60.206	20	232	414	645
60.227	20	TGGATCGACAATTAGCTGGA	59.226	20	185	309	493
58.78	20	CTACCCCCGTTGGAAAAGAT	60.18	20	222	17	238
59.988	20	TGGCTGGTTCTCAAAAGTCC	60.232	20	225	21	245
59.967	20	TAATCTTGGCCGCTGATTTT	59.682	20	227	1581	1807
59.985	20	GCTGCACACCCTGTTTTGTA	59.764	20	226	3450	3675
59.566	20	TCCTGATTTCACTTGGGAGG	60.042	20	218	120	337
59.839	20	TCCTTCAATGGAGGTTCAGG	60.042	20	173	370	542
59.381	20	ACCGATTTTCCCCCATTTTA	60.361	20	277	292	568
60.246	20	GTGTGATTTGGTGAAAGCCC	60.362	20	112	104	215
60.081	20	GAGGCTTGATGATGCACAGA	59.95	20	160	5217	5376
60.081	20	TGAAGTGGCAACAATTCGAG	59.84	20	276	920	1195
59.973	20	CCGACATAATACACCGCCTT	59.845	20	136	30	165
59.939	20	CCCTTATGGTGGCTTGTTTG	60.357	20	177	432	608
60.255	20	ACTTCCCGGACAGCATTAGA	59.694	20	226	376	601
59.549	20	GCGGCAGAATGAAGAAGAAA	60.469	20	127	273	399
60.073	20	TCCATGCAAGTCCATTCTGT	59.09	20	258	89	346
59.933	20	ATCGGTTATCACCGGATCG	60.697	19	209	1369	1577
60.277	20	CCGTGTCCGTGTACATTTG	58.394	19	269	139	407
59.435	20	TCAACCATTTTTGTGCTCCTT	59.601	21	152	259	410
59.625	22	GCGCGCTGTATATCTAACGA	59.104	20	153	62	214
59.992	20	TTTTAGAGCATCCCCAGTGTG	60.118	21	278	214	491
60.366	20	TGGCTCTGGTACCATGTTGA	60.112	20	218	6	223
59.229	20	CCTTCACGAGTGGTGACAAA	59.72	20	106	677	782
60.17	20	TTTTGGTGTTTTGCGTGTGT	60.05	20	241	25	265
59.555	21	AAGAGAAAACAAGAGGGGGC	59.691	20	102	3	104
60.042	20	GTTTACTTTTGGGACGGCTG	59.609	20	182	426	607
58.439	25	TCTGGGATAAGGAGCATCAGA	59.782	21	252	919	1170
60.03	22	GGGTTTGGAATGTTAGCTGG	59.429	20	267	304	570
59.752	20	GCTACAGCAGCCATTGATGA	59.979	20	128	644	771
59.955	20	TTGCAGATCTTCATCCAACAA	59.262	21	244	32	275
59.499	20	CCTCAATTCGATCCTGGAAA	60.006	20	179	48	226
59.664	20	GAATTGCGGTCGTCTTCTTC	59.82	20	254	825	1078
60.152	20	CAATTTGTTTCGAATTTTGCTG	59.64	22	172	257	428

60.156	20	CCCTGCTTCTGAAACCCTAGT	59.759	21	227	598	824
58.796	20	TCTTGGGAACCCTTGAGATG	60.042	20	257	965	1221
59.724	23	GGGAGTTTGCACCAGATCAC	60.52	20	276	19	294
60.095	20	TGAATCTGCATAGCCTCTACGA	60.003	22	188	161	348
60.051	20	AGGAAGGGTCTCGTGTGTATG	59.076	21	274	486	759
58.107	21	GGATCTCAAGCCATTTCATGT	58.998	21	222	469	690
60.363	20	TTGATCGACAGCATCCTAGC	58.979	20	228	330	557
59.113	20	ATTTCTTGAGTCGGGGGAAT	59.766	20	278	580	857
60.455	23	GGGAGATCTAGCAGGATACGC	60.209	21	239	247	485
59.91	20	GCGCCTAGAATTCGTCAAAG	59.982	20	260	228	487
60.029	21	TGTGCAGATCTAATGGCACAG	59.879	21	174	154	327
59.203	20	ACGCACGCACTCAGTTACAC	59.977	20	266	1203	1468
58.289	22	GACGCCAATGGAACCTTTTA	59.938	20	106	45	150
59.803	20	AAAATGGGTTTCCTTACCCG	60.048	20	220	138	357
60.29	21	AAATTGAGCTCCATAGCCGA	59.807	20	121	32	152
58.82	27	ACAAAAATGCCCTTGAATGC	59.945	20	265	0	264
60.081	20	CAGACCAGACTAGGGGCAAA	60.246	20	178	242	419
60.298	20	TTGATTTTTAATGGGGCAGG	59.767	20	280	66	345
59.894	20	CCGAATGCACTCACACAAAC	60.16	20	143	516	658
60.69	20	GCACCGGAGAAGAACTACCA	60.255	20	257	508	764
60.074	20	TTTCTCAACCGAGCTCACC	58.945	19	106	305	410
60.088	20	ATCCGCCCCTTATCTCTGTT	59.925	20	214	264	477
59.624	20	TTTCCCTCGATTCTCGTGTC	60.195	20	270	903	1172
60.042	20	GTGCTGCTTTTCTTCGGAGT	59.621	20	256	84	339
59.933	20	TCTAACTTGACCTCACCGCC	60.255	20	260	507	766
59.784	20	GATATTAAACGAGCGGTGGC	59.574	20	277	704	980
60.353	20	AAAATGCCCTTGTATGCTGC	60.103	20	224	457	680
59.989	20	CAAATTCCAATGAAAGGGGA	59.733	20	205	143	347
59.805	20	ATTTACGTCGATCTGCGTCC	60.103	20	168	64	231
59.923	20	GCACCGTGTGCAGTTATTTG	60.18	20	156	284	439
59.95	20	ACCAGCTGCACCTGTAACAA	59.365	20	170	3368	3537
59.914	20	TTCAAAGAGATGGGTCAGGG	60.042	20	168	1356	1523
59.779	20	GGGGTTCGTGCTTGTATTTG	60.365	20	241	404	644
59.829	20	AAATCGGTTAAAACCGGACC	60.055	20	179	71	249
60.147	20	GGCGCATCTGATCTTAAAAA	57.99	20	142	17	158
60.05	20	ACGGCTGTGGTTTCAAATTC	59.978	20	254	376	629
60.035	20	ACCATCGTAGGGTGTATGCC	59.7	20	218	34	251
60.074	20	GGAGAAGAACATGGATCGGA	60.011	20	127	86	212
60.194	20	ATATCAAAGGCGTGGATTGC	59.929	20	154	721	874
60.184	20	GGTAGCCATTTGAGTCGCAT	60.103	20	167	360	526
60.627	19	ACTTCATCCCATTGAGTCGG	59.927	20	103	2	104
60.627	19	CATCAAGAGCCTCCTCGAAC	59.95	20	125	2	126
60.074	20	CCGGAGCCTGTCAACTAGAG	60.005	20	256	3040	3295
59.997	20	TTGCTCTAACAATTCTGAAACGA	59.065	23	183	400	582
59.962	20	CGCCAGGGGAATTGTATTTA	59.789	20	216	1170	1385
58.623	20	GCAGCCATGGTATGGACTCT	60.104	20	279	548	826
59.63	21	TTATGTGGTTTGGTCCGGTT	60.088	20	143	21	163
60.206	20	GTGGATTTGGGGATGATGAC	59.995	20	257	362	618
59.59	20	CGTGGAGTCGACGACAATTA	59.716	20	198	1003	1200
60.185	20	CGCACAGATTGCTTGTGATT	59.871	20	242	597	838
60.072	20	GCCAAATGCCTACAAATTGC	60.465	20	237	1191	1427
59.688	20	TTGGCTTGTCGAGCTCTTTT	60.132	20	261	6193	6453
60.048	20	CCGAATGCTATCTTGGGGTA	59.916	20	248	323	570
59.664	20	TTTTGGCTCGTTGAGCTTTT	59.996	20	243	2350	2592
59.856	21	TGCAAAGCATACTAAAGATGCAC	59.463	23	185	385	569
59.966	20	ATTGTCTCATGGCCCAACAT	60.203	20	154	651	804
60.347	20	TTTGACGACCCATTCAAGGT	60.353	20	258	1480	1737
59.797	20	CGGTCTCCTTTGTCCAACTC	59.697	20	158	293	450

60.431	20	GAATAGTTGCGGATGCACG	60.235	19	177	156	332
59.973	20	CAAGCCCTAGTTCTTTCCCC	60.068	20	239	73	311
60.431	20	CGGTGGAAGGAGTGAGAGAG	59.978	20	103	4	106
59.931	20	AATCCGACACGAACATGACA	59.967	20	256	1659	1914
59.184	21	CACTACCAAGGGGTCTGCAT	59.989	20	131	340	470
59.976	20	TGGGGTTGAGCCCAATAATA	60.146	20	267	81	347
60.226	20	CCGGATATACAAACTACAGGGC	59.758	22	224	102	325
59.939	20	GGGATGAATTTCCACCATGA	60.526	20	183	564	746
57.16	27	TACATGATGGAACGGGGATT	60.014	20	155	2	156
59.993	20	GCATCTCTCTCTTGCTCTCATTG	60.665	23	110	370	479
60.762	20	ATCGGTTATTACCGGATCGC	61.031	20	199	198	396
59.967	20	TTCTTGGTGGCGGTAGGTAG	60.125	20	180	543	722
60.399	20	CAGCCGTCGGATTTAACATT	59.96	20	167	2364	2530
60.152	20	AATGCTTGCCATGAGAATCC	60.043	20	280	767	1046
59.784	21	TTAACCGTCCACATTGCAGA	60.111	20	166	435	600
59.971	20	CAGTTGGTTTTGCATCATCG	60.111	20	141	4573	4713
59.973	20	ACTCGGGCAGGAAAAGAAAT	60.074	20	184	869	1052
60.301	20	TTGAGGGATGACGGGAGTAG	60.065	20	263	39	301
60.637	20	AGGATCAATCCCCACAAAAA	59.22	20	271	159	429
59.028	20	GCGTGTGAGTGTTCGTGAGT	59.948	20	273	48	320
60.149	20	CTTTCTTCTTCATTTCGCCG	59.953	20	134	27	160
59.797	20	TTATCGATCTCCTGCATCACC	60.051	21	246	114	359
59.855	20	CATCACAGAGAATCAAACCAACA	60.023	23	120	325	444
60.045	20	AATGGACCAGCCACTACAGG	59.989	20	279	1375	1653
59.962	20	AACATCATCCAAATCCCAGC	59.756	20	202	644	845
59.966	20	ACTGTCCCTACCTGCCCTTT	59.994	20	256	1424	1679
57.885	21	TGAACCACTCCTCGCTCTCT	60.135	20	241	37	277
60.096	20	CCTTTTTGGGTGCGTATCAT	59.823	20	238	3169	3406
59.82	20	TTTAACAGCCATAAGCACAAGC	59.45	22	160	1713	1872
59.95	20	AGAGTCAAACATGCGATCCTT	58.806	21	190	381	570
59.96	20	GCCAATGGATGAACAGTCCT	59.934	20	191	693	883
60.054	26	ATGCCAATGGCCCAATAAT	59.994	19	244	5	248
59.827	20	GCAAGTGGTCACGTGAAATG	60.16	20	235	406	640
59.987	20	CCCTAATTTGTGAAAATGGGTT	59.141	22	274	69	342
59.964	20	GGTTCTCTGGTTGCACCATT	59.973	20	276	914	1189
59.955	20	CAAAACCCGTAAAGCGAAAA	60.102	20	231	861	1091
57.023	20	GTTCGAATCCTCTCTTCCCC	60.015	20	279	94	372
59.507	23	GTAGCCTTTCATTCCCTCCC	59.903	20	124	475	598
60.149	25	TAAAGCAATTTTGCCCAAGG	60.068	20	171	269	439
59.973	20	CTTGTCTCCATTCCATTGGC	60.461	20	231	85	315
60.001	20	AGGCTATAAAGGAGCGAGAGTT	57.926	22	260	929	1188
59.685	25	ACATATTTATACGCATATAGCAAA	57.577	27	197	1885	2081
60.223	20	TGACCCTATGAGGCCAAGTC	60.073	20	259	838	1096
59.691	20	CCGTGATGCCTGTGAAGTAA	59.716	20	254	2236	2489
59.694	21	TGCGAGTGTTAACCGTTTCT	58.432	20	260	0	259
59.939	20	CGACAATTTTAGAGACAACGTGA	59.322	23	212	2508	2719
59.803	20	CGAGGGAAGGAAGGTTTAGG	60.061	20	125	937	1061
58.912	21	TGTAGCCCGGTGCTAGAGTT	59.898	20	145	21	165
60.111	20	ACGTTGGACCTGAAAGAGGA	59.697	20	275	100	374
60.401	20	AAGGATGCCCAAAGTGTACG	59.993	20	235	8	242
60.243	20	CTTGTGAAATCAATGCACCG	60.111	20	202	98	299
59.854	20	GAGTTCGTCAAACCTCCCAA	60.088	20	184	259	442
59.883	20	TAGCCCATGAACACACCAAA	59.964	20	241	513	753
60.131	20	AGGCACGAACCTCTTTCTCA	59.989	20	145	8	152
59.118	22	AGCGGTTAAAGGTGGTGCTA	59.769	20	249	103	351
59.893	20	TTGGTTGGGTAGCTTTGGAG	60.103	20	278	404	681
58.013	21	ACAATCGTCGGATTTTAGCG	60.096	20	179	0	178
60.489	20	CGGATGGACCGGATGTATTA	60.544	20	250	13	262

58.882	20	CTCGGTATGCGAGAGAGAGG	60.111	20	209	57	265
57.552	24	TACGGCTGCGTAAACTACCC	60.152	20	271	16	286
60.132	20	CCCTAGCCTTTGCCTCTTTC	60.332	20	212	190	401
59.585	20	GGCTTGTCTGGAGTTTGCTC	59.997	20	277	65	341
60.011	20	TTAATGCGCGTACCAAATCA	60.096	20	274	925	1198
58.514	21	CACATGGAATTGCCTGAAGA	59.648	20	277	418	694
60.18	20	CCATGAACACATTGATTGGC	59.781	20	252	151	402
59.904	20	CACCCGAAAACCGAATAAGA	59.931	20	125	394	518
58.762	26	ACGGCCTGAATGACAGAAAT	59.556	20	280	10	289
59.871	20	CGGAGTGGGCTCATAAATGT	59.955	20	275	136	410
59.982	20	CATCCCAAGCCATACGAACT	59.955	20	250	56	305
60.089	20	CCTTTGTTCCTTTGGCACAT	59.971	20	242	1250	1491
60.203	20	ACACGGTCTCATGGCATAAA	59.002	20	254	425	678
60.074	20	GTTTCCTCCACAACGCTCTC	59.851	20	201	1936	2136
59.595	20	GCAATAACAAAACTCGGGTGA	59.989	21	253	63	315
60.088	20	TTCCTACTGGCTGTCCTTCG	60.388	20	227	962	1188
60.206	20	ATCCATGCATTCCCAACAAT	60.021	20	181	273	453
59.457	22	CAATAAGAAACACGCAACACAAA	60.082	23	200	221	420
59.25	20	GGGTCCAGACTTGAGACCAA	60.088	20	197	700	896
59.986	20	TGTGCGCTTGAGTGTGTGTA	60.096	20	164	676	839
59.697	20	TGACGTTCTTGCTGCTATGG	60.011	20	139	1633	1771
59.953	20	CACATGTCACGAATCGGTGT	60.45	20	274	108	381
60.118	20	TAAACAACCATGTCGGCGTA	59.992	20	279	235	513
59.001	21	GATCGACCAATTGTGTGACG	59.967	20	171	1003	1173
61.052	20	ACGTCCATGGGAGAATGTGT	60.246	20	228	68	295
59.381	20	AGGGCCACATGATGATAACC	59.635	20	252	61	312
59.888	20	TGAGCCTAAGGGGTGAAGTG	60.246	20	229	5579	5807
60.018	20	ATTTCTCTCGTCACACGCCT	59.874	20	205	949	1153
60.129	20	TCTTCGAATAAACCCCCACA	60.301	20	275	341	615
60.111	20	TGGAGGAAGAAGACAAGATGC	59.42	21	185	53	237
60.111	20	GGAGTGGCTTGCGAACTTAG	60.015	20	214	21	234
60.293	20	GTGCGTGTTTGTCGTGATTT	59.621	20	271	119	389
59.997	20	TAGATCACATTTGGCACGGA	60.073	20	164	265	428
59.238	21	GTCTTTGCGGGTGAAAAGTT	59.218	20	245	25	269
60.459	20	TCCAAACCAACAACACCTGA	59.976	20	136	107	242
60.096	20	TCCGTTATGGGCCGTTAATA	60.165	20	202	2707	2908
60.008	20	AAGGGACATTTTCTGCTTGC	59.316	20	215	1785	1999
60.015	20	ACATCTCCCTCACCCTCTCC	60.469	20	248	1167	1414
59.972	20	CTGAAACCACACCTCCACCT	60.002	20	272	722	993
59.966	20	GATACTCCGGCCAACTGAAA	60.074	20	280	1301	1580
58.866	20	TTGAACCTAGCCGGAGAAGA	59.948	20	237	32	268
60.016	20	GCTTGCCACGTCAACATAAA	59.735	20	136	2535	2670
59.853	20	TGACCGTTTCACCACAGGTA	60.001	20	234	14	247
59.659	21	AGATGTAGCAACCTATTTCTAATT	57.349	27	170	107	276
60.397	20	CTTGGACCAGATTGTCCCTC	59.505	20	233	346	578
59.907	20	GCATAGAAAAATATGTAAAATTC	58.929	27	178	356	533
57.795	21	ATCCATCCTACACAACCGGA	60.195	20	212	19	230
60.066	20	GGCACGATCACTTTAACCGT	60	20	170	1229	1398
59.803	21	TCCCAATTTAAGGGTTATTACCTG	59.555	24	145	1018	1162
59.893	20	TAATTGCATTCTCCCGAACC	59.901	20	271	268	538
59.836	20	AACCAGCTGTCAGAAGTGGG	60.298	20	266	1043	1308
59.897	20	CTTCTTGTCTGCAACGTGGA	60.025	20	140	668	807
60.184	20	GGCCTGTAGACCAATACCCA	59.813	20	107	42	148
59.67	20	TGACTGCCACAGTTTCCTCA	60.44	20	223	1545	1767
59.284	20	TGTGACCACTTGTCTACGGG	59.591	20	209	319	527
60.088	20	AAAGAGACTGAGCCACCGAA	59.989	20	251	346	596
59.989	20	AAGGACCAATGAGATGGGTG	59.779	20	248	66	313
60.018	20	TGAAGGTGACGAGAATGGTG	59.676	20	118	699	816

60.331	20	GGTGTGTGAGGTGTGTGAGG	60.045	20	103	40	142
59.973	20	TGCTCTCTCATTGTAATCTCTCTCA	59.688	25	251	109	359
59.673	20	CACACTGGACATCCCTTGAA	59.52	20	260	1698	1957
59.844	20	TGCTGCTGAACTTCTTGTGAA	59.773	21	203	4779	4981
61.188	20	TGCATATCTTCGTGTGTGCAT	60.158	21	242	133	374
59.381	20	CACCACTGCTTCTGCTTTGA	60.175	20	160	303	462
59.931	20	GCCGAGATTTGTTATGCGTT	60.103	20	169	329	497
60.331	20	CAAGATCCAAGGGCTGTGATA	60.081	21	190	705	894
59.96	24	CGATCCGGTCTGATCCAA	60.582	18	268	352	619
59.96	20	GCAGCCCATTCTATGCAAAT	60.067	20	209	1076	1284
59.924	20	ACGAAAAAGGGCATGAAAAA	59.564	20	280	381	660
60.158	20	TTCACACGAGAGTGCAGATTG	60.04	21	199	534	732
58.53	22	GCCAGAAATAGTGGATTTTGC	58.709	21	240	2170	2409
60.067	20	TTTAAGGGTTATCACCTGATTTTC	57.757	24	184	607	790
58.958	20	TTTTTAAAAGGAGACATTGCTGTT	58.494	24	227	246	472
59.901	20	TGTTGCAAGTAGTAAAGTAAAGG	59.475	25	182	528	709
59.847	20	AGAAGGTTATCACCGGATCG	59.006	20	250	1159	1408
59.901	20	AACCGCTGTTATCCCTCATT	58.53	20	152	674	825
59.934	20	GATGATTGGTTTCCACCACC	60.034	20	171	360	530
59.7	20	AACGCATTCTCCATGCTCTC	60.37	20	131	56	186
59.041	20	TTTTGGACAAAAATGCCCTT	59.429	20	251	43	293
60.05	20	GGCTGGGATGTCATTCATTT	59.756	20	263	150	412
59.472	20	GGTGTGGAAAAGGAACAACC	59.284	20	185	360	544
59.824	20	TCTTCTGTCTGTCCCTGGCT	59.986	20	265	347	611
60.051	20	ACAGCTTCACCGGTTTGTTC	60.156	20	231	1408	1638
59.591	20	ATGGCTGTTTTCCAATGAGC	60.081	20	167	528	694
59.938	20	GAGATTCGTGGTGAAAACCG	60.495	20	247	109	355
59.429	22	CAAATCTTAACCGCCGATCT	59.182	20	264	1274	1537
60.159	20	TTCCGTTTTCGACATCACTG	59.691	20	142	813	954
59.829	20	CAACAGTTTGGCATCAGAGC	59.445	20	143	97	239
60.278	20	GCCAACCACACAGTGAACAA	60.616	20	218	582	799
58.627	20	GTACAGTGGTGGTGTGCTCG	60.227	20	200	406	605
60.39	20	GGCTAATTGTTGGCCTTTGA	60.074	20	238	10	247
60.305	20	GGAGAATTCCAATGCCAGAA	60.014	20	171	307	477
59.938	20	TTCGTGGATGCTATGCTCAC	59.83	20	164	18	181
60.414	20	GCACAACTAATGCTTCCTGCT	59.536	21	250	150	399
60.032	20	ATTACATTGTTTCTGCCGCC	59.967	20	246	346	591
59.938	20	AGGTGATTGTGGTGGGTCC	60.649	19	155	35	189
59.297	20	GCCAATGCCTCATCCTAAAG	59.668	20	163	336	498
59.485	23	AAAAGTTTGGCGTCATCACC	59.978	20	213	2420	2632
60.278	20	TCGAGCTGGCTGAAGAATTT	60.096	20	212	568	779
60.195	20	ACGTAGGATATCACTAAATTGATT	57.146	27	279	1167	1445
58.055	22	GTGCAGCCTTATCTCTTGCC	59.985	20	207	93	299
59.967	21	TGGGTAGCATATGTCGATGG	59.375	20	161	68	228
60.257	20	GCGTTTTGATGATATATAGGTGTT	58.907	26	195	546	740
59.923	20	CGGGAGGGATGACTTTGTAA	59.926	20	233	971	1203
60.11	22	CCCTTGAAGAACTCATCCCTT	59.562	21	225	2837	3061
59.113	25	GTGGCAGAGGTTGGGTAGAA	60.111	20	216	18	233
60.312	20	CAGGGCTATCCCTCATCAGA	60.173	20	271	215	485
60	20	CATCGCTGCAAGATGGAATA	59.792	20	223	69	291
59.972	20	AGTTTTGTGGTCGAAGGTGC	60.156	20	202	151	352
59.813	20	CTCATTGACAAACCATGTCCA	59.405	21	276	122	397
59.96	20	AAACCCGTGTTCTTCAGTCG	60.149	20	256	19	274
59.504	20	GAGTGGGCATTATGGAGCAT	59.923	20	131	744	874
59.93	20	GACGAATCAAAGGTGCCAAT	59.939	20	173	73	245
59.739	20	GGGAAAGCCGATCAATTTTT	60.26	20	111	197	307
60.183	20	ATCGGTTATTATCGGATCGC	58.88	20	248	1258	1505
60.127	21	AAGGGTTCTGCTGAGAACGA	59.989	20	238	53	290

60.135	20	GTTAGCATGGGAAGGGAAGG	60.817	20	262	367	628
59.948	20	TAGGAATCACACGTGGTGGG	61.777	20	253	157	409
60.221	20	CAAACCCCGAGTCTGATGTT	59.966	20	202	1832	2033
59.127	20	AAGCCTTGTACCGAGCTTGA	60.015	20	243	1275	1517
59.95	20	ACCAATCTCGCATAGAACCG	60.096	20	274	1297	1570
59.656	20	CACAAATGGAGGTGATGTGG	59.806	20	251	317	567
58.955	22	ACTCAGGATGCCCACTGTTC	60.12	20	162	0	161
59.359	21	CCATCGTGAAGAACAGACCA	59.676	20	224	276	499
59.964	20	TTGACATGCCATTTTCTTGC	59.67	20	280	1028	1307
59.82	22	CCCCACTTCACCACTTCACT	60.002	20	219	142	360
59.862	20	AACAACCCTCATTGCTCTCG	60.255	20	278	121	398
60.157	20	CCCGGTAAGAAACCCATTTT	60.048	20	119	259	377
59.079	26	TGGGAAGAAAGGACAGGATG	60.042	20	188	4	191
59.09	20	TCGAGATGAAAACATTGGCA	60.197	20	218	113	330
59.411	20	CTTCACCTCCCAGATTTCCA	60.042	20	171	13	183
59.735	20	ATCCATGGTGAGGTGACTGG	60.806	20	145	390	534
59.707	21	TGCAGCTGCTCTAATCATGG	60.119	20	258	1254	1511
59.75	20	GGGGAGTAAAACGACCGAAT	60.187	20	231	74	304
60.067	20	AAGAACCGTGGTTTTTGTCG	60.008	20	251	298	548
59.146	20	TCCAAAATGAGACCAATCTTGA	59.546	22	248	164	411
60.298	20	CCGCGGCCTATCTTCTTAG	59.946	19	261	1972	2232
60.483	20	CTGTGTCCGGTTAAGTCCGT	60.028	20	213	1086	1298
59.866	20	ATGATTTTTGCAGCGAAACC	60.081	20	242	517	758
57.204	20	CAACAATGCCTTTGGTCTCA	59.691	20	152	328	479
60.49	20	GCTTGGGAGTCGAGGTACAA	60.255	20	264	963	1226
59.986	20	AGAGCGAGGTGAGAAGAGGG	61.061	20	260	113	372
59.826	20	CATCCTGATCCACACAGTGC	60.121	20	223	727	949
59.923	20	CCAACTGCAGAGTAACGCAG	59.658	20	232	2267	2498
60.067	20	GAAGTTAAAATAACGTACGTGTT	58.397	25	250	1080	1329
59.572	20	GGTTCGTGTCGTTTTCAGGT	60.012	20	189	165	353
60.051	20	ATGCCATCACAAGGAAGAGC	60.226	20	118	2103	2220
60.073	20	CCCGAATATTCTGTGCCAGT	59.955	20	138	2664	2801
59.212	20	TTGTCAGGAGAGGCGTTCTT	59.989	20	185	2496	2680
60.14	20	CCGCTGATGAAATGATCTGA	59.756	20	166	352	517
60.199	20	CTGGAGCCATTTTTGTGGAT	59.933	20	251	23	273
60.232	20	TTACCATTCGCGTGGACATA	59.953	20	104	421	524
59.973	20	GATTACTCCACCCTCACCGA	59.927	20	277	381	657
59.989	20	CCACCCTCAAACAACACTCA	59.565	20	211	16	226
60.009	20	TTACGTCCCGATCCCAATAA	60.146	20	202	2698	2899
59.847	20	ACCTTTTCACAGCAGAGGGA	59.844	20	233	726	958
59.801	20	TGAAGTATCGACGCATTCACA	60.272	21	238	545	782
60.006	21	AAACATTTTCAAAAACGCCAA	59.502	21	198	70	267
59.888	19	CACCACCACCGTTAAATTCC	60.088	20	224	49	272
59.975	20	AAATAGCTCCGATAACCGGG	60.292	20	198	165	362
59.772	21	GGGTTGATAGATCGGGTTGA	59.75	20	168	765	932
60.053	20	GCGTGCTGAATCTTATCCGT	60.243	20	251	204	454
58.986	23	GAGCATGATTTGGCTGGACT	60.226	20	261	78	338
57.484	20	GCAAATGCTTCTTACCCATCA	60.089	21	261	60	320
60.073	20	CCGGTAAAAACAATTCGCAC	60.356	20	135	117	251
60.395	22	AGAGAGAGAGTGTGGAGAGAGA	59.473	25	100	464	563
59.976	20	TTATACCACCGCCACCCTTA	60.202	20	144	1012	1155
60.657	20	CACTTTACGACCATCCCCAG	60.366	20	270	81	350
61.448	23	TTCTTGATGTGTTGGCAAGC	59.847	20	142	19	160
59.813	20	AAATGTTCGTGCGAATGTGA	60.119	20	136	440	575
59.986	20	TCATTCAAAAATTGATCACCCA	60.167	22	147	14	160
59.927	20	TAGATGGGAAATCCGACACC	59.75	20	250	2026	2275
59.836	20	AAACGATGTATGGGATTGATGA	59.162	22	222	153	374
58.32	21	AATCGTGCTGAAACGTGTTG	59.764	20	276	21	296

60.154	20	AAGGCCAAATGAGTCTGAGC	59.434	20	278	176	453
60.159	20	TCCATCTGCAAAATCCATCA	60.009	20	280	119	398
60.416	20	ACCCTGTGTATCCCAGCAAA	60.375	20	221	6	226
59.41	20	AAAAACACCAACACTTCTTGCAT	59.961	23	273	2325	2597
59.478	20	AGTTCCGGGGTCCATTCTAC	60.19	20	270	33	302
60.636	20	AGCGGAGGAGGAGGAAGTAG	59.972	20	246	43	288
59.997	20	ACTGCATCACTCTCAAGCCC	60.418	20	121	1119	1239
60.241	20	AAAACTCCGGTGTTCCATTG	59.83	20	116	374	489
58.111	21	AGACTATCAACAAGCCCCGA	59.694	20	227	3	229
60.009	20	GCCACCTGATCTAGCGATGT	60.249	20	156	2262	2417
60.483	20	CCAGGTGTTATGACCCGAAC	60.232	20	213	296	508
60.05	20	CACCACCATCACCCTCTTCT	59.962	20	203	96	298
59.943	20	TGCCACTTAGAAAAGTAAAAACG	60.101	25	243	315	557
59.572	20	AGGTGAATCGTCAAACGTCA	59.139	20	134	299	432
59.33	20	CCGTACCGGAAATTAACGAA	59.826	20	247	249	495
60.027	20	GAAATTCTGCAGTTCGGAGC	59.962	20	193	144	336
59.996	20	TTTGATTTTGGGGTCAGCTC	60.051	20	260	216	475
60.652	24	TAGTAGGGTGCAGGGGATTG	59.948	20	225	2391	2615
60.472	19	TAAGCCGCTTTGCCTAGAAA	60.109	20	280	1373	1652
58.974	20	GCTCCTCTTTCCCTTTTGCT	59.962	20	260	456	715
59.925	20	AGTCACAGGATCCAAGAGCC	59.258	20	219	232	450
60.133	20	CATTCCCAACTCCCAAAATTA	58.794	21	240	424	663
60.188	20	GGTGCTGCAACTCAACTGAA	60.032	20	216	869	1084
60.008	20	ATGAAGCATGCAATTCGACA	60.228	20	239	56	294
60.152	20	TCCACCCGAGCTTTAGTTTTT	60.116	21	178	1997	2174
60.011	20	CATCTGGTGGTCCAACGAC	59.945	19	178	2000	2177
60.21	20	TTTTGATGTTCGAAAATACCCC	60.056	22	152	102	253
59.903	20	ACATGCATGCTCGCAAATTA	60.245	20	130	34	163
60.352	20	GCAGCGTCAAATCAATAACCT	59.242	21	280	266	545
60.008	20	CGTGTGCAATGCATCTGGTA	61.713	20	226	69	294
59.152	20	ATGGTTCTGGCTTATGTGGC	59.962	20	273	288	560
57.613	25	ACCCAACCCAACCACAATAA	59.948	20	239	489	727
59.978	20	ATGGCCGAGATTTGTTATGC	59.929	20	108	1391	1498
60.389	22	TTGTTTGCTTGTAGATGTTGGG	60.032	22	183	799	981
59.551	20	CATTTGGCCGACTTTAGAGC	59.845	20	209	2649	2857
60.136	20	TGGCATGGGGAAGCTACTAT	59.551	20	230	80	309
59.955	20	TTCTCCCCAAAAGCTAATCG	59.292	20	277	148	424
58.646	22	GACGAAGAAAATCAACCGGA	60.051	20	159	4	162
60.532	19	AACTTTGAATCTGGCAACGTG	60.161	21	280	161	440
59.943	20	TTGTGTAATTGTGTTGTGTCGTG	59.468	23	237	101	337
59.933	20	AGGAGCTTTCTGCGTGGATA	59.978	20	118	2	119
59.815	21	TTGTTCTCTCGAAGCCCCTA	59.948	20	269	1823	2091
60.827	20	TCAGTTTTTGAGTTATGAATTTGC	57.598	24	188	244	431
60.138	20	GCTGGTGTGAGTTGTACGCA	60.939	20	247	233	479
60.096	20	CCAAATTTAAGGGTTATCACCTG	58.849	23	271	3642	3912
59.817	20	TTTCGACCGACAAAAAGGAG	60.22	20	107	717	823
60.23	20	CCAAAAGAAAATCTCCTGCG	59.817	20	200	702	901
60.111	20	ATAATTGATGGTTGTGCGGC	60.731	20	212	112	323
60.235	19	AAAAATGCAACCAGCATTAAAA	58.72	22	270	492	761
59.795	20	TACCCATTTGAAAATCCCCA	59.988	20	144	160	303
58.484	25	TCATGAGGAGCGTCAATCAG	59.942	20	141	9	149
60.234	20	AGTGCTGCCTCAAAGGGTAA	59.875	20	172	92	263
59.986	20	CGATCCTGTGTGGCCTAAAT	59.955	20	236	96	331
60.05	20	TTCCGTTAGGGGATACGATG	59.778	20	246	989	1234
59.816	20	GACACTTAGAGGGTGTTTTGACC	59.068	23	211	914	1124
59.762	20	TTCCAGATCCAAAATATCCACC	60.02	22	269	249	517
59.578	19	TGGATCATGTAAGGAACAATGTG	59.738	23	150	15	164
59.009	20	TTCAAGGCATTTGAGATCCAC	60.066	21	196	2356	2551

59.801	20	AAGAAGAAAAGACATTCCGGC	59.717	21	121	275	395
60.46	20	TAGGGTCAACCATCAGTCCC	59.779	20	186	250	435
59.958	20	GGTGGATTGTCCTTGATGCT	59.934	20	139	867	1005
59.596	20	GAAGATCCCGGTGAAATGAA	59.871	20	153	15	167
59.7	20	TTAAACCCTAAAAGCGCACG	60.251	20	257	228	484
59.978	20	CCCCCTAATCCCTAAATCCC	60.678	20	213	967	1179
60.025	20	CCATCTCCAACTTCATGCCT	60.073	20	252	0	251
60.118	20	ACGCAACCGTAAAGAACCTG	60.168	20	279	304	582
59.875	20	CCCGATCACCATCACTATCC	60.158	20	270	129	398
59.166	20	TGGTATCAGAGCCATGACGA	60.225	20	276	8	283
60.378	20	GCACGAAGAAGGTTAAAAGGG	60.116	21	252	651	902
60.134	20	TATCGTGCGCAATAGACGAG	59.999	20	178	1179	1356
59.483	20	CTCGATAGGAAAGGATGCAA	57.916	20	119	836	954
59.04	20	CAATCTTTGGGCGTGAGAGT	60.255	20	140	5	144
59.984	20	GTGCGTTGACCAGCATTTA	58.274	19	125	275	399
59.639	19	AAGGACGTAACGGCTCTCAA	59.875	20	253	8	260
61.078	20	TTTTGGAGATCTATGGCTGTCA	59.708	22	164	254	417
60.388	20	TAAGAATTCCAATGGGGCAG	59.894	20	280	127	406
59.585	20	AAAGTGGGAGTTAGGGCACA	59.592	20	219	62	280
59.809	20	TAGGTGTGTGCATCTTGGGA	60.112	20	217	513	729
60.132	20	GTGTTTGCATGGTGAACTGC	60.168	20	242	1485	1726
59.242	23	CGGATTTAATCGTGGCTGTT	59.96	20	140	31	170
57.296	27	CCAAATCAGACTGCGAACAA	59.84	20	246	1780	2025
59.999	20	CGGTTATTAGTTATCACCCGAAA	59.322	23	125	2896	3020
59.797	20	AGGAGGATTCACCACGTCAC	59.969	20	173	224	396
60.18	20	CAAACCATCCAACCACAACA	60.255	20	261	11	271
60.366	20	TCCTTCAATCTCAGCCTTTCA	59.94	21	250	963	1212
60.61	20	TTTCCCTACAATTTCGGCTG	60.067	20	195	145	339
59.827	20	CATATGGGCACAGACACTGG	59.984	20	153	21	173
59.827	20	CATATGGGCACAGACACTGG	59.984	20	153	21	173
60.066	20	AAAGGAGCTTCTTGCACTGG	59.615	20	261	1632	1892
60.235	20	TCCCAGAATATCGAAGGCAC	60.036	20	165	322	486
59.864	20	AGGGTTTTGAGGGTTTGCTT	59.976	20	253	438	690
60.051	20	AATCCCAACAAATGACCCAA	60.029	20	175	1155	1329
59.888	20	ATGCAGACGAATAAGCGAGG	60.374	20	218	119	336
59.691	20	CACCATCATCTTCATCCACG	59.918	20	258	85	342
59.928	20	ACCCACATAGTGCCGAGAGA	60.678	20	121	633	753
59.464	26	GAAAGCTAAAATTTGCAATCAAA	58.619	24	117	12	128
60.206	20	TCCTTGCATGCACATCATTT	60.08	20	263	34	296
59.685	20	GACAAAGCAGGCACACAACT	58.935	20	201	150	350
59.903	20	TTGAACGGAATCATGGACAA	59.9	20	167	79	245
59.055	24	TTTGTCTACCAGTTGCCCCT	59.592	20	234	798	1031
60.073	20	GGCATGATTCTGCTGGTTTT	60.081	20	278	1281	1558
59.215	20	GATTTGACCATGAGCGTTGA	59.654	20	157	157	313
59.9	25	AAATGGTCCCCTCATGAACA	60.173	20	139	8	146
60.013	20	CAACCAGCAAACAAAAGCAA	59.888	20	136	122	257
57.864	25	ATTTTAGGAAGGATCGGGGC	61.454	20	231	171	401
59.157	20	AAGCCTTCCATTCCGAAAAT	59.909	20	161	742	902
60.204	20	TTTTACACGGGACCGTCAAT	60.227	20	267	486	752
59.891	20	AGATGTTGGATCTGCAGCCT	59.834	20	253	591	843
60.015	20	AATCCTCCTGCTGTGGTGAC	60.12	20	230	4235	4464
59.276	20	CCGCAAGTGTACGGGACTAT	60.015	20	218	286	503
60.119	20	TCTTCTTCCACTCGCATCGT	60.945	20	237	864	1100
59.115	21	AAGCGCACGTTTGAGTTTTT	59.926	20	153	73	225
59.853	20	CAAATTGTTTGGGCTCGATT	59.938	20	226	340	565
57.656	19	CCAATGATGCATGGTTATGG	59.622	20	254	177	430
59.444	20	TTCAGCCATGGCAAATACTG	59.688	20	276	364	639
59.83	20	GCAGGTAAATATCAATTTTCGAG	57.112	23	272	211	482

59.875	20	TGCCAGCAGAGAGGAGGTAT	59.973	20	164	17	180
59.748	21	TACGCACGATGTTGGTGAAT	59.995	20	174	117	290
59.967	20	AATTAACATCACGGCCATCC	59.651	20	243	105	347
60.619	20	CCGTTGGAATTTTAGAGTTACG	57.9	22	111	578	688
59.979	20	GTGGGCTTCGACTCTCAGAC	59.993	20	184	566	749
59.993	20	CCAAAATCAACGTCCCAGAT	59.79	20	279	786	1064
60.039	20	GTGCTGAGGCGTTTCTTGAC	60.986	20	251	37	287
59.533	25	TGTTCGGATTTGGCGATTAT	60.289	20	276	219	494
60.074	20	TCCCTTAATTTCCTCACCCC	60.124	20	172	292	463
59.989	20	TGGACTCCGTGTGTATGACTG	59.606	21	203	478	680
57.849	20	CGCACCTTTCATGTGCAATA	60.665	20	280	1121	1400
60.096	20	ACATGATTTGCAAGATGCCA	60.08	20	249	519	767
58.532	23	CCGGCTCTGATACCATTGTT	59.955	20	270	687	956
59.713	20	TGGTCTTACATCTCCCAGGC	60.073	20	192	1510	1701
59.984	20	AACACGGTAACAAAATATATTGA	58.491	27	163	199	361
59.992	20	TCGGTTTCACCAATGGAAAT	60.17	20	110	304	413
59.733	21	GATCTCTTTTGTCAAGGGCG	59.813	20	119	4	122
58.315	21	CCCAAAATAGCTTTCCCACA	59.931	20	224	48	271
59.862	20	GGATTGTGCACTCAATGAATCT	59.059	22	256	198	453
60.195	20	TTCCTCCTTTCCTCTTATGGG	59.536	21	270	139	408
60.133	20	TCCCCGAATATTCCAACTCA	60.266	20	163	163	325
59.989	20	TTGGTGAAAGGAGACGAAGG	60.224	20	234	94	327
60.045	20	TGAGTGAACATGTGTGTGCG	60.373	20	159	250	408
60.401	20	ATCCAACTCCTGCATTTTGC	60.081	20	270	13	282
57.141	23	CGGTTAAAAATCGGACAGGA	59.931	20	260	1836	2095
60.671	20	TACGGCACCATATAATCGGG	60.548	20	109	86	194
60.012	20	AAAGTGGCCGACAAAAACC	59.963	19	275	559	833
59.803	20	GGATCGTTGATCGGGTTAGA	59.894	20	133	40	172
59.816	20	GATCTTTTCACTCGAGCCCA	60.34	20	252	93	344
59.799	20	CGACTGGCAAATACAAAAGTT	57.007	21	203	426	628
60.096	20	ATGGCTCCATTCTTCCTCCT	60.037	20	242	162	403
59.831	20	GGAATTGAAATCCCACCTGA	59.727	20	256	389	644
59.807	20	TATTTTCGGCCACCACTCTC	60.074	20	163	219	381
59.859	20	TCTCTTTCTCCCAATGAACCA	59.656	21	229	1614	1842
59.96	20	ACTCGTAACATCCCCATCCA	60.195	20	269	741	1009
58.775	22	AATTGTTGAAACCGGTCCAG	59.83	20	200	316	515
59.939	20	AACACCACAATTGGCCTCTC	59.973	20	130	230	359
59.894	20	AGCCTGCATTTGACTTTTGG	60.249	20	228	580	807
59.901	20	AGGAAGGGCGAAAAAGAGAG	59.955	20	273	31	303
59.599	20	GATGTGGAAAAGCCCAGAAA	60.051	20	272	1638	1909
59.986	20	TCCTTTCCGCTGAGCTTCTA	60.227	20	253	281	533
60.153	21	CCACCAAGCAGTGTTTATAGTAGC	59.308	24	217	155	371
60.011	20	TATCCCCTCATGCATTCCTT	59.344	20	200	1690	1889
59.387	20	TGGACCATTTGTCCTTCAAA	58.947	20	226	44	269
59.855	20	TGGTCAATACCAGAAAAATCCA	59.315	22	220	234	453
59.541	26	CCCCTTATTTGTGGTTCCAA	59.657	20	259	22	280
60.035	20	ATTACTGCGGCTGATGCTCT	60.007	20	254	56	309
58.12	20	AAGCCCTAAATGCACTCGAA	59.845	20	280	107	386
59.872	20	TCCACGAATTTGACACGAAA	60.088	20	162	1462	1623
58.471	27	TGAATTTTGTTTCCCACCAA	58.841	20	126	8	133
59.978	22	TTTGTTTCAAAGAATTTGTGGTAG	59.157	25	169	698	866
59.682	20	TGCTCCAGTTTCCTTTTGCT	59.993	20	116	52	167
58.765	20	CGACTTTTAATGGCGGTTGT	59.996	20	110	66	175
60.123	20	CCTAAATCATTGGGGCAGAA	59.894	20	220	3385	3604
59.721	20	TTGGGAAGGATGAAGTTTGG	59.903	20	142	1178	1319
60.11	20	GGTGCCGGTCCATAAAATAA	59.66	20	265	803	1067
60.573	26	GTGCTTGCATGAGAGATGGA	59.95	20	201	32	232
59.54	21	GTTGAAAAGAGCGCTGAACG	61.08	20	108	62	169

59.894	20	CAGCAACATCGAGTCGAGAA	60.136	20	260	1642	1901
60.215	20	TTCTACAACCACCCAAAGGG	59.824	20	251	109	359
59.878	20	GGATATCCAAAATATCCGAAAA	57.071	22	216	1066	1281
57.043	20	CGATCATATCCAATTTCGTTTC	58.449	22	149	156	304
59.973	20	CTTCATTACACCGGCAAGGT	59.993	20	277	922	1198
59.425	20	GGATCTGCGAGATAAGCGAC	59.946	20	229	471	699
60.081	20	ACCCTTGCAAATTATCGCAC	59.967	20	120	391	510
60.066	20	TTGCAATATGTCCTTGCACC	59.548	20	236	2340	2575
60.255	20	AACATGAGCGCACCAACATA	60.142	20	110	23	132
59.696	25	AAATTCTCCACTTCCCCACC	60.169	20	100	13	112
60.096	20	GGCTAATGTGTGGCAGGTTT	60	20	208	1536	1743
58.979	20	AACATCTCAAACATTCAAAGAGA	59.724	26	243	1757	1999
59.96	20	TACTGCCTTGCATTGGATCA	60.22	20	189	35	223
60.055	20	GGACTTATTACCAATCATCCCA	57.808	22	149	729	877
60.008	20	TCTCAGCTTTCTTGATGGGAA	59.94	21	197	1403	1599
59.992	20	CCCCCAAATTTTACAAGCCT	60.177	20	147	3190	3336
60.149	20	TTGCCTTGGCCCATTTAATA	60.275	20	119	1439	1557
60.377	20	TTGTCCATTCAATCCTGTGG	59.343	20	175	9	183
60.155	20	TCAATTAACAATAGACTGACGCC	58.335	23	179	320	498
59.481	20	GGAAAGAGTGTGTGTTTGCG	59.339	20	228	400	627
60.532	20	CCGTCGTATTTTCCCAACAC	60.227	20	266	7	272
59.322	21	TTGTAGCCCCTTTGAGCCTA	59.839	20	239	9	247
60.181	20	TTTTTCTTTCCACAACCCCC	61.05	20	275	68	342
60.352	20	CCATTGATTTGGTTGATTGAA	58.321	21	106	56	161
58.215	20	GACATTGCTAGCACCGAACA	59.871	20	177	93	269
59.789	24	AAAATGTAACAACTTTTGATCCCT	59.723	25	258	624	881
59.972	20	TTGTGATGTGGCAGCTTTTC	59.847	20	137	114	250
60.244	20	ACGCCAGATTTATCACCCAG	59.955	20	229	31	259
60.042	20	ATCGGAGTTGATTTGATGCC	59.9	20	277	134	410
59.872	20	TGGTGGGAAGGAGAGGTATG	59.92	20	154	989	1142
59.757	20	ATGCGTTTTGATGATATATAGGTG	57.255	24	100	706	805
58.341	21	TGAAATTTGGAACAAACAATGA	58.045	22	174	3	176
59.803	20	GCTATCAGCAACAAAACCCC	59.574	20	277	1011	1287
60.052	20	CACCCTAAAAATACGCCAACA	59.876	21	264	99	362
59.745	20	TCAAATGTAAAGCACTAGAGCCA	59.088	23	269	4579	4847
59.888	20	TGACATTGCCTAGAAAGTGGAA	59.747	22	279	117	395
60.022	20	TCTTTCGTGAACTGCTGTGG	60.025	20	102	1144	1245
59.757	20	GGCTTTTGTCCTCATGCACT	60.263	20	170	131	300
59.526	20	ATTCCATCCCTTGGCTCTTT	59.903	20	149	1311	1459
59.905	20	ACAGATGAGTGGCAGTCGGT	60.746	20	160	77	236
59.374	20	ATGTAATAGGGTTTGGGAAGG	57.006	21	196	823	1018
60.052	20	CCCGAAGAAGCCATCAAGTA	60.206	20	224	84	307
59.434	20	CATGACCACTCTTTCCTCCA	58.641	20	254	2352	2605
59.576	25	ATGAACTTGATGGTGGAGCC	59.934	20	276	219	494
59.806	20	GGATACAAGCAAGGGCACAT	59.962	20	104	1381	1484
60.111	20	GCTGCAGCATAAACACGGTA	59.902	20	238	137	374
60.352	20	CCCTTCACAAGTGGTGACAA	59.565	20	231	132	362
59.967	20	CGGTGTTGGATTGGTGAGTA	59.415	20	119	1123	1241
59.79	20	AAGACGAAGACGACGACGAT	59.874	20	218	538	755
59.955	20	ACTCCTTCACTCCCAGCTCA	59.986	20	203	811	1013
60.386	20	GGCAGCTCATCAAGTTCACA	59.992	20	167	10	176
59.679	20	TGATCCATGTACCCATGCTG	60.353	20	245	6	250
60.57	20	TCTTCACCAACTGTACGCCA	60.301	20	280	596	875
58.075	22	CAATTTGTTTCAGAACCCAAGA	59.108	22	246	4378	4623
59.933	20	AAATGCATGCACCTGATTACA	59.055	21	196	105	300
59.041	22	TCTTTTGCCGTAGCTTGTGA	59.609	20	243	44	286
58.117	22	CATTTCCTTTTCCACCAACG	60.336	20	215	19	233
59.328	20	CCAAGATCATATTCCGCCAT	59.745	20	190	892	1081

58.978	20	TTTTGATTTTATTGGGATTTGTTT	58.024	24	274	19	292
59.764	20	CGAGCCAAATCTTCCTTTTG	59.817	20	254	177	430
59.682	20	CGGTTATCACCGGATCGC	62.397	18	127	1345	1471
60.023	20	GGACTTTGAATTTGCTTGCC	59.691	20	266	338	603
57.557	25	ATCCAATTTGGGCCATTTTA	59.124	20	266	23	288
60.353	20	GACTTTTCCGATGGTGTCGT	59.973	20	199	100	298
58.035	19	CGTGGTTCGATCGTAATTGA	59.542	20	270	166	435
59.988	20	CTGCCTCCATTTCTTGCTTC	59.955	20	260	365	624
61.296	20	GTCTTCCTCGTAGCAGCACC	60.02	20	280	41	320
59.862	20	AGACCTTCTTTGGGTGCCTT	60.11	20	149	127	275
59.729	20	AGGGGTTATCACCTGAATGC	58.864	20	176	170	345
61.032	20	GTGGACGTCCCAGATTGTTT	59.827	20	173	9	181
59.953	20	TGTAAGCCCATCAACCTTCA	59.123	20	277	1378	1654
59.154	21	TGAGCCATGAACACCAACTC	59.682	20	207	338	544
61.031	20	TTGGGTTATCTTGTGGCTCA	59.123	20	114	21	134
60.074	20	CCACGATTCAATTATGTTCCG	60.195	21	180	1088	1267
60.048	20	CGCATTATGTTGCCTTTGAA	59.702	20	152	786	937
61.031	20	AAAGCCAAATGAATGGGGAT	60.511	20	126	21	146
60.195	20	TCCCCGAGTTATCGATCTTG	60.029	20	189	906	1094
60.008	20	CGAGAGAAAGAGATGGAGCG	60.232	20	236	61	296
59.851	20	TGATAACCATGACCTCACGA	57.442	20	256	488	743
58.882	20	TTCTCGTGTTCCTCCTCACC	60.238	20	103	0	102
60.029	20	AACAGCCATTAAAAGTCGGC	59.229	20	129	290	418
59.96	20	TGTACCAGGGAGTCTCGGTC	60.112	20	236	86	321
59.95	20	TCGATATTGTTGTTGCCGTG	60.523	20	278	572	849
59.61	23	CCAACTTGGATATTGGTGGC	60.192	20	264	454	717
59.963	21	ATACCGTTGAGACCACCTCG	59.989	20	279	108	386
59.84	20	CGGCTTAGCTGTTCGTTGTT	60.44	20	238	1323	1560
59.462	20	CTCTTGGGCCACACTTTCTC	59.844	20	266	146	411
59.88	20	CGAGCTCGAGTTTGAATTTG	58.649	20	280	679	958
59.84	20	CGCCCTCTCCACCTATCTCT	60.746	20	169	17	185
59.735	20	ATGGCAAAGAGCAAGTCAAA	58.502	20	252	91	342
60.071	20	TTTGTGTGACCCATCTTCCA	59.935	20	199	2232	2430
59.789	20	TTGCCATCCACTACACCAAA	59.964	20	269	551	819
58.807	20	CCGGGGCATTACATTATTTG	60.033	20	183	181	363
59.22	20	TGGGAGAGAGATCGATATTGTG	59.15	22	279	364	642
58.674	20	AATAACACGGCACCTACCCA	60.249	20	235	2798	3032
57.043	20	CAGAAACTACATCGCGCAAG	59.632	20	132	164	295
60.366	20	GGGGTTATCATGGGATCAAA	59.439	20	220	64	283
60.051	20	GCATGCTGATAGGCAACAAA	59.839	20	209	1339	1547
59.803	20	AAGTTGGAGGTGATGATGGTG	59.835	21	112	66	177
59.238	23	CGGGTTATGGCAGATTTCAT	59.784	20	142	5	146
59.101	22	TGTTGTTTGGAAAGTTGGAGG	59.994	21	237	641	877
59.579	20	TTCTGGTTTGGAAGGGAACA	60.465	20	216	133	348
59.485	21	CTGTCAAACGTGGTGAATGAA	59.6	21	276	164	439
59.697	20	GTCCACGGTGGTTTGAGAGT	60.009	20	141	38	178
58.625	20	TTGGACCTGCCACCAATTAT	60.192	20	229	739	967
60.005	20	AGCAATATCGATCTCGCAAA	58.483	20	207	48	254
59.947	20	ATGGATCAGTTAATCGGGCA	60.296	20	178	18	195
59.538	20	AAAATCAAAGGCCCACAATG	59.801	20	151	403	553
59.901	20	ATCTCAACGATATGGCTCGG	60.059	20	222	37	258
60.492	20	GCACACACCCACAAACACTC	60.055	20	220	103	322
59.966	20	TGAAGAGAGAGCTTCTGTCGG	59.876	21	278	177	454
60.103	21	GTGTTCGATACCGGGTTCTT	58.912	20	246	96	341
60.073	20	CACCCCACCTCATTTTCAAC	60.21	20	235	180	414
60.255	20	TTTTGAGATGGAACCACTTGC	60.103	21	164	6	169
58.994	22	TGCAAATACGGAAAATTTGACA	60.347	22	280	681	960
59.991	20	TTCTTCCTCACACCTCAGCC	60.386	20	237	240	476

60.251	20	TGAACAATTGAAACACCGGA	59.941	20	255	64	318
59.939	20	TGATCCATTCCGACTTCCTC	60.011	20	227	140	366
59.859	20	CCTCCATCAAACCATTGTCA	59.343	20	273	2329	2601
60.12	20	TTGAGCTATAGTTGGAGGGTAGC	58.986	23	176	6284	6459
59.882	20	ACATCTGTGGAGCTGCTGTG	60.055	20	254	1240	1493
60.255	20	CTTTAGGTGCATCTCTTGACGA	59.517	22	210	142	351
60.05	20	GTGATTCATGGCCGAGGTA	59.466	19	227	71	297
59.975	21	ATTTAAGCCCCATCCCCTAA	59.637	20	232	168	399
57.497	26	CTCAAGACCCGATCGGTAAA	60.066	20	254	50	303
59.487	22	GAGAGAAAACCGAGAAGCGA	59.694	20	260	41	300
59.836	20	AACACCTGTAATCGGGATCG	59.813	20	157	2	158
59.721	25	CGCCAAGTGAGTTATTGCAG	59.488	20	280	23	302
59.826	20	CGCGTCAGATTTGTTATGTGTT	60.06	22	253	90	342
59.873	21	TAAGGGTTATCACCGGATCG	59.778	20	108	0	107
60.288	20	GCGTCAATTACGTTCCATGA	59.548	20	241	1831	2071
58.928	21	AGGGGTCAAACCTCCACTCT	59.968	20	209	130	338
59.859	21	GTGCCAAAAATTGTCATCCA	59.375	20	228	127	354
59.806	19	AACTGGGCCATGATAGGTTG	59.813	20	246	0	245
59.969	20	GACTCCCTTCCTCAACTCCC	60.05	20	107	640	746
60.277	20	TTGGGCTACTGGAGATTTGG	60.066	20	162	3631	3792
59.939	20	TTTTGGGAAATGGGGTATGA	59.988	20	235	707	941
59.872	20	TACCTAATCTCCCGCCCTTT	59.924	20	277	148	424
60.193	20	GATCGGAGGAGATGAAACGA	60.158	20	112	148	259
59.934	20	ACATCAGAAGCAGTGGAGGG	60.261	20	254	80	333
59.822	22	GGAGGATCTTCTTGAGACACAGA	59.87	23	273	107	379
60.096	20	CATCCCTCGGTTCAAGGATA	59.887	20	274	2338	2611
59.874	21	TGCATCTTGGAGGTGAGTAGG	60.262	21	231	25	255
60.132	20	TGGTACCTCCAACAAGAGGG	59.959	20	279	87	365
59.901	20	CTGCTGACTGAAGCGGGTAT	60.419	20	258	509	766
58.879	20	CACCCCTTTCCTTTACCCAT	60.046	20	248	164	411
60.111	20	GTTGTAGGCAAAAGGGCGTA	60.131	20	162	363	524
59.63	22	ATTGTCATCCACGCAAAAAT	57.943	20	265	104	368
60.381	20	AGGGCAACAATCATGAGTCC	59.934	20	213	477	689
58.637	26	TTGTCATGTCCACCTCATTCA	59.951	21	182	501	682
59.943	20	CATCCAAGACATGATCGCAC	60.08	20	262	25	286
59.948	20	TTTAAACCCCAACACCTTCG	59.833	20	249	404	652
59.971	20	CTGGAGTGTCAAGCTGGGAT	60.261	20	198	103	300
60.332	20	CGAGGAAGTCGAGGATTGAG	59.943	20	220	25	244
60.281	20	ATAGCGTCTTCCAGTTTCCG	59.336	20	276	204	479
59.722	20	GATTATGTCGTGGATTTTGAACA	58.867	23	250	55	304
60.135	20	CCCTTTGAATTTTGCCTCTG	59.679	20	135	151	285
59.799	21	GAGTCAGCGGAGCTTTTACG	60.154	20	189	1	189
60.874	20	TGATCTGAGAATTCAGCAACAA	58.502	22	279	320	598
62.112	20	CGAACCATGAAAAACATGGA	59.371	20	230	25	254
59.826	20	AGGCACAATAGCCACGAATC	60.103	20	261	244	504
59.603	26	ACGAACTTGACACGAACACG	59.794	20	270	357	626
59.916	20	TATTCGGAGGGAGGGAGTTT	59.897	20	203	389	591
59.817	20	TTTGGGGCTACGTGTTCTTC	60.11	20	235	58	292
60.195	20	AGAGAAACTGGAACCCCCAC	60.349	20	181	122	302
58.843	20	CGGTTATCACCGGATCGC	62.397	18	250	836	1085
59.962	20	AAATAGCGCATTTTTGCCTG	60.226	20	232	903	1134
60.426	20	TTGCATGCTCAATAAAATGGA	59.159	21	251	1266	1516
59.883	20	ATGGGAATCTTGGGGAAGAC	60.133	20	194	232	425
59.838	21	GAATTTCCCAGTTCCAACCA	59.767	20	136	866	1001
60.833	20	GCAAGATCCAATGGTTGTGA	59.502	20	279	462	740
59.976	20	TAACCCATTTCAGCCGAATC	59.901	20	273	1923	2195
59.597	20	CCATCCTCCTCCAATAGCAA	60.029	20	218	1782	1999
59.464	20	GCACAGTGTCACCACAATCC	60.013	20	277	695	971

59.993	20	GACGGTGGAGATTGAGGAAA	60.05	20	197	1048	1244
59.238	21	AGTTTTGAATGGCTTGGTGG	59.971	20	241	592	832
59.709	20	AGGGAGGTGGTTGATCAGAA	59.505	20	279	122	400
60.169	20	ACGGCTGTGTAGTGTGTTCG	59.819	20	163	578	740
59.934	20	GCAAAAGCTGAGGTGTCAAA	59.05	20	245	11	255
59.947	20	TAAAAATGACCCTCGTTCGG	59.931	20	249	3	251
60	20	CAAGCCCGCATTAAAACATT	59.964	20	208	19	226
59.969	20	TAGTCGGCCGATAAGTTTGG	60.089	20	155	870	1024
59.299	21	CTTCGAGCTCCTCACATTCC	59.95	20	160	27	186
60.122	21	CGTGGAATTTCATGGTTTGA	59.371	20	222	18	239
58.734	25	TCATGTCCGTCCATTTTGAA	59.9	20	226	660	885
59.941	20	CAAGCCTAACACCACAAGCA	59.904	20	207	1755	1961
59.499	20	CTACCCTGCTGATGAAACCC	59.55	20	128	51	178
60.029	20	AAATCCATCCCATCCACGTA	60.014	20	216	296	511
60.051	20	AGCCAGCTAGTCGGTTTGAG	59.639	20	164	161	324
59.668	23	ATCGACCCTAATTCGAACCC	60.152	20	276	1190	1465
59.881	20	TGCATGTGAGTTGCACTTGA	60.029	20	209	456	664
60.161	21	TTTTGATGCAGCAACCATAAG	58.83	21	280	57	336
59.685	20	CATTGATTGATTCACAGCCCT	59.947	21	224	152	375
59.914	20	GAAAGTATGGCTGCTCCTCG	59.978	20	165	1915	2079
60.246	20	TTTGGGTGTTCTGTACACGG	59.46	20	165	182	346
59.23	20	GGGTCTCGCATAAAGTGGAA	60.074	20	278	124	401
58.92	20	TGATCTTGCTTGGTTGCTTG	59.988	20	260	2044	2303
60.051	20	CACATGTGGAGAGCTTGTGC	60.473	20	276	490	765
59.973	20	TTGCAAGATTTGACGATCCA	60.197	20	241	1710	1950
60.449	20	CCAACTTTGTGTTCTTGGCA	59.734	20	103	27	129
58.663	23	TTGTTAAAGGTTTCGACGGG	59.968	20	101	11	111
59.903	20	GAGGCTGTGAAATTGAGGTTG	59.726	21	101	277	377
59.359	20	CCACTTACCGGAGCTATCCA	60.088	20	241	181	421
59.864	20	ATGCGCGATTTTAAACCCTA	59.586	20	270	1579	1848
59.966	20	AATGCTTGCAAATTTTCGGT	59.592	20	136	407	542
59.313	20	AAGATGGAGAGACGGTGGTG	60.112	20	274	220	493
59.982	20	TGCCAATGGAATAGTGATCG	59.499	20	269	1664	1932
59.433	20	CCCACACTCACATGTACAAACA	59.385	22	152	324	475
59.89	20	TCCTTCCGGAGTACGAGCTA	59.971	20	111	36	146
58	20	TCGAACATGTAGTGGTCAAACTG	60.081	23	195	292	486
57.757	21	TGAACAATGAGATCCACAATCA	58.976	22	264	439	702
59.01	20	TTTTTACCTTCTCCAGGGCA	59.679	20	264	4236	4499
60.049	20	ATGTCACTGCCTTGCCTCTT	59.874	20	216	617	832
58.362	20	ATTTCAGAACGACACCGAGG	60.111	20	176	742	917
59.697	20	TGCCTTAGATCCACCGGATA	60.427	20	216	588	803
60.008	20	ACCCGAATTACCACCCCTAC	59.94	20	270	1898	2167
59.862	21	ACACACGAACACTCACCCAA	60.047	20	198	69	266
60.028	20	GGAAATCCAAACGAAAGCAA	60.053	20	213	60	272
58.983	22	TTGCCTTTTGATTTTCGGTC	60.053	20	280	697	976
60.044	20	GCAACCAAGTTGTCAACCAGT	60.066	21	251	65	315
59.322	20	TTGACTGAACTTCACCCATTT	57.16	21	199	175	373
59.853	20	CCTCACGAGTTTGGACAGTG	59.305	20	237	379	615
59.823	20	AGACCGGAGTAGATGACCTTC	57.321	21	218	250	467
59.505	20	GATTTTGACATCAAGATAAGGCA	59.525	24	220	408	627
59.836	20	AAAATCCAGCAGGCAAAGAA	59.823	20	231	103	333
59.255	20	TTGTCCTCAACTGAAAGAATGC	59.359	22	269	1679	1947
60.323	20	CCACAGCTTTCAACATCACG	60.301	20	261	77	337
59.933	20	ATCGGAGCTGAGAAAGCAGA	60.24	20	228	854	1081
60.208	20	CGCCATTCTCTCTCTAACCTG	59.087	21	171	279	449
60.011	20	GGCCAGATATCTCTCCATGC	59.616	20	253	2717	2969
59.874	20	CACCAACAGCTTGTCGAATG	60.301	20	159	1883	2041
60.011	20	CAAGGGCCGAGATTTGTTAG	59.702	20	202	1377	1578

59.938	20	TCCATTCCGAAAATCAAAGG	59.872	20	178	176	353
59.948	20	TGACGTTGGTGGATTGAAAA	59.941	20	154	322	475
60.249	20	CATCGGTTCATGTCACTTGG	59.96	20	185	5	189
59.623	21	TCTGAGATGTACACTGCGCC	60.016	20	160	17	176
57.44	23	GATAGGATACGGCCCATTCA	59.745	20	254	17	270
59.972	20	TCTAAATGGTGGCCGAAAAC	59.938	20	171	445	615
60.103	20	CAACGGCTATTTACATGGGG	60.202	20	266	681	946
60.192	20	TGCATGCTATACGGCACTGT	60.31	20	225	2771	2995
58.972	27	CTAATAGCAGGCAAAATGCG	58.609	20	241	2	242
58.028	22	TCAATATTTCCCAAACTCGGA	59.397	21	191	15	205
60.01	23	CGGATTATGTATGTTACTTTTGGG	58.797	24	173	14	186
59.625	22	CAAAATTTGGGGCAAAAA	57.057	18	277	742	1018
60.682	20	TCTTAGAAGGGGCCAAAGGT	60.068	20	101	6149	6249
59.307	22	CCAGAGGAAAATGGGTCAAA	59.903	20	254	130	383
59.928	20	CTCAGAGGCACCTCATCCTC	59.945	20	130	1788	1917
60.214	20	TCAAAATCAAGTCTTCCTCCG	59.298	21	200	339	538
59.255	24	ACCTCGCGAAAGAGACAATG	60.397	20	270	23	292
60.136	20	GCAAGACATGGTGTTGTTTGA	59.606	21	267	842	1108
60.246	20	TGTAGGGGACTCGCTTCAAC	60.255	20	166	76	241
59.556	20	GGGTTCCAGCGTCATAAAAA	59.938	20	277	317	593
60.984	20	TGGGTGATCTGAGAGGAAAAA	59.656	21	248	518	765
60.045	23	GGACCTCATCTGTTGTAACCACTA	59.726	25	273	390	662
59.779	20	CGGTGGAAGCTTTGTCTGTT	60.291	20	223	1065	1287
59.767	20	TCACGCTAAGGGGTGGTATC	59.955	20	187	371	557
59.993	20	TCCGTGCATGAGAGAGAGAA	59.656	20	280	1500	1779
60.742	20	AGTCTGCCATTCTTGCAACC	60.263	20	221	438	658
57.677	21	CGAGGATGTTGTCGAGGAAT	60.073	20	198	83	280
59.937	20	GAGGACACTTGGACCTGGAA	60.088	20	226	784	1009
60.112	20	GCTTCGTGTCTCTGTGGTCA	60.03	20	203	90	292
59.676	20	AATTGAGGGAAATGTCAGCG	60.074	20	199	1707	1905
60.175	20	CTTTTCTGTATTGGGGCTGG	59.564	20	238	465	702
60.042	20	GGTGGAGGAGGGTATTAAGATG	58.847	22	119	568	686
59.881	20	CCTCTGGACCGACCATTTTA	59.926	20	206	467	672
59.55	20	CGCAGAATCATGAGACACAAA	59.856	21	236	16	251
59.606	25	GCTGCTGTGTTTGTCTTGGA	60.032	20	216	292	507
62.18	18	TGGGTGAGAGAAAGATAGATGAG	59.371	24	238	447	684
60.321	20	CAGCAGGCAGATCACAGGTA	60.008	20	226	658	883
59.717	20	TTGGTCCACCAATCTTGTGA	59.935	20	260	894	1153
60.147	20	TCATTATTACTGCGCACCCA	60.096	20	138	19	156
59.861	20	TGAGGAGCGTTGATCTTGTG	59.984	20	234	354	587
60.758	21	AACCCGCTGTTTGTTTATCG	59.996	20	255	265	519
59.76	21	CATAATGCCTTCCCGTGACT	59.955	20	208	117	324
59.214	20	AACAATGATGGACACATGGC	59.223	20	143	539	681
59.722	20	GAAATGATTGGAGAAGGGCA	60.014	20	202	134	335
60.16	20	ATCCTTGCACCTCCTCTTGA	59.803	20	274	2185	2458
58.597	20	GCATCTAGCCACTGCTGTCA	60.168	20	245	274	518
59.91	20	GCACAACAATCTGCAATCTCA	59.862	21	253	1032	1284
59.879	21	CGCGTCCGACTCCTTAACTA	60.399	20	110	269	378
59.452	20	TGAAGTTTGGCAAGGAAACC	60.088	20	198	167	364
59.365	20	TGGTAGGCCAGAGCTTGATT	59.836	20	173	95	267
59.056	20	ATGCAATTTTTGTGGGCAAT	60.196	20	259	755	1013
59.816	20	TCAGCATGATATTGCGGAGA	60.329	20	217	26	242
59.989	20	CAACAAATTCCAATGAAAGGG	59.302	21	212	164	375
59.989	20	TCACATTCAACCTCAGCGAA	60.39	20	255	1278	1532
60.048	20	CTCTCTCTCCTGATGCAGCC	60.246	20	235	2656	2890
59.962	20	TATGTCGAGGAGGACGCTCT	59.973	20	240	3047	3286
60.008	20	TGTGGCTTGAGTGAAGTTGC	60.032	20	261	809	1069
60.292	20	TTCCAGCAATGGAACCAAAT	60.309	20	277	972	1248

59.875	24	TGCTGTGGACACGTTCAAAT	60.16	20	249	24	272
59.827	20	TGGGAACATTATGATGGGAAA	60.002	21	217	633	849
59.985	19	GGACCATGTACTGGACTGGC	60.395	20	244	1694	1937
59.993	20	CACCGGGTACTGAGGGATTA	59.807	20	251	325	575
60.324	20	CACGTGTAATTAATTCGGTTACCA	60.057	24	264	31	294
59.85	20	GGGAATTGGCCCAAATAAGT	60.02	20	262	51	312
60.184	20	CATCAGTCTACAGCCAGGCA	60.008	20	126	857	982
60.197	20	TTGTGCCGTGATGATGAGAT	60.08	20	263	261	523
60.242	20	ACTTTTGATGCCGAAGTACAA	57.439	21	254	103	356
59.019	20	ACACATGTCGCCTTCTGGTT	60.577	20	197	35	231
60.051	20	CGAGGAATTTGAAGAACACTTG	58.88	22	266	1390	1655
59.172	21	TCCATTAAGCCCTGAACCTG	60.066	20	272	163	434
60.199	20	TTGAACTCACGATCTCACGC	59.992	20	165	25	189
59.648	20	GCATAAATTGTGTTCCCCGA	60.701	20	268	183	450
60.257	19	GTTGGAGGAGAGCTGTAGCG	60.156	20	239	22	260
61.095	20	CTCGAAGGGAGGAAACAACA	60.224	20	212	21	232
57.38	23	ATGGGAAGAGGGGGTATGAG	60.147	20	239	1277	1515
59.843	23	GAGTGTGTCGGGAGTGAGGT	60.161	20	250	214	463
60.074	20	ACAGGGTCAAATCGAGATGC	60.081	20	206	778	983
58.917	20	AGGAAGAAAGAAGGGGCAAA	60.18	20	196	65	260
59.875	20	GAATGCTGCTGTTGTGCATT	59.878	20	268	2376	2643
59.74	20	TGACGGACCTTCATTTTTCC	59.91	20	188	526	713
59.903	20	ATGAAAGGGACACGTGGAAA	60.353	20	127	1381	1507
60.765	20	GGAATGGTGTGGGGAATATG	59.871	20	124	832	955
58.174	20	CGTAAAAGAAGTCGTTGCCC	59.747	20	222	183	404
59.913	20	GGGTAGTGGCGAGGTGAATA	59.955	20	113	71	183
59.962	20	GGCCCCTCTACTCCTGTGAT	60.477	20	272	114	385
59.851	20	GAACCACCACCACTGTTTCC	60.261	20	212	410	621
59.825	21	TGATTGATTAATTCGTTTGTTAGG	59.009	25	215	125	339
59.811	20	TCCATGAAGGAAAAAGTCGG	60.044	20	176	145	320
59.88	20	CTCCATTTCTTCTTCCTGCG	59.948	20	233	262	494
59.823	20	AGCTGGCTCAACTACTCCCA	60.012	20	246	2693	2938
60.042	20	CCTAGCTCTTGCCCCTTTCT	59.976	20	278	107	384
60.178	20	ATCGGAGTTGATTTGATGCC	59.9	20	209	594	802
59.855	21	TGTAAAGTGAACAATGGAAGCAA	59.677	23	215	4964	5178
59.971	20	ATTTGCTTGATCCAACGGTC	59.939	20	163	959	1121
59.939	20	CCAATTTGAATGGTTATCACCTG	60.457	23	157	1232	1388
60.177	20	ACAGTGGCGAATGTATGCAA	60.142	20	164	241	404
60.278	20	TTTCGTTGTTTCCAGCCTGT	60.668	20	239	2201	2439
59.903	20	TCTGCTTAGCTTTTGGACGTT	59.167	21	173	4369	4541
60.008	22	GTGAAGTGGGGTAGAAGGCA	60.111	20	264	50	313
60.045	20	AACATGCACACAAGCACACA	59.785	20	255	174	428
59.934	20	ATATCGTGGCACCATTGCTA	59.019	20	159	270	428
57.046	24	GCAGTTGGACTTTTCGCTTC	60	20	259	526	784
60.331	20	GCTTCAGCAAGGAAGATGCT	59.723	20	125	1434	1558
60.309	20	GAAACCCGTGAACTAAACGC	59.615	20	146	701	846
59.991	20	TGTGAACCTTTTTCAGCCGT	60.668	20	189	1443	1631
59.542	20	TCCAACGTTGTAACACACACA	58.508	21	134	4	137
60.356	20	TGAAGCACAACACCAAGCTC	60.032	20	247	284	530
60.558	20	GGGGAGGAAAGAGAGAGGTG	60.186	20	158	45	202
60.592	20	GGCAACTTTTGATTCTTCTCG	58.962	21	256	4356	4611
60	20	CCCAATAACTCGCAATAGTTTG	58.698	22	133	482	614
60.16	21	CACAATATTTGAGGGTTATCATTT	58.787	25	212	255	466
60.422	20	TTCCAATAACTCACAAAACTTTAA	58.364	26	185	270	454
59.802	25	TCAAAATCAGCAATCGGACA	60.197	20	233	3220	3452
59.558	20	ACGGCCGTGTACTCTGTTTT	59.662	20	131	416	546
59.133	20	ATCCCTCGACTTTCCCCTAA	59.897	20	187	1800	1986
58.049	24	CATGTTCCCAATTAAATAAATGTT	60.219	26	272	89	360

59.505	20	AAAGAAGGACCTCCCGTGAA	60.988	20	162	714	875
60.744	20	AATGGACGAAGATGCTCTGG	60.218	20	226	46	271
59.478	20	ATCTTCGCTCCTTCAGGGTC	60.735	20	277	450	726
59.924	20	CAGTTTCGAGTTTTGAAGTTAGGA	59.033	24	167	150	316
59.641	21	GAACTGGTGGCAACTGGATT	59.973	20	133	1027	1159
60.104	20	TAGGGCCGAAAACAACAAAC	59.975	20	154	4	157
59.801	20	CGTCCACGTGCATAATGAAA	60.523	20	245	3	247
59.914	20	GTGGCACCAATCAACTCCTT	59.973	20	128	497	624
59.85	20	TTGGAGAACAGGTAGCGGTC	60.255	20	158	32	189
60.006	20	CGGGAATGCACCAAGAAATA	60.827	20	113	89	201
59.266	25	GCCCACCATTTATCTAAACCTG	59.737	22	211	94	304
59.592	20	GGTTTCATTTCCACCTTCCA	59.767	20	217	338	554
60.204	20	CGACATTAAACACACGGTCG	60.027	20	156	5	160
59.973	20	ACCCACACATGCAAGACAAA	60.008	20	212	627	838
60.776	20	CATGAACCTCCAGGGAAGAA	60.042	20	277	389	665
59.894	20	GCCAACACCTACACCAGGAC	60.431	20	182	2977	3158
58.972	27	CTACGATCCGATCCAACGAT	59.917	20	176	3	178
60.625	25	CCCAAATTCAGGCTGTTCAT	59.933	20	186	1	186
60.019	19	CCTCCCCGTATCGATTATCA	59.739	20	268	62	329
59.966	20	GACTTGATGCATGCTGCTGT	60.024	20	214	1102	1315
59.817	20	CAAAATGAAGGCAATGAGCA	59.809	20	139	99	237
57.228	24	GCTATCCGCTGAAAAGCATC	59.951	20	204	79	282
61.298	20	CTGTCCACGGCTCCTAAAAG	59.869	20	277	1164	1440
60.469	20	TGGAACAACACTTCAACAACG	59.643	21	277	4151	4427
58.744	23	TTGCTAGAGGGTTTTGTTAATATG	59.12	26	115	1167	1281
59.973	20	TTGGTGGGAGATTGCTAGAG	57.894	20	278	18	295
59.712	20	TGTTTAATCAGGTAGAAAGTTGCA	58.854	25	233	1115	1347
59.992	20	ATGCGGCGCCTTTTTAAT	60.557	18	275	139	413
59.903	20	TCTTCTTCCCCAATCCTCCT	60.008	20	250	1574	1823
59.992	20	CATCCCATCACTACCCCATC	60.011	20	128	122	249
59.992	20	TTTCCCAAGGATCAGACGAC	60.05	20	224	2004	2227
60.005	20	CTTGCTCGTTTTATCCCTCG	59.839	20	236	416	651
59.685	20	GACGAGCAAGGATAGCGAGT	59.603	20	173	2	174
59.316	20	TTGGACACATAGTTCATGCCT	58.09	21	153	49	201
59.79	20	GCTCTCAAAGATGCGGAAAC	59.962	20	185	121	305
57.046	21	TCCCGAACTCTTTCAGCACT	59.989	20	239	104	342
58.48	21	CATCTTCTCATCTCAACTCCCA	59.284	22	277	2	278
59.631	21	AATGGAAATGAGTGGCGTCT	59.556	20	102	145	246
60.838	21	TGCCAAGTGTGTTGAACCAT	60.008	20	243	10	252
60.21	20	TTGAAGAAGCACAGGCAATG	59.988	20	244	101	344
59.823	20	TGCAAATTAAATCAACGGGG	60.671	20	271	227	497
60.008	20	CCGGCATCATCTGCTTTTAT	60.06	20	209	105	313
60.319	20	CCCGAATTCGATACAACAAA	58.48	20	133	65	197
60.025	20	TTTTTGAGGGAAAGTTGTGGA	59.573	21	280	40	319
59.66	20	GGTGAAATGACCATTTTGGG	60.029	20	239	2281	2519
58.995	20	GATCGTGAATGATCTACGTCCA	59.962	22	111	242	352
60.495	20	AATTCCCCATGACCCACAT	59.854	19	277	88	364
60.096	20	GGAAGAACACCCCATACGTG	60.232	20	276	132	407
60.617	20	TGTGCTAGGGTTTAGGTGGG	59.986	20	167	42	208
60.419	20	TTTGGCTGATTGAATTTATGGA	59.433	22	270	585	854
59.701	20	AGAATCGATTACTCCCGCCT	60.06	20	213	91	303
60.044	20	GCGGTCCAGATCTGCTACTCT	60.938	21	167	324	490
60.05	20	GAAGTGAGGATCGTGGAAGG	59.655	20	113	6	118
59.799	20	ATGCATTTTCTGCACACGAG	59.871	20	236	211	446
59.935	20	CACCAGCAGTCTGTCCTTCA	60.022	20	228	711	938
59.697	20	AAAGCAATGGCGGATACAAG	60.096	20	267	1	267
60.166	20	AAATTTGCCCTTGTGGATTG	59.801	20	252	2243	2494
60.246	20	GTTTGGGCTTTTAGCCTTCA	59.338	20	217	658	874

59.676	20	GGGATTTATTTTGGGGTACA	59.774	21	106	358	463
60.042	20	CCATCTTCCGTTGTCGATTT	59.933	20	251	114	364
59.092	25	GCAGCCGATTGAAGAACTTT	59.457	20	109	4	112
59.727	20	TGGAAGAAAAGGTTGCTGCT	59.993	20	221	188	408
60.044	20	GCGGTCCAGATCTGCTACTCT	60.938	21	173	338	510
60.08	20	TCTTCTTCCTCCCTGGGATT	60.008	20	170	112	281
59.676	20	TGCTGTTGATGGTGTTTGGT	60.008	20	267	1821	2087
60.035	20	ATTCTTCAATCAAGGCGTGG	60.074	20	235	854	1088
58.028	22	AGGCTCTGCATGCTCTTTTT	59.222	20	164	17	180
58.977	20	CAGTTGGGTCAGTGACATGG	59.997	20	203	3	205
60.054	20	AAAAATGGTTATTACTGGAACGC	58.564	23	258	440	697
59.933	20	TATGTGTGATTTTGGCTGGG	59.395	20	232	117	348
61.046	20	TATTGATGGAATTGGGGTGG	60.384	20	195	617	811
59.933	20	GGCCAATTCTTGGTAATTTCG	60.659	21	253	15	267
60.088	20	GTGAGGACTGAGGGCAGAAG	59.986	20	115	1588	1702
59.801	20	TGGGTTTGATTCCCAAATGT	60.029	20	176	309	484
59.6	20	AATTCATGGCTGCGACTTTC	60.221	20	268	265	532
60.37	20	ATTGAATTCGGATCTGACGC	60.043	20	264	321	584
58.799	20	CGCTTCCGGAGTGGATAATA	60.053	20	158	86	243
60.64	24	ATAGCGGACACTTGGACCTG	60.134	20	101	0	100
60.218	20	TTTCCGATAGGTGTTGGGAG	59.926	20	192	266	457
59.632	23	TCGGTCAAATTCAAACTCGT	58.201	20	239	1332	1570
59.697	20	TGTTGTTGGGTTGTTGGTGT	59.745	20	215	323	537
60.002	20	GGTCTAGGCCCCTCAAATCT	59.536	20	139	1127	1265
59.55	20	ATCGAACTCTTGCGTTGCTT	60.022	20	132	43	174
59.95	20	ACGTAATTTGGCGGTCTCAG	60.132	20	239	552	790
59.705	20	TCCACAAAAAGTGGGTGTGA	59.976	20	143	36	178
60.306	20	TCCAAGAGTCTGCAGTGTGG	60.022	20	100	22	121
59.964	20	GCTACCCCTCCCTACACCAT	60.212	20	208	595	802
59.648	20	CTTTTCACACGAGGTCACGA	59.873	20	199	82	280
59.83	20	TGCAATCCAGTGAAAACTCTG	58.912	21	190	48	237
58.328	20	TCATGTTGCATATTATTTGGCAT	59.256	23	241	60	300
59.981	20	ATTTCCCACCAAACAGCAAA	60.344	20	191	533	723
59.973	20	GGCACACATCTGTGACATCC	59.97	20	140	234	373
59.809	20	GGAGTTCAAATTCGGTTGGA	59.91	20	182	1159	1340
59.508	20	CACCAGATCACTCCCCTGAT	59.92	20	268	1303	1570
59.785	20	GCAGCTGCTGTGTGGATAAA	60.019	20	187	1147	1333
60.133	20	AGCGGTTATTACCGGATCG	59.93	19	163	479	641
60.111	22	CATTCAACTGGGCATTTGTG	59.964	20	206	27	232
59.496	20	CAAGGCTTGAAGCTGGTAGG	60.008	20	252	76	327
60.111	20	AACAACGGTATCACCTGAACG	59.906	21	151	3990	4140
58.826	27	CTTCTTTCCTTTCGCGTGTC	59.993	20	159	3	161
60.066	20	CACGGTTAGGCTCGAGAGAG	60.149	20	154	81	234
59.789	20	ATGGAGGAAGGAAGGAAGGA	60.008	20	276	15	290
57.439	27	GAGCAAGGCACCTCAATCAT	60.226	20	182	11	192
59.685	20	TACCGGCTGGGTACCAACTA	60.378	20	167	478	644
60.011	20	AAAAGGGCGGTGGTAAAACT	59.871	20	125	45	169
60.593	23	AATCGGTGAACAGTTCGGTC	59.973	20	224	1882	2105
57.155	22	CACCAAATTTCATCATTTTTAATTC	58.035	25	205	149	353
59.881	20	TTTCTGTTCCCGATCTGAGC	60.34	20	233	2095	2327
60.452	20	GGGAGAATCGAGATTTGTTTTG	59.945	22	274	271	544
60.081	20	AAATTTGAGGGGGTTCATCC	59.996	20	240	22	261
59.971	20	AGTCCCTTTTTGTTGCCTGA	59.711	20	128	369	496
60.326	20	CATGAAGCGCTGATTGTTGT	59.871	20	280	1301	1580
60.345	20	TAGCCGATAAAAATGGCACC	59.928	20	259	91	349
59.903	20	CGCTAACTTCCAAAATGCCT	59.361	20	262	799	1060
60.683	20	GCCCGTGTGCATCACTACTT	61.128	20	132	550	681
59.349	20	GCACCAAATAATTCGACTTGC	59.605	21	270	167	436

59.96	20	TCGCAGACTGATCTTAGCGA	59.847	20	203	772	974
60.14	20	GCATTGATGGGATTCCACTT	59.756	20	212	1085	1296
60.136	20	TCACTCCAAAATCCACTCCC	59.903	20	136	304	439
60.088	20	TGGGTGCAACTTTCTAGCCT	59.875	20	164	7	170
59.975	20	GGGTTTGGAGGGGTATCCTA	60.011	20	197	158	354
59.769	20	TCCATAGCCGGTAAAAATGG	59.789	20	188	8	195
59.757	20	GATTTGCGTGGTCCATTGAT	60.733	20	270	1	270
59.916	20	TCAGCCTCCATCAATTATCAAA	59.547	22	163	183	345
61.087	20	AGGGGTGACTTCATGGAATG	59.779	20	221	1922	2142
59.957	20	GGACCACAAGTTCGACAACA	59.571	20	194	169	362
60.95	20	CATGCTGCCGGAAGTAATTT	60.096	20	262	150	411
59.221	23	TGGACATATGGAGGGAAGGA	60.272	20	255	831	1085
60.074	20	TCCCTCTTGAGTGAGCTTTGA	60.119	21	263	2536	2798
59.642	20	GCATTTTGGGTACACCTGCT	60	20	250	1185	1434
60.449	20	CAACAAGAACCAGGCATCAG	59.288	20	271	146	416
60.622	20	GATGGACTCCGAGGATGATG	60.439	20	207	51	257
60.225	20	AGGGTTTCAAGAATCCACCC	60.169	20	126	1821	1946
59.92	20	TTTTTGACGATTTTGCCCTC	60.053	20	245	1642	1886
59.757	20	CCGACCTCGGTAAATGCTTA	60.089	20	206	626	831
60.232	20	GCATTGTGATGTTGTTTGCC	59.979	20	210	503	712
59.691	20	TCCAATCGAAGATTCGGAAC	60.014	20	202	98	299
59.708	23	TTTGTTAGAGATCTTGACGGGA	58.834	22	204	960	1163
60.018	21	GTGTGTATGAGAGCCGCAAA	59.871	20	189	1350	1538
58.513	22	CAACTCCTTTGGAGCCATTC	59.67	20	260	3	262
59.989	20	CTGGCACATCTGCAGTTCAT	59.862	20	228	287	514
59.322	20	AAGCTGTGGGAGATGGAGTG	60.261	20	237	646	882
60.022	20	GTGGATGGTCCTCAGCTGTT	60.12	20	183	288	470
59.967	20	TGTGGAAATTATGGTTCGCC	60.701	20	253	791	1043
59.964	22	TGCGTTTACATTCAAGCAGTG	59.926	21	100	43	142
59.195	20	GTCTTCTGGCTTCTCTTGCC	59.166	20	114	36	149
58.288	20	ATTTCGAAGATCAACGGACG	60.074	20	111	65	175
59.545	20	AAATCACAACTCACACGCCC	60.966	20	242	24	265
59.076	21	CCCCATTAGCTTCATCCTCA	60.029	20	236	780	1015
60.072	20	CGGGCATGAAAAGGTTAAAA	59.937	20	274	191	464
60.081	20	CAATACAACTGCCGAGCTGA	60.011	20	134	52	185
59.744	24	ATGATCGCTCTGTTCCGATT	59.658	20	275	681	955
60.11	20	GCAACCAGGTACTCATTGGC	60.526	20	160	781	940
59.988	20	AAACCCCAACGGACAGATTT	60.59	20	174	1832	2005
58.661	21	TTCCACCTGATCCTGGTTTC	59.903	20	166	2084	2249
59.881	21	TTTTCATTCATGTTTCGCCA	60.051	20	228	673	900
60.183	20	TCAAACCCACGGACTGTGTA	60.001	20	157	1596	1752
60.009	20	GATAAAACAGGGGAAAGGGC	59.777	20	223	96	318
59.976	20	TACAAAGCTGCTCGGTCCTT	60.015	20	227	101	327
59.74	20	CGTGCCTAGTCTTTGCTTCC	60.015	20	160	473	632
60.249	20	GAAAGTATGGCTGCTCCTCG	59.978	20	174	325	498
60.124	20	TCGACGATCACAATTTGTCC	59.502	20	193	439	631
59.839	20	CCCAAATTTTGACCATTTCC	59.111	20	176	0	175
59.72	21	AAAAACACATATGGTGACACGG	59.654	22	225	1285	1509
59.83	20	GTCGGTGGCTGGAGAAAGTA	60.255	20	155	2593	2747
57.118	25	CCCATAACTCCAAACCCAAA	59.657	20	269	52	320
60.142	20	TCACATGGAAACATGTGGCT	59.967	20	191	176	366
59.269	20	GGGAATTTAATTTCTGGCCC	59.621	20	147	2665	2811
59.829	20	CAAAAAGCTGGGTGAACTCC	59.711	20	223	247	469
57.055	25	TCTTAAAAGGGAGGGGCTAA	57.95	20	280	138	417
58.418	24	CGGTTTAGGTATTTTGATGTTTTG	58.937	24	136	83	218
59.347	22	CGACGAGAAAGTCGTGTCAA	60.025	20	232	117	348
57.664	22	TGGTTACAAGCAGTGGCGTA	60.316	20	162	4	165
59.644	27	ACATGGATTGTGCATTCGAC	59.379	20	280	31	310

60.066	20	AGGGGAGTGATCTCATGTGG	59.92	20	247	161	407
60.111	20	TGCTGCTGATTCACATAGCC	59.979	20	237	87	323
60.019	20	ACCATGGCAGATTCATCCAG	60.893	20	197	165	361
58.965	21	TTTAAACCTTCCCCCAATCC	59.992	20	277	1561	1837
60.009	20	GTATGTGTGGCTGTGGATGC	59.999	20	245	53	297
60.14	20	CCTATGGTGGTATGGTGTGG	58.569	20	190	5	194
60.049	20	TCTACCACTCCGAAACCTCG	60.246	20	238	82	319
59.658	20	GCGACATCCAGTCTGAGTGA	59.988	20	116	129	244
59.765	21	TGGTACCTCCTCCTAATTTCCTC	59.854	23	181	258	438
60.036	20	TATGATGGGAAGGGTGGGTA	60.006	20	263	1166	1428
60.05	20	AGCGAATGTTGTGAGAAGCA	59.596	20	242	25	266
60.688	20	CTCGACACAAATCTGCACAA	58.409	20	262	248	509
59.985	20	CGGTTTTCGGTTTTCACAAT	59.839	20	235	78	312
59.995	20	AGGGCTACAACTCTCAGCCA	60.012	20	265	627	891
60.209	20	CTGCATACGAGCATGGAAGA	59.972	20	273	588	860
59.799	20	TTGAGTGCGTGTGTGAGTGA	60.07	20	231	157	387
60.39	21	TTGGGAAGGGAATGTGTCAT	60.173	20	158	3705	3862
59.027	20	CAAACGCTAAACGACACCAG	59.386	20	279	2	280
59.336	20	AAGTTATGCTGGTGGTTGGG	59.853	20	263	344	606
60.147	20	CGCGTTCAATATTCTCAGCA	59.976	20	207	171	377
58.122	24	TGAGGAACTTGAGAGTGGGG	60.229	20	101	167	267
59.311	22	ACATTTTCGGTTCATTGGGA	60.17	20	145	25	169
59.813	20	CTCTCCATTTTCCCTCCTCC	60.008	20	280	470	749
60.005	20	TGCATGATCGATATTGTAAGGAA	59.468	23	184	56	239
59.95	20	GAGCGTTAATGCCGTTTCAT	60.103	20	172	192	363
60.119	20	TCCATTTCCTTTTTCGATTCC	60.246	21	195	998	1192
57.73	23	CGGACCCAGGATTTTAGGTT	60.18	20	262	14	275
60.048	20	TTGACGGCCCTAAACAAAAC	59.975	20	206	182	387
58.249	23	TCCGCCTTGACACCTTCTAC	60.255	20	162	0	161
59.671	20	TGTGAATCAAGTACCCCGAA	58.973	20	279	72	350
59.963	21	TCGAACCTGCCCTCATTATC	60.036	20	227	401	627
59.234	20	CTACACCCATCGGAATCAGC	60.483	20	271	91	361
60.938	20	TGTGGCCTTATTCATGCTCA	60.22	20	251	372	622
60.294	20	GGGCCACTTTGGTGACTAAC	59.454	20	252	326	577
58.358	23	CTCTCTGCTGGCCAAAAGTC	60.134	20	273	781	1053
59.58	22	CATTACAGCCGTGAGAAGCA	60.011	20	265	2	266
60.136	20	GGCAACGATCATTTCTGGTAA	59.952	21	271	1250	1520
59.995	20	ACCAAGGGTGAGAAGCATTG	60.111	20	227	288	514
59.694	20	CGTGTTTTTCCCCCTTTTTC	60.674	20	252	3826	4077
59.864	20	GGAGGACCTAGACAGCCCTC	60.216	20	254	1289	1542
60.124	20	CAGCCAAATGTTGGGTTAGC	60.502	20	221	145	365
59.528	20	ATTGCCCATATCAGCACTCC	59.923	20	279	795	1073
60.187	20	ACCCTCGACGTTTTCCTTCT	60.11	20	220	1106	1325
59.92	20	ATTTGTCTGCATACGGGCTC	60.103	20	184	1261	1444
59.978	24	TTGGATGTTCCAAATACAGGC	59.815	21	279	2551	2829
60.281	20	CTGGAAAAAGTCACCGGAAA	60.081	20	277	49	325
59.989	20	ATCCCATTTCCCTCCTTGAC	60.133	20	185	113	297
60.526	20	TGGATTTTCTGAATTGTGGG	58.395	20	254	846	1099
59.934	20	TTTCATGCAACAAAACCACC	59.42	20	261	1918	2178
60.691	20	TCAGCAACTGAACCTGGAAA	59.415	20	160	79	238
60.134	20	ATGCATCCGTTAGATCAGGG	59.917	20	233	104	336
60.008	20	CCAGCTGACGAGCATACTGA	60.16	20	247	205	451
60.138	21	TCTGAATCTGATTGCGTTGC	59.955	20	266	39	304
60.535	20	CCCGAGGACACATAAGCCT	60.081	19	280	165	444
59.109	25	TCCATTCCGAAAATCGAAAG	60.009	20	280	609	888
59.375	20	AAAAACACGCGTTTGTAGGG	60.032	20	232	104	335
59.96	20	TCCGGTGAAACATTGACAAA	59.941	20	249	1319	1567
59.662	20	TTAAAGTTCTTAAGTCCTGGCG	57.792	22	255	677	931

60.326	20	AGATGGTTGCACCATAACGC	60.925	20	183	298	480
59.96	20	GGCACCAATTCTCATAATACACA	58.891	23	142	266	407
58.823	21	TGGTCGCCGTGTCTGTAATA	60.134	20	195	3852	4046
59.52	20	CGACAGGTGGGAGAGTCATT	60.112	20	251	393	643
60.103	20	CACCGTTGTCTTTAAGCCGT	60.168	20	240	715	954
59.057	24	ATACGGATCTCTGCCTCTCG	59.41	20	155	3	157
59.928	20	TTGGTTGGATATTTTGGGGA	59.988	20	244	266	509
59.971	20	GAAATCCCATCCACAACCAC	60.034	20	165	203	367
59.971	20	AACACGAGCAAAACGACAAA	59.366	20	251	95	345
60.25	21	GGAAGAGGAGGTATGAGGGG	59.89	20	223	556	778
59.82	20	AAGGAGGTGTTATGAAGGGATT	58.028	22	157	291	447
59.72	21	GATGTTTTCCGGCTCAGTGT	60.119	20	269	91	359
59.898	19	CGGTGACGGTTGAGAATGAC	61.527	20	271	183	453
60.519	20	CAGGAACCACCTCAGGGTTA	59.959	20	250	39	288
59.751	20	GAGTTTTCATCTTACCTTGAGGG	58.333	23	271	70	340
60.464	20	TCAAAACGCATAAATAGTGCAAA	59.687	23	280	44	323
60.042	20	CATCAGATCCATACTCGGCA	59.629	20	241	18	258
58.58	22	GCGAACGGTATAGAATCGGA	60.06	20	278	56	333
58.823	20	TGGATGATTCACAACCAAACA	59.808	21	189	943	1131
59.975	20	TTGCTAAGTTGGGCCTATCG	60.223	20	272	1126	1397
59.903	20	CACTTCAGCGTCACCTCAAA	60.025	20	274	123	396
59.985	20	GTTTAGCAAGCACGCCTCTC	60.162	20	278	1222	1499
59.062	20	GGTTGTTTCATGACATTTGAGG	59.336	22	270	411	680
60.214	20	CTTCTACGCGAAGCACGTTT	60.575	20	264	1236	1499
59.273	20	CCGTTGCAAGAGTAATGGCT	60.27	20	185	2773	2957
59.943	20	AGCAGGCGAGGTGTTACAAT	59.763	20	242	57	298
59.923	20	TTGATTAGTTCGTGCAACGC	59.879	20	275	386	660
60.26	20	CCACCATCTCTCTCTCCCAC	59.638	20	179	1448	1626
59.587	20	GGGTGGCTGATGAAGAGAAA	60.195	20	262	705	966
60.051	20	ACACACAAATGGTTTGCCCT	60.277	20	218	69	286
60.029	20	TGGGTTGGTTTGCTTACCTT	59.471	20	260	150	409
59.525	20	TTTACGGGTCAAAAGAAACCA	59.478	21	250	678	927
58.842	22	TGGCTTGTGAACGTGTAACC	59.615	20	184	67	250
59.934	20	TGCATGCACATCAAATCAAA	59.648	20	253	40	292
59.316	20	GCAGTGGATATGCAATGTGG	59.955	20	217	88	304
59.667	23	TTACCATCATTCTTGGCCATT	59.287	21	244	169	412
59.955	20	CAAAATTGCGTCTCCAGTCA	59.84	20	238	1501	1738
60.272	20	TATCGGTTATCATCGGATCG	58.404	20	171	439	609
58.589	21	GGAATTTCCTTGATACACATACAT	59.918	26	277	619	895
59.974	21	GGGATCTACATGCTGGGAAA	59.894	20	135	134	268
57.268	20	CTTAGATGCCATCAACCCGT	59.955	20	184	22	205
60.073	20	CATCAAGAAGCTGCAGCAAG	59.888	20	269	769	1037
60.24	20	TCCCCTCAAAATCCCCTAAC	60.124	20	190	56	245
59.879	20	ATTTAAAGGCACGGGAACCT	59.835	20	275	1087	1361
59.926	21	CGTTAAGATCAACGCGGATA	58.794	20	210	2491	2700
60.111	20	CATGGAGATCGTACGTTTCGT	60.008	21	173	2001	2173
60.802	20	ATCTCCGAAGCTCAAAACGA	59.955	20	100	261	360
60.103	20	TCCACAGTTTTGTACCCACTTTT	59.827	23	233	1489	1721
59.823	20	TACACGCATATTCGCACACA	59.741	20	181	149	329
59.935	20	GGATCGGAAGGATAAGAGCC	60.003	20	135	442	576
59.988	20	CCACAAAACCACGTTCCTCT	60.005	20	190	268	457
57.552	24	GGGAAGTTGAGATAATGGCG	59.528	20	272	11	282
60.545	20	TGATGGCGGTAGGTAGCTCT	59.859	20	231	288	518
59.108	22	CCGACCCTCGTGTTTAATGT	59.853	20	129	13	141
60.184	20	TATGGGGACTCTCATCTGCC	60.034	20	248	1075	1322
58.864	20	ACCTCCCCTGCTCCATATTT	59.789	20	101	286	386
60.292	20	CGGACCGTGAAAGCTCTAAG	60.008	20	240	234	473
60.003	20	TCGTTTAGGAAGCCTCTGGA	59.948	20	261	88	348

59.291	21	TTGAATTTCGTAACGGGGAG	59.931	20	196	11	206
57.409	21	TCGGGACGAAATTTTTGTATG	59.818	21	274	2	275
59.337	20	GGCAACGGAACAACAACTTT	60.015	20	280	3145	3424
59.037	20	GGTTCAAATCCCACCAACAC	60.073	20	249	1192	1440
59.992	20	CATCCCATCACTACCCCATC	60.011	20	129	144	272
59.962	20	AACCGAATAACCGAACCAAA	59.315	20	235	25	259
60.612	20	ATTCTTGGCCAAAACGTGTC	59.978	20	241	148	388
59.957	20	GCTTTCCTCATCTGCACCTC	59.957	20	259	1291	1549
57.073	22	CTTCTGCTGGTAGAGCACCC	60.012	20	233	1228	1460
59.445	23	AGTTTATCATTTGGGCCGGT	60.562	20	140	21	160
60.074	20	TTTCTTCACCGTTTTCCTTGA	59.71	21	219	470	688
59.662	20	ATTCCAAGGTTTTGCTGTGG	59.971	20	177	3077	3253
59.84	20	CAACAGTTTGGTTTGGCTGA	59.734	20	255	708	962
59.861	20	AGGCATAAAATTCTCCCGCT	60.061	20	251	21	271
60.38	21	GCTTCAGGGGGTGTGAAGTA	60.111	20	254	90	343
60.155	20	CTCTCGCCCCAAACTTAGAA	59.448	20	255	401	655
60.319	20	TTACCTCCTCCACCATCGAC	59.927	20	272	273	544
60.05	20	GCCGAATATTTTGGGCCTAT	60.135	20	222	416	637
59.79	20	GAAAAGAAATGAACACCGGC	59.551	20	210	62	271
60.011	20	AACTTTGCTGAGTTCGGGTG	60.291	20	270	471	740
59.098	24	TACCCCACCGACATTTTTGT	60.088	20	126	343	468
60.345	20	TCCGTGAATATTTAACCCGC	59.795	20	254	1158	1411
60.132	20	TGCAATCACCAAAGAACTGA	57.806	20	118	340	457
60.025	20	TGTCCCCTATTTGGACGAAG	59.926	20	210	184	393
59.449	20	AGAAATAAAGGCCCAGCTCC	59.688	20	151	2176	2326
60.213	21	TGGCCCAGATTTGTTCCTAC	59.933	20	185	1360	1544
61.129	20	GGTGCGTGAATTGGCTTAAT	59.967	20	239	128	366
60.081	20	GAGGGTTATCATGGGATCAAG	58.32	21	162	470	631
60.089	20	CAAGCTTGTGGAGTACATGAGA	58.036	22	252	40	291
60.52	20	TGGTCGCATGTTACGTGTTT	60.035	20	179	1342	1520
60.111	20	AATTGCCAAGTTTGCGAGAT	59.713	20	259	622	880
60.073	20	ATTGGCTGAAATGGAGTTGG	59.933	20	236	497	732
57.828	22	GGGCCAACCACGTTAGTTTA	59.861	20	234	449	682
60.029	20	ATGCCCGGTTACCCTCTAAA	60.683	20	156	514	669
60.264	20	GTCTGGGACAGACAACCGAT	59.969	20	174	85	258
60.033	20	TCAATCCTTTGGAAACACTCC	59.017	21	178	155	332
59.79	20	TGCGTTCACACCTTCATATTTT	59.519	22	196	142	337
59.971	23	CAACTCGCCTACTCCTTTCG	60.008	20	154	445	598
58.62	20	TGCAAGCCTATGGTAGGTGA	59.297	20	115	103	217
60.049	20	CACTGATCGTACACGATGGC	60.144	20	182	403	584
59.813	20	CACCATCATCGACAATCACC	59.769	20	215	385	599
60.397	20	ATTTAAGCTGCACTTTTATTCAACT	57.118	25	240	140	379
59.415	20	TTCCACGTTTCATGTTTCCA	59.941	20	144	60	203
59.415	21	CTTGCGCCGCCTAAATAATA	60.202	20	189	809	997
59.797	20	AGGGGCAGGATGTGTAGTTG	59.989	20	273	437	709
59.991	20	CCCTCGGATGCTATGCTAAA	60.188	20	231	351	581
59.703	20	CTCTCGTCTCCTCCTTCCCT	59.945	20	170	28	197
59.46	22	AAGTTGGGGATCGTGCATAC	59.82	20	261	97	357
59.83	20	CCCCTATATCCCCATGACTCT	59.138	21	228	1301	1528
59.629	20	GTTGGATTCGAGCAGCTCAT	60.37	20	256	143	398
59.962	20	TCAGCCACCAAATCAAATCA	60.049	20	161	114	274
59.901	20	TAGTGGTATGATGTGGGGGA	58.643	20	203	196	398
59.75	20	TAGAAAGATGTGCGGCTGTG	60.011	20	153	2081	2233
59.966	20	AAACTCTTCCGCCCCTTCTA	60.2	20	151	135	285
59.843	20	AGGAATCCTGCCCCAAGTAA	60.817	20	146	324	469
59.784	21	TGATTGGTGTGGTGAATTGG	60.216	20	276	71	346
60.19	20	TCCGTCCCAAGAAATGTGAT	60.317	20	207	2175	2381
59.756	20	TTGGAATTTTTCGAGTTCCG	60.046	20	176	899	1074

60.051	20	CAATGTAAGGGGGAGCAGAA	60.066	20	254	124	377
59.755	20	AACATGTTTGCTGGTGCTTG	59.764	20	209	3746	3954
60.408	20	GGCAAGCGAGTAGGTTGTGT	60.321	20	161	242	402
60.424	20	GGGGTTGTTAAAATGTCCACC	60.326	21	156	607	762
60.111	20	AAAAACCTTGGCAACAGTCG	60.147	20	223	58	280
59.656	20	ATGTTTCATCAACGGACACG	59.42	20	280	477	756
60.159	20	GGAGAAGACGGAGCTTGGTA	59.43	20	245	722	966
59.579	20	AATGAACATGCTCCTATTTTAATA	58.22	27	280	735	1014
59.399	20	CCCAGTGAGGTTGTGGAGAT	59.962	20	130	1407	1536
60.307	20	ATGTGGCGACAAATTTAGGG	59.823	20	195	318	512
59.801	20	TGCATGGAGGAAATATGCAA	60.035	20	214	38	251
59.734	20	CCCCCTCTCTACACATTGACA	59.974	21	227	2892	3118
60.205	26	ATTCTGCATCAGGCCTTCAC	60.226	20	116	0	115
59.579	20	GGTGAGGTGAGGTGTGTGTG	60.045	20	157	395	551
59.986	20	ACCGGTTGACCCCGAATTAT	62.535	20	199	1244	1442
59.527	21	TCCATCTTCATGTTCCGACA	60.048	20	188	17	204
60.132	20	CTTGAATTATCGGCGGTGTT	59.96	20	153	143	295
59.871	20	TTTCACGCATTTCCACACAT	59.972	20	102	24	125
60.128	20	ATCGGTTATCACCGGATCG	60.697	19	280	73	352
59.587	20	CCCCAAGAACAGAACACCAT	59.82	20	112	1044	1155
61.096	20	GCGATTTCAATTCCGACTTT	59.162	20	279	1255	1533
59.962	20	CGGCCATGACTATCGTTTTT	59.96	20	242	181	422
60.265	20	TGCGCAAGTGTATTGTACCAG	59.807	21	259	2942	3200
60.21	20	CAACGCCATAGGGAAGTGTT	59.993	20	266	1562	1827
60.165	21	GGCAAATTGTGGGATGAGAT	59.756	20	212	86	297
60.413	20	TTAATTGGTTCGGGCTCATC	59.901	20	273	30	302
60.06	20	GACGTCGTCATCGAGACTCA	59.988	20	271	74	344
62.397	18	TCCGAAAATCAAAGGTCCAC	59.91	20	113	18	130
59.702	20	AATCGGAGTCTGTTTGGTGG	59.966	20	129	145	273
59.836	20	TGTCGCATGCCAATCACTAT	60.104	20	232	2549	2780
59.859	20	TCATTGAACTCCCCATCACA	59.893	20	251	1343	1593
60.012	20	CCTATGGTGGTATGGTGTGG	58.569	20	132	454	585
59.934	20	CACGAAGCATTGCCACTAGA	60.011	20	208	595	802
60.158	20	CATATCGGGTCAAAGCAACC	60.331	20	124	716	839
59.336	20	AAATCTCCACTTGGGAAATTTAGA	59.424	24	130	265	394
59.906	23	AACATTTTGGGTCTTTGTCG	57.578	20	190	1245	1434
60.812	20	ACATTTAATGCCCCAGCAAA	60.323	20	202	420	621
59.139	20	TGAACAGGTTGCATTTTAGATGA	59.639	23	254	2017	2270
59.955	20	CAACGGTACGTTCGGATTTT	59.861	20	212	519	730
59.97	20	CGACAAGAGAAAGAGGGTCG	59.982	20	142	393	534
59.14	23	AGAGCGTGGGATTGAGAGAA	59.95	20	226	900	1125
60.69	20	TGGAGACGGCTGTTTTCTTT	59.853	20	205	312	516
60.163	20	ATTGGGTGGGATAGTGCTTG	59.813	20	209	291	499
59.96	20	TAAGGGGCATTACCACATGC	60.721	20	218	490	707
59.799	20	GAGATATTCTGTCGGATAGGTGC	59.13	23	229	466	694
60.683	20	CACCGTTAATCGCAACAAAA	59.603	20	273	180	452
59.129	20	TTTGATGGGAATGGGAGGTA	60.126	20	114	15	128
59.778	20	CCTATGGTGGTATGGTGTGG	58.569	20	164	53	216
59.343	20	ATCAAAGCACCAGTTACCCG	59.993	20	279	182	460
59.894	20	TCTTCCTTTTCTCGTTCACATATT	58.4	24	221	198	418
60.309	20	TATGGGTTATCACCGGATCG	60.544	20	188	437	624
59.935	20	ACGCAGTTGCTCGGAAGTAT	59.904	20	265	39	303
59.282	20	TTTGATCCAATGGCCCTAAG	59.894	20	194	1	194
59.115	20	CTCAATCGTCGCCGATATTT	60.06	20	266	200	465
58.901	21	CACACCATGTGACGAAGGTT	59.441	20	271	627	897
60.088	20	TTTTGGTCACCGTGATTTGT	58.874	20	249	36	284
60.293	20	CACGATGAATTGTCGTGGTT	59.42	20	243	60	302
60.019	20	ATGCCAAATTGTGTTGGGTT	60.096	20	185	129	313

59.903	20	GATTGAAGATGTTGGGCGTT	59.939	20	167	1007	1173
60.16	20	ATTTCGAAGATCAACGGACG	60.074	20	214	2224	2437
59.727	20	TGGATTTTTGAAACGTGGAA	58.987	20	208	47	254
60.131	20	AAGCTTGCATTTTATCGGGA	59.682	20	220	248	467
59.973	20	GCAACAAAACAAATATTGGATCA	58.906	23	276	522	797
60.073	20	GTGCTGTTTTGGTTGGTGTG	60.049	20	244	480	723
59.307	21	CTGCCAGGACGAACTTGTAA	58.923	20	276	227	502
60.235	20	ACGTTGTAGTTGAGGCCCTG	60.171	20	276	1068	1343
60.081	20	TTCACGAATTCTTCTTTCCTTTC	58.919	23	276	951	1226
57.647	21	TCAACTCAATAGGTTTTCGAGTCT	59.732	25	198	8	205
60.199	25	ATTTGGCACCATTCTTCACC	59.797	20	266	331	596
59.769	20	GTCAGACGTCCTCCTGGTGT	60.161	20	108	39	146
57.201	23	CCGCGCTGTAGATTCAAAGT	60.407	20	124	40	163
60.149	20	GTGCACAGCTGAGACAGCAT	60.22	20	166	3909	4074
59.569	20	GGTTGATGGATCTGCGTTTT	59.939	20	240	154	393
59.938	20	AGGCTGAGATCTTTCCAACG	59.43	20	226	837	1062
60.134	20	CCAAATCCTTCGTTTCTTGG	59.541	20	271	105	375
59.528	20	GCCACATATGCAAAATATCAGC	59.486	22	280	163	442
60.104	20	AGGCCGAGGAGTAGGAAGAA	60.34	20	171	174	344
59.95	20	CAGGAAAAGCATCATCACCA	59.648	20	205	2039	2243
57.557	25	GACGTGACGAAAGTGGGAAT	59.973	20	196	11	206
60.314	20	TAAAAAGCGGCATTCGATCT	59.816	20	146	60	205
60.232	20	GTGGGGTGGGATTGAACTTA	59.647	20	272	23	294
57.395	25	AAATAGATGCATGAAACATTTTGA	59.012	25	280	28	307
60.281	20	AAGGAACAACTGGTGGATGC	59.973	20	201	1397	1597
59.837	20	TGTTGCGCGTGCTTTAAATA	60.401	20	155	246	400
59.831	20	AAAATTGCAAAGCGGTGTCT	59.752	20	246	2	247
60.142	20	TCCTAGCCCTCAATCTCGAA	59.91	20	236	251	486
60.014	20	AGATCCACCACTGCTTGGAG	60.261	20	217	280	496
59.704	20	TTGATTGTCTTTGCGTTGGA	60.234	20	227	127	353
60.081	21	ACGCGGACGGTACAGATTAC	60.022	20	189	171	359
60.155	20	GTAAAACGCTAGAAGGCCCC	60.095	20	124	9	132
59.952	21	AGGAACAATCCCAACTTCCC	60.169	20	248	273	520
60.074	20	TGATCTGGAACAAGGCAGTG	59.831	20	278	1276	1553
59.604	23	GGGTGTGATCTTGACCCTTG	60.363	20	216	473	688
60.461	20	CAAGCAAATCCCCTTCTCTG	59.807	20	141	849	989
59.542	20	CATGTTGCTTTTGCATGTGA	59.28	20	183	41	223
60.275	21	CAGATGGGGATTTGCTTCAT	59.894	20	224	2636	2859
60.461	20	CGACAGCGTAATTGAAGCAA	60.014	20	262	7	268
61.051	19	TCCGAAATATCCGGTTTTTATT	58.795	22	259	889	1147
58.456	24	AAGGGAGGGTTTCATTCTCA	58.568	20	277	54	330
59.229	20	CTGGCTCCCTATAGTGCTGG	59.853	20	266	1365	1630
58.613	21	CACATCCAGCATCAACCAAC	59.967	20	254	105	358
60.245	21	TTGCTGTAGGCCTTTTGCTT	60.018	20	117	157	273
60.238	20	GGGCAGCTGTAAAACCTTCA	60.249	20	250	154	403
59.485	20	CCTCCAGATTTGACAGGGAA	60.042	20	261	80	340
60.303	20	GAACGATTAGTGTAGGTTGGGC	59.898	22	177	348	524
59.938	20	ATGGCCTCTCCAGTTACGTG	60.134	20	129	138	266
59.875	20	TGTTGATTTATGGCGGATTG	59.377	20	173	1025	1197
59.976	20	TTTCTCATTGGCAGTCACCA	60.24	20	263	548	810
60.182	20	ACGGAAATCTAGGGAGCTGG	60.59	20	267	131	397
60.089	20	GTGGGTCCCTCTCTCACAAA	60.088	20	270	2739	3008
59.795	20	ATGAGTTATCACCGGATCGC	59.923	20	253	253	505
59.528	20	TGTTGTCGCTTTAGCTCCCT	60.015	20	267	430	696
59.547	20	GGGTTAAAAGAAACCCCCAA	60.027	20	233	257	489
60.067	20	ACAAAAATGCCCTCGTATGC	59.967	20	246	425	670
59.893	20	GGAATGGAATTCACTCCTAAAGC	60.316	23	223	2847	3069
59.445	20	GCCAGGCAGAGAGAAAGAGA	59.827	20	206	1142	1347

60.02	25	GGGTGGGATACAGCAAGAGA	60.073	20	106	44	149
59.101	20	TTGAAGAGGCAATTATCGGG	60.031	20	267	1677	1943
60.217	20	CGGCCCAGTCTAATTGGTAA	59.953	20	254	4	257
59.933	20	GCATTACGTGTGTGCGTTCT	59.794	20	268	51	318
58.536	20	TCAATCGAGCTACAAACGTG	57.506	20	108	16	123
60.192	20	AGGAAAGAGAAGTGAGCCCC	59.817	20	251	5474	5724
60.116	20	TTGTTGCATGTCATTGGTCA	59.516	20	216	268	483
59.467	20	GCGCATTTCTGATATCGTCA	59.799	20	159	675	833
59.226	20	TCGTGAATTATCCAAACTTTTCAA	59.885	24	155	414	568
60.032	20	GCGTTGGAGATGGTCTTACAA	60.125	21	146	546	691
58.595	20	CCAATGCGGATGCTCTTAAT	60.06	20	279	37	315
59.861	20	ACCGCCCTCCTATTTCGTAG	60.463	20	181	35	215
59.268	23	GGAGAGGGAGGAAAGACTGG	60.186	20	189	608	796
59.869	20	TCATGATCCCATGAACGCTA	60.033	20	252	194	445
58.897	20	AGGGGGTTATCACCTGATCG	61.095	20	111	448	558
59.586	20	TTTGATTTCTCCCCTACCCC	60.124	20	278	87	364
60.059	20	CCACCCGTTGATTTTTCACT	59.83	20	235	393	627
59.972	20	GCGTGCTGAATCTTAACCGT	60.278	20	141	1005	1145
60.006	20	TGGTTTCCATCGTTTGTTGA	59.941	20	143	451	593
59.003	21	GGCCGATATTTGCTCCTAGTT	59.606	21	272	145	416
59.972	20	AACACCTGGGTGAAACCAAA	60.246	20	164	312	475
59.542	20	CACCTAAAATATTGGTTTCTATTTG	57.121	26	139	281	419
59.562	21	GTCACGTGGCATCATGAGAA	60.698	20	199	336	534
60.02	20	TTGCCAGAGCAAAAACACAG	60.027	20	105	1622	1726
58.927	23	ATCTCAAACAGTGGGCTTGC	60.263	20	278	2836	3113
60.119	20	TGGCCCTTAGCCAGAATATG	60.053	20	165	916	1080
60.031	20	TCATGTACCCCGGATCTACC	59.629	20	280	828	1107
59.996	20	AAAAAGAAAAGAAAAGAAAGAAT	57.177	26	190	505	694
59.953	20	GCAAGTTGAGGGAGAATGGA	60.195	20	153	371	523
59.941	20	GTCTTTGGCTATGACCCACG	60.517	20	259	163	421
59.569	20	TGATTTTCATGTTTCGCGATT	60.45	21	216	81	296
60.112	20	GGACTCATACGAGGAAGCCA	60.218	20	196	2438	2633
59.956	21	CGTCATTGGAAAATAATGCG	59.029	20	218	65	282
59.407	20	GGAAAGAACTCAATGTCGGC	59.676	20	262	132	393
59.311	22	TTCACACAGTTCATCTCCCG	59.676	20	259	11	269
59.864	20	ATCTCCATTGCTGTTGGGAA	60.461	20	237	3106	3342
59.864	20	GGAATCCCTTGACACGAAGA	60.05	20	253	380	632
59.789	20	CCTATAGTGGTATGGTGTGGGG	60.365	22	194	180	373
59.2	20	GCAACCAAGGAGACTTGAGC	59.997	20	144	171	314
58.826	22	TGGCTAGCCTTTGAAGCAAT	59.982	20	149	24	172
58.667	21	CGTTGCTTCCTTCCTACTCC	58.934	20	204	186	389
57.904	20	TTGATGCACTCTTTTTCCCC	60.051	20	212	162	373
59.282	22	GAAGAGGGGGTATGAGTGGA	58.94	20	102	126	227
60.127	20	TGCGTTTTGACAATATTTAGTGTTT	59.109	25	188	281	468
60.032	20	TGCATATTTCTCGATCCCGT	60.435	20	249	5674	5922
60.11	20	TGAGCAAAACTGGTTCCCTT	59.711	20	269	966	1234
59.178	20	AGCAAGGTGTGTGAACGATG	59.751	20	274	525	798
60.014	23	TGAACACCCCTACTTGAGCC	60.111	20	185	0	184
59.534	20	GCGGATTGGATGCTTTAGTC	59.674	20	110	0	109
60.391	20	TCCGCACTAGTTCCACGATA	59.297	20	280	761	1040
59.817	20	GCCATGTTTACGATGAAATGC	60.345	21	205	487	691
59.96	20	CAACAAGATTCGATAGAAGCCAT	59.643	23	143	770	912
60.074	20	GATCTGCTGGCGGTCTTTAT	59.297	20	243	925	1167
59.469	20	GGCTCCTTGGATTCATCTTG	59.629	20	275	69	343
58.084	21	ATTCTTGCTGGCTGCTCAGT	60.164	20	125	9	133
60.147	20	GAGACGCGAATGTTGAGACA	59.992	20	210	3496	3705
59.793	24	CTTTGAGCTGATCTTGAAATGC	59.114	22	232	354	585
59.989	20	CTCCCTCTCTAAAGGGACGC	60.34	20	173	326	498

59.873	20	GCCAGTCTCTTTGGATCCTG	59.803	20	209	177	385
59.823	20	TGGTATCCATAGCAAAGCGA	59.281	20	249	158	406
60.365	20	GATTGACGGGATCACAGGTT	59.786	20	176	157	332
59.392	24	TTCTTACTGCCACACAAAATCAA	59.677	23	247	457	703
59.832	20	TGGTAAAAGTGCTCAAGACGA	58.566	21	277	93	369
59.136	20	TATTCCGCCGTGGTCTAAAG	60.089	20	267	145	411
59.304	20	CACTCTCCCTCACACACACG	60.358	20	143	1295	1437
60.124	21	CAAACTCGCTCAAAAAGACACA	60.453	22	222	1973	2194
60.008	22	CAAATAATGCTGCGTGATGG	60.096	20	200	11	210
59.934	20	AGCCCGATAAGTTCGCAGTA	59.867	20	204	257	460
60.483	20	CGGAACCAGACCGAATATGA	60.853	20	184	35	218
60.24	20	AGTCCGAAAATCCCAACAAT	58.36	20	270	271	540
60.138	20	TTAAAAATCGCCCGTGAGAC	60.074	20	267	3256	3522
60.022	20	ATCTTCTAATCACCGCCCCT	59.925	20	237	186	422
59.803	20	TTGTTTGAGGGAGAAGTGGG	60.081	20	220	3205	3424
59.795	20	TTTGGAGGATCGACGTTACC	59.933	20	260	67	326
59.846	20	TTGGATCATTCAAGGAATTTCA	59.388	22	218	918	1135
59.844	20	CGAATTCAAACTCTCCCGAA	60.184	20	266	14	279
58.44	24	TCACAACAGGTTTCGCCATA	60.111	20	199	142	340
59.624	20	ATGACTGCAAGCAACCTGTG	59.905	20	104	87	190
60.22	20	CTCCACCCTGGTTCTAATGC	59.55	20	275	937	1211
59.855	20	AATACCGGGAAGAATTTGGC	60.15	20	231	164	394
60.23	20	GACACGTTGGTGAAGCATTG	60.16	20	145	251	395
60.179	20	CCGCTATCGAAAATATAATCCC	58.9	22	272	112	383
57.122	24	TCCACGGGAGAGAATGAGAG	60.34	20	188	25	212
60.315	20	AAAAAGAGGGAGGGATACACC	58.452	21	274	59	332
59.928	20	TCACCCCACTCCTCACTTTC	60.088	20	116	283	398
60.02	20	GGAAAAGCAATCAAGATCCG	59.645	20	143	734	876
59.924	20	CTAAAATGGAAAGGGCGTGA	60.067	20	145	440	584
60.126	20	CTACCCGCAATGGTTCAACT	59.993	20	239	6672	6910
57.328	20	ACGGGTTATTACCTGATCGC	58.93	20	101	826	926
59.82	20	TTCCCAACTCCAATTGATCC	59.727	20	104	1119	1222
60.362	20	TCAACCTTTTCACACCACCTT	59.482	21	196	88	283
60.016	20	TACCCTTCATCTTCAACGCC	60.074	20	184	1341	1524
58.622	20	ACAGAAGGAGCAAAGCTGGA	60.134	20	262	621	882
59.942	20	TGTGCAGGGAAGATCAAGTG	59.831	20	191	7	197
58.898	23	GGGTGGAGTTATGGCTGAAA	59.933	20	235	150	384
60.328	20	CCATTTCAAGAATGCAGGGT	59.933	20	196	1510	1705
59.933	20	CGGTTCAACCCTTTTGTAGG	59.466	20	279	1497	1775
59.677	20	CAACACAAGAACTCACCTCCC	59.607	21	272	492	763
60.016	20	GGCCTAGCTGGGTCTTCTTC	60.349	20	187	5760	5946
59.942	20	TCTCGATCACTACAATCTTTGAGA	59.445	25	269	163	431
59.978	20	TGCCGTAACCTGTCATACCA	59.988	20	164	94	257
59.087	20	ACAAAGGCACAGAATGGACC	59.973	20	274	1449	1722
59.304	24	GAAGGAACGCTTACACGGAG	59.875	20	127	9	135
60.008	20	AGATGCTGGAATCTTCGTGG	60.218	20	191	20	210
60.081	20	TCTGTCACGTCTTCGTGTCG	61.092	20	177	254	430
59.662	20	CCTGGAACTGTCATCACCCT	59.962	20	264	1121	1384
60.15	20	TGGCTCTTCACCCTTGATTT	59.67	20	175	36	210
60.133	21	AGAAAGCCGGCAAACTGTAA	59.883	20	222	138	359
59.984	20	GCAGATGGCAGATTGGTACA	59.679	20	217	84	300
59.989	20	AACTGCCCAATCTGGATGTC	59.934	20	271	1139	1409
60.723	20	ATTTTGCAGTCCCTCCAACT	58.646	20	227	1192	1418
59.722	20	ACTTTTGGGGGACAAATCCT	59.668	20	226	265	490
59.844	20	GTCCATTGTAGCGGTTGGAT	59.82	20	250	96	345
60.197	20	GAAATGGCATTGATTGGGTC	60.141	20	226	2176	2401
60.096	20	TAGTCGCGTGCGATAATTTG	59.864	20	238	156	393
59.938	20	ACGTCCAACGATCATTCTCC	59.934	20	270	71	340

60.72	20	CTAAGGTCGGCGATAGCTTG	59.996	20	203	836	1038
59.894	20	CAAATGGGTCCATCACTCCT	59.779	20	184	308	491
59.997	20	TGCACGTGTGTAGGGTTTGT	60.072	20	271	1006	1276
59.972	20	GGAGGGCTGTGTGATATTGG	60.34	20	276	141	416
57.273	21	TGTTGCGCGTGCTTTAAATA	60.401	20	128	87	214
60.009	20	GGAACGAACCAAAAGTCCAA	59.948	20	271	509	779
59.853	20	GCAGGAGAAATGGAGACAGC	59.957	20	246	619	864
59.984	20	AGCAAGGTCTGGGGTGTATG	59.989	20	247	2105	2351
60.312	20	GCATCATCTTGTTGTATTCGTTG	59.532	23	223	2	224
59.864	20	TTTTTATGTGACACGCCCC	59.385	19	262	574	835
60.357	20	CCCTTGCTACCATCATCGTT	59.955	20	172	205	376
59.955	20	CTGTATTGTGGAAGGACGGG	60.366	20	241	266	506
60.096	20	TTGCAAACAATCCCATTCAA	59.907	20	235	1806	2040
59.993	20	GGGATGACTCCAAAAGGACA	59.903	20	237	169	405
59.829	25	TCGAACCTTGAACCAAAAGG	60.081	20	175	8	182
59.957	20	GCCTACGATCCAAATCCTGA	60.036	20	188	4143	4330
59.989	20	AGCCCCACATAATCCCACTT	60.578	20	254	56	309
59.956	27	TGTACCGCACCAAGATTTGA	60.111	20	169	1	169
60.021	20	TTGCAAGAAAAGCCACACAC	59.888	20	276	174	449
60.16	20	AAAAATTTAGTATGAGGTCACATC	59.925	26	235	657	891
59.134	22	AAGGGAGTTCTCCCAAATCAA	59.926	21	164	36	199
60.634	20	CATAAAGCCACCCCAACAAC	60.227	20	206	189	394
60.103	20	AAGGGAGCCCAATTGAAAAT	59.777	20	250	196	445
59.994	20	GAAAAGCTTGGCCATTCAAC	59.691	20	156	342	497
59.972	20	TCCCATTTGTGTGTTCTTCG	59.541	20	154	2458	2611
59.769	20	GGTAGGTGCTCTGACTTGCC	59.874	20	242	889	1130
59.953	20	GGAGGAGAAGGAACAAACCC	59.912	20	132	398	529
60.074	21	GAGCTTCAAGTCCCCACTGA	60.386	20	232	57	288
60.096	20	TGAGATTTGGACGGTTATGATTT	59.729	23	200	207	406
60.523	20	GCGAACTCGGCTAGAACAAA	60.523	20	116	695	810
59.694	20	CCCAATGATCAAAGACGAGG	60.452	20	272	201	472
60.119	20	CTGCAAGGGACAGCAAAATA	58.917	20	149	529	677
60.103	20	AGTATTTGCAGAGGCGGAGA	59.978	20	271	170	440
59.904	20	TTTCTGGTTGCATTTTGCTG	59.849	20	165	1610	1774
60.045	20	TCATTCTACAACTCATCCACATCA	59.499	24	267	266	532
59.96	20	GGTGTGCTCGGATTTTTGAT	59.939	20	161	279	439
61.113	21	CTATTTTCGCTGGCTTGGTG	60.762	20	279	210	488
59.74	20	TCCCATTTTCAGTGGAAACA	58.947	20	166	129	294
57.947	20	AAGGCGGTTTTTGATACGTG	59.996	20	275	346	620
60.096	20	TGTCTCAGAAACTGTAACCCTGA	58.898	23	260	2887	3146
59.945	20	TGAAAGGCAGATTTCCCAAC	60.051	20	204	189	392
59.973	20	GATGAAGATGACCACGGCTT	60.081	20	233	624	856
60.103	20	GTACGGTTGCATAAACGGCT	60.025	20	264	2458	2721
59.305	20	GGACACGTTGGACCTGAAAG	60.545	20	152	38	189
59.999	20	ATTTCGAAGATCAACGGACG	60.074	20	247	423	669
60.074	20	ATAAAAGCAAAAGACGGGGG	60.305	20	224	3215	3438
59.762	20	TGCCAGTAATTCACAACCCA	59.964	20	217	448	664
60.725	20	CAAGGGCTATGCAAATAAAAGC	60.114	22	276	83	358
60.544	20	TGGCAATTCTATGACCCTTG	58.572	20	135	22	156
60.132	20	CCGTTTTCCCCGTGAATAG	60.308	19	170	999	1168
60.021	20	TCTCTGTGTGTGAACCTGCC	59.872	20	271	795	1065
59.673	20	ACCATATTTAAGGGTTATCACCTG	57.552	24	167	773	939
58.464	23	TTGTGCATCGTGTTCTTGTG	59.298	20	127	0	126
59.913	20	GGGAAGGATGAAAGGGGTTA	60.124	20	104	177	280
59.869	20	TTGATGGTGACGTAGAACATTTG	59.912	23	166	44	209
59.482	21	CGTGTGTGTGGTGTGGTACA	59.95	20	146	65	210
59.939	20	AAAGTGCATGTGAACCTCCC	59.973	20	226	334	559
59.894	20	ATCAACACGTACGGAGATGC	58.599	20	240	214	453

59.813	20	TCATCTAGCATCTCTTGCTTTCA	59.261	23	184	390	573
60.074	20	GTGGAAGATTTCTTGGCAGC	59.82	20	193	756	948
59.847	21	CGACCACAAAATGGGAGAAC	60.353	20	152	1	152
57.432	24	ACGGCGTTAACTAACCTGGA	59.632	20	255	30	284
59.853	20	ACAATCCCCAGCTAATTCCC	60.152	20	273	334	606
59.972	20	GTCCCACCCAATCACATTTC	60.034	20	277	651	927
58.723	20	TATGTCGTTAGACGATGGCG	59.712	20	244	275	518
59.569	22	TAATGGGAATGGCTTGGCTA	60.415	20	277	909	1185
59.962	20	CGACTTGTCGTGGTTCGATA	59.716	20	276	44	319
59.394	20	TTCCTTCCCCACCTCTTCTT	60.045	20	232	854	1085
58.721	20	TTTCCTATGGACCGAAATGC	59.901	20	252	651	902
60.118	22	CGATTTGACCTCGGATAATCA	59.908	21	254	161	414
60.323	20	CATGTTATTCGCGTGCATGT	60.554	20	141	3658	3798
60.119	20	CACACCTCCTCCAAAGCACT	60.298	20	235	498	732
59.297	20	ACGGGAGGGAGAGGGAGTAT	61.214	20	111	371	481
59.278	21	GTTCTTGGTTGCCTTACGGA	60.11	20	275	138	412
59.853	20	GGTGAAGACGGATCGTCAAT	59.934	20	252	2605	2856
59.851	20	GAAGTGCATATGCGAGGTGA	59.83	20	139	734	872
59.933	20	GAGCCGTTGAATCCTTGTGT	60.119	20	265	28	292
59.864	20	AACCCGTTTGAGGTTGAACA	60.388	20	274	4	277
59.916	20	TCCCCTTGGTCCTAAATGTG	59.784	20	216	2372	2587
60.397	20	GTAAGCCAAAATCCTGCGAA	60.209	20	264	40	303
60.352	20	AAATGAAGGGTTGAGATGGG	58.836	20	204	2009	2212
59.375	20	TCATTTTACCTTTCTGTTTTTGGA	59.107	24	250	416	665
60.036	20	GGGACCATGATACATTTGGG	59.871	20	257	168	424
59.847	20	TTGTCAACCCTGTTGAGCCT	60.69	20	280	1856	2135
60.689	20	TCATGCAGGAAAAACCATCA	60.049	20	224	3338	3561
60.331	20	TGCATTTTATTTACGTGGTTACTTT	58.285	25	279	380	658
59.566	20	AATTTCGAAAATTTAAAGGTCCA	58.2	23	105	543	647
59.791	23	CATCGCATTCTCGATTCAAA	59.769	20	239	1492	1730
60.601	20	CACTGGCCAAGAATCAATCA	59.648	20	249	415	663
60.029	20	CCGTTGGATTTATCTTCTCCA	59.03	21	243	3503	3745
60.011	20	TTTGCTCGAATTCATATTTTTATGT	58.297	25	276	428	703
59.759	20	GTAGCCCGAGTCAGATCGTC	59.834	20	269	187	455
59.79	20	CCACCACACACAGGGTTATC	58.697	20	103	169	271
58.987	20	GATGTGTTTGGACGGTGAGA	59.525	20	147	815	961
59.656	20	TCCATTCCATTGACCCATTT	59.991	20	275	113	387
60.006	20	GATGAAAACGTGAGGCTGAA	58.85	20	259	137	395
60.16	20	TGATTTGGTTTTGGGGGTTA	60.024	20	251	12	262
59.967	20	GTGGCAGTAAAATTGTGGGC	60.374	20	243	80	322
59.978	20	CTACCACCTCCCATCACCAC	60.238	20	165	618	782
59.297	20	CAAGAACCCGGAAAGTGAAA	60.081	20	254	1581	1834
58.033	27	TAGCAGTGTTATCGATGGCG	59.856	20	177	446	622
60.132	20	ACTCTCCATTCCATCAACGC	60.081	20	249	286	534
59.844	20	TCCGAAAAATCAAAGGTCCA	60.418	20	236	458	693
60	20	GCCTTGTACGGTTGATTGGA	60.894	20	273	196	468
59.537	22	CAACTTGGTCACCTCCTTGG	60.536	20	111	66	176
60.193	20	CCCTGGATTTTGATTGAGGA	59.864	20	259	92	350
60.192	20	AGTTGTGCAGCCAGGATCTC	60.418	20	213	151	363
59.703	20	TGACGGGATTTAGGTGTTTTG	59.847	21	249	366	614
59.867	20	TTGTTTCGGTGTTGCTTCAG	59.881	20	265	357	621
59.499	20	TTGGGACACATTCACGAAAA	59.941	20	276	1994	2269
59.607	21	TGAGTTGGCCAAGAGAGTGA	59.545	20	224	342	565
61.035	20	GGAAAAATCAAACAAAAACACGA	60.238	23	257	1243	1499
59.148	20	GGCCCAAACAAAAATCTTGA	59.916	20	241	382	622
60.067	20	AATGCGATGTGAGGACATGA	60.08	20	239	1782	2020
58.374	21	GAGGCAGAGTAGGGGGAATC	60.037	20	137	22	158
60.041	20	CCTTCTGACAAAGGCGAAAG	59.986	20	198	2831	3028

60.169	20	TGTGCCATTTCTTGCACTTC	59.847	20	180	2250	2429
59.097	20	TTCTTCAACCGATCAATGAAA	58.201	21	278	844	1121
59.659	23	CATGAGATCCTGGGTAGTGGA	59.935	21	274	1521	1794
60.14	20	TGCCACGTGTCAAAATCTTA	57.763	20	154	757	910
59.5	27	GGGATTGGGATGAGAAGAGA	59.016	20	272	49	320
60.306	20	AGACTCACGCCCTCTCACTC	59.585	20	268	41	308
59.805	20	AATTTAGCGCAAACTGGTCG	60.264	20	264	190	453
60.298	20	GGGGATTTCAGACAGCAATG	60.461	20	239	1408	1646
57.188	23	CTCCGGTGTTAAAAGATGCC	59.569	20	260	2314	2573
59.84	20	CCCTCTTCTCCATCATCACC	59.46	20	226	134	359
60.009	20	CGATCGATTTTAGGGTTTTCC	59.795	21	197	773	969
60.005	20	CTTCTTTCCGCCTCTTTCCT	59.955	20	257	33	289
57.89	24	CATCAAGATCCAAGGGCTGT	60.073	20	201	4	204
59.954	20	CCGAACCCGATTACAGAAAA	59.931	20	196	16	211
60.344	20	TTTCAACAAACACACACGCA	59.765	20	274	505	778
60.05	20	AAAACCCATGGATGCAAAAA	60.167	20	275	468	742
60.067	20	TCACCCTTCGAGCTTAAAACA	59.869	21	183	361	543
60.583	21	CTTGTCTCCGTTCTGCTTCC	59.989	20	277	1245	1521
60.269	21	ACTTGCACTCCCTGTCACCT	59.756	20	208	966	1173
60.066	20	TGGAAACAAATCAATTGACCA	58.855	21	146	253	398
58.878	21	CACAGCAGTAGGGTCCAAAAA	60.154	21	156	7	162
59.097	20	CCCACCCCCAATATCAAAA	60.369	19	164	323	486
59.955	20	GTGGAGTTTGAAGGTGCCAT	59.973	20	241	561	801
60.043	20	GACCTGCGTAAGGTTCTTGC	59.882	20	194	2977	3170
58.973	20	CTATCTCATCCCCTCACCGA	60.027	20	104	28	131
60.022	20	TTATGGTGCTACTCCCACCC	59.813	20	240	132	371
59.971	20	CCAATCAACTAAACCCCCAA	59.657	20	222	1114	1335
60.002	20	AAAAGAGGAGGAGAGGCAGC	60.096	20	209	359	567
59.835	20	TGCAGTGGGTTTGATTGTGT	60.008	20	172	317	488
59.119	25	TTTTCAGTTAATGAGGTAATGCAA	57.967	24	199	22	220
59.951	20	GAAATTTTGGAGGCTGGACA	60.051	20	185	21	205
60.91	20	AAATGCCGCAGACATATCCT	59.556	20	246	14	259
59.942	20	TTGATTTGTATATAAAGAGGCTGG	58.367	25	276	2507	2782
60.16	20	GCAGCCTCCTCCTCTCTCTT	60.238	20	199	8	206
60.059	20	TTCTTCTAAGGTGCCCATCTG	59.322	21	247	2687	2933
60.21	20	GCATTGGATTCCTTTTATCCG	60.63	21	191	503	693
59.964	20	TACGCAGCCGGAGTAGTTTT	59.904	20	184	604	787
59.828	19	TTATGCCTATGTGGCTGCTT	58.414	20	280	550	829
59.844	20	TGTTAGGTGGTGGGGTTGAT	60.088	20	219	2	220
59.997	20	AGATCACCAAACCAACCAGG	59.82	20	270	1662	1931
58.325	20	TTGGTTTAAAAGTCGTTGTTGA	57.43	22	277	210	486
60.088	20	AATCTAACTAATGGCGCGGA	59.704	20	231	374	604
60.134	20	TCCAGCAGTTTCAATCACCA	60.24	20	239	1301	1539
57.557	27	GAAAAGGATTGGGTGCTTCA	60.051	20	123	4	126
60.046	20	CCTGCTCAAAGGGAGACAAG	59.982	20	144	153	296
60.049	20	TGTAATGGGTGCCAAAATCA	59.786	20	240	4666	4905
60.012	20	GGTGCAAGCCACAGGTTAAT	60	20	272	62	333
60.096	20	AAACAGTGCTTTTGTGATTCCA	59.654	22	146	885	1030
60.837	20	TGCAGATTTGTTGCACTTTTG	59.903	21	183	20	202
59.304	24	TGGGATAAATCTTCAACACCG	59.809	21	234	198	431
59.799	20	TTGTATTCGCAGTAGCCGTG	59.895	20	259	731	989
60.488	20	TTCACAGTTTTCATTTGATCACC	58.986	23	208	8	215
58.659	23	AGTGTTTTGACATGATTACTCGTC	57.373	24	247	1460	1706
60.081	20	GAAGCTAGCAACGAAATCCG	59.982	20	220	121	340
59.244	20	TTTATTAATCAATATAAGGTTGCA	59.344	27	271	613	883
60.089	21	TGGTTCGAATCCTCCACTACA	60.501	21	255	94	348
60.297	20	GGAACAAAAGGAGAACATCCC	59.797	21	272	2162	2433
59.343	20	CTCTCATGTGCGTGTTTGCT	60.056	20	223	127	349

59.848	20	TAGAGCCCTGCCAAACAACT	59.875	20	275	11	285
59.805	20	AGGATGGCATTCCAGTTTTG	59.933	20	276	9	284
59.836	20	TGCATTGTCAAAGTAGTTAACTCA	59.027	26	259	241	499
59.978	20	ATTCGTGCCAAGTTTATGCC	59.967	20	230	128	357
57.507	23	TGAGTGATTTGAAATAAAATTTGA	59.694	26	270	3473	3742
59.805	20	TGGTGTTACTGGCGGTGATA	59.988	20	222	93	314
59.966	24	CGAGTAAACCAAACACGTGAA	58.737	21	191	3146	3336
59.615	20	TGATGTTGGAGAGAGGACCC	60.048	20	258	339	596
59.234	20	AGTTAAAATCGAACCGAACCA	58.616	21	206	344	549
59.964	20	ATTTCAACCTTTGCCAACGA	60.481	20	278	880	1157
59.964	20	TCCCCTTTCTCTCGCTGTTA	59.948	20	205	302	506
60.119	20	TCCTCACCACTGTACCCCTC	59.962	20	243	434	676
60.128	20	CGAGATGGGGACAGTTGTTT	59.966	20	158	260	417
60.384	20	GGACAGCCAGCTGAAGAAAC	59.997	20	237	1310	1546
59.964	20	ATAGGCAAATTCGGAGGCTT	60.061	20	227	194	420
59.823	20	ACGAGACCGAAAGCAACAAC	60.299	20	192	385	576
60.046	20	GAGTGGAGGAAGATGGGGAT	60.278	20	265	525	789
59.762	20	TTATTTGGAAGTGCAACCCA	59.013	20	108	1909	2016
59.535	20	CACTCCAACTTTGCAAGAACA	58.96	21	230	1013	1242
59.612	20	CTTCTGTTTACTCACGCGCA	60.195	20	186	12	197
59.42	20	GGAGGGAGACCATGTGAGTG	60.527	20	206	2414	2619
59.405	20	TTACCACAGGCTTTTGGAGG	60.103	20	253	444	696
60.132	20	GGTGAGGTGGCTGCATTTAT	59.962	20	168	140	307
59.721	20	TTTAAAGGTCCCTCACCCGT	60.714	20	229	1562	1790
60.075	20	AAATACACAATTGAACCAACAAT	59.589	25	120	618	737
59.988	20	ATGTCCGCTCATACTTTGGC	60.103	20	176	196	371
60.25	20	TCCCTCTCCTCACCACACTT	59.682	20	266	536	801
59.789	23	GGGCGAGCAATCTGTAAGTC	59.843	20	262	183	444
60.544	20	TCCATTCCGAAAATCAAAGG	59.872	20	271	49	319
60.44	20	ATTGCATGTGCGAAAAGGAT	60.478	20	232	487	718
57.953	24	TGTGCAGGGTTGAATCTGAA	60.24	20	251	197	447
60.088	20	AACAAAACCAGGCACACACA	60.049	20	272	595	866
60.218	20	TTCAGACGAAGCGATCACAC	59.992	20	165	2	166
59.975	20	GGGCAGGTGGCTAATCACTA	60.096	20	139	1192	1330
59.989	20	TGCATGCTCACGCAAAGTAT	60.432	20	273	1895	2167
59.79	20	TCAAAATTGGGGAAATGACC	59.599	20	250	385	634
60.366	20	CCACGTGCTCCATACTTCCT	60.134	20	247	481	727
60.195	20	AAAGCCGACAGACAACAAGG	60.291	20	241	143	383
59.381	24	TCCGAAACAAAAGGGACAAA	60.452	20	167	38	204
58.836	22	CTCCATCCTCTTGCTTCGAG	60.088	20	219	1101	1319
60.204	20	ATGTGAAGAAGCTGCTGGCT	60.164	20	233	470	702
60.328	20	CCTACCTGCAATTGGACACA	59.566	20	262	4399	4660
59.935	20	AAATAGGCCCTTTTGCGTTT	59.97	20	150	1671	1820
59.363	25	AAAAATGAGTGGTTCATATTGGTT	57.968	24	134	719	852
59.691	20	CTTTAGGATCCCTTGTCCCA	58.978	20	226	268	493
58.215	20	CCCTTTGAAAGTTGATGGTTTT	59.39	22	266	202	467
60.074	20	TCGAGCAACATCTTGTGGG	60.823	19	135	839	973
59.748	20	TGAGATCACGAGGTCACGAG	59.98	20	192	437	628
60.882	20	GTTTTCAATCACAGCCACCC	60.362	20	127	170	296
58.475	20	CCAATTGTCCATATTTCGCC	60.153	20	204	347	550
60.01	20	TTTCGAGCACATTTTCTTCTCA	59.996	22	262	10	271
59.744	20	AGAGCATATCCAATGCCAGG	60.059	20	241	678	918
59.933	20	TGGAAAACAATGCCTAACAGC	60.124	21	247	143	389
59.377	20	TCCTACATTATTTGGGGATTAACA	58.735	24	135	10	144
60.118	20	CCACTGCACCACGAGATATG	60.136	20	189	6	194
60.035	20	CATCACATTCTCCAGTCCCC	60.326	20	252	774	1025
59.092	25	TGCAGTCGATATTTGCTCCT	58.477	20	120	1	120
59.997	20	CCCTTCTTTCCACAGCAGTC	59.844	20	279	25	303

58.172	21	TCTCGCGGTTTTCAGTTTCT	59.993	20	208	212	419
60.949	20	TGGCCTTCCTCAATCTATGG	60.029	20	146	2	147
60.991	20	TTGCAATTGAGACCGCTAGA	59.566	20	249	365	613
59.544	23	GAATGTTCAAGGCCATGGTT	59.797	20	227	133	359
59.172	21	TCGATCACACAGAAAACACGA	60.294	21	101	14	114
60.073	20	CTTCACTTCAAATGCCCCAT	59.933	20	275	2123	2397
58.161	22	CGACCAATTACACAAATCAACC	59.248	22	280	95	374
59.805	20	TGCGTTTTGACAATATATAGGTGT	60.083	26	170	306	475
59.967	20	GGCATGTGTGGGAGAAGAAA	61.046	20	171	7	177
60.126	20	TGCCAGGGTTATCTTGATCC	59.894	20	279	90	368
59.935	20	GGACAAGAGGTTGGGACAAA	59.943	20	122	170	291
59.91	20	AACTTTGGCGTTCTTGTGCT	59.92	20	108	955	1062
60.043	20	TGTTTGGGGGTGTTGAGTTT	60.246	20	182	2717	2898
59.526	20	TTTGCACCTGAGGAGGTGTT	60.69	20	131	1120	1250
57.733	24	TCCATACTCAACACAAGTCGAA	58.283	22	280	367	646
59.181	21	GTCCAGCTGCTCTCACACAA	60.187	20	173	3890	4062
60.082	20	TTTTGATTGCCACATTTCCA	59.907	20	248	691	938
58.89	21	ATAATGATATTTTGGAACGCATC	57.16	23	225	615	839
59.92	20	TTCACGAGTGGTGACAAACG	60.757	20	191	277	467
60.274	20	AATAAGGGTTTGGGCAGTCA	59.429	20	214	197	410
60.103	20	CCATCAAGGAAAGACGCATT	60.074	20	208	386	593
60.081	21	TCTGCCCTAAGATGAAACGG	60.206	20	178	99	276
59.82	20	TGAATCAATCTTGTGCGTTGA	60.25	21	183	19	201
57.09	25	TCGCCATAATTGACTGCAAA	60.215	20	108	18	125
60.162	20	CTGCAGTGCCTTTGGTAGTG	59.51	20	225	141	365
59.931	20	CACGTGGCATGATAATAGCG	60.118	20	213	390	602
59.005	24	GATGATCGGAACGTGAAGCTA	60.228	21	210	686	895
60.344	20	TCATCTTCTCCACCAAAGGAA	59.656	21	278	1231	1508
59.973	20	GCACGCAGCGAATAACAGTA	60.044	20	177	1108	1284
60.11	20	TGTTGAGACCAGGCGTACAG	59.897	20	216	180	395
60.553	20	TATCATTGTTTCGCGAGCAG	59.976	20	242	206	447
59.942	20	TTGATTAGAAAAATGCGCGA	59.424	20	175	97	271
60.237	20	CAGCTGCAGAGATGGAATCA	60.096	20	254	489	742
60.218	20	CGCGTTACGAATCCAAGTTT	60.131	20	177	344	520
59.28	20	ACTCCATGGTGCATTTCACA	59.967	20	264	4	267
60.209	20	TGGGTCACTCCTGTTTAGTGAA	59.633	22	276	14872	15147
59.971	20	TTGGCCATGTGAAAATCAGA	60.049	20	205	175	379
60.822	20	GCTCGGATATGTGGTAATCAAA	58.969	22	270	226	495
59.871	20	CGAATTCAGCCAGAACAACA	59.84	20	171	20	190
59.666	21	GGCCTAGGCACCAAATCTTA	59.182	20	188	1590	1777
59.96	20	ACCCACACCCTGTACCCATA	59.966	20	172	13	184
60.002	20	CACCATACAAGCATTCAGCG	60.28	20	253	284	536
59.978	20	CTTTCAATCGTTGATGGGGT	59.79	20	255	1153	1407
59.788	23	TGATGCAACCTTGCTCACTC	59.992	20	265	1459	1723
60.168	22	TGGTTTTATGTTTCTCTTTGGGA	59.865	23	248	1531	1778
60.475	20	AGAGATGCCGGGGAAGTAAT	59.925	20	227	144	370
60.073	20	TCTGTGAATCAAGCTCAAGCA	59.731	21	252	135	386
60.318	20	TTTCTCTCTTTTGGTGGAAGAAA	59.398	23	257	213	469
59.711	20	ACTGTGAAAGAGACCTCCGC	59.455	20	250	1095	1344
60.073	20	TATGGATCTTTGGCAGGTCG	60.992	20	240	195	434
59.941	20	TGGGAGTCTGTTTTCCCATC	59.903	20	100	178	277
60.24	20	CCCTCATAATGTGTGGCTCA	59.522	20	271	63	333
59.898	20	GGAATCTAGAACAGACCAATCCC	60.196	23	179	1339	1517
59.297	22	TGAGTCCATGACCCAACTTTT	59.439	21	175	753	927
60.051	20	AGAGATCCGTGCTTCACTTG	58.029	20	133	1469	1601
59.862	20	AAGGCGGCTAAATCAATCAA	59.682	20	268	283	550
59.064	20	CCTTGCACATTATCTGGAACAA	59.996	22	263	211	473
58.782	20	TTTCCCCAAGCTTCCTACAC	59.17	20	275	465	739

59.953	20	ACGCACCCACACTGTCAATA	60.032	20	135	60	194
58.054	22	GTGCGTTGTGTTGACGTTG	59.768	19	271	2325	2595
60.081	20	TTAGCATTTGACTACACTCCTCAA	58.151	24	186	272	457
59.914	20	TGCTGGAGCAGTCATTTTTG	59.988	20	140	1043	1182
59.269	20	TCCCGAAAATAAAAAGAAAAAGA	59.552	24	111	339	449
59.985	21	GATAACATGCCATCACACGC	59.963	20	269	873	1141
60.074	20	GGCTACTTGGCCCCTATGA	60.044	19	272	199	470
58.223	23	TGAACAGCCATCGAGCATAG	59.972	20	259	1211	1469
59.887	20	TCGGGTTAGGAATTTCATCG	59.894	20	272	1284	1555
59.842	20	TGTGATTTCATCCATTCGGA	59.859	20	227	262	488
60.64	20	CACACAATTGAGCACACACG	59.778	20	103	182	284
59.636	20	CCATCCACCACCGTCTACTT	59.844	20	252	72	323
58.976	22	ATGCGCAGATCTAATGGTCC	60.066	20	198	9	206
59.302	21	GGGTTTGCCTTTAGCCTCAT	60.451	20	239	131	369
60.43	20	TGGCCCTTTTGTACACTTCA	59.17	20	132	316	447
60.488	20	GTGCAGCACTAGGTCCATTG	59.318	20	277	127	403
59.587	22	ACGGGAGGTTAAAAATCGCT	59.966	20	193	24	216
59.814	20	GCCGCATTTCTTCTAACCCT	60.582	20	235	950	1184
58.474	21	AATATTTGCATGGCTCTGGG	59.923	20	274	1266	1539
59.973	20	GGGGCGTATAGACGCAAATA	59.95	20	168	638	805
59.912	23	GGCATCTTGGAATCACCAGT	59.934	20	172	1201	1372
60.31	20	TGGGGTTATTAGTGGATCAAGC	60.204	22	274	872	1145
59.255	22	TGCACCTCCTCTTCAACAACT	59.899	21	257	1022	1278
60.025	21	TGTTGCGCGTGCTTTAAATA	60.401	20	139	349	487
60.659	21	GAGCAAAGTGTTGAACTCTCGAT	59.942	23	121	7	127
60.088	20	AGAGAGAAAGTGGCAGTGGG	59.45	20	275	13	287
59.962	20	TCGCCGTGTTTGTATTCTTG	59.729	20	256	816	1071
59.989	20	AAACGCGCATTTTTAGGATTT	59.986	21	274	356	629
60.723	20	TCAGCTCGGGAAGAAAACTC	59.55	20	164	609	772
60.12	20	CGCTATGTGACCATCTGTGG	60.136	20	191	5217	5407
57.546	24	GTGCGTTCCACGTTAGGTTT	60.037	20	260	54	313
60.674	21	CGATTGAATTGGTGGGTTTC	60.17	20	170	78	247
59.827	20	TTTCTTCTCCCTCCCTCCAT	60.008	20	239	1548	1786
59.851	24	GTTAGGGCAATCAAGCAAGG	59.708	20	138	163	300
59.875	20	GGGCAAAACTGTAATTGCTCA	60.124	21	256	4053	4308
60.292	21	CACGAGATTTACGTGGTTCG	59.195	20	108	132	239
60.261	20	CATGGAATTGAAACTTTCGGA	59.924	21	156	16	171
60.604	20	CCTAGTGGCTTCCCCACTAAA	60.48	21	252	351	602
60.074	20	CGAACCATCGTCTCGTATCA	59.673	20	169	289	457
59.848	24	GGGGAATGGAAGAATGAGGT	60.133	20	244	1032	1275
59.311	23	TTGGCAAATTTTCTTGCACA	60.229	20	158	1028	1185
59.939	20	TATTGAACTGCCTTTCGCCT	59.845	20	193	113	305
59.542	20	AAACAGACTCCCATGTTCGC	60.119	20	280	153	432
59.933	20	AAGGGCTTTGTTGGTTTGTG	60.008	20	272	1049	1320
59.872	20	TTCATTCTTTGCATCCCTCC	60.014	20	111	3811	3921
60.05	20	GTGGTCGGAGAGTTGAGAGC	59.993	20	214	382	595
59.985	20	ACTCGAGCTGCAAAAACCAT	59.882	20	268	168	435
60.486	20	GCTTCCGCATTTTCTTTTTG	59.832	20	270	992	1261
59.853	20	CAAAACCTGACACGAACACG	60.19	20	271	850	1120
60.498	20	CTGAGGATAAAGGTGGCGAA	60.206	20	171	43	213
60.504	20	CCGGAAAACACCATCAATCT	59.79	20	279	581	859
59.521	20	CTCTCAGGGGCAGATACAGG	59.82	20	136	252	387
59.934	20	TGCAGTTGGTGGTAACCTCA	60.152	20	154	602	755
59.899	21	TGTTCTCGTATGATTACGCTCC	59.252	22	269	1024	1292
60.005	20	AGCAAGAAACCAGAGGCAAA	59.993	20	183	156	338
60.153	20	TTGTTATTGAGAGGGCAGGC	60.214	20	168	61	228
60.202	22	GATTGATGAGGGTTCCAAGC	59.488	20	253	94	346
57.278	21	TTATGCTGCCGTGTGTTTGT	60.18	20	228	0	227

59.375	20	CACACCTAGTGTGCTATCATCAAA	59.223	24	209	75	283
60.065	20	ATTTCCCGGAGAGGAGAAAA	60.011	20	210	1061	1270
60.146	20	CCAAATTGCCCTTCTGTGTT	59.971	20	265	454	718
58.658	21	CCAAGATTTGATCATGGCGT	60.864	20	272	584	855
59.089	24	ATAACATAATGGTTGGCGGC	59.688	20	125	19	143
60.051	20	AACCGTAAGGTAGATCCGGC	60.34	20	211	503	713
60.058	20	GTATTCGCTCTGCCACAACA	59.871	20	249	2574	2822
60.05	20	TACTCCTGCTCAACCTGGTG	58.879	20	132	378	509
59.955	20	CCACACCCTCTTCCTCTGAA	60.229	20	167	416	582
60.066	20	ACCAGCCTAGGGTTGAGGTT	59.994	20	250	1437	1686
59.049	21	TGTAAATCTGCCCGAAAACC	59.938	20	167	36	202
59.848	20	GGTTAACATTTCAGCGAGGC	59.713	20	185	0	184
59.93	19	AGGTTAATGAACGCAACCCA	60.365	20	119	66	184
60.73	20	CGTCCCATAAAATGTGACCA	59.247	20	241	824	1064
59.43	20	TGGTGTACAGTAAGAGGCAAACA	59.724	23	239	664	902
58.671	20	AAATCCTGCAATCATCACCC	59.756	20	234	259	492
60.036	20	ACGAAATGAGGAAATCGACG	60.074	20	254	67	320
59.691	20	ACCCGGACAATGAGCAATAA	60.331	20	199	276	474
59.883	20	TAATCCTCGTGGAAAATCGG	59.894	20	205	411	615
61.071	20	TGAACCAAACACCCGTGATA	59.816	20	244	87	330
60.032	20	TGAAATAAACATTGCCACCG	59.42	20	274	995	1268
60.042	20	CAAATCATGTGCGCTGAAAT	59.694	20	266	5404	5669
60.066	20	AGTTTGGTTCTGGCTCATGG	60.111	20	197	138	334
59.973	20	GTCAAGTCGACCACCCTTGT	60.009	20	123	30	152
59.452	20	TTACGAGGAGCAAGGTCGAT	59.836	20	191	385	575
59.985	21	CCAATTTGAATGGTTATCACCTG	60.457	23	272	1210	1481
60.103	20	ACGAGATGTGGAAGCCATTG	61.067	20	158	270	427
59.979	20	TCCTTCCCTGCATTTCATTC	60.014	20	214	1958	2171
60.005	21	TCATTTCAAAAATCAATGGATGA	59.291	23	193	2372	2564
59.917	20	GTTTTGTAGCTCTCGTCGGC	60.022	20	249	995	1243
60.252	20	TTCTTGGTTAGCTGGTCTGGA	59.861	21	224	1899	2122
59.931	20	TTTTGAACAATGATACCTTCTCC	57.314	23	215	36	250
58.694	22	TCATGGTGCTTGAAATTGGA	60.049	20	169	13	181
60.292	21	AGTTATGCTTGGACCGGTTG	59.993	20	277	146	422
59.764	20	GCTACGAACTACGGGGTGAA	60.132	20	259	82	340
60.698	20	GATTGGGATGGGCTAGGAAG	60.787	20	280	7	286
60.011	20	CTTACCACCATTCACCACCC	60.088	20	240	718	957
59.645	20	TACCAATGCCACAAAAACGA	59.969	20	254	79	332
60.533	20	GCATCACAAATTCCTGCAAA	59.67	20	276	185	460
59.867	21	CAGCTCTCATTATTTCCGGC	59.807	20	203	914	1116
59.585	20	GAGTGGAACTCGTCTTCCTCAG	60.427	22	217	776	992
59.111	20	TCACGATCGAACCACGTAAA	60.111	20	165	1440	1604
57.827	21	ACCTCTTTTCGGTTTGATGG	59.028	20	164	232	395
59.277	22	CGAATGATCTGGTGATGGTG	59.918	20	202	178	379
59.713	20	CAATGGATTAGGCCGAAAGA	60.031	20	177	1115	1291
59.871	20	ACCTGGTCTCCAAGTGATGG	59.962	20	243	2463	2705
60.038	20	GGGAATCAAAACCATTCCCT	59.996	20	280	393	672
59.809	21	GCCTGCCTTGGAAACTATTG	59.708	20	274	117	390
59.813	20	AAACTTGCGGGAATGAGTTG	60.11	20	228	637	864
59.951	20	GCTGCAGATCTAACGACCAA	59.028	20	130	368	497
59.679	20	TGGTAAGCGATTAACGGTCC	59.96	20	273	384	656
60.31	20	TTAGACGTGAATTGCAAGCG	60.014	20	272	181	452
59.994	20	AGGCCCATCATACCACAGTC	59.81	20	201	921	1121
59.998	20	CATTTTGTGGCCTGTGTTTG	60.004	20	206	2212	2417
59.934	20	GAGCTCACCGGTTCTTTTGA	60.375	20	184	134	317
60.015	20	CAACGATGTGCTAGTTGTGGA	59.773	21	221	4	224
60.051	20	AACACAAAAGGGCTCATTCC	59.031	20	221	93	313
59.95	20	AGAAGAGAGAGGGAGGGTCG	59.945	20	251	480	730

60.066	20	TTACGGCAATTTGCATCAGA	60.215	20	139	356	494
60.153	20	ACTTTTCACGGACTGCCAAC	60.156	20	132	1996	2127
59.895	20	GCCGGACTTGAAAATTGAAA	60.053	20	266	974	1239
60.34	20	TTGTCCTTTTGGGAACCAAG	59.942	20	226	471	696
57.662	20	TCACACACACGCACAAAGAA	59.912	20	107	74	180
57.628	22	GTTCGCCAAGAAACTTACCG	59.747	20	258	691	948
59.84	20	TGAAAAATGACGCCAAAATG	59.538	20	154	134	287
59.939	20	TCGAGTGGGACCAAAAGAAC	60.088	20	219	624	842
59.853	20	TGCAAGCATCAAAAATGGAG	59.809	20	216	759	974
59.191	27	ACCAAGTCATACATCATGTTATCTT	58.868	27	222	2	223
59.99	20	TTCTCACAGGATTTAGGTGTTCC	59.513	23	246	2	247
60.504	20	CTCGATGAGGAATGGGAAGA	60.15	20	278	69	346
60.523	20	TTTGTGTGATTTTGACCCCA	59.792	20	280	122	401
58.065	25	ATGGCGATATTGAAATGGGA	60.117	20	171	4	174
60.003	20	CTATCGTTTTCTCCGCCTTG	59.839	20	199	326	524
59.969	21	AAAACCGAACCAGGTCGTTA	59.471	20	225	231	455
59.654	23	ACGATTGTTTTGAATTCGCC	59.945	20	216	12	227
60.042	20	GTTGCTTCTTTAACGCTGGC	60.025	20	268	1016	1283
59.933	20	TGCATACAACACGCAAATGA	59.716	20	144	2397	2540
58.928	21	TTCGGAATTTATAATATGGGCA	58.4	22	276	99	374
58.836	24	GCTCGTGTGTTACAGGGGAT	59.997	20	249	703	951
59.03	27	AAATATGCCACCTATTGCCG	59.816	20	263	15	277
57.817	25	GGGTGGTGATATCTCCCTGA	59.737	20	270	19	288
59.901	20	ACGGCCCTTTCTCTTGAGTT	60.247	20	279	68	346
60.137	21	ACCATGGCGTGCAAGAGTAT	60.547	20	220	169	388
60.486	20	AATTAGTTGAGGCACGTGGG	59.993	20	233	207	439
60.235	20	TTTGCATCAAACATGGCTTC	59.67	20	253	1226	1478
59.901	20	TTGCGACTCAACACCAGAAC	59.88	20	196	454	649
57.557	25	TTCGATCTTCTTTCCTTTCCA	58.89	21	104	8	111
60.523	20	GTACAGGGTTCTCCAACCGA	59.966	20	177	138	314
59.96	20	GGTGGCCATTGATAGGAGAA	59.894	20	204	5491	5694
60.615	20	AAAAAGGGATTATCACGGGG	60.013	20	245	892	1136
59.367	20	GCGTTTTGGTGGATGAATTT	59.807	20	279	471	749
59.912	20	GCCATGCTCTATGGCAAACT	60.243	20	111	1149	1259
59.957	20	GGATTTTGATGTATGAGTTTGCAT	59.297	24	235	492	726
57.604	24	ATCAATCACAACCCCGTCAT	60.057	20	188	0	187
60.088	20	GGGTCGGGCTAATAGGCTAC	59.951	20	167	212	378
59.795	20	TCATATGGGTTGGTGTTGTCA	59.682	21	178	183	360
59.295	23	TGTGTTTTCAAAAGCCTAGACA	57.63	22	227	217	443
59.823	20	AGATCGCGGGCAAGTAGTTA	59.867	20	106	9	114
59.478	20	CCTCAGCAAAATGCAGTTGA	59.988	20	100	197	296
60.591	20	CTCACTAACTCGCACCACGA	60.049	20	264	101	364
59.888	20	TTTTGGAGGAGGCAAAGAAA	59.795	20	208	512	719
58.461	23	TGTAATAACCCTTATTTTCGTGCTC	59.834	25	265	69	333
60.252	20	TACAAAGTCGCCGGAAAACT	59.747	20	143	482	624
59.964	19	TCAAACCTCTTCCATCACCC	59.903	20	272	2135	2406
59.964	20	TTGCCAAATGGTGTAATGTCA	59.841	21	207	429	635
60.132	20	TTGACTCACAAACACACGCA	59.912	20	213	374	586
57.14	22	TCAAGGTGTTGATGCTTGGA	60.24	20	201	5	205
59.64	20	TGTGAGAGACGTCGTGTGTG	59.454	20	226	485	710
60.06	20	GCAAGAGCTTAGAACGGGTG	60.015	20	159	3004	3162
60.192	20	GTACGGCTGAGCCTGATTG	59.41	19	191	676	866
60.352	20	TTGGACAGGCTCCTTTATTTG	59.211	21	279	409	687
60.306	20	CCAGACATTTGTGGTGGATG	59.806	20	187	185	371
60.032	20	GTTGGGGTTGAGTTGTGCTT	60.012	20	194	570	763
59.836	20	ATTAATCCGATGGCCCTCAT	60.499	20	208	618	825
59.955	20	TCTAGGAAAGGGCGAATCAA	59.778	20	252	214	465
59.215	20	TGTTTTCTTTTACCTGTATTCAAGA	58.442	27	250	225	474

60.065	20	CGCCATAGCTTCTTGGTCTC	59.978	20	143	197	339
60.21	20	GAAAAGGGGAGGATCGGTTA	60.258	20	156	355	510
59.964	20	CGGATCACCAGATCCGATAG	60.439	20	202	520	721
60.263	20	TGAAAGAATATGAGTTTGAACGG	60.004	24	189	100	288
59.123	20	CCAACCAAATCCGGTTACTG	60.22	20	266	62	327
60.011	21	AGGCCTTGCTCTCTCTGTTG	59.745	20	278	63	340
59.982	20	TTTCTGGACCACTTTCTGGG	60.081	20	169	4	172
60.132	20	TTCGGGGTGAGAACTAGGAA	59.665	20	275	1291	1565
60.011	20	TGAGTTGGTGTGTTGGCATT	60.008	20	164	394	557
59.647	20	CGGTTGACAGCCGATTTTAT	59.96	20	280	557	836
59.894	20	TGGAGCATTAATTTGGAGGG	59.894	20	124	649	772
59.962	20	TGCTCAAGTTCTTGCCATTG	59.988	20	215	554	768
59.997	20	CCATCATCGTCCACATCTTG	59.918	20	270	659	928
60.244	20	GGTAGCCTGCTGATGCAAAT	60.243	20	250	121	370
60.511	20	TGTCAAAATATGGGCATCCA	59.745	20	276	611	886
59.993	20	GAAAGTTTGGGGTGGGTTTT	60.068	20	206	961	1166
57.824	20	TTTCATATATCACGTTAAGACATG	57.297	25	234	410	643
60.142	20	CCAAACGTATATGCCCTGGT	59.708	20	159	159	317
58.187	20	GCGTCGTTTCTTGAATTAGGG	60.962	21	206	1271	1476
60.053	20	ACAATACACGCCACACAAGC	59.646	20	220	1279	1498
60.008	20	AGCATTAATGGTGCCCAAAT	59.301	20	245	228	472
59.901	20	GCGTTTTGATGATATATATGTGTTT	59.956	27	198	971	1168
59.986	20	TAAGATCAAGGGCAACCTCG	60.206	20	244	2961	3204
60.964	20	TGAGAAAAGGTTGTACATGGCA	60.534	22	221	72	292
59.851	20	ATGTCCAAAGCTGGCAGAGT	59.874	20	137	576	712
59.923	20	ATGCATGCACGTGAATATGG	60.375	20	140	321	460
60.617	20	TTTTCATGTTTTGGAGCATCA	59.147	21	241	301	541
59.478	20	TCCCACCATTCACATCTTGA	59.893	20	255	482	736
59.916	20	GCATTCAAGATTCTGCCCAT	60.043	20	255	1550	1804
60.05	20	GGTTATCACCTGATTTCCTCCC	60.901	22	210	595	804
57.425	21	AATCCTTATGCCCCCAATTC	59.984	20	234	12	245
60.451	20	ACCCGGGTTTCGAAGTAGAC	60.361	20	190	1396	1585
59.688	24	TCCTTGCCAACAAGATAGTGC	60.264	21	248	2581	2828
60.646	20	CATTCGGTTTTCACTGGACA	59.541	20	276	45	320
60.074	20	TCGAAGGATGTGTTCATTGTG	59.556	21	260	1898	2157
59.937	20	AGTTGGGACGGAGGGAGTAT	59.817	20	142	339	480
59.966	20	GCACCATAAAGTTCAACGAACA	60.039	22	211	318	528
60.11	20	CAACAGGTCTCACCAATCCA	59.52	20	272	836	1107
58.642	20	TGACGAGTTAGAATGGCAAAGA	59.883	22	107	13	119
59.621	20	TCCAAGCTGACCAGTGTCTG	60.022	20	173	3756	3928
61.031	20	GCTGATCTTGGCCATGCTAT	60.207	20	172	38	209
59.598	20	TGCATATATTAGGGGAAAAATAA	58.877	27	277	896	1172
60.209	22	TCCTTTAACAAATTGGTGTAGTCA	59.056	25	195	216	410
60.443	20	TTGTGAATCGCCCAAATACA	59.93	20	222	802	1023
59.819	22	TGAGAGGTCTAGGGTTCGGA	59.797	20	243	642	884
59.786	25	CATCCGCCTGAGATTTTCAT	60.036	20	119	3	121
59.943	20	AAATGTGGATAGCAGAGGCG	60.235	20	164	47	210
60.151	20	GTCCACGGTGGTTTGAGAGT	60.009	20	151	41	191
57.162	22	TGTATGACATTTGGCTCCGA	60.073	20	227	499	725
60.011	20	AATTCCAGCCATGTAGGTGC	59.962	20	241	756	996
60.181	20	ACCCGATAATACCATAAAAGCA	57.629	22	265	1163	1427
60.05	20	TGCCCACTAATCTGTAAAGGG	59.098	21	184	927	1110
59.429	20	GCGGTAGGTAGCTCTTGTCG	60.037	20	201	170	370
59.848	20	TCCGTGAACCGTTCTTCTTC	60.232	20	233	476	708
59.823	20	GATTGTAAATCGGGCAAGGA	59.901	20	273	1558	1830
58.253	20	TCCGTTCATTCAACGAGGTT	60.495	20	280	50	329
60.278	20	AATTCGGGTACCATCGACAG	59.813	20	221	719	939
59.813	20	TCGGAAAAACTCCTGAGTGAA	59.838	21	182	380	561

60.66	20	TGTGGTGTTGACGGTGATTC	60.426	20	172	130	301
60.044	20	CCTGTAGCCATGTGATTGTTG	59.061	21	258	413	670
57.477	26	GGGAACATGCTTCCTGAAAA	60.051	20	158	7	164
59.907	20	CGTTCTTTCTGATTCGCCTC	59.955	20	149	484	632
58.694	20	TGGGCAATACGTGGTTTAGG	60.742	20	277	97	373
59.817	20	GAAGAGCAGGGGTGTCTTTG	59.844	20	268	207	474
60.304	20	TGCTAAATCTGCTCTGGCAA	59.712	20	244	755	998
60.032	20	TCATTCCCGAGAATCCTTCA	60.538	20	169	792	960
60.21	20	GCAAAAGGTTTGAAGTCCTGA	59.345	21	232	900	1131
59.636	20	ATCCCAAGTGGGTTTTTGTG	59.688	20	156	16	171
60.827	20	CATTAAATCTCATACCCTCAGTTT	57.435	25	249	224	472
60.133	20	ATCAAGAGCACGGTGGTTTC	60.119	20	224	210	433
60.119	20	TCACTCCATCTTCACACCCA	60.088	20	195	2614	2808
59.875	20	GCGCCGATAGACGATAAAAA	60.192	20	151	1180	1330
59.817	20	GCGGGGAAAAATAGGAAGAA	60.381	20	178	176	353
59.224	20	TTCCTCAATTTCTTCCACCC	58.956	20	236	164	399
59.272	20	GACTTTCCAAGCATCCAACC	59.532	20	280	59	338
59.933	22	TACTTTTCGCATCCGACTCC	60.214	20	114	2873	2986
60.119	20	TCTCGGTGAGCGAGTAGGTT	60.012	20	232	6	237
59.924	20	GGTTTTGACCATATTTACTGTTTTG	59.631	26	117	439	555
60.448	20	TTAGTTAGTACCGATTTCAGGGTT	57.499	24	153	1177	1329
59.179	20	GAGAACGTGAAAGCCAAAGC	60	20	187	9	195
60.081	20	TTTGACCTTTAAGGCCGATG	60.067	20	254	782	1035
59.84	20	TTGTTCTTTGGTTGCAGGAA	59.293	20	201	2802	3002
59.664	20	TGCCAGTGTCTCAATCCTCA	60.402	20	235	34	268
60.042	20	CCAAAACGTCCATTTTCCAA	60.702	20	273	572	844
57.369	23	TGGATTGAATGGATGTTTGG	59.175	20	102	0	101
60.111	20	TCACAAATACCCCTAAACCCA	59.188	21	148	356	503
59.962	20	TGTCATGGCATTTTTGTATGTTT	59.288	23	236	315	550
58.462	22	CCCTTTGGAATGTTCAAGGA	59.903	20	103	22	124
60.124	23	ACCAAGATTTGATCATGGGC	59.756	20	237	377	613
60.511	20	TTGTTAGAGGTTTTGACGGGA	59.595	21	192	241	432
60.103	20	GGGCTGCCTCCTAATCCTAA	60.542	20	254	348	601
59.431	20	TTATATGACCCCCTCCCCTC	59.974	20	154	1188	1341
58.258	20	ACTGCACCAAGGCAGAAACT	59.914	20	257	1191	1447
59.855	20	GTTTGGAGGAGCAAGTGGAG	59.844	20	148	1053	1200
60.348	20	CCATCATTTCATTCCCAACC	59.991	20	198	3610	3807
59.843	20	GCCCCAAACGACTTACGAT	59.947	19	203	326	528
59.694	20	ACACCCTCAAATGGCTCAAC	59.973	20	225	959	1183
59.982	20	TTAACAAAAGCAAACCGCCT	59.758	20	248	704	951
59.813	27	TTTCGAATGATTTTGCCCTC	60.016	20	218	0	217
58.98	20	TTGTTTACACACGGTGCGAT	60.035	20	253	85	337
59.679	20	ATTTTCCCCAAATTTGTCCC	59.867	20	150	13	162
59.894	20	CTTGAATTGCTCTCCCTCCA	60.331	20	229	183	411
60.011	20	ATTACGTCCAAATTGCTCGG	59.96	20	265	130	394
60.117	20	CCCTTGTATGCAGTCCGAGT	60.134	20	276	201	476
57.792	21	GCCACTCTTGTGCTTCCTTC	59.997	20	167	9	175
60.261	20	TTACATCCAAGCCACCTTCC	59.933	20	158	1059	1216
60.088	20	TCCTTTCTTCTTACGGCACC	59.312	20	251	790	1040
60.457	23	CGCGAACTCATAAATTGAACA	58.83	21	214	12	225
58.96	20	CGTCCGTTTTGAAGATCCAT	59.933	20	256	276	531
60.269	20	CCAAAAGTGTTATTTTTGTTTCG	57.875	23	146	64	209
59.165	23	TGTTAATCAGTTTATGCATCTTGG	59.917	25	149	24	172
59.028	24	TGTCCTCCATTAAGCAAGCC	60.214	20	114	1	114
60.03	20	TGTGATGAGAGAGAGGGGCT	59.945	20	235	104	338
59.953	20	CGAAGGTACGGTATGCGATT	59.982	20	172	62	233
60.408	20	CGGCGATAAGAGAGAGAAGG	59.17	20	161	422	582
60.663	21	TGGCAACTGCAAGTTCAAAG	60.027	20	269	514	782

60.109	20	TTTTGGGAGAAGTATTGGGA	57.13	20	183	56	238
59.415	20	CCAATTTGAATGGTTATCACCTG	60.457	23	107	1908	2014
59.978	20	GTTATGCGTTTTGACGGGAT	59.829	20	230	286	515
60.017	20	TGCATGGATGCAAGTTGAAG	60.812	20	229	138	366
59.964	20	AATAGCTTTGGGTGCATTGG	59.96	20	194	2862	3055
59.123	20	GGTTTGGCCGTTTTTGAGTA	59.975	20	225	13	237
60.081	20	TTCCGAAAATATGCTCCACA	59.112	20	166	801	966
59.939	20	AGAGGAGCCCCATTCATTCT	60.037	20	203	235	437
59.583	21	AGGTTGCGTACATCTGACCC	59.997	20	256	3	258
59.51	20	GATGGCTTCTCCTTGCAGAC	59.957	20	141	154	294
59.967	20	AGGGTCCCACCCTTTTGTTA	60.581	20	124	220	343
60.065	20	TATGAACCCACCAGCATTCA	59.924	20	131	1957	2087
59.83	20	ATTCTAAGCTCGAGGGCACA	59.978	20	238	327	564
59.234	21	GCTAGAGGGTTTTGTTAATATGTC	58.796	27	174	324	497
60.154	20	GTTAAGGCCAACTTCCCTCC	59.94	20	249	1543	1791
59.934	20	AGGAATGATGGGATCTGCAA	60.426	20	172	2082	2253
60.204	19	GGCGGCGTGACTTATTCTAA	60.23	20	262	208	469
60.035	20	GGGGGAAAATTATAGTTAGGGA	57.532	22	108	524	631
60.131	22	CGATAGATTCGATGAACCCC	59.344	20	226	665	890
60.038	20	GCAATTGAAGGTTTGACCGT	59.978	20	121	5	125
59.557	24	GGCCTATTGAGCCAAGACTG	59.836	20	279	972	1250
60.249	20	GTGCATTTTTGGGAGCAAAT	59.945	20	238	96	333
59.181	21	CAGAAACATGTCAACGTGAGAA	58.825	22	278	1114	1391
60.021	20	TCTCCGAGTTCTTGCTCTCC	59.679	20	228	352	579
59.966	20	CCTGGCTTCAAAACCAATGA	61.001	20	255	669	923
58.237	25	AATTGACCTTTGACGTTGGC	59.978	20	242	3	244
60.052	20	TTTTTATTCAGGCAAACATTCTCA	60.006	24	206	311	516
60.357	20	CGCTGGTTTTGGAGATCAAT	60.074	20	228	2294	2521
59.93	20	TCCGGTCCGATTACAATTTC	59.762	20	165	319	483
60.11	20	AGGCGTCTGTTGGAATTTTG	60.11	20	252	1446	1697
58.824	20	CTTCCAGAGGGATACCGTCA	60.065	20	198	634	831
60.066	20	TGTCCGGATTGTCACACCTA	59.96	20	225	90	314
57.557	25	TTGTAGTTGCTGGCCATGTG	60.72	20	105	21	125
59.773	22	TTCACTTTTACAACTTCCACATGA	59.959	25	205	96	300
59.992	20	TGGAAAGAACTAAATGCCCG	60.067	20	185	117	301
59.829	20	TGTGCATGTCTCATTTCGTTT	59.188	21	140	19	158
59.449	20	AGCCATGGTTCAATCATCAA	58.926	20	254	3115	3368
60.073	20	TCACAAACCCATGTCCCTTT	60.21	20	261	1440	1700
58.028	22	GAAGGAAACATTCTTTTGGGG	59.801	21	249	1914	2162
59.381	20	GCATGGTGATTTGAGGGACT	59.934	20	228	169	396
57.101	24	AGATTGGGTACCCGACACTG	59.844	20	175	5	179
59.839	20	AGATTCAAGGGCCGAGATTT	60.039	20	173	840	1012
59.916	21	TCCATAGCCGATAAAATGGC	59.892	20	217	6	222
60.057	20	AAAATCAAAGGCCCACAATG	59.801	20	139	11	149
59.829	21	GCGACAAATGCAAGGCTACT	60.416	20	177	20	196
60.001	20	GATGAAGGGTGGAAGGTTGA	59.903	20	160	456	615
60.073	20	ATGTGAGTGGCACGTGATTC	59.557	20	211	1611	1821
60.03	20	TATCATTTTGCCCAACCTCC	59.762	20	188	1324	1511
60.255	20	GGATGGCAAGCTTTTAGCTG	59.982	20	188	525	712
60.081	20	CGCATTATCGCTGTGAGTGT	59.895	20	224	1042	1265
58.337	20	AGCCTTGATTGGAACATGGA	60.461	20	252	102	353
59.939	20	TGTAACCCAAACCAAGCACA	60.004	20	247	2095	2341
60.21	20	AGAGGAGAGGCGAAGGAAAG	60.088	20	189	5	193
60.162	20	CCTATGGTGGTATGGTGTGGA	60.501	21	172	81	252
59.835	20	ATCAAAACCGTTACTTGCGG	59.996	20	260	814	1073
59.971	20	TGAATGCAGGACAAGAATGC	59.805	20	222	372	593
59.989	20	CTTTGCCCCTTTACTTGCTG	59.876	20	161	468	628
59.933	20	ATGCCCACATTTCAGAGTCC	59.934	20	234	692	925

60.315	20	TCAACCATTTGTTTTTGCCA	59.946	20	246	907	1152
59.986	20	TTAACCTCCCGTGGACGTAG	59.986	20	262	4	265
59.732	22	TGGTGGAGCGTCTGTTTTAAT	59.623	21	280	31	310
60.025	20	GACCAAGAGGCGTTGGTAGA	60.255	20	249	1943	2191
59.836	20	TCTAGGAGCGAAGGATTTGC	59.551	20	235	390	624
59.64	20	GACCGCAGGTTAATCCAGAA	60.074	20	240	1051	1290
59.806	20	TGTCTCCATTCTATTGGCCC	59.894	20	230	236	465
60.028	20	GATCTGAACCGACCGAACAT	59.934	20	255	206	460
59.986	20	ATTAGCGAACATGGAGGTGG	59.955	20	123	505	627
59.64	20	TCCGAGACAAGTTTCGTGAAC	60.284	21	270	63	332
60.122	20	AAAATCAAAGGCCCACAATG	59.801	20	265	391	655
60.17	20	TTATTGTGTGGGGCAGAGGT	60.375	20	226	139	364
59.685	20	TTTTCCCTGAGCACGTTAGG	60.241	20	178	404	581
59.239	20	GATTCTGTATCCGCCATTGAA	59.915	21	202	666	867
61.096	20	TGTGAAAGTCTTTGGATGGTTC	59.077	22	258	101	358
60.195	20	ACAGCTTCGTTGATGATGGA	59.245	20	247	474	720
60.894	20	CCGCCGATGTGATTTTAACT	59.96	20	273	242	514
60.133	20	TTCACACACCAAAATTCCGA	59.941	20	192	637	828
58.709	21	CATTTTTCCTCATGGAATGGA	59.748	21	188	1123	1310
60.362	20	GATTACAAGGCCCACCTCAA	59.933	20	239	124	362
59.744	21	CGGAATACAATTCGACAGAAAA	59.12	22	276	1051	1326
60.12	20	GAGGGGTGTTTCCAGACAAA	59.943	20	276	27	302
60.012	20	GTTGTTGAGGTGGTCTCCGT	60.009	20	268	585	852
59.829	20	TCCCGGCTGAATGTTACAA	60.057	19	176	10	185
58.028	22	GCATTGCAGGTTTCGAATTT	60.081	20	142	15	156
60.885	20	ACGAAAATCTCTGCCCAATG	60.074	20	165	221	385
59.762	20	ATTGCCACCCCTCACTACAA	60.375	20	246	488	733
59.923	20	AATGCCCTCAGATGCTATGG	60.059	20	249	384	632
60.129	20	CTGCCGATCAATGCAGTCTA	59.972	20	274	842	1115
59.822	21	CGTGTCAGAAATTGACAGCC	59.293	20	273	173	445
58.521	26	CAAAATTATGTGGCCCCAAC	60.053	20	274	87	360
59.522	20	GGGTCCCACCACCTAACATA	59.526	20	195	71	265
59.212	20	TCACTCCAGTTTTTCACCCA	59.109	20	206	902	1107
60.111	20	GGAAGCAAAAATGGCAGAAG	59.823	20	246	567	812
59.717	20	TGACTAAGTTGTGTGAGCAGGAA	59.966	23	262	741	1002
60.505	20	CGTAAAAATGGTTATTATTGGATC	58.395	25	254	909	1162
59.14	23	ATGCTGATGTTAGTGCGCTG	60.042	20	188	16	203
60.285	20	GCCCCCAATTTCTCTCTTTC	60.017	20	197	34	230
59.743	20	GATCGCATTGATCCCAACTC	60.435	20	167	605	771
59.978	20	CCATCTACGCAAACCCAGTT	59.993	20	213	150	362
60.117	20	AATTTCCAGATTCCCGTCG	59.879	19	173	1518	1690
60.569	20	TGTTGCGCGTGCTTTAAATA	60.401	20	134	1557	1690
59.813	20	CCACGACGGTTAAAGGAGAA	60.103	20	253	213	465
59.234	21	AGGGGGTTATCACCTGATCG	61.095	20	189	534	722
60.111	20	ATTTCTGCAATTGGGGTTCT	58.504	20	180	27	206
60.051	20	TGTACCGTGACAAGACCTTTG	58.687	21	100	887	986
59.901	20	CCACAACCCTTTCATCACCT	59.82	20	254	336	589
60.218	20	CATTGATGGTTTCGGAGCTT	60.074	20	280	232	511
59.002	20	CAATTACACTGCATGGGCTG	60.134	20	167	76	242
59.903	21	CAGCATTGATGGTCACATCC	59.925	20	217	118	334
59.94	20	AACATGGCCAACCCAAATAA	60.053	20	275	2488	2762
60.131	20	TGGCAGAAGTCGTTGAACTG	60.025	20	248	113	360
59.077	20	TCGGAGCCATAATCATCACA	60.033	20	225	696	920
59.595	21	TGGATCTTCGTATTTGTTACTTCA	57.899	24	129	213	341
58.977	20	GTTTTCATTTGATCACGCCC	60.318	20	106	24	129
59.972	20	TCCACTTTTCAATGGTGCAA	60.088	20	275	477	751
59.79	20	GAGATTGGGACAGACCCTGA	60.048	20	196	1667	1862
58.878	22	CGTCCAGTTCACTTCATTGG	59.135	20	113	1166	1278

60.269	20	CCTGAATTCTCCCCAACTCA	60.042	20	270	501	770
59.585	20	GAGTTCGTCAAACCTCCCAA	60.088	20	261	133	393
59.764	20	GAGGGAAATGGTGGGGTATT	59.881	20	107	1077	1183
59.82	20	AATCTTTGAACAGCCGATGG	60.074	20	208	577	784
59.722	20	CGAACCCTTCATCATCGAAT	59.894	20	100	570	669
60.103	20	AACCTCTTCGAGTTCGTCCA	59.844	20	278	390	667
59.829	20	AGAGTGCGCGTTTTCATCTT	60.022	20	108	442	549
59.518	20	TCACGACATTATTTCCCTCAAA	59.451	22	133	3481	3613
59.501	20	GCGGAAGCTGTGGTTTGTAT	60.14	20	270	228	497
59.129	20	AGATCTTAATCGTGGCCGCT	61.11	20	182	388	569
60.015	20	TCTTCTCCGTTTCAGTCCGT	59.844	20	226	560	785
60.073	20	TGAAGTTAGGAAATAAGGAGGTG	58.743	25	151	693	843
57.239	26	TAAATCATGTTTCACCGCCA	59.93	20	134	2	135
59.685	25	GACAATCTTCCAATTGGCGT	59.939	20	255	144	398
59.668	20	TCTTCGAGACGGAACCACTT	59.844	20	255	582	836
60.015	20	TGCAACTCCTCTGACCTCCT	59.986	20	125	2857	2981
59.75	20	CCACCACCAGAAGCAAACTT	60.149	20	143	247	389
60.46	20	CTTTATTAAAATGCGGGGCA	59.927	20	277	385	661
59.993	20	GAACAAGGGTAAGATGAACCCA	60.221	22	187	394	580
59.836	20	GCGGCTTCATCTTTACTTGC	59.988	20	239	167	405
60.032	20	TCACTGCTGACCGTGTTCTT	59.467	20	172	167	338
60.17	20	GTAAAGGGGGCACGAAAGTT	60.352	20	263	1643	1905
59.952	23	ATCAGATGGGCGAGCTCTAA	59.939	20	247	251	497
59.993	20	AGGCTGGATTTCGTCCCTAT	59.925	20	274	376	649
58.32	21	AAACGGTTGAAAAGCCCATA	59.451	20	247	18	264
59.25	20	TTTGGATGGAGTTTTGGAGC	60.051	20	199	186	384
60.012	20	CGTCACGGTGGTTCTTCATT	60.954	20	277	555	831
61.211	20	ATCCACGTCCTTGTGTCTCC	59.969	20	191	721	911
59.706	20	CCACAGCTGAAAACGTAGCA	60.05	20	225	2448	2672
60.066	20	TTGATGCACGAATTTGGAAG	59.664	20	228	198	425
59.067	20	ACCAGACCGTTAGGGGTGTT	60.66	20	277	50	326
59.803	20	CCACTTATGTCGAAGATTTTTGTG	59.933	24	261	1589	1849
59.994	23	TCTAAGGGATGATTGCACCA	59.075	20	125	322	446
59.897	21	ATGGCGCTATCTGGTTGTTC	60.103	20	109	6947	7055
61.118	20	AATTTGGGCCTCCATTATCC	59.984	20	213	416	628
59.647	20	GTTGTCTGAAAGGCATCGGT	60.119	20	225	155	379
59.992	20	CTTTTTGGTTGCTGTTGGGT	60.008	20	218	6944	7161
60.132	20	CAACACACAAAGCCACCATC	60.008	20	214	183	396
59.825	20	AGTGGTTATTACCGGATCGC	58.93	20	111	832	942
60.41	20	CTTGGAATCGTGAGAAGCGT	60.397	20	252	936	1187
59.831	20	TACAGGGGGATTTGGATGAG	59.744	20	149	567	715
59.809	20	TGCAGGGTATGCATGTTTGT	59.995	20	159	306	464
59.585	20	GGTTGCATACTGTGGGGATT	59.676	20	253	780	1032
59.716	20	CAAACAATGGGACCACAAAA	59.268	20	256	248	503
59.43	21	GTCTGGATCAGCTCGGAAAG	59.95	20	279	251	529
60.111	20	GTGGCTGTGGTTTTCGTTTT	60.015	20	279	181	459
59.901	20	AAGGCAATGGACATGGAAGA	60.461	20	244	1835	2078
60.045	20	GACAAGCACTCATGTGATGGA	59.698	21	193	3083	3275
60.119	20	TGCATCTCTAATTGGACCCC	59.894	20	122	205	326
60.112	20	GAAATGCAAGATTGCGACAG	59.425	20	131	1155	1285
59.297	20	ACCACCACCACCATTTTCAT	59.95	20	263	107	369
59.768	20	CAGTCATTGGATTGCATTGTG	59.98	21	159	342	500
58.959	21	ATGAAAATACGCGGGGAAAT	60.517	20	265	92	356
59.989	20	CAAAGGAAGTCGGTTGGTTC	59.569	20	166	17	182
60.201	20	CCCCCACCACACCTCTACTA	59.837	20	217	3485	3701
60.306	23	CCGAATCTTTTCGTGAATCAA	60.06	21	240	25	264
60.672	19	TTGAGATGAGGGATTTTGGG	59.864	20	197	3273	3469
59.654	21	CCAAGTAAAGCTCGAACCCA	60.241	20	265	1297	1561

60.17	20	TTTCATGATCCAGATGGACG	59.451	20	249	127	375
60.11	20	CTTGTGGAGCTACTCAGCCC	60.012	20	275	158	432
60.167	21	TGCGAAAAATTTGGTTCTTG	58.792	20	247	198	444
59.066	20	GTGGCACGATCATTGTTGTC	59.975	20	195	327	521
59.066	20	GTGGCACGATCATTGTTGTC	59.975	20	195	316	510
60.073	20	TGCTCTTGCATCACCTTCAC	59.992	20	268	396	663
59.817	20	CGTGCTCATGTCAGCAAGTC	60.627	20	164	23	186
58.812	20	TCGAAGATCAATGGTCCACA	60.048	20	134	118	251
59.561	24	TGCGTTTTGACAATATATAGGTGT	60.083	26	149	1376	1524
60.088	20	AGCGATAACATGGATGGAGC	60.066	20	275	2377	2651
59.832	20	GTTGGCATAAAATCCAACCA	58.335	20	244	512	755
60.152	20	GCTATCAGGAACCTATGTTTGG	57.774	22	207	1217	1423
60.514	24	TTCAAACAAGGCATAAAACTTTG	58.412	23	132	227	358
59.844	20	AGAGGCTTCATCTTCTGCCC	60.873	20	244	749	992
58.057	20	GCAAAGAAGGGACGACTGAG	59.989	20	238	885	1122
58.953	21	ACTCACGTGTCAGCACACAA	58.876	20	189	29	217
59.864	20	TTACAGCCCAGATTCCCAAG	60.066	20	277	231	507
59.81	20	TGATAGCGTTTTGCTGTATGC	58.998	21	202	418	619
59.82	20	GAGGTTGGTGACAGTGGCTT	60.159	20	272	484	755
60.393	20	ATCGCTTCTTCTTTCGCAGA	60.235	20	279	216	494
58.826	22	CCCCTGGTTGTTATCCTTGA	59.784	20	186	37	222
59.691	20	GTGTGACATTGGCCAGACAT	59.399	20	263	1022	1284
60.461	20	TCGATAGGACGTGTATGACGA	59.163	21	216	1687	1902
59.929	20	GGAGAAATTTGATTTGTTGGGA	60.164	22	274	205	478
60.073	20	TTAACCCTTGGATCTGAAGCA	59.693	21	269	49	317
59.984	20	TACTCTTCGATCCCGCGTAT	59.691	20	232	72	303
59.062	20	AGATGCTTTTTGTCGCGAAT	59.851	20	275	2434	2708
59.624	20	CGCCGCCATTATCTCTACTC	59.829	20	254	22	275
59.557	21	CCCCACTTTTAAATTGCGAA	59.937	20	280	710	989
59.864	20	GATTGCGTAGTCGTGTGTGG	60.183	20	267	561	827
60.702	20	TTAAACTACACATGTAATCCATAA	58.07	27	152	970	1121
60.913	20	ACAAAAATCTTGGTTTGGCG	59.975	20	266	115	380
60.17	20	CGCGTTAACAGTGGAAAACA	59.769	20	240	96	335
57.503	26	AATATCCTTTCGGGACACCC	60.017	20	148	13	160
60.066	20	ACACAGAATTCGCCCAAAAC	59.978	20	221	233	453
60.053	20	TTCCTACTCCCCTAGGCCAT	59.919	20	219	251	469
60.048	23	AAGGAAAGATCCGTCGAGTTC	59.705	21	170	3	172
60.123	21	GCTTAAGAATCGTGGCTTCG	59.982	20	199	220	418
59.457	21	AGCAAAAATAAAGGGGCTGC	60.566	20	278	609	886
59.109	20	GAATAAATGGACCCCCGAGT	60.017	20	164	427	590
60.008	20	ACGGCACATCAAACACCATA	59.847	20	217	4572	4788
60.145	22	ATGGAACATCTGATCACGCA	60.08	20	193	347	539
60.073	20	GCAACAATGGAGCAGATCAA	59.805	20	161	2273	2433
59.95	20	GCATCAAGAATCAAGCCTCC	59.78	20	262	714	975
59.579	20	TTGTATTTTGTCTGGCAGCG	59.872	20	215	159	373
60.162	20	GAAAAGGGAAAAGGACCGAC	59.919	20	173	368	540
60.203	20	ACCTCCCTCTTCTTTCCCAA	60.045	20	114	1144	1257
60.103	20	GATCCCGACGACCTCTCATA	60.034	20	139	539	677
60.017	20	AAACAAGGCATGGTTCATCC	59.797	20	238	840	1077
57.943	20	TATCCCTAAAGTGCCCTCCA	59.523	20	190	20	209
60.066	20	GAGTGCACCTCCTCAATGCT	60.418	20	244	1146	1389
60.074	20	GGGGTGAATTTAAAGGGGAA	59.992	20	259	261	519
60.014	20	ATTGACTAGGAGCACGCGAA	60.934	20	280	580	859
59.708	20	ACTGTCTGGGGCTTTGTTTG	60.149	20	240	88	327
60.206	20	CACACTCTTTCTCAGTGGACG	58.504	21	240	1020	1259
59.84	20	TTCCAGTTCCCTTCACCAAG	60.081	20	246	354	599
60.683	20	GGCATCACATGGTCTCTTGA	59.637	20	131	380	510
57.844	20	GTGCATGAGCTGTCTCTTGG	59.577	20	110	128	237

59.181	22	TTGACAATATTTAGTGTTTTGACAT	58.99	27	166	943	1108
59.438	20	AAAACGCGCAATGGATAAAC	59.971	20	243	179	421
60.11	20	TCCCATTCTACTGCCCAAAC	59.933	20	266	452	717
59.993	20	CGTAAATCCGGCTTGAATTG	60.448	20	217	300	516
59.874	20	TGCAGACATGAAGAGGGTGA	60.402	20	263	152	414
59.874	20	TACATGGCCAACGGGTATTT	60.074	20	260	177	436
59.939	20	TTCTCATCCTTTGCCTTGGT	59.67	20	235	395	629
60.173	20	GAAAATTGGCAGGATCCGTA	59.901	20	231	139	369
60.234	20	TTCCCACCATGATTTCAACA	59.75	20	220	1307	1526
60.152	20	TGTTTATGCCGTTGATACAAAAA	59.437	23	221	185	405
60.055	20	CCTAAAATTGGGTCCGATCA	59.756	20	242	293	534
59.475	21	TTTCCTGCAACAATTTCAACC	59.967	21	219	648	866
59.832	22	GGTTTGAACCATGATTTATTTGG	59.491	23	236	401	636
59.989	20	TTGGTTCGAGCCATTGTGTA	60.111	20	152	15	166
60.353	20	GTCCACAGTTACCCGCAGTT	60.035	20	239	497	735
60.263	20	ATCTCAGAACTCCCTTCGCA	59.95	20	219	1218	1436
59.943	20	AACTCCAAATTTTGATGCATGT	58.493	22	259	366	624
57.065	22	AACCAAAAACTCTCGACCCA	59.569	20	229	848	1076
59.676	20	CTATCCCCGAATGTGCCTAA	59.916	20	220	844	1063
59.943	20	TGAAGTTTACACAACAAATCTAAG	59.348	26	204	1628	1831
60.903	20	CTCTCAGTCCCAGACTTGCC	59.986	20	216	23	238
58.601	20	ATAGCTCAAGGGTTTTCGCA	59.845	20	208	259	466
59.984	20	GGGGACTGTCAATTCATTTTG	59.278	21	111	1388	1498
59.939	20	TGCAATTGTTCGTTCCTTCA	60.234	20	176	90	265
60.349	20	TGCCTACACAAATCCACCAA	59.964	20	133	921	1053
59.601	21	AAGGCAGTTATGACCGTTGG	59.993	20	158	29	186
60.088	20	TCACGCCTTCTCTCTCCAAT	59.95	20	257	617	873
59.746	20	CGGTACCGTCACCGTTATCT	59.875	20	232	126	357
59.767	20	AACCCTCAACCCTCTCCAAT	59.795	20	224	21	244
59.434	20	ATTGTGGCCCTCAGATTTCA	60.461	20	153	168	320
59.939	20	GCTCGTTTCGGACCAATCTA	60.214	20	271	214	484
58.9	25	TGCTTCCCTCACAACAACAA	60.278	20	268	1783	2050
60.457	23	GCGTTTTTGGCCTGATATTT	59.081	20	188	17	204
60.088	20	TGCATCTGTGAATGGAAAGC	59.805	20	278	76	353
59.989	20	CTGGGAGCATGTCAGTGTTG	60.309	20	224	763	986
60.206	20	TCGTTTGAGATCACGAGCAG	60.136	20	250	881	1130
58.858	20	TTTTTGTAAACCGCCTCGAT	59.586	20	193	584	776
59.869	20	ACAGGCCAAAGAGAGCAAAA	59.993	20	142	511	652
60.142	20	CAGAGAAAAGTCGTCGGGAA	60.366	20	221	117	337
59.926	20	GAGTTCCCGCGTCATAAAAA	60.074	20	256	498	753
59.882	20	GGGGAGAGTCAGGTAGGAGG	60.066	20	144	103	246
59.845	20	TGATGAATGACGACACATGC	59.037	20	266	316	581
60.175	20	ATGTGGTGTTCAAGCGTCTG	59.751	20	272	603	874
59.606	23	GCACGATCTCATGATTCCAA	59.61	20	255	21	275
59.396	20	TCATTTTTGACCGACGGTTT	60.344	20	188	23	210
58.789	22	CAATAAACGCCCACATGAAA	59.42	20	267	370	636
59.831	20	AAATTCCAAACTCCGACCAA	59.406	20	232	174	405
59.938	20	CGAGTGCCGTACTTGAGAGA	59.187	20	209	216	424
59.378	20	GCGCTATTTTTAACCCCAAA	59.11	20	214	204	417
60.12	20	ATTTCGAATGTCGCCTTGTC	60.081	20	242	1100	1341
60.012	20	TTGTCTCTTGCATCACTCCCT	59.859	21	259	488	746
59.481	20	CATGTGGCTTTGCTTTGAGA	59.988	20	160	191	350
59.728	20	CTCTTCACATTTCCTCCCCA	60.042	20	127	113	239
60.154	22	CTCGCCTCCAATACCAAGTC	59.694	20	272	178	449
60.827	20	ATGGCATTTCTTTGGCTTTG	60.074	20	257	524	780
59.7	20	CGGTATCACGGACGATTTTT	59.823	20	248	863	1110
60.031	20	TCTTCGTGTTCTTCGTCGTG	60.025	20	158	934	1091
57.943	21	CAAATCATGTTGAAAGGAACCA	59.839	22	272	728	999

60.05	20	TTGAGTGGTTCGGGGATTAG	59.926	20	205	242	446
59.397	20	TCGATAAATAGCCACATGCC	58.603	20	251	180	430
59.891	23	GGGACACCTCAGTGGTAGGA	59.962	20	264	59	322
60.119	20	TGTGAGGGACACAATTCTTGA	59.124	21	248	204	451
59.811	20	GGGGTGATTGGTAATAGCTCC	59.68	21	174	140	313
57.557	25	TTCAATCATGAGCGTTCGTC	59.805	20	136	16	151
58.486	22	TAATTCTGGCGAATCGGAAC	60.038	20	128	287	414
60.046	20	TCTTAATGAGGGCCCCTACC	60.278	20	263	125	387
59.298	20	AATTCCTATGGGTTTTGGGG	59.882	20	225	74	298
59.339	20	TGGGAGAAATCGATAATGGG	59.717	20	255	150	404
57.52	22	AAAATCAAAGGCCCACAATG	59.801	20	139	996	1134
60.025	20	GCGCAATTGCATCTATTGAA	59.809	20	177	2011	2187
60.198	20	CAGAATTGGGTGTAGCAGCA	59.864	20	175	263	437
60.005	20	CTCAAACCCCAAGAATCGAA	60.044	20	252	455	706
60.214	20	AATTAGCTTCTTCGTCGCGT	59.138	20	277	1389	1665
59.728	20	GTTCGCGAGATCCAGAAGTC	59.957	20	265	1445	1709
60.005	20	TGTTAATCTGTTCCGGCCTC	60.074	20	233	3245	3477
59.673	20	CTGAGGCCACTACCCGATAA	60.088	20	271	719	989
59.986	20	CAAAAGGTTTATCCCAGTCTCTC	58.333	23	108	3539	3646
60.036	25	TGAATTTTTGGAAATGGTGTTC	58.831	22	227	25	251
59.988	20	TAAGACACCAGGCAGTTCCC	60.111	20	202	263	464
60.125	20	AGCTTGAAACACACACACGC	59.953	20	252	307	558
59.469	20	ATGAAGAAAATCTGGCGCTG	60.352	20	244	615	858
60.036	20	GAAGTCGTCGTAGGAAAGCA	58.104	20	223	735	957
60.223	20	CAAAGCTCAAGCTGATGCAA	60.28	20	211	2993	3203
59.18	20	GGGGATTTCTGTCGCTTTTT	60.431	20	223	330	552
60.369	21	GTGATGATTCGGCTCGTTTT	60.081	20	194	558	751
59.523	20	CCATCATTCAACGCATTACG	59.953	20	274	2782	3055
58.755	20	ATAGGCCTACATCGAAGCCA	59.691	20	225	118	342
59.679	20	TGACCCTTTGTACCGTTCCT	59.449	20	181	113	293
59.96	20	AAGGAACGAACAAGTTTTCCA	58.73	21	270	654	923
60.526	20	TGAATGTTGTCGTAGCCTGTC	58.79	21	108	1358	1465
59.202	23	GACGCTAACGCCATTACGAT	60.124	20	255	531	785
59.708	20	GTGGCATGGGGAAGCTACTA	60.096	20	234	52	285
60.169	20	GAGCACGCAGAGAAGCAATA	59.326	20	238	378	615
59.688	20	GACAATCCGGCCAAATTAAA	59.773	20	276	196	471
60.089	20	GTGGAAGCGCCATGTTTTAT	59.967	20	240	130	369
58.8	20	GTATCAGCAGCCACCCAAAT	59.962	20	262	4780	5041
57.517	20	GCAAAGTGGAGATCATGGGT	59.934	20	229	631	859
59.861	21	GTCTTTAACCGCCACCAAAA	59.975	20	209	524	732
60.071	23	GAGAGCAGTTTCGGACATAAA	57.108	21	280	139	418
57.406	21	GCCAAAACTACCCCTTTCAG	58.694	20	176	414	589
59.657	20	CTTCAGCAAACCAGCTCTCC	60.134	20	247	44	290
59.938	20	TGCGAAGTTTGTTCTTGTGC	60.035	20	157	560	716
60.517	20	AAGGAGTTCACAGGTGGTGG	60.002	20	259	3	261
59.716	20	TCAAATTTTGGCTTTGCAATC	60.068	21	274	80	353
60.066	20	TGGAAAACACCCTTTTCTTGA	59.573	21	232	512	743
60.035	20	TGTCTCATTGTGCTCAAGCC	59.992	20	116	222	337
60.015	20	AGCTCGGTCGGGTAGAAAGT	60.268	20	246	91	336
59.758	22	GGGGTTATCATGGGATCAAG	59.055	20	266	2403	2668
59.939	20	GAGAAAGTGAAGAATCGATTGGA	59.717	23	123	370	492
60.235	20	TTCACGCAAACAAATTCCAA	60.088	20	161	242	402
59.982	20	TCAAGTGTTCCCATCACCAA	59.935	20	222	498	719
59.984	20	CCCAACTTTCTCCCCTCTTC	60.045	20	170	3415	3584
59.931	20	TGAAGCACAATGAAAACGGA	60.234	20	237	130	366
59.993	20	CCCACAACTTTTCTCTGCCT	59.328	20	212	1564	1775
59.738	23	CTCAACAGCGTGTTTGGTTT	58.825	20	280	1316	1595
60.089	20	TTTAGGCGTTCAAAAGGCAT	59.72	20	178	311	488

59.916	20	TCGAAGATCAACGATCCACA	60.201	20	177	799	975
59.988	20	TGTTGTGTGCAAGTTCCCAT	60.008	20	253	548	800
59.923	20	TGCACAACAAATAGGCAAAA	57.846	20	224	225	448
60.24	20	TACATTCCAATGGCAAAGCC	60.837	20	165	800	964
59.999	20	AACTCATTGTCAACCGCACA	60.16	20	217	566	782
59.878	20	ATTTCCAAGATCAACGGACG	59.933	20	169	496	664
59.989	20	AGGCTGATTGTGAACTCCAGA	59.859	21	250	2091	2340
58.743	25	GTGGACGCTCCAGATTGTTT	60.119	20	124	2	125
60.23	20	TCTTCCCAGCAAGAAAGGAG	59.545	20	268	95	362
59.992	20	AATTGTTCATTTGCAACGGC	60.876	20	273	802	1074
59.923	20	TTAAATATTCATGGGCACGC	58.513	20	209	158	366
59.924	20	CTCAGGCCTATCGAACCAAA	60.206	20	276	102	377
60.142	20	TGACCCGCCTCATCTTCTAC	60.218	20	197	1158	1354
58.743	25	CAGGTTTATCAACAAGGTTTTGG	59.795	23	140	24	163
60.312	20	AAGGCAAGCTAGAACCCACC	60.63	20	161	551	711
60.051	20	ACCTCCTCCTTTTCCTTCCA	60.045	20	265	787	1051
59.946	20	CCAGAGCTGAAAATCGAAGG	59.948	20	274	525	798
60.134	20	CGAATTCTAGGCGATTCCTG	59.801	20	218	1266	1483
60.016	20	GGGAAGAACGACGACGATAA	60.074	20	254	50	303
60.008	20	GGTTTGGTTGGAGAAAGCAA	60.088	20	188	296	483
59.828	21	CTTGAAAAGGGTTGCAAGGA	60.22	20	101	856	956
59.997	20	ACCCTGTGTATCCCAGCAAA	60.375	20	220	104	323
59.813	20	CTTTCTTGGACCAGATTGCC	59.67	20	240	3551	3790
59.28	20	TCAATCATGTTGGGTGCAGT	59.967	20	201	248	448
59.968	20	TACAAGCCTTGGACTTTGGG	60.103	20	173	1216	1388
60.181	20	GGACGTTGATTTGTTGGGAT	59.653	20	200	170	369
59.989	20	AACCATGTGCTTACACCACG	59.49	20	247	244	490
59.913	20	TGGTCGGAGACTAGGGTTTG	60.103	20	272	228	499
60.214	20	CCGAAACGATGAACGAGTTT	60.11	20	137	1001	1137
59.353	20	CTGCATGCACATAGAGTATTGG	58.346	22	274	380	653
59.96	20	TTCCAATATTCTTCGGAGCG	60.167	20	254	1879	2132
58.877	26	GGTACGTGGGGTATGGTCAA	60.495	20	276	610	885
57.036	22	TGAAGATCGATTGGCCATAA	59.065	20	237	268	504
60.17	20	TCTTTCTGCATCCACCACAA	60.24	20	258	110	367
59.702	20	TAGGCCCATAAATGCTTCCA	60.415	20	249	39	287
59.547	20	AACCGATTCTCACCTCTCCC	60.456	20	136	676	811
59.014	20	AGTCGAATCTGTCACGACCC	60.12	20	176	431	606
60.038	20	AACTGGCAATTGCTGGAATC	60.081	20	206	645	850
60.081	20	TCCCTACGAGGAAGTCAGGA	59.797	20	277	103	379
60.111	20	TTGGTTTTGTTTGGGATTGA	58.841	20	280	117	396
59.914	20	ATTTGTTGGAGGTTTGGTCG	59.83	20	223	57	279
59.157	21	TTTTTATTGTTTGCTCCGGG	59.937	20	138	48	185
60.224	20	GCCATTGGGGAAGGTAAGAT	60.152	20	143	371	513
59.955	20	CAACTCAAATGCATGGGAAA	59.518	20	129	237	365
61.031	20	TGTGCTGGATGTCGTTGATT	60.12	20	138	19	156
60	20	TCATTCATTCAGACTCAGGGG	60.058	21	113	935	1047
59.215	20	TGTTCACCTTTTGGCCATTT	60.344	20	195	30	224
58.897	20	CTTTCTGGTCAACACTCACGA	58.917	21	222	213	434
59.734	20	TGGGATAAAATAAGGGGTTTCC	60.241	22	255	966	1220
60.111	20	TGGGCTGCAAATGATAAAAA	59.146	20	204	88	291
59.494	22	CCGTCTCCTCCCTCTACCTC	60.208	20	245	843	1087
60.019	20	CAAGAGCAACACATGCCAAC	60.31	20	232	2586	2817
59.088	23	GTGTGTCTGGTGGGGAAGAC	60.421	20	166	15	180
59.638	20	GGGGCCAATCCAAATTTAT	58.563	19	192	618	809
58.285	21	ACTGAATCCTTTCACGGAGC	59.288	20	175	409	583
59.691	20	GTCGATCCCCTGAGTGTGTT	59.969	20	279	7	285
59.96	20	GGTCTCTCAAACTGGCCAAA	60.232	20	128	5861	5988
59.73	20	CGCCCCACATTGTTTCTTAT	59.823	20	119	70	188

59.161	20	GGAGGAATGCAAGTTGTGGT	59.973	20	280	263	542
59.845	20	TTTTGTTGGACGAAAATGTCC	59.831	21	248	1253	1500
58.743	25	TCTTAATTGGGGTGAAAGCG	60.067	20	260	6	265
59.916	20	TACCGACCATTAGCAGCCTC	60.235	20	189	557	745
59.304	20	CTCGCTTTATCCTCCTTCCC	60.166	20	258	1685	1942
58.243	20	TCGTCCAACTTTAAGTGATTTTCA	60.037	24	209	239	447
59.064	20	TGGTTTGGAATATACCGAAGTTG	60.115	23	115	4062	4176
59.875	20	GCGTAAGGGTGTTCGTGAGT	60.179	20	143	77	219
60.04	19	ATGCCATGACACGAACAATG	60.399	20	171	199	369
57.944	23	GGCCGAATTATGCTTTTGAA	60.04	20	261	94	354
59.738	21	TGTGTCATCTTACACTTTCCACA	58.201	23	136	20	155
59.229	25	ACAATCTGCGAAACTGGGTC	60.119	20	107	17	123
60.199	20	CTCGACAACCTTGCCCTATC	59.694	20	212	547	758
60.074	20	GAGAGTGCCTCACTTTTGTGG	59.899	21	203	177	379
60.035	20	GTCGTGGAGGCATGCTTAAT	60.103	20	275	682	956
59.978	20	CTTCAATTTCTTGGCGTGGT	60.11	20	267	393	659
59.985	20	TTCATCGCCTCTCCTCTTGT	59.95	20	275	35	309
60.096	20	CATTTGCAATGGAAAAAGGG	60.294	20	180	1720	1899
60.289	20	CGGTTATTACCGGATCGCT	59.93	19	196	61	256
59.141	20	AAGAGGTTGGGGGTGCTACT	59.994	20	254	669	922
59.997	20	CAAAGTCAATAGCCCAACCAA	59.982	21	238	320	557
59.629	20	CGTTTGAGCTTTGTTTTCTTGA	59.553	22	156	29	184
59.973	23	CCCTTTTTACCCACCGATTT	60.048	20	115	16	130
60.089	21	AAAATGCATCCTCGTGTGTG	59.572	20	277	260	536
59.202	21	GGCAAGACTCGATCAGGAAG	59.95	20	158	179	336
60.039	20	CCACTGTTCAAGTGGACGAA	59.72	20	214	119	332
60.34	20	ACCAAGCATTGTGGATGCTC	61.078	20	109	600	708
60.331	20	CCAATTTGAATGGTTATCACCTG	60.457	23	115	455	569
60.211	20	TCTCGTTTGGAGGAATTTGG	60.044	20	211	488	698
60.103	21	CCTCGTTTGCAGCAGTTACA	60.05	20	234	992	1225
60	20	GGCGTTACCGCATATGATCT	59.951	20	192	3205	3396
58.349	23	TGTTTTTCCGATTTCACCAA	58.987	20	177	33	209
59.26	23	TCCGTAGAATTTTAAAAAGAAGTA	58.158	27	267	61	327
59.7	20	AAAATCAAAGGCCCACAATG	59.801	20	168	369	536
59.655	20	ATCCCAAATTCCCAACCTCT	59.629	20	107	585	691
59.872	20	CGTGGCAGGCTAATATCCAT	59.945	20	168	85	252
60.203	20	AAATGGCCAAGCCTCTGTTA	59.708	20	253	805	1057
60.008	20	TCTTGTGGTAAGCAGCTCCA	59.591	20	194	1200	1393
59.712	21	TATATCGGGGGCTGAGCATA	60.403	20	146	248	393
60.081	20	CAAACTCCACCATAACCGCT	59.993	20	233	552	784
59.229	25	ACAATCTGCGAAACTGGGTC	60.119	20	109	17	125
59.84	20	AAGGGGACTTGCACAAACAG	60.149	20	244	100	343
59.091	23	CGATATTGTGCCGGTTTGAT	60.721	20	271	90	360
59.749	21	CGGGTGAGAATAATTTAAAGCC	59.049	22	179	2224	2402
60.179	20	CATCAGGTTCACTGGCAAAA	59.691	20	275	1120	1394
57.557	25	GGTTGGCCAAGTAAGGTCAA	59.971	20	244	15	258
59.496	20	TCAATGCAGATGGGATTCAA	60.009	20	201	421	621
60.068	21	TTCACGAAAGTTGCAAAACG	59.888	20	185	418	602
58.747	23	TTCATAATTTTGTTGCTTTTGC	57.131	22	272	1845	2116
60.081	20	AAATCCCAGCCACACATTTC	59.797	20	143	494	636
60.362	20	CATGATCACTTAGGCACTTAGGAA	59.687	24	279	547	825
60.068	20	CAGAGGCATGGTCTCAGTCA	59.98	20	239	610	848
60.481	20	GGGAGGACCATAGCTCATCA	60.034	20	187	467	653
59.535	21	GGAGATCGGAATCGAACGTA	60.036	20	199	466	664
60.144	20	GCCCACTCTTTCTAACCGTC	58.792	20	126	511	636
60.096	20	GCAGAAAAACCATGGGAGAG	59.67	20	106	451	556
59.934	20	AAAGCAAGCCTGGACTACCA	59.875	20	130	331	460
60.582	20	ATTTTCGATTTAGGGGCGAT	59.772	20	225	1417	1641

59.632	20	GGTTTTCAGATACACGTGCC	58.076	20	191	5	195
58.743	25	ATGAGGAGGAGGAGTTGGGT	59.929	20	224	3	226
59.842	20	CAAAGGCCTAGAAGTGTTTTGA	58.562	22	154	688	841
59.101	20	AGGAAATGCAGTGTTTTTCAA	57.411	21	259	216	474
60.103	20	GACAGTTTTCATTTGATCAAGCC	60	23	196	27	222
59.96	20	TTGAAACGGACCAACAATGA	59.941	20	266	1	266
60.692	20	GACCAGATGGGTGCTTGAGT	60.12	20	239	869	1107
59.927	20	TTCAATTGTATTAGCCGATTTTT	57.072	23	217	242	458
59.367	20	GAGAACCAAGGGTCAAGAAAAA	59.61	22	202	336	537
59.369	20	CAAAAATCCAACACCTCTCAGAT	59.513	23	228	1310	1537
60.04	22	TCACAATCGTCCATTTTTCG	59.518	20	273	244	516
59.978	20	TTGTGTGATCGAACCACGTT	60.008	20	179	118	296
60.118	20	CCGGAGCTTCAATATCCAAA	60.031	20	234	591	824
59.876	20	TGACTCAAGTCTTCAACCAACA	58.397	22	273	269	541
60.229	20	CGGAGGGTTGGTGTTAGAGA	60.103	20	180	1	180
59.939	20	CGGTGGAATATGTATGGTTGTG	59.996	22	221	6	226
60.457	23	GTGAGCTCTTCCGTGTCCTC	59.993	20	202	19	220
60.096	20	ACTTGCACCACCACTTCCTC	60.159	20	154	485	638
60.03	22	TGCCACGTAAGATCTCCAAA	59.272	20	280	609	888
60.785	24	GAAAGAAATGCACACGCTACC	59.766	21	220	1136	1355
59.813	23	GTTGGCTGTCCCACTCATTT	59.973	20	213	1128	1340
59.736	20	TTTAAGGGTTATCACCTGATTTTC	57.757	24	164	621	784
60.119	20	TTAAACTTTCCATCGTCGCC	60.074	20	246	1461	1706
59.833	20	ACGTTCTTCTCCATCCCCTT	59.935	20	179	218	396
59.685	20	GTACTGGCGACAGCGATACA	59.895	20	241	462	702
59.67	22	TGAAATTAGGAAATAAGGAGGTG	58.625	25	246	345	590
59.962	20	TGCCACGTAATCACAGCCTA	60.28	20	154	419	572
60.11	20	TCTGAGATTTTCATTTTGTCGG	59.202	22	198	713	910
59.901	20	TCAAATGCTCAAGGATCAATTC	59.162	22	250	1428	1677
60.576	23	GGCTGTGTGATCATGTTTGG	59.967	20	216	987	1202
59.124	21	AACGAAATCGAGACACCGAC	60.119	20	235	90	324
60.693	20	GATTCTGCTCTCGTGAAGGC	60.104	20	227	3555	3781
60.617	20	TGATCAATGTGGGATCATGTTT	60.059	22	224	955	1178
58.388	23	TCATGCTTGAATCAAAACAACA	59.206	22	193	1	193
59.691	20	AGGTTGTCCTGATGGTGGAG	59.962	20	114	2186	2299
60.088	20	TCACACACTCAAACACACGC	59.321	20	237	361	597
58.729	21	TTTTGCCATTTTCGAAATCC	59.886	20	253	1274	1526
59.854	24	GGAAATAAGGAGGTATTATGAAG	59.555	25	156	837	992
59.998	20	ATTGCTTCCAATCGAACACG	61.032	20	102	3550	3651
59.75	20	CACGAGCCGCCTAAAATAAA	60.218	20	270	203	472
59.935	20	GTGATGCAGTGTTGCTGCTT	60.064	20	239	2253	2491
60.104	20	TGCGAATGATAATCAACATGAA	59.032	22	269	206	474
59.573	21	GCAATTTCTGTTTCAGTATTTCAA	57.598	24	280	1003	1282
60.051	20	AAATATTTCACGCCGCTGTC	60.103	20	246	843	1088
60.073	20	CACGTACACCGACAAACACC	59.922	20	207	783	989
59.708	20	TGATCAGCAGCTATGGAACCT	59.851	21	258	83	340
59.945	21	TGATGGAAGCAATGCAACTT	59.276	20	171	173	343
59.937	20	TTGGCAAAACCCTATTCAGG	59.931	20	222	2852	3073
60.132	20	TTTCGCAAGGTAGAAACCGT	59.747	20	132	1257	1388
59.993	20	ACTGAACTCAGCAGCCTCGT	60.205	20	193	2510	2702
60.044	20	GGCCAAAACATTGCTCCTAT	59.046	20	175	2715	2889
58.108	22	TGGACAAATATGGTGATGGC	59.205	20	246	186	431
59.622	20	TTGGCTCGTACCAAGAAAGG	60.241	20	265	2305	2569
59.699	21	ATATCACATGCATGACCGGA	59.763	20	188	332	519
60.225	21	GCCCTAAGGTTGACTCATGG	59.55	20	211	25	235
59.882	20	GTTCCGGGATATCATCATGC	60.126	20	271	251	521
60.246	20	CGTTTGGCGGATAGTTTTGT	59.996	20	261	195	455
59.67	20	CGAAGGTGGGTTCTTGTGAT	59.966	20	217	11	227

57.797	24	GGGATCCATTGAGGATGTGT	59.593	20	266	2685	2950
59.91	20	GGGAGGGAATCTATTGTGATTG	59.666	22	198	577	774
59.05	20	TTGGATGAGATGATGGCAAA	60.009	20	236	1	236
59.99	20	GTGCTGCCCAAGAACTTAGC	60.022	20	242	639	880
60.053	20	GGCTGCATTTTTATCCCAAA	59.907	20	256	510	765
59.787	20	AAGCGTAGCATTGAGGGAGA	59.978	20	214	474	687
58.82	27	CCCCGACTTCTCCTTTGATT	60.434	20	253	1984	2236
59.84	20	AGAGGCGATTGCTTAGGTGA	59.978	20	269	66	334
59.007	23	GTTTTCGTTGTCCCCACAAT	59.694	20	161	199	359
60.038	20	CCAAGCCTACCGAGTCAATG	60.647	20	209	952	1160
59.907	20	TATACAAGCTGTGGCGGTTG	59.752	20	273	50	322
60.132	20	CGTCCAGTGCCTGTGAATTT	61.096	20	258	2258	2515
59.797	21	GGGTCGACAAGCTTGAGAAA	60.375	20	184	10	193
60.11	20	GCAGAGAGGGAGGGAGAGTT	59.952	20	237	123	359
59.866	20	TGGCACCCCTTTGTAATCAT	60.192	20	270	1035	1304
59.939	22	TCAAGATTATGGTGGGGGTG	60.572	20	274	878	1151
60.232	20	CACGAATTCCCCGACTTTTA	59.931	20	171	990	1160
59.945	20	TCACCCGAATCTTTCGTTTC	60.051	20	207	496	702
60.152	21	CGATCGATCATCGGAAAAAT	59.862	20	114	16	129
59.871	20	ATGAGGCCCATCAACACAAT	60.203	20	241	116	356
58.736	24	TGGCTGATCAAGCTCCTTCT	60.096	20	131	14	144
59.953	20	TCCCAAAGTTTCACACGTCA	60.128	20	216	501	716
60.042	20	TGGGATTGATCCTACCCAAA	60.126	20	262	2459	2720
60.03	20	TTTTCATGAATTGCCTTCCC	59.878	20	263	2855	3117
59.96	20	TTTAATTAGGTCCACGCGCT	59.742	20	103	123	225
59.988	20	TTGATAGTCCGGTTTTTCGG	59.931	20	238	179	416
57.278	20	TTGGTAGGTGTCCGTGATGA	59.96	20	249	836	1084
60.035	20	AGTTAGCATGGGGAAGGGTT	59.827	20	199	16	214
60.209	20	TCATCCCAAGTCCAGAGCAT	60.622	20	259	2726	2984
60.353	20	TTTTTCAGCTCACTTTGTGATG	58.081	22	229	647	875
59.903	20	CCAGCAATAGCCCTCTGTGT	60.277	20	267	4389	4655
59.992	20	TGCAAATGGTGATTGCTCAT	60.08	20	265	365	629
59.924	20	GACCGTGTGCAATGAAACAG	60.16	20	211	166	376
60.144	20	GTGGCATGCAAACGACATTA	60.532	20	107	2	108
59.938	20	CTGCAGATCTAAGGCCGAG	58.709	19	146	974	1119
59.773	20	GCTCGAACTCGATCACAACA	59.992	20	236	66	301
60.307	20	TCGCCAAAACATGATGAGAG	59.799	20	280	33	312
59.988	20	ATCGGAGTTGATTTGATGCC	59.9	20	261	1600	1860
59.005	20	TGGCGATTAATTTCCCTTCA	60.395	20	154	406	559
59.739	20	TGTCCAACTCAAAGAGGAAAA	57.441	21	260	130	389
59.065	20	ACAAAAAGCACAAACCCACC	59.875	20	259	1619	1877
60.059	20	CCAAGTTGATGCACGAGAGA	59.984	20	222	911	1132
59.722	20	GCTACCTTGCGGAGTTCAAG	60.015	20	188	59	246
60.36	20	CTCTCTCCTCCCACAACCTG	59.828	20	144	160	303
60.004	20	TGTGCATCAAAATAAACCCAA	58.922	21	144	1559	1702
59.756	20	AAAGCAGGTTCCCCCTATTG	60.312	20	207	270	476
59.024	20	TTGGGATTTCACGAAAGATTG	59.924	21	231	14	244
57.999	20	TTGCCGTTTTGTTCATGTTT	59.062	20	235	1925	2159
60.035	20	GGCTAATTGTTGGCCTTTGA	60.074	20	146	268	413
59.854	20	CCGGATACGGATTATATCCAA	58.659	21	249	383	631
59.918	21	CCTTAGATTCCACTTGGGCA	60.066	20	125	371	495
59.769	20	ACCTCCAACCCTTATCCCAC	60.052	20	146	8	153
60.111	20	GTCGATTCGCCACCTTTAAC	59.574	20	202	226	427
60.195	20	AGTTGCAATTGCCCGAAATA	60.456	20	175	250	424
59.606	21	AAGCCTACATTCACATTCCCA	59.443	21	241	418	658
59.82	20	TCCAGCGACTCATGTTGTTC	59.837	20	274	727	1000
59.079	21	AATCAATGAAGGGAGGGAGG	60.264	20	250	251	500
60.081	20	CCCAAGAATGGGTTATTATTTGA	59.14	23	149	778	926

59.972	20	CGAAATGCATGATTGAGGTG	60.073	20	249	722	970
60.074	20	TAGAGGTGGACGAGGAGGTG	60.252	20	224	274	497
59.369	20	TGACATGGATTGTGCTTTCG	60.665	20	233	2	234
60.051	20	TTGAGTTTGGGGATATTCGG	59.756	20	198	922	1119
59.917	20	TTTCTGGAAGGACCACCAAC	59.943	20	236	502	737
60.263	20	GGTTTCGACTGGTAACGGAA	59.971	20	277	390	666
57.297	26	AAGCGAAAGAAAATGGTTTGAA	60.108	22	280	5	284
60.073	20	CATGAAGTGAAAGGGACGGT	59.966	20	205	182	386
59.831	20	TTGAAGTAGGGCATTGAGGC	60.214	20	261	435	695
59.752	20	GATAGTGGAGTTGTGAGCATCTG	58.878	23	280	56	335
59.903	20	TGACGACCGATAATTGCTCC	61.003	20	174	44	217
59.817	20	TACTGCAGTGGAGTTGCCTG	60.049	20	250	1413	1662
59.052	20	CCAAAAACTGATAAATGATGCTG	58.687	23	253	423	675
59.971	20	TTTTTGGCCTTTGATCTTCG	60.181	20	262	95	356
59.864	20	TTCGTGAATAGTGCTGCCTC	59.028	20	235	512	746
59.978	20	TACCCATTCTTCGCCACTTC	60.074	20	209	1569	1777
60.264	20	CGGGAGAAAATGAAAACCCT	60.291	20	140	1025	1164
60.645	20	CGGTCTCGGTTTGGAATCTA	60.066	20	253	150	402
59.359	20	GGGATAGTACCGGAACACGA	59.813	20	186	877	1062
58.727	21	CGAACCTGGGTCTCTCACAT	60.112	20	164	118	281
59.882	20	GAGGGAGGGAAGATATTCGG	59.859	20	266	1447	1712
59.835	20	ATCCACCAAAAACCTGTCCA	60.21	20	173	1066	1238
59.923	20	AGAGTGAGAGTTGGCCTCCA	59.986	20	280	230	509
59.992	20	CGCTGCAACAAATACACACC	60.18	20	256	978	1233
60.11	20	TCCAACCTTGTTTTTCCGAC	59.948	20	227	573	799
59.903	20	ATCACCGATTTGCAAACACA	59.972	20	222	162	383
60.227	20	ATAGGATTTCACTGCCTGCG	60.235	20	247	140	386
59.903	20	TTGTCAAAAACTGCCAGCAC	59.888	20	265	2699	2963
60.074	20	CACCTGATTTTCTCCCTCCC	60.822	20	224	1547	1770
59.66	25	TGCACGCAGCATATTATGAA	58.88	20	216	578	793
57.587	21	TAGGCCTAAATGGTCGCATC	60.06	20	278	519	796
59.962	20	CAAATCCAAACCACCATTCC	60.029	20	224	156	379
59.839	20	GATTCTGCTCGATTCCCAAG	59.773	20	154	1348	1501
59.579	20	TTTGGAAAAACAGAGCACCC	60.088	20	134	342	475
59.992	21	GGCTTAATGGCCAAAAACAA	59.943	20	272	3788	4059
59.583	24	TGACATTTGTCTAACGATGGTG	58.554	22	269	70	338
59.851	24	TGTGATGCTCAGCAGTGTTT	57.976	20	208	48	255
59.826	20	GAAGCATTGGTAAGCCCAAA	60.074	20	197	21	217
60.194	26	AAAACGCGCTATTTTAAACCC	59.549	21	255	1	255
60	20	TCACTGCATTAAACCTACTCCC	58.264	22	263	3910	4172
59.174	20	GGTCTGGCAGTCGTGTTTCT	60.307	20	271	2751	3021
60.21	20	CAGACAATCCCGGAGGACTA	60.065	20	221	2622	2842
59.966	20	TGACACGGTGATTTACGTGG	60.427	20	242	248	489
59.833	20	CCTAATGAATCCTCCCCCAT	59.974	20	278	1154	1431
59.82	20	ATCTAATGCCCCAACACAGC	59.962	20	239	1130	1368
59.918	20	CTGTGCGCTAAAGGTTTTCC	59.883	20	145	77	221
59.661	20	TCCACTCCAACCCTTCTTTG	60.081	20	261	5285	5545
59.957	20	TTGTCTTCATCAAACGCCAG	59.84	20	183	787	969
59.933	20	AGGGAGGTGGCTCCTGTTAT	59.957	20	183	383	565
59.586	20	TGATTGCGAAACAGGAAAAA	59.277	20	168	85	252
57.796	21	GCCTGCTACACAGGGTTTTC	59.74	20	198	27	224
60.24	20	GAATGATGTGATTCGGCCTT	59.9	20	229	546	774
59.956	21	TGAGAAGAACACATAAATTCGCA	59.772	23	280	1610	1889
59.702	20	GGTGGAGACAGGAGGGTGTA	59.962	20	231	39	269
58.912	20	TCCAGCTGTTAAAACCCACC	59.971	20	235	1001	1235
60.132	20	TCGGAGTCTTCAGACAAATCAA	59.853	22	274	1919	2192
59.521	20	TGTGCTTCAGTCCTTGCATC	59.992	20	277	4899	5175
60.014	20	ATGGAATACCGGTGCAAAAA	60.188	20	201	1558	1758

59.864	20	ATTCTCTCTCCCCCTCCAAA	60.008	20	226	51	276
59.926	20	ATGCTTTCGTTCCATTGGTC	59.939	20	263	213	475
60.14	20	AATCCTGGTTCCTCGGAGTT	59.935	20	130	674	803
58.954	21	TATTTGCAGAATTTGCCACG	59.702	20	185	246	430
60.008	20	ACACCTGGGTGAGACCAAAC	59.859	20	181	742	922
59.723	21	TCCGATGGGGTATTCCACTA	60.148	20	182	180	361
59.989	20	GGCTAGGCTTGTAGCAAAAGG	60.389	21	234	71	304
59.916	20	CGCATTTTTGGCCTGATATT	59.928	20	221	776	996
60.431	20	TTTGAAAACGTTTCGCTTCA	59.462	20	269	646	914
59.293	20	TCCTTAATTCATTAAATACATACC	57.288	26	123	481	603
60.673	20	TGCAAACACAATGTCTGAAATG	59.632	22	269	698	966
60.147	20	CCCTCTCTCCCCTCACTCAT	60.605	20	240	58	297
59.439	21	GTGTGATTGGCAGTGACAGG	60.162	20	143	1036	1178
58.503	27	GCACGGCAGTGGAAGAATA	59.814	19	277	1015	1291
58.957	20	CTCAGTACAATGGAGTGATGGC	59.621	22	168	606	773
60.275	20	AGTCAGCCGAGGAAATTCAA	59.813	20	277	170	446
59.338	20	GCTGAGAAGATGGCCTTTTG	59.955	20	213	248	460
61.981	20	CGGCTGTCAACAGAAGTTCA	60.025	20	202	72	273
60.089	20	GGCATGTGGGGGTATAGTTG	60.074	20	256	1533	1788
59.934	20	GACACCCCAAGTCCAAAGAA	59.943	20	269	143	411
60.081	20	TATTTTCGGTTTATTGGGCG	59.799	20	171	76	246
59.939	20	TGGGACACTGTTTTCTTTGG	58.594	20	195	284	478
59.757	20	TCCCCTGCTTCTAAAACCCT	60.068	20	140	10	149
58.952	20	TGCCCAGATGTCAAGAATTG	59.648	20	271	223	493
59.362	23	GGATTTACGTGCAAGGGAGA	60.074	20	100	442	541
59.972	20	TGGCTTGGTCTTGATCTGTG	59.831	20	103	938	1040
57.299	27	TGGGAATAATGTATGAATGATCG	58.707	23	271	943	1213
59.74	20	CACGGTTGCCCTTTGTTACT	60.03	20	238	660	897
60.401	20	TGTTTGTGATCCCAATTGAA	57.35	20	234	608	841
59.989	20	TTGGTTCGAGCCATTGTGTA	60.111	20	155	44	198
60.081	20	TCCAGTGTTGCTTTGCCATA	60.257	20	254	1190	1443
59.941	20	AAGTCGAAATTTGGCAACAA	58.267	20	103	203	305
59.953	20	ATGAGCACATGCCAAAATGT	59.005	20	204	1838	2041
60.088	20	TGTGCTCCATGGCTGATAAA	60.22	20	226	189	414
59.258	20	GCTAATGGGAAAAGCATTGG	59.547	20	109	1461	1569
59.874	20	CATGATAATGCTGATAAAAATTGC	57.831	24	203	447	649
59.971	20	CTCCTTCTTTGGCTCAATGG	59.807	20	221	837	1057
59.097	20	ACTTGGAATCTGGACTCGGA	59.655	20	227	15	241
60.073	20	CAACCGGCAGCATTTTTACT	60.131	20	216	3487	3702
59.67	23	CGGGTGGGAATGTATTAGGTT	59.952	21	250	70	319
58.703	23	ATAAAAAGGACTGGCCTGGG	60.312	20	214	60	273
59.923	20	TTTGGTTGAAGGTGCATGTC	59.547	20	121	399	519
60.327	20	CTGCCCATTTGACTCCATCT	60.073	20	216	133	348
59.984	20	TGAGGCCACTGACTTGAATG	59.831	20	251	39	289
59.835	20	CAAATAATGTGGCAATCCCC	60.016	20	146	40	185
60.054	26	TTCATCTTGTAGCGTTTGAATGA	59.772	23	105	1	105
60.024	20	TGCATCATCTGCCATTTTGT	60.08	20	191	1438	1628
60.008	20	CACAAAGCTGCTCTCTTCTCC	59.367	21	280	27	306
60.544	20	CTACGCATGGTTTTCCCAGT	59.993	20	169	176	344
59.448	21	GGAATATGATCGGTCGCAAA	60.807	20	239	2	240
59.997	20	AAATCACAGGAGGACGATGC	60.081	20	182	850	1031
59.831	20	TTATCAACCCAAAACCCCAA	60.024	20	105	176	280
59.653	20	GCTAAAAGGGATTCTTGGGC	60.041	20	123	1186	1308
61.429	20	AATTTTGGAGATGGACCGTG	59.79	20	261	918	1178
59.9	20	ATCGCCTCCACCTCAAATTA	59.528	20	211	299	509
59.801	20	GCTGACTAACCCATTCTTGTTTG	60.048	23	240	917	1156
60.074	20	ATCTGAACAAATGGGCTTGG	59.933	20	205	2894	3098
59.96	20	ATACGACAGCGTGTTGGACA	60.183	20	255	1285	1539

59.861	21	CTACCCAAACGTCCCAAAAC	59.331	20	175	531	705
59.91	20	TTTTTGAATGGTGGGGGTAA	60.024	20	207	229	435
59.696	21	TCTTTCTTGGAACATCTCGTCA	59.853	22	255	595	849
58.922	20	CCTGGTTCATTTCAGGGAGA	60.042	20	155	211	365
60.142	20	AACACACAAACGAATGGCAA	60.011	20	275	404	678
60.241	20	AGGAAACCTTAAAGGGCCAA	59.939	20	256	1135	1390
60.129	20	GTGGTGGTGTGCGTTCATTA	60.436	20	176	185	360
60.081	20	TGAACATGCATCCAAAGGAA	60.049	20	214	214	427
58.605	23	ACCTGGAAACGCATATGGAG	59.955	20	260	2	261
60.056	20	CCTTTTCTGCATTTGGTGCT	60.249	20	251	584	834
59.875	20	GGGCTATCGACCTCTTTTCC	60.039	20	239	496	734
59.903	20	AACAGAGGCATTCCATGAGG	60.073	20	129	355	483
59.845	20	GCTTGAAGCGAAAAAGGAGA	59.708	20	218	228	445
60.79	20	CTCACCTGCACACACATTCA	59.265	20	280	1181	1460
59.989	21	AGATGGGGCTGTTGTGAAAG	60.111	20	244	2085	2328
59.789	20	TCAGTCAACCAACCAACTGC	59.726	20	212	21	232
58.601	23	ATTGCACCTCGTAAACACCC	59.859	20	111	22	132
60.042	20	AACTGGGAAAAGGAAACGGT	59.842	20	171	1532	1702
59.847	20	TTTACACCACAAAGTTGCCG	59.627	20	184	790	973
59.722	21	AAGGTCCTTCTCATTGGGCT	60.074	20	142	25	166
58.32	21	CCCATATTGGCAAGCATTTC	60.289	20	100	21	120
59.127	20	AACTCAACAACCCGTGAAGC	60.156	20	225	94	318
60.134	20	CGCGTGACAAATTCTTGAAA	59.849	20	154	275	428
60.175	20	AAGCCAGGCAGCATAAGAAA	59.982	20	212	47	258
60.833	20	TGCTTGACAAGTGACATTGAAA	59.366	22	146	446	591
59.948	20	ACTTGCAAATTACCAAGGGA	57.217	20	126	162	287
60.008	20	ACTGAAGCTCGAACCCCTCT	60.393	20	238	248	485
59.933	20	GTGGCAGGAAGCATTCACTT	60.263	20	260	1169	1428
59.875	20	ATGGGGAGGGGATATGGTAA	60.224	20	130	239	368
60.046	21	TGGTCCCTAATTCAACTTTTGC	60.344	22	208	68	275
59.742	19	GCTGGTTGCATACTTGCACA	60.876	20	205	8	212
58.315	21	TGATTCCTCCTACGGACCTG	60.065	20	159	2913	3071
59.882	20	TGTGCACTCGATGATGTTTG	59.248	20	235	2657	2891
60.06	20	CCAAACAACTCCCTACCGAA	59.964	20	233	481	713
60.064	20	TGTCACAAGCTCTTCATCGG	59.984	20	269	334	602
60.041	20	CTGATGCATGTGGTAGGAGC	59.271	20	220	4028	4247
60.238	20	CCATACAAAAGCGCCAAACT	60.131	20	188	1967	2154
60.244	20	CAATTGTAGCTCCTCCTAATTTCC	59.564	24	181	416	596
59.823	20	CCCAACATCATCCCTCACTC	60.326	20	174	150	323
60.448	20	GGTGGGCTTTTCTGACTCAA	60.232	20	271	19	289
59.587	20	AATTTTGGCAACCGATCTTG	59.938	20	212	2767	2978
60.044	19	CTACCCTTACCTGTCTGCCG	59.751	20	246	186	431
59.96	20	TCAAAAACCACAAACCACGA	59.981	20	222	445	666
60.277	20	GGCGGTATGCACTCAAAGTT	60.14	20	218	782	999
60.13	22	TTGGGTTTTGATGATTGCTTT	59.442	21	265	1016	1280
59.962	20	CCACCAAACCAGAAGCAGTT	60.149	20	161	3169	3329
60.151	20	TGTGGCCTTTTGTCACTTCA	60.278	20	280	131	410
60.449	20	ATGCATTTGGGAGGACAAAG	59.933	20	219	368	586
59.377	20	AGTGGAGTAGGCGGAAGGTT	60.132	20	277	832	1108
59.971	20	TTTAAAATGGCCTGTTCCCA	60.294	20	204	10	213
59.917	20	GGACGTCCAAAAACGGAAAT	61.08	20	231	455	685
60.003	20	GGGACTACCGTGATGGAAGA	59.927	20	138	76	213
59.875	20	CAAGTGAAATTGGATGGTGCT	59.985	21	219	355	573
60.431	20	GCTTGTTGTTCAAGCTGCTG	59.788	20	245	200	444
59.955	20	GGTGCGGGATCAATAGGTTA	59.784	20	203	4270	4472
59.869	20	AGGTGGGAGTGGAAACACAC	59.859	20	273	524	796
60.235	20	GTTGCTGTTCTGACCCGACT	60.307	20	140	465	604
59.846	20	CGGCATGATGCAGTAAGAGA	59.972	20	261	3250	3510

59.974	20	TCAAAATCCTGCCTTGTTCC	60.051	20	238	61	298
59.462	21	CCTTAAAACCCTCCTCGGAT	59.415	20	251	619	869
59.861	21	AAGGGCTTTGTGCATGAGAC	60.263	20	267	947	1213
60.074	22	TGCCTCAACTTTGTGTGCTT	59.49	20	264	1320	1583
59.894	20	TTGACATGTGGCATTGTGTG	60.003	20	155	1948	2102
60.315	20	TGTTGCACATTGCTTGTTGA	59.877	20	241	2179	2419
60.255	20	TCACAGGCAAATGACCAAGA	60.24	20	248	258	505
59.23	20	CTTCCACATGGATGAAGTGC	59.09	20	280	582	861
60.227	20	GAAGGCATGGCTCAGAGTTC	59.957	20	208	397	604
59.41	20	ACACCATGGTTTCCAATGCT	60.24	20	276	6	281
60.003	20	CCGTGATGGAACAACCTTCT	59.966	20	133	76	208
59.903	20	AATTCACAAGCTCACAAAACG	57.947	21	244	483	726
60.025	20	CCTAGCAAGGCTTCCATCTG	59.971	20	194	129	322
59.82	20	AAGGTGAAAGAGACATCAACCAA	60.026	23	105	539	643
60.155	20	CCGCAACTTGACAATGACAC	60.16	20	261	246	506
60.034	20	CATTATCTCAAACGAGCGGC	60.742	20	246	166	411
60.223	20	TGAATTGGCCTAAGCGAAAG	60.335	20	167	210	376
60.154	20	CGAACAAGAGTCTTCCGAGG	59.982	20	142	589	730
59.109	20	AAAGGCTCCTCTCTTCAGGG	59.95	20	163	2437	2599
60.755	20	GGAACTGCACAGGGTGATCT	60.12	20	133	617	749
57.15	24	GCAATGCATCAGAGACTCCA	59.95	20	228	161	388
59.955	20	TCCTAGGCGCTATTGAGGTG	60.365	20	276	92	367
59.065	20	CACATAAGCGAAAACGCAAA	59.88	20	237	3694	3930
58.927	26	TTAGTTTCATGAATGGAAGTGAAT	57.035	25	100	5	104
60.033	20	GGATCCTGATTCTCGACCAA	60.011	20	233	206	438
59.893	20	TGGAATTGCTACACCTGCAT	59.152	20	203	623	825
57.617	26	TGTTGACGAACGAGACAAGG	59.873	20	228	60	287
59.708	20	TTTCGACAAATCATTGCAACA	60.103	21	211	1310	1520
59.702	20	CGAGCACAAGTTCTCCACAA	60.025	20	131	2556	2686
60.018	20	AAGGCAGCATGCTTGAAACT	60.022	20	260	2003	2262
60.156	20	GGAAGTCCTGGCATTGTCAT	59.934	20	242	225	466
59.415	20	TAGGGATTTTGAAACGGTGC	59.938	20	264	27	290
59.673	20	TGGACCATTTGTGCACTTGT	60.008	20	262	1649	1910
59.801	20	AATTGCCCCTACATGCTGAC	59.962	20	242	387	628
60.31	20	TTTTGTGATTCAGGGTTCCG	60.863	20	280	221	500
60.172	20	TTGGGGATGAGATGGGAATA	60.088	20	227	6625	6851
60.145	21	AATGGCCCAGATTTGTTTTG	59.801	20	145	30	174
59.635	20	CGAGAAAAGACAAAGAAGGGAA	59.865	22	103	1325	1427
60.49	20	CATGAAGTGAAAGGGACGGT	59.966	20	259	9	267
60.159	20	CGTAGTTTAATTTTGCCGGG	59.489	20	209	871	1079
57.037	20	CTTGCGAGCAACTTGTCAAA	60.172	20	224	280	503
60.212	23	TTGGAGTCCATGAGCATCAG	59.787	20	268	36	303
60.074	20	GGGGTAAAATCGAGGGGTAA	60.013	20	221	1423	1643
60.397	20	TTGGGGAATGTTGAGAAGGA	60.43	20	269	966	1234
60.111	20	TGCTGGCATCAAAATTGGTA	60.073	20	184	560	743
59.753	20	AAGAGAGGACACCTCCGGTT	60.111	20	160	198	357
60.112	20	GAGTTGCATGATGGCATGAG	60.233	20	138	230	367
60.177	20	TTAGGGATTAAAAGCGGCAG	59.341	20	219	88	306
58.494	26	CTTGTGAAATGAATGCACCG	60.111	20	172	535	706
60.088	20	TATCGTTTTGCCGCCTTATC	60.061	20	256	1129	1384
59.81	20	GCACGCATTTGTGATTTTTG	60.118	20	217	1	217
60.128	20	GAGTTTGAGGCCTGACGAAG	59.989	20	126	262	387
58.935	23	CACAGTTCACCCCCATTTTT	59.688	20	224	198	421
60.241	20	TTGAGGTGTGGCTGGTATTG	59.566	20	238	214	451
60.461	20	GCAAACCACGCCAAATAGAT	59.967	20	252	567	818
60.06	21	GCCAGCAATAATCTCAGTGGA	60.228	21	264	700	963
60.312	20	CCTAGGCATACCAAGCCATC	59.551	20	154	1	154
60.176	20	TGCATGGCAAAGCTTCAATA	60.356	20	233	1032	1264

59.784	20	AGCCGATAAAAATGGCACAC	59.967	20	231	689	919
60.241	20	GATGAGGGTTGAAGTTGGGA	59.903	20	250	335	584
59.982	20	GATGATGAAGGCCAGACGAT	60.042	20	261	350	610
60.766	20	CAGAATGGTGGCAACAAAGA	59.691	20	133	586	718
60.046	20	TCGGAGACGAGAGAGGAGAG	59.81	20	190	574	763
59.614	20	CCAGGGCAGTTGTTTCAAAT	59.971	20	238	307	544
60.048	20	CCTCACTTCACCCTCACCAT	59.962	20	138	786	923
59.234	20	CGGGGTCGTATCATATTTGG	60.031	20	115	475	589
59.517	20	AATTTGATTGATGGTTTCGGA	59.264	21	105	130	234
60.975	20	GTACCAGCAGAAGACTGGGG	59.721	20	238	1407	1644
59.993	20	CGAGCATCAGTGAGACATCC	59.372	20	280	825	1104
60.146	19	CGACTCCCTTGTGGAGAAAC	59.697	20	275	251	525
60.268	20	TCCTTTTTGTATTCAAACTCAACAC	58.708	25	202	513	714
59.916	20	CAAAACCAACAGCCGAGATT	60.11	20	149	3	151
60.356	22	ACGTTTTGGTTGTTTGGAGC	60.015	20	162	2397	2558
59.826	20	TTTTTGACTTTTTATGGGGGT	57.539	21	264	198	461
58.385	22	AATAAGGGGGTGCATGTGAG	59.813	20	175	225	399
59.933	20	CGATGTCCAGAGGAACAACC	60.51	20	170	146	315
59.992	20	TTTGTGTCGCAAGGTGAGAG	60.025	20	267	2663	2929
59.685	20	TTTTCTTCACCCAAATTTAATCG	59.404	23	276	487	762
59.972	20	GACGAAGAAGGTGTTGGTGG	60.545	20	264	197	460
59.74	20	TTGACAATATTTAGTGTTTTGACAT	58.99	27	173	543	715
58.729	25	ACGCGTTAACTAACCGGGAT	60.741	20	261	1134	1394
59.969	20	GCAGGAAGAGAGGAGAGGGT	59.952	20	230	742	971
60.15	20	GGCATGTTTCGAGTTTGGTT	59.978	20	233	313	545
58.995	24	GATTCCGGGTTCAATACTCG	59.387	20	280	484	763
60.261	20	GAAGCTGCATTGGATGAACA	59.805	20	158	2124	2281
59.722	20	GGTTTCGTCATAAGGCGGTA	59.96	20	264	538	801
59.951	20	CAAATGTCTTCATCCCCACC	60.173	20	275	1652	1926
60.436	20	AAACCCCCTCTTAAGTCCTGA	59.088	21	254	292	545
60.081	20	CACCATCACCTCCTTCCCTA	59.92	20	241	960	1200
60.006	20	GTGGACGCTCCAGATTGTTT	60.119	20	113	29	141
60.045	20	GCCGATGATTTGCTACGATT	60.067	20	183	2942	3124
59.957	20	TGCTCACTCATCCTCCAGTG	59.98	20	219	699	917
60.042	20	ATTATCCAGTTTGGATTTTGTTCT	57.292	24	135	1896	2030
59.041	20	GTGTACCCTGAGGGACGGTA	59.844	20	146	93	238
60.181	20	AGTGGCATGATAATAGCGGC	60.088	20	255	419	673
60.299	20	TTTTAATGCTTTTCCGTGGG	59.937	20	190	2093	2282
60.044	20	TGGAAAGGTACGAGGTGGTC	59.966	20	187	402	588
59.805	20	TCAGCTTCAACATCACCAGC	59.992	20	264	1859	2122
59.901	20	CTATGTAGGGGCGTGCAAAT	59.982	20	203	29	231
59.592	20	TCTTTCATTCAACGGTATTGTCA	59.505	23	193	629	821
58.721	20	CCAATTTGAATGGTTATCACCTG	60.457	23	102	628	729
60.012	20	CAGCTCATCGTGGATGCTAA	59.972	20	170	1187	1356
60.453	20	ACCATAAGGCGCACAAAAAC	60.003	20	141	1193	1333
59.71	26	GTCAAAGAGACAGGGGTTCG	59.697	20	252	10	261
60.69	20	TGCATCCAACGCTACAAATC	59.694	20	143	38	180
60	20	TTTTAACTAACTCCGGCCCA	59.581	20	175	739	913
60.001	20	GTTTGGACAGATTGCCTGGT	59.973	20	272	1005	1276
59.499	20	ATGGCATCAGGAGGATCAAG	60.034	20	254	2279	2532
60.269	20	ACCAATGGTGGTATGGTGTG	58.984	20	132	181	312
59.679	21	TCTTGGAGCGACTCCTCACT	60.135	20	245	929	1173
59.694	20	GTTTGCTGACGCAGGGTATT	60.14	20	210	501	710
59.992	20	GATCGAACGGGTTCACCTT	59.918	19	175	2468	2642
60	20	GGCACACATTATGGTTTGGA	59.251	20	251	163	413
60.05	20	CCACATCGGTGAAGGTAACA	59.415	20	200	210	409
59.67	20	TTCACACCTCACCATTCGAG	59.676	20	161	443	603
59.851	20	ATTGTTCTTTCCCGTGCTTC	59.174	20	274	1937	2210

59.257	20	TGAGTCAGCACTGTGGTTCC	59.872	20	155	409	563
60.088	20	TTCCCTTTACTTCTTCCCCC	59.393	20	265	495	759
60.255	20	AGAAAAGAGTTTCAGCGCCA	60.132	20	214	1078	1291
59.805	20	AGCAGCTCGATGGAGGTAGA	60.119	20	246	2153	2398
60.321	20	GGGATAGTATCGGATCGCAA	59.885	20	129	69	197
59.24	21	AGAGTGATCAACCGATTGCC	60.081	20	200	14	213
59.924	20	TTGTGCCACATTTTTCCTGA	60.088	20	185	742	926
59.964	20	AACCCCACCTGTGCTAACTG	60.028	20	190	429	618
60.159	20	TTTGGGACGCTCTATTCTGG	60.206	20	108	258	365
59.705	21	CCGTCAACCAAACGTATTCTC	59.485	21	276	720	995
59.982	20	CCTGCACCAAATTTTCCATT	59.801	20	131	158	288
60.757	20	TCTATATGCCCAAGCCAACC	59.923	20	259	601	859
59.894	20	TGCTCATGAAATATCGTTGG	57.162	20	223	267	489
60.605	20	TGTCCCCGATAAAAGAAGGA	59.5	20	279	1149	1427
59.762	20	TTTTAAATGGACGTAAATGGATTG	59.218	24	126	15	140
59.924	20	TTTAAAGTGTTGAGCGCGAA	59.625	20	235	60	294
59.955	20	CGTTAGTCGTTCCTGGGCTA	60.262	20	189	2968	3156
59.927	20	TTTTGAGGTTCGGACCAGAC	60.088	20	181	265	445
59.097	20	CCTGATTAGAAGATGGTGATGAAA	59.502	24	207	740	946
59.915	21	CGCAATTATATTAACTTTGCGTCA	60.375	24	268	1478	1745
59.989	21	CCACGTGGAATTATGGGAGT	59.67	20	177	1708	1884
60.081	20	AGAGACTGTTGAAGCTCGGC	59.751	20	239	34	272
59.903	20	TCCTAGTGTCTTGTCTCCCACA	59.762	22	183	1017	1199
61.201	20	AATCGGCAAAAACCACAAAC	59.845	20	220	741	960
59.813	20	TGCTGAAGAATCTGACACCG	59.984	20	276	217	492
58.019	20	GTGATTCCTGAGGCCATGAT	59.893	20	229	1692	1920
59.415	23	GTTCCTGCTTTGTGGTGGAT	59.973	20	277	966	1242
59.942	20	GTCCCAACTGAAGTTCCCAA	59.943	20	166	283	448
59.651	20	TCCACAATGGAAAAATGCAA	59.907	20	209	2756	2964
59.992	20	TGCTGGTGATCAAGTGGAAA	60.24	20	254	367	620
59.955	20	CTGGAGCGGTAATCACAAGG	60.647	20	147	566	712
59.367	20	ACCCGAGACAAAAACCACAG	60.005	20	163	10	172
59.955	20	GTGAGGGAATGCTCTCCAAG	59.803	20	280	83	362
59.483	20	TTCCTCCAGAGGCTCAGTGT	59.986	20	203	2805	3007
59.945	20	ATACCTTTCTTTTTCCCGCC	59.442	20	182	2231	2412
59.827	20	GACCAGAACCTAATCTTGGGA	58.108	21	270	536	805
60.154	20	AAAAATCAAAGGCCCACAAT	58.418	20	264	591	854
59.942	20	CGTGTTATCCTACAGCCCGT	60.015	20	217	2625	2841
60.044	20	TACTCAATCAGCTCCAGCCC	60.362	20	202	1992	2193
60.073	20	CCCCTCATGTTGGTGGTAAT	59.526	20	271	255	525
59.988	20	AACATCATCGAGGTCGGTTC	59.934	20	192	919	1110
60.214	27	GAGACCAATTTTGCTATGTAATTTT	58.304	26	226	234	459
60.444	20	GAAATAAGGATGTGTTATGAAGG	59.656	25	145	512	656
60.118	20	AAAGAAAGCTTCAAGCAGCG	59.904	20	135	122	256
61.296	20	CCAAGCCTGGAGACCTAAGA	59.425	20	220	20	239
60.34	20	TGAGAATGGTGGGTGTGAAA	59.935	20	231	622	852
59.934	20	AATGCAAACCAGTGAAAGGG	59.971	20	166	1158	1323
60.088	20	CAGATTCTGGCACTGAGCAA	60.136	20	275	5356	5630
59.957	20	CACTAGATTTCTGCACCGCA	60.011	20	275	237	511
60.074	20	AATCTTGGGTCCAAACCCTC	60.169	20	230	248	477
59.691	20	GCTTGCTTCCACCAGGTCT	60.402	19	279	155	433
60.173	20	CGTCCATGCTCTGTTCTTCA	59.984	20	134	887	1020
60.17	20	TTCAGCCTCCATTTACCTCA	58.298	20	255	2688	2942
58.028	22	ATCGAGATGCTCTGATGCAA	59.507	20	277	20	296
57.372	25	AGCTAGACACGTGGAGACGC	60.621	20	249	931	1179
59.902	20	AGGGGAACGAAAATCTCTCC	59.513	20	221	2789	3009
59.575	24	TGGGTGATCAGGAAAAATCA	58.897	20	171	60	230
59.133	20	TGCGAGTGTTGCATCTGAAT	60.423	20	236	314	549

60.397	20	CCACGAAGAACCTGGTTTGA	61.064	20	277	866	1142
59.727	20	GGAGGACACCATTTCTCTGC	59.661	20	182	7747	7928
59.579	20	ATCGAAATCTAAACCCGCAC	59.046	20	251	672	922
60.324	20	TGAAGTTAGGAAATAAGGAGGTG	58.743	25	276	558	833
60.011	20	ACACAAGTATGACCAGGGGC	59.851	20	182	19	200
59.951	20	AAGAAAGTATCAGGCGCATCTT	59.42	22	187	26	212
59.973	20	CCGAAGGCAACACCACTACT	60.171	20	266	2007	2272
59.109	25	TGTTGAACGTGTACGTTGGG	60.463	20	228	590	817
60.223	23	AGCACGTGTGAATATTGGGC	60.925	20	255	299	553
59.779	20	CCTTCACACGATTGGAGCTT	60.255	20	275	660	934
59.803	20	ATTGTACACATGGTGTGGGC	59.143	20	151	1611	1761
59.874	20	TTTAGTGGCTGGAACCGAAG	60.241	20	220	517	736
60.205	20	TGGCTCAAAAAGTTTCATATTTCT	60.022	25	119	1980	2098
59.922	20	AAAAAGCCGCACTTACGAGA	60.018	20	251	11	261
60.187	20	TTGGGTTAATCCGTGTAATCG	59.707	21	230	361	590
60.543	22	AAGGAGGAGGTGAAGAAGCC	59.817	20	265	23	287
59.369	20	TTGGAGAGTTGGGTACAAGC	57.797	20	135	176	310
60.033	20	TGCATGCCGCATACTATTACT	58.368	21	241	1620	1860
60.615	20	TTTCCTCTTCCGATTTTTGG	59.131	20	253	918	1170
59.801	20	GATGTATGTGCGATGGGATG	59.763	20	179	825	1003
60.158	20	CCCCCAATTTGTTTTACTCG	59.311	20	223	1381	1603
59.984	20	CCTAATAAAATGGCCATGCG	60.295	20	147	1623	1769
59.875	20	CTTCTGGTTCCAGCAGCATT	60.397	20	124	252	375
58.94	20	CGGAGACAAAGGGTCATTTC	59.526	20	239	174	412
59.926	20	CCGCTGACAAACATCATCAC	60.12	20	230	5360	5589
60.177	20	CTCGATCAAGACCCTATCGC	59.797	20	183	1073	1255
59.989	20	TCGGATTAAAGCTAGGGCAA	59.81	20	279	1048	1326
60.008	20	AAACGAATCTGTCGGTGGTC	59.973	20	264	2696	2959
59.971	20	CAAACAAAAGGGCCTTCTCA	60.22	20	236	962	1197
60.232	20	TGGTAGGTTTTGGAGGGTTG	59.824	20	280	659	938
60.052	20	CACTCGAACCAGTCAAACGA	59.873	20	228	732	959
59.847	20	GACCACAACCAACCACATGA	60.27	20	246	742	987
60.096	20	CTCACGCGAGGTCTTTCTTC	60.134	20	153	34	186
60.089	20	AAATAGATCTTTTGTAAAGCCCG	58.02	23	112	2970	3081
58.813	25	ACAAATTTGCAGATGGAGGG	59.933	20	198	41	238
59.935	20	GATGAGGAAGAAAGGGAGGG	60.008	20	253	1010	1262
59.923	20	CGTGGCCTTGATTAAAATGG	60.315	20	201	442	642
59.091	20	GGAGGGAGAGAGGAGGAGAG	59.489	20	251	149	399
59.542	20	GCATCGTCTCAACCCTTGAT	60.081	20	184	660	843
59.831	20	CTCCCTCCAAATCGTTGCTA	60.206	20	101	634	734
61.146	20	TGATAGGGCACACAACCCTT	60.375	20	280	520	799
59.993	20	TGAGATATTTAAATCCTTCCGTTT	57.452	24	249	99	347
60.349	20	TCGTCCTTTCGACATTCTCC	60.195	20	169	2049	2217
60.366	20	GACTCCCATTCCCAAGCTCT	60.596	20	216	2437	2652
59.923	20	CGGATTTCGGAATTGATGA	59.415	19	215	634	848
59.978	20	GTGCCTTCTTCTAACTGGCG	60.015	20	220	502	721
60.053	20	TTCGATTCAACAAAGTCCCC	59.91	20	224	272	495
60.169	20	CTGAGACCCCTCATGTTGCT	60.261	20	197	425	621
60.081	20	TCCAAGTTGCCTTTCAACCT	59.711	20	173	623	795
60.074	20	AATTTGCATTGGGTTTCGAG	59.938	20	108	279	386
60.02	21	CTTCGAAGCGATGGAGTAGG	59.971	20	101	20	120
59.861	20	GTCTCCATGCTTGAGCCAAT	60.226	20	277	431	707
59.415	20	TAATTAAGTCATAGAGCAGGGGC	58.853	23	100	24	123
59.716	20	TCACGTCTTGTTGCATCACC	60.733	20	210	578	787
60.144	20	AGGTGGAACAAGTAACGCAA	58.283	20	207	449	655
60.074	20	TGAACCGGGTCTCTCGTAAC	60.111	20	174	2646	2819
58.214	20	CAGCCCTCAGATTTTAGCGA	60.481	20	277	410	686
60.634	20	TCGGTTGACCGAAAATAGGT	59.429	20	200	85	284

59.645	20	GGATGTTTCATTTTGCCTGG	60.309	20	249	559	807
59.885	20	TCCTCCATTTCCCACAACTT	59.381	20	230	293	522
60.088	20	GGCACATCGTGTGAATCAAG	60.12	20	162	242	403
59.871	20	CGGACGTTAAACGAAGGAAA	60.103	20	280	287	566
60.439	20	TTGTTGTAGTATGGCAAGATCCA	59.527	23	199	383	581
60.095	20	CCCAAGGCGAGCTCTAAGTT	60.884	20	201	139	339
59.48	26	CAGTGTAAAACCTTATTGGGGG	59.641	22	268	123	390
59.241	20	TCAATGCTCTTTTCAACCCTTT	60.109	22	209	403	611
60.214	21	TATCCTTGGATGGAAATCGC	59.862	20	183	805	987
59.365	22	ACTTCCCAGTCGTGGATGAG	60.112	20	210	337	546
60.119	20	TCCTGAAGAATTTCGGCATC	60.155	20	250	250	499
59.989	20	CCCCTAATCCGAACACAAAA	59.795	20	158	778	935
59.972	20	CCTCCCCAAATATCCCGAAT	62.062	20	278	2455	2732
59.927	20	AGTTCAATAGAGGCAGCGGA	59.978	20	217	797	1013
59.964	20	ATCGAAGATGAAAAAGGGCA	59.645	20	151	247	397
59.956	20	AACGGCCGAGATTTGTTATG	59.96	20	255	577	831
59.044	22	CGATTTCTACACCATTGTTCCA	59.861	22	211	2363	2573
58.227	20	GTTCGGGTGTGCAAAAATTC	60.352	20	275	361	635
58.571	24	AGGTGAATCCGATGATGAGC	60.042	20	181	3	183
60.074	20	CTCTTCCCTGCAGATGATGG	60.758	20	280	1442	1721
60.103	21	ATGACTTCCAGTGCCAGGAC	60.12	20	175	894	1068
58.808	22	TGCTCCAAAATGATTACGTGG	60.871	21	280	575	854
59.997	20	CCCGACAATTTCACCCATAC	60.051	20	234	239	472
60.019	24	CGTGGTACTCGAGCTGTCAA	60.049	20	219	8	226
59.967	20	CTGCTCCTGGAGTACATGACAA	60.312	22	228	309	536
59.734	20	TTGACACGAATATGACACAAACA	59.003	23	191	276	466
60.065	20	CTGCATCACCTTGCTTCTCA	60.136	20	177	733	909
60.34	20	GCTAACCCTCCGCTGTATGA	60.235	20	269	902	1170
60.005	20	AATGCTTCGGACTTGCTCAT	59.843	20	273	714	986
59.936	21	ATGCAAGAAAGACGTGGGAC	60.119	20	278	410	687
57.736	20	AAGACCCTTGTGAGTGGTGG	60.002	20	215	24	238
57.865	20	GGATAGGCGGTTGAGATTTG	59.528	20	221	1491	1711
60.13	20	TTGTTGTGATGTGAAGAATTGTAA	57.312	24	190	270	459
58.881	24	AAAATCAAAGGCCCACAATG	59.801	20	119	1264	1382
59.751	20	CACAACCAAACCAACCATCA	60.255	20	236	1730	1965
60.191	20	CTCGGATTTGGGTTTCTTCA	60.044	20	231	1278	1508
60.012	20	TTGAAACGGAGGTTTGGTGT	60.388	20	207	493	699
59.07	25	AAAACCGATGCAATTATGCC	59.801	20	280	101	380
60.059	21	CCGTTTGCAACAATTGAGAA	59.706	20	246	1465	1710
60.315	20	CAACATGTCGGCATGATAAA	57.988	20	246	286	531
60.3	20	GCATCGTTTATCCGATTGCT	60.067	20	248	16	263
59.996	20	TGTAAAATCAATGCACCGGA	59.93	20	252	473	724
59.993	20	ACAGGGGAGAGAGACAAGCA	59.986	20	192	36	227
59.995	20	CGCTGGTTTTGGAGATCAAT	60.074	20	157	526	682
59.745	20	TATAAACGCTCGTCTGCTGC	59.234	20	206	42	247
60.153	20	CAAGGGTAAGGGAGGTGACA	59.959	20	210	750	959
60.407	20	ACCGATCTCACCCCTTTTCT	59.935	20	134	585	718
60.008	20	TGAAAAGGCTTCAATTTGGG	60.046	20	184	679	862
59.836	20	GAAGAGTGTTTGGGGCTGAA	60.232	20	153	2110	2262
60.22	20	CCTTCATTGGGCAGTTTTGT	59.971	20	215	297	511
58.028	22	TTGCTTTGGGTTCAAATGGT	60.344	20	271	16	286
59.425	20	CACTTCAACACTCCCCACAA	59.565	20	267	2814	3080
59.988	20	ATCGGTTATTACCGGATCGC	61.031	20	157	601	757
59.373	20	CCAATTTGAATGGTTATCACCTG	60.457	23	253	450	702
59.848	20	TCGAGTTAGCGTGTCGTGTC	60.056	20	123	306	428
59.707	21	GTGGAGGGGGAGTATGGATT	60.015	20	265	140	404
59.224	20	CAAATGACAGAATCGCGGTA	59.688	20	246	95	340
59.49	21	GCAGTCAAAGGAGGAAGACG	59.989	20	269	573	841

60.012	20	AGTTCACAACCCTGAATGCC	59.973	20	168	690	857
59.797	20	GAAATGTTCACACACGTCGG	60.008	20	221	262	482
60.332	20	ATTGGCAATTAACCGTCAGC	59.967	20	124	394	517
59.853	20	GAATTTTGCCACCGATGTTT	59.807	20	109	1638	1746
60.088	20	CCTTGGGCAACTCACTCATT	60.111	20	262	42	303
59.955	20	TCCGGCAAAAACCAAATTAC	59.81	20	240	2671	2910
60.285	20	GTGGAGGGTTTTTGTCTCCA	59.943	20	278	3387	3664
60.073	20	CCATTGTCGTCTCCAACCTT	59.966	20	226	877	1102
59.894	20	TGCTGCTCTTTTCTGGGTTT	59.993	20	133	77	209
60.041	22	GCTTCAACGGTATCCAGTAACA	59.158	22	125	1000	1124
59.926	20	GATGCCAACGTCATATTTGC	58.997	20	252	3617	3868
60.073	21	TTGGCACGAAATTAGTTGTTTG	60.034	22	214	221	434
59.352	21	TCCCCCTCTCTCTCCTTCTC	59.883	20	127	10	136
59.146	20	TGTTGCAGCTCTTGCTCTTG	60.472	20	279	137	415
59.997	20	TTTACGTGTTTGCGGATTTG	59.603	20	258	276	533
59.996	20	GGCCGTTTTAAAATCGAGTG	59.586	20	206	703	908
59.906	21	AAATGCATGCACCTGATTACA	59.055	21	169	913	1081
59.697	20	GAGCTGTTATGCGTTTTGATGA	60.272	22	238	1700	1937
60.331	20	GGTTTAACTTTTCAAATGGAACAA	58.903	26	276	144	419
59.95	20	GGGCCTTGAAGTTCTCTGTG	59.844	20	134	271	404
59.986	20	ATCACCTCATCACCGCCTAC	59.957	20	222	191	412
60.081	20	ATGAAACACCCCCAAACAAA	60.066	20	208	3583	3790
59.41	21	ATCCGGAAGGTCCAAAACTT	59.805	20	221	564	784
60.218	20	TCCAACACAAAACTCTAAATTTTC	59.821	25	228	537	764
58.561	25	CGTCGAGAGATGCAACGTAA	60.011	20	106	8	113
60.104	21	CCTCACGTGATATTTTTAGCACA	59.197	23	188	914	1101
59.926	20	CGACGTTGCAAGAAAAGGTT	60.284	20	218	293	510
60.552	20	TGCAATGTACAGCAGAAGTGG	59.92	21	268	458	725
59.993	20	CCTTTCTCTCTCTTCCCCGT	59.811	20	158	35	192
60.06	20	CCAATTTGAATGGTTATCACCTG	60.457	23	130	807	936
60.014	20	ATCCCCTTCTCTTTCCCGTA	59.897	20	179	1209	1387
60.272	20	TAAAGGTCGAAAATGGCGAG	60.202	20	186	254	439
60.112	20	TCCCCTTTTAAGGTTGATGG	58.876	20	269	1063	1331
60.003	20	ATTAGGAAAAGGGGCAGACG	60.443	20	158	1269	1426
60.263	20	GCAGCACCCTTTCTAACAGC	60.022	20	167	2995	3161
60.255	20	TGCAACCATGAAAACAAACAA	59.999	21	275	3149	3423
60.051	19	TGCCGGAAAACACCAAAATA	61.214	20	280	390	669
59.929	20	ACGTGTCAGAATCTGGGCTT	59.727	20	223	611	833
60.203	20	CCGGTTCTCCTATCCGATTT	60.278	20	175	628	802
60.144	20	CCACTTTTGAACGTGTGTGG	60.041	20	249	2452	2700
61.304	20	GTTAAAAGTGGCAAGCGACC	59.752	20	247	145	391
60.567	20	GCTTGAGATGGACTACCGGA	60.218	20	279	45	323
60.035	20	TGGAATGAAGGGGTGAGATT	59.336	20	265	77	341
59.825	21	GCTGCTTTCTCGCTCATTTC	60.243	20	230	1377	1606
60.081	20	TCGCCCATTTTCTCAACTTC	60.192	20	272	685	956
59.95	20	ATCGGTTATCACCGGATCG	60.697	19	175	3832	4006
60.043	20	GGGATTCAGGAAACAGGACA	59.903	20	256	3394	3649
60.159	20	GCCGCAAAGACTTAATCTCG	59.982	20	150	972	1121
59.942	20	TTGCCACGACCAAAACCTAT	60.365	20	274	263	536
60.603	20	GCATCCTCCACGTTACCATT	59.82	20	157	269	425
59.72	21	TCCGACCTTGAAGAATGAAGA	59.799	21	279	951	1229
59.875	22	ACGACATACACAAGGGGCAT	60.263	20	233	661	893
60.261	20	GCATTGAATGAATGGAGGTTC	59.382	21	169	39	207
60.103	20	CGGATTTAAGGGTTATTACCTGAT	58.81	24	231	1785	2015
60.158	25	TCTGGAGGAAAGCACCAATC	60.195	20	114	19	132
60.017	20	TTTTCACCCGACAAATCACA	59.941	20	262	305	566
60.218	20	AACCTCATTGATTTGCAGGC	60.081	20	248	593	840
60.128	20	CTGCATCTTGTGTCCTGGAA	59.831	20	269	1370	1638

57.857	24	TGAGATTTGGGCAAGCTTTT	59.823	20	255	288	542
58.287	23	TGAAATCCAAATAGGTTAGAATTG	59.664	25	198	1012	1209
59.593	20	TGATATATGGCGTGTTGCGT	59.983	20	224	2209	2432
60.272	20	CGCTGGTTTTGGAGATCAAT	60.074	20	159	525	683
60.032	20	GGAAGGCAAGGAAACAACAC	59.574	20	272	578	849
59.973	20	AATTCTTGCACGCCATTTTC	60.081	20	237	653	889
60.11	20	CACGAAACGAGATCGCAATA	59.833	20	186	10	195
59.931	20	TGATTCATTTTCTGCACGGA	60.197	20	190	131	320
60.118	22	AATCGTGCTATTTTTGCCTGA	59.734	21	238	254	491
60.11	20	TCCTTGGCTGACTAGGTGCT	60.012	20	164	977	1140
59.127	20	AAAAATATGGCATCCCGGTT	60.389	20	233	539	771
59.955	20	GCTTTACGAGCTGTTGTCCC	59.882	20	212	931	1142
59.984	21	TGTAGCAGCGAAATGCAGTC	60.165	20	268	1119	1386
59.047	23	TCTTCCGGATTTTAGGAGGC	60.522	20	256	10	265
60.025	20	AGTGAACCCAGTGGGAGATG	59.962	20	226	725	950
59.962	20	GGGATTCTGGAAGATGCAAA	60.014	20	264	2265	2528
59.755	21	TCTAGGGGGTTGTTGCTTTG	60.103	20	230	1699	1928
58.825	22	TTCGGTTAATCCAATGGTCA	58.818	20	251	782	1032
58.882	20	GACAAAGTTGTAATTTGCGGC	59.644	21	270	907	1176
60.11	20	ACACAAAATGGCAATGCAAA	59.976	20	271	1116	1386
60.37	20	TTTATCGCACAAATATTTTGATTTT	58.231	25	272	403	674
58.326	25	TTGGAATGAATAAATGGAATGAA	58.357	23	255	17	271
59.345	21	GCTATATTTCAACCCCGCAA	59.928	20	152	1685	1836
59.784	20	TGCCGACTTTGTGGATGTAG	59.716	20	133	85	217
59.565	23	TTTGATAAAAATTTGGCGGC	59.913	20	276	5	280
59.942	20	TTCTCTCTCTCCCTCCACGA	60.064	20	278	752	1029
60.11	20	ACATGCAGAAAGAAGCCGTT	59.882	20	263	807	1069
60.46	20	CCACTTTCAGCTCAATCTTGC	60.008	21	201	16	216
59.795	20	CCATCTGTTCACACTCACGG	60.154	20	258	2476	2733
59.989	21	TTCTCAGCAATCATCGCAAC	59.955	20	276	616	891
60.003	20	TCCAAGTTTTGAAGATGACCTC	58.293	22	275	519	793
60.224	20	CATGAGCGAGTAAACCAGCA	60.011	20	222	428	649
60.755	20	GAGTGCGCTCTGGGTAAACT	59.501	20	159	432	590
59.937	20	TGTCCCACATTGGAAAATGA	59.75	20	240	112	351
60.169	20	ACGTGGATGTTATGCACGAA	59.995	20	254	510	763
60.11	20	AGTGCAATCCTTCCAATCCA	60.461	20	185	139	323
60.776	20	TGCATGACTGGATGAAGAGG	59.787	20	240	1153	1392
59.7	20	AACCAGAGACGCAGCATTTT	59.882	20	263	2353	2615
60.028	20	AGGAATGTCCACCGAGAATG	59.927	20	154	102	255
59.933	20	CCAACGGTCCCGTATTATTG	60.067	20	268	221	488
60.894	20	TCTCTTTTTGGGATCAACGG	60.044	20	258	1596	1853
59.141	20	TGGTACCTCCTCCTAATTTCCTC	59.854	23	270	102	371
60.235	20	GCCGGTAATTTCGTGTAGGA	59.96	20	211	473	683
59.42	20	TCATGATTCCAGCTTACCCC	59.894	20	227	1986	2212
60.048	20	CAATGCTCCCTTTTCTCAGC	59.955	20	213	1097	1309
59.596	20	GAGACGCTGATGGGATTGTT	60.081	20	276	693	968
59.166	20	TCCCGATTAAAGTTTCCATGA	59.397	21	230	433	662
60.156	20	TGGTGTGAGAGAGAAAAGGGA	59.829	21	159	1606	1764
60.046	20	GACCTCCGATTTGTCAAGGA	60.05	20	268	1469	1736
58.627	21	GTAGAGAGAAGTGGGCGGTG	59.867	20	146	24	169
59.767	20	TGATGATGGAGCATTTGGTG	60.481	20	109	585	693
60.074	20	AGCTTTGATCTTCGCCATGT	59.843	20	269	610	878
60.002	21	TCGCCTGTATAAATGCCTCG	61.113	20	274	535	808
59.13	24	ACCCCTCTTCCTCTATTGGC	59.536	20	256	445	700
60.644	20	CAGATCAAAGATCCAACGCA	59.799	20	209	17	225
59.946	20	TCCATGTCTTTTTCCCTTCA	58.117	20	187	1895	2081
59.677	22	TGAAGTTAGGAAATAAGGAGGTG	58.743	25	162	562	723
59.969	27	CGCTTATAAGAGCGAGCAAGA	59.903	21	274	226	499

59.505	20	GCCCTCGTGAACATAGGAAG	59.694	20	238	3240	3477
60.465	20	TTCGGTTTTACGGATTGAGC	60.074	20	212	817	1028
59.708	20	CTCATCGGGTTAATTGGGTG	60.184	20	277	884	1160
59.937	20	TCAAACAGAGTGGGGAGGAG	60.229	20	227	288	514
60.293	20	AGCACTGGTTTTGGAAGGTG	60.149	20	272	344	615
60.321	21	GGCTCCCATTGTTTCTCATT	58.984	20	276	1326	1601
59.201	20	CAACACCGAAGAGCTTCACA	60.025	20	223	206	428
59.88	20	TAAAGGGGGACCATTTTTCC	59.992	20	244	271	514
58.679	21	TGGTGAGGATTTAACGGGAA	60.301	20	210	124	333
59.864	20	TCGTGTGATGCCTTGGAATA	60.073	20	185	653	837
60.111	20	ACTTGCTTAGTTCATGGCCG	60.27	20	135	223	357
59.767	20	AAGTGTTGTCGTTTCTTTGGA	57.376	21	266	204	469
60.096	20	TGCCTTGCCTTTTAAGCACT	60.018	20	264	1554	1817
60.173	20	CGCAACTGTTATTCGGGACT	60.132	20	246	202	447
60.034	22	AAGGGGGTTATTAGTGGATCA	57.425	21	236	700	935
60.017	20	CCCACCCATGCCATTATTAG	60.031	20	277	1192	1468
59.943	20	TGTTGGGACAAAATGGTCAA	59.792	20	222	2019	2240
59.843	20	TCTCTGTTTGCGTGCTTGTC	60.183	20	203	279	481
59.551	20	TCGAGGATCAATCTCGGAGT	59.761	20	264	1106	1369
59.986	20	TAAGTTTCTATTCGCCCCCG	61.27	20	197	581	777
59.294	21	CCATGAATTCTTTTGGGGTG	60.162	20	129	732	860
60.836	20	AAATATTGAGGTGGGGGTCC	59.881	20	146	118	263
59.883	20	AGGCTTTGGCTCCTCAATTT	60.208	20	163	530	692
60.23	20	TATTGCCCCTATCTATGCGG	59.907	20	181	563	743
60.495	20	TTAGCATAAATTTAGCCACCG	57.12	21	128	583	710
60.457	23	TAACGATGGACTAGGGGCTG	60.088	20	219	11	229
59.795	20	CACCTCCCTGGGGATTTTAT	60.011	20	194	2492	2685
59.856	20	TCGCCCATGACTACACCATA	59.948	20	230	398	627
59.844	20	TAATGTAATTGGCCCCGAAA	60.144	20	234	270	503
60.011	20	TGGTTGTAATTGCACCAAATTTAC	60.045	24	104	344	447
60.035	20	AGCGTGAGCTCATTTTCGAT	59.985	20	206	2322	2527
59.726	20	ATGTGAATAGCCGTTGAGGC	60.103	20	256	30	285
59.155	27	ATGAGTTATCACCGGATCGC	59.923	20	213	794	1006
58.787	20	CAACGACCTTCATTCGATCA	59.648	20	102	2	103
59.797	20	GATGACGACTCCAACGACAA	59.682	20	203	1266	1468
60.081	20	TGGTGAAAACCCCCAATAGA	60.162	20	242	415	656
59.982	20	ATCGTACGTATCGCCGTCTC	60.125	20	253	477	729
59.997	23	GCACTCCATTCCAAAATTCG	60.448	20	211	150	360
60.299	20	ATCCTGCCAAACCAAGAATG	59.933	20	112	35	146
60.038	20	GTGCACTTGAAATTGCATCG	60.265	20	231	177	407
59.904	20	TCAGAAACAATCTTTGTCTGTTCT	58.992	25	112	1239	1350
58.746	20	CACCAAGTGGGAAATAGTGCT	59.111	21	145	1727	1871
60.045	20	ACCCTCTCTCCACTCACCCT	60.112	20	154	2369	2522
58.747	20	CTGGCATATTTGTGTTGGCT	58.651	20	233	368	600
60.096	20	GGTAGAAGAATAGGTGCATGAGA	57.533	23	269	781	1049
60.156	20	GGACCGTGATGGACTGACTC	60.537	20	230	2853	3082
59.946	19	CGTATCATACAAGTATGCTGTCCT	59.985	25	206	50	255
60.042	20	CTGAATTGGCTTGTGGGTTT	59.971	20	225	680	904
59.296	20	GTTGAATTTTCACCCCGGTA	59.662	20	262	1519	1780
59.101	21	AAGGAGGTGTTATGAAGGGATT	58.028	22	167	1236	1402
59.945	20	TTGCAACACAAAGCACGAAT	60.302	20	183	252	434
60.11	22	TTTAGTCCATTCTTTCGGCG	60.202	20	192	1994	2185
60.015	20	GAGGCTTATGCATTGACCGT	60.103	20	193	48	240
59.483	23	CATCTTTAATGGTGGCCTGG	60.323	20	221	2165	2385
59.992	20	AAAGATCGGCACAAAAATCG	60.074	20	127	944	1070
59.976	20	TTTGGGGACAACACTGACAA	59.976	20	188	351	538
59.755	20	CAAATCCTGCGACAAGTCCT	60.255	20	232	805	1036
59.813	20	ATGTAATGCCTCGCCCTATG	59.945	20	252	9	260

59.988	20	GAAGAAGGAAAGTTTGGGGG	59.912	20	217	1294	1510
59.971	20	TTCGGTACGAAAAATCGGAG	60.067	20	267	47	313
60.375	20	GGTTCACGATTTGGGAAAAA	59.778	20	258	2487	2744
60.3	20	CACCTCCATCTCCGATCATAA	59.902	21	202	695	896
60.125	20	TGTGAGGAATCCACTCTCCC	60.048	20	270	36	305
59.845	22	CACCAGATATTTGATGCGTGA	59.557	21	154	6	159
59.95	20	ACCGTTAAAGAAACCGGACC	60.221	20	255	1152	1406
60.157	20	TTGATCGCGACATTTGATTT	59.115	20	242	42	283
60.146	20	TGAGGCATCTCTCTCTCACA	57.05	20	244	318	561
59.966	20	TGAGGCAGTGTTGTTCTTCG	60.025	20	245	1321	1565
59.981	20	CTGCCAAGGAACCACAAAAT	59.971	20	229	1265	1493
60.014	20	CGGATTTAAGGGTTATTACCTGAT	58.81	24	255	747	1001
60.224	20	TTGGCCCTACTAACTTGAGCA	59.89	21	216	1489	1704
60.111	20	TGAAGCGTCAAATCACAAGC	59.995	20	229	350	578
58.792	20	CGTTTTGCTTCTCACCCTTC	59.853	20	241	1466	1706
59.43	21	ATTGACAAGTGCAACCCTCC	59.973	20	191	1237	1427
59.512	20	TCGTGTCTAGTGCAGCATGA	59.141	20	112	4751	4862
59.48	20	TTCTCATCCAACGAGCTGAA	59.522	20	248	316	563
59.955	20	GATCCTGTAAGCTCCACCCA	60.073	20	205	228	432
60.681	20	ATATGCACTGGCGGACCTAC	59.985	20	148	267	414
60.152	20	GGATTCCGAGTTTTCGATCC	60.777	20	279	441	719
59.92	20	CTTGTCGGCAGAGGCATTAT	60.235	20	233	811	1043
59.971	20	CGACTTCGGAAGCAAAATTC	59.823	20	133	2516	2648
59.739	20	AAAATTTGGACTCACAACTTCAA	57.841	23	257	63	319
59.648	20	GTGTTGGAAGAGGGGCATTA	59.933	20	274	853	1126
59.864	20	AGCAATCGTGATAGGCAACC	60.103	20	139	2362	2500
60.209	20	ATTTAACAACGGACGAACGC	60.003	20	267	252	518
59.805	20	GATGGGTTATTGATCACGGG	60.014	20	176	3815	3990
59.727	20	TTTGACCTCCTGCAAAATCC	60.051	20	197	167	363
60.214	20	ATCGAATCGGAAAGTTCCCT	59.903	20	259	296	554
60	25	CCAAAAGTTCACATCACTCCAG	59.633	22	190	3	192
59.774	20	AAAAGAACTTTCTCCTCTGGCA	59.521	22	219	200	418
59.463	21	CTGGTCAAATCATCCGAACC	60.317	20	243	4	246
59.992	18	TATCAGGCAAATCCTTGGGA	60.405	20	228	15	242
59.565	20	GGAGGCATTCGATCTTTGTG	60.603	20	178	197	374
59.979	20	GGTTGGAGTGAGCGAAGAAG	59.989	20	226	128	353
60.074	20	TTTTTAGGCTCTCGGAGCTG	59.724	20	241	179	419
59.834	20	CCTTCGTGCAATCATCTTCA	59.799	20	194	4442	4635
59.722	20	CCCAAGAATCAGAGGTCCAA	60.042	20	186	2249	2434
60.14	20	TTGGAAAGGAAAGCTCGAAA	59.931	20	246	1454	1699
60.032	20	GAAGTGAATCAAGTGATGGCTC	58.794	22	168	31	198
60.065	20	TGGAATGTCAAGTCAACACAA	57.556	21	179	891	1069
59.898	22	CTTCGTCGGAGCAGGAATAG	59.971	20	276	218	493
60.031	20	GTCATTGTATGGTGCGTTCG	59.995	20	112	321	432
60.149	19	GTCCCATGTTGCTGCTTTTT	60.118	20	219	46	264
59.882	20	AGGCACTGGCTTGGATTATG	60.096	20	280	146	425
59.415	21	TGATTGAGGCTTGGAACAAA	59.247	20	279	1724	2002
60.043	20	TTCACATTCCTGTCCTGCAA	60.24	20	144	1112	1255
58.411	22	TTGAATGCTCTGAATGCTGC	60.104	20	260	824	1083
60.278	20	TTGAGCATGATTTTTGCTGG	59.809	20	266	493	758
60.187	20	CAACCTCAAAAATGCCCACT	59.971	20	184	796	979
59.727	20	TCGAACCACGTAAATCCTTTG	59.982	21	279	988	1266
58.975	22	CTCTCTAGCACCGACCCAAC	59.867	20	232	15	246
60.022	20	CGTTAGCCTTCTGGATCAGC	59.978	20	213	208	420
59.935	20	TGTGAAATCCGAAAAATGGA	58.94	20	245	224	468
60.12	20	CTTCCCAAAGCCAGAGTGAG	59.982	20	272	1338	1609
60.033	20	AAGGTCTCCTCTCCCACCAT	59.929	20	139	470	608
59.891	20	CACAACAAAAAGCAACCCAA	59.603	20	276	226	501

60.853	20	GCGTGGAGCATTTAGCTTTC	59.988	20	223	0	222
59.84	20	CCATAACGCACCCAAGAACT	59.993	20	188	2129	2316
59.996	20	TCTCGAGAAAACGGGATTTG	60.184	20	226	629	854
60.183	20	AAATGGTGTGATCTTGGACCTT	59.735	22	279	1834	2112
59.833	20	CAACGTAACTGGCAGCAGAA	60.05	20	235	466	700
59.595	21	GAGCCTGACTGGTGTGGTTT	60.159	20	273	401	673
59.365	21	TTTTGTCAGCAGATGTTCGC	59.995	20	274	1922	2195
59.515	22	CTTTTAGCCAGCCCAGTTTG	59.876	20	274	48	321
59.935	20	TGTGGAGCTGAAAACCACAC	59.726	20	269	1051	1319
59.654	23	TGAATGTGCATGGAGGATGT	59.925	20	187	241	427
59.873	20	TTGTTCCTACGCACTCACATT	58.296	21	259	704	962
59.405	20	TGCAAGTGTGCAACAGATCA	60.029	20	271	338	608
59.942	20	GCAAGTAACCTAGTGGCCAAG	58.917	21	174	144	317
59.989	20	CACCTTCGAGATTGCTAGGC	59.978	20	185	1681	1865
60.395	20	CCGTTTACGTTTATCCATACCC	59.52	22	164	362	525
58.919	23	AATTCGTTCGGGGATAGAGC	60.419	20	280	337	616
59.836	20	GAAGAGGAGGCAGTTCATGC	59.957	20	256	185	440
59.94	20	CTGCCTACCATTTCAGCACA	59.864	20	235	409	643
59.425	20	TCATTAAAGCTAAGGCCCCA	59.677	20	252	1571	1822
59.385	22	TTCCGTAGTTGGTTTAGGTTCTTT	59.515	24	244	691	934
59.975	20	ACCATCAGATTCATTGTGCG	59.527	20	271	896	1166
60.03	20	TCACCTTCCAATTCACCCTC	59.903	20	108	568	675
59.891	20	AACAGAAGTGATGGGCTTTCA	59.726	21	230	85	314
60.05	20	CGAACACCATTTTCTTCGGT	59.971	20	175	135	309
59.945	20	GGCATCTCCTCTTGTCTTGG	59.803	20	237	2993	3229
60.656	20	GTCCGCTATAAAGCCCAGC	59.821	19	254	6640	6893
60.033	20	CATTGCAAAATCTCGCTTCA	59.953	20	276	88	363
60.388	20	TTTCGGTTTCTGCAATTTTTG	60.095	21	272	58	329
59.95	20	CCTCAGACAGCTTCAAATCCC	61.138	21	216	728	943
60.378	20	CATCACCGTCATCGTCTCAC	60.121	20	169	656	824
59.671	22	GCTTGTGAAGATGTGCAGGA	59.992	20	276	1	276
59.7	20	CCAGATCATACCTCCCCTCA	59.879	20	229	890	1118
59.694	20	ATCGCCGCCTCTTACTGTTA	59.867	20	191	57	247
59.989	20	TAACACGCAGTCAGTCCGTC	59.905	20	119	280	398
60.037	20	AAGCAGCCATAACTTGCCTC	59.481	20	194	583	776
59.852	20	GGAATTCTATCCGAGCACCC	60.797	20	243	1556	1798
60.022	20	AGACTTGAGAGAGCCGCAAC	59.751	20	191	778	968
59.759	20	GCACCCTCTCTCACTATCGC	59.981	20	234	1423	1656
59.951	20	CAACTTCAGTGCCTCCCATT	60.111	20	243	8	250
60.119	20	GAAGGAGAGTTCCAGATGCG	59.95	20	129	2688	2816
59.315	22	ATGTTATGCCCTAAGGGGGA	60.522	20	206	309	514
59.883	20	CGACTTTTCACTATTCTCCGC	58.986	21	151	19	169
59.911	20	GGGTCCTCCGTCATAAACCT	60.19	20	196	1432	1627
60.161	20	AAATTCCAACGACAATAATTCCA	59.616	23	255	589	843
58.536	25	GAAATAAGGAGGTGTTATGAAGG	59.323	24	152	1635	1786
59.907	20	GAAAAGCTTGGGAATGGTGA	60.051	20	247	1074	1320
57.73	23	CTTGCCACTTTATCCCTCCA	60.066	20	102	18	119
59.883	20	GTTAGATGATGCCACTGCGA	59.83	20	280	2748	3027
59.79	20	GCCTAGATAGGGAGCAGCAA	59.574	20	131	522	652
60.043	20	CTTCCCCTGCAATCAAAGAA	60.184	20	189	3625	3813
59.988	20	TTGCTGAAAAGCAAGCCTCT	60.27	20	222	564	785
60.16	20	CCCTCCTATGCACTCCAAAA	60.066	20	238	3637	3874
59.609	20	TGAGTGCGCTATGCCTAACA	60.566	20	279	172	450
58.296	21	GATACTCGCCATTTTCCCCT	60.286	20	268	496	763
60.025	20	GAGTCTGCAAAAGCAAAGCC	60.14	20	147	1659	1805
59.746	20	AACACACGTCGGTTCATTCA	60.008	20	226	3546	3771
59.993	20	TGTGGCATGTTCTTCGAATC	59.654	20	241	747	987
60.014	19	TCAGATGAAGCCAAAGAGGG	60.331	20	276	2066	2341

59.934	20	TAGAGTAGCGGCTGCAGGTT	60.176	20	178	13	190
59.763	20	CGCTCCCATTTTTGGTAGAA	60.067	20	124	587	710
59.263	20	CCAAACACCCCCTTAGTGTT	58.812	20	249	865	1113
59.828	21	GGGATGTTTGGAGAGACGAA	60.05	20	138	39	176
59.652	20	ATCAGCAGCAACCAAGTTGA	59.445	20	199	540	738
59.369	20	CACGACGAACTTTTCACTTCA	58.96	21	214	559	772
59.381	20	CCCACAGATCTTGGACTGGT	59.962	20	110	1408	1517
59.837	26	GGCTGGATCCAATGGTCTTA	59.894	20	256	453	708
60.221	20	GCTGACAACATGGTCGCTTA	59.871	20	153	813	965
60.141	21	AAGTTTGGGGGAGGAGAAAA	59.912	20	256	381	636
59.903	20	TGGTTGGAATTTTCTCCAGG	59.903	20	278	1174	1451
60.142	20	CCTCCTGAACCAAATCCAAA	59.903	20	146	565	710
59.966	20	AATTGTACATCAAAGGGGCG	59.823	20	173	947	1119
59.522	20	CAACGGTTGCAATTTGATTC	59.016	20	226	508	733
59.836	20	ACTCCATCTCTCTCCCGCTT	60.358	20	239	565	803
59.28	24	CAGGTGGAAGGAAGAGGAAAG	60.225	21	221	732	952
59.31	21	GAATCTTCACCAGTGCCTGA	58.802	20	280	6061	6340
61.339	20	CAATGGTGAATATTATAAAGGCA	59.607	26	216	192	407
59.411	24	TGCACTTGTGCCCCTAAAAT	60.502	20	270	1771	2040
59.992	20	AATTTCCCCGCGTTATTTCT	59.808	20	175	770	944
57.248	22	TTGTAAAAGGATTCCACGTATTTG	59.351	24	260	352	611
59.922	20	GACCAGCCTGACCTCAAATC	59.661	20	224	1059	1282
60.193	20	AGAGCTCAGGATCTTGCGAA	60.24	20	151	3401	3551
59.945	20	GCATGGTGAGAAGCGTTGAT	61.22	20	226	1292	1517
60.159	20	TCGCCTCCTCTTTCTTCTCA	60.21	20	108	1079	1186
59.66	20	CGCTTTCATACCATGCAAAA	59.702	20	227	376	602
60.119	20	AACTCATCCAACTAAGCCGC	59.34	20	259	1213	1471
60.051	20	GTGGCAAAGCAATCCAACTT	60.118	20	238	973	1210
59.894	20	TCCTTGTCGATGATGACGAT	59.04	20	112	341	452
59.971	20	TCTTGTTCACCCACCTTTATCC	60.221	22	243	3097	3339
58.028	22	TTTATTGTGCATGCCGTGTT	59.999	20	247	17	263
59.869	20	CAATTCCGAAAGAAGGTGGA	60.044	20	262	3328	3589
59.769	20	TGATTTCCTGGATTTGCCTC	60.014	20	263	70	332
59.79	20	GGCGGCTTACATTGTTTCTC	59.713	20	117	162	278
59.996	20	AACGTCAAACGGTCTATGCC	60	20	144	3195	3338
60.608	20	ACTAGCCATTGGCATGAAGG	60.096	20	150	882	1031
59.879	20	CGACGCCTCAAATTTACTCC	59.708	20	214	513	726
59.906	23	ATCAGGAGCTGCCAAAAAGA	59.955	20	265	6259	6523
58.896	20	CGGTAAGTCCCGACATTTTT	58.949	20	280	448	727
59.813	20	AGCTGCTCCTTTCAAGCAAA	60.27	20	274	453	726
59.805	20	GGTCGTTGCTGGTTTAATGG	60.365	20	143	338	480
59.711	22	TGCGTTCTGAGTTTGTTTCG	60.027	20	238	2766	3003
58.515	23	TTGAAAATTGTTTTATTCCACATT	59.246	25	197	14	210
59.23	20	AACTAGCGACACCCACCATC	59.997	20	153	25	177
60.088	20	TCAGTTATGCTCTTCTCCCCA	59.822	21	189	973	1161
57.29	25	CGAACTGACCGAACCGTATT	59.993	20	242	0	241
60.257	20	GACTGATTCAATCTCCTCCCA	59.079	21	212	2	213
60.378	20	TGGCGGCTAGGTTTACAGAT	59.73	20	239	367	605
58.923	20	GATCATGGGCTTGCAATCTT	60.043	20	255	3986	4240
59.957	20	AAGGAGAAGCAACAGCGGTA	60.015	20	208	444	651
59.22	20	CGATTCCGGCGTAGAAAATA	60.054	20	151	18	168
60.008	20	CCACAAGAAAGCAGTCCTCC	59.844	20	217	1130	1346
60.329	20	ATGAGCTCTTCGTCATTGGG	60.218	20	130	161	290
59.508	20	CGAGGGCGAAGTATTGTCAT	60.096	20	255	145	399
59.801	20	CGAATAACTGCAAAAGGCAG	58.582	20	201	856	1056
59.779	20	CCAGACTGGGAAGTCAGCAT	60.261	20	160	231	390
59.67	20	CAAAGCCATTAGCCTTGGAG	59.839	20	225	151	375
60.378	20	TCAAAGGGATCAAAATTCCC	58.808	20	202	3426	3627

59.322	20	TGAACGGTTAAAATAATTGCTGAA	59.91	24	277	189	465
58.618	23	CCCCTTGAGTATGTCCCATC	59.213	20	236	1316	1551
59.068	20	GGGAGGTTGCATTTCGTATG	60.331	20	271	298	568
58.418	20	TATACTTCCCAGCCACCCTG	59.948	20	142	9	150
60.192	20	CCATGTAGGCGTAAAAATAGGA	58.224	22	139	763	901
59.021	20	TACAGGCCCTGCAAGAATTT	59.708	20	206	19	224
59.747	22	CTCTTCACCTTCTTTTGCCG	59.986	20	201	566	766
60.142	20	CACCCGGCCTCTTTATTTTT	60.305	20	132	1400	1531
60.045	20	GGAGTCGCGGAATCAAATTA	60.038	20	205	349	553
60.837	20	CGGAGCTTGAAAGATGAAGG	59.948	20	254	333	586
60.291	20	CATGAGTCGATGATTGGCAC	60.08	20	138	53	190
60.02	20	CCACGTTTTGGGGTCCAC	62.219	18	279	573	851
59.96	20	TCAAACAACGTGAATGAGCA	58.835	20	250	347	596
59.953	20	GCAAGCAAATCTAACGAGCC	59.988	20	181	454	634
59.622	20	TCGTGTTTCCTATGCTTCTGG	60.256	21	138	747	884
59.195	20	CTCTCGTTCCAAATTCCCAA	60.044	20	264	1633	1896
58.494	26	TACGTCTTTGAGATCGCACG	60.011	20	100	12	111
59.888	20	CCCATTTCAAGCTTGCTCTC	59.955	20	223	283	505
60.015	20	TCATCCGGTTTTAGTTTCGG	59.931	20	157	3088	3244
60.111	20	GTGGACGCTCCAGATTGTTT	60.119	20	225	1562	1786
58.392	26	TCAACTGCCTGCATTGTTTC	59.847	20	218	609	826
60.657	20	ACCAGCCCTTTTCTTTCCTC	59.691	20	270	4275	4544
58.773	20	CACCAAATTTCATCATTTTTAGTTC	58.144	25	256	403	658
60.147	22	CGGGGGAAGAATAATTGGTT	60.013	20	136	57	192
60.038	20	CATGCATTGAGTTGGTGGAG	60.112	20	277	2223	2499
59.962	20	GCAAGTTCAACCTTCTTGGG	59.711	20	280	1377	1656
58.028	22	AATGCGTGCAACACACAAGT	60.23	20	156	14	169
59.962	20	AGTATGCGCCAAAACGAAAC	60.138	20	229	514	742
59.973	20	TGCACGTAGGCATGTTCAAT	60.142	20	251	110	360
60.081	20	AGTCCGATTTCAACCAGGTG	59.966	20	205	641	845
60.49	20	CATCCCCCAAAAAGAGGTC	59.322	19	278	833	1110
60.004	21	TGGTTATGCAAGTGGAACGA	60.111	20	276	192	467
60.06	21	TTCATGAGCTCGCTTTTATTGA	59.985	22	159	327	485
59.948	20	CCTATGGTAGTATGGTGTGGGG	60.365	22	193	12	204
60.045	20	GAAGGGGCGGAATTATCTTC	59.873	20	129	2403	2531
60.026	20	TGCGTTTTGACAATATATAGGTGT	60.083	26	253	634	886
59.856	20	CCCAAGCCAAACACTCTCTC	59.844	20	197	3751	3947
60.657	20	TTCGATCTCCGTCAGCTCTT	60.096	20	239	692	930
60.074	20	TTGCAGTTCAGCCTCTGCTA	59.888	20	261	249	509
60.353	20	CCACCGAGCACCAAGTAAAT	59.993	20	270	1096	1365
59.872	20	TTGCCTTGCACTTCATCAGA	60.539	20	266	235	500
60.06	20	TGATTCCTATGCCTCGTGGT	60.483	20	240	116	355
58.771	20	GGTCTCCGGTCCCTAAAATG	60.683	20	247	644	890
60.031	20	GATGGGGATGGGTCACTTTA	59.605	20	272	221	492
59.41	20	TAGGAATTTGCTGCTGCTGA	59.712	20	160	1089	1248
59.993	20	CAAACCGGGAAGAACTACCA	59.964	20	234	689	922
59.797	20	ACCCCGATGTGATGAACAAT	60.057	20	224	814	1037
59.778	20	TCATGGTTTCTCTGTTGCGA	60.39	20	170	821	990
59.49	20	GTGGCGTTGAAAATCTCCAT	59.939	20	177	632	808
59.246	20	TTGTTGGAGCTCATGGACAG	59.831	20	206	609	814
59.823	20	GCCGATGGAATCAAGAAAAA	60.016	20	188	2356	2543
59.849	20	TGATTCTGACGAGGCAGATG	59.942	20	137	1912	2048
59.244	20	ACTCGAAGAGTAGCGGTTGC	59.644	20	279	54	332
62.397	18	CCTTTAGCTGGCAGGCATAC	59.867	20	238	23	260
59.992	20	TCCCTCCCTCTTTAAAATCACA	59.939	22	144	3722	3865
58.951	22	GTCTCAAGCCCGCGTTATTA	60.23	20	270	963	1232
59.716	20	GACGAGCTGATCTTGGGAAG	59.95	20	235	1412	1646
59.778	20	GGTGTTTTTATGGGCTGTCC	59.292	20	271	3419	3689

59.382	20	ATGGTGGAGCAGTTTTCCTG	60.111	20	104	58	161
59.721	20	CTTTCCATCCTTTTTGGGGT	60.159	20	259	234	492
60.008	20	CACTAAGTTGAGCGTTGCGA	60.195	20	251	787	1037
60.34	20	TGGAAAAACAACCCAAATTGA	60.188	21	229	920	1148
59.953	20	CCGAACCGAACTGATTTTGT	59.971	20	149	142	290
59.816	20	TTGCAAACGTCAAACAAAATG	59.634	21	218	697	914
60.243	20	CGTCTGATTGGGAGAATCCA	61.004	20	276	1016	1291
59.971	20	CATAAGATGCACCTGCGAAA	59.833	20	254	319	572
60	20	ATTGACGGGGTTCACAGTTC	59.827	20	241	220	460
60.089	20	CAGACCTCCAAAAGCAGGAG	59.982	20	209	1227	1435
59.962	20	GAATCCGAAAAATAAGGGGG	59.616	20	124	385	508
60.246	20	ACCCACATCTCCCCTCTCTC	60.469	20	178	26	203
59.461	20	TGTCAATGAACAAATAGGTCACA	59.424	24	259	344	602
58.292	20	ACCCGAGACAAAACACGAAC	60.012	20	237	239	475
60	20	AATCACTCTGTGTGAGGCCC	60.12	20	229	651	879
59.184	21	TTGTCTAGTTGCAACCCCCT	59.592	20	276	2224	2499
60.44	20	GAGTAGAGCTCGGCGAGAAA	59.859	20	259	533	791
59.682	20	TGTTCATCCATGTTTTGGGA	59.75	20	176	206	381
57.172	22	TGCTGTTGGCCTGTAGTGAG	60.049	20	104	0	103
60.352	20	CGGTTCAATAAGATCACCGA	58.572	20	230	961	1190
61.029	20	AATACGACGACGAAGCCAAC	60.14	20	188	54	241
60.201	20	TGGAGATCGTGTGAGAGGTG	59.82	20	266	313	578
59.526	20	CCTCTCAGATGCAGAGGACC	59.945	20	156	12	167
59.378	20	TCTGAGGAGATTTTGGCAGG	60.331	20	241	557	797
59.648	20	TTGGACCACAAACCCCTTTA	60.198	20	167	392	558
59.939	20	TCATGGGAATTCACGAAACA	59.9	20	229	245	473
59.586	20	ACCAAGCATGCTCATGTCAA	60.272	20	127	145	271
59.933	20	CTGAGGTGACCTGGACCATT	59.962	20	269	34	302
60.206	20	TGCATGAAAACTCCCTCACA	60.24	20	224	585	808
60.21	20	GTGAAACAGACCCACAACCC	60.261	20	191	377	567
59.878	20	GAGGTGGGATATGATGGTGG	60.011	20	121	682	802
59.772	20	CCAATTCCATCAAATCCAGG	60.126	20	160	786	945
59.603	20	GGCTAGCTGTCCATACAATGC	59.75	21	221	296	516
60.517	20	ATGCGGTCGGATTAGAATTG	59.923	20	250	1305	1554
59.894	20	AAGCTAGCACGTAAATGGGG	59.248	20	145	515	659
57.15	20	ACGAGACCATCGTTCCCATA	60.34	20	233	2	234
60.363	18	TATTTTGGGCCTGAATGGAC	59.762	20	185	505	689
59.931	20	TGAGAATGTGCTCAGACCGT	59.42	20	255	1035	1289
59.746	20	GATTCGATTGCTTGCATCAC	59.234	20	256	280	535
58.65	20	AGCCACCCTCTCTCGTAGTG	59.474	20	280	196	475
60.186	22	TCGGTCAACATTGCTTTCAA	60.234	20	127	1333	1459
60.326	20	AAACTGGTGCTCATGCTTTG	58.926	20	236	2967	3202
59.918	20	CGTGGAGACAACGTGAAGAA	59.873	20	219	112	330
60.604	20	GTCGTAGTCTTCCTCGTCGG	59.867	20	135	1562	1696
59.903	20	GGGAATGGAATGAGCATGAG	60.426	20	249	73	321
59.927	20	TAACGGAACCGTGGGATAAA	60.181	20	208	270	477
59.871	20	GCACTCGAAGAGTAGCGGTT	59.644	20	254	2063	2316
59.948	20	AGGACGTCGAGGGAGAGAAT	60.216	20	206	560	765
60.186	21	CACTGCTTGGCCACTTATGA	59.864	20	266	32	297
60.08	20	CCTCCCCATGGCTAGACTAA	59.146	20	262	312	573
60.118	20	TTGCTCCATGTTATGCAATG	58.145	20	254	1295	1548
59.805	20	CATGCAACAAACCAACCAAA	60.393	20	236	398	633
59.147	21	GTTGAGATATTGGAGAAGATATG	57.119	26	265	1684	1948
59.847	20	CAACAAGATGCCAAAATAAACAA	59.076	23	186	670	855
59.779	20	CCAGTTCAAGAAAAGGCCAA	60.22	20	202	344	545
59.654	20	CATCCCCATTACCTTAGTTAGCA	59.424	23	231	556	786
59.624	20	TGACGACCGATATGTGCTTC	59.679	20	248	97	344
60.57	20	GCGAGGAAATCAGAGAGTGG	59.95	20	273	17	289

59.297	20	TTTCCTTTCATTACACGTGCC	59.989	21	266	39	304
59.82	20	TTGATGCAATGATCTCATTCTTTT	59.976	24	190	407	596
60.081	20	TGCACAAGCATGTTTTTCATT	59.22	21	243	288	530
59.15	20	AAACAGGCTAGGTCGGACTATTT	59.595	23	279	1510	1788
59.469	22	GAAAATGCAAGGGTGGTTGT	59.836	20	187	803	989
60.258	20	TCTGTTTTTGTTTTGGTTGCC	60.004	21	233	144	376
60.309	20	GCTAAAGCCATCTCCAATGC	59.813	20	261	299	559
59.7	20	CCTGGCAGCTTTTGATCTGT	60.397	20	154	74	227
59.549	20	ATGCTGCATCGGCAATAAAT	60.453	20	221	602	822
59.898	20	TAGCAAAGCCCAACCTCATC	60.214	20	147	880	1026
60.032	20	CATTTATTCCCCGCAACAAC	60.188	20	245	671	915
59.864	20	GATGACAGAGCAATCGGGTT	60.081	20	280	273	552
60.051	20	CACAGATCTGGTGGAGGGTT	59.962	20	154	519	672
59.858	24	GGCAGTTAACAGGACCCAAA	59.971	20	202	324	525
59.975	20	TTGGGGATTAGTTCGCAAAG	60.067	20	124	370	493
59.391	20	ACCGATTGCGATGCTTAACT	59.736	20	221	1373	1593
59.284	20	AAAGAAATTGGACAGTGGCG	60.11	20	169	3918	4086
60.121	20	ATCTTCAACCCCCACCTCTT	59.795	20	239	579	817
60.06	21	CTGCAATCCAAAAGGGAAAA	60.046	20	257	52	308
59.847	20	GGGAAAAAGGGCTTGTTGTT	60.332	20	196	3675	3870
58.957	20	TTTGAACACTCAATGCGCTC	59.995	20	274	940	1213
59.781	20	TTCTCGGACCTCAAAGTGCT	59.989	20	210	1299	1508
59.462	20	ATCGTGCCACTTTTCTGTCC	60.119	20	266	321	586
60.293	20	GATAAGCAGCGAGAACTCCG	60.118	20	229	28	256
60.049	20	CTTGAAGCTCCAGCAAAACC	59.993	20	142	926	1067
59.771	20	CAAACTCTTCCACCGACCTC	59.697	20	213	14	226
60.612	22	TGGGAATCCGGACACTAACT	59.405	20	246	326	571
59.96	20	AACCAGACCATTACCAAGCG	59.993	20	247	1032	1278
60.228	20	TGTATTAGGACCACCAGACCG	59.861	21	198	656	853
59.927	20	TACCCACCTCGAATATCCCC	60.901	20	140	308	447
59.973	20	CAACTAGGGGGTCCTGAGGT	60.363	20	144	1603	1746
60.235	20	TCACGTGACTTATTTGGTGGA	59.036	21	227	2858	3084
57.669	23	TCATGAATCATCAATTCGAAACTT	59.849	24	228	21	248
60.088	20	CCCCTGGTTGTTGAAGAAAA	59.942	20	116	1834	1949
59.912	20	TTCGCCCAATCTTCTCATTC	60.155	20	240	991	1230
59.545	20	TGTTTAATTTTTGTTAAGCATGCAA	59.958	25	203	387	589
59.801	20	CCGGGGTATGCTATAAACGA	59.81	20	189	17	205
60.031	20	GACAAGGAAAAAGAGCGCAG	60.132	20	201	1549	1749
59.967	20	CAAATGCGTGAAGATAGTGATG	58.32	22	219	446	664
59.955	20	CACCTAGTTGCCCCCTACAA	59.986	20	152	537	688
59.83	20	GCTTGATCGTCTCCTGCTTC	60.104	20	127	669	795
60.08	20	GTATCCTGCTGAGGTGGAGC	59.834	20	272	2083	2354
57.55	20	AATGCCCTCAGATGCTATGG	60.059	20	215	0	214
60.112	20	GTGGAGTGGTGGAGCAAGTT	60.159	20	141	825	965
59.344	23	TGAGACTTTGGTACGGGAGC	60.255	20	236	328	563
59.997	20	AGAGGCAGAGAGGTGACTGG	59.579	20	278	120	397
59.517	20	GGAATTCCATCCATCTCGAA	59.831	20	181	158	338
60.013	20	GGCATCCATACTTGCCACTT	59.962	20	269	1182	1450
59.91	20	GCATGCATACAAAACCAAACG	61.284	21	160	4358	4517
59.776	20	TCCTGCAATCTCTGAACCAA	59.369	20	230	410	639
60.195	20	GCATCATAGGACCCCAAAAA	59.762	20	209	391	599
59.903	20	GCTGCTTGATCCTGAATCCT	59.39	20	252	108	359
59.293	20	ACTACCATGCGGAAGGAATG	59.955	20	229	772	1000
60.142	20	TGTTCAGCACACAGAAACTTCA	59.534	22	272	554	825
60.074	20	TTTTTCTTTGGGTCATGTGATG	59.839	22	268	691	958
59.634	20	ATTTGATCCCCCAATTCAAA	59.067	20	128	45	172
60.081	20	ACTCCTCTTTCGATCTGCCA	59.95	20	212	2442	2653
59.996	20	GAGTGCAGAGTGCAAAACCA	60.032	20	135	511	645

59.98	20	TGGGATTCATGGGTCATTTT	59.991	20	208	746	953
60.025	20	AATGCCTTCTTTTGGCTGTG	60.249	20	168	831	998
60.14	20	TGGTCAGCATCCTACCAACA	60.112	20	207	1980	2186
60.031	20	TTCTGGATGCATGAAAATTGA	59.101	21	265	491	755
57.916	25	ACCAAATGGCTTAGGTGACG	59.993	20	169	1728	1896
59.874	20	ATCAAGTTTCCATTCTGCCG	60.074	20	155	74	228
57.972	20	TAGAGTCCTCCGATTCCGTG	60.21	20	277	602	878
60.037	24	TTGATGTTTGTATATGTTTCGTTCA	58.542	25	276	241	516
60.096	20	AATGAGGTCAATGGTCAGCC	59.934	20	197	1101	1297
60.307	20	GTGTGGCGTGCTAACTGCTA	60.081	20	220	236	455
59.95	20	GGCCCAACTCCACTAAATCA	59.933	20	201	60	260
59.807	20	AAAACTCCGGCATGGTACAC	59.859	20	272	594	865
59.059	20	CCGAACCACGTACATCCTCT	59.989	20	171	697	867
59.592	20	CCGTTCCATCAAGCATTTTT	59.938	20	234	1014	1247
60.053	20	ATTCGATGGATTTCGACGAG	60.036	20	119	7524	7642
60.032	20	CACCCCACGAGACAACTTTT	60.005	20	108	747	854
58.687	21	ACTAGTGGCAGCCATGTCCA	61.688	20	234	257	490
59.888	20	CGCCGATATATGCGTCTTTT	60.082	20	247	346	592
59.935	23	CCAATCCAAGTATCGTCGCT	60.096	20	258	769	1026
59.648	20	TGCCATCGTTCACTTTACCA	60.111	20	194	1279	1472
60.476	19	TGTTTCTGCCCAAGCTTCTT	59.993	20	280	997	1276
59.978	20	GTAGTGGTCGACGGGCTTTA	60.132	20	265	227	491
60.907	20	TCCAGTGTAGTTTACCCGGC	59.993	20	205	847	1051
59.818	21	ATTCCATGTCCAGACCCATC	59.593	20	253	1091	1343
60.038	20	ACGAACTCCTTCGATTCCCT	60.074	20	247	595	841
58.834	20	ATTCTGCTATTCCCGAGGGT	59.925	20	225	0	224
58.629	22	ATCCGTTCCGGTCTTCTACA	59.55	20	230	416	645
59.823	20	GAGGGCAATTCTGATGAACC	59.488	20	264	392	655
60.153	21	TTGCAAATATAAACGTAATGAAG	57.618	24	203	226	428
60.257	20	AGCTCCCAAGTCTGAGTGGA	59.986	20	184	435	618
59.937	20	ATTTGGGTGAGAAATCGCTG	60.074	20	269	1029	1297
59.662	20	CCCATTGAATTATGGGGTTG	59.872	20	108	1050	1157
59.042	21	GCGATGTGGACACCTCAGAT	61.116	20	275	42	316
59.146	22	ATGTCTGCCCAGCAGAGAAC	60.418	20	272	689	960
59.274	21	TGCACAATCATCACACATAACC	59.326	22	153	722	874
59.376	23	AGGAACGGGAGATTTTGCTT	60.074	20	186	267	452
60.42	20	TTCCGGAGCATTACCCTATG	59.916	20	279	1677	1955
60.049	20	AGGTGAGCCAGATGTAGCGT	59.898	20	238	656	893
59.939	20	AGAGCGACAGCGAAAATGAT	59.985	20	226	335	560
60.055	20	TGTGTTGAAACCCTCATCCA	59.935	20	250	1424	1673
59.923	20	TGGTTGCCAGCTTACTGCTA	59.632	20	200	326	525
59.838	21	TTGTCATGATTTGCGGGTTA	59.93	20	192	46	237
59.829	20	TGCTTGTAGTGGGAAGAGAGTG	59.538	22	184	710	893
59.903	20	GGATCTCCAAATCTGACGGA	60.011	20	238	819	1056
59.938	20	TCGGGTTCGATTCTCATTTC	60.014	20	257	10	266
60.015	20	TGGTAGTGGTGGATATTGGTGA	60.11	22	256	317	572
59.635	20	TGCTTTGACAATATTTAGTGTTTTG	59.216	26	280	3629	3908
59.955	20	CACATCCATGTTCGTGCTTT	59.572	20	263	163	425
60.18	20	CGAGCTCGGTGAAGCTATTC	60.118	20	244	166	409
59.894	20	TGGTGCACTGTTCCCAAATA	59.964	20	267	425	691
59.982	20	TGATTGTGGACCAACAGCAT	59.967	20	269	80	348
59.945	20	GTGTGGGGTGTTATTGGGAG	60.088	20	232	1330	1561
59.671	21	TGGACAAGGGAGAAAAAGGA	59.641	20	174	1724	1897
58.628	20	TGGCGTAGTGTTGGAGAATG	59.716	20	143	59	201
60.016	19	TCAATTAGGTGTCCCACCGT	60.232	20	197	337	533
59.901	20	CTTGAGTTCGGTCATCACCAT	59.981	21	154	963	1116
60.504	20	TGTCTTCCACACAAATCCGA	60.088	20	250	1404	1653
59.953	20	GGGTTCAAACTCCACTCAACA	59.997	21	177	618	794

60.073	20	TGTGTGTCATTTGTTTTGTTAGGA	59.464	24	268	114	381
59.931	20	GGACGATCCTCATCCTTGAA	60.011	20	219	119	337
60.205	20	CGTTGTAATGCCCCGTAAAT	59.72	20	193	1266	1458
60.414	20	GTGGAGTTCAAGCCCAAAAA	60.088	20	280	2108	2387
59.872	20	AAAGGTAAAGGGTCCTCCCA	59.799	20	214	1477	1690
60.299	20	TGCAGCTGTGGACCTACTTG	60.049	20	247	1033	1279
59.955	20	TTTATGTGCGTTTTTGGGAA	59.05	20	277	302	578
60.216	20	TTATCCTGTGCTTTTGCACG	59.872	20	211	2690	2900
60.278	20	CTCCTTCCTCCATTCCCTTC	60.008	20	139	74	212
60.323	20	GCTTATTTGGCATGCTCTCC	59.813	20	202	246	447
59.736	19	TGCGTTTTGATGATATATAGGTGT	60.054	26	271	724	994
60.103	20	TTTCCATCTTGGACCACACC	60.758	20	181	3669	3849
59.547	20	TATTCTCGCAAACAGTGCCA	60.401	20	278	2410	2687
59.962	20	TCTTGGATTTGGAGGAATGG	59.864	20	208	358	565
60.177	20	CCCTCGTATGCAGTGGTTTT	59.993	20	238	669	906
59.694	20	CTGCTGAAGCCCTTCTCATC	60.096	20	239	12	250
60.315	20	GGAATGTGGTGTAGATTTGTGC	59.364	22	183	221	403
58.976	22	ATCATGAATGACACATGGCG	60.362	20	226	10	235
59.942	20	TCACAAGGGTGAAAGGGAAC	59.943	20	206	97	302
59.84	20	ACCACAGTGGCATTACACGA	60.032	20	270	716	985
59.464	20	CTGCAACCGTTTCTTCACAG	59.485	20	114	403	516
60.549	20	CACCTTCATCGGCATCAAC	60.064	19	213	683	895
58.866	20	GAATAGGAATGGGGGAGAGC	59.866	20	221	959	1179
60.626	20	TGGTTGGAGGGTAACATCGT	60.232	20	248	985	1232
60.554	19	GCGAAGCGACATCACATAAA	59.839	20	140	25	164
60.294	20	AACTTGTGTTGGTGGCTTCA	59.187	20	132	2018	2149
58.044	22	TCAATCTCGTTGAAAAATGGTTT	59.871	23	261	818	1078
59.861	20	ACTCCCTCCTAAGGACCCCT	60.316	20	122	0	121
59.993	20	CGCTCGACTTTCTCGAAGAT	59.717	20	114	395	508
60.005	20	TCATGTCACGTTCCAGTTTCA	60.144	21	279	1565	1843
58.725	20	AAGGGAGTTTTTCACCCGAT	59.805	20	103	67	169
59.977	23	CATGTGCCTTCTCTGCTTGA	60.136	20	255	7	261
59.962	20	GGCCAACAAATCGTCAATCT	59.939	20	116	418	533
59.777	20	CGCTCAACAACCACAACAGT	59.794	20	260	21	280
60.318	20	CCATCGAAGCTCACTGTCAA	59.984	20	178	959	1136
60.17	20	TGATGTTATAGTAAGCAAACCAA	57.922	25	197	736	932
60.195	20	ATGCTGAAGGAGCCAAAAGA	59.955	20	158	290	447
60.12	20	CCGTTGCCTTACCTTTTTCA	60.103	20	229	518	746
59.609	20	GGACACCACGTTAGCATTCA	59.572	20	224	355	578
59.96	20	TGGGGGAGATTTTTGTTTTG	59.772	20	231	966	1196
59.323	24	ATCAAGAGCTCTCACCCACG	60.408	20	100	8	107
59.653	20	AAACTACCACTGCGTCCCAC	60.035	20	264	674	937
60.594	20	CGATAGGGATCTCTTCTGCG	59.933	20	241	335	575
60.315	19	GCACCTCCTGTTAGCGAGAA	60.538	20	263	393	655
60.103	20	ATTTCCACCATGATTTCGGA	60.133	20	258	603	860
60.12	20	TCCATACAGACACAACCCCC	60.634	20	197	271	467
60.483	20	TGTCTGGAATGGAATGTGGA	59.893	20	274	4267	4540
59.986	20	CCCCTACATTGGGAGTCAAA	59.784	20	210	911	1120
59.435	21	AAACATGATACCGCCGAAAA	60.323	20	227	159	385
60.317	20	ATTCAAGGTCACCATCCCAA	60.173	20	154	1421	1574
60.049	20	TGGAAAGCAACTCAATTTTGG	60.096	21	118	590	707
58.796	22	TGGTCGAATGAGGAGTGAAA	59.215	20	256	133	388
60.074	20	GCCTCTGCTTCACCAATTTT	59.316	20	265	241	505
60.056	20	TGCAGACGAAACTCACAAGG	60.025	20	138	660	797
60.068	21	GAAGGTGGTGTTGCTGTGAA	59.726	20	274	198	471
60.416	20	TCACCAAAAGGAGGGGTTATC	60.173	21	262	711	972
59.542	20	AGAAATGAGGGAGAAGGGGA	60.008	20	245	6310	6554
59.9	25	ACAAATGTGTTCCGCTTGTT	58.132	20	280	14	293

59.943	20	ATTATCGCAGCGAAGATGCT	59.973	20	202	47	248
59.439	20	GGATTGCAGAAAAACCCAAA	59.916	20	198	1502	1699
60.029	20	AATGTGATGTGAGCCACGAA	60.12	20	183	2520	2702
59.882	20	TCCCGCATAATTTGGATTTC	59.735	20	232	2	233
59.76	21	AAGCACTAACGAACACGGCT	59.943	20	276	599	874
59.694	20	TTCACGTGTAGGAGCCAATG	59.716	20	263	410	672
59.3	20	ATCCAACTCAAGCAACCGTC	60.119	20	258	7	264
60.564	19	GCATGCGTTGTCCAAATAAA	59.567	20	160	941	1100
59.966	20	CTTTGGGCATTGTTCTCTGA	58.847	20	227	122	348
59.709	21	TTTGGTCTCGTTGTATGAACAAA	59.544	23	244	432	675
58.707	21	AACATGGGTACTGTTTCGCA	59.05	20	135	996	1130
58.901	21	TTCATGTGTTCGTAATGATCG	57.082	21	272	344	615
59.272	20	GCACAATCAACTTGAGGCAA	59.847	20	180	27	206
60.156	20	GAAAGGGGAAGGAGAAGTGG	60.045	20	131	19	149
60.049	20	CCACGCTTGGCATTTAGATA	58.794	20	160	364	523
60.015	20	AATCCCATGTTGCTGCATTT	60.339	20	171	146	316
60.053	20	GATGCAACTTCGGGAGTGAT	60.081	20	276	923	1198
59.903	20	TGCCCCCTATGCAAAATATC	59.757	20	202	590	791
59.988	20	TGGCAACTCCATGAACAATTT	60.359	21	230	378	607
58.409	20	AACAGCCAAGTATTGGTGCC	60	20	273	1359	1631
60.001	22	TTCCATCTATCAATTCATTTTATTA	58.89	27	223	297	519
59.88	20	TGAAGTTAGGAAATAAGGAGGTG	58.743	25	120	854	973
59.859	20	CCACACCCCACACTCTCTCT	60.153	20	261	294	554
59.732	25	TTTGCATGGATTAACAGCGA	60.215	20	203	95	297
59.913	20	CTCACTCATTCCTCGCTTCC	59.95	20	129	1672	1800
59.935	20	GAAAAGGGGTGACCACAAAA	59.807	20	265	888	1152
60.049	20	TTCCACGAATACAAGCGTTC	58.773	20	240	330	569
59.685	21	TAAATTCGGGTCTTCCACCA	60.301	20	274	753	1026
59.911	20	TGTAGCCCGCATGACTACAG	59.888	20	238	968	1205
59.922	20	TCAGCAAGAACTCGAGCAAA	59.864	20	244	151	394
59.987	24	ACCGTCGATGAAAAATCTGG	59.933	20	264	994	1257
60.517	20	GGAGCAGGTTCGAAGTGAGA	60.533	20	275	4914	5188
59.459	20	AACTTGGGCCTGGCTATCTT	60.096	20	277	2089	2365
59.302	23	TCCAATATTTATGGCGATCTAACA	59.744	24	224	915	1138
59.973	20	AACATTGTGAAGGAGGCTGC	60.263	20	260	1125	1384
59.823	20	AGAATAATGCAGCGAGCGAT	59.973	20	242	1541	1782
59.929	20	GAGGGTGGCTCATCTTCAAA	60.195	20	278	1505	1782
59.925	20	TCAAGGGCCAAGATTTGTTC	60.051	20	148	122	269
60.14	20	TTTGCCCCACACAACTGATA	59.964	20	145	9415	9559
59.55	20	TACGAATCACACTATGGGCA	57.572	20	148	444	591
60.606	21	TTAAAGAAGGGTTGGCGATG	60.067	20	246	984	1229
59.098	20	CCAATTTCATTGATAACTCACCA	58.865	23	216	54	269
59.997	20	TTGCCCCCAACTGCTATTAC	59.96	20	191	282	472
58.148	21	ATTGAGCTTGCGTTTCCAAT	59.713	20	266	1203	1468
59.971	20	GGAGAGAAAGCTGGCTGATG	60.096	20	279	2676	2954
59.662	21	TTTGCACATGAGCTTTTCCA	60.379	20	207	1250	1456
59.33	21	GTCCGTTGGAAAAAGGATGA	59.91	20	221	369	589
59.585	21	GCCCGTGTCCATAACACAAT	60.646	20	274	1796	2069
59.055	20	TGCTTCTCACCAATCAGTGC	59.992	20	111	20	130
59.989	20	GGACAAGGGTCTGCATCATT	59.934	20	188	109	296
59.997	20	CCAGAATTTCGAACCTCCAA	60.044	20	202	1581	1782
59.679	20	GGAAGGCCTAGATTTGTCTTGA	59.725	22	197	2289	2485
60.046	20	GCAGGACTTGTAACCTTGGG	59.592	20	165	915	1079
59.805	20	TGGATTTTTGCCCTTGTTTT	59.429	20	279	315	593
59.809	20	GGCAAACAACAGTTGCAAAA	59.752	20	273	703	975
59.864	20	ACACACATGGGCTAGCTGAA	59.318	20	261	378	638
60.017	20	CCTCAGCAAAATGCAGTTGA	59.988	20	248	447	694
59.83	20	CATGGGGTTGGTTCCTATTG	60.044	20	227	563	789

58.924	22	ATGCACATTGTGTCCCAAAA	59.823	20	194	727	920
59.927	20	AGATTTGGACCCCACCCTAC	60.052	20	110	434	543
60.074	20	TGACAAGATTCAATAAAGCCACA	59.639	23	226	838	1063
57.955	22	GCCAGAGGAGTCCTTCACAG	59.986	20	161	215	375
60.493	20	CAAAAGCAAGCCTCCTTCAC	59.993	20	258	152	409
60.061	20	TTTTTGGTGTTTGATTGCGA	60.088	20	267	1924	2190
59.823	20	CCATCGCCACCTTTTGTAAT	59.823	20	247	3	249
60.523	20	GGAGCGCACGAGAATTTTAC	59.851	20	241	449	689
59.592	20	AAATGCATCTCAATTTTTGGA	57.239	21	228	539	766
60.201	20	TATCACCAAGAGATGCCCAC	58.516	20	112	407	518
59.993	20	GCAACGAGAAATGGAGTGGT	60.119	20	184	1927	2110
59.91	20	TCCTTTCCCAAGAGTCCAGA	59.773	20	154	1480	1633
59.969	20	TGTACAAAAGCTATGCTTTCACAA	59.045	24	188	119	306
59.927	20	TGCGACCTTGGTAGGTTTTC	60.11	20	163	123	285
59.833	20	ATGCTGCTTCTCCCTCACAT	59.834	20	170	2603	2772
59.957	20	GTCGATGGGGCAGAAAAGTA	60.074	20	142	589	730
60.024	20	TTCGAGTATCGCTCCGACTT	59.978	20	277	101	377
60.27	20	GATGAGAAGTGGCAAAGGGA	60.195	20	214	29	242
59.473	23	ATCTCTCAGCATTAGCCCCA	59.797	20	269	438	706
59.246	22	AAGGAGGTGTTATGAAGGGATT	58.028	22	275	693	967
60.059	20	AACTTTGCAGCTTCTGAGCC	59.763	20	231	239	469
59.864	20	TTCAGGACGCTTTACCGAGT	59.875	20	252	169	420
60.012	20	ACCAATGCGGATGCTCTAAC	60.103	20	263	3121	3383
59.872	20	GCCCAAAGATGAACCAAGAA	60.051	20	192	677	868
58.423	20	CCTTCGTCACCAACGAAGTT	60.149	20	265	647	911
60.184	20	CAGGTGATTGAACTCAAAGCC	59.726	21	273	3201	3473
60.074	20	GGTGGCAGGAAGTTGTACCT	59.065	20	212	1717	1928
60.112	20	GGCCACAAGCCATTAGTGAT	59.962	20	262	318	579
59.904	20	GGTGAAGCATGCAAAGATGA	59.805	20	260	888	1147
60.397	20	CCTAAAGTGACCCCATTCCA	59.784	20	279	828	1106
60.328	20	GGATGGAGAGATTGCAGCAT	60.189	20	181	232	412
59.486	20	CATCTATGCTCGCACATTCG	60.388	20	229	2656	2884
60.167	20	TCGCAATACTTCTGCCTCCT	59.978	20	145	1378	1522
60.343	20	TATCAAGCTTGTCAGCCCCT	59.836	20	248	1706	1953
60.122	22	GTTGTGATGCAATTTGAGCC	59.131	20	235	1133	1367
61.061	20	GCATCATTTGATTGGCAGTG	60.08	20	210	143	352
60.015	20	CCCTGTAACAGTTGGTGCCT	60.028	20	229	1278	1506
58.621	20	CCCTTGATTTAAGAGATCCAATG	59.004	23	278	210	487
59.827	20	TTCAGAAATGCAATAAATTCCG	59.11	22	274	1111	1384
60.131	20	AGCGCCTCCATATCAGAAGA	59.939	20	252	1660	1911
59.939	20	CCGGGAGGGTTTTGATAAAT	60.013	20	270	20	289
59.955	20	GGCCGTTTGTTTTATTGGAA	59.81	20	167	553	719
60.134	20	TCAAATAGGTGGGTGGTGGT	60.088	20	235	46	280
59.489	25	CATTCTCGCAGAGCATGTGT	60.016	20	280	1194	1473
61.08	20	CCAGGAACTAGATGGTGCAAA	60.118	21	195	476	670
59.712	20	GATGCCCTAGGGACGTATCC	60.682	20	247	425	671
59.67	20	ACCAGAATAGCCCAGTGGTG	59.989	20	246	312	557
58.261	27	TGTTTGTGTTTTGACGTTTGC	59.665	21	103	7	109
60.049	20	GACCGCAGGATAATCCAGAA	60.036	20	182	891	1072
60.628	20	TTGTTAGTTTTGGATGGTACGAAA	59.817	24	226	442	667
59.614	20	TTTTTGCAGGGAAAAAGCAT	59.699	20	266	2329	2594
60.156	20	TGTGATCAAAGAAGAAAAATGAT	59.549	25	279	874	1152
59.969	20	TAGTAAACCGGACGTGGCAT	60.386	20	125	665	789
60.074	20	TTCCTGCATATTGGAAAGGG	59.894	20	275	1850	2124
60.277	20	CAATGGTGTCCATCCCTCTC	60.326	20	277	3152	3428
59.639	20	GCACGTATCGACATTGCTTAAA	60.157	22	121	998	1118
60.365	20	AGCTAGGAGGAAGGGCTGAC	59.979	20	212	1	212
59.864	20	GCATCCAGCAGTGTAGGTGA	59.862	20	226	729	954

59.637	23	GCCGGAGTGATGCAGTAGTT	60.285	20	197	233	429
59.989	20	GCTCAATTTTAGTTGTGAAATCTT	60.065	26	138	2162	2299
59.773	21	ACTCACACACCTTCACACGC	59.789	20	143	60	202
60.256	21	CGATTACGCCTCTAAGAAAACA	58.589	22	240	193	432
60.029	20	TCGTATGGTCTCCCCAGTTC	59.927	20	268	456	723
60.11	22	TCCTGTATCGATTATCATTTTCAA	57.736	24	265	314	578
60.225	20	TCTCAGACAAAACCTTCGCC	60.375	20	228	1425	1652
61.025	20	GCTGATGTGCAAACAAAGAAA	58.956	21	264	2000	2263
59.236	24	TGGCTAGAGAGATTCCACGA	58.543	20	185	369	553
59.953	20	CAAGACCGGCCATTCTACAG	60.647	20	136	723	858
60.457	23	CCCAGTGAATGATAAGGGGA	59.744	20	202	12	213
60.111	20	CGATATGTTACGTAGGATGACGTT	59.374	24	220	1597	1816
60.025	20	ATGTGTTCCATTGCGGTTTT	60.235	20	253	1053	1305
60.154	20	TCTCAATAGCCCGTTTGGTC	60.074	20	151	113	263
59.296	20	TGAGCATTATTAGCACCCCA	59.136	20	269	2365	2633
59.992	20	GGGTCCTTTGATGGATTCCT	60.133	20	253	76	328
60.24	20	TTTTCTACGTCAGCACACGC	60.058	20	251	577	827
60.031	20	TCATCCACCACCCCTTTTTA	60.162	20	159	454	612
59.96	20	ACCCGTTCCACAACCTACTG	59.884	20	144	431	574
59.992	20	TCAACAGCCAGCATTGTTTC	59.847	20	174	58	231
60.232	20	CTGCACACACAAACCCTCAC	60.203	20	113	429	541
59.989	20	GAATGTCGTTTCAAAATAAAAGG	60.107	24	260	1191	1450
59.953	20	ATGCATTGCACAGCTAACCA	60.288	20	212	148	359
60.021	20	TCCGAAAAGGCGATAAAATG	60.033	20	226	74	299
59.971	20	TGGGTATGGGCTTAAAATGC	59.795	20	209	1075	1283
59.809	21	AATTGTGAACAGGTGGCAAG	58.623	20	245	547	791
60.032	20	CCCCTGATCAAGTCCATCAC	60.326	20	252	766	1017
60.127	20	ACAAAGTGATACATGCGCGA	60.288	20	206	602	807
59.933	20	TGAATGTTCCTTTGTGCTCG	59.84	20	168	484	651
57.795	21	TCTTTTCGGCAACCAATTTC	60.053	20	263	0	262
60.206	20	CAAGCGGATTTGATGGATTT	59.901	20	239	135	373
60.864	20	AATCCCAAATCCCATCACTG	59.605	20	224	428	651
59.635	20	TACCCATCTCTTTGCTGTCG	58.874	20	261	426	686
59.948	20	AAGGTCCGTAGTCCATCACG	59.989	20	233	3410	3642
59.767	20	TTCTTCGCGAGCTTCTTGAT	60.235	20	252	1180	1431
60.241	20	TGAAGCACCGAAAAATGTGA	60.234	20	254	1018	1271
59.982	20	AGCGACGCATGACCTTATTC	60.243	20	233	1757	1989
60.096	20	GATGGCACGGAGAGATGTTT	60.081	20	178	438	615
59.911	20	TGCTCTCAGATCCGGCTTAT	59.939	20	239	1301	1539
59.931	20	ATGGGTTATCACCAGATCGC	59.78	20	201	1013	1213
60.885	20	CGATTTACACACGCGCAC	59.859	18	259	17	275
59.966	20	CGCGGAGTTTAAGGAATGTT	59.225	20	213	1957	2169
59.924	24	CCCGATTGACATCCCTAATG	60.148	20	222	444	665
59.685	21	AAGATTGTGCCGATGGTGAT	60.348	20	173	459	631
59.2	24	AGGCTGAGACTGAAACCACG	60.444	20	235	888	1122
60.054	21	GTGACAAAAGGGCCTGAAAA	60.088	20	215	3131	3345
59.055	20	GTTCCTGCTTTGTGGTGGAT	59.973	20	234	35	268
59.81	19	TTGATCCGATGGTCCAAAAT	60.133	20	156	108	263
60.051	20	CCCCAAATTCCTAAGAACCC	59.639	20	275	4496	4770
60.183	21	ATCAAATGACAAAAACGCCA	59.016	20	228	393	620
59.773	27	AAAAATCCGTCACTAAATGGG	57.988	21	236	965	1200
59.311	24	CCAACAAATTGCATTGGACA	60.357	20	214	2	215
59.394	23	CAACGTGAGTTTGCCAAGAA	59.881	20	265	20	284
59.991	20	TGTGTTAACCTTTGGCTCCC	59.971	20	179	1215	1393
60.708	21	TTTTTCCAGACGTCGTCAAT	58.201	20	265	485	749
60.074	20	TGTTGGCATTCAAATCAACC	59.375	20	277	1178	1454
59.893	20	AATTGTCTTGCTTTCCAGCC	59.316	20	128	101	228
59.52	20	TGGGATGGACTTGGAATCAT	60.135	20	150	111	260

60.384	20	TTTAAGGGTTATCACCTGATTTTC	57.757	24	101	1173	1273
59.817	20	GCTCTTACCACGCCATTCTC	59.843	20	269	1393	1661
59.957	20	TCCCATATTGCCACCCTTTA	60.146	20	228	854	1081
59.638	20	GGCTGGCTCTGATCTTCAAC	59.957	20	248	2822	3069
59.141	20	GCCTTTTAGGAGCTCTCTGC	58.437	20	231	258	488
59.957	20	ATGCACAAACAATCCACGAA	59.972	20	214	2987	3200
60.033	20	CTACAATGGGCAAGGCATTT	59.96	20	264	627	890
59.997	20	TGTTGACCACTGTATCCCGA	59.96	20	216	711	926
57.422	20	CAAAACTCAGGCCACTTACG	58.431	20	265	1237	1501
60.036	20	AAATCCAGAAGCAATGCCTG	60.214	20	237	409	645
59.95	20	AGTTCTGATGGGGTGGATTG	59.779	20	150	1067	1216
57.059	21	CGGGTTGATTTTGTGTCTTG	59.021	20	278	1456	1733
59.743	21	CATTGCCTCCTTTCATGAGC	60.744	20	234	1215	1448
59.853	20	GGAAATTTTCGGGTGAACCT	60.166	20	223	1152	1374
60.124	20	TTGCATCGCATTCATCATTT	60.043	20	225	262	486
60.883	20	TTAACATCAAGGAAAGCCCG	60.067	20	263	701	963
60.073	20	ACTTGCAGGTTCTTGGCAAT	59.74	20	178	1644	1821
60.104	21	TGCATATGCGTTGTGTGTGT	59.621	20	235	4229	4463
60.088	20	TGGAATTGTTTGGCATTTGA	59.907	20	259	1097	1355
59.429	20	CCGCTTCCTACAGTACTCCG	59.891	20	153	1866	2018
60.149	20	TCGTCGAGAGTGAGGAGGAT	59.945	20	269	413	681
59.95	20	TCTCCTCTCACGCACTCTCA	59.846	20	269	710	978
59.561	20	TGTGGTTGTCGTCTCACGAT	60.162	20	128	1578	1705
59.924	20	CCTGAAATGGGGTTTGAATG	60.162	20	236	1177	1412
59.564	20	TTGGCAGAGGTGTGAGAGTG	60.022	20	154	423	576
59.657	25	CATAGTGGCTGACCACCAGA	59.701	20	242	461	702
59.82	20	TCTCCACAAGTTCCCGTTTC	60.088	20	112	2276	2387
60.103	21	TACGGTTGAAAACAATGGCA	59.969	20	236	786	1021
60.096	20	AGCAGCAGCAAACCAAGAGT	60.201	20	237	392	628
60.142	20	TTTCTGGTGAAACCGACCTC	60.088	20	257	414	670
59.041	20	CATTGGACGGATGGATTTGT	60.582	20	141	434	574
60.137	20	TCAGCCTTGTTTGATGCTTCT	60.008	21	192	1550	1741
60.544	20	GGTTCCCGCGTCATAAAAT	59.776	19	200	793	992
60.177	20	TTATGAAAACCGCAGCAGTG	59.872	20	197	318	514
59.871	20	GAAATTGAGCTCCATAGCCG	59.807	20	243	394	636
60.16	20	GTTGTGGGGCTGGAGATAAG	59.55	20	262	146	407
59.864	20	GCCTCTGATGCAAGTCCTTC	59.957	20	261	2507	2767
60.088	20	TCCTACCCATCTTTGCATCC	59.894	20	130	59	188
59.742	20	TCCTCTGATGCCGGAACTTA	60.734	20	233	2227	2459
61.137	20	GGTCTTCGGGTCTGGGTATT	60.19	20	229	1110	1338
60.624	20	ATGTCGGCATTCAAGGTTTT	59.434	20	254	1034	1287
60.028	20	TCAAAGCTTGAAGGCCTAGC	59.73	20	133	862	994
57.54	21	AAACCCATGCTCCACAAAAG	59.971	20	258	43	300
59.862	20	TCAAACTCCAAATGGTGCAA	60.088	20	243	36	278
59.247	20	TTACGTAAAAATGGGTTATTATTT	57.411	26	184	922	1105
59.49	24	ATATGGGACGTCCAAAAACG	59.685	20	130	2774	2903
59.983	20	CCAGATCTAATGGCCTCGTC	59.653	20	153	1133	1285
60.03	20	TAGGCGGATTGGTTTTTGAC	59.938	20	187	914	1100
60.003	21	ACCTTCCATAGGTTGGGAGC	60.328	20	111	87	197
60.958	20	AAAGAGTGGGGGAGGTTTTG	60.332	20	260	400	659
59.776	20	TTGTGAGAAGCCAAAGCTGA	59.716	20	168	3502	3669
59.685	20	GATCATTACTGGCCATGGGT	59.635	20	246	1128	1373
59.844	20	TTGTGTTCAAAACTTTGCGG	59.746	20	211	904	1114
59.939	20	TGGCATAGTCCTGAGTGGTG	59.701	20	246	479	724
59.971	22	TTCTTCTATCCCAATTTGCTTG	58.385	22	280	2706	2985
59.744	20	TCCCATTTCTTTTGTTCCCA	60.28	20	181	1152	1332
60.249	20	TTTTCTGCCCACCAGAAATC	60.051	20	201	2551	2751
58.541	24	TTTTTCTTTTTGCAGGATATTCG	59.646	23	198	410	607

60.24	20	TAGGTCACCGAATTCCATCG	60.853	20	279	46	324
59.517	22	TGCACTGCGTAATGGAGAAG	60.011	20	231	649	879
59.948	20	AAGGGAGGAATAGAGCCGAA	60.166	20	145	895	1039
60.286	20	TGACGGCCGATATTTACTCC	59.923	20	133	1096	1228
59.735	20	CCGTTGGTCAGAACCTTGAT	59.966	20	240	42	281
60.066	20	TTTTCGTTCTTTCTCAATTTCG	58.542	22	202	36	237
60.637	19	CCAAATATTAGGGTTATCACACG	57.562	23	217	836	1052
60.192	20	TTTGAGTTTGCATCTAAGAAGGTG	59.828	24	176	3217	3392
60.285	20	AGAGGGTGAGAGGGGACCTA	60.066	20	129	1516	1644
60.115	23	ACTAAATAGGCTAGGCCGGG	59.609	20	264	405	668
60.124	20	GGTTGTGGATTTGTGAATAAAAA	57.971	23	242	2451	2692
60.179	20	ATGGGCCCTCTAATCTCCAT	59.75	20	190	869	1058
59.968	20	GATGTTTTTCCAATGTGGGG	60.029	20	161	4224	4384
59.265	20	GAGCAAAGCTACCGAACTGG	60.015	20	178	610	787
59.874	20	CCCTTTTTCATGGTGGTTGT	59.688	20	199	4398	4596
60.008	20	CTAAATACCATGTGGCGGCT	59.982	20	275	10	284
59.166	20	GTAACCTGCCACCCCTGATA	59.813	20	260	1277	1536
59.882	20	TTTCGAATTTCCTAGGTCGG	59.155	20	165	2376	2540
60	20	TGGGACCCGTCTTCTTATTG	59.926	20	192	1243	1434
59.813	20	TCGTAGTAGGAGCACGAAAACA	59.941	22	265	21	285
59.996	20	GTAGCTCCTGAATCCCCTCC	60.037	20	249	580	828
59.955	20	CCCCCTAACATATCCACGTTT	59.952	21	105	474	578
57.02	24	CATCGGAGTTCACAAGTTCG	59.288	20	154	0	153
59.394	27	AAAGAACGAAAACCACACGG	60.008	20	190	0	189
59.322	21	TAGGGCCCATCCTATCACAC	59.773	20	271	973	1243
59.943	20	TGGGGGTGGGAGTTTAAGAT	60.549	20	250	372	621
59.933	20	GGGAAAACTTCCCACCAAAT	60.032	20	188	1036	1223
59.964	20	CCTGGATGATGCCAAGATTT	59.894	20	232	1908	2139
59.836	20	ATACATGCGTGTGCGTTCAT	60.026	20	269	2315	2583
60.134	20	TACCAATCCGGGTGATGTTT	60.051	20	211	1157	1367
59.99	20	ATCCCTGCTCCACTTTCTCA	59.803	20	112	491	602
58.869	20	TCTGATTTGTGCTAACCCTCG	60.256	21	242	392	633
59.969	20	TGATTGACTCATATGCCCGA	60.033	20	221	420	640
60.112	20	GCAATACCCTAATCCAGCCA	59.923	20	221	357	577
60.314	20	GTCCGGTAGGGTGCATAAAA	59.823	20	225	558	782
59.967	20	TGGATTGAAATAAGGGGTCG	59.756	20	138	229	366
59.679	20	GAAATCAGCACGAATCACACA	59.713	21	142	1010	1151
59.894	20	TAGGGTGAGGAAGAGGAGCA	59.943	20	193	465	657
59.978	20	AGTCAACCATGGCGTCTTCT	59.727	20	252	1394	1645
60.018	20	AAAACCGACCGCCTAGATTT	59.966	20	236	941	1176
60.096	20	GCTGAGCGGATTTAATCGTG	60.742	20	209	392	600
60.074	20	CACAAACATTCCAATGCAGC	60.119	20	269	736	1004
59.803	20	CGAGACATGGGAGCTCTAGG	59.966	20	192	2446	2637
57.743	20	GAATTTGTTGACGAATGGGG	60.17	20	277	748	1024
58.019	20	TGCGAGGATCTACGGACATT	60.624	20	268	737	1004
59.993	20	GCCGTTGTGTCGTTTTCTTT	60.154	20	198	74	271
59.869	20	ATCTCATCAGCAAGGCCAGA	60.914	20	221	1402	1622
60.228	20	GGTCAAATCGAGAACAACCC	59.386	20	251	718	968
60.005	20	GATGGTGCATTTTGTGATGC	59.939	20	260	523	782
60.344	20	TCTGTCATCGGTCCAGAGAA	59.34	20	277	2691	2967
59.496	20	TCAGGTTTCCACCTTTCTTGA	59.697	21	249	3334	3582
60.668	20	GCCATGGCCAAGAGTCTTAT	59.154	20	279	513	791
59.973	20	TGCTTCCAATGGTTGCATAG	59.688	20	248	9	256
59.986	20	TTGGGTGATAGGCCCAGTAG	59.948	20	169	501	669
60.088	20	TAGCCGACCCCAATTTAGTG	59.953	20	280	178	457
59.983	20	AGGTAATTTCGGTCGCACAC	60	20	255	208	462
59.803	20	CCACCACCATCTTACAAGCA	59.566	20	265	87	351
60.019	19	GAATTCAGCATTCCATTCCC	59.324	20	146	26	171

59.746	20	ATCACTTATCCCCCATGCCT	60.546	20	269	1254	1522
59.948	20	GTTGAAGGGGCTGACAACAT	59.973	20	196	1872	2067
60.762	20	AACATGATGAAGGTCCGAGG	59.927	20	188	1117	1304
59.945	20	TGTGCTTTGAGCAACTCCAG	60.175	20	280	211	490
60.104	20	TTGCGTGCAGGATCTAAGTG	60.011	20	272	201	472
57.894	20	TCAATTCCCCCACCAACTTA	60.162	20	262	459	720
57.681	27	ATAACGGGATTGAAGGAGGG	60.145	20	196	20	215
59.935	20	GCCTACATCCACTGGTCAAGA	60.126	21	280	2419	2698
60.478	23	TATCATTGTTTCGCGAGCAG	59.976	20	183	86	268
60.565	21	GGAGGCTGCTGACAAGATTC	59.957	20	231	394	624
59.994	21	TCTGTCCTTGCCTGATTTCC	60.195	20	275	264	538
60.265	20	TTGGGACCCCTTTCACATTA	60.162	20	175	1044	1218
60.14	20	GATCAGAGAAAACAAGCCGC	59.962	20	261	241	501
60.088	20	CCCCAGTTTTCCTTCCATTT	60.159	20	220	374	593
59.91	20	TGGAGTGTTGGATCTGTTGC	59.682	20	252	1040	1291
60.257	20	GCCCAAAGTTAGATGTGACCA	59.985	21	203	13	215
57.303	25	ACGAAAGCGGAGTTGAAAGA	59.993	20	249	484	732
60.14	20	GGAACATTAAGGCGCATGAT	59.929	20	252	368	619
59.816	20	TTCCCTCCTCTCTCTCTCCC	59.883	20	267	764	1030
60.231	20	TGATTCGAACGCTTGATTTG	59.809	20	224	834	1057
59.9	20	GACTAGCAAATTTCGGGACG	59.708	20	255	415	669
60.02	20	AATCCCACAATCCCTTCTCC	60.133	20	188	227	414
60.072	20	GCAGAGGTGTATTCTGTTGCC	59.755	21	177	1361	1537
59.05	20	AACTAATCCATGCTGCTGGC	60.243	20	212	18	229
60.448	20	TTTGCAAGACATCCAACATCA	60.104	21	196	1452	1647
60.073	20	TGACAATCACTTGCCACCAT	59.967	20	188	328	515
59.976	20	TCCCTGTGCAATCACTCAAA	60.24	20	169	2422	2590
59.734	20	CCCTCATTTGTACGGACTTGA	59.978	21	255	493	747
59.801	21	TAGGGACATCTGGGTGTGTG	59.388	20	182	2343	2524
59.883	20	TGGAGGACCTCACGTGTGTA	60.154	20	257	2238	2494
60.192	20	TCCTTGAACTTCTTCGGTGG	60.224	20	227	1462	1688
59.94	20	TCCGGCTCCGATCTATACAC	60.059	20	276	1687	1962
60.736	20	TGGTAAAAAGCGCTCGTACA	59.509	20	272	260	531
60.081	20	GGAGACCCCTACTTTGCCTC	60.074	20	186	761	946
59.72	25	CTGGTTTGAGGGGGAGTGTA	59.959	20	186	527	712
59.903	20	TCACTCTTCCGACTTCCGAT	59.803	20	231	600	830
60.134	20	CTCCTCCTCTCCAGCCATCT	60.891	20	208	1150	1357
59.795	20	TGCTGCTTCTGGTTGATGAC	59.992	20	227	95	321
59.862	20	ACAAAGCTCGAGTGGCATGT	60.865	20	103	5946	6048
57.201	21	CAAAACTATCGACCTTTTCGG	58.751	21	271	1236	1506
59.833	20	TGAAGTTTCCCCGAATTTTG	59.91	20	138	499	636
60.058	20	TTCAGAGTGCCTCTCTTGGG	60.523	20	148	2022	2169
60.119	20	GTTTGGGTCGAATTTGAGGA	59.91	20	264	66	329
59.673	20	AAGACGAGCAGCAGCACATA	59.77	20	276	42	317
59.485	20	ACCGGCCAAAGTAAGGCTAT	59.987	20	142	248	389
58.654	24	GTGGCGATATCCGACTCACT	60.104	20	206	666	871
59.935	20	ACCATCTCTCGCTCTGCAAT	59.981	20	212	978	1189
59.217	22	AACGGCAGGATTAAGTCCCTA	59.973	21	118	60	177
59.534	19	CGGTTTCAATCATGACTGTCC	60.368	21	198	3720	3917
60.182	20	AATGGTGTTTCCACTTTTTGC	58.986	21	202	641	842
59.775	20	TGCCGGATACAGATATGCAA	60.058	20	189	49	237
59.982	20	GTGAAGAGGAGCAAATGGGA	60.195	20	104	192	295
60.34	20	ACCCAACTCCACCCTCTTCT	59.968	20	191	516	706
59.831	20	CGAGTTTTGGTTCGGAAAAG	59.719	20	279	2155	2433
60.067	20	TTGATTTGACATTTTTGGAGAGAA	59.984	24	139	224	362
59.937	20	GGGAGGGAATTAGGGATTGA	60.089	20	264	115	378
59.542	20	TTTGAGTTGGGGGAATTTTG	59.772	20	243	332	574
59.143	22	TTTTCAGTTTCGAATCAGTTAGG	57.644	23	277	539	815

59.357	20	AACCCCTCCAAACCCTAGAA	59.799	20	233	416	648
59.773	20	TCTAGGCATCGAGATGCAGTT	59.992	21	135	591	725
59.816	20	CTATCATGGGCTGGAGGTGT	59.95	20	277	1086	1362
60.132	20	GAGGGATCGAGAAAGGGAAC	60.015	20	213	1302	1514
59.894	20	ACTCCAGGGTATTCCAGGCT	59.957	20	172	2338	2509
60.195	20	TTCTCTAGCTGTGCCCCTGT	60.012	20	107	625	731
59.789	20	GCGTTTTGATGATATATAAGTGTT	59.361	27	109	2594	2702
59.182	20	ATTTCTAATGGGCGCTGAAA	59.682	20	196	26	221
60.968	20	TCACGCAAGATGCAACAAAT	60.265	20	192	302	493
59.839	20	GCACCAATTATAGGATTTTGGG	59.588	22	262	5795	6056
60.112	20	TCCCTCTGCATATTTGTCCC	59.894	20	263	505	767
60.298	21	AATAAGTTTGCGAACCGCAG	60.264	20	143	501	643
60.132	20	TGCTGGAGCTACGATTAACCA	60.777	21	263	597	859
59.488	20	ATTCCTCAAGCATCATTCCG	60.036	20	130	985	1114
58.547	21	AACGGAGATTTGTCAAACGG	59.971	20	243	481	723
60.991	20	GGGTTGTCACGGCTAGGATA	59.955	20	278	159	436
59.813	24	ATTCGTGTTTGCAGTAGGGG	59.993	20	232	442	673
60.185	21	GGGTTTAATTTCTCGCATGG	59.411	20	217	1124	1340
60.08	20	GCTGTGCGTCGATTTCTTTA	59.066	20	220	876	1095
61.08	20	ACTCATGTGGATGGACGGAT	60.208	20	255	759	1013
59.198	20	TTGGGATTAAGGCTTTGGTG	59.931	20	190	2304	2493
59.849	20	GACTATGAAGGCTTGTCGGC	59.843	20	224	508	731
59.864	23	AACCTCTTCTCCTGCACCAA	59.844	20	275	20	294
59.726	20	AGGTTGGGAGTTGCTTCAGA	59.844	20	266	464	729
59.51	20	ATCGGTATAGGGCTTGGGTT	59.688	20	164	1174	1337
59.981	20	TCCTTGTGCTTTGGCTTTTT	59.861	20	209	4965	5173
60.827	20	TGCTGACATTGACGGCTTAC	59.871	20	276	1749	2024
59.888	20	TTCAACGAAGAAACCGAAAAA	59.723	21	239	796	1034
59.95	20	ATTTACGGGTTTGTGCTTGC	60.003	20	267	450	716
59.834	20	TCATCCCCATTGTTCTACCC	59.605	20	237	25	261
58.695	20	AAATGGGTGAGCCAATCACT	59.41	20	270	569	838
59.989	20	GTGAGTGCATGCAAGTGGAC	60.328	20	227	547	773
59.823	20	TGTTTGCAATTATTTCGTGG	57.176	20	194	394	587
60.111	20	GAGTTCTTTTGCTGGGATGC	59.82	20	270	260	529
59.52	20	CAATCCAAGAAGATGCACACA	59.707	21	264	1051	1314
59.445	20	GGCTGGTTTGCTTGAACATT	60.118	20	162	1547	1708
59.903	20	GCATCAGAGCAAAACGACAA	59.995	20	210	708	917
60.357	20	CACGACCCAACACACACATT	60.333	20	191	513	703
58.857	20	TGCATGATTGCTCCATGTCT	60.233	20	216	409	624
60.103	20	AAGCTATTGGCGGAGTATGC	59.347	20	276	383	658
59.445	20	CCTCGCGTAAACCCTTGTTA	60.124	20	267	2580	2846
59.78	20	GTTCATCTCAACCACGGGAG	60.51	20	259	356	614
59.917	20	TCTTCGGATATTGGGTCTGG	59.887	20	271	961	1231
57.809	20	ACCATGACCCTGAACAATGA	58.774	20	263	1640	1902
59.963	20	GGTGTGTGTGGAAACTGACG	60.047	20	266	191	456
59.278	21	ACAAGGCATCACTTCACACG	59.751	20	237	2260	2496
60.21	20	GATTGGTGGGGAGGTTAGGT	60.052	20	112	56	167
60.044	20	TTAACCCACCAAAAAGGTGC	59.839	20	194	472	665
60.111	20	AGCTCCTCAACTAAAGCCCC	59.848	20	116	330	445
59.812	20	CCGAATCTTTTCGTGGATCA	60.972	20	223	178	400
60.287	19	TTGAGGCTACCATGGGAAAG	60.066	20	260	157	416
60.517	20	TGGAGATTACCGGGTTTTGT	59.288	20	188	478	665
59.885	24	TCAAGCCATTTCCGAGAATC	60.155	20	260	724	983
60.22	20	GCCATTACGGGTGAGGAATA	59.784	20	278	1254	1531
59.91	20	GGAATGCTCTGTCTTGACCC	59.661	20	267	379	645
60.051	20	TGCTGTTCAAAGGAAGCTGA	59.716	20	249	2499	2747
59.975	20	TTTTGAGTTGGGATCTTCGG	60.044	20	274	788	1061
60.035	20	CATTTAATGCTTCGTGGAAAAA	59.151	22	279	1354	1632

59.676	20	GCAAATGGGGTACTTGGTTC	59.292	20	216	17	232
60.112	20	TGCCTTATCTGTCAGTCCCC	60.073	20	211	1210	1420
60.232	20	AAAAATTCTGGGAGGGGAGA	59.875	20	264	2122	2385
60.032	20	CCTCCCTCACCTCCACACTA	60.104	20	277	1137	1413
60.214	20	CCCTGTCGAGTCTCAGCTCT	59.732	20	272	2246	2517
59.953	20	CGAATTTGCAAAACCGAAAT	59.943	20	272	49	320
59.169	20	TTCGTTTAAATCGATTGGGG	59.767	20	166	1075	1240
58.663	23	GGCGCGACAGTTATAGAAGC	60.01	20	174	0	173
60.636	20	TGGATGTGAATAGGGTGGAAA	60.177	21	240	482	721
60.096	20	TCCTGTGAGCAGAAGGGAGT	59.986	20	165	143	307
57.624	26	GCGTAAATTTTGAAAGAAGCA	57.304	21	280	2	281
58.393	20	CAAGCGTGATTAGCCATCAA	59.833	20	247	210	456
59.872	20	TCAGAGGAGCAGAATTGGGT	59.803	20	253	6125	6377
60.053	20	AATGCAACGGTTTTAGTCGG	59.996	20	121	512	632
59.902	20	TTCATGTTTGCTTAGCCGTG	59.872	20	262	2451	2712
60.008	20	TGCAAAGTCATGGCTAAAGAAA	59.89	22	279	2284	2562
59.288	20	GGATGGTTCTGTGCAGGAAT	59.934	20	275	377	651
58.874	20	CGAACACAGGGCAATAGTGA	59.716	20	147	111	257
58.901	23	TGTCCATTGATTGCTTGATCC	60.859	21	274	23	296
60.006	20	AGAAATGGAAGATGCCATGC	60.043	20	195	130	324
60.757	20	TGGATACCAAAAGCTCCTGC	60.214	20	172	2192	2363
59.973	20	CAACAAGAAAAATGGCGGTT	59.975	20	172	138	309
60.194	20	GTTGAGGACAAAAACCCGAA	59.948	20	274	171	444
59.83	20	TCGAGTTCGGCCTATTTAGTT	58.039	21	224	167	390
59.927	20	TTCCAACTAAGTCATCGGGG	59.926	20	225	558	782
59.96	20	CGTTTTGACGATATATAGTGTTTT	58.68	26	157	1871	2027
59.988	20	ATTGCTGGAATCAGACGACC	60.081	20	249	1599	1847
59.893	20	ATAAATTGCAGGCCGATACG	59.95	20	275	1909	2183
59.266	20	TGTCACTGGGGAAACGATTA	58.973	20	234	584	817
59.44	20	GGAGTTAAAAGCACCATTGAGG	60.001	22	267	1121	1387
60.074	20	ATGACCCTCATTCAGCCAAC	59.934	20	231	114	344
59.717	20	TCAAATTTTCTTTCCGGTTCA	59.551	21	196	9295	9490
59.95	20	TGCTATAGGGGAAACAACCG	59.953	20	169	1773	1941
59.434	20	TAAGATTCGGTTCGGTTCCA	60.439	20	277	957	1233
60.003	20	TTTGAGTTTGCATCTAAGAAGGTG	59.828	24	214	2497	2710
59.031	20	AGAGGAGTTGGGAGAGCAGG	60.921	20	260	409	668
58.984	25	TCAATGGACTACTCCCAGCC	60.073	20	244	2	245
60.16	20	TGAGTTTGGTGTGTTGGCAT	60.008	20	241	315	555
59.944	20	TGATAATGCAATGGCCGATA	59.882	20	228	103	330
60.183	20	TCGATGATGACCTGCAGAAG	59.942	20	114	2570	2683
60.156	20	TGAGATGGTCACCCTTCCTC	60.048	20	213	723	935
59.751	20	CAGAAGTAAACAGACGGCCC	59.734	20	153	168	320
60.096	20	TTGGTCATCGCAATTCGTAG	59.688	20	102	346	447
60.119	20	TCGCAACAAGAAGTAAAAGGAA	59.052	22	258	270	527
60.022	20	TGCTAGAATGACCTGATGCG	59.972	20	155	62	216
60.476	20	GGAGGTTTCACACCCCAGTA	59.82	20	220	839	1058
59.126	21	TATATAAGAAACGGCGGCCA	60.424	20	109	1274	1382
60.066	20	TTGTTGGGGAAGGAGAACAC	59.943	20	179	553	731
60.015	20	CGTCAAGCAATGCCAGATAA	59.833	20	258	467	724
60.134	20	ATGATGCAACATCCCTTGTG	59.374	20	191	5049	5239
59.813	20	CAGAGGGTTTCCAAAATGTCA	59.956	21	204	1200	1403
59.851	20	GAAAAATGGCAGAGTGCTCC	59.82	20	237	2209	2445
59.971	20	CCTGGGTTCTTGGTTTTGAA	59.942	20	242	1294	1535
60.169	23	AATCCAAGGAGGCGAGATTT	60.039	20	216	8	223
57.499	24	GGGCCAGAATTTCAGTTTCA	60.051	20	178	9	186
59.671	19	CGATTAGCGAGTGATGGGAT	60.059	20	104	0	103
58.503	21	TGCTGTTTGCATTTTAAGATGAGT	60.186	24	185	827	1011
58.211	25	CTTGGCGCCTGATAGTCTCT	59.598	20	180	41	220

59.993	20	CACAAACTCACACAATGGGC	60.008	20	204	1769	1972
59.292	20	TGATCTTGGGGAATCTCTGG	60.003	20	127	13	139
60.227	20	AAAGGTTTTGATTTTCCGGC	60.292	20	123	49	171
59.945	20	ATGGGCTTTAGTCCCCTGTT	59.827	20	229	460	688
60.038	20	TGGCTTCTGTTTCTCCATCA	59.369	20	249	745	993
59.653	20	GGACTGGAAGGAAGGGAAAG	60.045	20	234	1149	1382
59.853	20	TCAGTGTCACCGTTCTCTGC	60.03	20	251	531	781
60.058	20	CGGTTGGAGAAGTCATGTCA	59.676	20	205	1651	1855
59.969	20	CTTGCAGGACATCAATCGAA	59.799	20	270	1505	1774
59.813	20	GACGTAGCAAACGCAAGGTT	60.313	20	256	1522	1777
60.142	20	TAGGGGCTAACCTTAGGGGA	59.918	20	218	218	435
60.034	20	CTGGCCATTGATTCTCCCTA	60.029	20	186	2153	2338
59.763	20	TCATGCTTATTTTGCAAGGG	58.769	20	239	8300	8538
59.942	20	ATACACGGCCGAGTGACTTC	60.142	20	193	800	992
60.051	20	ACCAGCTAGTCTTTTGCCCA	59.875	20	257	1609	1865
60.104	20	AGATTTTGCACCAACAACCC	59.836	20	170	1220	1389
60.173	20	TTGGTTTAATGCTTACGGGG	59.826	20	192	2664	2855
59.268	20	AACGCTGGAAGAATGTGACC	60.119	20	272	838	1109
59.668	20	AAACCGTGCATGAACTTTCC	59.978	20	129	296	424
60.315	20	CACAGAGCGCACTCAAAGAG	59.922	20	252	260	511
59.75	20	AAAACAGCAGCAGTATGCCA	59.493	20	246	3851	4096
60.126	20	CTATCCGCAGGCCAAGATAG	59.823	20	224	319	542
59.462	21	CAGCATGAATCAAACAACCAA	59.576	21	256	716	971
60.159	20	ATTATCTCGATCGGCCTCCT	60.024	20	253	126	378
60.067	20	TCACTGCGCTCATTGTAAGG	60.011	20	244	477	720
59.978	20	GCATCGGACATTGGAGCTAT	60.066	20	260	580	839
59.6	20	AGTTTTTGCGCAGGAATGTT	59.752	20	231	3370	3600
60.074	20	TAGCCGATAAAAATGGCACC	59.928	20	279	449	727
59.933	20	CATTCCATTCTCACCCTCATC	59.351	21	116	1578	1693
59.982	20	TTGTGCTTCAACACCCTTCA	60.278	20	181	891	1071
60.692	20	TGCGTTTGTTCTAACTTTATCAGG	59.734	24	268	2792	3059
59.737	20	CAGGGGGACTTTAATGGGAT	60.011	20	269	137	405
60.361	20	CCAAGTTCCAAGTGATCGGT	59.966	20	119	1142	1260
60.012	20	GCGAGCAAACTCGGTTAAAG	60.018	20	256	2654	2909
60.008	20	AAAACATGTGGAGGGCAGTC	59.973	20	233	227	459
60.111	20	TGTAATGCCTCCTTTCAGCA	59.42	20	267	942	1208
60.197	20	GGATTGCATGGTTTGCTTTT	59.945	20	273	224	496
60.121	20	GACAACAGAAAAACCACGCA	59.74	20	271	53	323
59.995	20	TCGGGGCGAATAGAGACTAA	59.801	20	179	317	495
59.546	20	GGGATTAATTCCCAGCATGA	59.722	20	238	1117	1354
59.984	20	GCCACGCTCTTTCATTTCAT	60.221	20	201	968	1168
60.142	20	ATTGCATTCTTGGTGTGTGC	59.577	20	270	1056	1325
60.924	20	TTTTAACGATGGATCATGTAAGGA	59.748	24	175	1408	1582
59.836	20	ATTTCACTTTGCCAGCAACC	60.118	20	140	785	924
59.264	20	CAGTCGGATTCGTTTTGGAC	60.495	20	202	1945	2146
59.853	26	CAGATCTGATGGCCCAGATT	60.034	20	114	490	603
60.495	20	TCAGGTTTAGTTGTTAGGTGTTTT	58.77	25	257	4870	5126
59.792	20	GCACAATCAAACCTTGCCTT	60.118	20	163	2259	2421
59.973	20	GAAAAGAGAGGGAGATGGGG	60.008	20	247	3217	3463
60.075	21	TCAACTCTTGTGGATAACTATTTT	59.968	26	279	1209	1487
58.12	20	GAACAGGTTGGTTTGCGTTT	60.015	20	106	6	111
59.974	20	TGCACAGCTCTAACAAACACAA	59.578	22	264	456	719
60.187	20	TTCTCAGTGCTGATGTTGGC	59.992	20	278	568	845
60.074	20	CTTGAAGCGCCTGTTTCTCT	59.757	20	228	245	472
59.955	20	CCTTTGCCAGATTGTTGAAA	58.745	20	200	2038	2237
58.836	20	CACAGCAGACGCAAAGAAAG	59.781	20	200	1881	2080
60.413	20	TGCGTTTTGATGATATATAGGTGTT	60.054	26	271	1314	1584
60.188	20	TGGAAAGAACTGGTTCAGGG	60.081	20	182	545	726

59.946	20	AAGGAGGGGAAGAATGGAGA	60.008	20	260	5715	5974
59.472	20	TTCCAAAATCGCAAATCTCC	60.016	20	224	0	223
60.066	20	TGGTGAAGAGTGTGTAGCCG	59.897	20	206	1090	1295
60.008	20	ACCCGAGAGAGAGATCGTGA	59.945	20	185	323	507
59.823	20	TGATAACAGTGAGGCCGGAT	60.483	20	261	559	819
59.955	20	TTATGATGCCTAGTGGTTGGC	59.974	21	252	367	618
59.984	20	GAGATCCCCGATGATTCTCA	59.971	20	226	552	777
59.937	20	CTTGGATTGAAGCTCAGCAGT	59.63	21	260	441	700
60.039	20	AAGCAAACGACTTGTTCCAGA	59.906	21	210	1661	1870
60.046	20	CAGATAATGGTGGGCCAAAT	59.645	20	101	535	635
59.984	20	TTCAAATGCCAGTTTTCACG	59.706	20	186	1007	1192
59.561	19	CATTTTTGGAGGAGATTCTTCG	60.068	22	104	1910	2013
59.587	20	GTTATGATGGGAATGGGAGG	59.055	20	113	1869	1981
59.873	20	CGTTTATCGATTAGCACCCG	60.468	20	216	713	928
58.874	20	TTTGCGTGTGAACATCAACC	60.562	20	210	2764	2973
58.673	20	ATGCAACGTCGAGGTTTTTC	60.118	20	243	224	466
59.906	21	GCATAGGAATGCCAATTCAA	58.577	20	268	32	299
59.157	20	TAATAGCCACGAAAGGGGTG	59.953	20	202	901	1102
59.967	20	CCCACTTCCCAACCATCTAC	59.259	20	262	481	742
59.72	21	TCCATTCCGAAAATCAAAGG	59.872	20	139	2	140
60.166	21	GATTCTTTGAATCATATTCCACCTT	58.865	25	275	256	530
57.452	26	CTCTCTCTTCCTCACCAAGCA	59.73	21	190	16	205
59.955	20	TGTGAGAGGGGTAAAGGTGG	59.959	20	256	1045	1300
58.775	24	GTTGGGCCCGTTAGGTTTAT	60.075	20	198	36	233
58.517	20	CCTCGGTCTATCTCATTTTTATCA	58.715	24	272	1022	1293
59.803	20	ATGATTGGGATGCCATGTTT	60.021	20	177	600	776
60.003	20	TCGAAATTCCTTGAGGTTGG	60.044	20	148	2152	2299
58.974	20	TGTGCACCCCATTAAAGGTT	60.227	20	167	903	1069
60.236	20	CCCAACCCTTCACACTCTTC	59.549	20	270	121	390
59.921	20	TACATTCCATTGTTTCGGCA	59.93	20	158	551	708
60.171	20	TGCAAATGAGAATTGGGACA	60.049	20	154	560	713
60.827	20	ATCTTCGGCCTCTCTCTTCC	59.919	20	124	2282	2405
60.158	20	ACGGATTCACCAGAACAAGC	60.119	20	254	1975	2228
59.91	20	AGTCAACATTTGGCCCACAC	60.823	20	198	194	391
60.022	20	GGGAAGACTGTGTGAAGGGA	60.088	20	143	68	210
60.011	20	GGTGTGCTCGGATTTTTGAT	59.939	20	162	262	423
59.313	21	TGCGAAATTTAAGCCAAGTG	58.958	20	228	559	786
59.82	20	CCTTTGGACTAAACCACCCA	59.824	20	203	1835	2037
59.992	20	ACTCCTTGATGGTGGAGGTG	59.962	20	219	1207	1425
60.081	20	GTAATCGAATCTCGCCCTCA	60.177	20	165	565	729
59.971	20	GGCCAACAACATGAAACTCA	59.547	20	196	1033	1228
60.346	21	CGGCGCTGTTTACTCTTCTC	60.154	20	221	1529	1749
60.197	20	CAACTGGCCCTGATGGTAAT	59.813	20	255	248	502
60.012	20	TCTCCACCACCATTCTCACA	60.088	20	242	1063	1304
59.866	20	TTGTTTTGTGCGTTATGTGGA	60.022	21	190	1126	1315
59.935	20	TCAACTTTCGGAAGCGTACA	59.464	20	271	391	661
60.525	20	CACGGTTCTTCAGCAACTCA	60.025	20	261	177	437
59.769	22	AAGGTGGAAAAGGGTTGCTT	59.976	20	264	574	837
59.889	20	CCGATCAAAGCCTTCTCTTG	59.948	20	174	878	1051
59.976	20	ACGGAAATTTCACTATGCCG	59.96	20	230	1411	1640
60.434	20	AAGCAAAATGGATAGCGTGG	60.096	20	232	105	336
60.203	20	ATAGATTCCAAGGGCAGGCT	60.06	20	266	1198	1463
60.249	20	GGAAGTGGTCCCAGTTTGAA	59.943	20	189	318	506
60.102	23	GCGGTATGACTTCATGGGAT	59.78	20	269	1176	1444
60.304	20	CTGTGACACGGAAATTTGAGA	58.761	21	191	2083	2273
60.014	20	TGTTGGATTTGGGATCCTCT	59.336	20	224	1493	1716
60.014	20	ATTTGCACATCAAACTCCCC	59.797	20	134	578	711
59.724	20	GCCTTTCTCGCTCTCCCTAT	59.947	20	270	5568	5837

59.945	20	GGTGGGGGTTATCTCCTGAT	60.015	20	218	505	722
60.025	20	AAAAACGGATGAGAAAGCGA	59.823	20	274	508	781
59.982	20	GTTGAAAGGAGGGACGAACA	60.088	20	181	19	199
60.17	20	CGTGTATATGCTCGAGATGGG	60.496	21	200	2155	2354
59.744	20	TGTGTGATGGAGCTTCTTCTTC	59.478	22	198	1246	1443
60.096	20	CTGCCACTCTGCAGGTACAA	60.049	20	265	635	899
59.803	20	CCCTTAGCTACCCAAAAGCC	60.089	20	102	1248	1349
59.317	20	CACACGCACACACAAAATCA	60.204	20	246	498	743
59.95	20	CAACTTTCCGCTTCTCCAAC	59.853	20	212	533	744
59.984	20	GGGGGCCAAGAAAAGAGTAG	60.068	20	200	883	1082
60.134	20	TAACAACTTCCTGCGAACCC	60.11	20	194	642	835
59.823	20	ATAAGAAGGGCTGCCGAAAT	60.061	20	240	1369	1608
59.609	20	ACCAGGAATCGAATCAGCAC	60.081	20	216	613	828
58.743	25	ATCAATGACCACCCAACCAT	59.91	20	197	0	196
59.967	20	CTTGCTTATCCCTCGTCCAA	60.206	20	176	1218	1393
59.054	21	GCCCAACACTAATTGCACCT	60	20	183	642	824
59.656	21	ACAGGTTGAGGCCCCTTAGT	59.994	20	124	74	197
60.037	24	CAAGAATAACACGCATCCGA	59.688	20	279	452	730
60.147	20	GCATGGCCCTGTCAATTAGT	59.962	20	209	3530	3738
59.297	20	GAATTGGGCAATGGAGAAGA	60.014	20	125	74	198
58.935	25	CATGGACCCCACATGTCATA	60.048	20	180	239	418
59.939	20	CGATTTCGAGTTCCTGGGTA	60.066	20	246	785	1030
60.089	20	GACATTCGTCGTTGAGGTGA	59.682	20	197	30	226
59.757	20	TCGAAAAAGGAAAAATAAAATTC	59.468	25	203	21	223
59.95	20	TTTCGAAGATCAATGGACGA	59.2	20	274	2114	2387
59.945	20	GCACAATGCACATACAAGGG	59.995	20	106	42	147
59.081	21	AAAGGAGACTAGTGGCTGCG	59.639	20	261	518	778
60.056	20	TGGCCTAATTTTGTGTGGTTT	59.37	21	219	1613	1831
59.597	20	TCATACTGAGCTGAATAGTTACCG	57.707	24	104	4	107
59.369	20	CAGGATGGAGTGCTTCAGGT	60.261	20	145	626	770
59.973	20	AAAAACATGAAGTCGGGCAC	59.978	20	199	30	228
60.195	20	ACAGATTCCCGTAGCCACAC	59.997	20	250	697	946
59.927	20	TACTTCGCACTTTTCCGTTG	58.964	20	205	687	891
59.823	20	CCACCCACTGCATTCTCTCT	60.261	20	189	761	949
59.588	20	CGAGGTTTGTACCGTTCAATTT	60.269	22	144	1016	1159
60.206	20	TGTTTTATCGTCCTGAGGCA	59.272	20	264	502	765
58.379	22	CCCTTCTTCTGATGTTACCGA	59.181	21	266	635	900
59.322	20	CATCTTATAGCGTGCGGGTT	60.117	20	176	1566	1741
59.813	20	CCGTTTCAATCGACACAACA	60.552	20	127	4973	5099
58.225	23	GGTTTTTGAGGGTGGAGTGA	59.943	20	234	2351	2584
59.997	20	ACCGTTGAGACAGTTGGGAG	60.151	20	253	1602	1854
60.012	20	ATCGGAATTGATTTGATGCC	59.728	20	210	102	311
59.978	20	TGCGTCTGCTAATCTCCCTT	59.978	20	267	1776	2042
59.709	20	CCCGTGTAACTGGTGCTTTT	60.03	20	245	2970	3214
59.966	20	GAATGAACTACGGCTTGGGA	60.074	20	207	123	329
60.029	20	TGCCCTAACAGACCTTGACC	60.111	20	249	392	640
59.706	20	TTGGCCAGGAACTTAGAAGC	59.452	20	234	289	522
59.878	20	TGTTGAGATGCCTCAATCAAA	59.262	21	274	427	700
59.95	20	GAACGAGCATTGGAGGATTC	59.635	20	102	3913	4014
60.073	20	TGGATTGGTTGAGAAGGGAG	60.042	20	141	1363	1503
60.214	20	TTGCCATTTTCAATGATCCA	59.867	20	264	2065	2328
60.012	20	CAACCACACAATGCTTTTGG	60.004	20	183	599	781
59.651	20	TTTGTTTTGTAAATGGTGCTTGA	59.562	23	101	3093	3193
59.172	21	GCTCAAGTTGATTGTAGCGG	58.529	20	260	136	395
60.277	20	GCAGAAATTTGAACCGGGAT	61.184	20	215	543	757
59.694	20	GCATAAGATTCAGACGGGGA	60.036	20	142	48	189
59.707	20	GTTTGCTGTGCTGTCTGCAT	60.064	20	275	321	595
59.807	20	GCTCTGCTTTGATCAGCTCC	60.249	20	237	448	684

60.095	20	CGCTGGTAATAGGACCCTGA	60.088	20	194	4462	4655
60.343	20	GACGGGGTTTCACTTTTTGA	59.948	20	233	369	601
59.978	20	AATGGTAATCCGATTGGCTG	59.784	20	162	673	834
59.492	22	CTGCATAGATGTCGAACCGA	59.823	20	275	607	881
59.933	20	AAATAAAGCGGCAACCACTC	59.229	20	179	1363	1541
60.096	20	TGAGATGTCAACAGGGAACG	59.676	20	171	885	1055
60.051	20	TTGCAAGTATTCTCTTCGCA	57.257	20	225	541	765
59.919	20	TCCATTCCGAAAATCAAAGG	59.872	20	222	2405	2626
59.391	21	GGGTTTATTTGCTGGCTAGG	58.718	20	262	625	886
60.036	20	TCCACCTCTCCACCAAATTC	59.903	20	211	3185	3395
60.034	20	TGACGCTCGCAGTATTTTTG	60.014	20	244	640	883
59.664	20	TGGCCTTGCACAAACTAAAA	59.344	20	280	1126	1405
59.941	20	GAATGGGAAAATGGAGGGAT	59.959	20	279	323	601
59.966	20	TATTTAATGCCGCACCTTCC	59.928	20	204	1210	1413
60.128	20	CCATTTCAAAATCCTGGCTC	59.505	20	222	2692	2913
60.155	20	TGCCAGAATGTTGTTCGTCT	59.293	20	261	612	872
59.851	23	TTGAATATATTATCAAATCCAATC	59.038	27	151	601	751
59.973	20	CGTTATTGCGTTACGGGTTT	59.89	20	178	776	953
60.014	20	TTTGTAACTGGATCATGGATGG	59.685	22	131	630	760
59.864	20	GTGAGAGGGAAAACGATGGA	60.05	20	170	1203	1372
60.066	20	ACCACCAGAAAACGGTGAAG	60.005	20	197	181	377
59.888	20	TCCATACGCACTGCTCTTTG	60.011	20	279	954	1232
59.84	20	TCCAAAATCAGAAAATGGCA	59.087	20	247	584	830
60.116	20	TCACACACACTCACACGCAT	59.772	20	265	457	721
59.722	20	TGTCAACAAAAGCTTAAAACTCC	60.192	24	211	654	864
60.009	20	CACGACGGATATTTGGCATA	59.401	20	276	627	902
60.206	20	GAATTTTAGTGTTCGGGCCA	59.938	20	272	224	495
60.088	20	TACTGGAGTGGTCTGTCCCC	59.962	20	174	590	763
60.54	20	GAAAAAGAGTGGCTTTTGCG	59.996	20	157	4818	4974
60.081	20	GAATGCCGGTCTGAAAACAT	59.939	20	275	12	286
60.243	20	TAGTTGGTGTGTGTGCTGGG	60.629	20	251	1147	1397
59.729	20	GATGTTTACTCGCCCTGGAA	60.074	20	236	460	695
58.746	20	GGCATATTTGGGGAGAGGTT	60.152	20	279	845	1123
59.779	20	CCCACACTCTCCTCCAAAAG	59.691	20	242	192	433
59.679	20	GTTCTAGCCCAAAACTGCCA	60.249	20	180	1459	1638
60.012	20	ATGATCTTCTCACGGGAACG	60.073	20	210	2345	2554
59.691	20	TAGAAAAGGTTCGCCATCCC	61.303	20	242	3138	3379
60.081	20	CTTCACCACCGTTGATTCCT	59.966	20	104	104	207
59.973	20	AATGTCCCGGTTGAGTCTTG	59.966	20	179	693	871
59.933	20	TCATGCAAGAAAACGTGGTT	59.174	20	184	1100	1283
60.192	20	AGAGCATCCACGTCAGCTTT	60.02	20	165	1360	1524
59.779	22	TTCGTGGAAAACCGTTTAGG	59.968	20	279	88	366
59.604	20	TCACAAACCCTTGCTTTTCC	60.088	20	163	1544	1706
59.88	20	TGAGGATGAAGTAGCGTTGG	58.874	20	185	635	819
59.855	20	GGACATATTTTGTGGGACGG	60.051	20	214	4035	4248
59.988	20	TAATGTCCTTGGAGATGGGG	59.744	20	123	1198	1320
60.096	20	GTCGCCTCTCTTTCAACGAC	59.997	20	229	922	1150
60.135	20	CGTATTCAATAGACACATTGCCA	59.903	23	239	1657	1895
60.05	20	CCAATTTTCCCCAACTCAAA	59.772	20	257	2278	2534
60.026	20	AAGCAAGAAACCGCTTGAGA	60.132	20	211	4626	4836
59.918	20	GGTCGATTACTCCACCCTCA	59.927	20	183	237	419
60.008	20	ATCTGTCAGCATTTGGACCC	59.934	20	216	1003	1218
60.111	20	CATTTGAAAGAATACAAAACGAC	58.295	24	280	255	534
59.778	20	TTTGTTCCACCACTCCATCA	59.935	20	211	86	296
59.615	20	ATGAGTGAGGCTGGAAGCTC	59.56	20	203	1115	1317
59.17	20	TCGGACAGAAATAACCTCCG	60.066	20	130	9	138
59.002	20	CACCAAATTCAAGCAATGGA	59.518	20	238	657	894
60.005	21	TTTACATCATGTGGTCGCGT	59.995	20	234	1407	1640

59.51	20	GGTACCGAAGTTGTCATCCG	60.375	20	225	1169	1393
60.639	20	TAAAAATTGCATGCACCTGA	57.788	20	268	1788	2055
60.059	20	ATCTCGCACGCGATAAAAAT	59.71	20	156	5015	5170
60.428	21	GGCTGTTGCTGAGTGTGAGA	60.187	20	279	482	760
59.903	20	GAGTATCGGCTGTGGGTTTC	59.556	20	264	2951	3214
59.572	20	GCCACACCTGACATTGCATA	60.549	20	187	692	878
59.621	20	TTCCTTTTCTTGGGTGGATG	59.903	20	259	4376	4634
59.9	25	AATAAGTGCTCCGACTCCGT	58.817	20	266	7	272
60.027	20	GGAGCATTGCCATTGTAGGT	59.962	20	247	1453	1699
60.066	20	TGTACTGAATGCATCAAAACCC	59.867	22	171	628	798
59.831	21	CCCCATTCCCTCTCTCTCTC	60.149	20	266	32	297
60.081	20	CAGGCTCTCCTCTCTCTCCA	59.81	20	259	1398	1656
59.928	20	GTGGGAGAAATGGGGAGAAT	60.133	20	274	624	897
60.359	21	TGCAATAGGTAGAGAAAAGTTGA	58.935	25	196	670	865
59.036	22	TGTTATTATTGGAACAGCACCC	58.878	22	216	1680	1895
59.637	20	TGTTGACTCCCACATGTTTCA	59.992	21	258	2101	2358
57.078	21	AGTGGTACACGTCGGGAAAA	60.41	20	249	406	654
59.882	20	ACCATCGATCTCTGCTTGCT	59.981	20	256	478	733
58.664	21	AAGTCAATTCCGTATGACAAAAA	57.752	23	194	62	255
60.407	20	AGCAAAAAGTTCTCCGGCTT	60.373	20	232	1321	1552
59.946	21	AAACTGCTGCCTTTTGCATT	59.889	20	232	739	970
60.19	20	CATCTGCACCCATTTCCTTT	59.933	20	188	706	893
60.199	21	CCGAGGAGAACTCTTTGGAT	58.323	20	269	1154	1422
58.649	20	TGTACTGCCACTTGGGTGTC	59.597	20	154	1396	1549
59.933	20	TGGATTCGTCCAAAAATTCC	59.739	20	240	22	261
59.924	20	GGCCAGATTAATTCTTTGCG	59.682	20	227	1811	2037
59.801	20	TCATTTGCGCTTGTCATTTC	59.816	20	279	757	1035
60.011	20	GGGCGCTATCCATTATGAAA	59.892	20	120	1250	1369
59.955	20	CAACAGAATTTGCGAGACGA	59.988	20	255	638	892
59.115	21	CGGCATTCTATTGTGTGAATG	59.052	21	232	1126	1357
60.219	20	TCTCATTTATGCATCACTAATTTG	59.142	26	231	111	341
60.118	20	CTGATTCCTTCCTCTTCCCC	60.008	20	251	4672	4922
60.228	20	GTGGACAAGAATGGTTTGGG	60.21	20	245	1890	2134
59.959	20	CTCAGATCCTGACAGCCCAT	60.223	20	276	1334	1609
59.904	20	CACACCCATGAAACTGCAAC	60.008	20	212	1528	1739
60.033	20	CATGGTCTATGAAATGCCCC	60.155	20	244	740	983
59.569	20	AAGCGAGAAGAAAGAGCGTG	59.898	20	274	1420	1693
59.756	20	GGGCAGAGAACGTGCTTTAT	59.34	20	239	1696	1934
60.11	20	CGATTTGGATTCGAATTCTGT	59.033	21	198	621	818
59.636	20	GAGGAGAAGGAGGGAGGAGA	59.883	20	169	1078	1246
60.183	20	GCCGACTCACCAACTTTCTC	59.851	20	212	39	250
59.722	20	TCTGACTCGCTTTGATGTCG	60.136	20	183	287	469
60.008	20	GATCCAACGGCTGAAAATGT	59.939	20	240	3177	3416
59.545	20	CACTCTCTGTTGCCCAATCTG	60.838	21	228	100	327
60.606	20	TGTGAAAACGTTGGTTGTGAA	60.035	21	228	4478	4705
59.817	20	CACACCGCACAAATTCTCAT	59.572	20	255	373	627
59.195	21	CAAGACTGGACACTCCACCA	59.705	20	114	1176	1289
60.088	20	CGGGAGAGCAAGTTTTGAAC	59.853	20	174	84	257
57.014	20	TGATGTTGATAAAACTGATAAATG	57.4	25	279	627	905
58.876	21	TCATCCAATGGTTTGGTTTG	59.222	20	275	700	974
60.362	20	ACTGTGAAAGGTGCCCAAAC	60.012	20	273	663	935
59.862	20	TTGGAGGAGACGATGAAACC	60.05	20	160	371	530
60.032	20	AGTGCCGATTGAAGTGCTGT	60.865	20	232	1879	2110
60.162	20	CGAAATAAGGAGGTGTTATAAAG	60.434	25	227	1717	1943
60.374	20	TTGCACGATAGCAGTAACGG	59.895	20	193	678	870
60.074	20	GCTACAGCAGCCATTGATGA	59.979	20	159	1968	2126
59.44	20	TGATTGCACCTTACATGGGA	59.924	20	255	2276	2530
60.104	20	GATAAATTAATCGCTGGCTGG	58.73	21	103	726	828

59.971	20	CATTTTGGAGGGAAAGTGGC	61.728	20	280	1706	1985
59.545	24	TGAATGGTAAATGAACCGCA	59.93	20	109	2	110
59.864	20	TACAAAACCATAACACGCGG	59.486	20	266	210	475
60.256	21	TTTTCCTTGCAAGTTCCGTT	59.724	20	221	0	220
59.595	20	GTCCCTTGTTGGGCAGTAAA	59.971	20	260	1343	1602
59.286	22	TCCACCCTCAGAAATTCAAA	58.117	20	273	1959	2231
60.894	24	CTTGCAGCATGGTCAAAGC	60.555	19	140	1695	1834
61.292	20	TCACCACAACCAAACACAAAA	59.889	21	274	1075	1348
59.496	20	TGCTCTCATTGTAATCTCCACC	59.198	22	161	1886	2046
60.036	20	CGGTTATCACCGGATCGC	62.397	18	190	3149	3338
60.073	20	ACTGAGATGCTCAAGCCGTT	60.02	20	209	1318	1526
59.882	20	TCTGTCGCCTTGAATGATTG	59.799	20	245	860	1104
60.016	20	TTTGGTACTTCATCATTTAAAAAC	59.446	27	255	733	987
60.195	20	CAATGCAGCAGGAACAAGAA	59.988	20	244	144	387
59.953	20	TAGGGCCCTTAGTTCGTGTG	60.125	20	230	443	672
58.331	27	GGAATTACTTTGGTTTTGGGG	59.575	21	233	378	610
59.198	20	TGGACTCTGGAAGCTGGAGT	59.986	20	231	1087	1317
60.06	20	TTGCCATAGATATGCACCGA	60.058	20	229	210	438
58.58	20	GAGCTTTGGTGGAAACATCC	59.532	20	149	56	204
60.088	20	ATGAACAGGTCCGCGAATA	59.09	19	169	650	818
59.953	20	GGTTCCAATTTCGTGTTGGT	59.694	20	173	4358	4530
60.352	20	CGGTGTGGATTTTGTGTGAG	60.001	20	238	890	1127
60.032	20	TGAACTGGTTTTTCGATCCC	59.91	20	183	5219	5401
60.008	20	ATCGGGTAAGCAACATGACC	59.82	20	279	275	553
57.297	27	AACATGTCATTGACCAGACCC	59.694	21	104	0	103
59.923	20	TTGTTGCCACGTATCCTCAG	59.716	20	199	2002	2200
59.708	20	CGTGAAGAGTTTCCCACCAT	59.966	20	212	2089	2300
59.805	20	CGTGGGACAAACAAAGGAAG	60.52	20	233	1277	1509
59.734	20	GGCAACAGTGGGATAATGCT	59.962	20	262	1540	1801
60.014	20	GCAGCAACAACGTTAACAGC	59.541	20	142	1976	2117
60.096	20	CCTCCAGAACCACAGCAAAT	60.111	20	180	66	245
59.651	20	CTCAACCAAGGAAGTGTTGG	58.187	20	277	618	894
59.967	20	GCAAAATTGGTCTAGAGAATTAA	58.51	26	158	1857	2014
59.933	20	CTCAAACGCATGTGCTTCTC	59.596	20	271	2098	2368
59.973	20	GACTCCCTTCCTCAACCCTC	60.05	20	167	5032	5198
59.933	20	CTTTTGCTGGGGAGGAGTT	59.269	19	276	2090	2365
59.935	20	TTTTCGTCAAATAATCCAAGCA	59.603	22	210	753	962
59.84	20	AATTATTTGTGGCGTCTGGC	59.967	20	251	416	666
59.966	20	TCGATTTGGTCTATTTCGGC	60.038	20	211	709	919
60.049	20	ACAGTTTCTGGCATGTGCTG	59.905	20	187	372	558
60.033	25	ATAAGGAGGGTCCCTTGCAT	59.789	20	236	41	276
59.862	20	ATGAATGTGGAAAGTGTGCG	59.572	20	186	255	440
58.201	20	TGTAGCAGGAACAAATGCCA	60.257	20	246	78	323
60.543	20	AAGGCACAAGTTCATGGAGG	60.111	20	112	767	878
60.124	20	ATCGGTTATTACCGGATCGC	61.031	20	225	1851	2075
59.864	22	TCCATTGATTGCCACTTTCA	60.049	20	268	324	591
59.813	20	ATGGTGGATGAGTAGGCGAG	60.096	20	262	1758	2019
60.111	20	GGTCACCCTAATGGCAGAAA	59.933	20	160	252	411
58.506	20	CGGAAATTTTCAACCAATTCA	59.797	21	237	4869	5105
60.187	20	CATGGTAGAGGCCCTGTGTT	59.989	20	227	4060	4286
59.988	20	AACACCCCATTTTGCTGTTC	59.836	20	223	293	515
59.816	20	ATTGGATTTGGTGTCGAAGC	59.939	20	204	15	218
59.962	20	TCAAAATGCCAGTCTTCACG	59.84	20	202	1862	2063
59.992	20	CCCATTTCCACTTCCATCAT	59.605	20	275	1458	1732
60.066	20	GAATTAGGGTGGGCGAAAAT	60.15	20	259	429	687
60.008	20	GAATGAGGGGAAGCATTCAA	60.014	20	256	753	1008
60.334	20	TTAGTGTTTTGACATGATTACTCC	57.936	26	263	2750	3012
57.944	20	CATCGAGAGCTTCCAAAAGG	59.948	20	251	803	1053

60.142	20	TTGCATCTCTTTTGTCGCTC	59.152	20	175	760	934
59.48	20	TGAAGTTAGGAAATAAGGAGGTG	58.743	25	201	5506	5706
57.59	23	ATGTTGGTCCAAGTCCAAGC	59.973	20	251	67	317
60.074	20	AGTTGAGGAAGCCGAACAAA	59.853	20	170	106	275
59.505	20	GTGTTTCTGCGGTGGAGAAT	60.119	20	182	365	546
59.938	20	AAATAGCCGTGTGGCATAGC	60.124	20	237	3169	3405
60.05	20	CATGTCCAGCAAGGGAAAAT	59.933	20	158	1308	1465
59.982	21	AGCACAGTGGTTTGCTTTGT	58.426	20	272	1153	1424
60.214	20	CCGAAGAAATGGATCCTCAA	60.006	20	267	184	450
60.067	20	AACAGTATGAGCAGCCAGCA	59.621	20	211	703	913
60.008	20	AAAGGTGTGAGAGGGTGGTG	60.002	20	182	1075	1256
60.497	20	TATGTGTGTGGTGGAAGGGA	59.806	20	276	6831	7106
60.088	20	GTCGGGCTAACGAGCTACAC	59.904	20	225	28	252
59.924	20	TCTAATCCTCTCCCCTGTCG	59.234	20	163	10448	10610
60.081	20	GGGGTTGAGTCCTTCCATTT	60.169	20	267	150	416
57.253	22	TGGGGGTACAAAGAGCTCAG	60.246	20	215	835	1049
59.953	20	GTGCGTGCATTTTTACGTGT	59.662	20	246	770	1015
59.926	20	TTTCAAAGCCATGCTGTCTG	59.988	20	275	1654	1928
60.088	20	ACACGGGCTTTTGAATTTTG	59.975	20	271	78	348
59.839	20	GGTTGGGACGGATAATCGTA	59.645	20	269	2885	3153
59.997	20	ATTTCCTTTCCCTGCCAACT	59.94	20	273	560	832
60.624	20	GCAGAAATCTGGACCCAAAA	60.051	20	228	2209	2436
60.331	20	GCACTGAAGTGGTGAGTGGA	59.872	20	184	2763	2946
60.977	20	TCAAATTTAACAGGCCGACA	59.157	20	190	584	773
59.866	20	CGATCCAGTTGCCAAGAAAT	60.074	20	161	862	1022
59.737	22	CATTGTCCGGGACTTTGTCT	59.966	20	189	1149	1337
60	20	AGTTCTTCTGGATGCTGGGA	59.803	20	256	1709	1964
60.044	20	AAAGCTAACCTCCCCACCTC	59.576	20	265	81	345
60.328	20	AATCTCTATCGGCATGTGGC	60.066	20	217	3991	4207
59.824	20	GGAAGACAAATATGGGACGG	59.244	20	160	40	199
59.797	20	TCCATGCATTTTTCATTATGTGA	60.199	23	279	292	570
59.871	20	TTCATTGGATAACAACCGCA	59.93	20	274	443	716
60.124	20	TGGCACCTTACCCATTTAGC	59.96	20	224	8	231
59.756	20	TGTAGCTGGACCAAGAGGCT	60.012	20	280	3511	3790
59.523	20	ATGTGTGCGTGTCCAAAAGA	60.16	20	215	781	995
59.606	21	TCTACTGCCTGGAAATGCCT	59.836	20	278	1042	1319
59.248	20	CCCTTGGTGCTGTTATGACC	60.375	20	253	2571	2823
60.074	20	GTCGTGGTGGTCTGATGATG	59.962	20	174	46	219
59.835	20	ATTTGGGTAGAGGATGTGCG	59.955	20	173	0	172
60.11	20	GGTCAAAACATTGACCATATTTAC	59.949	26	163	2284	2446
60.229	20	GGTGTGGAAGGCGAATTAGA	60.074	20	259	105	363
59.859	20	ACATGCCTCTTCCACAACCT	59.579	20	168	2330	2497
59.293	20	TCGTGCTGCCATCAACTAAC	59.871	20	154	8	161
59.882	20	TTCATGGGCGTTTCTTGATT	60.448	20	183	742	924
59.438	20	TAGCTGTTTGTGCGATGACC	59.871	20	211	1637	1847
59.648	20	TAGAAGGAGCTGATGGCGTT	59.978	20	229	226	454
59.903	20	GACGCCATTTCATCATACCA	59.355	20	231	1874	2104
59.055	20	TCCCGTCATGGAAGAAAATC	59.871	20	152	34	185
60.349	20	CCGCATTTTGTTATGCTTCC	60.456	20	269	44	312
59.879	23	CTATGTTCCGTTTGGTTGGG	60.22	20	274	100	373
60.352	20	CAGGCGCACAAACAGAAATA	59.872	20	246	47	292
59.939	20	TCCGCACCTTGGTTTAAAAG	60.103	20	218	4300	4517
59.75	20	GGTTTTCATAATGAGGGCGA	59.901	20	242	1627	1868
60.081	20	CGAGCAGACATAAAAAGGGC	59.845	20	224	432	655
60.123	20	GTTTCTCGCAGAAGGTGGAT	59.288	20	245	223	467
59.7	20	ACAGATTTGCCCCTGTATGC	59.962	20	165	859	1023
59.985	21	AAGCCTCCAAAGCATGAAAA	59.823	20	265	30	294
58.962	23	CTTTCACTCAGCATGCCATC	59.399	20	131	0	130

60.073	20	GGCCATCGCTAGGAAGTTTA	59.32	20	175	2637	2811
60.197	20	AAACAAGAGCCGAAAAGGGT	60.11	20	251	1746	1996
59.685	20	CAACAAACGTTGTCAATGGG	59.857	20	204	5382	5585
59.836	20	ACCATATTTAAGGGTTATCACCTG	57.552	24	256	1760	2015
59.95	20	GAGGCTGGAGCAAGAGAAGA	59.827	20	239	789	1027
60.014	20	CACATTCCCACATCCCTCTT	59.779	20	268	1229	1496
59.549	23	CAAAAGGTTGGGGAGTTCAA	59.942	20	226	69	294
59.467	21	TTCTTGCCACTTTCTCCGAT	59.813	20	163	2369	2531
57.71	20	GGGAACACCCTTGCTTGAGT	61.455	20	280	3478	3757
59.945	20	TTATCCCTTCGCTTTCTCCA	59.778	20	159	2339	2497
58.224	24	TTGCACATACACGCAGCATA	59.892	20	252	900	1151
60.014	20	CGCAACTGAAAAACCAAACA	59.746	20	256	621	876
60.14	22	AGTTCCGGGGGAGTTAAAGA	59.934	20	116	159	274
59.35	20	GCTGTTTTTGGGCAGTGATT	60.118	20	245	2211	2455
60.074	20	TGCTCTGCACTCAAATCTGG	60.136	20	273	761	1033
60.039	20	TTTACAATGCAATCGCCTCA	60.215	20	214	2709	2922
59.369	20	AGAGAGAAAAGAATCCCCGC	59.789	20	173	9	181
60.025	20	AACACTGAATCGCCTGGAAC	60.119	20	169	538	706
60.21	20	CCACGATAAATGCTTCGGTT	59.96	20	235	2525	2759
58.56	20	TCAACACCATTTATCATGTTTATC	58.367	25	277	1532	1808
60.119	20	TCAAGGGCGTTTTTATATTTGA	58.675	22	268	189	456
60.008	20	TCGTTTTACCTTTTGGCGAT	59.586	20	276	1961	2236
59.631	20	AAGTACATTGAACGCCCTGC	60.14	20	242	3040	3281
59.566	20	TGTCAGTTGCAACATTGCTT	57.896	20	267	1027	1293
59.89	20	CACTTCAAACGTCGTCCAAA	59.734	20	280	1956	2235
60.022	20	AATGAATCGAAAATGCTCGG	60.038	20	267	224	490
60.435	20	GAAAGCTCCAACCACTCTGC	59.997	20	213	1689	1901
60.124	21	AGGAATGTGGAGTTTGGTGG	59.82	20	253	726	978
60.011	20	CCAGCGTAAGTCCAACACAA	59.758	20	133	332	464
59.967	20	TGGGCTCTTCATCACTACCA	59.241	20	252	1331	1582
59.898	20	GCTGCAGCAATGAATCTGAA	60.104	20	261	745	1005
59.927	20	TTTTTCCGATTTGTGTTGGTT	59.348	21	214	730	943
59.654	20	AATCACAATAAGGCCCTCCA	59.387	20	198	827	1024
60.065	20	GATCCCGCACAAATGAGATT	59.9	20	259	68	326
58.709	27	CCTCGCTCTAATTTGGCTTG	59.975	20	194	20	213
58.559	20	GCACCCTGCTTAAACCAGAC	59.74	20	198	2039	2236
59.93	21	GCGTGTGGACTCCGTTTATT	60	20	146	579	724
59.556	20	TGCTTGTTTGTGACTAATGCAA	59.415	22	107	3159	3265
59.625	20	CCAAAATCCCTTCTTTGTCTTC	59.11	22	252	1729	1980
59.329	23	TTTCAATTCCTCGATAGCAAGA	58.966	22	210	1767	1976
59.941	20	TCGGTATGTTGACGATGGAA	59.924	20	225	208	432
59.988	20	AACCTGCAAAAAGAAGCACAA	59.912	21	158	478	635
58.228	20	CAAATTAGGCATCCACAACG	59.037	20	278	1341	1618
60.037	20	ATCGTAGCCAAGAAAGCGAA	59.982	20	272	269	540
59.887	20	CACTGGTGGTGGTAGTGGTG	59.907	20	241	340	580
60.096	20	CTTCGAGGGCGAGTGTTAAG	60.008	20	191	407	597
59.61	20	CTCAGCCTGTGTCGATTTCA	59.984	20	196	1364	1559
59.315	21	TCTTTACCGCATACACACTCTACA	58.901	24	210	2135	2344
59.376	20	TCCAAAGTTTGTTGGTGCAG	59.734	20	264	382	645
60.074	20	TTAGACCTCACACACCGACCT	59.631	21	243	1978	2220
60.004	20	GCTGCTACCTTTCAGTTGGTG	59.928	21	164	848	1011
58.93	20	CTTTCGGCATTCGTAAGGTC	59.708	20	200	7	206
60.232	20	ATTGCTTTTGCTTAGAGGCG	59.63	20	280	3774	4053
60.074	20	TGGACGCCCTAGATTGTTTC	60.074	20	180	21	200
60.135	20	GTGGTTGGAGTGGGAGACAT	59.817	20	153	2004	2156
59.349	20	CAAAACCACAAAACTGTGACG	59.13	21	273	367	639
60.035	20	CCGCATCCACTAAACCCTAA	59.953	20	250	440	689
60.096	22	GGGCTTCTTTTCTGGCTTTT	59.835	20	135	371	505

59.95	20	AAGTCCACCACCCTTGTGAC	59.859	20	227	1141	1367
57.971	22	TGCTATTCATCTCATTGCCA	57.8	20	229	1883	2111
59.973	20	TCTTGGATTGTGCGTCAGAG	59.984	20	254	254	507
59.87	19	TGACAGTGGAGGGAGAGAGAG	59.564	21	161	37	197
59.288	20	CCCTATGTCAAAAGTGTGGGA	59.838	21	242	1039	1280
60.096	19	AGAGGAGGCTCTTGGAGAGG	60.088	20	248	291	538
59.313	22	TTAGGCCCAGACTTCGACAT	59.694	20	225	3	227
60.096	20	GGTGAAGGTGTGGTTGCTTT	60.012	20	259	2768	3026
59.803	20	TGTCCCAACATCTCGTCTCA	60.246	20	264	897	1160
59.462	21	TCGACTGCCTTCAAGTAAAGC	59.646	21	278	785	1062
59.881	20	TGATCGCTTATGCATTCCTTT	59.696	21	253	2934	3186
60.067	20	TGGATGGTGGTAGGAGGAAG	59.92	20	232	946	1177
60.068	21	GCTGTGTTTTGTGGCATGTT	59.621	20	236	2013	2248
60.134	20	CATTCTGCAACACCAGCTTC	59.445	20	278	785	1062
59.736	22	CTCGGTTTCATTGCCATACA	59.542	20	206	185	390
60.052	20	GAATGCTCTCCTTGCACACA	59.992	20	118	266	383
59.973	20	TTGGGGGACCATTTTGTTTA	60.024	20	198	863	1060
59.988	20	CTTCCACATTTGAGGGGAGA	60.042	20	202	1774	1975
60.203	20	GTGCAACGGAACTGGTCTTT	60.156	20	145	666	810
59.09	20	TTTTGCAAACCAAGTTTCCC	59.953	20	152	4172	4323
59.993	20	TTTTATCAATTCGGGGCTTG	59.901	20	194	192	385
60.074	20	TGTTGGTTTGGTGAGTTGGA	59.976	20	267	909	1175
60.175	20	CCCTGAACAGGTATGGATAAGG	59.72	22	212	1089	1300
59.601	21	TTTTATGCACAAGTGGCAGC	59.879	20	251	4990	5240
60.136	20	AGGATCAAACCCAATCCACA	60.173	20	225	4172	4396
60.041	20	GTGGACGTCCCAGATTGTTT	59.827	20	138	1910	2047
59.94	20	GCCCAAACTACCGAATCAAA	59.938	20	266	2353	2618
59.632	20	ACGCGTATGCATTGGTCATA	59.983	20	232	980	1211
59.182	20	AAAAGGGCCTGAAAATCCAT	59.777	20	277	3176	3452
60.051	20	TATTAACACAAATCCGGGGC	59.66	20	235	2252	2486
60.032	20	ATGAGTGGCAGGGCAGATTA	60.624	20	279	2369	2647
59.688	20	AAGTAAAGGAAGGCCGAAGG	59.72	20	138	985	1122
60.24	20	CAGCACTGCACTTCTGAGAGTT	59.856	22	255	906	1160
59.924	20	TTGCATCTGATGATGCCAAT	60.041	20	234	2212	2445
60.212	20	TTTGGGAGTATGGTTGGAAA	57.917	20	235	1720	1954
60.177	20	TTGCGGAGTTTTCATTTTCC	60.053	20	168	1501	1668
59.894	20	TCGGATTCGATGCCTTATTT	59.507	20	252	170	421
59.903	20	CCGAAAATCCCAAAGATGAA	59.872	20	133	2211	2343
60.713	20	ATTGCATAAATGGGCCTTGA	60.289	20	259	870	1128
60.234	20	AAAGGGAATGAAGCAGCAAA	59.823	20	230	1380	1609
59.844	20	TCTGCAAAATCCAGGAAACC	60.051	20	185	1868	2052
59.83	20	TGATGGCATTTTTCTGGTTG	59.518	20	212	1092	1303
60.081	20	CACCTCGAGATGGTAGGCAT	60.096	20	212	539	750
59.995	20	GCAAGCCATCAGATTCCAGT	60.226	20	215	258	472
59.985	21	ATCTGGAGCTGGTGAAGCAT	59.834	20	259	3812	4070
59.989	20	GCTGGAGCCATTGAGAAAAA	60.331	20	222	1217	1438
59.337	23	CGAGGCTATTCTTTTTGCCA	60.335	20	223	61	283
60.299	20	TTTTCCCCACCAACAATCAT	60.029	20	273	1658	1930
59.972	20	ATGTATGGGCCCTTAATCCC	59.873	20	227	131	357
59.939	20	TTGCCAGTGCATTTTCATTC	59.67	20	155	484	638
59.973	20	TCTTGTGGCTGTACTCCGTT	58.37	20	276	1252	1527
60.232	20	GATGCACTTAGTGGTGCCAG	59.318	20	275	730	1004
60.111	20	ATTTTGGGAGTAATGGGGCT	59.666	20	135	360	494
60.854	20	CAAGAACCGGGGATGACTAA	59.926	20	211	579	789
60.038	20	TGCATGTGTATAATAACAACCGC	59.808	23	162	8535	8696
59.284	20	TATTGACCCACTTGTCTCCG	58.569	20	239	869	1107
59.992	20	AGGTTTTGGGTTTAATGGGC	60.055	20	244	314	557
59.962	20	CACAAGTACCCCTTTGCCAT	59.853	20	256	3171	3426

59.583	21	GGGTCCTGTTGATCTTTTGC	59.532	20	280	219	498
59.965	23	TGAATTGAAAGCTGAATCATGTG	60.124	23	238	22	259
59.933	20	ATAGCGTCCACTCCACCAAC	59.997	20	171	1828	1998
59.679	20	GGAAAATCTATTGCAGGTGCTC	60.102	22	278	1881	2158
60.28	22	TTTTCCTTCTCTTTGCAGCC	59.569	20	207	397	603
59.927	20	GGGGTAAAAGGGTGGTGTTT	59.955	20	280	1264	1543
57.222	23	TGTCGTCTGACATTGCCTACA	60.317	21	144	13	156
59.995	20	ATTCTCAACACCCACAAGCC	59.973	20	219	520	738
60.05	20	CCACCATTGCTAATCGTCCT	59.955	20	137	3444	3580
59.679	20	TTGCAGTTTTAGGCATATCGAA	59.753	22	246	104	349
59.799	22	ATGCATGCAGCAAGTTGTTC	59.878	20	212	938	1149
60.732	20	CAATGCAAGGGCTTAAAAGG	59.715	20	228	846	1073
59.94	20	AGAACAAACGACTTCCACCAA	59.624	21	227	2489	2715
59.934	20	CTTTCTGATGGGTGCCCTAA	60.066	20	233	587	819
60.038	20	GAAGGCTGGTAACCCATCAA	59.933	20	213	205	417
60.945	20	GGGGGTGTTTTAGAGCATCA	59.933	20	234	255	488
60.54	20	ACACATCGTCCCTTAATCGC	59.962	20	214	741	954
60.185	20	CCTACAATGCCACACCTCCT	59.989	20	198	72	269
60.351	22	TTGTGGTGTGGAAGATCTGG	59.52	20	212	1173	1384
60.006	20	ATTCCCTTTTGTCCCTTTCG	60.291	20	278	938	1215
60.009	20	ATTCAATCTGCACCTCCTGG	60.073	20	192	129	320
60.015	20	GGGTGGCTGTAATTGCTCAT	59.962	20	135	1036	1170
60.111	20	ATCGTGGATACGTTGAAGGC	59.962	20	234	46	279
60.743	20	CAAAAAGCGCTACAAGCACA	60.191	20	236	715	950
59.947	21	ATTGCGCTCAAAGATATGGC	60.203	20	205	2196	2400
60.007	20	CCAAAATTACATGGTTCGGTG	60.096	21	276	1483	1758
59.836	20	TCTGGTAACCGAATTGCCTC	60.074	20	179	1085	1263
59.82	20	TCAGGTTTATCAACATCATTTATC	60.138	27	202	14	215
59.943	20	GGATCTTTTGTTGCTGGGAA	60.051	20	224	1565	1788
59.872	20	AATGAAGGAAAAGGGCCATC	60.265	20	201	1950	2150
60.133	20	TGAAGTTAGGAAATAAGGAGGTG	58.743	25	279	3047	3325
58.671	20	TGAAGTGCTGACAAGGCATC	59.992	20	268	2380	2647
58.943	25	CCACTTTTTGTTTTGGAGCAA	60.131	21	237	367	603
59.955	20	CCCAACCTATTCTCACCCCT	60.183	20	135	1903	2037
60.744	20	GATTGGTCCAGCAGGTTTGT	59.973	20	232	638	869
59.93	20	TGCATCTCCTCCACCTATCC	60.034	20	171	434	604
60.088	20	GCACAGCATGTGGAGTGAAG	60.473	20	237	1418	1654
59.131	24	TTGTTGCGCAATGAAGACTC	59.995	20	251	17	267
60.016	20	CATCATTCCCCTCCTCTTGA	60.003	20	221	432	652
60.298	20	CATCCGTCCATTTCCAAGAT	59.75	20	249	2118	2366
60.205	20	TTGGGATCTTGCATGAACAA	60.049	20	238	487	724
59.61	20	AGCCATCATCCAACCACAAT	60.203	20	207	1039	1245
59.763	20	GGTCAAATTGGGGATGAATG	59.991	20	139	1116	1254
60.042	20	AACCCTTGATGTGGAGCTTG	60.111	20	238	1477	1714
60.111	20	CCGCAAAAATCCTTCACAAT	59.938	20	226	3735	3960
60.088	20	TATCCCCCTCTGGAGCTCTT	60.169	20	223	538	760
60.11	20	TGCCTTTCCATGAACAAAAA	59.133	20	253	1565	1817
59.537	21	TCAATATTGGGCAGAGGGAG	60.029	20	204	1828	2031
59.664	20	GGTTTGAGGCTGCTCTGAAC	59.997	20	274	322	595
60.134	20	AACAAGAAGGCCGGAAGAAC	60.61	20	179	380	558
59.778	20	GGCGTGACACTTTTTCGATT	60.118	20	280	3602	3881
60.015	20	ATTATCATTTCCACCGCCAC	59.651	20	280	2625	2904
59.429	20	TATAAATTTTGGCGCCGTTG	60.797	20	243	1152	1394
59.409	20	ACCCAAACATTTATTCCCCA	58.995	20	224	2376	2599
60.096	20	CGAACAAAGCACACATGAGG	60.301	20	219	5550	5768
59.918	21	TGTGTGCTGGATCATCTTCA	58.728	20	280	372	651
59.981	20	CCGAATTTCTCCCAACTCAA	60.044	20	214	4541	4754
59.82	20	TCCACATCTTTGGGATAGGG	59.744	20	241	141	381

60.06	20	CCGGAGAGAAAAAGACACGA	60.366	20	250	1971	2220
59.988	20	CGCTATGTACACGGTGTTGC	60.203	20	236	1012	1247
60.594	20	GTTTGCTTTGGGGTTGTGTT	59.875	20	277	1330	1606
62.966	18	GGTGCAGAATTCGAGGAGAG	59.95	20	192	9	200
61.016	20	TCATACTCTGGCTGCTCGAA	59.697	20	272	2202	2473
59.955	20	TTTGTGCATGCTTCAGTCTTG	60.042	21	209	2892	3100
59.948	20	AGAAGCCCATATGGCATGAG	60.059	20	234	463	696
60.184	20	TAGTGCATCCTGCCTGTTTG	59.864	20	229	1502	1730
60.294	20	AAGTGAATCTTGGTGGCTTCA	59.726	21	155	40	194
60.165	20	AAGGGAAATTCCAGGGAAAA	59.75	20	274	362	635
59.994	20	AATCACAGAATAAACGCCCG	59.96	20	254	3643	3896
59.622	20	AGAGGCTCGTGTTCTTTCCA	59.989	20	209	646	854
60.307	20	AGTTGTCGGAATGGAGATGC	60.081	20	182	108	289
59.992	20	AAGGACCTCAGCCTGCAGTA	60.012	20	189	2349	2537
60.081	20	ACATATGGTGGTATGGTGCG	59.152	20	134	176	309
59.605	25	TGCTTGATAGTGGGCATGTT	59.152	20	183	16	198
60.034	20	GCTGCATCCCGATATGGTAG	60.457	20	223	2196	2418
59.727	20	CGCATTGCACGTAGCTGTAT	59.925	20	248	1029	1276
59.933	20	GAGGAGGTGTAGATCTGGCG	59.827	20	270	550	819
60.11	20	TTCGACTTTTCAAGTTATTTTTCAG	59.74	26	275	72	346
59.155	21	ACCAATACGTTCGCTTCACC	60	20	279	403	681
60.187	20	TTTGGATGTTTACTATGGGGTG	58.74	22	251	1183	1433
60.999	20	AGCAACCTCAAACCACAAGG	60.149	20	182	3	184
60.232	20	TGCTGGATTCATAACACGGA	60.073	20	170	2271	2440
59.335	25	GACTCAGACCCTGAGCTTCG	60.135	20	164	21	184
60.134	20	TGCCATCAAATGCAAGTTTC	59.67	20	245	1159	1403
60.22	20	TATTGTTGCTGCTGATCCCC	61.003	20	239	759	997
60.051	20	CCCATCAGACCAGTTGACAC	58.94	20	158	993	1150
60.224	20	GGAAACCCTGAAGAAACGAA	59.146	20	195	1904	2098
60.057	20	ATTCAATCTCTGGGCTGTGG	60.073	20	225	5423	5647
60.199	20	CGCCCGAGTAATATTTTCCA	59.922	20	263	2375	2637
59.995	20	CTTCTCTCACATCCATCGCA	59.942	20	181	1199	1379
60.025	20	CGATACCAGCAGAACCCATT	59.955	20	127	1211	1337
59.967	20	TCCCATTTCCTCCAAATTCA	60.244	20	171	3682	3852
60.03	20	GCAACACTAGGCAACAGCAA	60.058	20	188	1756	1943
59.673	20	TTGAGCTCATGTCAGCTGGT	59.577	20	259	441	699
59.96	20	GCCTGCTCAACCTCAATTCT	59.434	20	150	2936	3085
59.037	20	TCAAACTGGTGTGTGTGGCT	60.203	20	277	9341	9617
60.405	20	TGCATGTGGTGATTGGTAGA	58.486	20	259	1353	1611
60.255	20	CCTCTGCTTTTTAGAGAGAGGGA	60.482	23	129	4109	4237
59.889	20	CTTCTCATCCTGCGAACTCC	59.95	20	256	633	888
60.209	20	GAACGCCGTTATGTTTCCTC	59.574	20	272	3394	3665
59.805	20	ATGTCCTTTTGCTTATGCCG	60.096	20	216	1734	1949
59.984	20	TTCCTAGCTCTCCCCCTCTC	59.912	20	271	2194	2464
60.081	20	TCTAACACGCAGCATCAAGG	60.011	20	236	2543	2778
59.982	20	TTGCCTTTATTTCTTGGCAGA	59.84	21	227	1126	1352
59.831	20	AATGCAGAGCAGCCAAGAAT	59.985	20	127	844	970
59.904	22	CGAGGCATATCATGTTCGGT	60.884	20	198	2234	2431
59.845	20	TGCTACCTCGCATTGTTGAG	60.011	20	275	289	563
60.181	20	CCCATCACCAAACAAAACCT	59.688	20	264	2588	2851
59.859	20	TGCAATCGACGGAAACAATA	60.073	20	191	1222	1412
60.183	20	GAAGTGCAGCATGAATTTGC	59.43	20	190	2802	2991
59.966	20	GCTCGAAAGCACCAGTAAGG	60.015	20	231	1278	1508
60.315	20	GATTCAAATCCCGATGGAAA	59.699	20	191	1355	1545
60.08	20	AAATTTCACCCACCCACTTG	59.688	20	114	2236	2349
60.148	20	GCATACGGCTCACTCTACGG	60.817	20	259	940	1198
60.096	20	CCCATTCCAACCATAGCAGT	59.813	20	223	3964	4186
60.103	20	TGGCATTACGCATTACCACA	60.926	20	169	72	240

59.916	20	CAAGAAACCTTGGCACGAAT	60.11	20	209	3292	3500
60.095	20	TTTGTTCGTGTTCCAAAGGA	59.145	20	278	4002	4279
60.05	20	TGTTTGGTTTGTGAATTGGG	59.268	20	234	73	306
60.159	20	TGAGCTGTGTTTAGGGCTGA	59.591	20	104	1837	1940
59.009	20	AAAAGGTGACGAGGGTGATG	59.966	20	279	3302	3580
59.485	20	CCCAATAACACCAAATATCCG	59.065	21	132	2780	2911
59.04	20	CCATAGCCAAGCACAACATC	59.152	20	203	3636	3838
57.466	20	GCAGTTGGAGTTGCTTTTGG	60.807	20	224	1310	1533
60.032	20	TCTGTGGGACCAACTTCCTT	59.549	20	193	5445	5637
60.11	20	ACACCCATTTCAAGCAGACC	59.973	20	252	534	785
59.67	20	GGTTTATTCAACTGCAAAAGCA	59.298	22	264	2151	2414
60.111	20	CACCCACCTTTTTGTCGTG	59.985	19	273	3800	4072
59.837	20	GCATATTTAAAGAAGGCCAAGC	59.301	22	221	3401	3621
59.603	20	GCGTTGTCTTGTGTGGTGAT	59.603	20	110	24	133
60.195	20	TGACGGGATTTAGGTGTTTTG	59.847	21	263	2627	2889
60.088	20	AGCATTAAAAAGGCCATCCA	59.547	20	195	2558	2752
60.006	20	CACCATTGATGCAGGTGAAG	60.112	20	212	3167	3378
59.973	20	TGTGCAAAATGCTACAGGTGA	60.309	21	224	4634	4857
60.12	20	TAGCCGTGGTTTGTCAAGTG	59.758	20	250	1229	1478
60.081	20	CATCATCGACTCGTCCCTTT	60.073	20	222	1324	1545
59.615	20	CCAACAGTTGAATATGCCTACG	59.536	22	261	710	970
59.964	20	CGGGAGATGGTTGTTTGAGA	61.034	20	232	3102	3333
58.961	21	CTGAAGCAGAAGCCCATCTC	60.096	20	256	2107	2362
61.119	20	GAACTTTGGTCGATCGTCGT	60.119	20	280	1289	1568
60.263	20	AGCACACCAATCCGAAAATC	59.939	20	272	3888	4159
59.938	20	CAAGAACAATAATCGGTGCAGA	60.131	22	225	2534	2758
59.585	20	CGCTTTGGTGCATCATCTATT	60.11	21	238	523	760
59.574	20	TTGGAGAAAATTTTGTGGGC	59.916	20	179	1630	1808
60.147	20	ATTCTCCGAATCCAGCACAC	60.081	20	260	1373	1632
61.155	20	GGAATCGGAACCCTTTTAGC	59.909	20	277	2519	2795
59.82	20	ATCTCAGGAACATTGCACCC	59.934	20	240	4974	5213
59.988	20	CAATCATGGACTTCACGTCG	60.112	20	280	3252	3531
59.894	20	GGAAAATGGGTGATGAGTGG	60.173	20	197	2032	2228
59.685	24	TGTTTCAATCGTTCCTTTTTCA	59.603	22	109	1620	1728
59.985	20	CCCAAGCTGGTGGTTATGAT	59.813	20	196	2791	2986
59.97	20	AAGACTCGTGTTCCAACATTCA	59.639	22	275	397	671
58.726	20	GGACCATTCACTGGCATTTC	60.326	20	218	3222	3439
60.127	20	TTCCAAAAGCTGCTCGAAAT	59.96	20	231	772	1002
59.706	21	GGCTAGCTGAAGGATTTCCA	59.41	20	258	2928	3185
60.073	20	GTTGCCTCTCTATCCGCAAA	60.352	20	275	21	295
60.049	20	CGTTGGCCCGATATTTAGAG	59.564	20	229	1186	1414
59.945	20	AACAGAGACGGAGGTGGATG	60.112	20	227	177	403
59.997	20	GCTGCTGCTGTCTAAATCCA	59.178	20	257	18	274
59.247	20	TGAAGATGGCACCTTGAGTG	59.831	20	237	804	1040
59.828	21	TCGTGCATCACATAGAATGGA	60.088	21	210	1162	1371
59.946	20	TTTTCTTCTCCGTCAACGCT	59.993	20	275	103	377
60.051	20	CGCACTGACACCATCAAACT	59.751	20	235	696	930
59.795	20	CTCCAAAGCTCGACAGATCC	59.95	20	264	1772	2035
60.096	20	CACCGATCCAGGTCATCTCT	60.072	20	260	142	401
60.045	20	GGGTGAAACCCAAACGTAGA	59.83	20	164	2635	2798
59.679	20	TGCGTAAATATTGGCATGCTT	60.478	21	252	4262	4513
59.445	20	TGTGTGTTGACCATGTATCGG	60.294	21	278	18	295
59.934	20	GAATTCGTGTTTGGTGGCTT	59.978	20	247	1297	1543
59.542	20	TGCGTTTCTGCGTTTTTATG	59.88	20	258	2631	2888
59.961	25	CATTCACGGAAAACTGCACA	60.699	20	239	1285	1523
59.727	25	ATGAGCTCGGTTCGAAATTG	60.214	20	249	1377	1625
60.032	27	ATCTTGGCAATCCAAAGCTG	60.214	20	138	2	139
59.621	20	TTAATCTTCGTCTTCGGCGT	59.845	20	277	715	991

59.849	20	GGCTGTATGGGCTTGGACTA	60.096	20	124	3902	4025
60.3	20	CTCTGTTATTTGCCTTGCCC	59.708	20	271	2108	2378
60.199	20	ATGAATTCCGCTGGAAACAG	60.074	20	268	2556	2823
59.901	20	GATGATTTATCACCGAATCGC	59.387	21	103	4112	4214
59.801	20	CCACCATGATTTCGACACAC	59.812	20	166	5815	5980
59.848	20	AAAATCATTGGAATCAGCCG	59.901	20	144	6076	6219
59.449	20	CCTCGATGTTTGAAAACCAGA	60.096	21	199	38	236
59.691	20	GTGCATGTGTGTGTGTGGAA	60.053	20	237	552	788
59.779	20	GCAACATGCTGATGGTGGTA	60.549	20	168	1124	1291
59.94	20	ACGATCATCACATGAACCGA	59.925	20	160	2269	2428
60.103	20	CGAAACGATTAGTTGAATGTGC	59.652	22	236	1957	2192
59.055	20	CGGAACACAATTCGACAGAA	59.691	20	128	21	148
59.301	20	CTGCTGCATTTGTTAAGCCA	60.014	20	193	6951	7143
60.073	20	CTGGGGTGCAAGAGATTCAT	60.073	20	264	2230	2493
60.439	20	TTTGTGCAATTTTCATCTCCC	59.93	21	102	1922	2023
59.735	20	TTCCTCACCCAAAATGGTGT	60.21	20	248	1798	2045
59.844	20	CACCTCGAAGGTACCACCAT	59.844	20	219	1233	1451
59.052	22	CTGAATTTGTGGTGGCAGTG	60.152	20	176	479	654
59.967	20	AGGTTCTCACTCTCTCTCAGCC	59.249	22	257	785	1041
59.622	20	GCATCGCCCTGTTAAGAAGA	60.352	20	254	2661	2914
59.962	20	CCACCCACTCTCCCCTTAAC	60.736	20	219	985	1203
60.019	23	GATTGGCCACTGGTGCTTAT	59.962	20	203	711	913
59.984	20	GAGGCAAACACCCAATTGAT	59.797	20	232	1215	1446
60.974	21	TCAAAACAAATGCTGTGGGT	59.024	20	265	1741	2005
59.954	20	TGTGACCAATATCACAGATTCG	58.502	22	277	9	285
59.962	20	CTGCATAGCTGATATGTCCCA	58.761	21	153	1763	1915
59.333	20	TCGGAAGGCAAGATCACTAGA	59.963	21	279	594	872
59.478	20	CTGACAATTTCCAGCAGCAG	59.591	20	267	2532	2798
60.096	20	CTGATTCACCTTCTTGCGGT	60.255	20	196	330	525
59.845	20	GGAAACCTTGCAAATGCTGT	60.118	20	262	2972	3233
60.64	21	GGAATGAATGGAGCGTGAGT	60.081	20	238	5322	5559
59.937	20	TATATCTCCACGGACCACCC	59.629	20	264	718	981
59.851	20	CCAGTCCTGTCGAAAATGGT	59.966	20	137	643	779
58.201	20	AGCTGCTGACTGCCAGTTTT	60.201	20	230	9045	9274
59.864	20	CTTCGCTTTTCGCGATTTTA	60.456	20	226	7849	8074
59.722	22	TGTCCAAAATTGTTGTCGCT	59.174	20	279	912	1190
60.151	20	ACTCGGCCTAGTTCGTTGAA	59.875	20	245	382	626
59.782	21	ATTACCTCTCCTGCCCCAGT	59.957	20	247	2562	2808
60.031	20	GATCCCTTCTTTCTCAGCGA	59.508	20	142	2081	2222
59.96	22	GGCTTCAGTTGGCAGGTATC	59.7	20	240	1403	1642
60.339	20	CAAGCATGAAAACAACCGTG	60.149	20	147	335	481
59.962	20	TGCTGTACTTGCATTGGAGG	59.864	20	255	641	895
58.743	25	CGGTATGGTGTCGTACCGAT	60.657	20	199	7	205
60.053	21	TTGCACAAAACAGTTCCACC	59.591	20	270	7392	7661
59.347	20	TTTCACCCACAAAATCATCA	57.35	20	279	2078	2356
59.629	21	TTCTCTAATTCACCACCGCC	60.074	20	258	292	549
60.103	20	TCCTGGATCACATTGGAACA	59.893	20	257	1979	2235
59.028	20	TGTTGTTGGTGGAACTTGGA	59.976	20	270	2194	2463
60	20	TGAGAAAACAAAAGTGGCCC	60.088	20	232	231	462
59.762	20	AGAGTCGGAAGGCATATGTGA	59.708	21	101	274	374
60.264	20	TGGGGAATGACTCACCACTA	58.93	20	211	4456	4666
59.912	20	GATTCGAGTTTTGCTTCCCA	60.192	20	182	2288	2469
60.111	20	CTTTGATTTCTCTCCGCACC	59.813	20	139	88	226
59.971	20	TTGACAATATTTAGTGTTTTGACAT	58.99	27	146	4685	4830
60.418	20	TGGGAATAGCGATTTTCCTTT	59.922	21	191	3254	3444
60.132	20	CACGCACACACAAATTCACA	60.204	20	193	1370	1562
59.971	20	ATCTGAAAAACACTCGCGCT	60.022	20	186	5080	5265
58.926	24	GTTGGAAAAATCTGGCCTCA	60.051	20	172	38	209

60.245	20	CCGGAAAAGAAAACCCACTT	60.324	20	225	281	505
59.724	24	TTGTTAGCGAATTTTTGGTGG	59.986	21	266	166	431
59.864	20	TCAGGTTGGCTCCATTTTTC	60.051	20	167	1026	1192
59.938	20	ACACCCGATTCGAGTAGCTG	60.277	20	273	2900	3172
59.009	23	AGCGCCACCTCAAAAGTAAA	59.883	20	204	1	204
60.103	20	TCCTCCTCCCTTCCTTCAAT	60.008	20	237	2253	2489
60.832	19	TTCCCAGCGGATAAAAATTG	59.901	20	241	20	260
59.986	20	AGATAAGGGTGCGATGTTCG	60.096	20	278	6770	7047
60.011	20	GGAATGTAGGGAACCGGAAT	60.017	20	251	3140	3390
59.894	20	ATTTTCTCCACGCTTTTTGC	59.343	20	276	1156	1431
59.316	20	CAACAAAAATCAAGCCATGC	59.161	20	264	2364	2627
59.984	20	CCTTCTTCCACTGCTTTTGC	59.993	20	243	14	256
60.165	20	ACCTCAAACCCTTCTGCGTA	59.734	20	224	1753	1976
59.995	20	GAAGCCGAGAAACAAAGACG	59.993	20	273	1642	1914
59.807	20	TAGTTAAACACCCCACCCCA	60.081	20	165	2372	2536
59.939	20	GCTTCAAACTGGCTCTCGAT	59.579	20	121	3686	3806
59.64	20	TCGGGTCTGCTCAAGTTTCT	59.989	20	237	162	398
59.933	20	AATCGCCATGATTCTCCAAC	59.9	20	262	2083	2344
60.332	22	TGAATTTGCCTTTGTACATTTTG	59.076	23	262	558	819
59.988	20	GAATAGCCCAAGACGAGTGC	59.843	20	191	1704	1894
59.801	20	CAATTCGAAAGTGACTCGCA	59.988	20	128	854	981
59.647	20	TGGGGTGATATAAGATGATGCT	58.419	22	243	58	300
59.925	20	CGAGAGGTGGGAAAAGTGAA	60.224	20	214	594	807
59.724	23	TTTGGTTCATGTAGCCGACC	60.894	20	123	271	393
59.993	20	CAATATGGGAACTTCGCGTT	59.96	20	210	210	419
59.963	20	ATCTTGAATCCCCTTCTCCG	60.401	20	245	33	277
59.784	20	AAGTCCCTCTCGGGTCGTAT	59.957	20	278	643	920
60.49	20	GGAAGCTGCTCTTGAGTTGG	60.134	20	239	277	515
60.263	20	ATCAAATTTTGGATCCGTGC	59.768	20	249	615	863
60.91	20	GGTTGCACACTCCAACACAT	59.446	20	275	196	470
60.608	20	TTCCATGATGCCTAGCATTG	59.646	20	102	51	152
60.103	20	TGGACTGATCAGCAGAGGAA	59.499	20	251	182	432
60.164	20	CCTCGCCTCTTACATCTGCT	59.598	20	173	51	223
58.999	20	TGGCATTGTCTTGGTTGTTC	59.547	20	270	1819	2088
59.679	20	TCTTCCTCATCTCCACCACC	60.048	20	223	526	748
59.967	21	ATGCATCAAACAACAGGACG	59.572	20	150	77	226
60.009	20	GCCAAAGAGTTGTTGGAAGC	59.859	20	162	1333	1494
60.04	20	ATAGGCGGTCTGGAGAGTGA	59.827	20	276	723	998
59.962	20	TAGAAGCATCTCCGAGGGAA	59.91	20	260	4999	5258
60.684	21	TCCAAGACCCCAATTTGATT	59.22	20	242	539	780
59.947	21	TCCAACCCATCTCCCATTTA	60.126	20	270	1136	1405
57.459	20	TGGTTGGATATTTCCCCCTT	60.37	20	221	306	526
59.996	20	AAACAGGGTTGGGAAGAAGC	60.476	20	160	9	168
60.111	20	TGCCATTGCAGCTAGTCTTG	60.157	20	178	452	629
58.717	20	ACTTTCACCACCGCGTACC	60.97	19	274	303	576
60.235	20	AATATGTCAACTTTCCGGCG	59.96	20	229	67	295
60.593	20	GGGCAAAAATGCCACTCTTA	60.074	20	144	78	221
60.074	20	TTTGTCGGAATTAGGGATGC	59.901	20	136	3538	3673
58.999	20	TTGTTGCACCGTGGAGATTA	60.111	20	153	84	236
60.036	20	AATAGCAGCCAAGGCAGAAA	59.982	20	217	1511	1727
59.297	20	CAATGCCGTTTGTGATCATT	59.4	20	243	7	249
60.082	21	TTGGTAAAGATAAATGCATCTCAA	58.244	25	246	359	604
59.04	20	TTGGCAGCAACTACTACCATACT	58.053	23	261	2353	2613
60.91	20	CTGTGGTTGATTTGTGGGTG	59.848	20	114	4	117
60.214	20	TGTAGCCGACCCCAATTTAT	59.297	20	202	1495	1696
58.479	26	GGTGCAGTCTCTTTCAAGGC	59.997	20	194	23	216
60.285	20	TTGGTCTCGGGTTATGTTTTC	58.938	21	263	156	418
60.606	20	TGGAGGAAATTTTGTAGCCG	60.067	20	110	91	200

59.955	20	CGATGCCCTTGAGAATCAAT	60.036	20	233	4249	4481
60.839	20	TCCCACCAAGTATTAATATGCTCA	59.768	24	185	0	184
59.971	20	CACGCTCCTCTCCTCCATAG	59.966	20	181	1851	2031
59.347	21	CCAGCCTAAATTCCATCACC	59.387	20	214	20	233
59.478	21	TTATCAGAGTCGAGCAAGCG	59.322	20	212	61	272
59.941	20	CCAATTTATTGGGATTAAGGC	57.539	21	119	1547	1665
59.803	20	TCGTGGAGATCAATGTCGAA	60.201	20	149	407	555
59.996	20	CGGTTGTATGAAACCGTTAGA	57.706	21	201	7	207
59.389	20	GCAGTTTGCTGTGCTTGTTC	59.646	20	253	1081	1333
59.776	24	CGAACTCGTAGCCCATCAAT	60.096	20	266	79	344
58.926	20	AGCAGCTAATCGCCTCTCTG	59.882	20	176	7	182
60.02	20	TGATGGGGAAATGGTTGAAT	59.991	20	166	863	1028
60.157	20	TTTATTGCACCCAATTAGGATAA	57.692	23	248	268	515
58.036	23	GAATTTGGGAAGAAATTTCAGTT	57.779	23	261	192	452
58.601	23	CGTGTGTGGGTGATCCAATA	60.24	20	237	30	266
59.993	20	CTTCACTTCCATCCTCTGCC	59.803	20	116	462	577
59.989	20	TTTAGACGGGCTCTTCTTGG	59.448	20	257	5708	5964
59.875	20	TCGACAACATCTCCGATCAC	59.637	20	240	1549	1788
59.83	20	TTTGATGGCTTCTGCCCTAT	59.668	20	144	324	467
60.801	20	CCTTTGATGCCGATGTTCTT	60.074	20	256	11	266
60.103	20	CGTAAAGAGGGGTAGGGGAG	59.949	20	231	1849	2079
59.745	20	TCGCTATTGCATGGATCAAA	60.179	20	256	695	950
59.953	20	CACCAATCCCACAACAACAA	60.255	20	114	1331	1444
58.283	20	TGAAATACCATCCAGTCTGTCC	58.912	22	265	12031	12295
60.375	20	CTTGCCTTGTGACTAGCGTC	58.677	20	260	2360	2619
59.95	20	ACACCAGCCGAGAACATCAT	60.542	20	274	127	400
59.702	20	GTCGATTTGCATAAGCCACA	59.694	20	197	21	217
59.538	21	CGTACCACACGATGTTACCG	59.904	20	232	641	872
60.22	21	TCTCACGCAAAGAACCGTATT	59.761	21	279	1347	1625
59.593	23	AAGCTGATCCGTTCCAAAAA	59.685	20	262	500	761
59.077	21	GCAATCAACAAAGCAACGAA	59.856	20	221	13	233
60.452	20	GGTTGAAAATGTAAAGGAAATCT	58.2	24	166	30	195
60.393	23	AGGCCTGCACTCAAAAGAAA	59.993	20	201	1	201
60.771	21	GCGGACCGGCTATATACTTG	59.592	20	276	387	662
57.539	21	TTCGATTGCTTAGATTGGTGG	60.081	21	172	14	185
60.214	23	GGATACATTGCATTTGGGAAG	59.287	21	237	414	650
60.111	20	GGGAGTCGGGCCCTATAGTA	60.299	20	276	687	962
60.218	20	TGAGTTGCAACCAAAACCAC	59.591	20	111	42	152
59.297	20	TCAAAATGGAAACGTGGACA	59.941	20	188	9	196
60.021	20	ATAGCTTGGCACCCTACCCT	59.983	20	220	3	222
59.371	20	TCATTCCTCTTGAATTTGGTGA	59.546	22	259	58	316
59.978	20	GTTGGGAGGTTTCGTCACAT	59.827	20	208	4	211
60.214	20	GTGGATGAGAGGGTTTACCG	59.405	20	258	1133	1390
59.827	20	GGAAGTGCATACGAGTGGGT	59.997	20	260	698	957
60.088	20	TGTGATGTGATTGGGAGAAATC	59.797	22	206	753	958
58.735	26	ATCCATTTCACACCGGAGAC	59.786	20	274	298	571
57.646	24	CTCGTTCTCTTTCCTTCCCA	59.401	20	241	10	250
59.893	20	TCTCCTTGGCCGAAAATATG	60.031	20	224	863	1086
60.009	20	CTGCACATGCTTTAGTCCCA	59.864	20	133	2025	2157
59.901	20	CAGGAACATCGTTGTTTGGA	59.541	20	227	184	410
60.006	20	CTGATGGTGATGGTGTTTCG	59.96	20	216	1990	2205
59.406	20	GCACCCCCACCTTACTTTCT	60.361	20	273	64	336
59.955	20	CCCAAGACCCCAATTTGATT	60.91	20	100	17	116
59.52	20	ACATTGGCTTGTGAGTTTCG	58.775	20	169	95	263
59.879	20	AGCTGGGTGACTTGGATCAG	60.261	20	154	166	319
59.969	20	CGGAGGTAGTTGGCATTTGT	59.993	20	231	324	554
59.463	21	GACGTGGTTTGCAGGCTATT	60.14	20	186	84	269
59.973	20	TGCTTAATTCTTAATGTAATATCC	59.009	26	243	524	766

59.212	20	AATCCTTTTGGTGATGCTGG	59.933	20	139	51	189
59.836	20	GCCACATCAAAACTCGGAAT	59.939	20	266	2961	3226
60.119	20	TTTTGCCAAGTTGTCTGCTG	60.027	20	258	275	532
59.784	20	TTTTTCACACCAGAAACCAAA	58.161	21	151	35	185
60.379	20	CATACTTGTGCCGGGTATGT	58.379	20	154	638	791
59.903	20	AGGGGAAAAGAGAGAGGTGG	59.671	20	255	21	275
59.873	20	TCAGAACCCGTCTCTGCTTT	59.989	20	238	1459	1696
59.22	20	TCTTCCATGACAAAATGCCA	60.049	20	209	703	911
60.401	20	GTTGGGCAGCCAAATATTGA	60.837	20	120	254	373
59.851	20	CTGTAGCGTTGCTATCCCGT	60.292	20	275	301	575
60.277	20	GATGATCGCTGATGTTTGGA	59.61	20	259	451	709
60.195	20	CCCAAGACCCCAATTTGATT	60.91	20	260	176	435
60.134	20	CCTCAACCAGCTTAAACCGA	60.241	20	278	389	666
59.964	20	AATGTGTGCACGAAGAGCTG	60.056	20	169	1754	1922
60.332	20	GCCTGAAATCTGTCAACCCT	59.141	20	241	202	442
60.008	20	CTTTATGCGCTCAGCTCTCC	60.257	20	232	219	450
60.132	20	GCGATTCGCCTTCAAATCTA	60.31	20	239	523	761
60.066	20	ACCGATGTAACGGAATGAGC	59.962	20	203	240	442
59.667	20	TGGAGGATAAAATTTGTAACACG	59.782	24	142	397	538
59.997	20	TGTAGCCGACCCCAATTTAT	59.297	20	147	1475	1621
60.073	20	GATGCTACTCCCACAAACCC	59.41	20	234	278	511
60.066	20	AAGTAGATTCCGGGCCATTT	59.799	20	203	564	766
60.218	20	AAGGAAACCACATCTAACCTGTT	59.817	24	273	3	275
57.079	21	TGCCCTATTTTTCCTCCTCA	59.64	20	188	20	207
59.923	20	TCGATCCCACGTATTGTGAA	59.924	20	143	37	179
59.898	20	CGATGCTCCTGTGTCAAAAA	59.84	20	247	1541	1787
59.931	20	AAGGTTGCGTACACCTGACC	60.035	20	133	249	381
59.972	20	ATCATCCTCATCCCCATCAA	60.096	20	164	156	319
60.003	20	ATGTTGAGCCCAACCCAAC	60.774	19	268	220	487
59.668	20	TATCGGTTCCAAATCACACG	59.395	20	172	2015	2186
59.658	22	TATTGGCTTTACAACTGGGC	57.781	20	257	6	262
60.02	20	AGGTTCGGGGAAGTCTGATT	59.935	20	265	67	331
58.576	20	TTCCTCTCCCAAGGTATTTCAA	59.939	22	208	1230	1437
59.833	20	GCTCGGTTTCAGAGGAGTTG	59.989	20	189	305	493
59.2	20	AAATTGTGGGCTACTGGTGC	60	20	231	86	316
59.718	20	CCCAAGACCCCAATTTGATT	60.91	20	162	819	980
59.836	20	GCAAGGGATCCTCTCCTTCT	59.778	20	203	534	736
59.95	20	CGTCGGGTAGACCAATGACT	59.989	20	265	37	301
59.933	20	TGTAGCCTACCATTCCGTAGAA	58.787	22	246	1199	1444
59.96	20	TTGAAGATTCGGACGATGTG	59.648	20	172	1609	1780
60.754	20	TTCGGCATAAAAATTGGTCA	59.004	20	267	71	337
59.107	24	TTGATTGCTAATTCAATTTTTATAC	59.326	27	206	60	265
60.134	20	TGCAGACACTTCAAAGTTCCA	59.475	21	169	31	199
59.821	20	CCGGATCGGTCTTAACTCTG	59.688	20	231	964	1194
60.91	20	CTCCCCAACTTGCAACCTAC	59.592	20	153	4	156
59.867	22	TGCAGTATTGAATTACTTTCCG	57.065	22	250	59	308
60.169	20	GCCTGATCTACAGCCTCGTC	59.981	20	266	86	351
59.316	20	TGGATGATCAAGGCTCTCAA	59.322	20	251	293	543
58.999	21	CGCGGCTAAATTTGAAAGAG	59.979	20	218	70	287
60.182	22	GAATCAAGCAAGCGGAACTC	59.962	20	138	400	537
60.545	20	TGGCAACTGTACAAACAATTCA	59.132	22	150	683	832
59.789	20	ACATGTCAATTAAAAAGAAGGAA	57.538	25	185	383	567
59.938	20	TTTTCGTCCCTTACCCTTTG	59.061	20	225	3	227
60.096	20	CTTGCAAGGGAAGACGAAAG	59.986	20	254	206	459
59.491	20	AAGTAATGTTGGTGTCCGGC	59.859	20	108	0	107
60.112	20	GGCGATTGTCAACTTGGTTT	59.978	20	224	98	321
60.063	19	GGGTTTAGGGTTGTCAGCAA	59.971	20	276	28	303
59.911	20	TGAATATCACAGAATTTGGGAGG	60.19	23	147	253	399

60.11	20	CTCCAGGCTGATGTTTCCAT	60.073	20	160	44	203
60.029	20	ATGCATGGTGTAGGATCACG	59.399	20	121	526	646
59.955	20	ATGGCCATTTTTCCACCATA	60.016	20	160	2748	2907
60.529	20	CCCAAGACCCCAATTTGATT	60.91	20	268	652	919
59.297	20	AAAATATAGCCAGCCCAGCC	60.428	20	240	1	240
59.92	20	CAGCCAACACGATCAAACAT	59.572	20	275	808	1082
59.978	20	CTTCAGCAATTCTTCCTGCC	59.955	20	227	513	739
59.807	20	TCTATTTCCTGCATCCTGGC	60.177	20	177	4395	4571
60.474	21	ACTTCCTGGCCAGACCTTTT	60.11	20	189	6	194
58.201	22	ATTGTGCAATGGGAATGGAT	60.021	20	278	698	975
61.032	20	TGCAAAGCGAAGAGAGACAA	59.864	20	246	292	537
59.986	20	ATGGATTCCTTGTTCGATGC	59.9	20	108	397	504
59.986	20	CCTTGGAGAAAGTTGCGAAG	59.986	20	224	260	483
59.967	20	ATGTAGCCGACCCCAATTTA	59.297	20	263	1735	1997
59.726	20	GAGAGAAGCCAGGGATGACA	60.349	20	215	4	218
59.803	22	GCTCTAATTGCATGGTCGGT	60.103	20	154	141	294
60.945	20	ATGTAGCCGACCCCAATTTA	59.297	20	194	3484	3677
60.049	20	ATTCTTCGGTTGGAGGTGTG	59.966	20	185	470	654
60.664	20	CTCGGGAAATTGAAAAGCAA	60.181	20	176	154	329
59.546	20	TCAATCACCAATCAACAAAACC	59.708	22	205	154	358
61.034	20	CGAATGAGAAAAACTGGGGA	60.044	20	244	52	295
59.367	21	CGACGGATTGATGCTAATTG	59.136	20	249	706	954
60.088	18	ATAATAACCCCGCAAGGGTC	60.041	20	183	13	195
59.971	20	TTACGGCCAAGGAATGAATC	59.901	20	274	959	1232
58.929	20	TGTAGCCGACCCCAATTTAT	59.297	20	278	2429	2706
60.218	27	ATGTAGCCGACCCCAATTTA	59.297	20	105	14	118
59.241	20	GTGTTTTCTAGAGGCACGGG	59.734	20	161	869	1029
59.717	20	CAAGTAAATGCTCGGCACTG	59.488	20	186	1822	2007
59.297	20	CACACAATACGCACACACCA	60.071	20	235	0	234
57.142	24	TGGACAGTAGCAAAGCCACA	60.449	20	276	330	605
59.726	23	GCAAAATTGTTTGTTGTTCTGTT	58.273	23	108	318	425
57.291	20	ATCATTCAGGAGGGCGGTAT	60.682	20	260	1915	2174
60.362	21	AGAGACAAGCCAACGCAAAT	59.882	20	266	1521	1786
59.654	22	TGCTTCCCAAAAGTCATTCC	60.051	20	217	186	402
59.933	20	CAATGCATGAACCACACTCC	59.967	20	168	23	190
59.837	20	ACCAAAGAACTTGCCCACAC	60.012	20	270	1230	1499
60.073	20	GGAAATTGAAGGGCAGTTGA	60.051	20	206	53	258
59.592	20	TAAACCCTTTCCCCGAATGT	60.534	20	105	2216	2320
59.259	19	TGAAATTCCCGATAAGTTGGAA	60.645	22	211	0	210
59.878	20	GGGATTGTTATCGTGATGGC	60.163	20	242	156	397
60.366	20	GAAATCAGAAGAACCATGCCA	60.066	21	259	288	546
59.992	20	GCATTGGTGACATTGATTGC	59.939	20	185	2796	2980
59.556	20	TGAAATATCATGTCCAGGTTTCT	57.62	23	190	56	245
60.91	20	CTCCAAGCTGATGCAACAAT	58.877	20	178	6	183
59.599	20	ATGGAAAAATTTGCAGAGCG	60.209	20	229	2918	3146
60.39	20	TTATCGGTTTAGCCAGCACA	59.325	20	266	770	1035
60.27	20	AATATGATGGTGCGGTGGTC	60.613	20	273	71	343
59.96	20	CCCAAGACCCCAATTTGATT	60.91	20	142	389	530
60.159	20	CCAAAATGTAAATCGGCCAC	60.188	20	242	1372	1613
58.264	22	ATCCGCCCTTGATACAGGT	59.376	19	179	2266	2444
60.384	20	TCAAGCAAAAATTGAACCCC	59.916	20	214	156	369
60.032	20	GTAGAGGCGTGACTTTGGCT	59.501	20	224	304	527
60.016	20	GGTGTTGAACAACCAGACATAAA	58.917	23	266	746	1011
59.585	20	TCAGCAGCCATCTGTTCTTG	60.136	20	183	104	286
59.076	20	GGACACCCGTGTTGAAGTTT	59.867	20	200	21	220
59.927	20	CGACCCGTGATACCAGACTT	59.989	20	211	115	325
59.832	22	CCATCACTCTGTGAACCGAC	59.101	20	128	59	186
59.486	20	CATTTTATGCAGCGAATGTTG	59.227	21	164	22	185

60.008	20	TTCACTGTCGTCAAAGCTGG	60.025	20	252	324	575
59.939	20	TCGATCAAAATAACACCATTGC	59.838	22	195	1470	1664
59.992	20	GATTTTCGAGTTGCAGAGGC	59.962	20	183	1649	1831
59.759	19	TCAGAAGGGGTTATGTCCTCA	59.536	21	263	107	369
60.226	20	TCAAGGTGGTGTTTTCCACA	59.976	20	238	32	269
59.993	20	GGCAGCCTAATATTGAGCAGTT	59.784	22	252	19	270
59.927	20	GGACCTAATTTTCCCCAAGG	59.639	20	219	1458	1676
59.945	20	ACCAATGGTGGTATGGTGTG	58.984	20	131	201	331
60.156	20	GAGATGGGAGGTGGTCTTGA	60.048	20	181	20	200
60.187	20	CAAACCGGTGCTCCTTGTAT	59.993	20	280	2107	2386
59.805	20	GCACAATGCCAAGTAGCAGA	60.019	20	156	994	1149
60.469	20	TCAGCAGCCATCTGTTCTTG	60.136	20	161	17	177
60.529	20	TTCCTAGCTAGCTTTCCAATTCA	59.549	23	227	725	951
60.035	20	CGATCCCATCAAATCTGAGC	60.57	20	245	2799	3043
58.823	21	TCACTCATGCATCTTCCACAA	60.256	21	249	8745	8993
59.297	20	CCTACTTGCATTGTGCTCCA	59.864	20	111	1	111
59.989	20	AAAGTCGCAATCAGCAACAA	59.469	20	181	1650	1830
60.118	20	TCTTTTACAAGGTGGGTGGC	59.971	20	162	412	573
59.101	20	GACTGGGCTTTTTGGTTCAA	60.088	20	120	351	470
60.074	20	TGTAGCCGACCCCAATTTAT	59.297	20	149	489	637
60.449	23	CCCAAGACCCCAATTTGATT	60.91	20	109	9	117
60.096	20	GATGGACGTCGACGATTTCT	60.081	20	263	156	418
59.329	24	GTAACCAGCAGTCCCCAAAA	59.971	20	149	227	375
59.948	20	CGACGAGAAAGTCGTGTCAA	60.025	20	178	306	483
60.317	20	TGCACCAACTTCCTCTCCTT	59.844	20	197	1	197
61	20	GGAAGCCAATTTGTTTGCAT	59.945	20	219	782	1000
59.91	20	CTTCCCTCTCAAAACCATCG	59.665	20	238	27	264
60.138	22	CCTTTAGAACTTGCTCCACCA	59.364	21	268	16	283
60.051	20	AAGAGAAACAGAAGTTGCAGCAC	60.109	23	107	2543	2649
60.11	20	ATTGGAACGACATTTGCCTC	59.939	20	240	1264	1503
59.829	20	ACGTAGGGTTACCGGAGCTT	60.019	20	192	271	462
59.904	24	TGATGCAGACTCGAGGTACG	60.008	20	246	478	723
59.917	25	CCCAAGACCCCAATTTGATT	60.91	20	102	15	116
59.67	20	TCTCCCCAATTCACCCTACA	60.309	20	236	121	356
59.874	20	CTCAAGTGGCTTCTATGGGC	59.836	20	102	4	105
61.171	19	GTAAGCACCTCCTTCCACCA	60.111	20	177	31	207
60.24	20	ACGATGTTGAACGGAAAAGC	60.118	20	196	437	632
59.297	20	CCCTTGACTTTCAACCCAAA	59.942	20	222	12	233
58.837	23	CCTCGAACCTTCTGCAAAATA	59.348	21	180	406	585
60.056	20	CCCAAGACCCCAATTTGATT	60.91	20	235	584	818
58.294	20	TTCTTTTATGTGGGTTGCAAAA	59.511	22	224	1258	1481
59.297	20	CTTCCTTGCATTCGTCATCA	59.799	20	203	4	206
60.365	22	TTGATGGAGGCCTTATTTGC	60.038	20	258	295	552
59.547	20	GGGATTTGGTGGTGAAAATG	60.029	20	150	469	618
59.923	22	CAACCCCTACTCTTTTCTTCCTT	59.222	23	173	32	204
59.292	20	ATTGGGTATAACCCCGAAGC	60.041	20	224	2012	2235
59.7	20	CCATGACCGGTGATTCTCTT	59.927	20	269	5637	5905
59.637	20	CAATGGATGAAATTCCCGAG	60.266	20	261	307	567
60.208	20	TCCAGGTCCTCTGTCGTTTC	60.238	20	145	101	245
59.735	23	TTTCATTCCTTTTTCCTCCTTT	58.307	22	166	335	500
59.938	23	ACCTCATCGCCACCTAAATG	59.955	20	251	20	270
60.91	20	GGTGCAGATTTAAATGTTATACAG	59.731	26	185	4	188
60.91	20	TGCCTGATGAACATCCAAAA	60.049	20	268	4	271
60.91	20	GCCCAAATACCACTTGAAGC	59.574	20	280	4	283
60.034	20	ATCGAGTTGGTGGAGTGGAC	59.969	20	219	471	689
60.91	20	TGTTTCACATTTTCAAGCGG	59.706	20	189	2	190
59.297	20	CGATGCGCAAATAAAAGACA	59.842	20	120	229	348
59.377	21	CCCAAGACCCCAATTTGATT	60.91	20	100	23	122

59.013	20	TTTTGCATCTGGGTTCCTTC	60.051	20	129	3072	3200
60.088	20	GCCTGAGATGGTAGACACCG	60.678	20	271	1034	1304
59.371	22	TGCTGCCTTTGTTTTGTCAG	60.027	20	171	37	207
60.054	20	ATTGTACCTGGACTCCTGCG	60.134	20	242	703	944
59.945	20	CAGCGAAGAAATTCACCCAT	60.074	20	237	3405	3641
60.699	20	GGGCGAGTCTCAAGAAACAG	59.989	20	155	31	185
60.196	20	CAATGACGAATAGCAGCCAA	59.833	20	188	20	207
60.91	20	CCTCGATCGCTTGGATCTTA	60.309	20	229	7	235
59.726	21	TTTGTGTCATAGAAGGCCCC	59.933	20	252	1526	1777
59.305	20	ATTACAGCATGAGCAGTCCG	58.903	20	201	27	227
60.088	20	CCGAGGTGAGATTCAAAGGA	60.187	20	241	1586	1826
58.187	22	GACAATGTACGCACGGAATG	59.995	20	246	3	248
59.155	22	ATCTATGGCTTCCGCTTGTG	60.235	20	278	27	304
60.293	20	CATAAATGCATGCAACGTCC	59.96	20	113	264	376
60.91	20	AGCAAAAATCGGCACTAACC	59.229	20	163	7	169
60.218	20	CCGAAGTGCTAGACCCAAAG	59.869	20	179	73	251
58.119	21	TTTCACGTGGTTTGGTCTGA	60.128	20	140	33	172
57.413	27	TGGAGTGATTAATATGCAATTTTC	60.563	26	245	35	279
60.399	18	GCATACCTATCCGAGGGACC	60.682	20	178	31	208
60.91	20	GCTTTCTTCAGCATGTTGTCC	59.874	21	168	7	174
59.924	20	CCCAAGACCCCAATTTGATT	60.91	20	114	3	116
58.761	27	CCCAAGACCCCAATTTGATT	60.91	20	111	6	116
60.074	20	CCCTGAATTTGATCCTGGTG	60.309	20	238	1840	2077
60.074	20	CTGCTTTCTTGTCCTCGTCC	59.989	20	170	244	413
59.055	21	TTCGACAATGTGTCTACATCCA	59.05	22	198	69	266
59.957	20	CCATAATTACCGGCGTCATC	60.175	20	183	313	495
60.053	20	TCTGCACATCTGAATTTACAAAA	57.528	23	238	150	387
60.051	20	AGCCCTCACACAACCAATTC	59.973	20	194	772	965
59.901	20	CAATGATCGGTTTCAAGGGT	59.79	20	207	1409	1615
57.268	25	CCTCTTCGGTTGGTTTTGAC	59.569	20	225	24	248
59.697	20	ATACCTCTCCGTCCACGATG	59.95	20	272	358	629
59.638	20	ATGTTCGACTGATCAAGGGC	60.081	20	183	5633	5815
59.355	22	TGGAGGACTAGATTTGGGGA	59.478	20	104	20	123
59.429	20	AACTTTGTTGAATGAGCCCC	59.031	20	279	501	779
59.74	20	GCCATTGGATTCGATTTTGT	59.768	20	201	2	202
60.036	20	TGAGGAAAGTGATCCTTGGG	60.042	20	112	16	127
59.133	23	ATTTTTGGGCTACGACAACG	59.996	20	210	168	377
59.647	23	ACGTCGACACTAAGGCCAAG	60.312	20	117	6	122
60.045	20	AATGATGACCTCATCTCCGC	60.042	20	167	914	1080
60.088	20	CCCAAGACCCCAATTTGATT	60.91	20	268	454	721
60.175	20	CCCAAGACCCCAATTTGATT	60.91	20	111	6	116
59.787	20	GCTGCATCAATGGAGCTTCT	60.514	20	280	1493	1772
59.984	20	CCTTGAAATCGAACTCTCGC	59.955	20	216	951	1166
59.96	20	TGGGAATAATCCAGGAACCA	60.126	20	237	293	529
60.066	20	TTACGCTAGTCCGTGGGTTT	59.632	20	156	1051	1206
60.51	20	TCCAATGAGACACACTCCCA	60.088	20	223	1624	1846
60.767	20	TTCTGTGCATTGCCATTGAT	60.08	20	255	23	277
60.39	20	AGGTGCATCCATGGTTCATT	60.203	20	253	826	1078
60.112	20	ATGCAAGCTTTCCCACTCAC	60.263	20	266	3193	3458
60.17	20	AAATGGTTCGTAACTGCCCA	60.365	20	222	353	574
60.196	20	GGGTTTAGACGTCATGCACA	59.572	20	224	44	267
58.789	22	CCCAAGACCCCAATTTGATT	60.91	20	104	17	120
59.297	20	TCGAAGAAGCGAAAATCACC	60.331	20	122	1	122
60.365	20	AAGCTTCGTAATATGGGCGA	59.704	20	150	2053	2202
59.907	20	TGGGAGTCAACTGATTGCTTC	60.248	21	178	707	884
60.022	20	GTCGAGACGGGACTGTGAAT	60.12	20	267	2144	2410
60.91	20	GAGGATGGGCACATACTGGT	59.81	20	178	4	181
59.297	20	CCGATCGAGCTGAGAAAAAG	60.088	20	280	4	283

60.045	20	GATTTTCTTGGATCTCATGCC	58.586	21	262	614	875
57.335	25	TCCGCACTTGAAATTCCATC	60.983	20	243	35	277
60.77	20	CCCAAGACCCCAATTTGATT	60.91	20	134	1	134
60.011	20	TCTTACTGGTGCCGGAAATC	60.074	20	183	292	474
59.248	22	CCCAAGACCCCAATTTGATT	60.91	20	100	23	122
60.127	25	CCCACACTTTGTGTCACCAC	59.89	20	265	518	782
60.91	20	AAAAGAATGCAGCGCAAAGT	60.025	20	213	6	218
60.91	20	TTTGCCGGTCGATAACTCTC	60.214	20	252	771	1022
60.817	20	GCATGGGCTTGTTTTCATTT	59.945	20	156	29	184
57.86	24	TGTCTTGTGCTGAAGATGGTTC	60.299	22	262	27	288
59.88	20	TACTGCTCTCTGGGGCATCT	59.973	20	194	1527	1720
60.443	22	AAGCAATTGGAAGATGGTGC	60.081	20	213	651	863
59.995	20	GCCCATTTTGATCACCATCT	59.756	20	247	445	691
59.146	20	TATCGGATGGCTTATCCCAA	60.247	20	206	4966	5171
59.856	21	AATCCGTTATTTCTCCCGGT	59.666	20	258	723	980
57.698	20	GAGCTGATGGAAACACTTCG	58.443	20	276	1789	2064
60.91	20	AAGCTTCAGCAGCTCTTTCG	60.037	20	175	7	181
59.94	20	AAAATCGCACGACGAATACC	59.967	20	180	738	917
59.997	20	CCTTCAATTGCCCTTCACAT	59.933	20	244	710	953
60.839	20	CGTTCCGACCCTTCAATAAT	58.903	20	216	6	221
60.112	20	GATTCGAATAGGAACGCGAG	59.807	20	210	2644	2853
59.84	20	TTCCCAGCCACAATGTGTAA	59.964	20	249	110	358
59.505	20	AGGCTGGTCTAAAGCGCATA	60.003	20	231	496	726
60.124	23	TCTGATGTGAAATGTGTGGATAC	57.465	23	178	19	196
57.488	20	TGTAGCCGACCCCAATTTAT	59.297	20	253	467	719
58.609	21	GCATTTTTCACTTAGCCGAGA	59.488	21	225	29	253
59.966	20	GGGTGAGGGAGAAAAAGGAA	60.414	20	236	131	366
59.546	20	TGTCGAAACCATCGTTCCTC	61.046	20	271	55	325
59.668	22	AATATAGTTATCACAGGATCACCA	58.111	27	209	1409	1617
60.355	21	GGGATTTCATCCAAAAACCTG	60.528	21	275	2145	2419
59.955	20	GAGCAACTTCTTGGCTCGTT	59.621	20	255	18	272
59.609	20	GTAGATCCATGTGGCCGTTC	60.348	20	195	985	1179
59.957	23	TCTTCATCTGCCAGTGCTCA	60.711	20	136	18	153
60.082	21	TTGTATGTCGAGTCGAGTGTGA	59.365	22	139	205	343
59.964	20	GTTCGATCGTTTGTCCTCGT	60.119	20	268	51	318
59.871	20	CGGCTTAGGGCAGATAACAG	59.861	20	127	1837	1963
59.982	20	GCAACACCGGATTCACTTTT	59.978	20	210	2658	2867
60.006	20	GAGAGGAGCGACACCAGTTC	59.993	20	141	340	480
59.297	20	GCTGCACATATTATGCTTTGC	58.485	21	257	6	262
59.799	20	CTCCTGCTTCACCTCGATTC	59.95	20	225	174	398
58.997	22	ATGATCTGAAGAAGCGTGGC	60.37	20	260	89	348
60.346	23	ACCCTAATCCCACCCTTCAC	60.052	20	123	2	124
59.812	20	AGCATTGGCAAAGACGACTC	60.406	20	279	870	1148
59.931	25	TCACAAAAATATTTCCCGGC	59.773	20	195	38	232
59.887	20	GAACAAAACATTTCGGGGTG	60.206	20	221	3812	4032
58.649	20	TAAAGGGCAGGGTGAAGTTG	60.103	20	205	9	213
60.377	20	GTTCGTCTTTCCCGTTCTCA	60.232	20	208	231	438
60.91	20	AATAAAATGTCGTGAGCCCG	59.96	20	151	9	159
60.096	20	TCTCCGTTGGAACAATAGGG	59.926	20	273	628	900
59.846	20	GTGAGGAGGACGATGAGGAG	59.792	20	176	196	371
57.318	22	GGCGTGTTTGGGATGTTTAC	60.235	20	214	12	225
60.894	20	ATTTGGCATCCATGTACGGT	60.081	20	168	2001	2168
59.34	20	AGCTTCTGCCTGAATTTGGA	59.955	20	208	286	493
59.958	20	AGAACATCACCTGCCTCACC	60.12	20	255	3311	3565
60.142	20	GATCGAGCTAGCCCAGTTTG	59.978	20	216	74	289
60.206	20	GCCTCAAGGTATGAAGCAGG	59.836	20	265	25	289
58.987	26	GCCAAGTTGACACACACAGG	60.203	20	144	36	179
60.502	20	GCTTGGGCAGAGTTTTGGTA	60.249	20	155	16	170

59.297	20	TGTGTCATTGTTTCGTGGAA	58.514	20	100	3	102
60.469	20	CAAAAGGTTTTTGACTCTTACCAG	60.077	25	137	444	580
60.401	20	TGGGCTTTTAAGGAAGACGA	59.817	20	231	521	751
57.883	25	ATTGCGTTGCTTAATGGGAG	60.096	20	275	263	537
58.054	24	GCAGCCAAATACACTCAAAACA	60.173	22	253	162	414
59.933	20	GACTCCGCATAGTGGGAAAA	60.074	20	258	4604	4861
59.297	20	CGACGCTGAATGAGCTAGAA	59.322	20	212	0	211
60.051	20	AATCGAGAATGTGGACGGAG	60.073	20	223	826	1048
59.773	20	GAGCGTGCGGAGCTAGTATC	60.147	20	198	127	324
59.934	20	GGTAGGCTGGTAAGGGCTTC	60.096	20	162	7990	8151
60.415	20	GGTGGTATGCTGTGGAGGAC	60.395	20	184	1	184
59.875	20	CCCAAGACCCCAATTTGATT	60.91	20	249	529	777
59.917	20	TTGCTTCCGTGTTTTATCCA	59.157	20	112	46	157
59.612	20	CTGCAGCCATCTGTTCTTGA	60.136	20	204	3	206
60.111	22	TGGTGCTGGAGGTGACAATA	60.112	20	268	368	635
58.736	21	CAGACGCCAATTACAGGTGA	59.716	20	232	32	263
59.933	20	CAAAAACGAAAGCAAGCTCA	59.226	20	257	4483	4739
60.91	20	AACAAATCCTTTGGCACAGC	60.118	20	138	8	145
60.117	20	GCTTCAGCGATCAACAAACA	59.995	20	180	1354	1533
59.297	20	CTACCACAACACATGAGGCG	60.175	20	176	9	184
60.57	27	AACCGTGTGCCCCTAAAAAT	60.593	20	231	7	237
60.036	20	TGAGGAAAGTGATCCTTGGG	60.042	20	112	11	122
59.784	20	CCCAAGACCCCAATTTGATT	60.91	20	173	1218	1390
59.982	21	AATGCTATTTGGAGCCATCG	60.06	20	209	32	240
59.547	20	AATGGGGTGTGAGGAAATGA	60.173	20	189	571	759
59.966	20	AATTCGAAAGTTTGCCAAAAA	58.773	21	106	287	392
58.348	24	GGCCGATATTTTGGCCTTTA	61.096	20	206	36	241
59.721	20	TAAAGTTTGGTGACGACCGC	61.06	20	273	924	1196
59.897	20	ACTATGGCCACCGTCACACT	60.453	20	146	496	641
60.073	20	CATTTCCTCCTCCGGTGTTA	59.926	20	188	920	1107
61.103	21	AATGGAGTAGATTTTCCCATGA	57.552	22	153	204	356
60.588	22	TTAATTATGGGACGGAGGGA	59.227	20	152	16	167
59.545	20	AGCATGTAACTCATGTGTCCCT	58.603	22	269	1136	1404
60.05	20	GGATTCGCAAGATCGACAAT	60.043	20	253	1071	1323
60.065	20	AGTAAAGGGTTTGCGCTTGA	59.883	20	236	965	1200
59.694	20	ACGAATTAGCGTTTGATGGC	60.103	20	279	2492	2770
60.274	20	CTCCTGCACCAGAACTCTCC	59.986	20	244	178	421
60.12	20	AAACATCTTGCCACAGGAGG	60.111	20	212	132	343
59.329	21	TCCAAATGTAACTCGACCCA	58.973	20	185	1339	1523
59.971	20	GAGCAACTTCTTGGCTCGTT	59.621	20	114	513	626
59.901	20	GAGGCTCCTTCAAACACTGC	59.997	20	234	287	520
60.461	20	CCCATCACCCACCACATAAT	60.317	20	191	3173	3363
60.066	20	CTCCCCGTTTCTCTCTCCTT	59.811	20	207	691	897
60.067	20	CCACCCCTAGCAAAGTTGAA	60.103	20	244	2593	2836
59.824	21	AGATTCGTCCCAAAAACACG	59.971	20	208	177	384
59.32	20	TGCTGGTCGCTATCTCTGAA	59.697	20	171	1780	1950
60.051	20	TTGCTGACTCTTCAGCCATC	59.116	20	211	466	676
59.881	20	AGCTAAAGTCGGGCCAAGAT	60.228	20	245	918	1162
60.43	20	TGAAACTCCACTGCCCAAAT	60.495	20	208	2	209
59.865	22	CTTCGAGGGGAGTGTTGAAG	59.837	20	276	43	318
59.648	20	TGAAATGGTAGAAATCGCCG	60.961	20	212	47	258
59.887	20	TGGATTATGTAGCTGACCCCA	60.337	21	125	318	442
59.988	20	CCCTCGCTAACTCTTTGTGC	60.015	20	261	749	1009
59.577	20	GTGAGAAATCGAGGTCCGAA	60.195	20	146	551	696
59.297	20	ACGGGATTGAGTTCACGTTC	59.973	20	232	4	235
60.323	20	ATAGGGCAGGCCTAAGGTGT	59.983	20	246	403	648
59.764	20	GCCACACGAGGAATAGGAAA	60.074	20	222	736	957
59.869	20	GGTGAATCAGCAGGGGTTTA	59.933	20	109	996	1104

59.453	24	TCAAAAGTTATTTTCGAGGACGA	60.115	23	243	34	276
59.75	20	TCCCAATTTCACCTTTCCAC	59.767	20	272	2809	3080
59.566	20	GGTCATGCGTTCAAGGTTTT	59.978	20	254	344	597
60.011	20	CCACAGTTGGATCTCGACAA	59.676	20	259	349	607
59.717	20	ATCCATCTGTCCTCCATTGC	59.893	20	242	1205	1446
60.91	20	AGCTCGAAGTGGAAGACGAG	59.745	20	222	8	229
60.074	20	ATGATCCATATAGCCGACGC	59.914	20	244	1950	2193
59.955	20	CCTTCAGCAGCCTTTGTCTC	60.134	20	188	1105	1292
60.16	20	AGGGTTAAAGAAGCCGAAGC	59.856	20	255	57	311
60.067	20	TCGGAAGCTTCAAGTCCAAT	59.813	20	247	282	528
59.843	20	AACCGGATACAGCCACAAAG	59.993	20	144	249	392
59.7	20	GAGAGGCCGGATGATCTACA	60.181	20	218	1	218
60.223	20	CCTGAGGACTGATGGTGGTT	59.962	20	235	1214	1448
60.24	20	AAGGACAGGACAGCCGTATG	60.134	20	267	821	1087
59.297	20	GGTGAAAAACCCGAGTTCAA	59.948	20	115	3	117
59.955	20	TTGCTCAACTAGGCAATCCC	60.214	20	230	251	480
59.302	27	AACCCTAAATCTTCATCACACG	58.124	22	277	632	908
60.014	23	TCATGTAGTCGACCCCAATTT	59.302	21	101	387	487
59.488	22	AAAAAGATTTTACGTGTTTCACGA	59.169	24	110	61	170
59.894	20	CTCATTATGATGCTCCGCCT	60.199	20	109	209	317
59.971	20	CCTCTTGCATATTGTGGCCT	60.096	20	270	161	430
60.024	20	TGCATTGGCTGAAGAAAGTG	59.988	20	111	2194	2304
59.903	20	TCTTTGAGGGACATTCGGAC	60.05	20	142	349	490
59.649	20	ACAGCGCTATAGGTTGCTCA	58.703	20	140	836	975
60.938	21	CCCAAGACCCCAATTTGATT	60.91	20	179	2188	2366
59.297	20	AATCAATACGGACTTTGCCC	58.906	20	274	375	648
60.263	22	CATGTCCCCAGAGATGAAAGA	60.058	21	208	6	213
60.899	19	TGACAGGAGGAAATAATGAGATT	59.502	24	269	412	680
59.738	20	ATGTAGCCGACCCCAATTTA	59.297	20	220	311	530
59.917	20	TGACTACAACGACGATTCGG	59.716	20	251	118	368
58.502	21	TGATACTTCGCATCTCACGG	59.823	20	157	1	157
60.91	20	CACGGTCCCTTATCACGACT	59.989	20	110	2	111
59.784	20	TTTGATTGGGAATAATTGGG	57.289	20	237	279	515
60.647	20	GGCCTGAGCAATGGAATAAA	60.038	20	267	164	430
59.297	20	GGTTGCACATAATAGCTGCG	59.353	20	228	0	227
59.973	20	TCCCGGTACGACGAAATTAG	59.953	20	170	666	835
60.257	20	CCTTTGTTGCACTAAGTTCCAAAT	60.746	24	261	270	530
59.673	25	TCGATTGTCCACAATTGCAT	59.931	20	169	1519	1687
59.297	20	CGGCTAAAATCGGTCAAAAC	59.586	20	247	1	247
59.799	20	ATGAGGATTCTGTGGTGCGT	60.542	20	233	2	234
59.93	21	TGTGGATATTCTTTAATTTGTGCC	59.318	24	205	566	770
60.132	20	CCAGCCTTCCAAATTACCCT	60.312	20	221	3213	3433
60.411	20	GGCTACCGTGGACATGAGTT	59.997	20	165	3872	4036
59.929	20	CCCGGATTGACACTCCTAGA	60.065	20	231	43	273
59.917	20	CCAGCTCTTTCTGAACCCTG	59.982	20	252	448	699
59.578	21	CCTGAAACGAGTGATGCTCC	60.801	20	137	65	201
59.359	21	TTGGGACAAAAGAAGCTGAA	58.475	20	280	1930	2209
60.049	20	GGATCGTTCTCCTCCTCCTC	60.157	20	271	502	772
58.698	22	CCCAAGACCCCAATTTGATT	60.91	20	100	21	120
60.883	20	ATGGTTTTTGCACCCATTTG	60.597	20	135	105	239
58.623	20	CCAAGTTGAATTGTTAGTATCCGA	59.453	24	279	381	659
60.218	20	TGTAATGCATGGGGGAGAGT	60.34	20	226	38	263
60.155	20	GGTCCATGAACCCTGGACTT	61.152	20	145	314	458
58.508	20	CCGTCTCACTCCAATTGACA	59.676	20	246	158	403
60.427	20	TGCAGATATGGAGCAATTTTT	57.413	21	244	15	258
58.067	19	GCGTGACTCAACAGTGTGGT	59.789	20	182	0	181
59.989	20	CCCAAGACCCCAATTTGATT	60.91	20	201	111	311
59.496	22	CCCGTGGACGTAGATCAGTT	59.989	20	237	288	524

59.799	24	CGTTACTTGCTGGAGCTAAAAAG	59.64	23	158	58	215
59.894	20	GGATGCATCAGTTGGAAGGT	59.934	20	271	842	1112
59.969	20	GGAAGAGTGGGGGAGAAGAC	60.05	20	250	488	737
57.442	20	CTCTAACCCAGCAGCAGACC	60.012	20	238	30	267
60.112	20	TGCTCATTATTTGATTGGCG	59.662	20	214	14	227
58.518	22	ACGATGCACAAGACATGAGG	59.707	20	167	237	403
59.872	20	GGCAAAATTCGTTGGAGAAA	60.053	20	218	533	750
60.52	20	GTCGACAGGCATAAGCTTCC	59.843	20	271	491	761
59.505	20	TTGGTGCGATAACAATGGTG	60.379	20	244	489	732
59.415	21	CCCAAGACCCCAATTTGATT	60.91	20	225	2612	2836
59.688	20	GGTCACAACGGAAACAACCT	59.867	20	230	1609	1838
59.786	20	CACCCAAGTTTCTTCCAAGG	59.563	20	280	2159	2438
60.419	20	AAACCCCTCGTGTTGTTTCA	60.388	20	247	1235	1481
59.894	20	TCAGCAGCCATCTGTTCTTG	60.136	20	255	228	482
59.992	20	CATGCGGAACCAGTTACAAA	59.585	20	274	369	642
59.502	20	CTTAATGGGTGAGAGACCCG	59.545	20	147	1080	1226
60.197	20	CTTCCCGCAAAACGTTGTAT	59.996	20	155	417	571
58.783	22	ATTTCCACCGTTCAGACAGG	59.966	20	275	52	326
60.443	22	TAGCAGGCCAAAGAGGAAGA	60.088	20	150	45	194
59.948	20	AATCAGAATGGTTGGTTGGC	59.797	20	190	83	272
59.888	20	GGGCCTGTGCTCATAGAGAG	59.973	20	269	885	1153
58.965	20	TGAGGCAAGCATCAGAAAGA	59.673	20	235	122	356
60.053	20	GCTAGTTGCACCCCTGTCTC	59.874	20	160	969	1128
57.968	20	TGGAGAAGGAGGATCCATGT	59.46	20	184	35	218
59.801	20	GGAAACCCCATCCAGAAGAT	60.133	20	175	680	854
59.734	20	AAAGCTCGAACTTGTGGCAT	59.882	20	271	1559	1829
59.528	23	TCCTTAGCCCAAGTTGTACCC	60.359	21	167	182	348
59.711	24	GGTGAATTGTGTCGCTCCAT	60.935	20	272	2	273
59.145	21	AAGTTTGCCCTATCAAACAGGA	60.001	22	279	2150	2428
59.297	20	TGGTGGGAATCTTTTCATCG	60.832	20	164	9	172
59.254	20	TGGGGAATTCACGGAGATTA	60.266	20	157	66	222
59.924	20	CGCCTGAATATAGCCTTTGC	59.838	20	234	1346	1579
59.989	20	TGGAAAACCATCATCAACCA	59.75	20	230	6892	7121
60.001	21	TCCCTGTGCATTAATTTTTCA	58.148	21	237	50	286
60.02	20	CCTCCGATTTCTTACCATGC	59.528	20	212	23	234
59.639	22	TTGCTAGCCTCATCATTCCA	59.375	20	252	933	1184
60.051	20	GCAAACAGAAAATGAGGGGA	60.051	20	149	523	671
60.068	20	AACCAGCGCTAACACGAAAT	59.775	20	145	212	356
60.397	20	TCCCACCAATTTGTCCTAAA	57.917	20	132	560	691
60.27	20	ACTCAGAATTCCGATCGTGG	60.073	20	230	46	275
60.11	20	CCACTATGACCATGCCCTCT	59.95	20	261	43	303
59.218	20	AAATCCCACAAACGGAAACA	60.206	20	185	1475	1659
59.973	20	GCTAGCACCTCTTCTATTGCTGA	60.183	23	119	108	226
60.221	18	AGAAGAGGATGTTGGCGATG	60.218	20	185	28	212
59.198	20	ACTTCATCATTGAGCCCCAG	60.073	20	280	217	496
60.053	20	CCGTCGGTTTCTTGGATTTA	59.931	20	133	8305	8437
59.978	20	ACTGCCCTTTCAAATGTTGC	60.118	20	274	992	1265
60.143	20	GTCTCCAACGGCATCTCAAG	60.801	20	259	453	711
59.924	26	AAGTGCACAAGCACTCGCTA	59.812	20	267	17	283
59.186	20	GCAAGGCTGGAACTGAAAAG	59.993	20	226	13	238
59.542	19	AACGTGCAACGAGAACTTCA	59.49	20	189	2510	2698
60.301	20	GTAGTGGTATGGTGTGGGGG	59.966	20	277	646	922
59.872	20	CAAAATTCCATGACAACCGA	59.371	20	272	1132	1403
57.289	20	GCGTCCAAATAACCGACACT	60	20	271	65	335
59.939	20	CTGATAGCTCCGACAACCGT	60.277	20	204	181	384
59.065	20	ACCTTCGTCAAGGCAGAAGA	59.989	20	214	4	217
60.467	24	GGTATGGGGTGATGTCGATT	59.488	20	277	108	384
59.82	20	TGATCCACCCTATTTTGCATT	59.287	21	249	959	1207

58.188	24	TGAATTCTTGCACGTTCTCG	59.988	20	254	451	704
59.872	20	ATGTAGCCGACCCCAATTTA	59.297	20	261	5784	6044
59.856	22	TTGTTTTCATTTGAATAAATACGTG	58.972	26	255	166	420
58.177	24	TTGATTCGTGAACATTAGGCTC	59.229	22	135	55	189
60.134	20	TCAAACCCTAACCCTTTCCC	60.159	20	246	15	260
59.914	20	CAATTGAAGGGAAGGAAGCA	60.184	20	222	2230	2451
59.705	26	GCGATATAATCTCTGACGATTGC	60.102	23	112	9	120
60.328	20	TCGAGAAGTAATCGTCGGCT	59.978	20	245	484	728
60.162	20	CACTGGAATGTCAAGGCAGA	59.831	20	101	163	263
61.968	18	GAGCTACATTCCCGCCTTTA	59.32	20	194	8	201
59.425	20	AGCGTTCTTTCCCGAGTCTT	60.382	20	101	9	109
60.008	20	ATGTAGCCGACCCCAATTTA	59.297	20	207	71	277
60.002	20	TGTCCTATTTCCCAATCCCA	60.126	20	166	627	792
59.894	20	GCCGAGACCAACTCTCTACG	60.012	20	178	1218	1395
59.623	20	AGCCAATCTCCTCTCAGCAG	59.703	20	244	60	303
58.874	20	TCTACGCGGCCATCTCTATT	59.829	20	215	2051	2265
60.051	20	CCGGCAGTTACATATTCGCT	60.117	20	231	30	260
59.836	20	ATAATCAAGGGTGCAGTCGC	60.103	20	167	644	810
60	20	AGGTTGCGTACATCTGACCC	59.997	20	109	20	128
60.066	20	TGAAACGGCTCCTTAACTGG	60.241	20	269	236	504
60.545	20	CAAACAATTCATTGGTGTTCTTG	59.411	23	178	410	587
60.315	20	TCATCTCTTGCATCACTATGGG	60.096	22	265	98	362
60.074	20	TCAATCGACAGCACTTCCAG	59.984	20	247	678	924
60.742	20	GTTGGGCAGCCAAATATTGA	60.837	20	155	81	235
59.297	20	GGTGTGTTGTCTGGTGCAAG	60.203	20	100	4	103
59.882	20	CCTCGAACGTGTGTGTTAGC	59.365	20	233	1961	2193
59.96	20	ATTGACATCGAAATCCTGGG	59.75	20	254	3	256
59.124	20	AAACTTATTTATGGGTGGCCG	60.082	21	204	1310	1513
60.263	20	AGCTTCAGCTCCTCACCAAA	60.134	20	172	24	195
59.916	20	TTCCGACAAAATCAACACCA	59.941	20	240	6006	6245
60.153	20	CAAGTTGAATCAGAACGGCA	59.84	20	225	515	739
60.014	20	GGTTCAAGTGTTTGGGAGGA	59.943	20	124	389	512
59.735	20	CCACTAGAGATGACCTACAAGGA	60.063	25	177	608	784
60.573	20	TGGTCTCTGTCCATTGTGCT	59.261	20	159	44	202
59.867	22	CATCCAACATGAGGGAAGAG	58.071	20	202	2499	2700
58.943	20	CGAGGTTTTTGCTTGCACTT	60.42	20	180	21	200
59.933	20	TGATCAGATGCGAGCAAGC	61.257	19	134	2255	2388
59.455	20	GGAAGGACCTAGGCCTGAAC	60.074	20	221	884	1104
59.536	21	TTCAAGCAATAGGTCTTTAATATC	59.499	26	149	13	161
59.108	22	TCTGATCCCCCAAGACCC	60.835	18	110	19	128
59.897	20	CGAACCAGGCCGACTAATAC	59.592	20	220	1218	1437
59.903	20	ACTTTGAAGCTCGGAAACGA	59.993	20	218	38	255
60.249	20	CCGCATCGGCCTATTTACTA	60.075	20	158	272	429
60.255	20	AGTCACGAGCATGTTTGCAG	60.056	20	234	1793	2026
58.496	20	TTTCCCTGTAGAGGCAATGG	60.066	20	243	41	283
61.63	20	GCCAAGATTTTTGCTCCTTG	59.823	20	274	3	276
60.015	20	TCGTTGATTGTACGAGTCGC	59.871	20	183	108	290
60.692	20	GGTAACGTTTTCCGACCAAA	59.839	20	193	29	221
60.006	20	GCGAAAGGTTTTGGAAATCA	60.053	20	183	1413	1595
60.309	20	ACACATAGGGACGGTGGTGT	60.159	20	269	4485	4753
59.525	20	CCACAGATTTCCCATGACTTG	60.36	21	167	392	558
59.615	20	GATGACAATGATCCCCAAATG	60.006	21	272	1403	1674
59.927	20	ATTGCACCATGCATTCCATA	59.775	20	257	89	345
60.021	20	AGGTTGCGTACATCTGACCC	59.997	20	199	3355	3553
59.573	21	TGTACTCAATGAAATAGGGTGTGT	57.629	24	245	581	825
59.859	20	TTTTAGCCGACCCCAATTTA	59.429	20	100	321	420
59.95	20	TGTCACACGTATTTTTGCAGC	59.79	21	252	66	317
59.909	20	TCGAGGCAGAGAGGAGAGAG	59.962	20	247	60	306

60.597	20	TGTAGCCGACCCCAATTTAT	59.297	20	161	317	477
59.989	20	TACAGTCCGTGTTCCGATGA	60.112	20	157	17	173
59.35	21	ATGTAGCCGACCCCAATTTA	59.297	20	134	90	223
59.955	20	CGCTTGAAGAGCAGTCAGTG	59.922	20	118	656	773
59.943	20	TCAGACGTAAGGAGCGTGTG	60.049	20	186	186	371
59.955	20	ACGCAGTCTCTGGATCGAAT	59.834	20	213	59	271
59.864	20	GCAACGGAAACAACCTCTTT	59.218	20	171	154	324
59.724	20	ACCCTGGGGGCTATCTAGTG	60.34	20	175	3	177
59.952	20	GCTCCCACCACAACCAAT	59.318	18	157	455	611
60.157	20	TGTCTCCTTCCATTCCTTGG	60.042	20	136	549	684
60.017	20	TGAGGGGGAAAAGAGAGGAT	60.008	20	168	607	774
60.103	20	AGCCGACTTCACATAGTGGG	60.134	20	170	529	698
59.844	20	CTCGAAACCACTCAACCCAT	59.966	20	230	436	665
59.979	20	CGACGGAGTTGGAGAAGAAG	59.982	20	215	74	288
59.679	20	TCCCGAATCAGATTGGTCTC	60.011	20	239	4	242
59.922	20	TCGATCTTAGTCGGTCCAGC	60.362	20	269	881	1149
59.927	20	GTTGGTGGGATTTGAACCTG	60.21	20	208	1301	1508
59.411	20	GCGTGCTGAATCTTAACCGT	60.278	20	234	575	808
59.966	20	AGAATTCCGGTAAGCCCAAT	59.799	20	229	3711	3939
59.973	20	TTCATGTAGCCAACCCCAAT	60.192	20	139	7215	7353
60.009	20	CCCAAGACCCCAATTTGATT	60.91	20	269	32	300
60.073	20	AACAAGACCAACAAGCACCC	60.012	20	160	674	833
60.003	20	AGAGCAGAGCAAAGCAGCTC	60.187	20	275	873	1147
59.861	20	AGGTTGCGTACATCTGACCC	59.997	20	101	324	424
60.171	20	TTTATTGGGGGAGAATTCTTGA	59.782	22	255	79	333
60.119	20	TGGGAGTGAGTGAGTGTGTGT	59.181	21	260	2	261
60.074	20	GACATGGAGGAGGGACGG	61.494	18	230	97	326
60.17	20	AATGCTGTTAGGTGCATTGAA	58.307	21	205	221	425
59.138	20	GATGATGATGCCACTCTTGG	59.04	20	134	58	191
58.697	20	ATCGAAAAGAGGTGAGCGAA	59.955	20	250	567	816
59.604	20	CTTTGCTTGAAAATGCCGTT	60.244	20	247	200	446
60.119	20	ACGGTAGGGGGCAAAAATAC	60.075	20	262	54	315
58.292	25	TGGCTTGATTTAGCCCATTT	59.547	20	210	1	210
59.845	20	TTTCCTCAACCTCGTATTCTTAGG	60.02	24	260	729	988
59.541	21	GCAGACGTAACCTCGCAAAT	60.278	20	100	341	440
60.103	20	GCACAAGTTGGATTCCATGA	59.502	20	101	989	1089
60.034	20	ATCACGCACTGTTGTTGCTC	59.912	20	101	208	308
60.587	20	CGCAACGGAAACAATCTCTT	60.249	20	132	56	187
61.383	20	TAACCCAATCGCAGATTTCC	59.901	20	198	2	199
57.113	19	TTTGCATACCTTCCGATCAA	59.112	20	244	12	255
59.809	20	TGCAGATTGCGATGGATAAA	60.179	20	103	252	354
59.654	25	TCCCAGCACTCATCTGTTTTC	60.248	21	243	1051	1293
59.881	23	TGCCTAATACTGTTTTACGTAGAG	58.155	25	276	121	396
59.81	20	TGTAGCCGACCCCAATTTAT	59.297	20	158	3161	3318
59.84	20	TGAATGCACAGAGAGATGGAA	59.384	21	193	11	203
59.772	21	TGCCATGCTATCCTAGTATTCG	59.257	22	225	466	690
60.905	20	AGGTTGCGTACATCTGACCC	59.997	20	117	1	117
59.639	20	TGTCTATGTGCGTTTTTGGC	59.735	20	268	909	1176
58.989	25	TAATCCCAAACTCCCCAACA	60.162	20	276	3	278
58.359	23	TGCGACAAAACATTTAGGCA	60.251	20	269	188	456
59.603	20	AAATTTAATGAACGCGTGGC	59.971	20	202	665	866
60.019	22	TGCAAATTTTCAGCCATGAG	59.809	20	108	70	177
60.251	20	ACCATCTTGGTGCCGTACTC	59.997	20	263	1093	1355
60.721	20	TTTAAGTTTATTCATTTATGTTGAT	57.211	27	274	156	429
58.544	21	GGCATCATCAATAGCTTGGG	60.435	20	243	42	284
60.074	20	GATGAGGCTGGGAACCAATA	59.894	20	164	7	170
59.768	20	TTCCCAAATCATCTTCACCC	59.727	20	243	87	329
60.736	18	TCTTCGCCTTTGTCTGGAGT	59.989	20	100	4	103

60.997	20	TGAGAAAAATGGAAGTGCCC	60.051	20	200	364	563
59.183	20	CTTTTGGGCAAAGGATCAAA	60.046	20	266	67	332
59.476	20	CCCAAATCCCCTTTTGACAT	60.91	20	117	568	684
59.933	20	TCGTCAGGATAAGGGTGGTC	59.927	20	182	166	347
60.015	20	TTGTCATATGAATCATGAAATTGA	57.088	24	188	1	188
59.903	20	GATGGTACAAGAGGCCGAAA	60.074	20	190	21	210
60.032	20	ATCATACTGCACCCCTACGC	59.985	20	220	171	390
60.331	20	TCGATGCCAAAATGTAGCAA	60.215	20	257	96	352
60.118	20	GATCCTCATCCTCCTCCTCC	59.973	20	210	306	515
60.036	20	TTTGGATAAAGTTATCAAGCTCTTT	59.326	26	141	1280	1420
60.656	20	TAGCAGGCCAAAGAGGAAGA	60.088	20	171	298	468
60.053	20	CATGGACTTTACACATGCCG	59.988	20	195	3237	3431
60	20	TGTGGCAAGGTTTTAGGAGG	60.103	20	208	3823	4030
59.575	24	GGTTTACCACACAATTCAATCAA	58.776	23	147	26	172
59.161	20	TTTCCCCAACCTCAACATTC	59.767	20	195	0	194
59.762	20	GGTGACCAAGTGGCATTCTT	59.973	20	275	118	392
60.711	20	TGACATTTTTATGCTAGTTTGAGCA	60.189	25	266	540	805
59.894	20	TTTCGAAAGGCACAAGATCA	59.395	20	215	1136	1350
59.891	20	CCCCGCTACAAAAGATTGAA	60.067	20	254	1176	1429
60.211	20	AAAACCCTCAACATCCATGA	57.835	20	153	563	715
60.254	22	TTGTTTTATCTGTGCCGTTGA	59.216	21	140	17	156
60.263	20	ATACGTCGCACAATGACCAA	59.995	20	206	2445	2650
59.326	20	TTCTTGCATGGGTATTGCTT	58.241	20	277	820	1096
60.088	20	TCCGAAGTCTCAGTTGGGTT	59.697	20	272	433	704
59.955	20	CTACCCTGGGTTTGTTCCTG	59.444	20	198	200	397
60.02	20	CTCTCTCGCCCTCAAATACG	59.971	20	270	1243	1512
59.862	20	AACACGATGGCGATGTATGA	59.955	20	136	294	429
59.694	20	GGAAATAGCCTCTCCGATCC	60.003	20	237	731	967
59.909	19	AGCCACAAACCTGAACCAAC	60.012	20	280	503	782
60.024	20	TCATCATCGGGAGGAGTAGG	60.027	20	200	1109	1308
59.68	22	TGTTAATAGGGCAAAATGCCA	60.321	21	199	21	219
59.017	22	CAATTTCAAGAACCCCCAAA	59.772	20	254	18	271
59.598	20	GGAAACCACATCTAACCTGTTC	57.578	22	120	11	130
59.74	20	AAGGATTCCAGCCACAAAGA	59.67	20	260	2306	2565
59.894	20	TCTCCTTTGTCATGTGCTCG	59.984	20	242	1415	1656
59.973	20	CGCATCCAAATACTTGTTCG	59.182	20	252	251	502
60.11	20	GAGCAACTTCTTGGCTCGTT	59.621	20	123	141	263
59.649	20	CACGGGCACATAATGAACTG	59.988	20	220	1648	1867
60.277	20	GCAGTGATCGGTTCTTCACA	59.837	20	244	298	541
59.994	20	TTAGTTCATAGGCCCGTTGG	59.953	20	200	1097	1296
59.29	21	GGATTCTTGAGCCAAAAACG	59.685	20	253	53	305
60.049	20	GTTTCAGGGCAGACTTGCTC	59.997	20	256	251	506
59.598	20	AAAGGGGCTTCCAATCATCT	59.903	20	119	110	228
59.631	20	TGTTGCAGCTCTTCTTCGTG	60.324	20	179	1455	1633
60.257	20	AAGTTGTCATTTCGGCCTCA	60.636	20	243	574	816
59.996	20	TCTCGGCATTCTCATCCTCT	59.91	20	229	2367	2595
59.184	21	TCTTGGTTAATGGCGATGGT	60.331	20	271	186	456
59.465	20	CCTGAAACGAGTGATGCTCC	60.801	20	216	14	229
60.407	20	TTGTTGAAATTGGACCAGCA	60.088	20	234	2326	2559
59.996	20	TCTTGTTTACCGGCCTATCG	60.089	20	177	35	211
59.911	20	TGGATTTGGATTTCATGGGT	59.991	20	252	1570	1821
60.111	20	AGGCTTAACCAATTTTGGGA	58.556	20	266	56	321
60.022	20	TCCATAGTGTGCGGTGACAT	59.992	20	183	2202	2384
59.455	20	CAAAATAGCCCGAGGTTGAA	60.067	20	143	92	234
60.014	20	GCATGTGAGGGTGGTTGAGT	60.999	20	273	464	736
59.661	20	TTCGTGATTAATTCCGACCG	60.827	20	167	411	577
60.196	20	CTGCAGCCATCTGTTCTTGA	60.136	20	174	34	207
60.315	20	TAAGACCAGTTTTGCCCTGG	60.103	20	175	763	937

60.399	20	TCAACGACGAGCTGCTTAGA	59.888	20	121	9	129
60.307	20	TGTGGGTTCTTTTATTAATTCACTG	58.605	25	276	309	584
60.374	24	TGGAATTGTTGTAATCTCGCAC	60.003	22	255	27	281
57.829	27	CTTTTGTACGGGTCGGGTTT	61.114	20	177	51	227
58.585	22	TTTGCTTACGGAAACAGCAA	59.486	20	202	43	244
59.789	20	CGCAATTTACAACCATTATCTTG	58.625	23	161	2282	2442
59.396	20	TGATATAATGGCGTAGCGCA	60.219	20	270	19	288
60.036	20	CGACTGGTCCGAATCTGAGT	60.261	20	241	752	992
60.131	22	GCGACATTTAAGAGTTGGGG	59.569	20	259	1097	1355
61.032	20	CCAAGTTCAGTCTTCTTCATCCA	60.646	23	263	771	1033
59.688	20	TTGGAAATTCTCCTCCCTTTC	59.519	21	178	1	178
59.903	20	TGGGAAGTTCAAGGAGGATG	60.042	20	139	178	316
59.963	20	CCACCAATTTCTATTTCCTTGC	59.844	22	224	12	235
60.176	20	TGTAGCCGACCCCAATTTAT	59.297	20	148	763	910
60.224	20	ATTTCGCACTCCAAGACACC	60.119	20	178	297	474
58.544	21	CACCAAAGCCTTAATCCCAA	59.931	20	128	38	165
60.033	20	TGAACACAATCAGTATCGTAAATA	60.514	27	159	137	295
60.155	20	TTGCCAACCTCATTTGTTTT	58.12	20	280	90	369
60.088	20	TGTAGCCGACCCCAATTTAT	59.297	20	140	271	410
60.27	20	GTACGCAATCATGCATCACC	59.963	20	147	89	235
60.096	20	AGATGATCCGAACGCAAAAC	60.081	20	228	7	234
60.326	20	GCCGCGTACTCTTGTCTCAT	60.428	20	255	163	417
60.096	20	TCATGTAGTCGACCCCAATTT	59.302	21	221	67	287
59.943	20	AAGTCCTCTCCGCACTTCAA	59.989	20	278	9	286
60.894	20	GCTTCTCGATCGGTTCAGTC	59.957	20	163	15	177
60.238	22	TGTGTTGATGGAGCAAGAGG	59.831	20	171	55	225
59.799	20	AGGGGGAGAGTTCTCTTGGA	60.186	20	199	146	344
59.882	20	ACTCCCACCAGCACGATTAT	59.434	20	217	10	226
60.046	20	GCTGGAGCAAACTCTTCTGG	60.134	20	152	281	432
59.713	20	CATTGATCGTATTTGGGATCTTC	59.693	23	136	199	334
59.767	20	TGCAATGGCTTTTCATTGTT	59.161	20	195	210	404
60.012	20	CGTGGCTGCCATCAGTATAG	59.322	20	184	14	197
59.518	20	TCTCCTTCACCACCTCCAAC	60.088	20	268	177	444
59.536	21	GGCCATTGCCATCAACTTT	60.859	19	262	7	268
60.12	20	AAGCTGGAGCTAAGGGCTTC	60.117	20	171	160	330
57.787	23	TCCCACATTCACGTTCTACG	59.566	20	223	772	994
60.467	20	TCATGTGCAACTGTGTATGCT	57.779	21	235	25	259
59.649	27	AGATCATCAAAGCCCCTCAA	59.629	20	101	10	110
59.623	21	TTCCACTTGCTCGACTCTGA	59.701	20	269	15	283
60.044	20	AGGAACAAAAATGGTGGCAG	59.971	20	173	574	746
60.081	20	AAGTCTGCTTGATGTGGCCT	59.874	20	225	605	829
59.744	21	TGATTTCGCAATATGGTTTGA	59.018	21	274	226	499
59.957	20	TCCCATCTCCTTTGATGAGG	60.003	20	181	28	208
61.195	20	CAACATGCAACACCAAACAA	59.017	20	181	381	561
59.905	20	TGGTGAAACCGGAGTCTAGC	60.255	20	205	82	286
60.081	20	TGATGTTCCTGAAACGAGTGA	59.278	21	184	19	202
59.297	20	GTGCGGTACGGAAAGGAATA	59.96	20	195	5	199
60.017	20	GGTAAGAAGCGGTGAAGCTG	60.015	20	167	634	800
59.984	20	TTTTGAGGATTCTGGATGCC	60.014	20	160	11	170
60.184	20	CCGGACAAGGATCTTAGCCT	60.59	20	101	82	182
59.562	20	TTCTCTCTCACACACACGCA	59.126	20	119	66	184
59.869	20	TGGATCACTTGTCCCATCAA	59.893	20	156	10	165
59.366	21	GAAAGGAAGTGGAGTCGCAG	59.989	20	166	189	354
59.882	20	AGCATCATGAGGAGGAGCAT	59.792	20	171	85	255
59.89	20	GCGGTTCTTCTCCATCACAT	60.081	20	260	38	297
60.142	20	CTCTGCACTTCGTCCTCCTC	60.135	20	228	106	333
60.015	20	ATGTAGCCGACCCCAATTTA	59.297	20	110	259	368
60.224	20	GAGGCGGGAAGGGTTGAC	62.969	18	237	182	418

59.867	23	TTTTTCTTATTTTATCCCGATTTTT	57.886	25	273	1586	1858
60.003	19	CATATCTCTCTTTCTCCTTCTCTCT	59.63	27	198	32	229
60.051	20	GACCCCACATAGTGGGAAAA	59.647	20	243	3372	3614
60.119	20	GTGGGGAAAATGAGATGGAT	58.641	20	236	12	247
59.904	20	GATTCTGTGGTACGTGCCCT	59.997	20	194	467	660
59.997	20	GTTGGGCAGCCAAATATTGA	60.837	20	269	318	586
60.074	21	CGAGCCTGGATTCTTCTCTG	60.088	20	274	48	321
59.861	20	TTTCGAAATTGGGGGTTTTT	60.5	20	236	26	261
60.239	20	GCCCCTCGTATATAACTAAAGAA	59.539	26	126	779	904
60.073	20	TCTGCGTCTCCAAGTTCTCA	59.701	20	183	734	916
59.21	20	TGGAGAAGTTAACCAAGGGG	59.024	20	106	230	335
59.95	25	TGAACACTCAGTTGCATGCTT	59.505	21	257	417	673
59.993	20	CCCCCAGTGAACGAAAATTA	59.795	20	133	480	612
60.786	20	TCTGCAGCCATCTGTTCTTG	60.136	20	160	20	179
60.075	20	TGCCGATAAGACCTCTATGTGA	59.73	22	234	506	739
60.183	20	GAAGATGAAGTGTCGTTGCG	59.445	20	235	1404	1638
60.051	20	TTGGGATTAAGGCTTTGGTG	59.931	20	233	709	941
60.235	20	CGCTCGTTCTGATTTTCTGA	59.148	20	143	487	629
60.321	23	GACATTAGGGCAAAAGCCAA	60.074	20	120	54	173
58.654	24	TGTCACGAACGGTTTTGATT	59.024	20	241	17	257
59.927	20	TTGTTGTTTCCATTCCGTGA	59.941	20	157	405	561
59.82	20	ATGACAGCTAGAGAGCCCCA	59.973	20	174	9	182
59.989	20	AGAGAAGGAAGGTGACGGGT	60.111	20	133	608	740
59.813	20	AGAGGTCGTGGACGAGGTAG	59.325	20	162	44	205
59.874	20	GGCCTTCAACTCTCTGCTTG	60.134	20	120	304	423
59.716	20	TTCATGTAACCGACCCCAAT	60.051	20	165	4052	4216
59.682	20	CTTTGACGTCATGGATGCTG	60.263	20	224	60	283
60.199	19	ATTCCCTTCAGTTTTGTGCG	60.11	20	216	25	240
60.11	20	ATAAGGAGGAGAGCGGTGGT	60.096	20	177	92	268
57.789	22	AGGAAATGATCACAGGCCAT	59.366	20	236	245	480
60.192	20	CAGCCGCAACTGAATTTATG	59.325	20	187	2269	2455
60.036	20	AAATCTCCTAGCCGGAGACC	59.674	20	144	47	190
59.943	20	GAAACAACCGAGCAGAAACC	59.717	20	151	338	488
60.483	20	GGAGATGGAGGATGTGAAGC	59.617	20	166	56	221
59.834	20	TCCCCATCTAAGAATGGTCG	59.887	20	252	43	294
59.96	20	CCCAAGACCCCAATTTGATT	60.91	20	164	1803	1966
59.469	20	CGTTACTCCCACATGCACAC	60.032	20	269	356	624
60.36	21	TGACAATTTATCATTTCCTGTAAC	58.939	26	250	2472	2721
59.794	20	GATCTCCCTATCTCCGGGAA	60.367	20	140	48	187
60.669	20	TATGGTGGATTGGTGTGGAG	59.215	20	132	399	530
57.096	21	AAACCAAACATGCTTCCACA	59.024	20	239	427	665
59.972	20	GAAGGGGGAATTCATGGAAG	60.632	20	233	862	1094
60.103	20	CCGGTACATGACTTCGAGGA	61.055	20	122	356	477
59.95	20	CCAAGATTTCCGAAACCAAA	59.91	20	213	4	216
59.752	24	GCTGATGATCCTGAGAAAACTG	58.936	22	116	14	129
60.28	20	TGCACTTCATTTTCAATTTATGC	59.167	23	232	28	259
58.863	24	GATTTTGTGTGGCGGGTTAC	60.235	20	214	19	232
59.988	20	GCCCAATTTGTGAGAGTGGT	59.973	20	237	871	1107
60.188	20	ATCTTCTCGCGATCAGTGCT	60.127	20	246	83	328
59.82	20	ATAGTGGCAGCTCCATGTCC	60.104	20	266	197	462
60.637	20	CAGGTTGACCTGTTTATGCAA	58.687	21	237	458	694
59.843	20	ACGGTATTCAGGCTCGGAC	60.088	19	113	391	503
60.096	20	CCGTTTGAAGAGTTATGTGCAA	60.166	22	142	228	369
60.088	20	ACCATGAACTTCAAATGGTGA	57.908	21	196	1030	1225
60.088	20	TTTTTGCCACATTCCCTCTC	60.051	20	168	173	340
60.124	20	GTTTGGTCCGGTTAATGCAC	60.235	20	255	530	784
60.78	20	TACGCTGCGCTGCACTAATA	60.706	20	257	7	263
60.301	20	GAAATAGGGGGAATGCACAA	59.762	20	218	803	1020

59.861	20	GCGAAAAATATTTCCAGCAA	57.92	20	193	805	997
60.22	20	TACCGAAACAAGATCCGTCC	59.933	20	250	1141	1390
60.29	21	TCATGATGCATACGAATGATAAAA	59.373	24	238	1266	1503
60.571	20	ACTCTTGGCGGTTTCGGT	60.656	18	131	57	187
60.081	20	TGCCTTTTCAACCATTTTGAC	59.967	21	200	3134	3333
59.712	20	TCAGATATTTAATTTGGCGGAGA	59.947	23	240	2046	2285
59	20	TAGCAGGCCAAAGAGGAAGA	60.088	20	277	104	380
60.044	20	GGAAATGGACCCACAACATC	60.034	20	234	2043	2276
59.04	20	ACATCCTGCTGCATGTTCTG	59.862	20	235	3	237
59.621	20	TGGTTTGATGTAACATTCCGA	58.881	21	259	297	555
60.095	20	AATAGAGATTGCACTCGGGC	59.297	20	261	794	1054
59.813	20	CAAATATTTTGGGCTCCCCT	60.143	20	218	181	398
59.973	20	TTTTCCCTAACTCTCATCCTTTT	57.568	23	163	535	697
59.67	20	TCAGCAGCCATCTGTTCTTG	60.136	20	257	40	296
59.685	20	GCATCATCATCATCAAGCATC	59.049	21	272	360	631
59.992	20	TTCTCAAGAATTTGGCACCC	60.051	20	189	3707	3895
59.962	20	AGGTTGCGTACATCTGACCC	59.997	20	231	1002	1232
59.938	20	CGTGCAAGCATCTAAATGGA	59.833	20	222	709	930
60.966	20	AATTCTCGATCCAAACCACG	59.933	20	267	48	314
60.189	20	GGTGAATCAGCAGGGGTTTA	59.933	20	145	285	429
60.046	20	CCTGCTATCGCTTGGAGAAG	60.11	20	255	61	315
59.411	20	GCGAGTTCAAAGCTGTTTCC	60	20	164	141	304
62.522	18	GGTTAATCGGGTCGGAATTT	60.02	20	174	15	188
60.206	20	TCCAACCCTATCTATGGCTCC	60.293	21	256	225	480
60.274	20	CGTAGGCGATTAGTGGAAGC	59.867	20	274	1042	1315
58.969	20	TTTTTCTTGAAAGTACGTACACTTT	58.23	27	243	768	1010
59.436	26	ATGGGTTGGATTTGGTGTGT	59.95	20	185	4	188
58.997	22	GGAGAAGGAGAAGCAGCAAA	59.694	20	276	329	604
59.709	21	GGCAGCTTCTTCGTCAAAAC	60	20	146	583	728
58.259	23	TTCATTTGGGGTTTTTGTGC	60.712	20	122	174	295
59.341	22	AGCCTTTTGTGGAGGATGAC	59.141	20	279	112	390
60.225	20	TGTAAGCTCTGGAACGGAGG	60.388	20	258	31	288
61.106	20	CTCGGGATCAATGACATTCC	60.281	20	180	4	183
59.992	20	GTACCCCACACGAAGACACC	60.284	20	213	469	681
59.038	20	GAGTGGCCGACATTGAAGAT	60.081	20	261	100	360
58.556	24	GCCGAACCCACTGTGATATT	59.82	20	221	35	255
59.499	20	CACTGATCGTACACGATGGC	60.144	20	128	670	797
60.015	20	CTTTTCGGGTATTTTCGGGT	60.177	20	131	84	214
59.799	20	AGGGGATCGTAAAGCCTGAT	59.925	20	264	0	263
59.894	20	ATATGTGGGGATAGGGGTGG	60.652	20	155	105	259
58.865	26	CAATTCCTTACTGAATTTGGGG	59.711	22	187	276	462
60.112	20	GGGTCACCCTAGATGGGTTC	60.575	20	202	30	231
59.315	21	TTGTGGGACGGACCAAAAT	61.152	19	262	142	403
60.461	20	GGGGCTATCTTGTGAGTTGC	59.7	20	233	0	232
60.025	20	GGAATTGGAGTGGTCTGTGG	60.363	20	176	70	245
60.21	20	TTTATGTAGATATGGAGCGATTTTT	57.561	25	241	364	604
59.978	20	TTCATCGACTCTCGCATCAG	60.096	20	262	416	677
58.307	21	ATAGAGCTCCAACAGCTCGC	59.746	20	260	621	880
59.897	20	TTATTTTTGCGGTAAAGGCG	60.089	20	187	380	566
60.063	19	AACACGAACTTGCCGATTTT	59.615	20	279	25	303
59.784	20	AATTGCAGGGGAACACAAAG	59.971	20	158	1728	1885
59.83	20	TTTTGTAACTTGAGCAATTTATGGA	59.966	26	203	1624	1826
59.04	20	TGTCCTCAGTAATCGCCTGA	59.394	20	256	79	334
59.923	20	CGCCCAGTTTTGGTCATACT	59.993	20	140	45	184
59.313	20	TTATTGAAAATCCTGATTTGATGA	57.712	24	190	3	192
60.11	20	ATGAGTAAGCTGAGCCGGAA	59.978	20	268	202	469
60.03	20	GCGTGCACAAAATGGTAAAC	59.09	20	263	39	301
59.405	20	ATTTAAAACCGATCCCACCC	59.888	20	277	160	436

59.971	20	CAACGCCAAAACATCAAATG	59.969	20	239	72	310
59.982	20	TCGTTCATTCACGTAGAAGTTCA	59.799	23	236	667	902
60.159	20	TTCAGCGGATTGAGTGTCA	58.88	19	208	32	239
60.169	20	AGCTGGATTACCAGTGCGTC	60.285	20	231	271	501
59.973	20	AGTTGCTTTTGTTTGGAGCG	60.42	20	174	471	644
58.621	20	GCCGCACACAGACCATACAT	61.966	20	268	1083	1350
60.843	20	CGAAAGAAACACACGTGAGAA	58.96	21	226	224	449
59.993	20	CATCAACTCAACAAAGCCGA	59.84	20	180	1084	1263
60.192	20	GCCTCCCTCTTTAGCCATCT	59.811	20	169	227	395
59.691	20	TTGAATCCCAGATTGCATCA	60.009	20	181	660	840
59.779	20	GCAACGGAAACAACCTCTTT	59.218	20	160	700	859
60.204	20	TCCCATAGCATTTTTCAGCC	60.038	20	197	618	814
59.479	20	AAGATTTCATTATCCACATTGGG	59.113	23	273	90	362
59.827	20	TTGTGTGCATGTATTGACAGGA	60.035	22	172	2436	2607
57.069	20	CCTCGAACCTTCTGCAAAATA	59.348	21	280	713	992
59.823	20	TTTTTGTATGGGTCGGGTTC	59.662	20	220	84	303
59.736	20	GGCAAGAATCCTCACCAAGA	60.195	20	185	1012	1196
59.811	20	TTTTCACACGTTTCGCATTC	59.712	20	179	6	184
59.166	20	GATGAACTTGTCCCCAGCAT	59.934	20	239	6	244
59.893	20	CCTGAAACGAGTGATGCTCC	60.801	20	214	93	306
59.981	20	TGTAGCCGACCCCAATTTAT	59.297	20	191	841	1031
60.074	20	GGGTTTAGACCGATGTCGTG	60.375	20	180	2410	2589
59.946	23	GGAAGTTGGAATGGCATCAA	60.843	20	271	20	290
59.873	20	GCATCACAGTTGAATGTGGG	59.967	20	164	279	442
60.422	20	CTTAGGAAAGGCACGACACC	59.734	20	278	50	327
60.05	20	TCGTAAACGAGTGTTGGAAAAA	59.663	22	278	323	600
60.081	20	CCCATAAAGCGAAATGGAGA	60.031	20	251	1189	1439
60.025	20	GACAACACTGGAGCTGTGGA	59.872	20	240	4850	5089
59.964	20	GGAGTGCATGCTCCAGACTC	60.989	20	153	52	204
60.053	20	GCAGACGTAGGAACGGAGAG	60.012	20	125	17	141
58.072	26	TTTACTCGCTCTTGCTCGGT	60.154	20	161	0	160
59.195	20	TTGTCATATGAATCATGAAATTGA	57.088	24	211	288	498
59.465	20	TATCATCCTCGGAGGCAATC	59.998	20	230	153	382
59.823	20	GGCAGTACTTGAACCTTCGC	59.882	20	123	47	169
59.897	20	ACAGGAAACGTAAAGGCCG	60.118	19	215	42	256
59.697	20	GAGCGCATGTTCCAGACTTT	60.406	20	105	5	109
59.983	20	CATCTCCATGCCTTTGGTCT	60.073	20	129	458	586
59.968	20	CCAGGTAGATGCCGTGATTT	59.955	20	245	0	244
59.808	20	TGTAGCCGACCCCAATTTAT	59.297	20	268	277	544
60.336	20	CTCACCGGAGAAAACCTCAC	59.697	20	204	103	306
59.982	20	CACTGTGGTGGCATATCAGG	59.984	20	270	1	270
60.133	20	GGAGGAAACAGTGGTGGAAA	59.943	20	249	600	848
60.202	20	CCCGAACACTAGTGGGGTTA	59.846	20	265	212	476
58.019	20	CACTCGTTTAATGTTACACTTTGA	57.266	25	280	192	471
60.431	20	TTTGTTTATCGTTTCCGTGTTTT	59.809	23	275	307	581
59.691	20	CCCGAACGATGTCAGTACCT	59.989	20	129	202	330
59.75	20	GGAAGGTTCTAGGGCCAAGT	59.576	20	194	52	245
58.936	21	TGGAATCCGAGAAAATCAGG	60.006	20	196	4	199
59.95	20	AAAAGTTTCCACACTTGCCG	60.147	20	271	83	353
59.705	20	TTCAAATATTCGACTCCGGC	60.038	20	217	36	252
60.042	20	GAGTCTTCCGACAAACCGAG	59.844	20	197	127	323
59.978	20	GGTGGTCATTTTGGGGATATAA	59.787	22	180	114	293
60.303	20	TAGAGGTGCCTGTGGTGACA	60.309	20	195	10	204
59.823	20	TTTTTGGATCCACACCTTCA	58.947	20	259	836	1094
60.425	21	CACCACCCCAACCAAATAAA	60.452	20	206	19	224
60.68	20	CCCACTAAGCTAGCTCCCCT	59.864	20	113	81	193
59.861	20	TATTTGTGCCTCGTTTCGTG	59.729	20	204	21	224
59.945	20	CGACCTGCTCCTTTTCAATC	59.813	20	223	1137	1359

59.844	20	ATAGCCGATCCCACAGAGTG	60.096	20	224	2365	2588
59.875	20	TTTTGATGAAGGCGGGAATA	60.395	20	270	2462	2731
59.297	20	GGATTCGAAAAGACATCCCA	59.871	20	101	7	107
59.679	20	CTAGGAAACAGCCCTCAACG	59.869	20	213	5033	5245
58.733	23	CATGCCGAGTTTTTCTCATTT	59.215	21	276	344	619
60.134	20	CTGGGCAGCCAAACATAGAG	60.786	20	105	100	204
59.42	20	AACAGGGATTTTGAAGGTGC	59.031	20	163	498	660
59.822	21	CCGACTAGGACTAAGGGTCCA	60.493	21	101	389	489
59.406	22	GTGAAGGTGCTGGGAGAAAA	60.232	20	133	287	419
60.058	20	AAGAGATGGGGGTCAAGGAC	60.314	20	190	231	420
60.915	18	GTCGTCATCCCCCTAGTTCA	59.927	20	198	1	198
59.945	20	AACTCACACCAAGTGGGTCC	59.859	20	249	1058	1306
60.096	20	TCTCATCTCGAGCCTTTGGT	59.95	20	108	1038	1145
59.442	21	CGTCAGTTCCACCGAAATCT	60.111	20	213	36	248
61.42	20	GATGAGCCATGACCCTCCTA	60.034	20	194	6	199
60.119	20	GGAAAAAGTGACTGGGCTTG	59.711	20	238	245	482
60.167	20	TTTGGTGGTTAGGGAGCTTG	60.103	20	161	673	833
60.133	20	ATTGTCAAACCAGCGAGAGC	60.406	20	216	323	538
59.948	20	ATCATGTTGTCCCCTTCTCG	59.927	20	264	3588	3851
59.788	20	CATTTTCACGTGACCCTATTGA	59.861	22	250	654	903
59.95	20	CGTCGGAGGGTTCAATAGAG	59.688	20	256	26	281
60.012	20	GCTGCTGTCCATGAAGTTGA	59.992	20	233	84	316
59.571	20	ATGTAGCCGACCCCAATTTA	59.297	20	132	874	1005
60.135	20	TTGGTTAATGTAGCCGACCC	59.823	20	116	134	249
59.637	24	TGGAATCCGAGAAAATCAGG	60.006	20	259	3	261
59.994	20	CAGATCGGTTTACCACGACA	59.566	20	138	401	538
59.157	20	GTGTTCCGATAATCGCCAGT	59.962	20	138	22	159
60.218	20	AACAACATTAACAATCATGCCAA	59.288	23	210	1180	1389
59.817	20	CTCCTCGCCTCCTACATCTG	59.966	20	200	644	843
61.387	19	CCCACTAAGCTAGCTCCCCT	59.864	20	123	8	130
59.823	20	ATGTTAACGCACAATATTCCAA	57.175	22	274	438	711
59.287	21	TCAAGGCAAATTCATTGTGTG	59.576	21	164	1171	1334
59.957	20	TCCTTCCCTTTCCTGGAACT	60.045	20	256	77	332
60.151	20	TCTGATCTCCGGTCGACAAT	60.622	20	169	3128	3296
60.186	20	GCACAACAACCACTAATCCG	59.05	20	111	108	218
60.386	20	CACCAACTTGGCTACCCCTA	59.986	20	201	160	360
60.042	20	TTGAACCCGATTTCTTGTCA	59.097	20	182	314	495
60.103	20	ACTCCATGGCAGAATGTTCC	59.934	20	157	3672	3828
59.972	20	TAAATTGCCGTGTGAAACCA	59.969	20	240	769	1008
60.562	20	CAAATGCATGTTTGTCGTCC	59.972	20	267	2885	3151
59.929	20	CAGCATTGTCCAAAAGCTCA	59.988	20	253	1548	1800
59.457	20	GCAGAAGCACGATGCTCTTA	59.326	20	149	771	919
60.081	20	CTATGCAAATCAGTGCCGAA	59.833	20	158	236	393
60.339	20	TGTTTGAAATTCCTGCCTCA	59.247	20	234	56	289
59.578	21	GGTCAATGCAAATCCAATCA	59.33	20	280	456	735
61.087	20	AGGGCTAAGAGGAAAGACCG	59.842	20	251	20	270
60.496	20	CCATAATTACCGGCGTCATC	60.175	20	120	106	225
60.11	20	TTCCCATAATTACCGGCATC	59.621	20	259	76	334
59.439	20	CGTCAGAATATTTATTCCATGTGT	58.462	25	270	160	429
60.386	20	GCAAAGGGGCTTATCCAAAT	60.28	20	191	47	237
60.644	20	ATGTAGCCGACCCCAATTTA	59.297	20	118	2398	2515
60.43	20	ATTGATACGGGCATTATCGG	59.643	20	186	958	1143
60.034	20	ATCCCGGAAGAAGAACGAGT	60.074	20	265	858	1122
60.11	20	TGTAGCCGACCCCAATTTAT	59.297	20	188	1195	1382
60.206	20	GCTCCGCCAGTGACTGTATT	60.285	20	265	1299	1563
59.978	20	CCACGTCAGCTGCTTTATCA	60.011	20	249	393	641
60.147	20	TCTATTTCCAAGGCCAATGC	60.038	20	235	1689	1923
59.938	20	TTTCCTAAATCATGATGGTGAATA	59.123	26	264	105	368

59.971	20	GGTTCGAAAACCGTTGTTGT	59.875	20	225	741	965
59.728	19	CGGATTTTACGTGGTTCGAT	59.823	20	190	10	199
59.238	20	TGGGGGAATGTAATATCATTGAA	60.261	23	270	346	615
59.955	20	CTTGGCTCATTGCAAGCATA	59.976	20	177	808	984
60.504	20	CTTCTTCTCCCTTGTGTCCG	59.837	20	178	5	182
59.988	20	CTCCCCGACTTCTCCAACTT	60.619	20	194	0	193
59.814	20	GTTCGAGTCTCAATGGGGAA	60.05	20	110	1904	2013
60.309	19	GTCGGCATTCAGCAAGAAA	59.94	19	262	1796	2057
59.364	21	AGATTTTCGGAGTCACGACG	60.255	20	241	79	319
60.272	20	GGGCCATTTCCCATTAGC	60.238	18	278	61	338
59.836	20	ACCAATGGTGGTATGGTGTG	58.984	20	125	105	229
60.183	20	GCCATTGCCACGATGAATAC	61.27	20	258	1178	1435
60.025	20	TCTTCGGGATTCTCCATGAC	60.011	20	247	14	260
59.942	20	GCGGGCAAATTTCTTTTTCT	60.547	20	223	227	449
58.307	20	GTCTTCTTGACGCCGCTC	59.663	18	100	26	125
59.467	21	TCTAATGTTTCCTCCACCGC	60.074	20	203	58	260
60.156	20	GCAACAAGACTAAGGCGGAG	60.015	20	275	215	489
60.143	20	GATAAGCAAATTTCGGGACG	59.547	20	268	8	275
59.52	20	GTACAGCTAAAGCGGGGGA	60.22	19	169	9	177
60.261	20	TCCCTCTGGTGGTTTTATGC	59.933	20	164	40	203
59.67	20	AAAACCCAGTTCCCCTTGAT	59.668	20	145	1139	1283
59.32	20	GAGAAGCCTTTGTTCTGGGA	59.405	20	117	2	118
60.011	20	AATGGGGACAGACGAAAGTG	59.966	20	164	761	924
59.91	20	TCGATTCCACATATCTCCACA	58.938	21	260	387	646
60	20	AGAAGACCCAAGATGGCTCC	60.596	20	172	498	669
59.971	20	TGGGTACAGGTTGTGGGTTT	60.126	20	200	90	289
59.923	20	TCCTGCATGGCTGTAAACAC	59.722	20	273	486	758
59.172	19	TGGGTTGCAAAATTAATCCG	60.671	20	230	654	883
60	19	CGTCAGTTCCACCGAAATCT	60.111	20	246	108	353
59.823	20	CTCCTCGCTCTCTCCTCTCA	59.962	20	134	701	834
58.68	26	CACAAAATTAAGCGCAAGCA	60.017	20	175	73	247
59.853	20	CCCAAGACCCCAATTTGATT	60.91	20	218	48	265
58.695	24	AAATGATGTCATGGGAGCTT	57.043	20	189	58	246
59.869	20	TGAAGTTTTGGCTCATCTTATCA	58.888	23	150	24	173
61.167	20	TCAACCGTCTTGAGATGCAG	59.984	20	163	211	373
60.126	21	ACCCACTAACACCCCTCACA	60.275	20	192	54	245
59.761	20	TACGGTGGAAGATCGGAGTC	60.073	20	220	43	262
60.331	20	GTGCGAGGGAGATTATGAGG	59.653	20	236	69	304
59.297	20	CACCCACTCGTAGAATCCGT	59.989	20	155	6	160
57.925	24	ACCAGGTTTGAAGTTGTCGG	60.005	20	161	3	163
58.858	20	CCACCAGGTTGTACAGCAAA	59.609	20	272	1056	1327
59.112	21	CAACTTGATCCCTATCACGC	58.173	20	222	18	239
60.193	20	CAGGGCGTGACAGTAACTCA	59.897	20	275	756	1030
60.034	20	GGAGTTCACTGTGGGATCGT	59.969	20	268	614	881
59.571	22	CCTTCTCGGTTGAGTCTGCT	59.598	20	265	1424	1688
59.925	20	CGGGGAGGAATAGAATGCTT	60.411	20	181	22	202
59.933	20	AGCAAATGGTGGAAATGAGG	59.933	20	145	128	272
58.965	20	ACAGAAGACCCGAGCCTACA	59.867	20	229	701	929
59.929	20	AAAAGCAGGAGATGACAGCC	59.434	20	228	544	771
60.857	20	TCATAACATCGATGAGTGTGGAC	59.874	23	101	265	365
59.015	24	TGGGGCTTTTTAGGGCTACT	60.089	20	256	67	322
60.088	20	GGCCAACTGAAATTTGAAAGA	59.192	21	176	3	178
59.396	21	CAAATCGGCATTATTTAATGGAA	60.052	23	176	562	737
60.065	20	TGGGTCTTGGCTTATTGGTC	59.933	20	215	1635	1849
59.813	20	TGCACATTTGGATTTACCGA	59.93	20	201	829	1029
60.076	24	CCGTCTAGGGCTTCAACTTC	58.934	20	179	66	244
59.893	20	TTCAAAAACTCCCAATTTATAACA	60.042	26	222	1035	1256
59.853	20	CCATCAAAACCATCACCTCC	60.173	20	268	104	371

59.297	20	TTTTTGTCAATGTGGGATTGAT	59.182	22	257	182	438
60.008	20	GACGATGGTTGCCTTTGTTT	59.978	20	145	227	371
60.109	22	GGGCTTCAACATCTCAAATCA	60.066	21	124	108	231
59.284	20	CGAGAAAGAGAGAGATGGGG	58.963	20	102	282	383
60.21	20	CTAGTCCGGTCCAAACCAAA	59.964	20	170	2220	2389
59.886	20	CAAGACCCCAATTTGATTGC	60.309	20	149	95	243
59.989	20	GAAGAGCGCCAGTATGGGTA	60.235	20	196	3974	4169
60.721	20	GTTCATGTAGCCGACCCAAT	59.82	20	230	2587	2816
60.822	20	TCTGCACCTCATCAATGCTC	59.95	20	280	907	1186
59.903	20	GAGAACCAGATTGTAGCGGC	59.843	20	117	400	516
60.149	20	TAGTGGATTGGGGAGGATGA	60.272	20	235	1817	2051
59.995	20	TTAAGCTGATGATCTGGGGG	60.029	20	209	16	224
59.962	20	ATGAGGTGACAGCCCTTGAG	60.261	20	117	0	116
59.969	20	CAACAGGCTACCTCCTCCAC	59.721	20	198	282	479
59.297	20	ACCTTGCGCCCTTTAAAACT	60.129	20	108	6	113
60.393	20	GTTGACGAGAGAAACTGGGC	59.851	20	277	547	823
60.074	20	CAGAAACCGGTGTTCCATTT	59.83	20	266	407	672
60.796	20	CAATCAACCATCACATCCCA	60.177	20	228	0	227
60.111	20	GAAATCCGATCCTGGACCTT	60.272	20	266	72	337
60.111	20	CCCCAATTTACTGGGATCAA	59.617	20	197	529	725
60.186	20	GCTGGGAACCAATCATCCTA	59.894	20	207	27	233
59.844	20	ACTCACCTCTCCCTCGACCT	60.258	20	232	16	247
57.552	20	TGATGCTTGGGATCTTAGGG	60.029	20	187	7	193
60.357	20	AGGTGAATTTGGTCCTTCAAA	58.54	21	278	672	949
60.91	20	GTGGCACCTCCTGATTCATT	59.934	20	104	0	103
58.315	21	GATTACACGTTGGGCCTTCT	59.056	20	181	2059	2239
59.998	20	TGAAAATAGTTGTGCCTGGG	58.623	20	208	246	453
59.969	20	CTCCTCCCTGACGATATCCA	60.027	20	263	1112	1374
60.755	20	AAGGGATATGTGGGTGGTGA	60.05	20	140	853	992
59.39	22	TCTTCGGGATCACAATTTGG	60.832	20	275	413	687
60.439	20	TCAAACTGATTGTTCGCTGC	59.995	20	280	394	673
59.985	21	GGGTTATCACCTGATTACTACCCA	60.352	24	242	241	482
60.195	20	AACTTTGGTTCATGTAGCCG	57.757	20	105	282	386
60.801	20	CACAAACCAAAGGTGCATGT	59.465	20	218	16	233
60.232	20	ACCAATGGTGGTATGGTGTG	58.984	20	205	0	204
60.035	20	CTTCTCCTCCACAGACTCCG	59.978	20	277	275	551
60.362	20	TAACGTTGTGTGCACCTTCC	59.615	20	253	2714	2966
60.211	21	TCATCAACGTTCTTGGGTTCT	59.583	21	160	57	216
60.119	20	AGCCTTATTTCCCACCCACT	59.827	20	192	4056	4247
59.405	20	GGAACTGCTCAACTTGCTCC	59.997	20	254	38	291
59.505	20	ATTGGCTGGATGTATTAGGATATT	57.193	24	153	97	249
60.34	20	TGCGTCCTCATTGTTTATGC	59.694	20	274	968	1241
59.933	20	AAATGGTGGTTCATTTGGGA	60.029	20	172	2302	2473
60.883	20	TGTAGCCGACCCCAATTTAT	59.297	20	280	37	316
59.805	20	TCTGTTGAGCAGCAGCAACT	59.929	20	245	841	1085
59.869	20	AACACTGGTAATGACGCTTCG	60.183	21	233	11	243
59.399	20	TTTGTATGCTTGTAGTGGTTCCTT	59.162	24	228	261	488
60.227	20	AGGCTCGAACCATGCATATC	60.066	20	202	2140	2341
60.12	20	GGCACAGTTTTCGATCTGGT	60.119	20	263	1802	2064
60.142	20	ATTCCTTCCCCGTCATCTCT	59.896	20	239	1682	1920
59.864	20	CTCCTCGCCTCCTACATCTG	59.966	20	234	174	407
58.381	25	ATGGTAGAAATCGCCGCC	60.973	18	196	6	201
60.11	20	TCCACCAATTTCTCCTCTGG	60.042	20	274	251	524
59.797	22	CCACAAGTTATCACACCCCC	60.088	20	249	204	452
59.758	20	GAGGACTCTGGAGAAGGGCT	59.952	20	239	328	566
58.487	20	TATATTCTCGAAGGCGGCTG	60.323	20	264	656	919
60.27	20	GTGTAGCCGACCCCAATTTA	59.823	20	102	254	355
60.132	20	GTTTACGGAAGCATGATGGG	60.331	20	116	3175	3290

59.789	20	GCCTGAAAATGGTCGTGATT	59.939	20	256	15	270
59.664	20	TATCGATTCCGGTCACACCT	60.34	20	245	40	284
60.142	20	CGCAATGGAAACAACCTCTT	60.11	20	246	2201	2446
60.21	20	GCGATAGAGTTTCTGGTGCC	59.843	20	262	1437	1698
59.717	20	AATGGAATGGTACGAGGGTG	59.67	20	144	617	760
59.998	20	AGGAGTTTCCGGAGATCACA	59.655	20	145	187	331
58.726	25	TTGTCCACCCCTCAATTCAT	60.173	20	263	18	280
59.971	20	ATAATAGTGCCCCGAAAGGG	60.164	20	167	184	350
59.344	20	TAAGCGTGACGACGAGAATG	60.011	20	167	41	207
60.014	20	TGGATTTTGTATTGCCCGTT	60.188	20	183	47	229
60.05	20	TGGAGTTGCAGATTTTTGGA	59.247	20	181	4690	4870
57.077	24	ATCTGGCGCTTCAATGTTCT	59.843	20	159	10	168
59.708	20	TCTGCAGCCATTTGTTCTTG	59.988	20	213	300	512
59.988	20	GGTGGTTTTATGCACGCTTT	60.003	20	215	87	301
59.966	20	ATGTAGGCAAAGGCTGCTGT	59.904	20	111	11	121
60.338	20	TCCCAGAAAATTCTTTTCCTTTC	59.943	23	199	375	573
59.942	20	TTGGGGAGGATGAGAATGAG	60.003	20	216	5304	5519
59.966	20	TTGCTCCTTAAAGCTCCTGC	59.73	20	195	2137	2331
59.938	20	TTCAGCTCCAGGGTTTTCAT	59.67	20	250	414	663
59.95	20	CACTTTGTGTTAATTTAAAGGTCG	57.158	24	168	111	278
59.679	20	GGGTGTTTGGTGGAGCAGTA	60.954	20	197	275	471
59.997	20	GCGTCTCCAAGATCCCATAG	59.653	20	210	61	270
58.109	20	ATGTAGCCGACCCCAATTTA	59.297	20	174	1686	1859
59.297	20	TGAAGGTTTTGAATTCCATTGAC	60.21	23	279	657	935
59.724	22	TGACAATTCCTATGCTTAAACTCA	59.262	25	188	132	319
60.966	20	CCTTTTCAAAGTGGACTATCAATT	59.472	25	170	185	354
59.853	20	GTTCGGTAGATCGACTTGGC	59.7	20	140	927	1066
60.243	20	CTGTAGTGAAGTGGGACGGG	60.557	20	181	22	202
60.074	20	CGTCCTAGTTCTTGTATCAAGTGA	58.941	25	190	16	205
59.297	20	TTTTTCTTGGACCAGGTTGC	60.088	20	162	4	165
59.948	20	TGGGGGATAAAGATGCAAAG	59.894	20	160	1009	1168
60.91	20	GTCTCCACCAGGTTTTTGGA	59.943	20	234	2	235
59.712	21	TGAACGCATGAGGTAATGGA	60.073	20	272	0	271
59.945	20	CAACCGAAACGCCTGTATCT	60.132	20	271	512	782
59.629	20	CAACGGCTGGTCCTTGTATT	59.993	20	257	41	297
60.144	20	CACGGGAATAAATTGTTGGA	58.334	20	169	535	703
59.924	20	AATCATGTACACCCGCTTCG	60.914	20	196	147	342
59.971	20	TCTGGAGCTGGATGATGATG	59.743	20	230	731	960
60.032	20	TGAATGTACTTTAACCACTGCACC	60.327	24	212	556	767
60.02	20	ACCCCAATTTGTTGGGATTA	58.995	20	240	766	1005
59.711	20	AATTGATGATTCCAAAGCCG	59.901	20	234	849	1082
59.934	20	GTGGATCATCAAGGTGAGGG	60.326	20	213	460	672
60.265	19	CCATATAGTTGACCCCGCAT	59.668	20	164	229	392
59.985	20	TGCAATGGCTTTTCATTGTT	59.161	20	227	186	412
60.226	20	TGTGTGTGTCCCATATTCGC	60.399	20	229	4603	4831
59.42	18	CCTCTCCTTCTAGCAACCCC	60.204	20	193	4	196
58.969	21	CGCAATGTACCTTGGCTATG	59.206	20	147	704	850
60.807	20	GGGGCTCAATTCTAAAAGCC	60.041	20	187	1574	1760
58.881	21	TGGAGCTAAAAAGATTTTCACGA	60.238	23	167	83	249
59.121	27	CATCGGTTTCTGGACAAGGT	59.966	20	268	15	282
59.867	20	CACCATTATCTCCAGCTCCA	58.67	20	255	253	507
60.375	20	CATCAAACCCAAACCAACCT	59.688	20	163	278	440
59.993	20	TGTAGCCGACCCCAATTTAT	59.297	20	222	796	1017
60.056	20	GCCCAATCCAAACAAATCAG	60.309	20	179	631	809
60.063	19	AGGTTCAAATCCCACCAACA	60.21	20	265	17	281
59.692	21	CTCTCAATCCCAGACTTGCC	59.803	20	245	550	794
59.257	21	TTTTGGAACGGGATTCGAT	60.259	19	211	498	708
59.948	20	AGCCCCTTCGGTAAAAATGT	59.835	20	227	856	1082

59.452	20	CGAAATCTCACGACGCATTA	59.833	20	109	1674	1782
59.96	20	AACCGTGTACACCCCTACCA	60.149	20	262	814	1075
60.209	20	CCCAAGACCCCAATTTGATT	60.91	20	228	2412	2639
60.125	20	TGCTCGAGATCCCAATATCC	59.998	20	230	265	494
59.985	20	TCATCACCACAAAAATCCCA	59.75	20	184	1167	1350
60.232	20	ATGTCGGTCAGCGATTCTTT	59.7	20	268	980	1247
59.73	20	AATTCAATTACCTGCCGGA	58.024	19	128	105	232
59.332	21	TGGAGGGAAGGAAGTTGTTG	60.081	20	187	1825	2011
59.95	20	GTGGCAGAGATGGAGGATGT	60.08	20	245	2	246
60.272	20	TTTGCCAAGCTATCCAAAGG	60.202	20	234	823	1056
59.879	20	AAGCAGAAGAGTGCATTAATCGT	59.471	23	232	278	509
60.349	20	CCAACCAAACTCCCTCTTCA	60.081	20	244	4765	5008
60.025	20	CAAAGACTACCTACAGATCCCCC	60.241	23	264	65	328
60.328	20	GGTCAGAGTGACCGTTGGTT	60.009	20	272	3883	4154
59.911	20	CAGCTACCCATCTGCCAAGT	60.277	20	108	541	648
59.297	20	CATGCAACAGAAAATGCCAC	60.119	20	266	2	267
57.46	22	TGCAAAGCATACTTACAGAAACC	58.516	23	223	4	226
59.946	21	CCGCTGAGATAATGCTCGTT	60.374	20	268	4226	4493
59.845	20	CGATGGGGTCTTCTGATGAT	59.886	20	207	792	998
59.816	20	TTTAATTAGTTCCACGCGCC	60.095	20	246	2217	2462
57.999	20	CATGATGCAAAAATTTAATTAGCA	59.485	25	230	1074	1303
59.82	20	GTTCACCAACTCCCACTCGT	60.009	20	227	21	247
59.988	20	CAAGATTCCTCTCACCCCAA	60.042	20	213	502	714
59.962	20	AATTGTGTCTGCTTCGGACC	60.119	20	248	977	1224
60.11	20	ACAAGAACTCGATTTTCGCC	59.316	20	204	692	895
59.933	20	GCCAACACCTCCTTGATGAT	59.934	20	142	789	930
60.014	20	ATGGTGACAATCGTGCTGTC	59.557	20	214	1047	1260
60.096	20	GAACCTCCTCTGTTCCCTCC	60.05	20	261	2283	2543
60.517	20	TGAGAGGACACCCAAGTGGT	60.563	20	172	3	174
59.284	20	TGAGAATTAGCAATTGAAGTTGA	57.791	24	266	534	799
60.051	20	TTGCTGGCAGTGAAGCTCTA	59.888	20	209	625	833
60.074	20	CCAAATAGCTTAGGAGGCCC	60.055	20	237	16	252
60.042	20	TCCTCAGCCGGTGTAGAAGT	59.867	20	241	513	753
59.946	20	TGCTTGTGGACCAAAGATTG	59.691	20	145	1459	1603
60.636	20	CCCCATCCCTAAGAACATCA	59.744	20	257	164	420
59.767	20	TGTAGAGTTTTGGGTTCGGC	60.11	20	112	470	581
60.017	20	GACAACGATGGATACCCCAC	60.057	20	237	56	292
60.088	20	AGGCCACGTAAATACGAACG	60.018	20	256	806	1061
60.333	20	TGCTTTCTCTCTCCTCCCAA	60.065	20	250	1589	1838
60.051	20	GGAGGTGGGCTCTCATGTAA	60.073	20	185	330	514
59.574	20	ACCTGTGTTCGGGCTAAATG	59.993	20	133	29	161
60.24	20	CTATGGGCCGATCCTATCAA	59.878	20	161	1006	1166
59.933	20	GACCACCTGCATTCACAGAA	59.682	20	266	612	877
60.687	20	ATTTGGAACCTTGTGCGTGT	60.419	20	181	200	380
61.059	21	TTCCCTCAACCTAGACCTCG	59.28	20	138	31	168
59.3	20	TGCATGTCTGATTCTGAGTACG	58.952	22	250	967	1216
60.299	20	ATGCCACATAACGCATTCAA	59.96	20	263	573	835
60.034	20	ACCAGCATTTTCAGAGCCAC	60.263	20	159	269	427
60.065	20	GCAACCACGTACCATGACAG	60.032	20	200	5713	5912
59.84	20	CCCAAGACCCCAATTTGATT	60.91	20	106	2447	2552
60.188	19	GGAAACATCAACACACGCAT	59.425	20	152	618	769
60.212	24	TGAGTGCGTTTGTACTCAACCT	59.842	22	181	99	279
59.49	20	GCTTGCAAATCACGTCAGTC	59.45	20	205	12	216
58.012	25	AAAACGCATTTTGGAGTTTG	57.81	20	187	43	229
60.44	20	CCACCATACTGGGTGCTCTT	59.989	20	156	835	990
60.019	20	AGGCGGGACTGTGAATAATG	59.955	20	146	469	614
59.599	20	CAATGAAGACTGAATCTCGGAA	59.312	22	203	1040	1242
59.982	20	CTCGAAGCAGGGAAAAATTG	59.817	20	248	44	291

60.015	20	CAAGACCTACTGAGCCAGCC	60.012	20	240	332	571
58.147	20	GATATCCGGTTTTGCTCACC	59.391	20	188	325	512
59.871	20	AACTCCCCTCCATTCTCCAT	59.755	20	249	939	1187
58.998	20	CGTGTTAAGTTGTTAACCAATACG	59.456	25	170	94	263
60.77	20	ATCCTTTTCCGTCGCTTTTT	60.075	20	236	110	345
58.31	25	CAAGTGGAATTCATGATGCG	60.073	20	134	31	164
60.436	20	GTGCACAATCACCAAGATCG	60.12	20	234	875	1108
60.599	20	GATTTTGTAAACTGCCCGGA	59.938	20	135	487	621
58.997	24	GCCACTGAACTAGCACCACA	59.905	20	208	1	208
59.551	20	CAATACTTGCCGTCGCCTAT	60.117	20	280	31	310
60.155	20	GACGTGGTTTGCAGGCTATT	60.14	20	235	62	296
60.291	20	AGGTTGCGTACATCTGACCC	59.997	20	239	1231	1469
60.224	20	TTTCTGTTGTCAGCCCACTG	59.873	20	140	765	904
59.945	20	TTTTGTGGATATTTGTTTATTGTCT	60.054	27	189	647	835
59.493	20	TTATGCGATGATTGCAAGGT	59.14	20	265	477	741
60.135	20	TAGGCATGGATTGCATTTGA	60.035	20	113	335	447
59.783	20	CAACATTGGATTCGAAAGGG	60.301	20	218	172	389
60.066	20	GCTCGGTTTGGCTAGATTTG	59.845	20	248	7	254
59.457	20	TCTTCATTTTTCTAGTGCGCTG	59.669	22	273	962	1234
58.761	25	AGCCGAAATTTTTAGGTATCG	57.509	21	267	9	275
59.979	20	CCGTGTGATAGGAACCATCC	60.195	20	246	546	791
59.948	20	ACTACGATGTTCGCCACCTT	59.621	20	209	38	246
59.73	20	GATGAGGACGCTTAGGTGGA	60.218	20	258	80	337
60.132	20	CCAATATGGTTTAAAATTCTTCCG	59.976	24	265	35	299
60.255	20	ATCTCACATACATATAATTGAGCT	57.101	27	221	237	457
59.6	23	AAGTAGTTGTTCCAGTGGCAAT	57.804	22	197	286	482
59.996	21	TTGATGAGGAAAACAAGTGGG	59.956	21	165	478	642
59.933	20	CAATCCTCAAAAGAACCCCA	59.903	20	232	2637	2868
59.429	20	CATACGGAAGCCTTTGTGCT	60.27	20	232	3	234
59.966	20	GACGATCACCGGTTCTTGAT	59.934	20	239	189	427
59.914	20	CCTGAGGATGAAGTGGAGGA	60.191	20	267	9	275
60.117	20	TCGCACCACTTCACTTTCAC	59.88	20	234	293	526
59.864	20	TGAAAATCCCACTCCCACTC	59.903	20	240	587	826
59.823	20	ACCTTCAAGGGCATCATCAG	60.073	20	221	168	388
58.325	20	GATGATCCACGCAACTCAAA	59.654	20	101	233	333
60.118	20	AGGTTGCGTACATCTGACCC	59.997	20	100	17	116
59.957	20	TCCAACTGGAGGATCAGGAC	60.048	20	272	6	277
59.931	20	AGGAGGTGCCATACACGAAT	59.434	20	280	2604	2883
60.559	20	TGTCAACACTGCCTTCTTGG	59.873	20	224	388	611
59.914	20	TCAGTTCCATGCTTGTCTGC	59.992	20	112	438	549
57.158	20	GCGGATTTACAATTCGTGCT	60.103	20	229	904	1132
59.875	20	GGAAAATCGGCTGAAGTCTG	59.813	20	275	2084	2358
59.325	20	TGTAGCCGACCCCAATTTAT	59.297	20	171	273	443
59.883	20	CTAGCCGATGACCTCCAAAG	59.83	20	189	376	564
59.962	20	CCAATGTAGGATTGGGTTGC	60.192	20	276	941	1216
60.132	20	AAAGGTCAGATATTGAACATCAT	59.647	25	180	4383	4562
60.008	20	GGTGATGATGGTGCTTGTTG	59.967	20	196	938	1133
59.606	21	AAATTTTCACCCGCAAAGAA	59.564	20	222	2527	2748
60.065	20	TACCGACAATTTTTGCTCCG	60.989	20	168	294	461
59.14	21	TGCAGTGGTGACGGAGTAAG	59.897	20	265	23	287
59.914	20	GACACACACCATTCCCAACA	60.27	20	213	1272	1484
59.566	20	CATTAGGCTTGGGAGACGAA	60.206	20	193	673	865
59.907	20	TGACAAGTGTTTGAGGGAGG	58.695	20	106	916	1021
59.898	20	GAGCTTCTTGATTCCATGTCAA	59.316	22	252	973	1224
60.066	20	GGTCGTACTGGTGCCTGAAG	60.711	20	180	750	929
58.5	27	TCACTCCGGATCAAATAGGC	60.036	20	114	7	120
60.24	20	TGGTGGTAATGCCAAGAGAG	58.722	20	187	298	484
60.112	20	TCGAACTTGTTCAGGCACAC	59.88	20	239	1454	1692

59.989	20	GACACAGAGGCTGACGATGA	59.988	20	116	14	129
60.019	20	CCGCCTCTATTTCCGTAACC	60.811	20	211	217	427
59.883	20	CCGATCGATCAATCTGAAGG	60.56	20	177	434	610
59.955	20	GGAAATAAATGGATTTTCGTGA	57.992	22	266	447	712
59.864	20	TGTTCCTTTACCAGAGGCGT	59.734	20	175	87	261
58.871	20	GATCCGTAAAACACCGTTGG	60.227	20	237	25	261
59.948	20	TAATTGCCACAGGGAAAAGG	59.931	20	279	2547	2825
60.91	20	CCATTGGTACAAAAGTTTGCC	59.37	21	110	6	115
60.206	20	CGCAACCGTACCCTTGTAAT	59.883	20	165	2095	2259
60.673	20	GGCACTGTCACCGGATTATT	59.82	20	276	240	515
58.456	21	TGTAGCCGACCCCAATTTAT	59.297	20	126	7	132
59.42	22	TGGATAAGAAATGGATCCGAA	59.355	21	237	278	514
57.992	20	TTTGATTGGGAATAATTGGG	57.289	20	280	1731	2010
60.792	20	GGAAGAATTAGTGGAGGGGC	59.903	20	164	195	358
60.04	20	TCGTGTGGTTCGAATATGAAA	59.027	21	150	38	187
59.244	21	CAAATGGGACAATCCATTCC	59.991	20	123	89	211
59.297	20	CCTTATGGGGTACTGGGCTT	60.2	20	229	55	283
60.373	20	TGTAGCCGACCCCAATTTAT	59.297	20	154	276	429
59.862	20	GGAAGTGGGTTCTGTCCAAA	59.943	20	274	3874	4147
60.755	20	GCCAACTAAGCGATCCATGT	60.103	20	166	927	1092
60.332	21	TGATGAACCCCACATCCAAT	60.995	20	231	47	277
59.65	24	ACCCTGGCCATCTTCTTTCT	60.074	20	135	7	141
60.003	20	TCACAAGGAGGGTCGAAATC	60.05	20	165	1307	1471
59.734	20	ATAGTGGTATGGTGTGGGGG	59.405	20	197	354	550
59.79	20	GCCTGCATGATTTTTATGGG	60.289	20	274	3319	3592
60.26	24	ACAACCATTCACCATCCACA	59.656	20	163	0	162
59.756	20	TAGGGGTTGGCTCTCTGATG	60.21	20	277	322	598
59.739	20	TCCACTTTTCGAATGTCCCT	59.526	20	272	6089	6360
61.63	20	ACACAAGAAAATCCATCGCC	59.939	20	102	3	104
59.297	20	AAAGCCATATGCGGTAGGTG	59.982	20	276	1	276
59.326	27	GAATACCAACAACTAAATACGCTT	57.217	25	266	196	461
60.278	20	TGCACCGTGTGCAGTTATTT	60.18	20	220	126	345
60.401	20	TTCCCACTAACCAGCTCACC	60.111	20	273	2104	2376
60.91	20	TCTTTAGTTAGCCCTTTGAGCC	59.079	22	234	1	234
59.894	20	TCCTTTTGACACAAGAAAACCC	60.365	22	225	169	393
59.973	20	CGACCTCCACCTCCTGTTAG	59.715	20	274	199	472
60.11	20	AAACGAGAACTATGAAGCACCA	58.906	22	214	17	230
59.42	20	TCCCAAACTCCATAGGTTGC	59.933	20	251	574	824
59.933	20	CCAGCCTTGTGAGACAGTCA	60.022	20	134	794	927
60	20	GGGTCAGATGTACGCAACCT	59.997	20	247	987	1233
59.962	20	AATCCACATTATTTCTCACTCACC	58.455	24	104	150	253
60.174	20	TCATCCTCGGAAGCAATCTC	60.303	20	197	104	300
58.442	24	TTTAGATAAGCATACACCATCACA	59.08	26	190	542	731
59.918	20	CCGTGCCAGTACCTCCTCTA	60.269	20	253	74	326
60.607	20	CTGGGTAAACCCACGGACTA	59.846	20	113	8	120
61.099	20	CTCCACCCCTTACAAGCAAA	60.103	20	230	304	533
57.655	22	CAGGCACCAACCAAGAGATT	60.111	20	194	231	424
59.664	20	CCAATTTCCGGTCTCACAGT	59.966	20	264	147	410
59.077	20	GCTTACACACGTTCTTGAGGG	59.788	21	243	509	751
59.356	19	ACGATGACGTGGAAGTCGTT	60.577	20	251	2	252
59.789	24	ATTTTACGTCACACAACTCGAA	57.364	22	140	2784	2923
60.074	20	TCAATGGTTAAATTGGTATTTGATT	59.073	26	199	108	306
59.797	20	CCTTCTGCGAATCGTTCAAT	60.214	20	246	3	248
57.292	24	TTAGGCTGAATTGGAATCCG	60.031	20	211	720	930
59.779	20	ACTCGCTCGATCGTTGTTCT	60.02	20	202	479	680
58.932	23	CCGAGACCCCAATTTGATT	59.735	19	118	21	138
58.46	21	GAATGCAGCATCATCACACA	59.202	20	262	1793	2054
60.06	20	GTTTTCCGGTGATCTTAGCG	59.708	20	231	351	581

59.933	20	TCATTGAAGTGACCCAACCA	59.935	20	243	2467	2709
60.011	20	CTGCAACCCGTAAATGGAAC	60.365	20	217	3138	3354
60.111	20	CATCCCAACCACGTTAGCTT	59.993	20	182	1622	1803
60.235	20	AACTGATGCTGCTGCTGCTA	59.918	20	183	51	233
59.588	22	TCCAATCAAGTCGACAAACG	59.691	20	134	162	295
60.184	20	TGTAGCCGACCCCAATTTAT	59.297	20	233	397	629
59.871	20	ACCTTCATCATCCTCATCCC	58.741	20	250	3159	3408
60.278	20	AGGAGGCTTTCCAGGTCATT	60.074	20	115	3679	3793
58.446	24	CGTGGTTCGTCACGCTACTA	59.928	20	260	301	560
61.08	20	AGAGTGAGGCGATAGGCAAA	59.978	20	223	264	486
59.813	20	CCTGTGTCAGGGCTAGCTTC	60.012	20	200	515	714
59.225	22	AAGGCAGCGACTGGAAATC	60.355	19	126	7	132
60.91	20	GCGGTGTATGTCCCTCAACT	59.997	20	249	5	253
59.55	20	TGCAGAGATGGACGTGTTGT	60.319	20	185	1515	1699
59.903	20	ATAATCCGGTCCCTTCCAAA	60.502	20	243	157	399
60.469	20	CTTGCTCGAATTCTTAGCCG	60.11	20	168	254	421
60.088	22	CCAACCCGCCTTATCTAAAA	59.075	20	230	448	677
59.316	20	GGAACTTGCGAAAATGGAAG	59.685	20	129	88	216
60.025	20	GGCAACCCATTCGTATCCTT	61.072	20	182	121	302
60.066	20	TCACTTCATAAAGTCCGCCC	60.074	20	130	146	275
59.989	20	TCCGTCGTCTTTCTTTGCTT	59.993	20	151	4032	4182
60.493	21	TTCCTCTCGATCCTCGTTACA	59.822	21	104	8	111
60.118	20	TGTTGCTCATGACAAATTCAATC	59.996	23	105	1384	1488
59.671	22	CATGTCAGAAATTGGGAGCC	60.461	20	189	158	346
59.651	20	GGGTCACACGAAAGTTTACAAG	58.675	22	194	461	654
60.149	20	CACTGTGGTGGCATATCAGG	59.984	20	271	32	302
59.43	20	CGTTCAAATCACCAACATCG	59.964	20	280	360	639
59.168	25	AGTTGGAAGCCTTGACATTGA	59.726	21	221	18	238
60.117	20	GGGGAGAAATGAAAAAGGGA	60.237	20	169	25	193
60.599	20	AAGGTTTTAACAGTCCTCCGA	57.854	21	227	4096	4322
60.035	20	CGAGCTCTAACTCCCCCTTT	59.842	20	200	231	430
60.175	20	CCAAGAGCAAGACGACAACA	60.025	20	156	3643	3798
58.759	21	CCAAATGAGCTCGGTTGATA	58.721	20	280	582	861
60.164	20	GGACCGGCCGTATTTATGAT	60.903	20	272	188	459
59.415	21	TGAACAAGCCTATTGCCTCC	60.214	20	273	74	346
58.987	20	CTTCACACATCCAATCCAAGAA	59.971	22	261	489	749
60.293	20	TTCACATTAGAGCACATGGAGG	60.132	22	219	331	549
60.032	20	CATGCTTTTCGTCTCGCATA	59.976	20	141	182	322
60.465	20	GCTAAAGTGCCTCGTGCTTC	60.162	20	159	4289	4447
59.89	20	TACATGGATTTCCAGCAGCA	60.22	20	268	10288	10555
59.964	20	TGAAGCAATTCAATTCAAGCA	59.434	21	233	328	560
60.251	20	TGCACTGCATTTCCTTCGTA	60.401	20	251	71	321
60.005	20	TCAGCAACTCCTGCATATCG	59.972	20	201	479	679
60.271	20	CAGGTTGGGATGAAAGGAGA	60.042	20	212	0	211
59.971	20	TGAATTTGATATGGGGCACA	59.745	20	250	4272	4521
60.326	20	GCCAATTCGTCTCGTGATTT	60.081	20	137	329	465
59.415	20	ATTCTCTCTTCTTCGCCACG	59.574	20	259	70	328
59.951	21	GGTCCCAAAATCGACGTAAA	59.801	20	252	120	371
60.315	20	TGGCATATAGTGGCCTCCTC	60.059	20	220	11	230
60.021	20	TGATCAAAATCGAGAAAGCG	58.991	20	256	442	697
60.173	20	TGAAAATGAATTGGGGTGGT	60.029	20	181	1975	2155
59.813	20	ATTCAGCCCTTAACTGCCAA	59.708	20	261	3	263
59.598	24	TGTTCCATCTAAGGCTCCCA	60.594	20	253	1	253
59.72	20	CTTTGCACATGAACAATCACAA	59.632	22	278	682	959
58.334	20	GCCATTGAAATTACCTGCAAA	59.957	21	122	21	142
60.378	20	GTCGTTGGTTCTTCGTGCTT	60.299	20	177	338	514
58.623	23	TTCTCGCCCTCTAAGGTTTTC	59.843	21	272	568	839
60.145	20	GATTCTTTCGTGGAGTCCGA	60.195	20	257	275	531

57.589	23	TCCAACCCAAGGTGAGTAGC	60.111	20	150	107	256
59.105	20	TGAGGGGGAAAAGAGAGGAT	60.008	20	211	1187	1397
60.249	20	AAACCAAAAACCCAAGACCC	60.068	20	264	2585	2848
59.415	20	TTTTCCATTGGCATAGTTGAA	58.148	21	263	956	1218
59.925	20	GGATGAGCTTTGGCTTCTTG	59.955	20	185	940	1124
60.197	20	AACTCAACCCAACGCAAATC	59.978	20	157	36	192
60.326	20	TGGGGGATTGTTGGAATTTA	59.988	20	157	199	355
59.82	20	CAGAGCGCACTCGAAGAGTA	59.49	20	150	184	333
60.91	20	TCAACATACCCAATTATTCCCA	59.055	22	133	11	143
60.02	20	TCCTCCATAACTTTTTCCTCACA	59.987	23	232	66	297
60.073	20	AAGAACTCGCAGGTTCCTTG	59.473	20	167	99	265
59.99	20	GGTGAGAAGTACGCATGCAA	59.871	20	169	530	698
59.926	20	GCAAGAGAATTGAAGAGCGG	60.096	20	269	17	285
60.11	20	TCTTCCCCAAAAGTCACCTG	60.081	20	184	701	884
60.158	20	TCGTTGCCGGAAAATGAATA	61.319	20	264	255	518
59.767	21	ATGTAGCCGACCCCAATTTA	59.297	20	102	42	143
59.871	20	GGATTTGCTGTGGTAGGTGG	60.375	20	249	435	683
60.91	20	CCGTGTGCATTTGTGTCAAT	60.436	20	105	1	105
60.016	20	TCACTCCCTCCACATCTTCC	60.048	20	178	246	423
59.971	20	AGCCCATGTTTTGAGAAATTG	59.077	21	207	105	311
60.008	20	TTGGGAGAAGGGTTTGTGTC	59.943	20	150	416	565
60.172	20	ACCAGATTTTTCCGGCTTCT	60.074	20	225	200	424
59.971	20	GGAGAAGCACCTCCTCTGTG	59.986	20	227	255	481
59.671	21	TGCCCATGTCCACTCAATAA	59.924	20	182	22	203
60.074	20	CAGCCTCCCAGCAAGTTATC	59.836	20	167	834	1000
59.674	20	TTAAAAATGAAACCGGCCAA	60.287	20	235	1768	2002
59.957	20	AGGTTGCGTACATCTGACCC	59.997	20	244	3030	3273
60.212	20	CTCCGGATTTGGAGACTCTG	59.797	20	221	84	304
59.301	20	TCAGACTTGGTGGCAATCAG	59.831	20	241	76	316
60.774	19	TTCAACATTCAAAATTGGTATGAA	59.665	25	272	18	289
60.045	20	TCAAGTTTTTATTAGCATTTTAAAC	58.796	27	225	601	825
60.009	20	GGCGATTGTCAACTTGGTTT	59.978	20	206	78	283
59.218	20	CATGCAGACCACTTTTGGTG	60.152	20	247	52	298
60.111	20	GCCTCGATCCTAACGTGTGT	60.142	20	173	1613	1785
59.336	20	TCACCCCTCATTCACATCAA	59.893	20	230	547	776
57.86	23	CCATCTTCAAGCAAACAACA	57.316	20	248	1	248
60.065	19	ATGGGAAGGGGTGGAGATAC	60.015	20	114	308	421
59.927	20	CGGTTGTCATAAGACCACTTCA	60.03	22	119	7	125
60.103	20	ATGGGATAAATTCGCTCACG	59.923	20	178	5069	5246
59.244	20	AGGGGTAGGGGGTAGACCTT	60.068	20	115	108	222
60.074	20	AGGACTGCCGACCTCTTTCT	60.393	20	246	371	616
59.953	20	AAAAACATTAAATCAAACTGTACC	57.811	26	231	239	469
59.93	20	AAGGGAGCTACAACCTTTCATC	58.783	22	229	196	424
58.948	19	GAGAATATATCCCGGCACGA	59.885	20	155	0	154
60.074	20	GAGTCATTAAGTGTGGTCTCGG	58.721	22	139	967	1105
59.861	20	AACTGACTGTCGACCCTGCT	59.907	20	216	20	235
60.022	20	CCCAAGACCCCAATTTGATT	60.91	20	174	2648	2821
60.089	20	TCAGCAGCCATTTGTTCTTG	59.988	20	164	231	394
60.039	20	TGCATTACCTTTGAAGCACG	59.872	20	242	2019	2260
60.712	20	TGCTGTTTTGTTATAACCCCG	59.876	21	250	59	308
59.907	20	TGCTTCTGGTAGCAATGGTG	59.864	20	264	380	643
60.112	20	GAATGAATTCGAAGTTTGGGA	59.009	21	149	408	556
59.726	21	TGTAGCCGACCCCAATTTAT	59.297	20	125	1057	1181
59.03	21	TTGAACAATGGTACCTCCTCC	58.898	21	134	11	144
60.096	20	TTATAACGTGGGAACCAGCA	59.037	20	242	687	928
60.119	20	AGAATCAAGCAATGGATGCC	60.043	20	196	598	793
60.439	18	ACGGCGATGGCTAGAGTGTA	60.817	20	105	11	115
59.968	20	AGGAAATGCGAGAGGGATTT	60.039	20	172	321	492

60.221	20	TGAAGGCGGAGGTTTCATAG	60.206	20	200	202	401
59.931	20	GGATTTTTCGAAGCACTCCA	60.192	20	249	262	510
59.645	20	AGTGCGGGGTAAAAATGTTG	59.861	20	209	230	438
60.043	20	CTTTGTTTGGAGCGCGTG	61.555	18	133	171	303
60.623	21	GGTCTTTAATATCCCCATTTGA	57.032	22	136	211	346
61.713	20	ACTCGTTCAAATCCTGCCAT	59.556	20	217	5781	5997
59.993	20	CCTTGGGATATTGTTTGGCA	60.692	20	179	59	237
60.036	20	TGGGATTATGTTTGGATTTCA	57.804	21	119	13	131
59.002	20	TGGCTTCTTTTGCACCTCTT	59.993	20	274	711	984
60.352	20	GTCATTCCCTCGTCTCCAAA	60.05	20	191	124	314
60.134	20	CTCCTGCTTCACCTCGAGTC	60.135	20	202	84	285
60.24	20	GCTGAGAGCAATACCGATGG	60.765	20	277	1784	2060
59.752	20	GTGGGAAGAATGCGAAGTGT	60.119	20	244	789	1032
58.781	23	CGGCTCAAAGGACAGATAGG	59.83	20	262	277	538
60.011	20	TGAATCAGCTCCGTAGGCTT	59.978	20	177	228	404
60.067	20	TCCACAACCTCTCATCTCCC	60.048	20	247	241	487
59.371	20	TCCTCACTGAGTCTTGATATTGTT	57.06	24	269	512	780
60.008	20	GAACAATCAGCACCGTCAGA	59.837	20	196	1537	1732
59.823	20	GCGATATCACGTTTAACGGC	60.485	20	242	19	260
59.166	20	ACCTTCCAATCAGCCTGCTA	59.836	20	150	65	214
59.886	20	CACAATAACCATTCGTTCTCAA	57.692	22	240	157	396
59.42	20	GAGAGAGGGAGAGAGATCGGA	60.043	21	131	206	336
59.988	20	TGTGCAATGCAACAAGATGA	59.833	20	151	77	227
60.187	23	GGAATTGAGCAGCCTTTTTG	59.823	20	240	346	585
59.923	20	AACAATGGCTGCTGTTAGCC	60.278	20	158	428	585
59.962	20	GAATAGCCCAAGGGAGGAAG	60.032	20	188	1639	1826
59.74	20	TGAGACTCGAACCTGTGAGC	59.129	20	219	30	248
59.853	20	CCTGAAATTTGGTAGGCGTG	60.493	20	221	1273	1493
60.024	19	ATTACCTGCCGGAATGTTGC	62.128	20	110	33	142
60.073	20	TCGCTAGAATCTCATCCAGTTG	59.476	22	280	211	490
60.223	20	GATGTACGCACTTGGTGGTG	60.032	20	100	636	735
58.775	20	CCACAAAATAATAAGGCGGC	59.455	20	211	2	212
60.21	20	TCCACAAATCATGCGAAAAA	60.051	20	211	23	233
59.939	20	TCAACAGAGCATGAACCAGC	59.992	20	262	41	302
58.759	21	TTGCCATTATGCTCCAATGA	60.035	20	182	1739	1920
59.41	20	TGTTGGCATCAAGCTTCAAA	60.379	20	133	2369	2501
59.885	20	TTCCCATCATTCACGACAAA	59.9	20	244	132	375
59.722	20	CTGAGCCATCGAGGTATGGT	60.096	20	280	230	509
60.111	20	GTTACCAAACAGCCCACTCC	59.454	20	279	676	954
59.916	20	AAACAGAATTGTGCTTGGGC	60.118	20	267	3048	3314
60.037	22	TAGCAACAGTTGGAAATGCG	59.872	20	128	6	133
60.301	20	AAGCTTGATGGTGGATGTTTG	59.985	21	239	207	445
60.049	20	ACCGTACTCCGAATGAATGC	59.962	20	162	2374	2535
60.277	20	CGGGACCGTGAATAATGACT	59.813	20	262	937	1198
59.853	20	AAAGTGAAGGTGACCAACGG	60.005	20	216	1430	1645
60.029	20	TGATTTGATCATCCCTGCAA	60.009	20	111	40	150
60.11	20	AGTCTCCTCGCTTTTCCTCC	59.957	20	279	3647	3925
60.096	20	AATTGTGCTATTATCTGCGCC	59.251	21	142	244	385
60.015	20	TGTAGCCGACCCCAATTTAT	59.297	20	133	127	259
60.326	20	TGCATGCATCTTTTTCTCTTTT	59.013	22	267	41	307
59.059	20	CGGTAAAGGGTTCGATTTCA	59.931	20	269	870	1138
58.639	21	TAAGAGCCTTGCGCTCTACC	59.752	20	213	287	499
60.096	20	GACAGGCCTGAGTTCGGTAG	59.867	20	249	3253	3501
59.859	20	CTTGGCATCCTCATGGAAGT	60.073	20	271	3948	4218
59.942	21	GAATGCATTGAGTCAAACATAAG	58.323	24	190	612	801
60.118	20	TTTCTTTTGGCCAATGTTGA	59.133	20	265	191	455
60.206	20	CAAGAATGTTGACCAAGAGCA	58.912	21	215	242	456
59.813	20	GCTCTTACACCCATCCGAAA	60.074	20	244	304	547

59.047	20	AAAACGGACACCAAATCAGC	59.978	20	277	12	288
59.557	21	GGGTGTCCTCGACATTTTTC	59.386	20	271	87	357
60.192	20	ACGAAGTGGCTGAGGAAATG	60.255	20	278	59	336
60.413	20	CTGCAACTTTCCATACGGCT	60.27	20	277	121	397
59.96	20	AATTACCTTCACTCACCAGAAAA	57.008	23	277	78	354
59.749	21	AAATTACAAACCCGCATCCA	60.188	20	210	417	626
59.443	23	GGAGCAGAATGTGGAGAAGG	59.803	20	137	14	150
59.375	20	TGCAGATGGAAGATGAGCAG	60.096	20	148	930	1077
60.11	20	CTTGATATGGATCCGAGGCT	59.105	20	202	550	751
60.258	20	ATGGGGGATGAGTTTGTGAG	59.779	20	219	58	276
60.076	20	GGAAAGTGACCTCTGAAGCG	59.989	20	170	980	1149
60.31	20	GAAAATTGGGGATCACATCG	60.133	20	232	90	321
59.926	20	CCGTTTGATTCATCGGAAAC	60.309	20	110	837	946
60.195	20	GGGTGGACTTGATTTGCACT	59.973	20	187	336	522
59.7	20	ACCCGACCACAAAGGAATTA	59.288	20	262	363	624
60.044	20	GATTCAAGCCCCAAAGTCAA	60.051	20	174	1069	1242
59.369	20	ATGTAGCCGACCCCAATTTA	59.297	20	187	174	360
60.362	20	TTGATTATCATGTCGCTCGC	59.799	20	111	983	1093
59.901	20	ACTGATTGTACACGATGGCG	59.596	20	237	241	477
59.609	20	GCGGATAAGCTCGAACAGTC	59.985	20	181	5	185
59.247	27	CCCACATTTACTTGATGCATTCT	60.25	23	111	11	121
60.209	20	TGTCAGGATATTGACAAGGTGC	60	22	170	2052	2221
57.334	23	TGAATATCGGTTTCATCGCA	60.035	20	100	40	139
59.931	20	ACCCAACACCAAATTATGCC	59.551	20	227	20	246
59.978	20	GGAGCCACGCTACAGACAGT	60.476	20	250	4003	4252
59.962	20	ATTTAATCCCGTGCAACGC	60.852	19	218	59	276
60.042	20	CTTCAGGGCCAAATGTGAGT	60.111	20	270	4724	4993
60.448	20	TGAAAGTGATTAGCATGACCCA	60.502	22	241	251	491
59.967	20	CTGGTAAGGCTGTTGGGGTA	59.986	20	218	1333	1550
60.198	20	CTCCTGTGGCCAAACAATCT	60.111	20	222	3478	3699
59.834	20	GAAATTGGCTCCGAAATTGA	60.016	20	191	403	593
59.933	20	AGCCATAAGCTCGGATAGCA	59.967	20	130	194	323
59.853	20	CGTCCTTTTCAGTCAGCCTC	59.989	20	229	123	351
59.985	20	TATCGTCGGAGGAGGAGCTA	59.933	20	177	941	1117
59.297	20	GACACTTGGTGTGCAAATCG	60.16	20	201	3	203
60.221	22	GCGATGGTGTTTGAAAGGAT	59.939	20	204	19	222
59.827	20	ATCTGCAAAGTGCTGCTGTG	60.207	20	247	23	269
59.903	20	TCTAGGGTTGACCCACCTCA	60.501	20	175	1689	1863
60.102	24	TTTGGTTCGATCACGCCTAT	60.469	20	262	110	371
59.887	20	GTGCTCAAGGTTTGAACTCG	58.497	20	280	1261	1540
59.926	20	TAGTCTCTGCCAAGTGGGCT	60.012	20	233	227	459
60.214	20	TTTCCAAGACCGGAAACAAG	60.081	20	261	310	570
59.799	21	AGAAGGCTTTCGCCTTTTTC	59.966	20	258	76	333
59.67	20	CAATGGCGAAGGCAGTATTT	60.096	20	111	577	687
57.669	26	GGTTCTCAATTATGTTATTAGCAT	57.053	26	253	84	336
59.302	21	TGGGCGTAAAATAGAGGTGC	60.096	20	225	5710	5934
58.738	20	GGTACCGTCATTCCAATGCT	59.82	20	269	50	318
60.081	20	TCGCTCCTCCAAGAACAACT	59.989	20	110	66	175
60.058	20	CAACCCTTCGGATGAAGAAG	59.665	20	203	2430	2632
60.081	20	CCTGCAGATCATTCACATGTTT	60	22	186	55	240
59.927	20	TTCGATGTATTGTTGGATAATGTG	58.808	24	216	404	619
59.813	20	TTGGCTTTCTTTCTCCCTGA	59.926	20	275	352	626
60.468	19	GCTCGGCGATACTTGTCTTC	59.985	20	244	16	259
60.176	20	GCCCTCTGCTTTCAAATTCA	60.331	20	252	860	1111
60.018	20	TCACCATCACCATCACCATC	60.189	20	259	744	1002
59.439	21	CACTAACCTGAAGCCATGAGA	57.966	21	239	14	252
60.173	20	TCAAATTTTTCAGCTTCGCC	60.323	20	181	354	534
59.492	22	CCCAAATGGATTGGGTTCTA	59.617	20	115	89	203

60.053	20	TTCTTATCGTCCGATTTGCC	60.038	20	189	439	627
60.046	20	CCCCTTTCGGTGTAGACAAA	59.964	20	275	972	1246
59.126	22	CCCGAGGGAGTCACAATTTA	59.926	20	236	55	290
59.702	20	CGCACGTTTGTATTTTTATTTTT	57.532	23	108	263	370
58.998	20	ATTACGCATCAGCACAATCG	59.718	20	277	92	368
59.831	20	GTTACATCCCACCGGATTTG	60.051	20	269	217	485
59.522	20	CACGTCTAGATGGCAAGCAA	60.011	20	209	2031	2239
60.375	20	CTTCAATCAATCCCCCTGAA	59.864	20	261	4160	4420
60.039	20	AAATGCACTGGTTAGGAGGG	59.052	20	195	1090	1284
59.78	22	TGAGCAAACTAAATTACAACGAA	59.322	25	252	3716	3967
59.91	20	CCATGGCTTTTCAACCAGAT	59.933	20	255	707	961
58.906	21	TAGCAGGCCAAAGAGGAAGA	60.088	20	271	61	331
59.991	20	CACTTGCTTTGCCCGTTTAT	60.131	20	145	876	1020
59.955	20	TTGTTTGATCTGTGGGTGGA	59.935	20	204	140	343
58.783	22	ATTTTCGTCGCCCCTCTTAT	59.93	20	228	71	298
60.037	20	GGTGGTATGGTGTGCAGAAA	59.42	20	115	458	572
59.867	20	AAGTAGGGTCAAACACGTGAAG	58.304	22	262	37	298
59.955	20	GCCCATCTGACGATAGAAGA	57.834	20	172	594	765
60.339	20	CACTCCTTTCGTTGCCAAAT	60.11	20	209	228	436
59.67	20	CTAGATCATCAAATGCGCCA	59.792	20	273	586	858
59.823	20	TTTGGTTCATGTAGTCGACCC	59.845	21	274	909	1182
59.925	20	GGACTGACAGAGATCGAGGG	59.792	20	249	24	272
59.945	20	TCCATGGTGTCACATAATTGC	59.266	21	174	223	396
60.241	20	TTGCATTTAGGAGAATCCCG	60.031	20	248	11	258
59.916	25	TCGAAATCATGGTTCGTCAA	60.049	20	253	969	1221
60.051	20	GAGGCCAGTGATGACACAGA	59.827	20	143	3962	4104
60.189	20	TTATCCAACCCAGCCAACAT	60.192	20	254	477	730
59.4	20	TCTGTCTAATGTTTCCGCCG	61.157	20	238	773	1010
59.864	20	GGTAGCTACTTCAGTGGCGG	59.898	20	187	59	245
60.511	20	AGCATCGGCTGGTGAATTAT	59.556	20	273	104	376
59.247	20	TCGTCCAGCTGATGGTAATG	59.673	20	222	15	236
59.795	20	TCCCAAAGAGCAAACAGCTT	59.993	20	245	821	1065
59.67	21	TCGGCCTCCGTCATTATTAG	60.053	20	268	253	520
60.096	20	AGGCTGTGCTCATCCGTAGT	59.898	20	218	399	616
60.112	20	TGTAGCCGACCCCAATTTAT	59.297	20	180	315	494
59.997	20	CCATTTTCAAGATGTGCCCT	59.933	20	204	395	598
60.108	24	TTGTTGCCACCACTGTTGTT	60.049	20	255	2	256
60	20	CAGCTTCCCCCAATACTCAA	60.066	20	140	453	592
59.933	20	TCCCCGTACACAGTGATTTTT	59.345	21	224	959	1182
59.43	20	GCAGGCCAAAGAGGAAGAGT	60.903	20	244	243	486
59.844	20	TGTTCCAAGCTTTTCTCCTCA	59.978	21	219	176	394
60.103	20	TCACATTGCTCTGCAAGTCC	59.992	20	221	108	328
60.776	20	ACAAGACCTGCTTCATTGGC	60.263	20	138	996	1133
60.184	20	GGCAGCAGCCTCTTAATCAC	59.985	20	107	371	477
60.91	20	TCAACCCAGCATATTCCACA	59.924	20	209	10	218
59.402	22	TCGAACTTCCATCAACACAATC	59.978	22	206	417	622
60.088	20	CCTGCGAACTTTCCTAGCAC	60.015	20	101	275	375
59.827	20	AGCAGAGGAGGACGATGAAG	59.555	20	219	236	454
60.31	20	CCGCACTTGACTACTCAGCA	60.199	20	267	551	817
57.404	20	TCGGGATCTTGATGGTTCTT	59.483	20	275	187	461
60.37	20	TCTCGTTTGACCAAATTCCC	59.91	20	277	428	704
60.285	20	GTGGAACTGCAGGGCTAGAG	60.012	20	268	453	720
60.27	20	ATCTACAATCATGCTCGCCC	60.066	20	134	11	144
59.71	20	TACCTTGTCGGTAAATCGCC	59.96	20	192	355	546
59.955	20	GGGCTAATAATGCCCAAGGT	60.171	20	154	241	394
59.981	18	CTTCAGCTTGGTTTTGGAGG	59.846	20	109	9	117
59.72	20	CATACACGGTCACGTCTCGT	59.622	20	157	336	492
60.745	20	ACCATAAAAGTGCCCGACTG	59.993	20	250	27	276

60.199	24	GGCCAAAGTGGTGAATCAAG	60.495	20	279	2	280
60.257	20	ATGTAGCCGACCCCAATTTA	59.297	20	232	268	499
59.971	20	AACACAAATATGCCATGCAA	57.506	20	269	223	491
59.912	20	CGATAGCAAACCTTTCCGAG	59.839	20	218	1163	1380
57.65	24	GTTGAGGAAGCTGTTGGAGC	59.997	20	197	62	258
59.968	20	GTCAATCCCAATGACCATCC	59.995	20	211	204	414
59.138	22	TCCCATGCAAACTGAATCCT	60.461	20	220	1309	1528
59.904	22	AGTGGCTCTTTCGCTTACCA	60.015	20	123	3227	3349
60.232	20	TGAGTAAGACCCTCACCAGTTG	59.253	22	187	39	225
59.855	20	AGTTTGAAGAAAACCCGCCT	60.11	20	206	483	688
59.36	20	GGAAGTTAGAGGAGGTGGGG	59.928	20	274	569	842
59.572	20	TCCAATTAGGACAATCAAACCC	60.055	22	212	204	415
59.989	20	CAGCTCGGTTGTCAAGTCTG	59.616	20	199	216	414
59.848	20	CATGTGTGGGTGGTTCATGT	60.138	20	279	917	1195
59.322	20	TCGTCGCAGAGCTAGTGAAG	59.49	20	268	803	1070
59.807	20	AAACAGCAATTGGAACTCACTG	59.286	22	229	335	563
59.576	20	CATGCTGGGAACTGTACTGG	59.161	20	276	1623	1898
59.297	20	AACAAACATATGCTTTCCCAAGA	59.891	23	142	4	145
60.032	20	TAGCCAAGACCCCAATTTGA	60.439	20	144	2218	2361
59.959	20	AACACGCGAGTTTAAGGGAG	59.378	20	224	121	344
59.955	20	TAGGCCATGTGTAGCGACTG	59.888	20	277	326	602
60.201	20	TTCGGGGAAGTCTGATTTTG	60.044	20	129	427	555
59.837	20	TGCTAGCACCTCCTCTATTGC	59.629	21	216	71	286
59.073	24	AGGCCCCCTTGTCAAATACT	59.827	20	161	51	211
59.836	20	CACCGACAAATCCGGTAAGT	59.853	20	234	1450	1683
60.12	20	TTTCCCTTAGCCATGAATCG	60.031	20	210	539	748
60.128	20	GGCGATTGTCAACTTGGTTT	59.978	20	207	1095	1301
59.752	20	AAGCAAACCAATGCAACACA	60.157	20	263	1947	2209
60.074	20	CTCTTCCACCTGTCTCACCG	60.85	20	275	5778	6052
59.574	20	AGGTTGCGTACATCTGACCC	59.997	20	106	34	139
59.734	20	TGATGCTTTTGCGTTTTCTG	59.992	20	259	1505	1763
59.401	20	TTGTTAACCCATTCCCACAA	58.719	20	185	121	305
59.645	20	AAAGAGTTGACAGGGGCAAA	59.711	20	275	233	507
60.08	20	TGGCTGTTGTTGAAGTCGAG	60.025	20	229	2192	2420
60.048	20	TCTCCCTCGATCCTTATCCC	60.367	20	127	1199	1325
57.589	25	TTGATATCTTGGGCAATTGTAGA	58.642	23	193	32	224
59.95	20	CCTCTCATTCACCCTCATCC	59.46	20	212	11	222
59.555	20	TCATCTTCTCCCTCCACCAC	60.048	20	151	178	328
60.646	20	CCTTTCTGGACATGGATCGT	59.927	20	251	1195	1445
59.574	20	ACGGTATTCAGGCTCGGAC	60.088	19	108	41	148
60.34	20	AACCCACATACTCGAGGCAC	59.997	20	229	143	371
60.129	21	ATACGTAAGGCCGAGAGCAA	59.867	20	136	212	347
59.762	20	CTTGAAACCGGGGTAGGATT	60.18	20	245	34	278
59.978	20	CGTGTTCGTTCCTAGCTTCC	59.875	20	231	245	475
60.263	20	GATCGGAGATGGTGACGATG	61.474	20	210	1310	1519
58.502	20	CACTTTGAGTGGCGATGGTA	59.716	20	250	31	280
59.853	20	ATGGTGATTTGATGGGCATT	60.021	20	226	43	268
60	20	CTCGGGATCAATGACATTCC	60.281	20	226	209	434
59.799	20	AGATGCTGGTGGTACTTGGC	60.142	20	252	260	511
60.91	20	ACGAACAAATCATATGGCCC	59.651	20	227	34	260
60.074	20	ATGCGCTCTAACTTTCGCAT	60.01	20	205	964	1168
59.823	20	AGGCAGGACACAAACGAATC	60.119	20	191	675	865
58.768	22	TGACGTGCACATTTGTTATGG	60.43	21	106	4	109
59.88	20	TGTGCTTGGAGGAGTGTGAG	60.022	20	267	277	543
59.997	20	TCATGATGGTCCTGATGGAG	59.425	20	255	94	348
60.096	20	ACCAATGGTGGTATGGTGTG	58.984	20	231	37	267
60.073	20	TTTCTTTTTCCCCGTCCTCT	60.046	20	210	485	694
60.175	20	AGAGTGGAGGAGTTGCAGGA	59.986	20	193	2293	2485

57.065	22	TGTGGACAAAATTTCAAAGTGG	59.876	22	271	4	274
60.529	20	CCTCCATTATTGTGGTAGGACC	59.593	22	215	746	960
60.206	20	TTTGATTGGGAATAATTGGG	57.289	20	127	24	150
60.042	20	ACATTCGGGGGAGAAGGTAT	59.651	20	207	2	208
59.95	20	GAAGACGACGATGTTGGGTT	59.973	20	201	402	602
58.776	21	GCCACCTACAAGAATGCCTC	59.7	20	277	5	281
59.476	20	AAGCAACATCCATCGAATTGT	59.448	21	271	1114	1384
60.066	20	TTTGATTGGGAATAATTGGG	57.289	20	173	730	902
60.37	20	TGGGTTGGGATCCTCAGTAG	59.92	20	132	17	148
60.263	20	GCAACCGAGCTCTAACAAGC	60.162	20	249	80	328
61.269	18	TCTGAACAATTTGCAGCTCG	60.134	20	120	8	127
59.443	20	CTCTGCTTCAAGCTACTCGGA	59.906	21	187	2615	2801
59.838	20	GTGGGCACTAAATCGGGTAA	59.823	20	267	2333	2599
59.405	20	ACAATTGTGGTCGTGGGAAT	60.096	20	124	58	181
60.14	22	AAGGTGTAGATCTGGCGGG	60.081	19	161	1113	1273
59.864	20	CTCGTGCATTTTCCTTGACA	59.84	20	260	896	1155
60.08	20	GATCTTCATTGCGGGGATTA	59.862	20	134	1822	1955
60.074	20	GAGGTGGAAGCACTTGTGTG	59.31	20	166	312	477
59.953	20	TGCATCATGTGACTTTCATTTG	59.59	22	226	483	708
59.991	20	ATCACAGCCCCGATAATGAG	59.917	20	202	372	573
59.518	20	TCTGCACAAAACCTTTTCCC	60.088	20	272	1034	1305
58.875	22	GCAAATCCATTTCTCTCCGA	60.155	20	149	47	195
59.6	21	TTTCGTAATCCTGGATCGCT	59.668	20	258	327	584
60.27	20	GCATTCCGAGTTTTGGATGT	59.939	20	180	11	190
59.918	19	CCACTGCGCCATAGGAACTA	61.176	20	253	1435	1687
59.271	20	TAGTTATTCCGCAACGGAGG	60.089	20	231	2914	3144
60.032	20	CTCAAAACCGAATGGAGGAA	60.044	20	174	556	729
59.297	20	ATGGACATGATTTGGAGGGA	60.135	20	205	6	210
59.599	20	TTGATCGAAATGGGAGTATGC	59.915	21	108	17	124
59.992	20	ATTCTGCTGCTGTGACGATG	60.016	20	253	204	456
59.74	20	GCGACTAGTGCTGTAGAAGGC	59.304	21	182	131	312
59.639	23	TGGTTCTCCTCCCCTTTTCT	60.045	20	137	14	150
57.341	23	AGGCCGAACCACCTATTTCT	59.962	20	219	0	218
59.49	20	TCCCTCCCACATTCACTTTC	59.903	20	134	4	137
58.777	20	TTGTGCCGATTCCCTTTTAC	59.938	20	244	4050	4293
60.011	20	AGAGGTGGGTGGATATGCTG	59.95	20	175	592	766
58.741	24	GGACGATTGCGTCACTGTTA	59.722	20	274	8	281
59.499	20	CATGTAGCCGATCCCAATTT	59.784	20	116	234	349
59.218	22	ACAACCAGTCTAAGCGGCAT	59.763	20	272	2481	2752
60.024	26	CCCTGCATGTCAAATTGCTA	59.688	20	170	21	190
60.414	20	TCAATGTCGCATATATTACTTTCC	59.79	25	209	245	453
60.05	20	AATTCACAAGCCCAAACGAC	59.978	20	227	1760	1986
59.059	24	AACATGCGCTTCTTATATTTTGC	59.695	23	230	30	259
58.602	22	TTCCTCATGTCTTTGGCCTC	60.195	20	241	5	245
60.832	20	TGAAGGATGCATCTTGCTGA	60.504	20	134	5	138
59.998	20	TTTATCGATTGTTGCCCTCA	59.112	20	261	43	303
60.435	20	TCAACTGGGAAAACCTGGTC	59.943	20	268	1731	1998
60.272	20	GAAGGTGGTCGTGTCGAAGT	60.159	20	193	722	914
59.93	20	CCGACGACCAAATGGATAAC	60.192	20	162	455	616
58.836	20	ATCATGTTCTGCCTGTGCTG	59.862	20	279	3	281
59.624	21	TCAATTCATGATGGTCATTTCA	58.82	22	230	992	1221
59.53	20	TAGTCGTGGCACACAGGAAC	59.751	20	162	706	867
59.598	22	AGGGACGCTATCGATTTGTG	60.096	20	253	3	255
60.066	20	CACAAAACATGCATCAGCCT	59.722	20	228	49	276
60.012	22	ATAGCAGGCTCGACCAAGAA	59.978	20	208	358	565
60.226	20	TTCAGGGCTGCTGAATGATA	59.375	20	277	808	1084
60.891	20	ATGGCCAAGTCAAAGTCACC	59.973	20	162	331	492
59.478	20	AAATGCAACATGTGATCTCAAAC	59.013	23	221	475	695

60.218	20	TAGAGGCTGCGAATTTCCAT	59.807	20	278	363	640
60.131	22	AGCCATCTCAAGAGTCGTGG	60.408	20	271	350	620
59.851	20	GATAGCCACCGTGATGCTCT	60.249	20	179	3246	3424
59.886	20	CCAAGAATCTCGATTCCCAA	60.006	20	269	1071	1339
60.096	20	CATCATGTTTAACTGGATTGTGC	59.397	23	202	190	391
59.097	22	CACCAAAGCCTTAATCCCAA	59.931	20	151	6	156
60.111	20	GGAAGTGGGGGTCGGTATAA	60.929	20	198	323	520
60.02	20	GGTATGCTTGGAGGGTTGAA	59.933	20	195	366	560
59.297	20	ACCTTTGAATGGATTGCTGG	59.933	20	130	7	136
59.855	21	GTTGTTCACAATTTGGCGTG	60.011	20	222	263	484
60.111	20	CCATGGCAAGTGACTCAAGA	59.831	20	205	4486	4690
59.962	20	ATCAAGCAAGCATCTCAGCA	59.704	20	163	808	970
59.585	20	AACTGGAGCACAAACCGAAT	59.598	20	257	815	1071
59.975	20	TTTTGCAATCGGAGCTCTTT	59.96	20	103	1000	1102
59.831	20	GGTCGTTGGTAATTGGACGA	60.755	20	121	775	895
59.318	20	GCTGAAAAATGCCAAGAACC	59.691	20	238	15	252
59.846	20	TGGCTTGCAGAATCAAGAAA	59.542	20	241	967	1207
60.025	20	GTGGTCATTTTAGGGGATGC	59.249	20	228	151	378
59.297	20	CTACCCACCCAGGTCATCC	60.183	19	270	9	278
59.332	21	CTTTTGTGAGCCATCTGCAA	59.988	20	210	49	258
60.038	20	TGGTTCGTGATTGACGTCTC	59.682	20	233	544	776
59.934	20	TCGTTGGAGTCTGAAAACCA	59.262	20	244	928	1171
59.87	20	GGGTGTGACAGCCTAACCAT	59.851	20	221	13	233
59.84	20	TGCAATGGCTTTTCATTGTT	59.161	20	259	96	354
59.552	23	ATATTAACAGTCCGGCGTGG	59.845	20	237	180	416
60.336	20	GTGGCGGTGGAGACTTGTAT	59.997	20	117	37	153
60.067	20	TCCAAGAATCCCTTCCAAAA	59.476	20	272	235	506
59.574	20	CGAAGACGTCAATTTGGTCA	59.691	20	243	1216	1458
59.943	20	TTTTTAAGGTGGGGAGAATGT	57.596	21	250	43	292
59.659	23	TGTAGGCATAACTATGATTGGGA	59.768	24	117	2	118
59.761	21	TCCAACTTATTGCATGTTGAACT	58.688	23	260	710	969
58.937	20	AGTGACCCTGGGGCTATCTT	59.957	20	215	18	232
59.405	20	GTTGGTGGGATTTGAACCTG	60.21	20	219	473	691
60.08	20	TTTGCGTCCTTCTGCTATGA	59.566	20	260	105	364
59.894	20	CCTCCCTTCACCTTCAAACA	60.081	20	229	3207	3435
60.48	20	TCCGCGTGTGCAATAAATAA	60.096	20	110	2998	3107
59.249	20	CATATCACGCGGATACCACA	60.366	20	230	719	948
59.957	20	ACCTCAGGTTGCTCCGAACT	61.219	20	179	288	466
60.005	20	TTACATATTTCTTGCGGCCA	59.169	20	115	476	590
60.459	20	AAATTGGTTGCAATTCAGGG	59.801	20	269	448	716
59.456	22	CGGGCTGATGTAGAGGAGAG	59.966	20	202	55	256
60.212	20	CTCGTTTACAGCATACGCGA	60.037	20	199	60	258
60.133	20	CTTTATCAAGGGCTGGGGTT	60.312	20	273	959	1231
59.943	20	AAGGAGATCCACTCTCGCAA	59.95	20	221	139	359
60.045	20	GATGAGCTACTGGAGCGAGG	60.119	20	272	388	659
59.83	20	GACGTTCGACTTCTTTCCGA	60.375	20	138	1360	1497
60.066	20	TCAACGCTCACCTTCACATC	59.837	20	209	76	284
59.297	20	GCGTGGTTCCATCTCAAAAT	59.939	20	153	8	160
59.962	20	CTGGCCAACTCTCCCTTCTC	61.299	20	204	386	589
59.297	20	CCAATGGCTACTTCTCTGCG	60.924	20	138	2	139
60.641	20	TGAATGGGGAAGGAGAATCA	60.395	20	214	1001	1214
60.16	20	TGGTGATTTGGGTTTGGAAT	60.029	20	274	88	361
59.853	20	CAGCATTCTATCTGGGCCAT	60.059	20	217	4463	4679
60.125	20	TCAGGCAGAAAATGGGATTC	60.014	20	276	903	1178
60.074	20	AGCCGTCCACAACACTTACC	60.035	20	241	61	301
60.232	20	GTACTTCTGACCCCGCAAGA	60.255	20	254	31	284
59.94	20	CCCAAATCAGAAACGCCTTA	60.067	20	247	57	303
60.096	20	TTACCGGTCGGTTACCAGAG	59.986	20	218	23	240

59.691	20	GAACGTGGGAGGTGAAGAGA	60.238	20	272	35	306
59.562	20	GGGATAGCACGTCAATAATGC	59.452	21	279	815	1093
60.103	20	TTTTTCTTGCACCAAATAGGTT	57.875	22	228	332	559
59.454	21	CGCTTACCTAGATGGGAGCA	60.365	20	216	0	215
59.309	20	AAAAGTCGCCGTTACTGGTG	60.168	20	229	399	627
58.368	20	CCCGAGAAATTGGTCTCAAA	60.044	20	222	541	762
59.569	20	TGCAAGGTCTTCTCCAACCT	59.844	20	211	46	256
60.271	20	AATTTACGGGACCCTCAAGC	60.32	20	212	293	504
59.691	20	GTCACGGAGAGCCCTGTTAT	59.166	20	130	939	1068
59.973	20	CAAGACACTCGCTACAGGCA	60.199	20	195	451	645
59.823	20	AGTCCTCCAATGAAGTCCCA	59.505	20	249	449	697
59.546	20	GGGGAAATGTGCCAGTTAGA	59.933	20	250	293	542
60.046	20	AATTTGGATTGAAAATGAGAGATT	57.344	24	201	791	991
59.96	20	ATTTTGAATTCGGCTTGTCG	60.074	20	267	860	1126
60.11	20	TCAGGGTTTCAACATTTCAGC	60.103	21	278	272	549
60.06	20	AAGAAAAGAGAAGGCTCCGC	60.096	20	277	366	642
59.224	21	GGGGAATTGATGGACATGAT	59.42	20	147	258	404
59.708	20	TGATGCTCTACCACTGCACC	59.862	20	124	265	388
59.955	20	AGACTACGGCCTCATCTCCA	59.827	20	156	892	1047
59.439	20	GCGAAGACAACCACGGTAAT	60	20	262	2824	3085
60.051	20	GCCCCTGTTTGCAATGTAAT	59.829	20	224	480	703
60.212	20	TGGTTGGTCTGATGATTGTGA	59.951	21	197	4	200
59.749	20	TCCTCACCCCCTCTCTTTTT	60.045	20	247	14	260
59.499	22	AACTTTGACTGCTATGCCGC	60.416	20	159	40	198
60.177	21	AGAGCAAGAAAGCATGGGAA	59.955	20	185	2721	2905
60.096	20	TCAGTCCCACCAATCACAAA	59.935	20	209	638	846
60.014	20	AGAGAGGGCTTAGAGACGGG	59.972	20	250	13	262
59.973	20	GCCAGCGTGATACTGATCCT	60.249	20	144	371	514
59.966	20	GGATCAGCAGTGGCTTTCTC	59.957	20	124	871	994
60.122	20	ATTCTTCGCATCAATCCCAC	59.9	20	277	244	520
59.387	20	ATGCTCTCGTTTGCCTTGTT	59.882	20	254	8	261
59.805	20	TCCACAAACGTGAAGTACGC	59.764	20	189	1171	1359
59.871	20	GCTTCTCATGCCTCTAGGGT	58.5	20	243	79	321
59.571	20	GGGTTTTGGTGATGTATGTGG	59.963	21	105	37	141
59.875	20	TTGAACTGAAAAAGTGGGCA	59.293	20	147	5186	5332
60.073	20	TGGCTAGCACAAATGAAATGA	59.315	21	250	71	320
58.056	27	TTATTTTGCATGTGATATTGGAA	57.2	23	252	2	253
59.022	20	GCAGGGTCGACTCAAAAATC	59.676	20	256	77	332
59.916	20	GAACCCGATGAGGAAGATGA	60.011	20	205	149	353
60.032	20	CCCAATGAGAAAAAGGCAAA	60.046	20	196	797	992
60.378	20	GTCTATGCTGGGATCACCGT	59.957	20	238	2286	2523
58.751	21	GGAGGGGTATTTTGGGGATA	59.846	20	124	33	156
60.088	20	CATTTCCCGAAATAGCCAGA	60.031	20	273	123	395
59.855	21	TTCGGAAACACCTAGAACGG	60.103	20	120	156	275
59.988	20	TGCAAAGTTCACATTCAGTCAG	58.975	22	183	1599	1781
60.006	20	GGGCGAAATGACAAAAATTG	60.302	20	255	1847	2101
59.708	20	CAAAGCAGCACAAGTTTGGA	60.027	20	269	1363	1631
60.074	20	TTTTTAGGAGTCCCGAACCA	59.541	20	129	852	980
60.05	20	AAGTGCACCTGAGCCATTCT	59.874	20	233	2126	2358
60.199	20	ACGGAGGTCTCTTGGGTTTT	59.972	20	182	448	629
59.579	20	CCAGCACGACGAGTACGTTA	59.928	20	206	282	487
60.111	20	TTCTTCTTTCCATTCACCCG	60.044	20	237	26	262
59.387	20	TTCTTGTCCATCATGCTTCG	59.799	20	182	140	321
59.931	20	CCGGTACATGACTTCGAGGA	61.055	20	240	91	330
60.464	20	GGAACCATTTCGTTAAAATTATGA	59.264	25	269	192	460
59.639	21	GGTCCAATAAATGTGGGCCT	60.94	20	270	1619	1888
59.855	21	TTCGGAAACACCTAGAACGG	60.103	20	120	115	234
59.751	20	TGGTCTGGGAGAACTCCACT	59.682	20	221	968	1188

59.066	20	TCACATTTAACCTATGAGTCTGCC	59.565	24	109	692	800
60.221	20	CTTTTGGTGATTGGGATGGT	59.647	20	199	459	657
60.34	20	TTTGATTGGGAATAATTGGG	57.289	20	153	128	280
60.016	20	TGTTTTGCGCAGTTATGGAG	59.872	20	248	41	288
59.997	20	TGGTACCACGAGGAGGAAAA	60.486	20	154	726	879
59.302	21	TCACCCAAGTCCAATCTATTCA	59.429	22	267	81	347
59.939	20	AACGGGGAAAAACAAATTCA	59.292	20	278	52	329
60.005	20	GGGTGCACTGGTTAAGCATC	60.526	20	238	455	692
59.978	20	CAAGGTGACTGCATCATTGG	60.112	20	197	83	279
59.946	20	CCAGCACCTCCTCTATTGCT	59.454	20	267	16	282
60.11	20	AGCGTGCATTTTCAGAGGTT	59.882	20	126	661	786
60.03	20	CCTTGAGGAGCAATGGAGAC	59.803	20	275	3776	4050
60.214	20	GGTCTCTGGATCAGGTTGAGA	59.243	21	175	324	498
59.42	20	TTTGGAGGATTGACTATATCGGA	59.816	23	271	233	503
59.172	21	CCCAAGACCCCAATTTGATT	60.91	20	276	1730	2005
60.126	20	ACGTTAGAGGGAGTCAGGCA	59.867	20	186	1653	1838
59.51	20	GCTTGTTATATCCCGCCAAA	59.928	20	227	28	254
60.154	20	GAGGTGATCGGTTCATTGGT	59.786	20	267	5475	5741
60.22	20	CGTGTCTATTGAAACGATGAAAA	59.175	23	274	270	543
60.159	20	TGCCTCTCTCCCTTGTGTCT	59.986	20	229	3121	3349
59.972	20	CTGGAAGAGGTGGAATGCTC	59.803	20	200	728	927
60.067	20	TGTTCTCTACAACCATGGCG	59.716	20	186	1030	1215
59.837	20	TTCTAAAGTGCAGGATGGCA	59.42	20	224	43	266
59.549	20	ATGTAGCCGACCCCAATTTA	59.297	20	191	2468	2658
57.423	27	GATCACCTCGAACCTTCTGC	59.81	20	275	3240	3514
60.241	20	GCTTGTTTGTGGGCGATAAT	59.967	20	134	101	234
59.805	20	GGAACACATCTGGTGCATTG	59.967	20	200	36	235
59.688	20	AAGAGAAGCTCGAAGGGGTC	59.957	20	173	207	379
59.487	21	ATGCAGGACAAACCCAATTT	59.292	20	226	1	226
60.12	20	ATCTGCATTGCAAACTGTCG	59.871	20	272	5	276
59.997	20	ATCTAGGAGGCTCATCCGGT	60.059	20	247	1554	1800
60.009	20	ATGTTCCAGATCCATTTGCC	59.756	20	265	330	594
59.297	20	TCGAGGTAAGTCGATCAGGC	60.362	20	110	2	111
59.697	20	AAACGTGAGGTTTTGACGAGA	59.766	21	223	133	355
59.275	22	AAGAAAGCCCACCTGATCACT	60.125	21	166	56	221
59.836	20	TTCATCTGTATTCGACTTCTCCA	58.847	23	280	69	348
59.948	20	AAAAAGTGCCTCCCTCGATT	60.074	20	158	1629	1786
57.809	27	CGTTCCAGTGGTTCAAGTCT	57.771	20	280	186	465
60.843	20	GCGAAACACGCATCTTTATG	59.329	20	248	21	268
60.495	20	GCGATCTTGTCACTTACGCA	60.019	20	280	89	368
59.997	20	ACCCACCACCAACATCAAAT	59.95	20	173	36	208
60.426	20	CTCATGGATCTTCATCGGCT	60.181	20	273	379	651
59.454	21	AATCAAATCGCCATGGAAAG	59.901	20	220	247	466
59.997	20	GCATCATGCTTTCCATACTCAA	60.103	22	140	934	1073
59.866	20	GATGCCAACCAACAAGCATA	59.548	20	254	3200	3453
59.655	20	ACTGCCCAACACCGACTTAC	60.035	20	175	325	499
59.911	20	AGCCTGCAAGGGAAGAAGTT	60.382	20	212	243	454
59.717	20	TGTAGCCGACCCCAATTTAT	59.297	20	239	479	717
59.816	22	CTGACATGGGGGTCTGCTAT	59.95	20	258	304	561
60.011	20	TTCTTGATACATGGGCGTCA	60.073	20	162	519	680
60.134	20	ATTGCTTACTGCCGGATTTG	60.096	20	161	95	255
59.562	20	ACCGGGATCCTTTTCAACTT	59.805	20	189	309	497
59.434	20	GGTGTGGCTCCTTGAAATGT	59.973	20	118	2149	2266
59.41	20	ATTGATGACGATGACGTGGA	59.925	20	119	888	1006
59.377	25	GAAACTTCAAATGAATCTTCAACA	58.769	25	107	429	535
59.955	20	TCCTAGAATTCCAATACGTGGTT	58.941	23	108	376	483
59.967	20	TCCAAGCAAGAGATTATCACTCC	59.739	23	208	85	292
59.75	20	ATAGAAGCCTCTGAACGCCA	59.978	20	190	880	1069

59.904	20	AGCCTTGCTCACGCATCT	59.688	18	267	663	929
60.096	20	TGGATTGTTGATTTTTGCCA	59.907	20	265	13	277
60.046	20	AAAAAGCCCGAACCTGACTT	60.11	20	203	38	240
60.309	20	GCTGTCTTGATTTACCTTCACG	58.906	22	206	1188	1393
60.027	20	TCAGCTGCGTTTCATTCATC	59.955	20	154	2413	2566
60.192	20	AATGGTCACACCCTACAACAA	57.841	21	260	394	653
59.682	20	TGTAGTCCTTCCTCACAAAGACA	58.898	23	260	134	393
59.508	21	GGCACGTAGGCTACAGCTTC	60.044	20	205	84	288
59.945	20	CAAAAGGTGGAAAGTCACCAA	59.994	21	211	3140	3350
59.945	20	CATCCTCTGCGTCAGAATCA	59.942	20	247	261	507
59.727	20	TCAAAGTCGATCTCGTCGTG	59.984	20	217	613	829
59.948	20	CCCAAGACCCCAATTTGATT	60.91	20	259	2165	2423
60.353	20	GCTTCAGAACAAGGAAGCCA	60.517	20	202	1236	1437
59.988	20	TCAGTTGACTGCCCTCACAG	60.022	20	265	155	419
60.171	20	GTTTGGACAAAGAGGGGTCA	59.943	20	272	455	726
60.081	20	TCGGAAATCTGGTCATTGAA	59.049	20	229	533	761
60.219	22	TCCTTTCTGTGGTTTGGGTT	59.425	20	259	541	799
60.15	20	TGATTTAAATAAAAATATGTTGCC	57.023	25	135	1587	1721
60.21	20	AGCATCAAGCCTGCTCAACT	60.164	20	121	1221	1341
60.197	20	TCCTCTCCCCACTGAACAAC	60.088	20	120	996	1115
59.17	22	ATTTCTCAAATGGCGAGCTG	60.352	20	105	358	462
59.95	20	GCAAAAAGGAGCGTATCGAG	59.982	20	142	337	478
58.601	23	CACAAAATGAACGTGGTTCG	60.004	20	236	19	254
60.011	20	TCGAATCAAGATTTCTCACGC	60.346	21	134	321	454
59.392	20	ACACATCCTTCTCTCCGTGG	60.112	20	243	6	248
59.91	20	GCAAGACTGGTTCCAAAAGC	59.859	20	198	9	206
60.01	20	CGAACTAGCTCACGAGTCGAA	60.715	21	174	3094	3267
59.878	20	GGATTGATGCTCCATTGCTT	60.043	20	198	442	639
59.971	20	TTCAGTTGGGCAATTGGTCT	60.495	20	118	54	171
59.924	20	CAGTGGGCAAACCAGATTTT	59.971	20	212	2055	2266
60.003	20	ACACCTCCGTCAACACCTTC	60.009	20	280	271	550
59.95	20	CATACGATATCACCGACCCC	60.036	20	261	535	795
59.813	20	TTCTTGGCTGTGGAATCCTT	59.67	20	263	421	683
59.823	20	CCAATGATTGTGGAATGAATGA	60.564	22	195	1169	1363
60.112	20	TACGGTATCCGAAGAGGGTG	59.948	20	224	1972	2195
60.255	20	GAATCTGAGCTGGAGTTGGG	59.803	20	234	655	888
59.405	20	TCCGCACAAAGAAAATGATG	59.664	20	111	1184	1294
60.025	20	TGGTTATGGAGGAGGAGGTG	59.92	20	203	142	344
60.226	20	CCTCGATGATGATGTTGGTG	59.918	20	264	98	361
58.995	20	TCTCCGCAATTCGAAAAATC	60.153	20	262	71	332
59.891	20	TTGACTTTACCCTCGGACCA	60.486	20	139	852	990
60.055	20	CCCAAGACCCCAATTTGATT	60.91	20	109	65	173
58.2	23	TCAGTCACAGATGCCCTGAG	59.98	20	243	0	242
60.025	20	GGCTAGTAGTAGTGGGAGGAGAA	58.139	23	277	130	406
59.87	20	AGTCGGTTAGCGTTGCTTGT	59.943	20	143	52	194
60.258	20	GGAACCCAGGCACTGACTTA	60.111	20	231	150	380
59.927	20	CTTGAAAAATCTCGAAGCGG	59.953	20	152	62	213
60.005	20	AGCAATTTCTTGGCTCGTTG	60.386	20	235	553	787
60.012	20	CCTCCACCTAAGCACCCATA	59.948	20	273	131	403
60.249	20	TTTCCAATCCAATTCCTTGAA	59.374	21	259	4	262
58.579	23	GCGATATCCGTGTAGCATGA	59.676	20	242	453	694
60.251	20	AACTTCTGCTTATCGCCTGC	59.62	20	185	140	324
60.353	20	TCATGAAAATGAAAAACGCAA	59.179	21	140	817	956
60.21	20	GCCGGTCCCATAACAAGTAA	59.823	20	253	1857	2109
60.063	20	CCATATTGCACCCAGAGCTT	60.096	20	225	840	1064
60.247	20	CCCAAGGCTGATGATCTTTT	59.126	20	209	1735	1943
59.218	20	TTGCTGGATCTGATCTGTGG	59.787	20	223	173	395
60.073	20	TCGTTCTTAAAAGTTATGGCACC	59.569	23	109	2959	3067

59.984	20	GAGGTGTGTAAAAAGGCCGA	60.11	20	111	504	614
59.959	20	CCCAAGACCCCAATTTGATT	60.91	20	184	1431	1614
61.479	19	GGAGGTGGAGGATTAGGAGG	59.89	20	177	721	897
59.518	20	ATGTAGCCGACCCCAATTTA	59.297	20	236	242	477
60.011	20	ACACATTTACAACCCGGCAT	60.118	20	242	3122	3363
59.433	20	ATTTTGGTGCGAGTCTACCG	60.132	20	227	1144	1370
59.966	20	CTCAAGATGCGAAGCAAACA	60.134	20	268	85	352
60.469	23	TGCCTGTATTATGAACGCCA	60.096	20	100	125	224
60.073	20	TAGCATGGAGTTGTGCATGG	60.687	20	133	320	452
58.997	20	GGGGATTCCTACAAGAAGCA	59.126	20	280	740	1019
59.988	20	GGATTGGATACCAAAAGGGG	60.37	20	174	972	1145
59.548	20	GCATTACAATGAACCACCGA	59.4	20	249	1928	2176
59.562	20	CAAACACCAGAATTGCCCTT	59.971	20	150	76	225
58.971	21	GTCGTTGCATGAGATGATGG	60.08	20	236	2401	2636
60.924	20	TGTCATCCCAATAACGTCCA	59.774	20	103	49	151
60.69	20	GCATGTCAATTGTCGAGCTT	58.879	20	273	25	297
59.351	20	CAACTCTTGTGTCGGGTCCT	60.151	20	165	3	167
60.155	20	TCCGATGATCAGTTGTTGGA	60.048	20	127	2185	2311
58.66	21	TGTAGCCGACCCCAATTTAT	59.297	20	280	1437	1716
59.933	20	AGTCCGCATAGGTTCGATGT	59.579	20	227	189	415
59.993	20	AACCTTATCCCCAAATTCGC	60.15	20	119	446	564
60.91	20	TGCATTTCTTTTTGAGTTGGG	60.096	21	200	6	205
60.035	20	ATCAATTCCCCAATCCCTTC	59.959	20	116	403	518
59.297	20	GAGTGGGCGTTATGGTGACT	59.997	20	149	7	155
59.583	21	GACCGGGAAAATTACATAAACAA	59.182	23	280	26	305
60.319	20	TGTAGCCGACCCCAATTTAT	59.297	20	206	1958	2163
59.691	20	CTTCCCGTGATATTCCACTGA	59.94	21	221	1078	1298
60.192	20	GTCGATCACAAACAGCCAGA	59.837	20	240	9	248
59.396	20	GGTGGGATTGGATTTGATTG	59.991	20	144	93	236
57.927	20	GTTCATATAGCCGACCCCAA	59.784	20	144	1322	1465
59.997	20	AAACGCATTCCCATCCATAA	60.153	20	121	42	162
59.933	20	CAGCCATTCCCCTAAAGTCA	60.066	20	276	1233	1508
59.966	20	AATTGTTGCTTCAAGGCTGC	60.395	20	201	1107	1307
59.813	20	TTTGATGATGTTGCCTGGAG	59.648	20	259	119	377
60.015	20	GACTTGCCGGAAAATCAAGA	60.192	20	273	235	507
59.676	20	GAGAAGAACATCCTCAGCCG	59.95	20	146	859	1004
60.375	20	TTCGTGTGTGTTTCCTCTCG	59.873	20	179	57	235
59.948	20	GACCGAGCTTGGATTTTTCA	60.192	20	224	1000	1223
60.345	20	TTTTGCTCATCTTGTCTGGG	58.847	20	279	65	343
60.031	20	CCACCTTGTTGTGGATTCAA	59.389	20	186	494	679
60.406	20	TTGCCATCATCTTCAATGGT	58.926	20	197	139	335
60.406	20	TTGCCATCATCTTCAATGGT	58.926	20	187	139	325
60.853	20	CCAATAAACAAGGAAGGCCA	59.931	20	187	107	293
59.873	20	TTGCATATTGAATACAATGTCGAT	59.675	25	277	244	520
59.903	20	AATTCTGGCCAGTCTCAAGC	59.434	20	170	1091	1260
60.299	20	GCCCTCAATTTTATACTCGAAA	57.495	22	265	126	390
59.823	20	TCATGGACCTGTTCGTCAAA	60.088	20	258	2613	2870
60.238	20	ATCTCCATCCCTTTCCCCTT	61.002	20	120	20	139
60.051	20	GTGGCTAAGCCCATGAAAAA	60.074	20	169	1182	1350
60.495	20	CTCTGTGCACCATCAAACTCA	59.889	21	203	914	1116
60.088	20	AGGGCCAAGTCAATTGATGA	60.461	20	213	148	360
59.297	20	TTCAAGACAAATGCAGACGG	59.84	20	275	5	279
59.971	20	GAGCATGTGGGTCAGCAGT	59.844	19	257	109	365
59.897	20	TTCCTCATTCTCCGCAGTTC	60.34	20	189	2461	2649
60.073	20	CCCAAGACCCCAATTTGATT	60.91	20	163	2133	2295
59.967	20	CATCATCATCCTGTTGTCGG	59.918	20	248	143	390
59.938	20	TATCGATGCACAAGATTCGC	59.799	20	237	505	741
60.035	20	CCCTTTCGGGACATCTACAA	59.926	20	102	71	172

59.592	20	TGCTTGCCTCGTTTAATTTG	58.958	20	146	647	792
59.827	20	TTTTCCCCTAAGCACAGCAT	59.708	20	179	113	291
59.907	20	GCAACCGAGAGGTTATCGAC	59.7	20	168	2704	2871
60.173	20	CAAGCACAAATCTCGATTACCA	60.131	22	187	269	455
59.055	21	CAAATTCCATGTGTCGCCTA	59.542	20	262	610	871
59.992	20	AAGAACTGCCAAAAGGCAAG	59.494	20	273	1635	1907
59.95	20	ATGCATTCCTATGCCAGTCC	59.923	20	187	993	1179
59.993	20	TGTAGCCGACCCCAATTTAT	59.297	20	217	1650	1866
60.914	20	TCCCAAAACATCACCTCCTC	59.903	20	110	29	138
62.247	18	ATTCCTATAATGCCCCTCGC	60.267	20	121	28	148
59.942	21	CAAAGAAATCATTCACATTCGG	59.451	22	115	159	273
59.745	20	GGAGGTGTTGGACAGCCTAA	60.111	20	274	115	388
59.743	24	AATGGCCAATGACCAATACC	59.51	20	242	67	308
60.054	20	AGTTGAATTTATGGCGGGTG	59.823	20	270	6	275
59.878	20	TTCTGTTGATGCCAAATCTTGT	59.615	22	200	4164	4363
59.981	20	ATGTAGCCGACCCCAATTTA	59.297	20	278	52	329
59.845	20	TGGTTTCCATTCCTTCCTATTG	60.177	22	197	45	241
59.83	23	ATTTTCCCAGCCCTTCACTT	59.94	20	280	474	753
59.978	20	GCACTGATAACTTCTCCCGC	59.843	20	203	100	302
59.989	20	TGCACGTAGATGTCAGAGGG	59.855	20	231	82	312
59.974	20	TAATCGCCCCTTGCCAAATAG	60.054	20	182	1316	1497
59.964	20	TCCCAATTACGGGAGATTCTT	59.785	21	223	4796	5018
60.042	20	GGGACCTTTCAGTCACCAGA	60.088	20	126	1579	1704
59.72	24	TCGGCATACTAATGATAATGTGA	57.274	23	271	2829	3099
59.874	20	TGGTGCCATCTTCTTCACAA	60.24	20	108	918	1025
59.967	20	GGTTGCACAAAGTAGCTTCACA	60.347	22	212	81	292
60.195	20	TACCAACTTTTGCCTTTCGG	60.103	20	276	1088	1363
59.752	22	ACGTCGTAATCCGAAGTTCC	59.056	20	270	895	1164
59.867	20	TGTGAGAATCCACAATCGGA	60.048	20	241	128	368
59.931	21	ATCTCGAGCATGTGGTGGTT	60.542	20	280	487	766
59.886	21	TGTGGAGCTTGATACGACGA	60.413	20	223	2179	2401
59.375	21	TGAATCCCTATTGTCGAGAGC	59.283	21	192	875	1066
59.931	20	TGAAACTGCGAGTTCAATCA	57.968	20	155	218	372
59.931	20	TGAAACTGCGAGTTCAATCA	57.968	20	155	217	371
59.397	24	TTGAAAAACCCTGGTCCTTG	59.942	20	120	4	123
60.072	20	AAAACCGTAATTTCACCCCC	59.924	20	215	1332	1546
60.081	20	TGAAATCGATCCCGATTATTCT	59.772	22	228	896	1123
59.962	20	CGATGCGAACAAAAGGTTTC	60.617	20	237	1878	2114
59.297	20	TTAATGGCTTGTGAATACGGC	59.978	21	263	14	276
59.297	20	ATATCATTCCCCGAGAGGCT	59.888	20	162	134	295
59.711	20	CAAACTCCACCCAACCACTT	59.861	20	240	2238	2477
60.17	20	AGGTTGCGTACATCTGACCC	59.997	20	183	139	321
60.157	19	TTTCGGCCACCATTGTTATT	60.188	20	279	467	745
59.521	21	ACCACCCTTGACCCTCTTCT	59.968	20	237	2664	2900
60.172	20	AGGTCCATCAATGCCCATAA	60.155	20	196	127	322
60.517	20	AACAAAGGAGACGAGTGCGT	59.914	20	274	121	394
59.824	21	TCGTGGGTAAACACACCAAA	59.857	20	235	386	620
60.05	20	AGGTGGTGTGGTTTCAGGAG	60.002	20	227	413	639
59.855	20	ATGGCGAAAAGTGCAAAATC	60.081	20	124	840	963
60.195	20	TTGTTTAGGGTTTTGGGCTG	59.968	20	269	1127	1395
59.912	20	CACAACAAGGACTTGCATGG	60.152	20	100	56	155
60.15	21	TTTCCAAAACACATTGTTTCAA	58.097	22	186	207	392
59.762	20	CGTGAATTGTCCCACATTGA	60.367	20	235	450	684
60.148	18	TGGGAGTTCCGACCTGTTTA	60.486	20	245	3	247
61.329	20	ACACCACGCATGTTTTTCAA	60.011	20	210	1725	1934
59.55	20	TACATGCTTTTTCAAGCCCC	60.074	20	268	125	392
60.874	20	CTCCTCCGCTTCTTCTTCCT	60.088	20	261	812	1072
60.089	20	TGTGCTCATGATAGCATTTGA	57.874	21	204	334	537

60.384	20	CGCAATCTTGAACAGGGTTT	60.11	20	265	2158	2422
59.818	21	AGTCGACCTTACGTAGCGGA	59.898	20	207	563	769
60.074	20	GCGAATTTCATCCGTTTTTG	60.436	20	141	977	1117
60.118	20	ATCCTGCACCACAACAAACA	60.008	20	205	1492	1696
60.005	21	GAGGCTACTACATTTTGCCCC	59.979	21	192	25	216
59.697	20	CCCAAGTCGGTTTCAACTTT	59.073	20	213	306	518
60.036	20	CTCATCATTGGCTCCCATTT	59.894	20	178	97	274
59.302	23	TCAGTATGTGATCCGCCTTTT	59.583	21	216	0	215
60.15	20	CACGGATTCGAATTGTCTTCT	59.184	21	269	734	1002
60.029	20	GCAACGGAAACAACCTCTTT	59.218	20	169	142	310
59.688	20	CCATTACCAACGGTCTTGCT	59.993	20	180	50	229
60.185	20	TTCCGGCAGACAATGATATG	59.499	20	246	282	527
60.197	20	GGTTGTGTACATCTAACCCCAAA	60.028	23	116	706	821
59.82	20	CCCGCTTCTCTTTCTCTCCT	60.088	20	267	411	677
59.091	22	AGATACGACCTTGCTCGCTC	59.603	20	154	320	473
60.734	20	TGTGCTCTGAATAGGACCGA	59.394	20	228	3523	3750
60.138	20	AGCACACCACAGACACAAGC	59.948	20	144	491	634
59.668	20	TTTTACGCTTAAACTGGCCG	60.251	20	255	355	609
60	20	ATTCTCCCATGCCCATCAC	60.708	19	182	219	400
60.06	20	GCAAGAGATTCTTTGTCGCC	59.962	20	254	1265	1518
60.481	20	CCTTCATAATTCTCGAAAGGTTC	58.342	23	215	24	238
60.012	20	GGAGGAGGAGGTGGTGATTC	60.86	20	222	446	667
59.957	20	TCAAACTCGTGTGAACCCAA	60.128	20	144	345	488
59.833	20	GTGCCGCCAATAAGTTGTCT	60.14	20	245	474	718
59.986	20	CTGAACCAGAAGAGCCGAAG	60.126	20	236	1649	1884
60.041	20	GTCGTTGTTGGTGTGAGTGG	60.047	20	210	704	913
60.118	21	CCACCTTCTCTCCTATCCACC	59.943	21	116	3	118
59.976	20	TTCCCACATGCATTCAGAGA	60.201	20	262	420	681
60.025	20	AGGTTGCGTACATCTGACCC	59.997	20	124	55	178
59.098	23	ATTGTTTTGGCGTTTTCTCG	60.11	20	178	254	431
59.914	20	TGTCTCAGGGAAGAGGCAGT	59.986	20	246	116	361
59.966	20	ACCCAATTGTTGTGGATGCT	60.24	20	219	827	1045
60.27	20	TCCGATGGAGCCTTAAAATG	60.031	20	205	1889	2093
57.39	20	TCCAAATTCGTGTAAGAAATCA	57.314	22	109	266	374
60.214	20	GACGTGGATCGATGTGATTG	59.925	20	139	1432	1570
60.014	20	TCGAAACCGCTCTTCTTCAT	59.955	20	214	791	1004
61.146	20	TTTGGTCACTTTGCACCTAAAA	59.663	22	168	500	667
59.888	20	CCACCACCCACTCCAATACT	59.697	20	224	164	387
59.859	20	TTTTGCGTTTTCGACTTGTG	59.888	20	110	733	842
59.533	20	TCCACCGACTGTACGACTCA	60.309	20	108	0	107
59.993	20	ATTGAAGAGCGATTCCGAGA	59.917	20	107	83	189
59.988	20	AATTTTCGCCATTTGCTTGT	59.592	20	216	410	625
59.823	20	GCATGGACAAGACGGGTAGT	59.997	20	172	1822	1993
60.197	20	ATTGAGGTCAACCCAACGAC	59.827	20	131	901	1031
60.104	20	AATTCGATTGCCTCTGCAAC	60.221	20	280	1328	1607
60.049	20	TGCCATAACGGCTAGTCTCA	59.444	20	250	102	351
59.928	20	TGCATTATATGGCCGTGACA	60.896	20	167	396	562
59.973	20	AGATGCGACTTTTGTTTCCG	60.249	20	262	2169	2430
57.539	21	CCGACGTGGAATCTGAAAAT	59.933	20	123	5	127
59.824	21	CTATTTTTGGGCCTTTTCCC	59.782	20	256	560	815
59.948	20	CGGGAAGACCAAAAAGTCAA	60.081	20	231	48	278
59.904	20	TATTTGCTTAGTCGTGGCCC	60.096	20	157	750	906
60.031	20	TTGCACTTTTTATGGGGGAG	59.931	20	268	47	314
59.935	20	TTAGCTACAGGTGGGGTTGG	59.986	20	258	98	355
60.048	20	AAAGTGGAAGCGAAGGACAA	59.853	20	258	822	1079
59.651	20	TTTTACGCAAATCCGAAGGA	60.56	20	178	544	721
60.103	20	TTCGTTGCAAAACGAGTGAG	60.027	20	211	146	356
59.933	20	CAAACTGCACCTCGTGAGAA	60.025	20	217	3480	3696

58.647	25	CTAATTGGATTCCCTCGGGT	60.145	20	167	1846	2012
60.348	20	AGAGGAGGTGGAGGTGGATT	59.929	20	263	569	831
59.973	20	AAGGCCTTATCCCCTAAGCA	60.055	20	112	24	135
59.585	20	AATTCTTCCTTGGTGGGCTT	59.94	20	209	467	675
59.933	20	GAAAATGCTGGAAATGAGGAA	59.148	21	160	269	428
60.329	20	CACATCTCCGTTGGTGTCAG	60.154	20	239	118	356
59.646	20	GCTCCAAGCACGGATATCAT	60.066	20	273	831	1103
59.967	20	GTGGATGATGGGATTTCTCG	60.281	20	261	1496	1756
60.162	20	TCAAGGGATCAAAAGCCAAC	60.051	20	153	339	491
58.845	20	ACATTTCATTGCCATTTCCA	58.82	20	195	630	824
59.91	20	GGTTTTGATAAATACGATTTGCAT	58.457	24	127	1220	1346
59.903	20	CCTGCCATTCCATGTCTTCT	60.073	20	235	2294	2528
59.964	20	CGGGGATCAAATGAAATCAA	60.64	20	248	555	802
60.21	20	CCTCACAATTCCATGCACAC	59.967	20	131	422	552
59.901	20	GACCCCACATAGTGGGAAAA	59.647	20	236	9812	10047
59.685	20	TGTAGCCGACCCCAATTTAT	59.297	20	181	341	521
59.959	20	GGAGAATGGGTTGCTCTGAA	60.195	20	207	783	989
58.933	20	AAACCAAGACCCCAATTTGA	59.264	20	107	12	118
58.586	21	AGTTCATGTGGTTGTTGGCA	60.008	20	100	14	113
59.953	20	TGCCAAAGTCTCCCATTTTC	60.051	20	239	3792	4030
60.022	20	TGAGGAGCAACCATTACCAA	59.123	20	234	116	349
60.11	20	CCCCGTCATGTAAAGTTTCG	60.357	20	188	93	280
59.971	20	CAGAGCGCACTCGAAGAGTA	59.49	20	110	386	495
60.12	20	AACCTACCCTCCCCATCATC	60.015	20	110	11	120
60.344	20	GGAGTGGGAGAGAGATGCAG	59.945	20	275	129	403
59.042	21	TGCCTCTTGGCATCTTTCTT	59.955	20	270	1884	2153
60.318	21	TGAGCATGCACAACTAAAAAGC	60.437	22	100	554	653
59.697	20	AGGTTGCGTACATCTGACCC	59.997	20	174	7	180
60.326	20	GATGATCCCCCGATGTAGAA	59.709	20	249	174	422
58.224	22	ACATGCAATGTTGGGCACTA	59.995	20	273	767	1039
59.794	20	CCCCGAACAATTTTTCCTTT	60.157	20	236	150	385
59.62	20	ATGTCCGCCTTATGAGGTTC	59.009	20	279	1143	1421
59.997	20	ATGGGTTGGTGGTTTGGATA	59.91	20	181	118	298
59.75	20	AGGTTGCGTACATCTGACCC	59.997	20	125	32	156
58.952	22	CACCTTAAGAGCCATCGTCA	58.874	20	217	132	348
59.195	20	TTAGTTCCAAATTGTGCCCT	57.217	20	249	2472	2720
60.137	22	GGAGGGTGTTGAGTTTGAGG	59.549	20	211	665	875
59.773	20	AAAAGCGTTGGAAAGCTGAA	59.996	20	182	85	266
60.78	20	CCACCATGGAAAGTGCTTGT	60.954	20	272	74	345
60.218	20	GCGTCATCTCCCACTCTCTC	59.952	20	117	249	365
60.17	20	TGGATATCATTGTCGCTGCT	59.256	20	206	133	338
60.17	20	TGGATATCATTGTCGCTGCT	59.256	20	209	133	341
59.993	20	TCCTTTTCTTCATCCTCATCC	58.174	21	184	65	248
61.006	20	AGTCGACGGTCAATTTCCAG	60.111	20	108	8	115
59.517	20	AGAGATTGCCAGATAGGCGA	59.939	20	271	625	895
59.297	20	CACGACAACCCAACACAAAC	59.897	20	212	9	220
60.131	22	TGTTTCATCTGCTTGTTCGG	59.84	20	121	173	293
59.847	20	TCGAAAATGGTATTCGAGCC	60.038	20	223	301	523
60.3	20	ATTTCGGTTGACCTCACCAC	59.827	20	225	285	509
59.935	20	AGAGGTATTTGCAGCGCAGT	60.044	20	210	1313	1522
60.025	20	ATTACCTTCTCTCGCCGGAA	61.08	20	224	90	313
60.118	22	TACATTAGCCGTAAACCGGG	59.847	20	272	51	322
58.946	22	TTGAAAAGTTTGGATAATTCACGA	59.885	24	268	26	293
59.905	20	CGGGACTGTTTCCTGAGTTC	59.697	20	123	1042	1164
59.729	23	ATCATTCTCGGAGTTGAGCG	60.362	20	209	1055	1263
59.997	20	ATTCGAAGCATAGATGCCCA	60.574	20	219	636	854
59.891	23	TTTGGGAGGTTGGATGGATA	60.126	20	160	0	159
60.117	20	GGAGTCTTCTGCATTTGGTTG	59.726	21	113	938	1050

58.297	25	AGAAAAAGGGAGCATGAGCA	59.955	20	181	2	182
58.475	20	CCCAAGACCCCAATTTGATT	60.91	20	194	2816	3009
60.088	20	TCCTTGTTCGATTCCAAACC	59.91	20	181	307	487
59.551	20	GGGACAAGCTTCATTTGCAT	60.081	20	228	927	1154
60.036	20	TATACACCATCATGACCGCC	59.23	20	144	868	1011
61.33	20	TGGATCTGCAACTTCAGCAG	60.136	20	137	16	152
60.185	21	GATACAGAGTCGGACGATGACA	60.142	22	278	261	538
59.927	20	AGATTGCGTAAACCTGACCC	59.056	20	189	722	910
59.893	20	CCCAAGACCCCAATTTGATT	60.91	20	110	1206	1315
59.67	20	TTGGATAGTAGGATATGATAAGG	58.812	27	246	175	420
60.488	20	ACGTGGCCAAAACGATTCT	60.511	19	273	62	334
58.741	20	GGAGACCCCTTCGAAAAATC	59.881	20	165	115	279
59.297	20	TAAGGTTAGCAGTTTGGCCG	60.257	20	255	206	460
59.993	20	TGAAGAGGAGGGGAATGATG	60.003	20	265	128	392
59.984	20	GAATCCGCCACATTGCTTAC	60.478	20	134	127	260
60.195	20	TGTAGAACCTTCCAATCCGC	60.074	20	266	186	451
58.991	20	GCTTACCGGCGACTATCTCA	60.374	20	224	483	706
60.91	20	GCCATGAAATTCCCATCACT	59.756	20	248	8	255
60.301	20	TGTGCACCGACAGTTTTTGT	60.199	20	271	642	912
59.762	20	CCAATTCGAAGCCCAAATTA	59.901	20	200	256	455
59.934	20	ACCCAGAAAAACGAAACACG	60.008	20	158	147	304
59.934	20	ATACGCGAGACCGTGTAAGG	60.154	20	164	306	469
59.919	20	TAACAATGCACCCGAGATGA	60.073	20	217	26	242
59.95	20	TCACTTTCCTTTTTCGGACG	60.22	20	241	8	248
60.048	21	CAAACCAAGGCAAAGAGAGG	59.846	20	241	295	535
59.697	20	CGAGGTGATTTGGACCAGTT	59.966	20	112	1797	1908
60.372	20	TCATAACAGTCTTCGACTAGCTTC	57.073	24	262	98	359
59.297	20	TGATGTATGCCTGTGGGAAG	59.522	20	162	8	169
59.141	24	TTGTGTGGAAAAGGGGAAAG	59.942	20	280	59	338
60.162	20	GGTGACCAAAGAGGTGGGTA	59.82	20	243	229	471
60.692	22	AATTGTTATCTCAGGCTACGCT	57.267	22	266	441	706
60.133	21	AGTTTAAACCCTCCCAACCC	59.191	20	218	87	304
59.957	20	CGAGCAAACTAGTCCGTTTCTT	59.948	22	227	375	601
60.124	22	TCACCAAAGGGACACACAAA	59.976	20	243	72	314
59.997	20	CCTAACCTGCGTTGGAACAT	59.993	20	171	144	314
59.957	21	TTTTGAGCAGGAATGTTCTTCA	59.861	22	252	70	321
59.838	20	TCCTCAATAATCAAACCTCGG	59.03	21	214	947	1160
58.725	25	TGAATTTGCGACATTATTCATTG	59.854	23	256	12	267
59.933	20	CAAGTTCACATTGAAATCGACA	58.675	22	270	231	500
59.767	20	TACAGTTGCCGAAAAATGCC	60.999	20	124	16	139
57.104	26	CGATAGGTCCTCGATTCACC	59.508	20	223	298	520
57.289	20	TTTGTGTTAATTATGTTTCAGTTTT	58.306	27	250	1744	1993
59.959	20	ATTGACTCCCACCAGGAGTG	59.962	20	144	461	604
59.757	20	TCCCACAAAACCAAACACAA	59.834	20	262	1076	1337
59.873	20	TTTCATCAAAGCCTGAAGCA	59.542	20	266	152	417
60.192	20	CTCGGGATCAATGACATTCC	60.281	20	277	702	978
60.133	20	GTTCTTGCTTCTCACCCTGC	59.997	20	163	1406	1568
59.992	20	TGGGTTCATTATCAAGAATTGC	58.946	22	250	6	255
59.94	20	GGGTTTTAGAGGGGAGTTGG	59.799	20	153	763	915
60.352	20	AACTGGATTGACTTCACGGC	60.119	20	271	366	636
60.464	20	AGCATGTGACATTTCCCGTT	60.384	20	277	1109	1385
59.693	22	GAAAATGAGGTGGGATGTCG	60.317	20	170	290	459
59.991	20	TCTCTGAATCCGGCCTAGAA	59.91	20	218	2444	2661
60.176	20	CTTCATATTGGGGCCCATC	60.103	19	251	470	720
59.901	20	TGCCCTAATCACACATTTCCT	59.443	21	172	237	408
60.12	20	AACAACATAAGGGAAGGGGG	60.046	20	229	1455	1683
60.152	20	AAGACCGTGGCGAAAATATG	59.96	20	108	1398	1505
59.993	20	GTGGGACCTTGCTACTGAGC	59.874	20	261	1582	1842

59.901	20	TTGGGAGAGGGAGAGAGACA	59.913	20	132	98	229
59.933	20	GTTTTCTCCCAACAGGACCA	59.943	20	248	3494	3741
59.592	24	ATTAAAATGGTGCGAATGGG	59.66	20	263	1	263
59.344	20	CGAAATCGCGGTATCTTGTT	60.096	20	222	290	511
59.982	20	ACATACAGGGGTGAAAACCG	59.711	20	175	3656	3830
59.712	20	TCAGCCTTCGCCACTACTCT	60.156	20	266	6780	7045
59.805	20	GGAACCATTGAGAGGAGCAG	59.803	20	238	459	696
57.327	21	CAAATTATTTTCAACCCTCATACC	60.324	25	244	1439	1682
59.971	20	GCAGTTGTTGCGGATAGTGA	59.871	20	271	86	356
60.408	20	TGCGTGTGTAACCGAGAGAG	60.049	20	278	406	683
59.831	20	TCCAAGGAACTTTTCTCCCA	59.641	20	271	2615	2885
60.02	20	TACCCTAGCCCTACCGGAAC	60.332	20	249	553	801
60.008	20	CTCTCCCACTATTCCCACCA	59.92	20	139	210	348
60.481	20	TTTGCCAAGAGACACGACAC	59.88	20	200	1931	2130
59.892	20	CCACCTCACGTAAAGCACAA	59.758	20	246	802	1047
58.595	21	CGAATTGAATTAATTTTATGAAGC	59.807	26	212	99	310
60.066	20	GCCCCACCAGAAAAAGGATA	61.173	20	104	20	123
59.887	20	ATTAAGGGGTTGAGGAGGGA	59.761	20	179	898	1076
60.081	20	ATGAAGCTGAACTCGCTGCT	60.307	20	205	538	742
59.42	20	ACCCGTTAACGACACAAACC	59.757	20	155	24	178
59.992	20	GAAACACAGCGGGAATCAAT	59.939	20	266	1427	1692
59.182	22	TCGTTGATGATGCAAAGAATG	59.679	21	252	180	431
59.716	23	GAACCAAAACTTGCTGACCC	59.574	20	100	50	149
58.754	23	CCAAGTCCCCCTCATACAAA	59.784	20	166	0	165
60.184	20	GACATCTGGCCCATTTTCAC	60.326	20	270	150	419
59.688	20	GGTGAAAGACCCGAATTCAA	59.91	20	270	74	343
59.563	20	AGGTTGCGTACATCTGACCC	59.997	20	115	46	160
59.819	20	GGGCTTCGTTTGATGACTGT	60.119	20	214	62	275
60.053	20	ACACGGGTGGAAGTGAGAGT	59.604	20	194	435	628
59.982	20	CATCCACAGTGAAGACCACG	60.154	20	262	15	276
59.277	20	CTACTCGCCCTCTCCATCAG	59.966	20	248	1219	1466
60.074	20	ACACGACGGACGTAGAGCTT	59.937	20	161	72	232
59.751	20	TGTGCTATAATGGACTACATCAAA	57.873	25	182	1556	1737
59.853	20	CTTGGGAGTTGCTTCGTAGG	59.869	20	173	239	411
59.997	20	TTGGGTCCTATCCAGTTTGG	59.784	20	151	3843	3993
60.111	20	GTAATCCCAAACCGAACACG	60.227	20	153	284	436
58.822	22	TGCCATACAACACCACTTGC	60.584	20	144	348	491
59.682	20	GGAGATTCTCTTGGGCACTG	59.803	20	251	154	404
60.012	20	TAGATGCACCGGTTAGGAGG	60.088	20	147	112	258
60.173	20	TTGACCGTACAAGATTGCGA	60.257	20	219	1016	1234
59.941	20	TCTACCACTGCACCACGAGA	60.463	20	260	102	361
59.641	20	CTGCAAAATGAGCAAAACCA	59.849	20	257	31	287
59.967	20	TCCGGTCAAAAACAGAAACC	59.948	20	148	378	525
60.361	20	CCTTCTTTAGAGGTTGGGGTG	59.977	21	242	158	399
59.694	20	TTGGTATCTTCCTTGCCGTC	60.074	20	145	28	172
60.067	20	CTTTGTGCGACCACTAAGCA	60.05	20	184	2541	2724
60.991	20	TCGATCCTTTATGGATTGGAT	58.33	21	277	872	1148
59.297	20	CAACTTGACATAGCATTCCCAA	59.996	22	112	2	113
60.214	20	TCCTCTCACGCATTCTCTCA	59.656	20	137	413	549
58.158	20	CCCAAGACCCCAATTTGATT	60.91	20	195	1	195
59.67	23	AACCAATTGACAATGAGAGGAGA	59.99	23	251	95	345
59.703	20	AAGAGTGCAGCCATCGTACA	59.47	20	184	185	368
59.685	20	TGCCCTAGATCTCACACACG	59.855	20	211	450	660
58.746	20	TGGTGATATTATTGTGATTCCCC	59.801	23	266	368	633
60.074	20	TATGGATGCACCGGTTATGA	59.769	20	247	23	269
59.975	20	TTTTCATTTTTACTTACGCGTCT	57.35	23	214	166	379
59.985	20	GACACGAACCCCTATCCAGA	59.927	20	225	306	530
59.182	20	TGACGCACACAAACACTTCA	59.912	20	274	89	362

59.543	20	TCCTTGAAATGCCGACTTCT	59.813	20	192	1320	1511
60.386	20	AGAGACGGTGACGTATTGCC	60.142	20	137	588	724
59.722	20	TGGGTTTTATTTTTGCCGAG	59.937	20	277	1958	2234
60.111	20	TCTCCAAAATCGCAAACCTC	60.192	20	143	403	545
59.955	20	GGACAAGGGTTCGAGTCTCA	60.238	20	113	15	127
59.934	20	TCCCTAGAAGCGCACGAGTA	61.06	20	169	277	445
59.846	20	CAGCAGTCTGGATCTCCCTC	59.945	20	252	4	255
59.823	20	TAAAAATGAACGAGTCGCCC	60.074	20	252	1151	1402
60.601	20	TGACCACCTTTCTTTCCACC	59.943	20	139	16	154
60.187	20	TTCCTATTTTTCAGAGTTGAACCA	59.203	24	249	186	434
59.989	20	TGGGTTTGGAGTGAAAACAA	58.995	20	272	1781	2052
59.916	20	CACCTTGAATTGACTGCCATT	59.985	21	162	483	644
59.206	20	TAACCCTAACCCTCGCCTTT	59.96	20	265	51	315
59.955	20	AGGCACGGTTCATGTGTGTA	60.032	20	252	420	671
57.717	21	TGCCAGAACACATAAATTTTGAA	59.524	23	220	212	431
59.846	20	TTAATCTGCGTCTCCAGGCT	59.978	20	143	335	477
60.014	20	AACAAACCCATCACTCCGAC	59.827	20	257	1434	1690
59.405	20	TCTCATTCTTACGAGTGCCG	59.024	20	217	186	402
62.174	18	GAGGGTTTGTAGGTGCGAAG	59.734	20	133	0	132
59.943	20	CTCTTGGTTCTGGTGGTGGT	60.002	20	250	730	979
60.11	20	TTGACGCGCTTGAAGTAGTG	60.195	20	143	131	273
59.234	21	CCTTTGAACAAAGAGTGGGG	59.563	20	260	65	324
59.632	20	TGTAGCCGACCCCAATTTAT	59.297	20	177	238	414
60.017	20	GGAGGCATAAAAACCCCAAT	60.02	20	252	69	320
59.88	20	TATATGCAGGTGTGCCTTGC	59.718	20	253	1881	2133
60.326	20	GGTGCAAGAATTTCCCAAAA	59.916	20	248	4	251
59.984	20	CACAGGGCTTAGGAATGGAA	60.066	20	208	410	617
60.025	21	ATAAGGGAAGATGCAGGCAG	59.292	20	201	504	704
60.576	21	TGGCAATGATAAATGGGGTT	60.016	20	136	5	140
60.502	20	ATGCGCTGCTAGGTTCAAAT	59.873	20	267	350	616
59.938	20	GAGTCATCCCCAACCTTTGA	59.903	20	280	800	1079
60.005	20	GGAGTCATCCACCTCAGGAA	60.048	20	253	396	648
60.008	20	TGTAGCCGACCCCAATTTAT	59.297	20	187	2349	2535
60.508	20	TTCACGCCTAATTAAACCATTG	59.044	22	267	317	583
60.052	20	ATGAGCAGGGTGGAGAGAGA	59.945	20	162	764	925
57.394	27	GCTCAGGTTGTGCACGATAA	59.871	20	105	12	116
60.149	20	CATTATCTAATGATTAACAGTTCC	58.894	27	159	296	454
60.073	20	TCAATGATCCAATCCCCACT	60.135	20	174	1047	1220
59.997	20	TCTGTGTTGTGGGTTGCAGT	60.203	20	193	1608	1800
59.656	26	AGGGTCCCTCCTTATTGACA	58.446	20	201	156	356
60.089	26	ATTTTGGTCCAGTGGCAGTC	59.973	20	221	211	431
59.971	20	GGTCGAGTAGAAGAACCCCC	59.935	20	193	310	502
59.803	20	CTAACGCAAACCAGCAATCA	59.872	20	278	3473	3750
59.596	20	TGTAGCCGACCCCAATTTAT	59.297	20	219	729	947
60.221	22	GATTCTTGAAAATCGGCAGC	59.791	20	237	1446	1682
59.7	20	AGTTTCGACATCGCATCTGG	61.208	20	279	407	685
60.173	20	TGGGGATTGAACCCAGATAA	60.126	20	129	602	730
60.074	20	GGTGGCTGTTATCGAAGGC	60.619	19	245	344	588
59.801	20	AGGTACTGCCCTCGAGGATT	60.096	20	202	227	428
59.817	20	GAGTTGGCTCACGATACGGT	60.142	20	246	66	311
59.984	20	GGAACAGAAGAAGCGGATCA	60.34	20	258	417	674
59.297	20	TGCAGCTCCTCAAAAAGGTC	60.517	20	227	6	232
59.773	20	TGGGGGTGCATTTAATGTTT	60.053	20	176	1689	1864
59.873	20	CAGAGCGCACTCGAAGAGTA	59.49	20	220	821	1040
60.339	20	TCAAAAGAATAACGTGGGGTG	59.847	21	275	704	978
59.969	21	GTTAGCCGACCCCAATTTTT	60.184	20	111	34	144
60.163	21	GCAATAAATTTCTATGTTGCTCCA	59.562	24	207	695	901
60.133	21	AGTTTAAACCCTCCCAACCC	59.191	20	239	99	337

59.971	20	GGGACAGAGAAAGAATGCCA	60.195	20	273	0	272
60.181	20	TGTAGCCGACCCCAATTTAT	59.297	20	264	148	411
60.116	21	TCACACGTGACAATGAAAAGG	59.6	21	189	14	202
58.976	24	CTCCCCAATTCATGACCCTA	59.744	20	237	151	387
58.956	20	GTGGCTTGCAGGAAAGAGTC	59.997	20	242	660	901
61.826	18	AGGCCCCCTTGTCAAATACT	59.827	20	199	2	200
60.057	23	TGCTCAAATATTTCAAAAAGCAA	58.963	23	276	2	277
60.019	20	CCTCCCGAAAGAGGAGACTT	59.811	20	263	483	745
59.959	20	AGCGATTCTCTTCGAGCAAG	59.859	20	152	136	287
60.11	20	TCTCCCCAATTCCTCTTCCT	60.008	20	100	31	130
60.073	20	GGCAAGATCCACAGCCTTAG	59.836	20	279	164	442
59.788	24	AAAAAGCCACGACCTCTTCA	59.853	20	267	873	1139
60.364	20	TCATCCCTTCCAACTTCTGC	60.195	20	224	938	1161
60.429	19	CAACCTGTTGGGAGATTTCG	60.486	20	172	31	202
59.807	20	GAACCATTGAACTGCCGATT	59.939	20	256	145	400
59.75	21	TCGCATTCTACTCCATTTTCC	59.172	21	268	112	379
59.17	20	ATGGCAGCATTCATGTAGCA	60.251	20	235	84	318
60.032	21	AAGCCGATTTGTAAATTTGAGG	59.52	22	277	345	621
60.91	20	GTTCAAAATGGCCTTACCGA	59.938	20	199	4	202
59.96	20	TGCCAAAAGGAAAGATCACC	60.051	20	101	432	532
58.768	21	CCCAATGAAAATCTGTCGGT	59.79	20	173	32	204
60.584	20	TTTGATTGGGAATAATTGGG	57.289	20	136	1686	1821
59.476	21	AAAACAGACCCACCAAGAACA	59.482	21	276	6	281
59.485	20	TGTAGCCGACCCCAATTTAT	59.297	20	122	615	736
59.966	20	TTCCATTATTGCTTCCACCC	59.762	20	210	1498	1707
59.82	20	GGGAGGTTTCGTCACACAGT	60.009	20	119	9	127
59.903	20	GCAAAGGTTTTCCGATCAAA	60.053	20	219	77	295
59.746	20	TTCTGGTTTCAGTCGCTGTG	60.025	20	228	872	1099
58.148	21	GTAGAGGTGTCAAAACGGGC	59.598	20	279	91	369
59.931	20	GAATTTGAAACCGAACCGAA	59.916	20	186	352	537
59.763	24	GGCAAACCACCCTTTTCTTT	60.332	20	175	298	472
59.763	24	GGCAAACCACCCTTTTCTTT	60.332	20	205	299	503
60.207	26	ATAAGCAGCAGGGCATGAAT	59.696	20	215	376	590
59.933	20	CGACGAAATCGATGACTGTG	60.263	20	255	503	757
59.953	20	GATGCTCGAAGCGACAAAA	60.088	19	161	31	191
57.789	22	TTTGGAAATTTTTCAGAACACG	59.14	22	167	0	166
59.186	22	GGCGTGTGGATGATTTCTTT	59.939	20	268	840	1107
59.993	20	TCGAGTCCACTGTGCAAGAT	59.42	20	162	1118	1279
59.398	23	CTTGAAGGGACCCGTGAGTA	60.103	20	249	1248	1496
59.062	20	TGGCCTCTTCAGAAGGAGAA	60.065	20	145	109	253
60.186	20	AATCTCGCTCACGACTCGAT	59.981	20	189	12	200
59.993	20	GGTCATCTCTCCCAAGTCAAA	59.126	21	257	160	416
59.535	20	CGCTGTCTGTCCTCCTTCTC	60.135	20	277	85	361
60.517	20	TACCTACAACGTGAAGGCCC	59.993	20	246	18	263
59.938	20	TTCTCAGCCTCAGCTTCTGG	60.812	20	187	816	1002
59.322	23	GCTCAAATCGGAATTCAAACA	60.067	21	167	8	174
59.6	21	CGACTGGGCCTATCCTATCA	60.051	20	273	570	842
58.902	22	ATGGGCCCAACACCAGATA	61.143	19	211	661	871
60.111	20	AAAATCCTGTGTAGCAGGGC	59.198	20	268	500	767
58.646	20	TTTCCAAGGTTTGGGTTTCA	60.314	20	235	428	662
59.002	20	TTTGATGCGCTCTAGTTGGA	59.566	20	222	104	325
60.91	20	CCCAAGACCCCAATTTGATT	60.91	20	204	1	204
59.205	22	AATCAACGAAATGAAACCGC	59.945	20	165	270	434
60.02	20	ATCCGAGCAGCCTAATGAGA	59.939	20	217	581	797
59.978	20	TCATTGCCCGAATAGAGTCC	60.036	20	221	119	339
59.89	20	TGGGAATATCCATTCGTTCC	59.581	20	147	257	403
59.935	19	TTTCATTTGATATTTCCAGAGACC	58.566	24	262	300	561
59.881	20	GGGAGGCTATTTTGGAGAGG	60.032	20	168	828	995

59.773	20	GCCTAAGAATGACTGAAACGG	58.847	21	202	273	474
60.073	20	AAATTGGGCACCAGAATCAG	59.933	20	205	187	391
60.014	20	CTGGACAGACAACTGGCAAA	59.873	20	273	2267	2539
59.314	21	ATGTAGCCGACCCCAATTTA	59.297	20	211	2321	2531
59.452	20	CCCAAGACCCCAATTTGATT	60.91	20	181	1060	1240
57.456	25	GAAAAATACAGCTAATCGGTCCA	59.533	23	239	283	521
59.993	20	GTGCAGCAATACCAAACCCT	60	20	182	173	354
59.839	20	CATGTCAACCACCCTTGTCA	60.416	20	203	803	1005
59.134	22	ACGTGAGTTGGAGGAGTTGG	60.151	20	267	2146	2412
60.232	20	TGTTGGGCCTTTGACCTTAG	60.103	20	164	509	672
59.366	21	TTCTTCAGCTCCAAGTCGGT	59.989	20	244	61	304
59.312	21	GCTTTAGTGGGACATCCGAG	59.694	20	254	1882	2135
59.982	20	TACAATGGCCTGAGCAAGTG	59.864	20	175	565	739
60.074	20	CTCTTCGAGCGAGTTCAAGC	60.419	20	151	258	408
59.911	20	TTCACCCCGATTTCTTTTTG	59.91	20	266	534	799
60.291	20	AGCTTTGCCGGTGTCATAAT	59.597	20	273	2225	2497
59.829	20	CGAGAAGTACCGGATGGAAA	60.066	20	190	730	919
59.993	20	ACGACCTTGCTCATTGCTTT	59.882	20	277	297	573
59.288	20	GCCGTTATCACTCAGTTTTCG	59.761	21	263	454	716
60.192	20	TTCTACATGCCGGAATTCGT	60.469	20	170	23	192
59.94	20	CACCGCAAATATACGAAGCA	59.725	20	160	861	1020
60.393	20	CCCGGAGCTGATCTCAAGTA	60.353	20	226	525	750
60.088	20	ATGCTGCATGCACTATTTGG	59.718	20	111	781	891
60.132	20	CGGAAACTGACATCCACCTT	59.966	20	221	90	310
60.269	20	AGTTCGAGCAGGAAATGTGG	60.255	20	276	1396	1671
60.238	20	GGGACAGGCTCTTGTGTTGT	60.159	20	155	21	175
60.012	20	GATCGGCAGTGGCATTTT	59.61	18	117	498	614
60.612	20	AAAAGAACGTGCAAGGATGC	60.257	20	216	1283	1498
59.682	20	CCTAGCTGTGCACACCACAT	59.776	20	271	3603	3873
59.817	20	CGGAACAACCTATCAGGCAT	59.955	20	260	3343	3602
59.013	22	TCTCTTGCAGCACTATGGGA	59.547	20	148	12	159
60.125	24	AAAACGGTTGATTGCAGAGG	60.11	20	262	42	303
60.055	20	TTCATATTCCTGGCGAATCC	59.862	20	233	2100	2332
59.18	23	TTGTTTTAATGCATCGGCTG	59.702	20	157	1072	1228
59.844	20	GGTGGTGCTCCAAATCCTAA	59.933	20	221	1725	1945
59.297	20	TTGGGGACAAAGCAAAATTC	59.916	20	137	16	152
59.993	20	GTTTCGGAGGTGTTGGACAG	60.545	20	275	95	369
60.048	20	CAGAAAGGGGCAGATTCTTG	59.807	20	129	3316	3444
60.23	20	ATGTCCCACCAATTTGTCCT	59.116	20	122	81	202
59.95	20	TTCCCTCATTTGAACAAAACG	59.961	21	256	1106	1361
60.184	20	CAAAATGAAGCAGACTGCCA	59.988	20	208	251	458
60.489	20	ACATCAGATCTCCGTCAGCA	59.372	20	189	18	206
57.746	22	TGATCTTGAAACCGTGATGG	59.496	20	263	3414	3676
59.894	20	AAATGGACCCAACGTTGAAA	60.206	20	236	550	785
60.056	20	TCCCTAATGCAAGGATGGAC	59.894	20	218	400	617
58.594	20	CCTTGCTGTGCATTTAACCA	59.729	20	225	81	305
59.997	21	TACATGCAACCTCCTGCTTC	58.877	20	242	1433	1674
59.247	20	TGAGACGAGAGAGGGGGTAA	59.797	20	260	286	545
59.823	20	TGGTTTTGGCAAACTGTGAG	59.734	20	240	320	559
60.406	20	TTGCAAGAAAACTGTCCCGT	60.668	20	232	72	303
59.82	20	CCCAAGACCCCAATTTGATT	60.91	20	149	65	213
60.006	20	CCGCAGAGGCGATCTCTA	60.201	18	165	218	382
59.731	20	AATGGGGTAGCCTGGAATTT	59.666	20	214	385	598
60.088	20	TGATGGAACCGGGAAGTTAG	59.926	20	259	107	365
59.809	21	CCAACCGAACTAGCAGAAAA	58.027	20	280	12	291
61.176	20	CCATTGCTTAAGCTCCCTTG	59.839	20	203	260	462
59.874	20	AAATTAAAATTGGGAGCGGG	60.142	20	275	45	319
59.199	20	CAACCATGTCAGCCGTTAAA	59.585	20	118	178	295

59.657	20	CATCGCATTCAATTACCCAA	59.377	20	161	436	596
60.014	20	TCCAATTTATTGGGATTAAGGC	59.217	22	280	791	1070
60.056	20	CATATCCATGGGTACGGAGG	60.029	20	222	909	1130
60.075	20	CGTTGCAGAAGTTTGCTTGA	60.172	20	103	111	213
60.599	20	GGTGGTATGGTGTGGAGGAC	60.096	20	168	9	176
60.051	20	AAGTGGTAGGCGGATTCCTT	59.962	20	247	684	930
58.041	21	TGATTGGTTAGAGAGTATGTGAA	59.971	27	131	705	835
60.144	20	TAATGGGGGTTTGAAGTTGG	59.657	20	116	200	315
59.7	20	TGATCGGGTTCATTCTGGTT	60.317	20	152	324	475
60.555	20	GATCACAACCAGTAAATATTGTA	58.64	26	221	624	844
60.195	20	CCAAACACCACAAATTGCAG	60.004	20	198	972	1169
59.926	20	TTCTTGCTTTTTGCCATGTG	59.849	20	172	794	965
59.943	20	AGAGATGCGCTGGATAAGGA	59.939	20	167	84	250
60.514	23	AGGCTCGAGATGTTTCAACG	60.397	20	274	81	354
57.751	23	TATGCATGGATGGTGTACCG	60.22	20	260	1060	1319
59.853	20	AAACGATCGCCTACGAGAAA	59.845	20	210	49	258
59.742	20	CAATTGCAAGGAATTTCCCA	60.807	20	231	253	483
59.803	20	TGTTTAAAAGTTTCCTGCACAA	57.571	22	239	889	1127
59.992	20	GCATCTTCTTTTGGGGATCA	60.014	20	122	1114	1235
59.945	21	GGGACGAATAGGAGAGGGAG	60.03	20	199	10	208
60.688	20	AGGCAAAACCCATGAAACAG	59.971	20	175	441	615
59.094	21	CGCCGATCCCTACTTTTCTC	61.08	20	240	664	903
59.648	20	GACCAAGAACCACTGCGTTT	60.156	20	280	778	1057
60.468	20	AAAAGTACGTGGGTCGTTGC	60.037	20	220	372	591
60.156	20	TTCAAATTAGCAACAAAAATGAA	58.007	24	252	297	548
59.79	20	AGTTGTCTGGTGAAAACCGC	60.156	20	251	811	1061
59.996	20	AGAACTCCGATAATCCGCCT	60.06	20	272	1376	1647
60.103	20	AAGGATGCCAATGCCATAAC	59.791	20	244	126	369
60.501	20	TCCTCTTCTGCCATTTCAGC	60.483	20	202	1415	1616
60.299	20	TGTGGCAGATGATCAAAGGA	60.201	20	207	3747	3953
58.054	25	CTCAGGGAGTTCCATGACTCT	58.327	21	101	595	695
60.405	20	AAAAAGCGACGAAGAACGAA	59.996	20	269	229	497
58.365	23	AAAATTTTCATCAGTTATTTGCTC	58.388	25	177	28	204
59.56	21	CCTTACATAAGGGCGGGAAT	60.164	20	266	178	443
58.188	22	CGTTAACCGGTACGAGCAGT	60.19	20	206	11	216
60.746	20	CTTCTCCCCGTAGAAGCCAC	61.142	20	278	81	358
59.95	20	AAACACCTCCTCCCCATACC	60.052	20	205	602	806
59.545	20	ACTTGTTGCTTGGGAGCTTG	60.431	20	212	307	518
60.008	20	AGTAACGTGTAGGCCGCATC	60.162	20	226	1158	1383
60.05	20	TGCATGCTCATAATGCCATA	58.679	20	101	846	946
59.717	20	GATGGGGACACTTCCAGAGA	60.048	20	221	364	584
60.365	20	ACCCTTGCGAATCTGAAAGA	59.813	20	222	242	463
60.173	20	TGCTTGTTTCTGCTTTCAGG	59.195	20	271	64	334
60.029	20	ACTTCCGAGTTTTTGGCAGA	59.853	20	267	443	709
60.067	20	CGCAATGTACTTTGGGTCG	60.119	19	171	347	517
60.91	20	TGAGACAGGTTCTCGTCGAA	59.545	20	176	6	181
59.701	20	AGGTTCGCTACTGGTCATGG	60.134	20	256	418	673
58.465	22	TGAAGTTGAGGGATGCATTAAA	59.586	22	139	9	147
60.147	21	AGGTCAGAGGTGACGGTTTG	60.151	20	245	797	1041
59.907	20	AAAAATTTAGGGCGTTACGAA	57.906	21	276	1003	1278
60.014	20	TTCAAACATTCTCCTTCCAAAA	58.716	22	122	24	145
59.964	20	ACATGTCTTGCCTCAAACCC	59.973	20	206	163	368
59.763	24	AATCCTTGCACGAACGAATC	60.081	20	250	2683	2932
59.471	20	GACAAAAATTTGGCGATGCT	60.081	20	274	57	330
60.035	20	CTCCCATAACTCCAACCCCT	60.183	20	210	490	699
60.134	20	GGGTCGTTCAGCCAATCTAA	60.074	20	260	2090	2349
59.976	20	TGTAGCCGACCCCAATTTAT	59.297	20	260	334	593
59.105	20	ACGGTGACATTCTCTTTGGC	60.119	20	272	374	645

59.831	20	TTCCTGACGCTGAGGAAGTT	59.989	20	197	341	537
60.517	20	CAATTGGAGGTTTGTGGTGTT	59.743	21	222	1	222
59.67	20	TCCGAATATTCATTGCCCTC	59.862	20	278	173	450
59.882	20	ACATCGAATTCTTTGGCGAG	60.214	20	241	1238	1478
59.94	20	CCCACTATTTCCCCTGAACA	59.784	20	266	421	686
60.074	20	CCCAAGACCCCAATTTGATT	60.91	20	171	4969	5139
60.498	19	TCGCTAACATGGTTCGTTTTT	59.639	21	277	1222	1498
60.492	20	CTTGCTCCCTTTGTTTCCAA	60.22	20	170	858	1027
59.926	20	ATGTAGCCGACCCCAATTTA	59.297	20	191	268	458
59.942	20	GATATGCGTACTTATCCTTACCG	57.031	23	252	510	761
59.697	20	AAGACCTAAGCCACAAGGCA	59.875	20	168	258	425
60.059	20	TTCGCCTTCAATCGTACTCC	60.214	20	211	144	354
60.326	20	TTGTCAACCCAACGCTACAC	59.615	20	232	4809	5040
59.673	20	ATCCACCCTAGCATGTGGTC	59.81	20	176	370	545
59.733	20	TTTTCCCATTTTGGTGCAAT	60.167	20	141	396	536
60.134	20	CCCTCCAACATTCGTCTTCA	61.034	20	237	923	1159
60.678	20	TCATCCAAGTTCGTGTGAAATC	59.978	22	219	19	237
60.188	20	TCCAAAATCTCGGCTTCAAT	59.645	20	208	893	1100
60.066	20	TTTTCATGGCCCTTTGTCTT	59.546	20	267	175	441
59.297	20	GAGCTCGTTGAAGCTGGAAG	60.277	20	196	6	201
59.009	25	TTCTGATCCTTTGCATTTAGCA	59.853	22	280	478	757
58.281	20	GGTTGCCTGCACCAAGTAAT	60	20	160	3	162
57.727	23	ATGTCCTTTATCTGTTATGTTTTCT	57.249	27	279	1371	1649
59.637	20	TGGTGATCTACATCTCTTCCCA	59.55	22	105	332	436
59.439	20	TTTTGGAGGATTTGGAATGC	59.878	20	212	1207	1418
59.931	20	GCAAGGTGATTCCTTGTTGTT	59.091	21	207	54	260
61.021	20	TCGGACAACAATTCATTGAGA	59.112	21	204	450	653
59.502	20	ACTTCCCACTCCACCACTTG	60.002	20	101	9	109
60.41	20	CCCAAGACCCCAATTTGATT	60.91	20	151	1220	1370
59.94	20	TGAAGGAAGAGAGAGAGGCG	59.82	20	208	381	588
59.297	20	CCGTCTGCGCCTTAAGTTAG	60.032	20	208	4	211
60.517	21	TCACGGAAAACCTAAGTGGC	60.11	20	234	573	806
59.556	20	ACGCTTCATTTCATCCCATC	59.9	20	222	849	1070
59.993	20	TATCGATGGAGCAGCAATCA	60.329	20	252	2274	2525
59.988	20	CTCGTCTTCCGTGGATAAGC	59.836	20	102	290	391
60.005	20	AAAGGAAATCCCCTCACCTG	60.298	20	211	197	407
59.711	22	TTCAGGTTGAAGTCTTGGGC	60.232	20	267	481	747
58.89	22	CATCGACCGGCTTCATTTAT	59.923	20	223	1272	1494
59.926	20	TGTTATCTCCGACTTTGGGG	59.926	20	215	1293	1507
59.723	20	CACAAAAGCAAGATTTCGCA	59.992	20	252	705	956
60.02	20	AAGTAAAAACAGGCGAGGCA	59.883	20	249	863	1111
59.807	20	GAACCCAAATCACGGAGGTA	59.79	20	208	836	1043
59.443	24	CTTCTTTCCCTCACAGCACC	59.844	20	146	0	145
59.985	20	CCCCAATACCCCAATTTGAT	60.614	20	223	968	1190
60.298	20	TTAGTTGCTGGTGTGGTGGA	60.152	20	272	2385	2656
59.617	20	AAACCAGCTCATTTGTTGGC	60.118	20	165	2375	2539
60.051	20	ACGCGGATTTGAAAATGAAA	60.436	20	213	822	1034
59.762	20	TCGTATTCTTGGGTGAGCAA	59.272	20	269	2304	2572
60.119	20	CTGATCGCATGCCTTAACAA	59.833	20	105	14	118
59.359	21	TATTGGGGCGGGATTACATA	59.998	20	275	523	797
59.926	20	AGGATTTTGAGGATGCGTTG	60.074	20	102	459	560
60.39	20	CTGATCGGCCAAAAACTAGC	59.845	20	272	1861	2132
59.989	20	CATGATAAATTAAACGTAAGTGA	59.371	27	154	331	484
60.181	20	CACCAGCTTCGACACACAGT	59.94	20	178	1841	2018
59.971	20	TTGAGTATGGATCCACCGAA	58.923	20	260	1041	1300
60.042	20	GGGAGTGGCTGAGCTTGTAG	60.012	20	115	446	560
59.523	20	CAATCAAACCCCAAGACACA	59.389	20	206	581	786
59.521	20	TTGTCTGGATCCTTTTGCCT	59.67	20	248	1699	1946

59.971	20	CCTCCGCCTAGACTCCTTCT	59.972	20	277	347	623
59.084	20	GCACTCTCACTTTGCCCTTC	59.997	20	230	1547	1776
59.945	20	GAATCAGAGCCTTGTCCAGC	59.957	20	234	1235	1468
59.757	20	GTCTGAAAAATCGGCGACAT	60.081	20	265	671	935
60.28	20	TAAACGGCTCCGTGTAGACC	60.132	20	201	155	355
60.453	20	AAGGGTGCCGACCAGTAATA	59.452	20	252	2897	3148
59.762	24	TGCTAACAAATATGCATTCCAAA	59.526	23	267	197	463
60.713	20	TTCACGTTCAATCCCTCACA	60.088	20	275	25	299
61.263	20	AGCTGAGAGATTCGGGTTCA	59.95	20	157	2991	3147
59.992	20	ACCCTTGTGAACAAACTCGG	60.005	20	132	143	274
59.948	20	TCCACTGTGGTAGATGCCTG	59.701	20	247	824	1070
60.155	20	TTTTGCGTGAATTGAGCTTG	59.992	20	175	411	585
60.154	20	TTTTGGAAGGAGTGGTGGTC	59.943	20	138	1361	1498
60.159	20	TGAAGCGAAAACTGAACGTC	59.05	20	279	58	336
60.074	20	ATCCCCTCCAAATTCCAAAC	59.996	20	172	475	646
60.469	20	TGCTTTCATCACTGGCAGAC	59.992	20	158	853	1010
59.978	20	AATGTCTCCCGAGTTTGCTG	60.255	20	110	307	416
59.007	20	TCAATTACCTCCCCAGAACG	59.926	20	273	4410	4682
59.84	20	GGTTCTGGGCTGTAACCAAA	59.971	20	265	1070	1334
59.123	20	TCATGAGCTCCGTGTTGAAA	60.39	20	234	131	364
60.126	20	CCCATACCCACATTTCCAAG	60.044	20	109	1843	1951
60.157	20	TCTCGGCATACCCATTCTTC	60.036	20	219	1186	1404
59.131	20	TGTAGCCGACCCCAATTTAT	59.297	20	160	1275	1434
59.927	20	CCACCACCACCCAATACTTC	60.088	20	220	114	333
58.409	22	AAAATCCTAATTGCTTTGCACC	59.525	22	240	500	739
60.013	20	ATAATTTATCCCGCAAGGGG	60.002	20	268	34	301
60.278	20	TGCCAAGGGATATACCCAAA	60.146	20	242	1015	1256
59.617	23	AAATGGAGGAACATGCCAAC	59.797	20	270	1946	2215
60.096	20	TGTCTTTTGGTGTGTGGGAA	59.976	20	234	186	419
59.955	20	AACCGACTTGAAACCTAGCG	59.378	20	220	104	323
59.978	20	GGAGTACCACCACTTAGCCG	59.615	20	229	2658	2886
60.483	20	ATGTCCACCTCTCAGCCTGT	59.713	20	268	137	404
60.836	20	AGAAATCAACCACGTCCCAG	59.966	20	127	18	144
60.066	20	ATGCCTCTGTTCTTCATCCG	60.218	20	265	2221	2485
59.853	20	AAAATGAGGAGTGGGTGTCG	59.966	20	268	1095	1362
60.215	20	GCCGAATTCAGTTTTTGGAA	60.053	20	228	1810	2037
60.074	20	GATTGGTGGGAAGATGATGG	60.135	20	280	525	804
59.597	20	TGACACAATACCCCTGGTCA	59.806	20	255	1060	1314
60.237	21	ACGCCAATGGTTTAGAGACG	60.132	20	202	306	507
59.62	20	ATGCTAACTCCCCTTCCCAT	59.789	20	261	29	289
60.91	20	GTGAACTTGGGAGCTTCCTG	59.844	20	178	3	180
60.043	20	TCTCCTCGTCATTGGAGAAAA	59.799	21	228	1383	1610
60.066	20	CCAAACCCTCATCTTCCAAA	59.903	20	251	262	512
59.809	21	CGCTTATTTTTGTAATGGAATTTG	59.049	24	266	12	277
61.217	20	TCCATATAGCCGACCTCACA	59.101	20	263	253	515
60.042	20	ACAGGATGCCAGTTATGGGT	59.288	20	224	232	455
59.995	20	TTGCTTCAACACAAATTTCACA	59.25	22	213	423	635
60.243	20	AGCCAAAATTTCCTCCAAGG	60.423	20	253	1405	1657
59.83	20	TCCGACATCAATGGCAGTAA	60.073	20	202	1062	1263
59.831	20	CACTGGGACTAAGCGAGAGG	60.005	20	224	3223	3446
59.967	20	CTCACCCCGCACTTCTTAAC	59.734	20	276	1081	1356
60.136	20	TTATTTCGCGGATCCAAGTC	60.038	20	219	225	443
60.91	20	AATTTGGAACCCGCAACATA	60.188	20	156	9	164
60.162	20	CTCGCCCCTTAGAAGAGGTT	59.842	20	195	91	285
59.745	20	TCAAGCAACATCGCTTCAAC	59.995	20	247	89	335
60.001	20	TAAGGCAAGGAAAGCTCGAA	60.089	20	146	7	152
59.415	20	GCCAAAGGATGAAATGGAGA	60.014	20	278	2341	2618
60.036	20	GCAACAAAGATGGCCAAGAT	60.081	20	185	1446	1630

57.596	26	TCGTATTCCTCATTAAGCCCC	60.286	21	256	7	262
59.897	20	CCCTGGACCTGCAAAAATAA	59.931	20	203	339	541
59.279	20	TTGAATCCCGAGATGGTAGC	60.036	20	127	1269	1395
60.221	20	CGGAAGTCTTTCCCATCAAA	60.044	20	221	404	624
59.836	20	ACTAGGGAAGTTGGGAGGGA	59.928	20	237	173	409
60.096	20	TTATGTCATCTTCCGCTCCC	60.036	20	136	577	712
60.05	23	GAGGCATGGTTAGGTTTGGA	59.933	20	220	726	945
60.096	19	CCAAAATCTCGGCTTCAATC	59.645	20	242	723	964
60.91	20	TGAATGTCTCTAGCGACCCA	59.394	20	117	9	125
60.032	20	TTTGGGATGATGGTTTGGTT	60.029	20	139	8590	8728
59.861	20	CCCAAGACCCCAATTTGATT	60.91	20	179	1716	1894
59.878	20	AGGAACAAAAGGGAATCGGT	59.805	20	221	950	1170
60.34	20	CTCCAAATGTGATGTCACCG	59.96	20	155	40	194
60.486	20	AAACTTTGGTTCATGTAGCCG	59.144	21	100	2146	2245
59.679	20	AGTTTGAAGAAGCCGTGGAA	59.853	20	184	3851	4034
59.791	20	CATCCATCACCGTTAATCCC	60.014	20	260	803	1062
60.025	20	CAAAGAGTTGTTTTACAGACCATC	59.626	25	210	472	681
58.213	22	CATGCGTTGTCCATCATCTC	60.08	20	155	1422	1576
60.014	20	AGGAGGAGAAGCCAAAGGAG	59.95	20	192	554	745
60.049	20	CAACAGGAAGCCGTCAATTT	60.11	20	184	320	503
59.697	20	CTCATCGTCAGAACAGGCAG	59.571	20	265	84	348
60.903	20	CAGGCCAACTGAAATCTGAA	58.847	20	223	0	222
60.375	20	TCGCTGGTCGGTTAACTCTT	59.875	20	264	185	448
59.934	23	ATGTGCAGCTAGTCCCTGCT	60.043	20	242	185	426
59.995	20	TTCTGTGCTCAGCTTCTCCA	59.855	20	165	1077	1241
59.182	20	GCATAGTTCGAAGGACAATATGA	58.287	23	280	1489	1768
60	20	GAGCCAGACAATGCAGTGAA	59.992	20	231	83	313
60.317	20	TGATGTCAAAAGCGTTCTCG	59.988	20	202	149	350
59.297	20	CAATCGACCACCCGATATGT	60.603	20	252	139	390
59.83	20	ATTCTATGCCTTCAGCAAATG	57.031	21	164	5	168
59.96	20	GCTGAGCAATCTGGGACTTC	59.957	20	200	193	392
58.567	22	AACCAATTGACAATGAGAGGAGA	59.99	23	258	125	382
59.874	20	AGGCCAAGAAGGGAACATTT	59.94	20	258	88	345
60.366	20	GATCTTTCATTGTGCTGCCA	59.805	20	250	888	1137
59.723	21	AGAGGGAGGAAACTTGACCC	59.534	20	202	1	202
58.658	21	TGTGGTCACACACTCCATGA	59.518	20	264	381	644
60.03	20	GCAGTTGGATGACTGGGTTT	59.973	20	186	816	1001
59.955	20	TGGAAATTGTCGTGTAGTGGTG	60.837	22	260	457	716
59.933	20	CAGAAATGGCAGCAGAAACA	59.988	20	279	1372	1650
59.945	20	GGTCATAGGAATTCGAGGCA	60.036	20	154	480	633
60.263	20	GTTGCAACTTCCCACCTGAT	59.973	20	267	599	865
60.56	20	TGATTCATTCATTTGTCAACACG	60.777	23	219	109	327
59.972	20	TGTGCAGTATGTTACCGCGT	60.203	20	232	383	614
60.21	20	TCTCTCTTCCGTGTTGGTCC	60.238	20	217	347	563
60.081	20	CCGCCTGTAGTTCCTCTCTG	60.005	20	235	386	620
59.43	20	GGTGGCTCATAGGCTATCCA	60.059	20	276	57	332
60.567	20	TTCCTCGCGAAATTAGCATT	59.816	20	275	170	444
59.992	20	AGACATGTTGCGTTTCCCTT	59.598	20	219	1920	2138
60.221	20	TCTCTCCGGAATTTTTGACG	60.184	20	267	3099	3365
59.429	20	GTTCATGTAGCCGACCCAAT	59.82	20	129	810	938
59.91	20	AGCTTATCGAAACGCTCGAA	60.117	20	200	628	827
60.111	20	TGATATTCACTTGCCCCTTCTT	59.966	22	216	253	468
59.034	20	AGATTTGCGGCTTCTCACAT	59.843	20	257	102	358
59.94	20	CAGCCGGAATCTCTTTTCTG	59.948	20	233	988	1220
59.653	20	CGTTCACAACAACACACATGA	59.042	21	202	2688	2889
60.014	20	GGTGTGAAAAAGAGGGTGGA	59.943	20	187	12	198
60.228	20	ACCTCGTGCAAAAATTCCAG	60.11	20	260	351	610
60.223	20	TCGATTCCGATTTTCTGACC	60.014	20	273	162	434

60.129	20	TTTTCTCATGAACCATCCCC	59.727	20	104	3754	3857
59.881	20	GACTTGAGGACATACATAGTGAA	59.96	26	250	457	706
60.037	20	TCAGTGGCTCGCTCATACAG	60.16	20	199	541	739
60.096	20	AACTGCTCCGTCTGCATCAT	60.833	20	262	1378	1639
59.864	20	GCAGGGTTTTCGACAAAAGA	60.227	20	259	614	872
59.691	20	TTGCTTAATTCCTCATCCGAA	59.668	21	217	325	541
59.991	20	CCGGATGTGAGGTTGAAGAT	59.927	20	278	5886	6163
60.065	20	GTCCTTTTTCTCGAACGCAG	59.993	20	203	276	478
59.725	22	GGATATCTATTTGCGCGCTT	59.331	20	230	112	341
59.983	20	GCTCTTCGACGACCTCAATC	59.957	20	186	687	872
59.882	20	AGCGTGAGAAACCCATTTTG	60.11	20	258	60	317
59.955	20	TTCCCATTTCTCCTTGCATC	60.014	20	235	116	350
58.969	20	GTTTTCCGGTTGACAAATCG	60.344	20	208	1575	1782
60.008	20	ACACCACCAATTTCAGAGCC	59.973	20	280	1290	1569
58.758	21	GGTTGGTAGTGGAGCTGGAA	60.111	20	128	828	955
59.495	21	ACTCCATCACTTGGCCACTC	60.12	20	100	0	99
59.962	20	TCGAATGCTCACGTTGAAAA	60.379	20	139	47	185
60.563	20	GAGTTGTCAGAGGAGGCCAG	59.986	20	183	1959	2141
59.964	20	AATTCGACAGCCATTCAACC	59.939	20	166	933	1098
59.83	20	ATTCTCGTTTTCCACATGCC	59.939	20	199	256	454
60.075	20	GTCATCGAGTGCTGCAAAAA	59.995	20	214	1069	1282
59.966	20	TCACCATGTTGATGAAGCGT	60.12	20	123	172	294
60.581	20	TGGAGTTCACGTAGCAAAACA	59.376	21	241	665	905
59.813	22	TGTAGCCGACCCCAATTTAT	59.297	20	240	1166	1405
58.528	20	CACCTCTTGCGGGGTATTAT	58.928	20	215	898	1112
59.927	20	AAGATGAATGCTTTGACCGC	60.221	20	106	3022	3127
59.943	20	AGCCCTTGCTTTCACCAGTA	59.875	20	255	739	993
60.015	20	ATCATCCTCATCCCCATCAA	60.096	20	273	402	674
59.469	20	GGCCATACCTTCAAAACCCT	60.187	20	141	411	551
59.955	20	TGACCAATGAGTCGACTTGC	59.837	20	210	333	542
59.938	22	CCGTATTTCTATGCCACGGT	59.845	20	262	190	451
60.258	20	TATTGTGGTTGGATGGTTGG	59.097	20	274	10	283
59.995	20	ATTCGTCGATGGATGACTCC	59.893	20	238	307	544
59.774	20	TTGGCATTTGATGTATATTGGA	57.92	22	184	602	785
60.049	20	CCCGAGATCTATCATGGTGC	60.448	20	125	370	494
59.971	20	CTCAGTCTTCTCCGCCTCAG	60.275	20	134	228	361
60.22	20	CTCCTCGCTCTCTCCTCTCA	59.962	20	131	755	885
60.241	20	CCATCCTTTAAGTACTTTGACTTTT	58.83	26	217	66	282
60.317	20	CCCCAAATTCGACAAACAAT	59.662	20	221	194	414
59.297	20	GGGGAAGAACTCATGAACGA	60.05	20	128	13	140
59.962	20	ACCACAAATTAATCGGGCAC	59.691	20	129	434	562
59.587	22	TGGAATAAGGCAAAAAGGAAA	58.726	21	277	2998	3274
59.116	20	CTGCATGTTCTTTTGCCAGA	59.988	20	222	1178	1399
60.215	20	AAGATGTCATTTTGTCGCCC	59.939	20	279	35	313
57.789	21	TGCGTGTTTGCATCCATTAT	59.96	20	220	4453	4672
59.845	20	CCACTCACTCCAACAGAGCA	60.022	20	195	463	657
59.882	20	GCTTGAAGCTCTATGCAAATCA	59.636	22	179	332	510
59.939	20	TGCATTTGACAATCGCATTT	60.081	20	104	501	604
60.144	20	CCTCTCCTCGAAAACCCTCT	59.811	20	229	437	665
60.187	20	CATACCGGAGCAGATCCAAT	59.917	20	274	92	365
59.61	20	AACCCCATATTGGTGGCATA	59.901	20	223	1816	2038
59.933	20	AGCGTTCGCTTGAAACTGAT	60.022	20	111	354	464
59.935	20	ATGTTGAGCCCAACCCAAT	60.188	19	214	1452	1665
60.388	20	CAGCTGTCTCGCACAAGTTC	59.776	20	246	964	1209
59.297	20	TCTTCCCCATCTCATCAAGC	60.158	20	185	7	191
59.81	20	CTACCCGGACTTGGATGTGT	59.844	20	194	120	313
59.483	21	CCATGTGACAGAACCAATCG	59.96	20	230	217	446
60.412	18	ATGGCAAAGGCTTGTGTTTC	60.118	20	137	20	156

59.964	20	TGTGGAGTGGACCTCATTCA	60.088	20	196	100	295
59.9	20	CCCTCAAGTTCACCTGCATT	60.111	20	198	594	791
59.986	20	GGTTCAAGTGTTTGGGAGGA	59.943	20	279	741	1019
60.002	20	TGCGATGAAGAACAAGACCC	61.188	20	221	574	794
59.96	20	ATGGTATGTGGGATGGCACT	60.081	20	244	4170	4413
59.415	20	TTCCAACACACCATTCCTGA	59.935	20	271	420	690
60.029	20	ATGAGCACCTTGACAATCCC	59.934	20	216	1869	2084
59.297	20	AATTGAAGAAAGCCGCACAT	59.713	20	141	8	148
60.012	20	CAACACTCCCCACAACTCCT	60.002	20	123	813	935
59.973	20	CGCCGCACTCCTCTATACTT	59.499	20	136	68	203
59.957	20	CTTCCAATGCAGAGTCCCAT	60.073	20	135	1003	1137
60.382	20	CCAATCAAGGTCAATGCAGA	59.648	20	272	113	384
60.088	20	GGGTCCATCATTCCCTTTCT	60.133	20	264	1094	1357
59.992	20	TTGCAAAGGTTTTGGGATTC	59.916	20	176	896	1071
59.297	20	TTTTCTGCATTAGGGTTTAGGG	59.515	22	115	3	117
59.983	20	CCAGTTGCTTTCTTTCCAGC	59.993	20	229	527	755
60.24	20	TGTTCCAATGGAGGAGACAA	59.059	20	238	1820	2057
59.716	20	GCCCATTTACATCATTTGGG	60.016	20	199	412	610
59.708	21	GGAGTGGACAACGTAGGGAA	59.966	20	261	535	795
60.478	20	ACAAAAAGGAAATAGGCGGG	60.305	20	112	723	834
59.997	20	CACAGCCGATCACACATTTC	60.12	20	181	36	216
59.84	20	AAAAGGAAACAAAGCAGCCA	59.861	20	263	1456	1718
59.297	20	GAATTGTGGAAACACCTCGG	60.353	20	120	4	123
60.628	20	TGCAAACAAACCCGTACAAG	59.627	20	231	338	568
60.034	20	CAGAAAAATAAAAGACATACGAA	57.384	26	225	205	429
59.504	25	ATCGAATCCGCTTTCATGTC	60.043	20	170	399	568
60.051	20	ACCCCATATAGCGGGAAAAA	60.508	20	148	1413	1560
60.111	20	CTTCCAGCTGAAACTGTGAGA	58.229	21	199	398	596
59.787	20	TCAAAGCATCCCTTCTCTTACA	58.973	22	215	675	889
59.934	20	GCGCATTGCAGAGATTGATA	59.944	20	222	2300	2521
59.85	20	ATATGTTGGCCAGGCTGAAG	60.096	20	267	1037	1303
60.91	20	TTGCAAGTACACTCCATTTTGT	57.364	22	258	8	265
59.957	21	TTTTGAGCAGGAATGTTCTTCA	59.861	22	234	131	364
60.088	20	ATACAATGACGAAAACGCCC	59.829	20	168	432	599
59.297	20	GTACCAACGCAAGGCAAAAT	60.003	20	147	3	149
59.882	20	CATCGAGTGATCCATTGTGG	59.918	20	228	194	421
59.959	20	ACATCGGATTCCAACTCTCG	60.073	20	200	585	784
60.038	20	CCCAAGACCCCAATTTGATT	60.91	20	184	1131	1314
59.873	20	GCCCTGTCATTTTTGAGCAT	60.081	20	226	1112	1337
59.655	20	CTAATCACCAACGCCCACTT	59.993	20	222	546	767
58.919	22	AGAAAGCCTCTCCCTCCAAG	59.95	20	135	173	307
60.214	20	GCATGCTATTACGCTAGCCC	59.866	20	232	8	239
59.874	20	TTCAAATCTCGCCTACACCC	60.074	20	180	1124	1303
59.955	20	AACATGGACGACCACGTGTA	59.88	20	184	571	754
59.101	23	AAACAGCTTTCTCGGATGGA	59.813	20	164	1461	1624
59.981	20	GTTCCCCAGAACGTCACACT	60.009	20	228	482	709
60.015	20	ACTGCTAGGAACGCAAGGAA	60.015	20	268	302	569
60.263	20	CGTAAGCCAATGCAGTGAGA	60.011	20	279	2515	2793
58.819	20	CCCACATATTCTTCAAGCGAA	60.081	21	252	42	293
59.835	20	TTTCACGGATCCAAGTTTCC	59.91	20	137	1009	1145
59.989	20	TTATGCCCAAACCTACCGAG	59.953	20	113	190	302
59.838	22	TTTCTCCATTCGTTACTGCAT	57.379	21	272	514	785
59.901	20	TGGGTGCCTTTGTTCTTTTC	60.088	20	184	60	243
60.575	19	GTTGAACGGGAACGGAACTA	59.971	20	259	241	499
59.711	20	GAGGCGTATGAGATGGAGGA	60.181	20	186	405	590
60.184	20	TCGATGAAGGGAAGAAGGAA	59.744	20	247	960	1206
59.928	20	AACATCGAAGCTTTTGGCTG	60.386	20	263	679	941
59.933	20	CCCAAGACCCCAATTTGATT	60.91	20	271	1080	1350

60.123	20	AATCCCTCTTCTCCTCCACC	59.492	20	225	1633	1857
59.857	20	AGCACAAGAAAGAAACCCTGA	58.969	21	236	48	283
59.992	20	CAGGTTAGATGCCGACACAA	59.716	20	259	1727	1985
58.233	27	AGAGTAGCTGCTGCGGGTT	60.171	19	268	902	1169
60.015	20	GATTTCCCAAATCCCGTCTT	60.131	20	232	2808	3039
59.996	20	GCAATCTCTCAAAAGCAGCC	60.103	20	280	54	333
59.991	20	TCACAGCTGTTGGTGGAGAG	60.022	20	243	1427	1669
60.152	20	AGTTGGGCCTCTTCCAACTT	60.11	20	275	709	983
59.456	20	GCGGCGGAGATAGTCTACTG	60	20	130	234	363
59.79	20	ATTCCACTCCACCACCTACG	59.844	20	172	2062	2233
60	20	AGTAGACTCCACCGCCTTGA	59.867	20	273	501	773
61.263	20	ATTTCATTTGGTGCTTGCCT	59.574	20	184	3	186
59.698	23	CGGTATATAAGTCATGTGTTTGGT	59.625	25	258	218	475
59.966	20	CCTTGGTCGATCTCATCACA	59.631	20	236	1336	1571
60.035	20	TCGAGTTGATCTTGCCTTTG	58.999	20	252	68	319
59.861	20	GGAAGAAAAGTGCGATGACG	60.776	20	229	414	642
60.269	20	CCATACATGTGCTGGCAAAC	59.995	20	196	335	530
60.081	20	GATGAGGGAGGCACTAGACG	59.827	20	111	352	462
57.211	21	CCATGCCTTGTGTTTGTACG	60.027	20	173	14	186
59.935	20	AAATGACTAATCTTGAACATGCG	60.03	24	255	106	360
59.098	24	GAGCCACGACTACAGGCAAG	60.996	20	238	192	429
59.767	20	TGCACTCATTAATTGTTTCGG	58.688	21	116	433	548
59.864	20	CCAGCTTAAGCCTGCATTTC	59.982	20	230	116	345
59.995	20	TGTCGGGTGGTGTGTAGTTG	60.477	20	223	64	286
60.074	20	TGTAGCCGACCCCAATTTAT	59.297	20	231	1027	1257
59.859	20	ATACAGTCGCCGTGGAAAAC	60	20	175	1	175
60.448	20	TTGGTAACGGTACCCACCAC	60.529	20	110	38	147
60.081	20	ATGTAGCCGACCCCAATTTA	59.297	20	196	552	747
59.297	20	AAAATCATCCCAATTCCCAA	59.067	20	147	15	161
59.791	20	ACCTCGACAAACTCCACACC	60.009	20	246	614	859
59.297	20	TGTGGAAGGCGGAAAGATAC	60.074	20	218	4	221
60.029	20	CTGCTCCAGCGCTTTTCTAT	59.752	20	260	178	437
60.636	20	GAGAAGGCGGTGTATGGTGT	59.997	20	212	740	951
60.261	20	TCATTGGGAAAATGATTTGG	58.255	20	215	1910	2124
59.566	20	GAAGGAAGATGGATCGTGGA	60.011	20	219	510	728
59.808	21	AGTCGAACCGGATCATATCG	59.917	20	242	81	322
60.419	20	CAATCCTTTTGAGCCTGGAC	59.67	20	220	23	242
60.156	20	CGAGGATGCTCTATCCGAAG	59.933	20	169	486	654
60.91	20	TGGCTGACAACTTGTTCTGG	59.873	20	195	2	196
59.706	22	ATGAGAATCTCCACCTCCCC	60.278	20	192	5	196
59.511	20	CTTCCCTCATTCCCTCCTTC	60.008	20	257	1971	2227
59.989	20	GTGAAAGCGCCATTCTTCTT	59.457	20	244	1812	2055
60.074	20	GCGAAGAATTGGTTGAGGAA	60.192	20	207	317	523
59.512	19	AAGGGGCAGTTAAAAATCGG	60.305	20	102	0	101
59.844	20	ACAGGCAATCTGCTTAGCCA	60.934	20	221	2149	2369
59.929	20	TGTAGCCGACCCCAATTTAT	59.297	20	280	660	939
59.938	20	AGGTCGTGATCCAGAAGGTG	60.112	20	155	555	709
60.786	20	TGCAACACCTCCATCATCTC	59.637	20	260	566	825
59.809	20	TTAGGAGTCGTGGGTGGTTT	59.449	20	106	418	523
60.036	20	CCCATCCCTTTATCGGAAGT	60.145	20	246	90	335
60.21	20	TAAGCTGAACCCCAACCAAA	60.472	20	212	341	552
58.307	23	CAATTTAGCTGAAATCTCAACCTT	59.296	25	243	429	671
60.036	20	CATTTCAACGTCTCTGCCAA	59.84	20	277	90	366
57.114	27	TTATGTGGTGTCCATGTGGC	60.249	20	279	1017	1295
59.875	20	CTTCCCCGCATCTCTCATAG	59.79	20	138	18	155
59.83	20	GCTTTTGAAGTCCTTCCACG	59.853	20	201	37	237
60.375	20	GCCAACCTAACGCCACCTTA	62.257	20	270	137	406
60.16	20	CTTCCCCCTCTTTGAACTCC	60.045	20	106	8	113

60.206	20	TCAACACATTCAGCAGGCTC	59.992	20	193	149	341
59.648	20	CTCAATCGCAACTGCAAAAA	59.992	20	279	44	322
60.426	20	AACGTTCGCTCCAAACAATC	60.118	20	276	126	401
59.853	20	CGCAATTGAATAAGAGGGGA	60.031	20	270	158	427
59.997	20	TCTTTAGCAATGGACCTCGC	60.352	20	190	342	531
60.132	20	ACCGAGATGCAAATTCAACC	59.939	20	275	972	1246
60.174	20	TGCAATGCTCCGAGTATGAG	59.972	20	250	311	560
59.966	20	TTGGAGGAAAGCAAGGAAGA	59.926	20	231	582	812
60.104	20	GAACGGTGCTTATTACGGGA	59.96	20	191	315	505
60.195	20	TGAGGAAGATGTCGCAGTTG	59.984	20	195	1	195
57.624	26	AAATCACGTGTCTACATTTTTAAT	59.769	26	230	426	655
59.933	20	TTGGGATTAAGGCTTTGGTG	59.931	20	186	895	1080
58.56	25	GTCTTCCGCGTGCGTATAAT	60.124	20	226	38	263
60.125	21	CGTTTGATTCGCCGATAAAT	59.928	20	257	379	635
58.06	24	TGGTGTTTCAGCAGAGTTCG	60.025	20	109	0	108
59.097	22	GCCGGTTCTTTGTGAATCAT	59.939	20	256	26	281
59.887	20	TTCGAATTCAAAAACTCCCAA	59.551	21	226	355	580
59.988	20	ACGGCTATGCATCCAAAAAC	59.967	20	148	702	849
60.17	20	GCTCCATTGTACGTTTCCCT	59.056	20	135	125	259
60.015	20	GTTCAACAGGAGGTGAAGCC	59.703	20	212	2261	2472
59.813	22	GGCGCACATTAGACATCCTT	60.103	20	151	16	166
60.266	21	AGGCTTTACTCGGTTTGGGT	59.998	20	279	179	457
60.34	20	TCCTCCAATGTCTCGTACCC	59.927	20	236	561	796
60.353	20	CACTTCCGCCACCATAAGAT	59.955	20	261	115	375
59.297	20	CACAGGAGAAGATTTTCTTTTCAA	58.971	24	193	0	192
60.126	20	CTGTCATGCAAGCAGCAACT	60.207	20	255	343	597
60.434	20	CCGGAACATAAGTGCCAAAC	60.365	20	266	335	600
60.91	20	TTCGATGCAGTGTTCTCCAG	59.984	20	245	5	249
59.925	20	CTTGGAACAACTTGGACGGT	60.005	20	132	493	624
59.964	20	GGCCATTGTTGTTGAGCTTT	60.118	20	239	1449	1687
60.048	20	TTCTCTGCTTTGATGGAGGG	60.331	20	203	104	306
60.91	20	TTTTCTGTTTTTGTTCTCCTGC	58.539	22	263	5	267
58.897	20	CGTCGATCACTTCAACCTTT	57.797	20	227	604	830
59.992	20	AAGTGGGGAAGTCTCGGATT	59.935	20	167	576	742
60.285	20	TCTTCATGCACGACATCCTC	59.794	20	280	882	1161
59.903	20	TCTTCCAAGATCACACAGCCT	59.859	21	249	1170	1418
59.978	20	ATCCTTCAACCCCAAATTCC	59.996	20	242	1198	1439
59.986	20	CGTGATAGCAGAGAAAGGGC	59.978	20	122	740	861
59.971	20	CGAGAATATAGTGTGCGCGA	59.999	20	150	366	515
60.357	20	AGTAAATTCCGGGCCATTTC	60.15	20	124	870	993
57.539	21	CAACCCCTGATAAGCAGAGC	59.836	20	148	6	153
60.534	22	TTCCTTTCTTAAGCTTGTGAACTT	57.936	24	152	937	1088
59.553	20	GTAGCCAATGAGTTGGGGAA	59.933	20	237	213	449
60.081	20	AGGTACGTTCCTGATCACCG	59.989	20	210	173	382
59.955	20	CACAAAAGGGCCTCTGAATC	59.67	20	230	137	366
60.235	20	GAGAAGCTGCGGAAGAGGTA	59.717	20	242	3659	3900
59.172	21	ATGAGCAGACTTGATGCGTG	60.016	20	276	197	472
60.132	20	CCCTCTTCCCCTTCAAACTC	60.045	20	241	968	1208
59.884	20	ATTCGTACACCCAATCAGCC	59.82	20	199	201	399
59.443	20	GCCACAGACCACAGTGCTTA	59.905	20	204	300	503
59.729	20	ATTCAAACCGCCAAATTCAG	59.938	20	261	95	355
59.823	20	GCGTGATGAATGTCACGAAC	60.128	20	211	384	594
59.792	20	AATTAAACAAGCCCCTGCCT	59.966	20	244	333	576
59.368	20	TTTTCCATGCACATGTAAGTTTTT	59.822	24	106	119	224
59.955	20	CTTTGCGGGTAAATCGAAGA	60.202	20	118	529	646
59.918	20	TGACTGGCTTGTGAGAGGTG	60.022	20	205	455	659
58.304	24	TGTAGCCGACCCCAATTTAT	59.297	20	170	1325	1494
59.748	20	GAGTCGGCGTTAAGTGAACC	59.74	20	255	132	386

59.132	22	ACTGTCCAACCAATGCACCT	60.431	20	168	462	629
59.813	20	ACCTGATCGGTGCGATTAAC	59.962	20	272	420	691
60.123	20	CCATCCCATCATTCCATCTC	60.096	20	265	800	1064
60.125	20	TGGAGGAGGTCGCTAAAGAA	59.948	20	253	467	719
59.791	20	TTCACCCTTGCCTTCATAGG	60.066	20	139	2145	2283
60.181	20	AGCAGTCGACGATCCTTCAT	59.834	20	212	494	705
60.255	20	CATACCTCATCCCGCAGATT	59.917	20	269	1803	2071
59.92	20	CGTGGAAGGGTGACTTGAAT	59.966	20	192	159	350
59.183	20	GCTGACCTCACATATTGGGAA	59.947	21	247	10866	11112
59.32	20	AGGGAGAATTAGTGGAGGGG	59.392	20	151	346	496
59.703	20	TCGGGGAGAGTCAAGAGTTG	60.377	20	268	456	723
59.474	22	CGTCTCCAAGGAAAAAGCAA	60.357	20	157	9	165
60.015	20	TTGTTGCTGCAGTTGGTCAT	60.31	20	271	149	419
59.933	20	TGGGCCAATTGAGTTTTTCT	59.546	20	200	534	733
60.264	20	TTTCAATCACCATCAGGTGC	59.502	20	196	5825	6020
60.624	20	TGCAAATACATCGAGCGTAGA	59.481	21	236	141	376
61.245	20	CCTTTGGAACAGGGTATGGA	59.784	20	148	693	840
58.978	20	AAGTGATCAGCCGAGGATTG	60.218	20	255	1041	1295
60.134	20	CTCCGCCGGAAATTTTGTA	60.946	19	214	370	583
59.935	20	AAAAGGATATATTCACTGGGTTGC	59.668	24	272	120	391
60.119	20	GGGGCATAGCATAGCCATAA	59.913	20	208	904	1111
59.715	24	TGGAAGGCAACTGCTCAAAT	60.776	20	184	22	205
60.214	20	CCCAAGACCCCAATTTGATT	60.91	20	137	2397	2533
60.008	20	TGATCATAGGGTTCTTCGGC	60.036	20	165	2384	2548
60.011	20	GCAACACCAACAACAACAGG	60.049	20	149	736	884
59.573	21	TCTAGCTGTGAGATGTCTCTTGC	58.903	23	271	557	827
59.894	20	GAGTGCATTAGGGTGGCAAT	59.962	20	268	1028	1295
59.933	20	CCTTCCTTCGTCGATGTTGT	60.111	20	150	810	959
59.955	20	GCAAAGGAAATTCACGAGGA	60.192	20	187	161	347
59.918	21	GGTTCATGTAGCCGAAACCA	60.894	20	150	2174	2323
59.829	19	GTCGTTTGCTCCTCTTTCCA	60.375	20	200	28	227
59.434	20	GAGACATTTGGGGTAGACGC	59.556	20	251	188	438
59.835	20	AACTCCCAATATGGTGCTGC	59.962	20	274	2016	2289
59.35	23	CGGAAGTGATCACAAGGGTT	59.966	20	168	20	187
59.995	20	GTCCTGATTAGGGATGCCAG	59.508	20	273	4335	4607
57.473	25	GGGAAATTTGAGTGGATGCT	58.984	20	255	516	770
59.551	20	CGTCGTCGTCGTCATCTTC	60.419	19	199	153	351
60.152	20	TGTTTGAACGACTGCCTTTG	59.881	20	153	461	613
60.469	20	GCCGACCCATTACTAATCCA	59.784	20	246	649	894
57.172	24	CGGTATTCTCAAATGCACGA	59.688	20	199	1076	1274
60.21	20	GCTGGAGCTGGAGTGGATAC	59.834	20	158	742	899
59.934	20	CTGCTGCTGCTGTTGATGAC	60.778	20	195	408	602
59.957	20	TTAGGTGAAGCCAACATCCC	59.933	20	153	1731	1883
60.331	20	GTCTAACAAACGGCGGTGAT	60	20	101	69	169
59.297	20	GCATAGCAAAAAGAAGGCCA	60.343	20	171	6	176
59.674	20	GATGCGGAGGAGGATCATAA	59.998	20	162	1250	1411
60.209	20	GATGGACTCCGATGACGATT	59.893	20	264	10	273
59.964	20	CCTCTCTCTTCGTTCATCCG	59.943	20	138	319	456
58.227	21	GAAAATTCAAAGATTTGGGGG	59.645	21	149	1	149
60.081	20	TCCCTCCAAGATCCAGATTG	60.003	20	259	43	301
59.779	20	GCACATGCGGTCTGTATCAC	60.152	20	132	387	518
59.955	20	GAAGACGCGAAGTGTGATGA	59.992	20	257	5	261
60.195	20	TGGCTGAGTTAGATGCCCTT	59.836	20	279	1998	2276
59.73	20	TTTGCAGCCGAACTACTGAA	59.609	20	257	565	821
58.071	20	ATGTAGCCGACCCCAATTTA	59.297	20	183	854	1036
59.661	20	ATGACGACAAAGCTGAGGCT	60.02	20	225	1907	2131
60.066	20	GATGCTAGCCGGAGATGTTC	59.803	20	153	352	504
59.601	21	GGAGCTATTGATGCCACCAT	59.923	20	230	2970	3199

59.688	20	AGAGAGGGTGGGAATGGACT	59.929	20	267	0	266
58.894	20	ATGTATAGGCTCGACGTGGC	60.125	20	216	149	364
60.517	20	TGGCATAACACTGAAGTGACAA	59.245	22	271	18	288
59.927	20	GCCACAAAAACACTTAGGCA	58.822	20	267	32	298
60.05	20	TCCAGTTAAACCAACCTCGC	60.11	20	204	1650	1853
59.75	20	AAGAGAGAGAAAGGGGCGAG	60.088	20	142	1234	1375
60.197	20	TTCCATGCAACTTTCTACCAA	58.28	21	266	78	343
59.974	21	TGGCATGTTGTCTTTTCCAA	60.088	20	106	27	132
60.108	24	TCTGTGATGCAATGCGGTAT	60.104	20	233	310	542
60.088	20	CCCGGGATTTCTAAATGGAT	59.978	20	240	965	1204
59.973	20	GAAGAAGAATCTGAGCCAGCA	59.708	21	155	1097	1251
59.917	20	GAGGAAACAGAAGCACTGCC	59.997	20	252	818	1069
59.297	20	AGGAAGTGAAGTCGGACGAA	59.844	20	111	6	116
60.187	20	GGCGACTCACTTAAGGTTGTG	59.788	21	245	52	296
60.031	20	TAGCACAATTGCCTCTGCAC	60.019	20	255	23	277
60.246	20	TCCTAACTTTTATACCCGAAACAC	60.161	25	208	662	869
59.178	20	TTATCTCCATTTGTTGCCGC	60.971	20	150	694	843
60.214	20	ACACGATTAACTGCCTCGCT	59.904	20	120	2287	2406
59.94	20	CCCCAATTAGTCGTAGCCCT	60.332	20	149	1473	1621
59.995	20	TGCTGAAACTGGTGGAGTTG	59.873	20	115	1979	2093
59.989	20	CCTCAATTGCCACCAATTTC	60.309	20	252	935	1186
57.578	22	TGGGAAAGATTGAAGATGACG	60.059	21	258	116	373
59.297	20	CAACATGTGTGGAGTGGTCA	58.928	20	107	13	119
59.992	20	ACGTCTCTCGCACTCCTCAT	60.017	20	117	6	122
60.036	20	TGCAAATAGAAGGCCAGCTT	59.982	20	150	2254	2403
59.511	21	TTCCGGACCAAACTTTAATGTAG	59.441	23	270	856	1125
60.435	20	TGTGGATGAGCTGTTTGGAG	59.831	20	244	2233	2476
60.012	20	TTTTCAAGCAAAATTTCAATTAAG	59.911	25	276	297	572
59.95	20	CCAGTAATGGCATCCTTGGT	59.813	20	198	40	237
59.745	20	AATTTTTGGTTGAGGAGGGG	60.159	20	280	2837	3116
60.068	20	TGTAGCCGACCCCAATTTAT	59.297	20	117	2537	2653
60.008	20	TTAGGGGAGCTGCAACAAGT	59.875	20	198	1469	1666
60.326	20	TGCAAACCTCAAAACTCAAAAA	59.774	22	207	3	209
60.207	21	AATGACCGTCTTGATCGTCC	59.934	20	233	378	610
60.129	20	ATCATCAATGCCCATCCATT	59.982	20	205	240	444
59.916	20	TGACAGTGCCATTCCATCAT	59.925	20	257	998	1254
59.688	20	AAACCCATGCATTTGATTCC	59.628	20	221	519	739
60.016	20	GAAGCCACATGGGAAAAAGA	60.051	20	256	36	291
61.585	20	GGATCTAGTGCGGGTTACCA	59.955	20	181	31	211
60.012	20	ATTTGGTAGACCTGAGGGGG	60.183	20	209	3263	3471
59.691	20	TGAGTTTTGGGAGCAAATTACA	59.625	22	249	399	647
59.978	20	CGCCTTCACTGCCAAAATAA	61.12	20	108	17	124
59.572	20	ACCTGCCAACCAAAAACAAG	60.008	20	219	253	471
60.419	20	CAGCCCAAGAAAAGATCTGC	59.955	20	210	152	361
59.673	20	AAGGGGAATGAAATGGAACC	59.996	20	231	53	283
60.118	20	AATGTAGCCAAACGCCTCC	60.088	19	206	638	843
59.784	20	CCGGTTCAGTGGTCATTTCT	59.966	20	141	25	165
60.015	20	GCTGGCTGTGATAGGCTAGG	60	20	216	794	1009
60.134	20	GCTGAGCAGGTGGAAAAGTG	60.975	20	225	1202	1426
59.993	20	ATTCTGTCTAGGCGCTGGAA	59.978	20	237	182	418
58.687	23	TCAGCCCCAAATGAAGAATC	60.014	20	277	262	538
60.19	20	AGTGGTCTTCCTAGGTGGCA	59.721	20	123	1021	1143
59.929	20	ATGGTTTGTGCCTGCAAACT	60.559	20	226	977	1202
59.862	20	GCACCAACTCTTATTGGGGA	59.933	20	124	68	191
59.853	20	AAATGTTCCTCATCATCCCG	59.75	20	105	719	823
59.629	20	GTTGATTTGGATCAAGGCGT	59.939	20	267	673	939
60.166	20	AGTTTTTGGAGTCCACCCCT	59.834	20	280	732	1011
59.897	20	CAGAGCCATCCCATTCAAGT	60.073	20	141	53	193

59.845	20	TGATGCTGCGGAGTCAATAG	59.972	20	166	266	431
60.125	20	TGATGAAGTAAAATAGTGAGTTA	57.311	27	258	158	415
59.971	20	ACGTGGAGAGTGGTGGATTC	59.969	20	198	259	456
59.98	21	ATGGATCGAACATTCACGAG	58.516	20	194	257	450
60.234	20	CATCGCTTGCTTTCCATTTT	60.209	20	189	746	934
59.948	20	TATTTGAAATGCTGAGCCCC	60.038	20	208	227	434
60.14	20	AGACTGGTGTTGCTGCTGTG	60.096	20	276	74	349
59.569	20	ATCAATGGGCGGTGTAAAAG	59.823	20	166	712	877
60.096	21	GGATACGCTGGAAATGTTGC	60.478	20	279	704	982
60.081	20	CCAACCCAGTTGGTTTCATC	60.21	20	233	680	912
60.065	21	GCAAAAATTCAAGCCTTTTCC	60.069	21	216	167	382
60	20	CCCAAGACCCCAATTTGATT	60.91	20	165	463	627
59.685	20	TCAACAACACATCGTCTTCCA	60.144	21	165	72	236
59.957	20	ATTCGAACATCTTCATCGGC	60.043	20	206	1775	1980
60.019	20	GCAATGGAGAAGCAGCAAAT	60.361	20	244	1863	2106
59.957	20	ATGGCCCTAAACACAGCAAG	60.132	20	137	554	690
60.91	20	GGCGTGATGCTGGATGTAGT	61.099	20	211	4	214
60.91	20	TCTTTATCCCTGGTGTCGTC	57.58	20	280	4	283
59.665	20	AAGGAGGTGGTGGTGATTTG	59.82	20	217	1586	1802
59.989	20	CAGGGAAATCCAATTCATGC	60.274	20	245	216	460
60.651	20	CGATATGGCTCGTTTAGGGA	60.053	20	123	29	151
59.91	20	CGGGTTTGAAGGGGATTTAT	60.013	20	240	1199	1438
60.269	21	TGCAGTGAGATGCATAAGGA	57.937	20	280	1330	1609
59.898	20	GCTACCTCATTGGCTTCGAG	59.978	20	245	473	717
60.21	20	CGACATGAACTGCTAAGCCA	60.011	20	269	1054	1322
60.511	20	TTGCATTCAGGTAGCACGAG	60.011	20	220	422	641
60.074	20	CAGCCCATTAGCATTCCATC	60.435	20	208	159	366
60.175	20	TATTGGAAAGCAAACCCTGG	59.931	20	213	400	612
59.711	20	GAGTGTGTCTGGCAACATGG	60.162	20	136	57	192
59.548	20	AGTTCCTGCAGCTCTTCTGC	59.898	20	145	1235	1379
60.132	20	TCCGATCATAAGAAATCGCC	60.001	20	141	415	555
60.91	20	GACACATGCTCGAAAGGGAT	60.081	20	180	7	186
60.271	23	TGGGTAGGGAGTTTCACCAA	60.345	20	243	395	637
60.91	20	AAAGGGGAGCAAGAGGAAGA	60.319	20	112	9	120
60.362	20	TGCACCGTATCTTAGGAGGC	60.235	20	187	396	582
60.34	20	GTCAGGTTTCTGATCCGAGC	59.81	20	124	173	296
59.948	20	TGCTCATCAACACTGCCTTC	59.992	20	232	1102	1333
60.191	20	TGGAATAGGTTTCTTTGGAGACA	59.987	23	118	44	161
59.425	20	AACCAACATGATGAGTGACCC	59.694	21	182	68	249
59.621	20	GTCTTCGTCACTGCCGTCTC	61.021	20	186	413	598
59.502	20	CACAACTATTGCGCGACTCA	61.009	20	167	247	413
59.939	22	CTTGGTCATTTAATGGGATCA	57.415	21	269	511	779
59.797	20	CCCAAGACCCCAATTTGATT	60.91	20	176	145	320
59.966	20	TACAACCCAAAAACCTTCGC	59.975	20	268	548	815
59.881	20	TTTGGAGGAGCCATGAGAAC	60.195	20	208	372	579
58.808	21	GTTTATGTAGCCGACCCCAA	59.823	20	184	492	675
59.963	21	GGGTTATCTATGGATCACTACCC	57.813	23	212	542	753
60.046	20	GAGGAGGGGTGGTTTGAGAT	60.314	20	147	81	227
59.67	24	ATGTAGCCGACCCCAATTTA	59.297	20	175	3607	3781
60.11	20	TGTGCACATCATGATTTCGTT	59.987	21	252	1385	1636
59.579	20	CCCCGTGTAAAATTCATTCG	60.181	20	266	760	1025
59.297	20	GCCCGAATGTAGATCTGCTC	59.803	20	161	4	164
59.693	24	AAGATGAGCACCATTCCTTTG	59.184	21	100	56	155
60.285	20	AAGACCACTCAGTCGAACGG	60.298	20	207	49	255
59.877	20	GCTTCTGGTGCAGCTCTTCT	59.898	20	256	154	409
59.823	20	ATCGCTCACCGTAGCCTCTA	60	20	194	537	730
59.341	22	AAAATGATTGCTTGGCTTGAA	59.712	21	253	589	841
59.962	20	TTTTTCTTTTTCCTCTTGTCATCA	59.307	24	253	563	815

60.507	19	CACCCAAAAATCCTCTTCCA	59.903	20	170	81	250
59.958	20	TCATCCTCCATTTCAGCTCC	60.158	20	186	175	360
59.247	20	GACCCCACATAGTGGGAAAA	59.647	20	164	790	953
58.901	20	TCTCTCATTCTCCATTGCCA	59.322	20	272	138	409
59.571	23	GACGGCGTCGTTTTCTTG	60.39	18	257	145	401
59.79	20	GACGGTGAAGCGTTTAGCAT	60.278	20	266	3017	3282
59.304	22	GGTAGCCGACCCCAATTTAT	60.041	20	217	393	609
59.424	20	CCACGATTTTGACTGGGATT	59.79	20	240	429	668
60.033	20	GATCGTTCTCGGATGCATAAA	60.052	21	182	735	916
59.933	20	CACAGTCTCCTCAATGGGGT	59.962	20	170	614	783
60.015	20	GTAATTTCAGCGGGGAACAA	59.938	20	155	4965	5119
58.888	23	CGTCATGTGACACCTCATGC	61.206	20	207	125	331
59.993	20	GAGTGCCCCCAAAGAGGTAT	60.328	20	248	1083	1330
60.001	20	TTTTTAGGCGTTGAAATGGC	60.075	20	188	463	650
60.032	20	AGCTTTTGACCAAGGAAGCA	59.993	20	161	191	351
61.067	20	ATCCAAGTCCATCTCCTCCC	60.278	20	243	268	510
59.823	20	GATTGCGAGGGATGGTCTAA	60.036	20	280	19	298
60.91	20	AAACTTCGACCCCTGGAACT	59.972	20	256	9	264
59.939	20	GTTGCGTACATCTGACCCCT	59.997	20	173	3790	3962
60.066	20	ATGTAGCCGACCCCACATAG	59.836	20	101	714	814
60.096	20	TGTTCACCGAGCTCAGATTG	59.984	20	238	3070	3307
60.195	20	CCCATGTGACACTTCAGCAG	60.309	20	145	597	741
60.033	20	TGACGGTGAAAAATAGCGAA	59.301	20	248	201	448
60.22	20	CCCAAGACCCCAATTTGATT	60.91	20	177	157	333
60.126	21	AGTGTGGAATGGTGAGAGGC	60.12	20	111	1594	1704
59.67	20	ATCCTTTTCTTCTTGCACGC	59.457	20	260	1281	1540
59.49	20	TTCATTTCCTTTGACTTGCG	58.892	20	109	427	535
59.725	20	TTTCAATATTTAACTGAATTAACG	57.55	26	280	445	724
59.571	20	GAATGGAAAGGTGGGAGGTT	60.169	20	196	17	212
59.625	22	TCGAGAGTTCGGATTTTTGAA	59.809	21	118	342	459
59.526	20	CCCAAGACCCCAATTTGATT	60.91	20	130	3022	3151
59.297	20	AGCTACCGTATGAAAGGGGC	60.471	20	192	41	232
59.924	20	CCCAAGACCCCAATTTGATT	60.91	20	257	4790	5046
59.297	20	GTCATGGGTATGCAGGGAAC	60.203	20	186	7	192
60.557	20	TTGTGTTTTGAGCACTTCGC	60.035	20	239	497	735
60.263	20	CCCAAGACCCCAATTTGATT	60.91	20	171	1971	2141
59.845	20	AATGGTGTCCACTTTCCACC	59.679	20	193	628	820
60.044	20	TTTTGAGAAGGTTCCTTAATTCTTT	59.227	26	254	257	510
60.053	20	ATTAGCAAATTTCGGGACGA	59.547	20	270	384	653
59.273	20	AAGAGCGTGCTTCAATCGTT	60.022	20	123	915	1037
60.27	22	CCTCAAAAACCAATAAATGAATG	60.871	24	166	112	277
59.556	20	TGCTGACAATGATATGTGTTCAT	58.039	23	222	557	778
60.016	20	TGGCATCCAATCAACAAGAA	60.049	20	274	139	412
60.831	20	TTGAAATTTCGAGTTGGACG	58.745	20	274	609	882
59.297	20	TGGCCAAATACCCGAATTTAT	60.385	21	206	5	210
59.853	20	ATGTAGCCGACCCCAATTTT	60.562	20	163	978	1140
60.081	20	TGGAAGTTTTACGAGAGCCG	60.378	20	228	260	487
59.988	20	AACCCAGCGTAGAGGAGGTT	60.132	20	198	4806	5003
57.916	20	TCGCGACAGTCAAAGAAAAA	59.585	20	169	0	168
59.851	20	GCCGACCTCACATAGTTGAAA	60.125	21	223	320	542
60.455	20	CCCGAATCCGTTACAAAAGA	59.931	20	209	86	294
59.773	20	TCCTAATCCCCCGAAATACC	59.978	20	271	545	815
60.278	20	GTAACGCGGTGGAGAGAGAG	60.012	20	253	529	781
59.984	20	TGGGGTGATTATGGTGGTTT	59.91	20	255	185	439
60.081	23	ACACTTTCGAGATATAAATTCAGT	57.327	27	256	470	725
58.528	21	TGTTTATGTTTGATGTTATGTATTT	58.499	27	278	0	277
60.061	21	TGGTTGCAAGTCTTTGGTTG	59.734	20	266	9	274
59.872	20	GAAGCTGCCCTAATTCATCG	59.807	20	150	68	217

58.515	20	CCTTTGACGTGGGAGTCATT	59.966	20	222	1173	1394
60.036	20	CTCCTCGCTCTCTCCTCTCA	59.962	20	247	461	707
60.044	22	GCACGTGCGTAGAGGGTAGT	60.343	20	224	470	693
59.789	20	AAAATGACATGCAAGGAAAAA	57.299	21	228	950	1177
60.91	20	TCTCCTTGTTTGGGAAGTGG	60.081	20	153	8	160
60.517	20	GTCGATCTTTACGACCCCAA	59.933	20	193	76	268
59.864	20	CCCAAGACCCCAATTTGATT	60.91	20	219	3385	3603
60.328	20	ACTAACTGAGCTTGAGCGCC	59.786	20	219	180	398
59.257	22	TTTCACCTATGCATTTGCCA	60.073	20	275	3265	3539
59.982	20	ATTCATTCCCATCCGTCAAA	60.133	20	215	1764	1978
60.058	20	ACATCAGTGTGTTCGGTGGA	60.005	20	182	3545	3726
59.297	20	TAGTCACACCAGCATTCCCA	60.112	20	210	2	211
59.91	20	TCGATTAACGAAGTCTCTCCC	58.398	21	274	695	968
60.088	20	CCATCAGAGCACGACAAAAC	59.293	20	214	1597	1810
59.569	20	TGTCATCAACAAAACCCCAA	59.792	20	273	518	790
58.844	23	AACTCCGCAATCACTTTGCT	59.882	20	208	630	837
59.995	20	CCCCCATTAAAACAATGGTTAC	59.374	22	280	8218	8497
60.162	20	GCCTCAGTTTTCAGCTTTGG	59.993	20	264	706	969
59.807	20	ACCTACTAAGGCCTTCCCCA	59.955	20	276	171	446
59.77	20	CCGATACCCTTGGATCTTGA	59.887	20	271	540	810
59.973	20	TCATCCATGTCCAAGTCCAA	59.893	20	275	6185	6459
59.002	20	ATGTAGCCGACCCCAATTTA	59.297	20	262	431	692
59.297	20	CAAGGCTCCCCTTCACAATA	60.066	20	272	2	273
59.849	20	ATGTAGCCGACCCCAATTTA	59.297	20	267	2321	2587
59.993	20	CATACCCTTCACCGAGTGGT	59.844	20	189	731	919
59.662	20	TCCAATCTCAAGGGGATGAG	60.003	20	262	205	466
59.964	20	TGCATGTTGATGTGTCTGCT	58.816	20	271	948	1218
60.11	20	TCCGACCCATCTACCAAGAG	60.065	20	253	253	505
60.025	20	TGCATCAGAAAAACTGGCTG	59.988	20	201	428	628
59.962	20	TCTACTGGGATAGTTGCGGC	60.235	20	192	663	854
60.603	20	CTTGGCTTCTGCTTCTGCTT	59.898	20	198	778	975
60.103	20	GACTCAATGCTCCACCCAAT	59.934	20	232	1322	1553
60.006	20	TCCTGCATGCATTTATTGGA	60.035	20	261	1656	1916
60.381	20	TTTTCCAAGATGGGTATTCG	57.551	20	222	502	723
59.779	20	CGACAGGGAGTTCCACAGAT	60.112	20	233	3604	3836
59.226	20	AATTGGTTTGAAATTACGCGA	59.485	21	249	2675	2923
59.971	20	CATCTCCACCTTTTCCCTCA	60.042	20	171	220	390
60.284	21	GTTCCCTGAATGCCCTGTTA	59.933	20	221	79	299
59.297	20	ATCGACAAATGAATCCCCAA	60.133	20	109	6	114
59.42	20	ATTGCTTCGTTTCATGGAGG	60.074	20	236	572	807
59.993	20	CAGCAAGATGAGATCACCGA	59.942	20	266	4355	4620
59.853	20	AGTGGCTGGTACGGAATACG	60.015	20	157	691	847
59.894	20	TTCAAGAAAGCCACCGTCTT	59.853	20	145	509	653
59.739	20	CAGGTGCCTGAAAATCACAA	59.691	20	262	281	542
59.464	20	TGTCCTTAAAACCACCGGAC	59.83	20	125	456	580
60.052	20	TCACCTCCATTGCTTTTTCC	60.051	20	166	981	1146
59.794	20	AAGGAAGGCCTTAGTTGGGA	60.068	20	279	1259	1537
59.926	20	CTGAGAGAAGTCTGGGAGCG	60.275	20	209	931	1139
60.218	20	TGCCTAGCTTGTGTTAAATTGC	59.45	22	196	107	302
60.08	20	CACCGTCTCATCGACAAATG	60.112	20	225	412	636
59.392	21	CACATTTGGGGTTGTGAATG	59.667	20	269	287	555
59.78	20	TGACAATTAGCAACCCACCA	59.964	20	187	1291	1477
60.413	20	CGAACTTCGTGACGTGAACA	60.906	20	148	160	307
59.703	20	TTGGATACTGCACGTGGAAA	60.111	20	241	319	559
57.914	21	GCACAACAATGATTTTTCAGTCA	60.032	23	270	1076	1345
59.682	20	TGAATATTTAAAGGGATTGTTTAG	60.006	26	235	915	1149
59.757	20	TCAATGACAAAGGAAAACGATG	59.975	22	210	1	210
60.17	20	ACCGTAAGGTTGCGAACATC	60	20	130	1260	1389

60.331	20	CCCACTTGCATTCTCCACTAA	60.118	21	168	2181	2348
60.074	20	GACGGTGTTGTACGTGATGG	59.88	20	168	312	479
60.388	20	TAAAAGCAAAAAGGGCATGG	60.068	20	256	89	344
58.131	21	GGCTAGGTTATGATGAGCCC	58.624	20	227	1339	1565
60.195	20	CCCAAGACCCCAATTTGATT	60.91	20	131	1882	2012
59.94	20	TAGGGGTGCTTCTGCTTCTC	59.574	20	156	719	874
59.982	20	CTTCCCTTGCCTGAAACAAA	60.22	20	180	1	180
59.725	20	TTGCAGAATGAAGAATTGCG	59.953	20	254	629	882
59.871	20	TGGGTCCACTCCAAATCTTC	59.903	20	203	424	626
59.254	20	AAGGACCGAGTTGCAAGAAA	59.853	20	182	60	241
59.662	20	CACATGTTAAACAACCCCACC	60.001	21	258	442	699
60.008	20	TTTCATGATCACCAATTTGCTC	59.945	22	235	186	420
59.862	20	CTGGATTCAAACCCTCTCCA	60.042	20	245	229	473
59.055	22	TCTGGAATGTTTTGAGTTAATGC	58.311	23	236	512	747
60.91	20	GCCTATGCAATGTCACAACG	60.142	20	182	5	186
59.075	20	CGAGTTCAAGTGCAAAACCA	59.881	20	164	71	234
59.572	20	TGGGTTTTTCACGTGTGCTA	60.149	20	187	3299	3485
59.897	20	CAGCAGCCTCTTCATCATCA	60.096	20	230	574	803
59.993	20	ACCTCTAGCCCGGTGAACTT	60.132	20	209	4	212
59.79	20	GGAGACCGAATTGGTAGCCT	60.464	20	200	41	240
59.42	20	AAAAGCGAAGAGAGCGAATG	59.73	20	263	186	448
60.066	20	ATCGAATTACCCGTTTGTGC	59.829	20	109	828	936
59.569	20	CAATCGGCCAAAATGTATCC	60.153	20	110	127	236
59.983	20	AATTCTCCCACCATGCAATC	59.756	20	252	3733	3984
59.808	22	GAATCCACGACAAGGTGGTT	59.827	20	150	11	160
60.444	20	AAGAGAGTTGCGAGAGCGAG	60.035	20	259	1981	2239
60.374	20	CAGAGCTCGCTGTGTGAGTC	59.922	20	216	979	1194
59.881	20	TTGTGTTGAGCTCCTTGTCG	60.025	20	142	3641	3782
60.049	20	TCATACGCATGAGGGATAAAA	58.122	21	237	127	363
59.297	20	TCAAAAGGCAACATCCATGA	60.049	20	143	3	145
59.127	20	TGGTGTAGATTAACACAACTTGTA	57.939	27	254	536	789
58.914	23	TGTAGCCGACCCCAATTTAT	59.297	20	214	307	520
60.11	20	TTATGGGAAGGAGATGCAGG	60.029	20	219	122	340
60.331	20	GCGTTCCAAATCCAGAATGT	59.939	20	213	2428	2640
60.117	20	TCTTCCTGCCTCTCTGCTTC	59.827	20	258	2185	2442
59.946	21	CCACGGTCATTTCTAGGGAA	59.926	20	275	682	956
59.077	23	GCCCCTTGATTAACATCCATT	60.034	21	279	150	428
59.682	20	CCCTACCCTGAATTTTTCCC	59.639	20	265	26	290
60.187	20	GTGATGAAGCGTGTGAGGTG	60.319	20	120	1409	1528
59.116	23	TCAAAACAGGGGATTTGAAGA	59.532	21	267	241	507
59.997	20	GAAGGGCCTTGTCTTCCTCT	59.817	20	258	280	537
59.943	20	GGGAACTATTTTCTGCAGCG	59.845	20	162	824	985
59.711	20	ATCCCTACCTCAAGGGGATG	60.147	20	111	1208	1318
59.934	20	GAGCTGCAACTAAGGCCAAC	60.022	20	220	129	348
59.966	20	TTTTAATCACTATACCCGATTTGG	58.455	24	245	1181	1425
59.96	22	TGTTAGCCCACATTGGATGA	59.924	20	269	392	660
60.049	20	TGGGACCAGAAAGATGAAGG	60.042	20	232	501	732
59.957	20	GAGAACAAGTGGGTGCTCGT	60.307	20	199	39	237
60.117	20	ACGATGATTCCTCCGATGAG	60.034	20	128	1773	1900
59.889	21	CAATCTTGCACCACATTTGC	60.119	20	138	5009	5146
57.99	27	CCCATTGCCCTCTTGTTTTA	59.931	20	182	226	407
59.297	20	CGAGTTTATGACCATCCGGT	59.813	20	109	14	122
60.836	20	GGGTGAACCTTCCATCATTC	59.192	20	124	3	126
59.973	20	TGGATTTATTCGGCTCAACC	59.901	20	246	364	609
58.997	21	CATAGTTGGCCTGGAAAACG	60.493	20	213	417	629
61.079	21	AACCGTCGGAATTACTGGTG	59.853	20	172	30	201
59.424	21	AGTTCACACCCGAATCCAAG	59.966	20	173	254	426
60.232	20	CCACATCATGCAAGGCTTTA	59.688	20	266	790	1055

60.011	20	TGACATGATGGGGGAAGAAT	60.135	20	224	251	474
59.379	22	ATAGAAGGGGGATCGGTTTG	60.145	20	229	874	1102
59.839	20	AAAGCGAATGCCCTTTGTAA	59.72	20	245	2652	2896
60.051	20	CGCCTTTGCTGGTGTTTATT	60.131	20	233	448	680
59.297	20	ACGGAGAATGGAGATTCACG	60.073	20	251	14	264
59.974	20	TCTGCTGCTTCATCTGCATT	59.704	20	139	1080	1218
59.823	20	TGTCGGTGTTACCCCAATCT	60.232	20	171	1361	1531
59.807	20	CAAAACATCATTCACGACGC	60.119	20	250	331	580
59.95	20	TGGGTTTATTGATGCACCTG	59.395	20	217	545	761
60.179	20	TTCATCAAGAGATTACGTTTTATT	58.427	27	148	112	259
60.353	20	TGATATCGGGCTTTGAGCTT	59.807	20	206	578	783
59.911	20	TCGGAGGAAGAAGACGAGAA	60.065	20	201	462	662
59.955	20	CAAGAAAACAGTGGGGGAGA	60.081	20	216	1157	1372
59.851	20	CGCATGTCATCACTCGCTAT	59.854	20	261	863	1123
60.073	20	CCACTGTTGCTGCTGCTAGT	59.264	20	117	122	238
59.329	21	CTGGGTAAACCCACGGACT	59.829	19	275	810	1084
59.978	20	CTCTCCAAATCCCACCAAGA	60.042	20	248	1976	2223
60.148	20	CGGGGGTGTTAGTTCAGAAT	58.909	20	272	49	320
59.955	20	TCCCTCGAAGGTAAGAGCAA	59.948	20	164	131	294
60.395	20	GCGACCAAATCGATACCCTA	59.923	20	235	415	649
60.969	20	GCTAACCACCTCCAACGGTA	59.993	20	234	1638	1871
60.036	20	AAAAATAAGCGCCACGTCAC	60.138	20	218	1105	1322
60.21	20	GCTTGGAGAGAAGGAAGCAA	59.694	20	244	104	347
59.997	20	ATTGGAATGTGAGAAACGCC	59.939	20	191	2501	2691
59.833	20	TCCGTACACCTGGAATCCTC	59.927	20	273	1911	2183
59.985	20	TCGTGCCTGTCCTAACAATG	59.716	20	114	502	615
59.318	20	CCAACACTTGTGCAAACTTCA	59.79	21	211	977	1187
59.969	20	ATTCGATCGTAAAACAGCGG	60.096	20	159	196	354
60.366	20	GCCCTGTTACATATTTTCCCA	58.82	21	213	543	755
59.957	20	TGTTCCTCAAGTCGACAACG	59.873	20	219	2265	2483
60.159	23	TTTCGCCCCCTATTTCTTCT	60.034	20	267	53	319
59.297	20	TCTGCTAAAAATATGATGAATGC	60.008	25	205	7	211
59.837	20	AATACGACGAGGCGGTTTTA	59.609	20	271	1459	1729
60.232	20	CGAACAATTTTCAAACGGCT	60.11	20	250	1318	1567
60.208	20	GTAAATGGCCGAATCAGGAA	59.901	20	143	1656	1798
59.55	20	GCAGTGCGACAAGCATTAAA	60.021	20	178	783	960
59.579	20	GAGTCGGGCAATGCCTAATA	60.06	20	137	943	1079
59.262	20	AAATAGTACAGTGGGTTTTGCTAC	59.023	25	216	1119	1334
59.297	20	CCACTCCGTCTTCTTTTGGA	60.224	20	241	23	263
60.042	20	TTTGATTGGGAATAATTGGG	57.289	20	172	1008	1179
59.747	20	CTTCAACTTGGCGCACTGTA	60.05	20	190	704	893
59.935	20	AAACGCGTCCTGATAGGAAT	58.672	20	217	282	498
59.297	20	CTAATGCAGGTCACCAGTCG	59.314	20	277	2	278
59.505	20	CCAATTCAAGTCAGTGTTCCTTT	59.552	23	257	262	518
60.642	20	GGGTCAGATGTACGCAACATT	59.874	21	270	279	548
58.878	22	AATGGGCCAACTACAGTGAA	58.076	20	250	2160	2409
59.271	22	GAGATGGCCGACGTTAAAAT	59.046	20	177	0	176
57.778	27	AGGACTTCCAACATTCGTGG	59.966	20	170	4	173
57.85	20	TCCATTGAAGACGGACAACA	60.088	20	218	462	679
59.91	20	TCACCGGTTTGTGAGTGGTA	60.001	20	255	134	388
59.996	20	CTCCATCTCCATCCACGTCT	60.072	20	214	1847	2060
59.955	23	AAAAAGTCCATCCCAAGAAAAA	59.013	22	254	325	578
59.93	21	TACCCACTGGAGGTGAAAGG	59.959	20	273	1880	2152
60.376	20	ACCCTACGAAGGGGAGACAT	59.817	20	276	351	626
59.934	20	TTTCTTGTCTGCATTCAGCG	60.134	20	196	345	540
57.853	20	CTAATTTTACAAATTTAACGAGTG	57.347	27	184	299	482
60	20	GCCTGTCTTTGGAACACCAT	59.973	20	176	5639	5814
60.229	20	ATTGGAAGATTTCGCTGTGG	60.074	20	128	554	681

59.602	20	AGTTCCTATGGTTGTTGGCG	59.993	20	228	1145	1372
59.218	21	GGAACCAAATTAATGGAGGAAA	59.207	22	145	670	814
60.91	20	CATTGAATCCCTACTTGGCG	60.46	20	222	4	225
59.442	20	CATCAAAAGTTTTCCAACATCAA	59.02	23	263	364	626
60.073	20	GAGCGATTCAACTTGCATGA	59.955	20	252	567	818
60.545	20	GCCTTCATCATCTTCTTCGC	59.923	20	228	175	402
59.392	21	CGGAAACAGAGCACATCAGA	59.984	20	229	342	570
60.201	20	GATTCTCCACTCTCCCCTTTTT	59.947	22	169	953	1121
60.27	20	AGGACAGTTCACATGCAACA	57.64	20	241	5924	6164
59.993	22	TGCACGATTTACGCATTGAT	60.103	20	152	1810	1961
59.001	20	CCGCGCAACAACAGTAACTA	59.934	20	113	61	173
59.688	22	TCCAATCATTACCCTTGGCT	59.387	20	186	60	245
60.149	20	CAATCCTACGCACTCCCATT	59.955	20	164	1900	2063
57.96	22	TGTAGCCGACCCCAATTTAT	59.297	20	241	572	812
59.239	20	GTGTGCAGGGAGACTGGACT	60.315	20	249	622	870
59.464	20	TTCAAGTTTTGACAATGGGC	58.599	20	256	23	278
60.765	20	ACAGGAAAAGCAAAGCGAAA	59.996	20	276	908	1183
60.388	20	CACCGTCGAAACCAACTTTT	60.008	20	147	2895	3041
59.948	20	AACGGCGTTTTGAATACTGG	59.996	20	175	526	700
59.545	20	AAGGTCAAGTTCACACCAAACA	59.538	22	125	52	176
59.996	20	GCGGAGAAATCTTCTTGTCG	59.955	20	233	533	765
60.012	20	GCAAGAACACATGGGGAAGT	59.973	20	148	319	466
59.735	20	TTGGGATTAAGGCTTTGGTG	59.931	20	280	359	638
59.297	20	ACACAATCAGCACAGTGCAA	58.871	20	127	4	130
59.313	20	CTTCTGCGGTTTCTCTCGAC	60.134	20	104	248	351
59.939	20	AGACCTTGACTCGCAACACC	60.307	20	272	56	327
59.864	20	AGGGAAGCTCTTCGTCATCA	59.95	20	177	480	656
59.834	20	CAATGCTTATGTTCCCTCCC	59.387	20	235	851	1085
59.971	20	TTGGTTCCTATGTTGTCCCA	58.821	20	225	961	1185
59.624	21	GGGCTTTCAAGCTATTGCAG	59.982	20	253	3325	3577
59.615	20	TAGGGAGATGATGAGGTGCC	60.034	20	133	1654	1786
59.799	20	ACGAGCCATTGTTGGATAGG	59.955	20	146	498	643
60.053	20	TTTGCAAATTCAATTGGACG	59.538	20	207	5	211
60.088	20	CACCGCCTCCTCCTTATGTA	60.088	20	171	168	338
59.42	20	TCCATTTTGCCATTCAAGGT	60.309	20	231	969	1199
59.95	20	GAGAAGGTGCCCTGTTGAAG	59.844	20	220	2522	2741
59.985	21	GATGAACCGAAACCTCTCCA	60.05	20	213	30	242
60.226	20	TGGAGGCATCAATCTTGTGT	59.09	20	235	793	1027
59.907	20	GAGGCGTCAGCTTACATTGG	60.796	20	266	848	1113
60.11	22	GGAGCCATGAGACTAGACGG	59.827	20	208	281	488
60.045	20	TTTTGCAATTTTCATTGGCTT	59.595	21	127	290	416
60.331	20	TGAGTTCAAAATGTCAAAAGTATT	60.614	26	242	463	704
60.703	18	CTTGTCCTGAACCACCACCT	60.002	20	183	11	193
60.074	20	AGTTTGGGAGGTTGAATGGA	59.381	20	211	77	287
60.017	20	TCCTCCACCAGCTTCTGAAC	60.386	20	118	1948	2065
59.78	20	GGCCGCCTCATACTTTGTAA	60.096	20	151	209	359
60.263	20	CGTTCTCTCTCTTGCTCGCT	60.035	20	158	333	490
59.592	20	AAGCGCAAATATATCCCGTG	59.95	20	226	5167	5392
57.117	20	ATTGTTTTCCGCCATTCTTG	59.938	20	198	535	732
60.11	20	TTGCTTCTTCTCCCTCCTCA	60.065	20	128	832	959
60.008	20	CGTCTACGAGGACGTGCTAA	59.097	20	225	1100	1324
59.989	20	TCCTTTGTCAGGTTTGGCTC	60.232	20	226	1397	1622
60.427	20	GCATTGTATATTTGCGCCCT	59.956	20	275	893	1167
59.964	20	CTCGAAGCCTTGACCTGAAC	59.989	20	224	1532	1755
59.031	20	TATCGGAGGAGGATGTGGAG	60.027	20	241	554	794
60.349	23	TTTTCCTTGGGTAAATTGCG	59.937	20	267	742	1008
59.793	21	TGCCGGTACATACATGGAGA	59.948	20	224	54	277
59.769	20	GTTCTTGGTTGGGAGGTGAA	59.943	20	252	2926	3177

59.844	20	TTTTCAAGCAATTTCTGCCA	59.42	20	170	854	1023
59.566	20	CATCTTTACTGCACCACCAGAA	60.168	22	261	1370	1630
60.042	20	GCTGCCACCATCTTTCTTTC	59.82	20	184	1389	1572
59.966	20	TCACGCCCAAAAATACTTCC	59.938	20	228	4	231
59.297	20	AGTCATTCATTTCCCGTGCT	59.556	20	262	12	273
59.335	25	TGGGAAGTGGGCAAAGATAG	60.066	20	249	1277	1525
60.074	20	GAATTGGCCTTGCTTGCTTA	60.343	20	264	245	508
59.504	20	CAGCATACCTAAACCTCCCTG	58.73	21	245	31	275
60.24	20	TTTGGACCAAGTCACACGAA	60.128	20	131	608	738
59.816	20	GAGGAGATTTTACGGTGGCA	60.074	20	124	513	636
60.059	20	GCCTACAGCAACTCCTTTGC	60.022	20	145	1224	1368
59.958	21	GCAGCGTGTTAAAGTTTACGAA	59.489	22	206	921	1126
59.716	20	TCCAGTCCCCATTCGTATTC	59.75	20	223	1353	1575
59.901	20	GGTTCATGTAGCTGACCCCA	60.924	20	197	793	989
60.132	20	ACTTCCAGCATACCTCCCCT	59.957	20	131	16	146
61.012	20	AAAATGACGTGAAGTATGAAGGC	59.557	23	242	1000	1241
60.041	20	TTGGGAACAAGAGATTTCGC	60.192	20	177	326	502
60.066	20	ACGGGTTGAGTTCTTGTTGG	60.005	20	203	511	713
60.61	20	CAAGCCATTAAAGGTTGGGA	59.931	20	158	288	445
59.972	20	GCTCTGACTTGTTCTTGGGC	59.997	20	160	97	256
60.006	20	AATGGCGATGAAGGAGAAGA	59.773	20	247	933	1179
60.066	20	GGCATGACTGGTCAAAGGAG	60.656	20	174	711	884
60.008	20	TGTTACCGTTGCCGTTGTTA	60.029	20	231	370	600
60.91	20	CAACAAATCCCTTTTTCCCA	59.772	20	235	9	243
59.734	20	AGGAATCCCTCTTTCTCCCA	60.008	20	276	683	958
57.286	27	TGCTGAGCTTAGGCTTAGTGG	59.799	21	241	1668	1908
59.694	20	TTCGAGCTTCGTTGAGGACT	60.134	20	246	27	272
59.909	21	TGAGAATCATCAGCGGTACG	59.823	20	168	614	781
59.691	20	CAGGGACTGCTAAAGGCAAA	60.378	20	195	1187	1381
59.988	20	GTGTCGGCATCGATCATGTA	60.513	20	278	713	990
59.967	20	AAATGGAGGCACTGATCTGC	60.226	20	272	691	962
59.859	20	CCACATAGCAACGAAGCAGA	60.011	20	239	2326	2564
60.05	20	ATGTAGCCGACCCCACATAG	59.836	20	162	1066	1227
60.059	20	TTCGGGTTTCACAATTCACA	59.941	20	211	957	1167
59.72	20	TTTTTCGAAATCGTGCACCT	60.617	20	237	771	1007
59.971	20	AGGCTTGTTGACCGCTTAGA	60.015	20	272	113	384
58.673	20	GTGTAATGGCGGTGGAGAGT	59.997	20	115	258	372
59.229	22	GCGAGTTGATGGTTTTGGAT	59.939	20	149	118	266
59.996	20	CGACCTCCACTCTTCTCCAG	59.978	20	247	730	976
60.424	20	GTTTCTGTGAAGAGCGGAGG	59.989	20	197	803	999
60.41	21	AACAGGGTCCCTTCGTTTTT	59.842	20	206	567	772
60.91	20	TCATTTCAGTTTGCACTAAGCC	59.406	22	224	6	229
59.656	21	TGTTGGTTCAAAACTAATCCAAT	57.617	23	117	2516	2632
59.395	20	CCTAGGCTCTCAGACACACG	58.621	20	229	296	524
59.984	20	GTTACATCCCACCGGATTTG	60.051	20	272	919	1190
60.123	21	CCCTCATTTGGGATCTACCC	60.517	20	257	359	615
60.154	20	AAAACAAACAAATGGCCGAC	59.845	20	209	1966	2174
59.602	20	TCTGCTTCTGTTGCTGCTGT	59.929	20	113	3414	3526
60.91	20	TCTGAACATGGGGAAAGACC	59.903	20	279	0	278
59.82	20	CACGATTCATATGTGCTTCCA	59.557	21	249	46	294
60.206	20	GGATCAAGTGGGCAAAGAAA	60.051	20	278	4497	4774
60.002	20	CCCACGTACGATCTCAGGTT	59.989	20	205	199	403
60.111	20	TCTACGATGATTTCCCTCCG	60.029	20	279	1512	1790
59.953	20	GTGACCCCACAATCCAAATC	60.034	20	136	9	144
57.409	23	TGGTGTTGATAACGGCCATA	59.809	20	256	1759	2014
59.644	20	GAGCTGGCCGTAGTTTCCTA	59.476	20	279	404	682
59.768	20	TTTTGCATGTGAAAAATGGTTT	59.385	22	207	968	1174
60.214	20	TGAGGAAAATGGGTGGAAAG	59.903	20	268	677	944

59.947	21	AGCAATCTCTACAAGCGGGA	59.978	20	208	69	276
58.858	22	GCTGTGCATTATCACCTACCTC	58.747	22	275	666	940
60.051	20	GCAAGCATTTTCACCACCTT	60.118	20	258	392	649
60.28	20	GCCTGAATAACGAATGTTGGA	59.952	21	134	356	489
59.872	20	AAAAACAACAAACAACCACTTCA	58.621	23	153	222	374
59.488	20	TGGAGGTCTTCAGAGCAGGT	59.986	20	132	1359	1490
59.586	20	TAGAAATTGAAATGGCCGGT	59.411	20	259	419	677
59.893	20	TTGGAGAAACAGTGCTGCTG	60.175	20	192	991	1182
60.416	20	AGGGCTCTGCTAAAACGACA	60.015	20	212	196	407
58.529	25	TATTTTAAATTAAGAGCCACCCA	57.076	23	180	400	579
59.95	20	ATGTTCCTCGGAATCACCTG	59.927	20	227	647	873
59.953	20	ATAGGCCTAACTCGAAGCCC	59.709	20	211	370	580
59.83	20	AAAACCAACATTCACCACCTTT	59.653	22	232	487	718
59.957	24	AAAATTTATTGGGATTAAGGCTTT	59.995	25	194	754	947
60.042	20	TCAAACCAGATGACCCAACA	59.935	20	205	875	1079
60.152	20	TGTAGCCGACCCCAATTTAT	59.297	20	111	2141	2251
59.074	21	GCTGCTGTCCACATAGCTGA	60.168	20	182	67	248
59.913	20	TGGAGGATTTGTATGCGACA	60.073	20	157	2420	2576
59.933	20	GATTTCAGCCATGGTTGCTT	60.081	20	216	439	654
59.903	20	ACCACTGCACCCTAAGATGG	59.989	20	235	496	730
59.993	20	GGCAGCATTGAGGATTGATT	60.043	20	173	104	276
59.993	20	GCTAAGGCTGAAAGCAATGG	59.982	20	175	698	872
59.938	20	TCACTTCCACGAAACCCTTC	60.088	20	264	4820	5083
59.989	20	CCTTCTTGGTCTGAGCTTGC	60.134	20	279	182	460
60.073	20	TTGATCCTGAGAAAGCCGAT	59.773	20	274	436	709
60.074	20	CTCCATTCCCATCTCTTCCA	60.003	20	214	1408	1621
59.845	21	AGACAGGCATAACCATTGCC	59.962	20	263	17	279
59.882	20	CCTGGAACCTTCTTTTGTGC	59.711	20	254	1768	2021
60.395	20	GATGAAAGGGAGGTTCGTGA	60.05	20	133	534	666
59.927	20	TGTAGCCGACCCCAATTTAT	59.297	20	185	1375	1559
58.432	20	CCCAAGACCCCAATTTGATT	60.91	20	250	1864	2113
59.734	20	TTGCCTCCTTACACTTATTTATCAG	59.631	26	204	2436	2639
59.927	20	TTTCACCGGTTATCTGCCTC	60.074	20	127	252	378
60.011	20	CCGCCTCTCCTCCTCTCTAT	59.935	20	279	1158	1436
59.762	20	CCGACCCCACATAGTGAAAA	60.745	20	166	0	165
58.223	24	AGGCAACACGCTTCATTACC	60.14	20	157	7	163
60.255	20	TGCAAGCTGATAGGTGTTCAG	59.087	21	278	2179	2456
60.733	20	GCTCTCATGCGTACAAGCCT	60.569	20	279	611	889
60.262	20	GCTCCGTCACTGCTACATAGTG	59.965	22	172	926	1097
59.988	20	TATGACGACGGCTCTGTCTG	60.008	20	259	192	450
58.48	20	TGTGAACGGCACGACATATAA	60.006	21	265	196	460
59.989	20	CACACACAATACGGGAGACG	60.025	20	279	2537	2815
59.964	20	AGCGGAAGTACAAATGGACG	60.132	20	273	1459	1731
60.119	20	GCAACATCATCCAGATTGGT	58.36	20	220	677	896
59.61	20	GGTTGCCAAAAGAGGTTGAA	60.088	20	271	579	849
59.923	20	AAATATTGCCGCTCATCAGG	60.06	20	279	622	900
59.059	20	GTACAGGCTGGCATCCCTAA	60.096	20	191	2276	2466
60.134	20	TGGCCTACGTTACTCAACCC	59.993	20	149	1069	1217
59.688	20	TGCTATGCTTGGAAGTTATGTGA	59.793	23	112	2594	2705
60.02	20	TGCAAGAGAGCTTTGTGGTG	60.175	20	277	33	309
59.039	21	AGGTTGTCACCCCAATAGCA	60.375	20	258	103	360
60.015	20	CCCAAGACCCCAATTTGATT	60.91	20	124	2184	2307
60.102	22	CAGCACAAAACAAAATGCTGA	59.903	21	279	654	932
60.014	20	CCTTAATTTGCGACGGGTTA	59.958	20	247	166	412
59.903	20	CCCAAGACCCCAATTTGATT	60.91	20	110	1104	1213
60.074	20	CAATTCTTTGGTCGGGTTTC	59.406	20	108	2377	2484
59.948	20	AAGCTGCCCAGAGAACTTGA	60.134	20	103	1884	1986
60.11	20	ATGGCAAGAACAGTCCCAAC	59.973	20	186	996	1181

60.128	20	GGAGCACTGTGAGCTATGTGG	60.87	21	279	1080	1358
59.655	20	ACCGCCTGATGATTTTGAAC	59.939	20	213	109	321
59.959	20	CGATGATGCTGAGGGAAAAT	60.036	20	121	1505	1625
59.47	20	GTCATGCTGCGTTGTGAGAT	59.87	20	275	7552	7826
59.677	20	GGAACCGTGCGATTTTCTTA	60.074	20	214	203	416
59.702	20	CATTGGCATGTAGTGATGGC	59.955	20	145	463	607
60.005	20	TTAACGTGGGCGTTTTTCTC	60.11	20	166	13	178
59.522	20	GCCTCGATCAATGTCCTTGT	60.081	20	189	104	292
59.242	22	ATGGACTGTGGTGCTGCATA	60.144	20	237	100	336
60.162	20	TGGGCTAATAATGGAGCTGG	60.053	20	280	6109	6388
59.297	20	TGTGGTTATTCCAACGACGA	59.964	20	273	0	272
59.297	20	GGGAATTGGGATGAAAAGGT	59.996	20	204	43	246
59.247	20	CCCAAGACCCCAATTTGATT	60.91	20	185	942	1126
60.155	20	AAACACAACTGGCATCCCTC	59.973	20	182	15	196
59.978	20	TGAGAGTACGCACAGCAAGG	60.199	20	187	42	228
59.895	22	AAATAAAATATATATGGGGTTCCA	58.563	27	172	95	266
60.462	20	TTTTTGGATGGAAAAATGGC	59.751	20	137	1537	1673
60.082	21	TGTAGCCGACCCCAATTTAT	59.297	20	166	1291	1456
60.05	20	TACCACCGTAACCACCACCT	60.149	20	277	632	908
59.297	20	TGCACCACAAGATGGTGAAT	59.967	20	188	8	195
60.344	20	TTTTGAGGTTAGTTTGGCCG	60.103	20	127	586	712
59.938	20	ACCGTCTCATAGCCCATGTC	59.957	20	219	49	267
60.051	20	TCTTGTCGTTTCCCTTTTGC	60.227	20	173	167	339
60.444	20	TTCAGATCATCCACCCACAA	59.893	20	152	590	741
60.05	20	GGATCACCACAAACTCCCAG	60.363	20	280	2871	3150
60.143	20	TTCACCGAAATGGTGTCGTA	59.964	20	232	2131	2362
59.978	20	CAAATTAATCAATCTCCTCCTCC	58.164	23	250	1898	2147
59.525	20	AAGGAAGCTTTGCACCTTGA	59.993	20	104	577	680
59.84	20	AATTACGGCGTGGATTTTCA	60.323	20	215	38	252
60.039	20	ATAATCAGCCTTTGCGTTGG	60.096	20	182	1669	1850
60.31	20	AAAACACGTGTGGAAGGAGG	60.005	20	152	408	559
60.12	20	TCCACGTTAATATGGATGCG	59.401	20	278	2494	2771
59.694	20	TTGTCCAGCGATTTATTGGA	59.112	20	277	2845	3121
60.089	20	GAGGTAGAGCTGCAGATGGC	60.127	20	188	107	294
59.724	20	CCCAAACTTCTCCCATCTCA	60.042	20	197	867	1063
59.297	20	GGGTCTTGGGGGTTAGATGT	60.052	20	127	3	129
59.934	20	TGAGGATTCCTACCCAGTCG	60.065	20	189	144	332
60.292	20	GGGAGAAGAATTCACGAGCA	60.34	20	232	21	252
60.11	20	ATGTTGCATGTGAGGTGCAT	59.999	20	264	327	590
59.813	20	ATTGTGCATGCATGTGGTGT	60.896	20	135	1549	1683
59.112	21	CATGTGGAAGTGTGGAATGG	59.806	20	266	341	606
59.962	20	TTTGCAAAATGACACACGAAA	60.14	21	268	1468	1735
59.928	20	TGCCACCAAGGAGAGTACAA	59.288	20	144	403	546
59.9	20	TGGGGATCTCATGGACATTT	60.135	20	245	835	1079
59.962	20	ACACCTGACCAGACCTGACC	60.006	20	123	496	618
59.973	20	CTCGTCACAATTTGCTTCCA	59.84	20	261	662	922
59.83	20	CCCAAGACCCCAATTTGATT	60.91	20	201	1394	1594
60.365	20	ACATCTGACCCCTCAAGACC	58.95	20	177	375	551
59.955	20	ATCAGAAGATCCAGCATGGG	60.034	20	172	508	679
60.734	20	TTGAATTTGCCTTAATAATTACCC	59.991	25	269	20	288
60.035	20	GGTTGCGTACATTTGACCCT	59.859	20	175	3292	3466
59.967	20	CTCGGAAAATTCCAACGAAA	60.046	20	272	896	1167
60.059	20	GAGTATCGGTTTTGGGGGAT	60.017	20	178	1061	1238
59.259	22	ATTCTTGCGTGCTCACCTTT	59.882	20	192	2089	2280
60.046	20	ACGGACATGATACGACACGA	59.992	20	196	87	282
59.92	20	CTCAGCCCTATTGTAGGCCA	60.227	20	236	1402	1637
59.858	20	GCACGAACGTTTGAACTGAA	59.888	20	208	626	833
59.82	20	ACCACAAGCTTCCACCAATC	59.973	20	277	209	485

60.029	20	AGTGGAATGTGGGGAGAGTG	59.962	20	219	740	958
60.363	20	TATTACAGGGCCATTCACCC	59.645	20	169	525	693
58.646	22	AATTTGGTTGATAAGGCCCC	60.02	20	275	191	465
58.465	22	GCTTATGGATTTCCCCCAAT	59.984	20	207	5	211
60.045	25	TTCCATTCGTAGATCCTATTACCA	58.945	24	226	1256	1481
58.055	21	CGGGCGGTTTTTAATGTTTA	59.835	20	236	86	321
60.201	20	GAATAAGGAATTCGCACCGA	60.038	20	189	17	205
60.352	20	TGAAACCGTTCGTAAAAGGC	60.11	20	185	640	824
59.882	20	TGCATTAAGGGTTGGAGACA	59.123	20	203	447	649
59.828	21	TCGAAACCACTCAACCCATT	60.353	20	212	86	297
59.955	20	AAGGCATGGGCAACTTAGAA	59.708	20	259	863	1121
59.984	20	GGGTTTGGATAAGCCTGTGA	59.933	20	268	812	1079
60.162	20	ACAACGAACAGCCGGTTTAC	60.037	20	175	272	446
59.297	20	TCTTGGGAGTGCATTTTCCT	59.67	20	264	8	271
60.721	20	TCGTCAAAATCTTGGAGGCT	59.813	20	241	17	257
59.989	20	GACCGTTTAAACAGACCGGA	59.971	20	145	708	852
60.019	20	TACTACCCCATCTTCGCACC	59.955	20	219	396	614
59.988	20	TTTCATGGCTGTGCACCTAC	59.722	20	252	787	1038
60.042	20	CAAGAGCATCCCACTTCACA	59.831	20	200	945	1144
59.807	20	ATGAAAGTTTTCCCGTGCC	59.925	19	103	316	418
60.34	20	CGAGGAAACAAACGACCTGT	60.149	20	264	829	1092
60.074	20	ATACAGCACGCCGAGAGACT	60.043	20	101	105	205
59.988	20	TGCATATTAGTCTGCGGCTG	59.999	20	195	1134	1328
60.91	20	CAAGCTGTGTGCCTCAAGAA	60.175	20	158	5	162
60.356	20	TGAAGCTGATGTTGGCGTAG	60.011	20	238	387	624
59.986	20	CAAATAATGGCTGCTGCAAA	59.842	20	212	827	1038
60.05	20	GGTCTCGTGGTGGCTAGAAG	59.867	20	204	534	737
59.347	24	TCCATGAAACATAAATCTTGCC	58.946	22	160	10	169
59.964	20	AGCTGCATGAGCAGGAATTT	59.985	20	139	1144	1282
60.104	21	GGCCATGGAGAAGAACAAGA	60.195	20	280	570	849
59.297	20	TCCAGGTTATGTTCCACGGT	60.232	20	205	1	205
60.103	20	GAAGGGTGGTTGTTCTGTGG	60.399	20	246	1205	1450
59.297	20	TCACCATATGTTCAACCTGTCA	58.9	22	245	9	253
59.928	23	AACGTAAATAGTTGCGCCTCA	59.793	21	258	4339	4596
60.234	20	GCTGATACCGGCTTCTCATC	59.803	20	157	601	757
60.065	20	CACCTCGCAGCTATCATCAA	59.972	20	228	87	314
59.992	20	TGTCTCGTCCTGCAACTGAC	60.03	20	163	1200	1362
60.048	20	GCTTCAATTCCCCTGACAGA	60.195	20	252	863	1114
57.017	20	CCTCCAGCATCCGAATATGT	59.917	20	160	476	635
60.517	20	GGTGGGGAGGTGTAGTGGTA	59.697	20	235	3760	3994
59.978	20	CATTGGTGAAGAATTTGGGG	60.162	20	176	1930	2105
59.873	20	TGCTTCAAAAATTCAGCCAA	59.42	20	178	534	711
59.79	23	CAAGAAACATCATCATGCCG	60.073	20	146	53	198
59.93	20	TGGGCCTCCTCCTTAAGACT	60.204	20	276	502	777
59.918	20	GTTTTTGTCGAGCCTTGAGC	60	20	218	155	372
59.405	20	ATTCGACACCAATTTCTCCG	59.933	20	167	546	712
60.267	20	ATGTGGGCTTATTGGGTGTG	60.636	20	203	160	362
60.111	20	CTTTAACCCCTGCATCCTGA	60.066	20	116	1071	1186
59.844	20	GGAGGGATGTTTCCAACTCA	59.903	20	257	1000	1256
59.934	20	TCCACACCTCCACCTCCTAC	59.962	20	262	224	485
60.134	20	CCCAAGACCCCAATTTGATT	60.91	20	116	3012	3127
60.349	20	CACCTTAGTTGTCAGGGGGA	59.959	20	136	1986	2121
59.569	20	AGGTTGCGTACATCTGACCC	59.997	20	200	2366	2565
60.024	21	TCCCGATATGGTAGACGGTT	59.269	20	244	847	1090
60.381	20	CAGCTGAGGGAGGAGTTTTG	59.982	20	140	2987	3126
59.855	20	ACAGGGTTGCTGGTTTCATC	59.973	20	166	525	690
60.096	20	AACTACGGGTGGGGCTACTT	59.886	20	225	702	926
59.78	20	GGTGGATCTTCGGTGAGCTA	60.218	20	228	557	784

59.955	20	GGACGAGTTGGATCGTCTGT	60.12	20	263	2066	2328
59.297	20	TCCTCTGCAAATGAACATTGA	59.262	21	268	7	274
60.91	20	CATGCAATAAGTTGAGAAAAATG	58.378	24	111	4	114
59.297	20	TTCCAATTGCTTTCCTCACC	60.051	20	181	7	187
60.37	20	TCAAATTTCCCAGCAGGACT	59.67	20	279	2169	2447
60.913	20	CAGAGAAGTGGAAAATCCCG	59.665	20	119	474	592
60.102	24	TCCATGGTCGACGAGTTGTA	60.112	20	267	658	924
59.697	20	TTGTGCCCTTACCCAGTAGG	59.986	20	233	740	972
60.31	20	AGATGTACTGACGGATCGGG	59.95	20	221	282	502
59.894	20	TGCTGTTGATCAATGGGTGT	59.967	20	209	3603	3811
59.569	20	TGACCACTACAATGTTCGCC	59.572	20	266	477	742
60.05	20	TGGCAATGCTCATCAGGTTA	60.22	20	269	226	494
59.812	20	TGTAGCCGACCCCAATTTAT	59.297	20	198	2200	2397
57.804	20	TTTCCCACCCACTCATCATT	60.173	20	263	3	265
60.91	20	TTGTGGGAAATGGTTGCATA	59.786	20	213	5	217
60.416	20	TGGTGGCTCTTTCAATTGCT	60.776	20	253	1518	1770
59.697	21	GGGGAAATTCTGACAATGACAA	61.08	22	188	5765	5952
59.369	20	CGTCTGATATGTTGGACGGA	59.522	20	218	1107	1324
59.807	20	CTGGTGGAAGGTTTGCAAGT	60.149	20	188	1148	1335
60.34	20	AGCTTGTTCGCTTCGACAGT	60.201	20	212	467	678
59.995	20	GGCTTGCACCCTACTAAAGC	59	20	278	1069	1346
59.541	20	CCCAAGACCCCAATTTGATT	60.91	20	122	3834	3955
60.081	20	TTGTCAATTTTGAGTCCCAGG	59.956	21	257	521	777
59.903	20	GAGATATCGTGGGCCTTCAA	60.036	20	134	3209	3342
59.297	20	AGTTGGCATCCCAAAGTCAT	59.41	20	188	12	199
59.784	20	TGTAGCCGACCCCAATTTAT	59.297	20	245	392	636
58.914	21	GTAAGGAGGGAGGGAGATGG	59.89	20	200	624	823
59.962	20	GCGTTTGGTGAAATCGTCAT	60.905	20	259	227	485
59.797	20	GCAGCGGACTGTAAGTTTCC	59.882	20	218	384	601
59.546	22	TGGCACCATGAGAGAGAATG	59.787	20	265	586	850
61.124	20	TTCATGTAGCCAACCCCAAT	60.192	20	199	3346	3544
59.986	20	GGAGCTCTTCGTCGAGATTG	60.096	20	262	678	939
60.02	20	CAACAACGAATCTGCCAATG	60.111	20	248	660	907
59.415	20	CAAAAATGGATTATGGGCAA	58.344	20	226	287	512
60.188	20	CTTCTCCTTCGTTGGCTTTG	59.986	20	274	1339	1612
59.647	20	GTTTGAAAGGCGTGGAGAAG	59.853	20	224	1805	2028
60.448	20	GGATGTGGAGTTGTCGGTTT	59.827	20	261	728	988
60.238	20	ACTGCTAGGCATCAAGGCAT	59.866	20	168	756	923
60.376	20	GATTCGGGTCTGGTGTCTGT	59.969	20	237	471	707
59.972	20	CAGAAATCCGAAGCACGATA	58.869	20	239	249	487
60.044	20	CACCGTCTGATGAAGAAGCA	59.984	20	275	563	837
59.813	20	CTCCCCTATCTCCGCATACA	60.051	20	172	284	455
59.23	21	CCATCATGCATTTTTCTTTCA	58.613	21	275	3222	3496
58.151	23	AAGGGCCATAAATTGTGGAA	59.273	20	244	1085	1328
59.992	20	TGTGGCCAGTACCACTACCA	60.025	20	254	284	537
60.599	20	TCCACAGTCTCAAAGTGCAAA	59.475	21	279	3209	3487
59.609	20	GTTGTACGTCGAGGCCGTAT	60.022	20	159	2012	2170
60.111	20	GCCATCAGCACATCCCTATT	59.923	20	209	1398	1606
59.395	20	AGAAAAGCGAAAACCTGCAA	59.996	20	248	164	411
59.133	20	TGTAGCCGACCCCAATTTAT	59.297	20	263	2980	3242
59.978	20	CACGGATTCTCTTCCCTTCA	60.187	20	274	291	564
59.843	20	TTGGTTTGGTTGGTGAGTGA	59.976	20	274	710	983
60.291	20	ATTCGTTGAAACCTGCTGCT	59.882	20	217	607	823
60.029	20	TACTACTTCCGTCCAACCCG	59.986	20	176	125	300
60.801	20	TCTGCGTCTGAAATGTACGC	60.019	20	133	1012	1144
60.003	20	AACCAAGACCCCAATTTGATT	59.563	21	273	3209	3481
59.996	20	GATGGACCTGCTTCAGCACT	60.418	20	244	1288	1531
60.472	20	CCAAACAAAACCAGCAACCT	60.008	20	218	1243	1460

60.27	20	AAGTTGGGAGTCTCCTGCAA	59.844	20	274	3	276
60.111	20	ATCAAGCAGCCCTTTGTCAT	59.7	20	219	2283	2501
58.062	21	TTGTATCACCTCCGCCGTAT	60.352	20	230	248	477
60.103	20	TTCCTGTGCGTGAATTTTGA	60.234	20	280	872	1151
59.55	20	CCAATCACCCTTCTGAGGAA	60.042	20	235	567	801
59.95	20	CCCACTTCCGTCATTGAGTT	59.966	20	279	5651	5929
60.126	21	ATGTAGCCGACCCCAATTTA	59.297	20	216	5360	5575
60.081	20	AGACCATGCAAGTGGTTTGT	58.058	20	133	302	434
60.052	20	GAAGATGGTGGCGGAGAG	59.291	18	244	979	1222
58.158	20	CCCAAGACCCCAATTTGATT	60.91	20	160	544	703
59.7	20	CGCGTGGGCTGTTAGTTTTA	61.166	20	272	1828	2099
59.644	20	TGAGGAAAACCAGGAGCTTG	60.366	20	251	44	294
59.926	20	ACCCTGATCATCCTTTGACG	59.927	20	199	1153	1351
59.9	20	AGAGCTCTCTCACAGGCTGC	60.041	20	235	30	264
59.685	20	CACTTGTGGCTTTTGGAGGT	60.149	20	276	1304	1579
60.606	20	TCACGAAATCGAAGTGAACAA	59.307	21	257	635	891
60.223	20	GCCTTCTTGGTCTGAACCTG	59.844	20	218	1393	1610
59.795	20	AACCCGTTTACGTTAAATTTATGA	58.113	24	243	2986	3228
60.91	20	GAGATGATGGCAAGGAAAGC	59.78	20	125	6	130
59.939	20	GTCACCGGAAGAGAAAGCAG	59.989	20	260	372	631
60.042	20	TGGTTCATTTAGTCGACCCC	59.79	20	100	2019	2118
60.111	20	CAGGTTTACGGGGCAGAATA	59.953	20	277	1122	1398
60.191	20	TCGATTCTGTGCCAGTTCAG	59.984	20	177	900	1076
60.022	20	ATGGAACTCCAAAAGGGGAC	60.169	20	155	2255	2409
60.91	20	TGTAGCCCTTAAAACTTGGACA	58.809	22	272	1	272
59.009	20	ATATTTTGGGGAAAGGGGTG	59.882	20	168	1126	1293
59.926	20	TGACACTGATGAGAAAGCCG	59.984	20	187	1193	1379
60.333	20	AGCACGAGCCTCAAAATCAT	59.843	20	273	960	1232
60.893	20	AGAGAGTCGATTGCTTGGGA	59.95	20	191	1193	1383
59.864	20	AGAAGGTCATGACGTCCCAC	59.969	20	135	669	803
59.989	20	ACGTGAAGTGGGACTATCGG	59.989	20	232	126	357
60.688	20	TGGAGAGTGCAGAGATGTCG	60.138	20	105	84	188
59.722	20	ACACAAACGACACAAGTCCG	59.641	20	230	2277	2506
59.962	20	CCGACCTCACTTAGTGGGAA	60.103	20	187	1069	1255
60.088	20	CTTATCGGAAATCGAGCTGC	59.945	20	231	1132	1362
59.48	21	CAGGCTTGCCTTCACATCTC	60.945	20	159	2070	2228
59.988	20	GTGAGGGTGCTACCTTCCAA	60.111	20	266	556	821
60.461	20	CCCAAGACCCCAATTTGATT	60.91	20	213	1750	1962
60.709	20	TGCCTGCAATCAAATCTCAG	59.948	20	195	521	715
59.244	21	GTTGAATATGGCGGAAGAGG	59.528	20	280	422	701
59.928	20	TAAAGCCGTGTACCTCCACC	59.993	20	207	2567	2773
60.051	20	TGTCCTTTGGGTTCGTAAGG	59.964	20	259	2747	3005
59.757	20	TCTGCAGAAGTCGTGAAACAA	59.624	21	187	2236	2422
59.993	20	CCCAAGACCCCAATTTGATT	60.91	20	193	561	753
59.297	20	CGAGATAGCCAAAAGCGAAG	60.11	20	114	7	120
59.833	20	ACCCCCAAGTTCTTCTTCGT	59.972	20	220	293	512
59.537	20	CATTTGCTTGAAACGTCCAT	58.625	20	279	981	1259
60.08	20	TGATCCCTGCCCTAAATCTG	60.029	20	223	2487	2709
58.409	20	TCGCTGTGTATGCATGAGTG	59.436	20	226	475	700
60.469	20	TGGCGAGTTTTATGCTGAGA	59.566	20	197	275	471
59.927	20	AAACCCCACATGCAGAAGAC	59.973	20	255	474	728
59.111	20	ACAAATGGGGAGGAGGACTT	59.795	20	273	1857	2129
60.096	20	TCGAGAGCAAACTTTTTGGAA	59.982	21	280	139	418
59.872	20	TGATTCAATATTAGCCGTCCC	58.912	21	272	828	1099
59.945	20	TGAAAACTTTGGGATGGGAG	59.903	20	248	213	460
60.315	24	GCAGGTGGTGTTTTCCAAGT	60.012	20	136	0	135
60.366	20	TCCTCTTCTCCTCGAGATGC	59.636	20	148	53	200
60.91	20	GCGGAACCGTCCTAGTTACA	60.132	20	257	1	257

59.807	20	TCATCATCAGCCAAACGGT	60.064	19	240	967	1206
61.003	20	GCGTTTTCCAGACCAACAAT	59.978	20	198	13	210
60.038	20	AACAAGGGTAGGGGAAGACC	59.299	20	258	4979	5236
60.009	20	CTGGTAAACGGGTGTGGACT	59.884	20	189	2	190
59.655	20	GTGTGCAAGGTGGTCAAAGA	59.726	20	273	68	340
59.297	20	GCATGATACGAGCACGAGAA	59.979	20	206	11	216
59.42	20	AAGGCTTTGCAGGACAAGAA	59.993	20	201	1803	2003
59.931	20	TGATTGTTTAGGCCAGGGTC	59.933	20	140	36	175
60.058	20	TGAATTGAAAGCCACTGCAA	60.379	20	233	434	666
58.226	20	CCCAAGACCCCAATTTGATT	60.91	20	142	656	797
60.019	20	ACGATGATGATGAAGGAGGC	60.042	20	228	511	738
60.019	20	TGAGGAGAGTGATGGTGGAA	59.18	20	226	2176	2401
59.962	20	GTGGGTAGTATGCCGTGCTT	60.022	20	214	1575	1788
59.823	20	TGTTGCAATTTGAGGCTTTG	59.849	20	133	4	136
59.939	20	AAAAACCCCTCGACCATCTC	60.306	20	260	338	597
59.876	22	GTTGAGTCCAACCCAACCC	60.207	19	228	347	574
60.034	20	CCAGATCCATCTTTCCTCCA	60.003	20	131	1381	1511
59.734	21	CGAAGGAATGCGTAAGAAACTT	59.793	22	259	1585	1843
59.844	20	AGCAATAAGGCAGCAGCAAT	60.01	20	167	643	809
59.903	20	CTGCTTCAATCCTCCGACTC	59.95	20	180	359	538
59.955	20	CATTATTGGAGCCCATGCTT	59.923	20	273	1748	2020
59.758	20	CCCAAGACCCCAATTTGATT	60.91	20	248	1729	1976
59.992	20	TCTTGAATGGGCTTCTGGAT	59.629	20	239	4759	4997
60.179	21	AGAAACAGATTGGGTGGGTG	59.82	20	142	1459	1600
60.11	20	CCATGGATGCAACAATGACT	59.374	20	251	962	1212
60.074	20	TTCATGCAACATTAAGCCGA	60.215	20	199	4460	4658
59.901	20	AACAAACGGCCAAGAATCAC	59.978	20	223	433	655
59.955	20	TGATGTTTGCATTTTAAGATGAGTT	59.143	25	260	4637	4896
59.66	20	GCATGGATGAATGGAGCTTT	60.043	20	157	1579	1735
59.526	20	CCATTTTTGTTGAAGCCCAT	59.801	20	254	619	872
59.951	21	GGTCGCCTTGGTTCTTCTTT	60.61	20	250	5869	6118
60.91	20	AAGCATAAAAGGCATCGCTC	59.461	20	126	4	129
59.972	20	ATGGGACCAAAACATGCAAT	60.059	20	216	3768	3983
60.644	20	TCAGACCGCCGGTATAACTC	60.096	20	267	1608	1874
59.779	20	TTGTCGATTGGTTAGGGCTC	60.074	20	118	459	576
59.924	21	TGGCATTGCGTATGAAAAAG	59.702	20	190	1596	1785
59.955	20	ATCCAGGATGGTGGAAATCA	60.135	20	215	4606	4820
60.375	20	GAAGCGAAAAGCATTTGACC	59.829	20	276	496	771
59.989	20	GCCAAGATCAGCAGATCACA	59.95	20	186	801	986
60.14	20	TGCAACATGGTCAAACTTGG	60.552	20	129	381	509
59.807	20	AATCGACACTCCCACTTTCG	60.111	20	183	357	539
60.91	20	TGTGGCCAATCTTTTGTTTT	58.12	20	258	5	262
59.473	20	TGCTGCCAAACTAACTGCAA	60.578	20	279	1818	2096
59.807	20	CAATACGCTGAATGCAAAGC	59.472	20	280	372	651
60.91	20	AAAATGGATGGTGCTTTTGC	59.945	20	167	9	175
59.883	20	TGCATGTTTTGTGTGTGTGG	60.046	20	278	1391	1668
60.415	20	AGAGAGGTGGTGCAGATGCT	60.017	20	202	1202	1403
59.708	22	GCTGGAAGAGTGCGGATAAT	59.297	20	202	4	205
58.762	25	ATGGAGACATCTGGTGAGGG	59.92	20	211	1675	1885
59.239	22	CGGCATCCATCTCAATCTTT	60.036	20	223	96	318
60.374	20	TCTTTCAAATTCCCTTCCCC	60.237	20	264	766	1029
59.49	22	TGACAGCTGAATCAGTCGGA	60.557	20	238	1928	2165
59.82	20	AAGCCCGTGAAAAAGGAAAT	59.945	20	253	1774	2026
60.04	20	CTTTTGGCTATCTCGCTTCG	60.11	20	103	1944	2046
60.979	20	AACTGCCACATGGACCGTAT	60.263	20	192	875	1066
60.17	20	GGTAGCCGACCCCAATTTAT	60.041	20	236	1954	2189
60.11	20	CCCAAGACCCCAATTTGATT	60.91	20	189	2576	2764
59.591	20	TTTCACGAATTTTTCATTCAGG	59.098	22	209	906	1114

60.517	20	CTTTAGCAACACCAGCCACA	59.904	20	226	1	226
59.226	20	CATTCGCTTCCATTCATCTG	59.226	20	275	4929	5203
59.991	20	CGCGAACAATGATATAGGGG	60.302	20	217	312	528
60.284	20	TGTAGCCGACCCCAATTTAT	59.297	20	222	2948	3169
60.074	20	TTGACACACTCCCTCTGCTG	60.022	20	144	5314	5457
59.297	20	TTTTTCAAGTGAAAGGTGCAA	58.451	21	155	7	161
59.943	20	GTCCAAATCCGACAGATGCT	60.081	20	202	1431	1632
60.014	20	ACGGAGAGAGCCAAGTCAGA	60.135	20	190	1672	1861
60.892	20	GAGAAAGCCCAAATCCTTCC	60.017	20	270	0	269
58.963	20	TTTCTGGATCCCATCTGAGG	60.003	20	151	837	987
59.986	20	GAGAGTGTCACGGACAGCAA	60.03	20	229	624	852
59.297	20	CAAATGGCAGACAAAAACGA	59.706	20	239	5	243
59.735	19	TGGGTCTTCCCTGATTTTTG	59.903	20	260	7	266
59.297	20	ACGACGACCAAAGGAATGAG	60.111	20	259	29	287
59.297	20	TCAATGCAGCATCCTGAAAC	59.805	20	133	4	136
59.297	20	GCACTTTGAGCTGCATTGAG	59.746	20	152	3	154
60.032	20	CCCAAGACCCCAATTTGATT	60.91	20	120	2993	3112
59.734	20	TAGCCTCCAGGAATCAAGCA	60.874	20	183	3154	3336
60.111	20	TGCATACCCAAGATTGTCTCC	59.947	21	276	517	792
59.955	20	GGATTAATGGCCACGAAGAA	59.901	20	276	63	338
60.044	20	GGTTTATGAAGCCAATCCCA	59.762	20	131	794	924
59.774	20	ATTGCACCGACAAAAGAACC	59.978	20	234	3650	3883
59.457	20	CCGGAGAGGGCATCATAGTA	60.051	20	206	1862	2067
60.152	20	CCCAAGACCCCAATTTGATT	60.91	20	171	5787	5957
59.989	20	ATTCCATCACCATGATCCGT	60.018	20	108	605	712
60.134	20	AAGCCACAACCAATCAGCTC	60.263	20	131	2121	2251
60.134	20	GTGATCGGGAGAGTCTTTGG	59.655	20	249	1099	1347
60.131	20	GGTTGCTGGTAGTTTGCCAT	60	20	184	904	1087
59.297	20	AGCACAATCTTCAGGTGGCT	59.874	20	260	8	267
59.973	20	CTTTTGGGCAAAGGATCAAA	60.046	20	191	30	220
59.604	20	TTTGTCTCCTGGTGTTTGGA	59.109	20	180	2231	2410
59.752	20	GTCCGAGAAAAAGTGGTGGA	60.088	20	136	1570	1705
60.226	20	GGAAGATGCAGAAGCGAGAC	60.104	20	254	697	950
59.993	20	CCGTACCCTCCTCCTAGACC	59.95	20	178	674	851
59.931	20	AGATGGAGTCGTGTAGCGGT	59.751	20	142	23	164
60.103	20	TGTGAAAAACACGTGACATCAA	60.05	22	116	2240	2355
59.82	20	GCAGAAGGAGCCAAAGAAGA	59.694	20	272	908	1179
60.15	20	TGTTGTTGGATCCGTGTGTT	59.855	20	218	2835	3052
59.724	20	TCGCTTATGGTTGGAGTGTG	59.716	20	276	280	555
59.994	20	AGGCCAACACTGAAAACCAC	60.012	20	234	3770	4003
57.317	24	GACAGCGAGTAAGCTGAGGG	60.156	20	147	118	264
60.353	20	CTGTAGGCCCATAGCCACAT	59.978	20	220	138	357
59.297	20	TTGCGTTCAACGATTTTCTG	59.849	20	150	7	156
60.053	20	TGGAACAGCACAGACTGGAG	60.022	20	156	211	366
59.866	20	CTGCTTTTTGTGATTGGGGT	59.971	20	162	226	387
60	20	CCTTCACACCAAACTGCAAA	59.734	20	225	3486	3710
59.988	20	ACGCGGTGATAAAATCTTGG	59.96	20	277	1658	1934
59.993	20	CCTCCGTCCCTCTCTCTCTT	59.945	20	219	3108	3326
59.93	20	TTTGCATCATGGTGTGTGTG	60.003	20	233	3803	4035
59.988	20	ACAGCAGCAGCAATCATCAC	60.024	20	181	2626	2806
59.948	20	TCATGACGAGCAGTGTCTCC	59.988	20	147	1770	1916
59.927	20	TCAGCCTTCAAAAGTTGCCT	59.993	20	247	501	747
60.002	20	CCGAATCCATCACATTCAAA	59.325	20	111	3717	3827
61.042	20	ATTAACACCGGCATTGCTCT	59.597	20	234	2707	2940
59.893	20	AATCCCAATCCCAATCACAA	59.991	20	114	699	812
60.241	20	CCAATTTATTGGGATTAAGGC	57.539	21	265	3817	4081
59.955	20	TCATATGACGCAATGCACCT	60.104	20	251	502	752
60.285	20	TTGGAATGCAACTCAAACCA	60.088	20	161	20	180

59.184	21	AAAGTGCGGAATTTGCTTTG	60.244	20	197	1229	1425
59.978	20	TCCTAATACGACTGCCCACC	59.955	20	222	160	381
60.011	20	TGAGAGAAGGCGAAGAGGAG	59.82	20	203	781	983
59.297	20	TGCACATTTACAACCAACAAAA	59.027	22	140	3	142
60.112	20	TTTCCCTCTTTCGTCCTTGA	59.784	20	267	2779	3045
59.955	20	ATGTAGCCGACCCCAATTTA	59.297	20	157	3318	3474
60.096	20	AAATCATAGCTCCGCCATTG	60.06	20	205	667	871
59.716	20	TTCGCCCCTTATCTACATCG	60.053	20	171	487	657
59.823	20	ATTATGCGCTTACCGTGGTC	59.988	20	171	134	304
60.606	20	TTGTGCCTTGAAGATTGCAG	59.988	20	237	1573	1809
58.663	21	TGAAACCCCATGTGTTCAGA	59.935	20	271	1336	1606
60.149	20	CGGAAGTAGGAAAACACCCA	59.964	20	239	744	982
58.804	20	GCAGCAATATCAACCTGGCT	60.243	20	226	2951	3176
59.165	20	AACCATGCTCTTTCCACCAG	60.111	20	238	580	817
59.769	20	CCACTTCCATTCTCTTCCCA	60.042	20	156	2336	2491
59.861	20	GCCCAAGTGTAAGAGTCGGT	59.212	20	238	158	395
59.831	20	AGCGGCATCCTCATAAATTG	60.06	20	248	1781	2028
59.476	20	GCCATGTCGTTTACTCCGAT	59.962	20	264	346	609
59.521	20	TCCCCAACTTTTTGCATTTC	59.916	20	221	1310	1530
59.855	20	TTTTGACACCCAGTGTTGGA	59.976	20	274	327	600
59.973	20	CCGACCCCAATTTATTTGAA	59.633	20	123	1998	2120
60.664	20	GGTTGCGTACATCTGACCCT	59.997	20	263	1012	1274
59.779	20	TCAGTCAAACCACTCGGTCA	60.285	20	194	1759	1952
60	20	CTCCCAAAGTCACCTGCATT	60.111	20	160	604	763
60.175	20	GGTTTTGCTGCGTTTGATTT	60.117	20	130	148	277
59.297	20	ATCCCATGTGCTGTGATGAA	59.925	20	224	4	227
60.91	20	GAGATGCTCTCGAATGAATGC	59.938	21	239	10	248
59.297	20	CTGGAGTAGGGGTCATTCCA	59.92	20	167	7	173
60.328	20	AATGATAAGATCAAGGCCGA	57.244	20	125	269	393
60.049	20	GTTCTGCAAAAGAAAAGGCG	59.996	20	212	580	791
59.967	20	TTCCATGTCGAGTTTGTTCG	59.691	20	207	964	1170
59.96	20	CAAAATCAACCATATTTTCGCC	60.533	22	233	390	622
58.132	22	TTCTAAACAATTGGCTGCTGAA	59.89	22	235	5622	5856
59.272	20	CGTAACATGCCACCAGTGAG	60.175	20	269	2293	2561
60.05	20	GAGGAGAATGCGAAGGAGAA	59.508	20	227	3104	3330
59.586	20	GATGCTGACGTGACGACTGT	59.905	20	251	41	291
60.049	20	CGAACCCCTTGTTCAAAAGA	60.081	20	254	2601	2854
60.051	20	AGCCTCCCTTTGGAGAAGAG	59.95	20	280	13	292
60.074	20	ACACTTGACTTCCCGTGTCC	60.009	20	241	905	1145
59.873	20	CAACTGCAAGATTCAGCGAC	59.596	20	228	1674	1901
59.888	20	ATGTAGCCGACCCCAATTTA	59.297	20	165	2972	3136
60.773	20	GTCGGTAACAGTCTGGCACA	59.751	20	180	2	181
60.136	20	CCCGATCCCAACTGAAATAA	59.756	20	278	734	1011
59.982	20	TGCTGCGGACAAATAACTGA	60.401	20	256	16	271
59.135	20	TTGAGTTGAGGTATGAGAAAAGTT	58.919	25	280	311	590
58.992	20	CTTGAAGCATGCACGATGAC	60.423	20	107	3	109
60.028	23	TCAATGCAGGATGATTGCATA	60.05	21	181	21	201
59.297	20	ACTGTTGCGTTATCCAAGCC	60.14	20	237	6	242
60.162	20	CTGCTTCACTAAATCCCCCA	60.066	20	118	156	273
59.985	20	CTGGCTCCCCAAGAATTACA	60.066	20	271	429	699
60.035	20	ATCTCTGTCCCCCTCGTTCT	60.073	20	213	595	807
59.765	20	CGTTGCTGCATTTCTAGGGT	60.27	20	252	2396	2647
59.883	20	TTCGCCACCTCCATTTCTAC	60.074	20	150	488	637
59.716	20	ACCAAACTCTCCTCCCGAAT	59.935	20	247	706	952
60.017	20	GCAAGCACACACGTCGTAAT	59.794	20	252	2552	2803
59.845	20	AGACCAACAATTCCAGGTGC	59.973	20	276	1263	1538
59.966	20	GTGGCAGTTATAGCGGTGGT	60.022	20	177	1699	1875
59.986	20	TCTGCTAGCACTGCCCTTTT	60.154	20	149	3199	3347

59.775	20	CGACTAGCCACGTTCAATCA	59.864	20	215	1222	1436
59.524	23	TTTTACCTTAATCTTCACCCTTTTT	57.969	25	256	1648	1903
60.528	20	AAAGAGGTTGTTTCCGTTGC	59.218	20	229	1192	1420
60.335	20	ATCATCGCCACATCGTGTAA	59.955	20	130	426	555
59.795	20	TCGTATCTGGTTGAAAGTTGTTG	59.187	23	258	1364	1621
60.187	20	TTGAACACGATGGGCATTTA	59.93	20	226	2088	2313
59.795	20	TTGATTCCACCTCTTCACCC	59.903	20	200	1311	1510
59.971	20	CCCTACATAGGGGGAAAAGG	59.655	20	134	1947	2080
60.339	20	ATGGATGCACCGATTAGGAG	59.917	20	188	2139	2326
59.297	20	GCTACTCCCGACCATTCAAA	60.074	20	136	14	149
60.011	20	TGGCAGGAAATCACACAAAA	60.088	20	255	3323	3577
60.036	21	TCCAATAAAATTTTGCCCCA	60.123	20	219	216	434
59.962	20	TAATCACCATGGACTTCCCC	59.605	20	145	2744	2888
59.603	20	ATTTGATTAATTGGTGGCCG	59.66	20	105	1513	1617
60.033	20	AGTTTGGGGCCTGAGTTTCT	60.11	20	158	293	450
60.046	20	CAAGTCACCTTTGACTCGCA	60.025	20	275	3710	3984
59.964	20	TCGAGAGCTCTGGTGTTTTG	59.161	20	204	2448	2651
60.523	20	AATTCTTGAACGCGAGGAGA	59.955	20	258	371	628
58.163	21	CCTACAAAATGGGTCTCTTTGA	58.238	22	165	2660	2824
59.641	21	TCTTCAGAAGCTTGCTGTGC	59.47	20	267	2765	3031
60.91	20	ATACCTCCATGAGCAATCCG	59.917	20	268	9	276
59.931	20	TCTGAGCAGCCACATAAGACA	59.606	21	276	24	299
59.993	20	TTTCCGGCTGTTTCAAAAAT	59.564	20	273	112	384
60.074	20	CTCTCAGTCCCAGACTTGCC	59.986	20	209	1361	1569
59.938	20	GGTTCATGTAGCACATCCCA	59.374	20	167	4478	4644
60.066	20	CTTCAACAGCTGCAATTTCG	59.609	20	273	3119	3391
59.982	20	AAAGCCCAAGCACCTTTCTT	60.242	20	214	1110	1323
59.522	20	CACCCACACTTTAATCTAAGGGA	59.42	23	280	2597	2876
60.104	21	TAAATGTGGAAATCGCATGG	59.377	20	263	1183	1445
60.227	20	CAGTCAAGTTCGGGGAGAAG	59.837	20	249	446	694
59.297	20	CACCCCAAATTCTCATCACC	60.173	20	178	7	184
58.711	21	AAAATGAAAGGAGGGGTGCT	59.94	20	125	1078	1202
60.088	20	TTGGTTCATGTAGCCGACCT	60.517	20	106	3438	3543
58.698	22	CCACGGTCTCCCAATTCTTA	59.926	20	276	2776	3051
59.934	20	CTGCCAAATCTGGGACTGTT	60.111	20	176	139	314
60.036	20	GGGTGAGGGGATGTCTATCA	59.737	20	109	323	431
59.985	21	TCGCATTGTGTCCAATAGGT	59.002	20	210	837	1046
60.187	20	CGGTCTCTCAGTTAAGTCTATCTC	59.98	25	117	670	786
60.91	20	TAACACCTTTGATGGCCCAG	60.883	20	236	8	243
59.344	20	CATTATGCAGGAACTCGCAA	59.833	20	267	5116	5382
60	20	AGCCGGTTAAGGAGGGAGTA	60.089	20	267	125	391
59.496	22	TTCAAGATTCTGAAAATTGCGA	59.832	22	247	2802	3048
60.029	20	AGGCTCGCAGACAACAGAAT	60.02	20	218	2577	2794
59.556	20	GATCGATCAGCTCCGAGAAG	60.057	20	267	1688	1954
59.112	20	CTTCAGGTTGAACACCCGTT	60.005	20	229	122	350
59.526	20	AGGATACGTGGATGGAGACAA	59.42	21	154	692	845
59.138	20	TTTGGTATGTGACCCCAACA	59.667	20	252	870	1121
60.111	20	TGCACAAAGTTTTGTTTCCA	57.794	20	229	1848	2076
59.978	20	TAGGGCTACCGGACACTACG	60.147	20	279	3700	3978
60.081	20	CCAAGGCAGAGAAGTTGAGG	59.982	20	266	5968	6233
57.289	20	AATCTCGACCATCCTTCCCT	59.896	20	155	5	159
59.92	23	AGGGAAATGTGCAGGAATTG	59.933	20	215	1796	2010
60.272	20	CCCAAGACCCCAATTTGATT	60.91	20	164	1897	2060
59.215	20	ATGCTCGTTGAATTTCCGTC	60.081	20	186	1974	2159
59.301	20	AAGTCCTACACACCAAGTTCATCA	59.964	24	216	1513	1728
59.989	20	CTCAACCTCATTGCCCATTT	59.933	20	221	1060	1280
60.012	20	AGGATGGTACAGTTGGCTGG	59.989	20	162	3913	4074
59.297	20	TGCCTCGAGAGTAAGAACCC	59.43	20	167	7	173

59.493	23	CGAGCATAACAAGACTCGCA	60.157	20	241	466	706
59.744	20	TGATGGTAGCAAGCAAAAGG	58.917	20	246	148	393
59.971	20	CCCAAGACCCCAATTTGATT	60.91	20	152	2071	2222
59.297	20	CAGTCCTGCAGCAAGAAGAA	59.314	20	203	0	202
59.96	20	TCCCTAACCATGTACCACCC	59.526	20	211	4354	4564
59.297	20	TGGTGTAGATTGTGAATAAAAAGC	59.016	25	100	12	111
60.111	20	GCAAAGAAATCAAAGGACCC	58.622	20	263	3314	3576
59.91	20	TTGATCATTTGGGAACACCA	59.75	20	259	5353	5611
59.605	20	CCATTTGCAATGGACAAAAA	59.396	20	149	1582	1730
59.986	20	ATCATGGGTGGTGTCACCTT	60.096	20	258	8588	8845
59.297	20	CCGCCCATCTCGAAGTAATA	60.053	20	176	6	181
59.988	20	CAGGAAGAAGGTGGGCAGTA	60.246	20	197	1965	2161
59.879	20	TCATTGAAACCTCCTCCTCG	60.187	20	206	2784	2989
60.132	20	GTTTGAATACGTTTGGCGGT	59.867	20	105	2185	2289
59.803	20	ACTGAGTGCAAACAAGAGCG	59.239	20	194	23	216
59.933	20	GCGGTATCAGAGTTGGCATT	60.103	20	261	1028	1288
59.894	20	GAGTTTTGTGGCGGATTGTT	59.978	20	233	111	343
58.288	20	GTATTCACGGGCAGTGGAGT	59.997	20	248	955	1202
60.074	20	ATCTCCCGGGATGTTAAAGC	60.286	20	167	2567	2733
59.297	20	CGTTTCCTCTCATTTGCAGG	60.766	20	224	9	232
59.162	22	GCTTGTTAGTTTGGTTATGTCGC	60.076	23	227	3095	3321
59.711	20	GGAATTCCTTTGCAGTCAGC	59.82	20	277	2874	3150
59.962	20	TTCACCAGTCCCATCAAACA	59.935	20	156	4387	4542
59.297	20	CGCCTTCCTTGCTCTTAGAA	59.724	20	242	1	242
59.748	25	AGGGAGAATTAGTGGAGGGG	59.392	20	134	35	168
60.11	20	CAACTAAATTGCCCCATGCT	59.96	20	212	3284	3495
59.925	20	TGGATCCAGTGTGAAGGTCA	60.088	20	249	112	360
60.112	20	ACACACCCAATTCTTCAGCC	59.973	20	224	316	539
60.103	20	ACGCTTTCACTGTTGTCGTG	59.946	20	275	521	795
59.916	20	TCATTTCAATTCGAACGCAG	59.809	20	269	801	1069
59.849	20	GCATGCCCTTACAACGAAGT	60.14	20	174	604	777
59.98	21	CCGGTTTTGTTAGGGTGTGT	59.751	20	139	1264	1402
60.255	20	TAGAAACACCTTTGCGGCTC	60.386	20	223	1511	1733
59.82	20	CAAGATAGGCCCGAAATCTG	59.662	20	232	685	916
59.992	20	GGCCTTCAAAAGCATAACCA	60.074	20	269	934	1202
60.074	20	GAGCCATCTTGTGACTGCAA	59.992	20	269	265	533
59.452	20	AAAACCCATTGAATTTGCCA	60.167	20	266	67	332
59.23	20	CTAGACATCGCCGAACGAAT	60.235	20	275	1129	1403
60.186	21	ACGGCAAATTAAAATGCGTC	59.971	20	268	1179	1446
60.365	20	AAATTTGCCCTCTCCCTCTC	59.651	20	154	0	153
60.119	20	GAGACTGTGGATGGGGAAGA	60.048	20	278	534	811
59.213	20	GATGAAGACTTGAAGTTGGTGG	58.695	22	244	385	628
60.525	21	TGTTTTCGGATCAAAAGTTGG	59.961	21	265	2709	2973
59.679	20	ATGCCTTTTTCTGCCATGAG	60.214	20	269	2282	2550
59.049	21	AATATTGCTGAATCGAGCGG	60.196	20	193	1458	1650
59.979	20	GGTCGGAGATGATGGTCCTA	59.886	20	166	1201	1366
59.787	20	GGTCCGAATACCAACACCAC	60.096	20	257	997	1253
60.012	20	CAGAGAGAGAGAATGCCCCA	60.488	20	272	260	531
60.357	20	GCTTCTTGATCAAATTCCGC	59.791	20	274	926	1199
60.073	20	AACCATCCGCGTGAAATTAT	59.301	20	258	798	1055
59.541	20	ATGCCCACCCCTACTCTTCT	59.957	20	215	739	953
59.828	21	GGGGAGGGAGTTTTTGTTTC	59.783	20	270	3825	4094
59.984	20	GCTGTTTGGTTTGGCAACTA	58.822	20	208	369	576
59.955	20	TTTGATGACCAAGGAGAGCC	60.195	20	215	128	342
60.112	20	ATCAAATCGAAGACGCCAAG	60.214	20	182	378	559
58.165	23	TGTGGAAATACCCTAAATTGGT	57.44	22	211	1339	1549
60.488	20	TTCCTACCTTCACTAGTTTTCATGG	59.946	25	187	322	508
60.025	20	AGGCAGCAATGGCAATAAAC	60.103	20	263	801	1063

60.594	20	GTCGAAGGCCTTTTCGAAGT	60.743	20	148	576	723
60.011	20	TGAATCTGCAATTTTCTTGTTGA	59.75	23	141	331	471
59.813	22	TGCAGAAGGTCAGAGGAGGT	59.986	20	162	505	666
59.875	20	CACACAAAATTGTGCCTTGC	60.157	20	255	25	279
60.008	20	CGGTTGATTTTGAAGTGGCT	60.11	20	118	216	333
57.41	24	AACAATTATTTGAGGCGCAAT	58.643	21	184	737	920
59.706	20	GGGATGGTGGAAGAGCAGTA	60.073	20	223	1342	1564
60.142	20	TGCTCTACATTCGGTGGAAA	59.272	20	103	612	714
60.176	21	CACAACTCGCAAGACTCCAG	59.616	20	236	1006	1241
60.225	20	CCCCGTATTTTCACAAATAAAA	58.001	22	237	89	325
59.859	20	TTGTTAATGGGGTGGGGATA	59.872	20	278	701	978
59.899	21	TATGGACGGTTCGGTCTAGG	59.948	20	271	1985	2255
59.559	20	CCCGTATTTTCTTCGGGTTT	60.177	20	200	50	249
57.338	20	TGTTTATTTCCCCCATTCCA	59.988	20	265	544	808
58.969	21	TGGTGTTTGTGGGTGATGAA	60.829	20	170	292	461
59.769	20	ACATGGGGTTCGAGAATGAA	60.317	20	175	798	972
60.004	22	CATATTCGTGATGGATTGGCT	59.799	21	211	33	243
59.496	20	TGCAGTACAAATTTAGCTGGACA	59.829	23	130	257	386
60.081	19	ATTTGACGAAGAACGGCTTG	60.249	20	237	8	244
60.235	20	CCCCCTGCCTTTCTTTCTAC	60.068	20	143	470	612
60.34	20	AATCTTCTGGCTGCTTCGAC	59.579	20	202	256	457
59.746	20	CGCAGTCTCCTTTTTCTTGG	59.986	20	193	342	534
59.644	24	TGGGCGTTGTTCTGTACTTG	59.758	20	244	8	251
59.805	20	TTTGATGGATTGTCCGCATA	59.891	20	208	1611	1818
59.626	22	TCGGAGAGCTAACAGAGGGA	60.088	20	231	26	256
59.993	20	TGCGCGTATGCATAAGGTAG	59.886	20	238	4347	4584
59.813	20	CAGAGCGCACTCGAAGAGTA	59.49	20	243	335	577
60.074	20	AAAACACCTGGGACCACAAT	59.162	20	213	224	436
59.003	20	GCCAAGAATTGAAAAGGCAA	60.188	20	178	865	1042
59.195	20	GGATTCAGCTGGAAAAACCA	60.051	20	183	132	314
60	20	TGATCATCCTCAGTTGTTGATTG	59.985	23	225	436	660
58.495	22	TAGTTCCGAAATGATTGCCC	59.901	20	252	2206	2457
59.837	20	CTTGTTTCCATTCCACCTGC	60.495	20	256	5815	6070
60.694	20	AATATGTTTGAGGCTGCGCT	59.873	20	261	1260	1520
59.934	20	GCCTTTCTCCTTTTCTTTAACCA	60.114	23	278	857	1134
59.939	20	TCTTCCGTAAAGCGAAGGAA	59.953	20	256	755	1010
59.903	20	ATCATTCACCAACACGCAAA	59.972	20	103	3060	3162
59.989	20	CCCGTTGAAAAAGTCTGGAA	60.081	20	195	6515	6709
60.133	20	TGTTGCAGATGTTTCTTCGG	59.84	20	186	757	942
59.848	20	TCGGACTCCGTCCATAACAT	60.34	20	172	1506	1677
59.829	20	ACGGTGTTGATTGTTCGTCA	60.008	20	219	12	230
59.996	20	CGGTCAACCGATTCCCTATT	61.061	20	246	637	882
60.051	20	TTTGTGGACCTAACGCATGA	60.111	20	146	390	535
59.752	20	GGTTGGATGAAATAGTGCCG	60.331	20	160	11	170
59.933	20	AGGGACGGTGCTATTTAGGG	60.332	20	245	98	342
59.894	20	TCCGAGCCTGAGTCAATTCT	59.95	20	141	274	414
59.799	20	CAATTTGGTTGGGTGCTTCT	59.971	20	203	32	234
57.372	23	CGGATGAGATGCAAGAAAAA	58.843	20	278	1930	2207
59.806	20	GAACCACTGAACCACGGAGT	60.009	20	103	706	808
60.149	20	TTCAGCAGGCGTAGACATTG	60.011	20	239	279	517
59.923	20	TTGCGGACGTCAAAATTCTA	59.301	20	170	2172	2341
60.21	20	AATGGGTTGTCCCCTTTTTC	60.032	20	199	115	313
59.892	20	TTGCACCCTGAGCAATAACA	60.257	20	275	533	807
60.012	20	TGCGTTGTCGAGTGGTGTAT	60.183	20	171	697	867
60.786	22	GATTCTGCGAAACATGACGA	59.805	20	276	2031	2306
59.945	20	TGTTAGAGTGGCCGAACTCC	60.255	20	204	168	371
59.541	20	TTTGGGTCAATCATTTTGGTT	59.168	21	250	510	759
59.903	20	CACGACCCAAATCAACTATTCA	59.861	22	236	1824	2059

60.156	20	TGTCCTTTACAAGGCGGGTA	60.493	20	247	101	347
60.267	20	GAATCCGAACCCTTCTCCTC	60.015	20	165	25	189
60.014	20	CCTTGAATCTCAGCACCACA	59.831	20	230	898	1127
59.894	20	CTTTCGTTTCCAATGTCGGT	59.971	20	260	2511	2770
59.948	20	TCCGTGTGGCTAACAATTCA	60.111	20	262	77	338
60.11	20	TTTGGCATTCCTTTTTCAGC	60.188	20	105	42	146
58.973	20	TGATTTTGGCCTTTCAGCAT	60.585	20	261	2650	2910
60.008	20	TCTGGCACGAATGGTGAATA	60.073	20	234	610	843
60.081	20	TGCGGGTAAGGAAATTTGTC	59.938	20	130	1732	1861
59.882	20	TGCAATCTGCTCCATTTAACA	59.315	21	225	371	595
60.671	20	TCTCAAGTTCGCCCTTTTTC	59.429	20	260	1074	1333
59.772	20	TGCTTCCAAATAATGGCTTCA	60.574	21	228	118	345
60.791	21	CATACATTTTATCATCCATTCGC	58.405	23	249	13	261
59.997	20	TGTGAGCGTGTGTGAGTGAA	60.07	20	271	224	494
59.868	19	TTTTGGCATAATCTGGACTAAACA	59.904	24	238	177	414
60.801	20	AAAATACCATTAACACGCAGGA	58.567	22	240	538	777
59.974	21	CGTCCCCTCTCTCCCTTAAC	60.067	20	222	48	269
60.046	20	GAAAGGAAGAAACCGGCAAC	60.968	20	252	109	360
60.15	20	TTGACAACAACTTTGCCAGC	59.888	20	156	412	567
60.173	20	TAGAGAACACGTGCAGAGGC	59.191	20	191	2684	2874
59.696	20	TGGGGAGAATGTAATAGCCG	59.916	20	271	1433	1703
59.98	20	TGATGACCTGGAGTTGTGGA	60.088	20	227	6797	7023
59.894	20	AAATCGCACACATACCAGCA	60.142	20	115	450	564
60.089	20	CACCATATTTGTGTTTCTCATTCG	60.625	24	209	127	335
60.263	20	CCATGATCAACCATGCCATA	60.159	20	250	440	689
57.547	24	TCTATCTCGGATCCAATGGC	59.998	20	224	1067	1290
59.907	20	TGAGATTGGTTGGTGCTGAG	59.831	20	253	786	1038
60.088	20	AACCTTTCGATGAGGCCCTA	60.949	20	160	965	1124
59.903	20	CCCCAGTTCCCTCCCTACT	60.312	19	122	227	348
59.762	20	TAGTATTGTCCCTCCACCCG	59.807	20	279	1629	1907
59.799	20	TCATAAGGATTCGGCCAGAC	60.036	20	245	7	251
59.973	20	TGCCAAGCGAATGACATTTA	60.215	20	208	226	433
60.797	20	TCTTCAATGCCACAAGTGCT	59.445	20	263	1579	1841
57.987	27	TCGTACCAAAATGTGCAACAA	60.022	21	126	0	125
60.11	20	TTTCCCCTTCATGTCCTACG	59.926	20	241	190	430
60.796	20	ACGGTGAGGATTTGTGAAGG	59.966	20	256	82	337
59.037	23	TCATGGAATGAAGTTCTCAAGC	59.316	22	107	563	669
57.578	20	TGGAATTTTCCAAATCTGGCT	60.788	21	192	333	524
59.971	20	TCCCATGTATGTAGATTGCTTCC	60.218	23	174	230	403
60.173	20	TCTCGTCCTGACAAACTTCAA	58.483	21	214	82	295
60.027	20	CTCTTGCGAGAAGTTGGAGG	60.126	20	238	49	286
60.117	20	CGCCTTCAAGATCCACATTT	60.074	20	151	389	539
60.39	20	TTCGAGTATTGGTTAATGGCA	58.174	21	216	1349	1564
59.931	20	TCACCTTATTTCGCAATTTTCA	59.603	22	158	650	807
60.088	21	CCGTAATGCGCCTGAGTAAT	60.117	20	262	1416	1677
59.939	20	GGACCCAAAATGCCTATTCA	59.762	20	186	695	880
60.853	20	GTACGGTAGCCAGTTCCCAA	59.993	20	170	13	182
60.439	20	CCCATTTGAATCAACCCCTA	59.617	20	100	647	746
59.747	22	GGTTGTTCTCTGGAAACTGTTG	58.744	22	273	312	584
60.395	20	CAATGTCACATCCCAAGCAC	59.967	20	110	107	216
60.001	20	ACGGTTCATGATATTGGGGA	60.014	20	261	877	1137
59.813	20	CCCCAAAATTTCCCATTTCT	59.992	20	276	1365	1640
60.134	20	GGGGGAATTTATCCCGACTA	59.978	20	121	446	566
59.382	20	ACCTCCGGTTTTCCATTTCT	59.805	20	198	1348	1545
59.326	19	ATAGGCCGGACTTTCGACTT	60.096	20	203	180	382
59.429	22	ATGTCGGTTTGGTTTAACGG	59.724	20	173	11	183
60.066	20	TGACCAAATCAAGGGGCTAA	60.439	20	235	1721	1955
59.03	20	TGTCCCACATTGGAAAAACA	59.792	20	246	338	583

59.337	21	GGAACATTACAGTTGGCAAGC	59.629	21	241	2517	2757
59.997	20	TAAAGCGTTGTCTTTGAGCG	59.25	20	243	1355	1597
59.95	20	AGGTTTGAGGGCCATGACTA	59.55	20	238	754	991
60.125	20	GCTTGTTACACCACACTGGG	59.06	20	157	1038	1194
58.111	25	GACGCCCACGTGTAAAGACT	60.179	20	133	0	132
59.49	20	AGGTGTCCCATACGGACTTG	59.844	20	154	0	153
57.696	20	TGTAGGCAATTCAAGAAGCAA	58.57	21	177	729	905
60.188	20	TGGTGAATTTCTTTTTGGCA	59.133	20	273	0	272
58.733	21	TTCGGACGAGATCCTAATGG	60.029	20	211	323	533
60.036	20	GCAAATATTGCAGTCAGCCA	59.839	20	192	482	673
58.654	22	GTTTTGTCAGAGGCCACCAT	59.973	20	186	1177	1362
60.936	19	TCGAGTTTAGTTCTTCTGTAATGTT	58.319	27	223	397	619
57.066	23	CAACTAGGGGTGTTCACGGT	59.884	20	204	712	915
60.257	20	AGAGGAATGTAATCCCCCGT	59.651	20	228	160	387
59.19	21	GGCGAATTAAAATACACCACG	59.376	21	202	622	823
59.976	20	TGCATTCTAAACTGCCAACG	59.872	20	212	686	897
59.931	20	CCCAATTTTTGGGAAATCCT	59.992	20	164	496	659
59.077	20	GCTTCCATGTATGAAGATCGC	59.688	21	181	17	197
59.973	20	GGATCGAAAGGTTGTGGAAA	59.91	20	180	188	367
60.184	20	TGGTGATTTTTGCCGTGATA	59.93	20	277	534	810
60.671	20	GTTGCGGCCCATATAGTTGT	59.851	20	245	130	374
60.386	20	GTTCTGAATTCCTCCTCCCC	59.874	20	230	224	453
60.02	20	CCATTTGATCTTGGCATGACT	59.947	21	266	1740	2005
60.156	20	AAATAGCAAGTTGATGGCGG	60.096	20	168	224	391
60.406	20	TTCTTACGTTTCCTTTGGTGC	59.257	21	264	1189	1452
59.855	20	AAAGTGCTTTCATATGCGGC	60.238	20	159	2	160
60.034	22	TTTCAATCTTCATCCGAGCC	60.155	20	164	0	163
59.795	20	ATGGGTTGTTCCAAATCCAA	60.029	20	202	214	415
60.088	20	CCCATGTCTTAAATACTCTGCCA	60.369	23	269	1598	1866
60.461	20	GGTTTGGGAGAAAAGCATCA	60.051	20	265	444	708
60.104	20	CCCACTGACTCCTTCCATATCT	59.461	22	222	375	596
59.94	20	AGGAAGGGGGAAAAGGAAAT	60.122	20	186	608	793
60.49	20	CCCTATCAAACCCAGCAAGA	60.066	20	280	38	317
60.192	20	AGAATCGACAGTTTGGACGG	60.111	20	226	586	811
59.875	21	GCAATTTTGTTGTTTTGTAAACTCA	59.539	25	273	593	865
59.569	20	AGGCTCTGGTCTGCAACTGT	60.057	20	195	1385	1579
57.189	22	TCATGATTCAAAGCAGTTGATTG	60.124	23	275	229	503
59.768	20	TTTGTACGCAGCCATTACCA	60.133	20	223	940	1162
60.249	20	TTCCAGAAATTGTGTTGGCA	60.088	20	263	2016	2278
60.126	20	ATTGTCTCCCACCTGAGACG	60.112	20	229	2446	2674
60.014	20	CATGGCTAATGGACTTCACAA	58.637	21	262	1089	1350
59.962	20	GCTAGCAGCCTTGTCTGGAT	59.603	20	254	817	1070
60.538	20	AAAGTCGCGTATTTTTCGTGA	59.772	21	249	353	601
60.594	20	GGTGTCCCATTTCCAATGTT	59.508	20	228	2440	2667
60.894	20	GGCATGTGTATCAGGTCGTG	59.992	20	157	6	162
60.199	20	TCCAATTAATCCTAAACCACATTT	57.985	24	234	323	556
60.724	20	GGGGTCTTGGCGTACTAACA	59.993	20	248	142	389
59.411	20	TTCTTTTTGACTTTTGAGCAGATG	59.933	24	267	547	813
60.074	20	TGCTTTACACCCCTCCAAAC	59.971	20	162	1795	1956
59.844	20	CGATTTTTCACAGTAGCAGCA	59.122	21	279	835	1113
57.547	24	TCAGTGTTTGAATCACCTAATGG	59.007	23	184	691	874
59.888	20	TGGGTTTCCAACACAAATCA	59.792	20	167	121	287
60.353	20	TTTTGTTCCATGTTATTGCCA	58.922	21	212	4585	4796
59.992	20	AAACTCCCACATGCACACAA	60.008	20	149	222	370
59.532	26	GAAGTTTTGGAGATCCGACG	59.67	20	127	290	416
60.253	19	AGGGGCAATTTGTAGACACG	59.993	20	280	813	1092
60.204	20	ATCAAATTCCGACTTGCCAC	59.939	20	243	115	357
60.27	20	CCCATTGTTAACCCAAAACG	60.081	20	134	37	170

58.749	20	TTAACGCGCGCCATATATTA	59.233	20	225	2883	3107
60.249	20	AGTGAGACACTGAATGATATGAC	58.279	24	240	214	453
60.209	20	TTGTGAATTCAATCGAGCCA	60.197	20	159	253	411
59.532	20	GCTAAAGGCGGAACTCAGTG	60.015	20	193	3272	3464
60.12	20	CTCCAGCTGTTGATGGGATT	60.073	20	274	949	1222
59.962	20	TTGTTATTTTCATTAAGTTATTAGC	57.628	27	136	3149	3284
59.933	20	TAGCCAGAAAACCCCAGATG	60.066	20	258	471	728
59.79	20	TCGTACACGAGGAGATGCTG	60.008	20	274	1087	1360
60.795	20	ATGCAGCTTTAGCAGAGGGA	60.118	20	280	233	512
59.504	20	TCTGCCATCATCCACCATTA	59.883	20	182	166	347
59.824	20	TTTCGGATGTAACACAGGCA	60.111	20	130	1691	1820
60.395	20	CCACCCTCTCTTTTTCCACA	60.081	20	275	62	336
59.727	20	CTTCCCTCTGGATGGTGCTA	60.21	20	239	149	387
59.247	20	TAATAGAAGCGGAGGAAGCG	59.586	20	225	827	1051
59.6	23	TTGGAATTAAAACCGAGCCA	60.427	20	210	719	928
60.089	20	CAATCCAATTCCTGTATGGAAAA	60.062	23	267	583	849
60.043	20	TAGCAACTCGCTCTCCCAAT	59.978	20	198	103	300
59.935	20	GAATGCAACGACACTCGAAA	59.847	20	202	1443	1644
60.029	20	GAGAGCAAACACCCCAAGAT	59.141	20	132	49	180
60.06	20	TGTGGGATGCAATGAATCTG	60.481	20	167	5358	5524
59.935	20	ATGGGAAAGGAATTGCAACA	60.309	20	205	825	1029
60.05	20	TTGATGGAATTAAGCTGCGA	59.401	20	250	201	450
59.986	20	GCCTCTGCTTTCTCCTTCCT	60.096	20	276	2175	2450
59.793	21	CTGTTGGATTTCAACTCGGG	60.486	20	241	1141	1381
59.995	20	GCAGGCATACACTCCCACTT	60.142	20	173	384	556
59.964	20	GTTGGCCCCCTTAGATCATT	60.152	20	202	607	808
60.045	19	TCTAATGGAGATCAAGTTCGCTC	59.87	23	263	1674	1936
60.16	20	CAGCCAATCAGAAAAGTCGG	60.766	20	140	3007	3146
60.195	20	TTGCTTAATTACCATAAATGCTGA	58.866	25	240	1405	1644
57.953	22	TCCACTCCATTGGTTCTTTTT	58.54	21	280	844	1123
59.982	20	CGGGTAGGAATCAGTTTTCG	59.564	20	154	1124	1277
59.939	20	AAAATGTCAAATAAATTCTCCGAA	59.359	25	255	6398	6652
58.962	21	TATCATTAACGCCCGTAGGC	59.95	20	274	3241	3514
59.966	20	CTTTCCAAATCCCTATGCGA	60.031	20	134	1124	1257
59.685	21	CACCTCGCAACAATAAGACG	59.342	20	183	2130	2312
60.206	20	TTGCCCACCCCTAACAATAA	60.181	20	234	3	236
60.282	20	TGGTTAGGGGTGTCAAGAGG	59.959	20	251	74	324
60.27	20	TTTCGTGTTTAGCCTTTCGC	60.376	20	257	13	269
59.286	20	TTCCACCCTCTCCTTTTCTG	59.255	20	219	402	620
60.874	20	GGTTTCGCTGATTTTGTGGT	59.978	20	256	638	893
60.074	20	CCAATGGTGGTATGGTGTGA	60.088	20	214	173	386
60.573	20	CAACACCCATGTGATTGCTC	59.967	20	186	5	190
57.132	27	TCAATACCCGAGAATTGCAT	58.038	20	253	41	293
59.84	20	AACTCCCACCGACAGTTTCA	60.545	20	268	345	612
57.432	26	ATGCAAAAATACGGAAACGC	59.971	20	271	3	273
59.996	20	ACTCGACTTGATTGCGAACC	60.263	20	249	0	248
59.276	20	CCACTTTTGTGGGTTCTCGT	60.005	20	263	41	303
59.956	21	ATCAAGTCAATCCGAGTCCG	60.073	20	243	142	384
59.823	20	GCAGCCCGAGAATTGTCTAC	59.843	20	229	1902	2130
59.892	20	CCGAAAGAAACGGTGGTAAA	59.968	20	219	1369	1587
61.616	18	ATTTGAACCCACGCCATAAA	60.188	20	174	0	173
57.743	23	TGGTTTCCTTCATGCTTTTTC	59.192	21	235	360	594
57.242	22	TGCCAGGGAATTGGAAGTAG	60.066	20	105	0	104
59.716	20	CAGACCGAATAGGAGTGCAA	58.874	20	215	161	375
59.862	20	GGGAGAGTGGATGTGTAGGC	59.535	20	260	1201	1460
60.138	22	CCTTAGTGGATTTCATGGGC	59.387	20	280	1868	2147
60.34	20	CCGTGGAATGAAATTGAGTCT	59.042	21	257	960	1216
59.95	20	TGTCCAATCAAGAGGCAACA	60.24	20	149	73	221

59.864	20	TCGTTTCGACATCCGTTACA	60.111	20	279	35	313
60.362	20	GAGTTCGGTGGGTATGGATG	60.195	20	204	77	280
58.929	27	CCCTCCAGCATACCTGCTTA	60.227	20	226	1241	1466
59.839	20	CGCATGTTACGTAAATCGTTAAA	59.149	23	250	201	450
60.001	22	AAACTGCCATGCACACCATA	59.995	20	278	308	585
59.77	20	CCTTTCTTTTGACTGATGTGGA	59.215	22	223	174	396
57.963	22	TGGAGTGGCATTGCAAGAG	60.975	19	168	878	1045
60.14	20	CATCAGCAGCAGCAGAAGAG	60.032	20	156	127	282
60.096	20	TCGCTATTGTATTTAGGCAGG	57.163	21	116	316	431
59.599	20	CACCCTTGAGGTGTTCATCA	59.52	20	176	159	334
59.925	21	GCGGTTGATGATAGTCGGTAA	59.974	21	265	818	1082
59.824	22	TCTCCATCTCCAACTCCACC	60.048	20	157	47	203
59.988	20	TAAAATGGGCGAGAGTGAGG	60.206	20	128	1108	1235
59.894	20	AAGTTCACCTTCGGAGATCG	59.284	20	271	336	606
59.917	20	TATATTTCGAGGCGGAGGAA	59.638	20	268	1211	1478

FORWARD PRIMER2 (5'-3')	Tm(C°)	size	REVERSE PRIMER2 (5'-3')	Tm(C°)	size
CGAATTGAAATGAATTCTACGTT	57.426	23	TACCCCTACCCTTTGGGAAC	60.046	20
CGAACGCTCCAAATTAGAATG	59.728	21	CGATCCCCTTACCACCCTAC	60.569	20
TTCCACCATTTCCCGATTTA	60.124	20	AAACACGACCATTTTCAGGC	59.978	20
AGCCGATCTGAGTCTGCTTC	59.709	20	TTCTCATACTAAAAGGTCTTTC	59.662	27
TGAATTCATAACCTTCCCATTCA	60.533	23	AATTTCCAGAACTTTGGGGG	60.159	20
AGCTCCACCTCCAAACAAGA	59.844	20	GGCATTATGCTTCTGCCATT	60.067	20
CTGGAGCAGCATCCAAAGTT	60.397	20	GCTTGCATTCACCCAAAATC	60.457	20
TGTGTTGTGTGGAATAAAAAGTTT	60.217	25	AATAAACGTGCCAAAAACCG	59.868	20
TCTTCGTTTCTGGTCTGCCT	59.989	20	CCATGCGCTAAAAAGTCACA	59.872	20
TGCAGCAATGGTTGTGATTT	60.119	20	TGATTCTCCCTCTAATCTGTTTT	57.985	24
TGAGTCACGAGACACTTGGC	60.03	20	GCGTCTACGGTGCAGAAAAT	60.278	20
CCCTCGACACACACTCACAT	59.577	20	TGTGCGTGAAAAACAGATGG	60.699	20
TAAATCATCAGCCCACGTCA	60.073	20	CCATCGATTCTCTCTCCTCG	59.903	20
TGTTTGGCCAGCAGTAATCA	60.257	20	CAATCTCGAAAATGGATGGC	60.414	20
TTGACCGGAAGGTATGAACA	58.973	20	CGTGAGAAGCAACCAAATGA	59.84	20
TCGCTGACATCATCTTATGGA	59.241	21	TTTTATCCTTACGCAATCCCA	59.442	21
CAAGGGTTCAAGCATTGGAG	60.626	20	CCCCACACCCTCATTCTCT	59.905	19
TTCAAGCATTTGAGGGGTTT	59.546	20	CAACACAAGAACTCACCTCCC	59.607	21
CGGGGACACATAAACCTCAC	60.232	20	TTCCACCGGTGTTCTTGAAT	60.353	20
TTTCCCCTTTGCCCTCTATT	59.903	20	TTGGGAGGGAGAGATTGTTG	60.042	20
CCCACTGATTTGTGTGAGGA	59.52	20	TTGGGCTAAGTGGAGTGAGTG	60.297	21
AGTTTTCATGGATGGATGCC	59.756	20	TCTCCATTTACTGCTTTCCGA	59.831	21
ACGCTCTTTAACCACGGAAA	59.747	20	TGTTGACTTGCTTTCTTGGC	59.05	20
GATGACCATATCTCGGTTTAGCA	60.346	23	GCTTAATCTTTCAACGCCGA	60.343	20
TTTAATGGGCGGTTATGGAA	60.144	20	CAAATATGCTTTCTTGATCATC	58.646	25
GACATATCGTCGATCGGCTT	60.066	20	GGTGCATGACACAGACCATC	59.97	20
ATGGGTGGATGACTTTGGTG	60.634	20	AATGATCTCATGGTGGAGGG	59.737	20
TCTAACCCAAACCCAAACCC	60.938	20	CGGTTTGACTTGCCCTAAAA	60.103	20
TTTCGTCCCGAAATTTTGTT	59.429	20	CATCCCCTTTTTCAGACGTT	59.028	20
AGATGACAACCTTCGGCTTG	60.255	20	CGCGAACTTTACAGGGCTAC	59.904	20
AACTTGGCCCCTAAGCTTGT	60.13	20	TTGGGCTCGAATCTCTTGTT	59.813	20
CCATCTATAGCGGTTAGCGTG	59.772	21	CGGAAGAATTAGAAACGGCA	60.202	20
CCCACTTAGGAACATTTAGGGA	59.368	22	ATCCAGCCAATTTTATCCCA	59.23	20
TTGATACCTCCTCCCACGAC	59.927	20	TCGTAATGATCCCCCAACTC	59.75	20
GTTAGCGGAGTGAATGAGGG	59.694	20	GGCCGTTTTAACGGTTTTG	60.342	19
AATTGATCATGGCTTCTGGC	60.043	20	AAAATCGCGCTTACATCACC	60.103	20
GGAGTTTGACACCTAAAGCCC	59.99	21	CTTTGGATGGATGAACTTGGA	59.918	21
ACAGGCTCTTTGGAAGACGA	59.989	20	AAACCAACAGCCGAGATTTG	60.11	20
TGGTTATTACTGGAACGCGA	59.182	20	CCGATATGCTATGCTTTTGCT	59.38	21
TTTGTTGGCTAACAGGTCCC	59.971	20	CCATGTTGTAATTAATGTAGG	57.155	24
CGTGAAGGCTGGGACATACT	60.134	20	GGTCACGAGAACACGCATAC	59.169	20
ATTTGACATCTAATACCCAACTAT	57.03	27	CATCCACTCGCATCACAAAG	60.263	20
GCGCTCTCTTCTAGCCTCAA	60	20	CAAAAGCGCACAGAGACAAA	60.172	20
AGGATACCCTCTCAAACCCTAGT	58.616	23	CGGAAACAAGCAACTACAGC	58.58	20
GGGGCGTGACAAGTTATGTT	59.859	20	ATGGATGCCGATATTTGAGC	59.891	20
ATCAAACAGCTGAGGCTCGT	60.02	20	ATTCCCATCGATTGAACCAA	60.133	20
TCCAAATGCAAATCAGTGGA	60.049	20	ACCCCACTAAACCCAAACTT	57.435	20
AATTCTAACCATCTTCTTTTGCC	57.932	23	AGCCATTTTCCAAGAGCTTAA	59.416	22
ATCCTCCCACCCCACTTAAC	60.052	20	CGACACGAACGGTTTAGGAT	59.993	20
GAGAGTTGTAGGGCGACTGG	59.867	20	CTTGACTTCAAACCCCAACG	60.52	20
GACTGTTCGAGCTTATCCGC	59.985	20	AAATGAAGTGCAGGGTGGAG	60.111	20
CGTACTGGCCTAAATAATGTCAA	59.05	24	TCAGTGGTTGTAACATTGGCA	60.019	21
GGAGAGCATGAAGAATGAACC	58.731	21	CACCCGAAAACCGAATAAGA	59.931	20
TGGTGAGATTTGTGGTTTGG	59.389	20	GACCCTTAATGCAGGGTTTG	59.429	20
TCGGTCGAAACCGAATAAAC	59.938	20	AGCGGCTACGCTAATTCTGA	60.138	20

ATTGGCAAAATATCACCGGA	60.153	20	TGATCTCAACGGTATGCTCG	59.823	20
CAATAATTTTGTTTCCCACCAA	58.76	22	CAATCTGGATCGTTTGATACC	57.015	21
ACGATGTCCTCTATCACCCG	59.95	20	TCCAAAAATCAAAGCTTGAAG	58.987	22
TTCACAAACCACGTTGACATC	59.455	21	CGTCAGCATTTACCCCAACT	59.993	20
GATAGGCCCTAACTCGACCC	59.925	20	CATTTTACGAACGAACCACG	59.083	20
TTGGGGTGATGACATTGAAA	59.75	20	GAGCAATGTTGGTTGCACAT	59.577	20
AGAGAAAGATAGGGGGCGAA	60.166	20	AACAACAACCCCACCCATTA	59.948	20
GGGATGCCATTCGTTAGTCC	61.606	20	CAAATCCCTCGTGTTCTTCC	59.526	20
AATTCGGGTTTTCCACGTAA	59.315	20	ACCGTCCATCTTAATGCAGC	60.103	20
CCCCTTTGTCAACTTAGGCA	60.103	20	CAACAGTTTGGCATCAGAGC	59.445	20
AGTTGATTCCTAGGCGGCAT	60.978	20	GGTTGTATGAAACCGTTAGTT	59.826	23
CGGTGGAGTGGTTTCACAG	60.137	19	TCACTCCGCCAACTAACAAA	59.317	20
CAGAGGATCCAAATCCGAAG	59.623	20	TCCCATGAATGTTTGTGGTG	60.216	20
GCTACCTTATTGATCCATTCCTC	58.188	23	GCGCTTCTTTTGTATCCCAG	59.845	20
GCATGAAATTGTGTATTTTGGTG	59.288	23	CATAAGACGATGCGAGGTGA	59.823	20
TTGCCGGGAAAGTTTTCATA	60.427	20	GCCCCCTTCTGAATCTCCTA	60.537	20
TCTCTCTTTTTGGTTGGTGGA	59.697	21	GATTCAAGCATGGAATCGCT	60.185	20
TTGTGAATTGGGTATGTGAATCAT	60.352	24	CCCATTCCCAAATCCCTTAT	59.846	20
AAAATGTGCAATCTCAGCCA	59.276	20	GTCTTGCACGATTCTCCACA	59.837	20
ATGGTCGTTGACACGACAGA	60.162	20	TTATTGCCTACCAACCAGCC	59.96	20
TGCAAGAATGGGTTTTTGAAT	59.442	21	CACACATAAATGGGTTATCAA	60.232	24
TCTGCAGAAATAAGGGGTTCA	59.693	21	TCCAACAATCTCCCACTTGA	59.059	20
GAGCACTCGAAAAGTAGCGG	60.154	20	ATATGCCAGTGCGTGTTCTG	59.746	20
CGAGGAGAACCTTGGAGTGA	60.377	20	TACGATCCCAACGGTATGCT	60.352	20
TGAGTTTCAATTGCGTAGTCAAA	59.808	23	TCCCTCTCTCTCTCTCTCGGT	59.694	21
TCACAGACGGAGAGAGACACA	59.587	21	GTGGCGAACGAGAGAAGATT	59.434	20
TCGAACTTACCTAGGCCCATT	59.973	21	CGGTTTTGGTTTGTTCCTACA	59.884	21
TATTTTGGACGATTTTGCCC	59.773	20	GGGAAGGATTTGCACGACTA	60.074	20
TCGTCCGCTGCAGTAATATG	59.856	20	TCGGTACTGGGGCAGATAAG	60.088	20
GTGGATTGTGTCTTGCAGGC	61.684	20	ACATTTTTGTGTTGCTCCCC	59.836	20
ACGGAAATGACCCTCATTCA	60.317	20	CCATACCTAACCTGTACCGTC	60.652	22
CCGATCCCACCTTGTTTTTA	59.795	20	GCTATCGAAACAACCCCAGA	60.074	20
CCCCTCACATGCAATAAACC	60.192	20	CCTTTTTCTTGCAAGGATTGA	59.325	21
AAGGTGAACTCAAACGGCTC	59.333	20	GTTACCCGACCTGAAGGAGG	60.872	20
CGTACAACTGGTTTCATCCG	59.047	20	ACCGGCAAGAAGAAAACTGA	59.853	20
TCTCCCTCTCAATGCACCTT	59.803	20	TCATTAGCCATGTGTTCCCA	59.924	20
TTAAGGAGCGGATTCACCAG	60.206	20	CATGAGCCGCTAGATTGACA	59.972	20
TGGAAATTAGACGATTTACACAA	59.048	25	GTGCGTGCCATTTATAAAACA	58.622	21
ATTGGACACAACCCACACCT	60.135	20	CAGCCGAAAGAAGCAGGATA	60.481	20
ATTAAACCACCGCGCTACAC	60.025	20	TACGGGATCTCTTTGGTTCG	60.066	20
AAAAGGTGGTGGTGGTGTTC	59.721	20	TCCTCTTCCTTCTCTCACGC	59.679	20
GTTGGGGTTAGGTATCGCCT	60.208	20	ATTCCTCCTCAACCAAACCC	60.169	20
ATTCCCCCAAAACCGAATAA	60.361	20	GATGTGCAAAGCTGCTGAAG	59.746	20
TTGGCAACTAGATCACTCGG	58.874	20	TGGACGTAAATACCCTTTTACC	59.667	23
TGGAAATTCATCCACGTTCA	59.9	20	GGAAACCCACAATCATCACC	60.034	20
TGACTATAAGGGGTGTTTTGACA	58.551	23	ATGCGCGCTGCTTTAATAAT	59.873	20
CGTGTGTGTTCCTCTCGTGT	59.782	20	TGGGCAGTAGAATACCTCCG	60.088	20
CCCAAACTTCGTGTGTGTTCT	60.058	21	TTTTGTTTGGGACAAAAATGA	58.032	21
AAGCTTGGCCATTCAACAAT	59.574	20	TTCGAGTGACACAAGGCAAG	60.025	20
TGTTTCCTAATCTACCATCGCA	59.609	22	ATTAGGCGACAACCAACTCG	60.132	20
GATTAAATTGGCGGGTTTCA	59.773	20	AGAGACGGCAGAAGGTGAGA	60.135	20
TTTTGTTTGTTCCCAGGTTG	58.5	20	ATGTCATTCTGTTGCGGGTT	60.384	20
CCCATTATGGAATCTCACGG	60.148	20	TCACGGTCTATCTCAGCCAA	59.394	20
ACAGCCGTCCATCTCCAATA	60.483	20	TGAAGTTAGGAAATAAGGAGG	58.743	25
AAACAACAATTCATCAAATATCC	59.194	24	TTCTGGGCCCAAATCAATAC	59.762	20
ACTTTGCATCCCAGTCAGGA	60.656	20	TTGGCCTTGCCATGTATATCT	59.447	21
TTTGAGGTCCCAGCTGAACT	59.844	20	GGGAAGCTATGATGGGGAAT	60.117	20
TCACCGGAGAAGCTTAGGAA	59.948	20	TTGGGCTTTCATTTTTCAGC	60.188	20

TTCCCAATGATCCTGAGAGC	60.158	20	CAACAGTTTGGCATCAGAGC	59.445	20
GCAAATGTAGCACGCAGAAA	60.021	20	AGGTAACGAGTGATGCTGGG	60.134	20
TTGTGCACTTCATATCGCGT	60.288	20	TGTCAGATGACAAGGAAGAGG	59.844	22
AAGTGAGAATGATGAGGGCG	60.218	20	TCGGATCACATCACCACATC	60.349	20
CTTCCTTTAGGCCATCCACA	60.066	20	TCTCTCAATGTGGCAACGAG	59.984	20
CACTGACATCCATCCATTGC	59.925	20	CATTCCACCGTTGAAAGATCA	60.878	21
AGATAGTATGCCAATTTTTCGTGA	59.113	24	ATTTATGCTGACCGGAGTGG	59.955	20
TGGCACATTATTGGTCTCTCA	59.138	21	TGTGCGAAACAACCCAATTT	61.292	20
ACGTACGTGTGTGTGTGCATT	60.009	21	ATTCCCTCCTCAACACCCTT	59.795	20
AGAAGAGCAAATGGTGGTGG	60.111	20	ACCCCACTCCCTACATTTCA	59.259	20
ACGAATTTGGTGTTGGAATTG	59.716	21	AAGGAGATGACACCTAAACCC	59.864	22
CAACGGTTGTCATTGTTTCC	58.874	20	TGGCTGTCATTATTTCTCATTTC	58.262	23
CAACATTTCGTGGCCTTGAT	60.894	20	GGAAATAATAAACACAAACAC	59.233	24
CGGCCGGAATATCTAAAGTG	59.564	20	AATCCTTGAACCATTCCATCA	59.234	21
ATATTGGATGTCTTGCGGCT	59.556	20	GAGGGCCAAAATCTTTAGTGG	59.952	21
CGAAACTCACGAACCAAACA	59.734	20	TCTACGTGGCATGTGGACTC	59.707	20
TTGCTTTCCAAAAAGTTGTACG	59.333	22	CTTGAATTGAATTGGAGCAAA	59.231	22
CTTGTCGTGGTTCGGGTATT	59.853	20	TATAACCGTCGGCTTGCTTC	60.23	20
CAATTTCCATGTTCCGCTCT	60.074	20	ATATCCACGAGAATGGCAGC	60.066	20
CATCCCAAACTCTCTCGCTC	59.95	20	AGCGGTTAGTGTCGATGGAG	60.277	20
AACATTCCCCTCAACACCTG	59.82	20	CCCAAGACCCCAATTTGATT	60.91	20
CGTCGATCCTTCCTCATCTC	59.761	20	TCATCGACACCACTCATCGT	60.121	20
TCCGCCACTGATCATTACAA	60.073	20	TTTGCTGCAGTCTGTCATGG	61.023	20
CAATAACCCTTGGCTCGAAA	60.067	20	TGTCCGTTGCATGGTGTATT	59.847	20
CGTCTTTATTTCCACCCCCT	60.18	20	GATGTTGGGTCTGCAGAGGT	60.12	20
TCTTCCCCAAATTGGTTTCC	61.023	20	AAGCCCGATCTCAAACTCCT	60.212	20
TTCCGAATTAACCACGACCT	59.429	20	TTAGCTTCACACCAGCAACG	60.05	20
GTTTTGGCTACGACAACGGT	60.037	20	TTGCCTAAAAAGTTGCTCCC	59.338	20
TCTGTGCTCTCTTTCTCAGTCG	59.93	22	TTTACCGACGTCTCACCATC	58.57	20
AGGGCTACTTGGCCCCTAT	59.933	19	GAAGGTGTCTTCAATGGAGGT	59.484	22
TTGGGAGGATTTTCTCTTGC	59.244	20	AATCCGCACATGTTCCATCT	60.348	20
TTCCTTCATCTGTCACGTCG	59.831	20	CGAGCAATAATTTAACAATTTT	57.678	25
CGACGAGCATGGAAGAGTAA	59.024	20	CTTAGCCCCCAAGTTTTCAA	59.198	20
TGACGAGAGCAGAGCAGAGA	60.162	20	AACGCTAAAAGGCGACAAAA	59.89	20
TGTCCTGTTGAGGTGGAACA	60.129	20	CGACCCGTCTCTTGTGACTT	60.298	20
TCCCACGTAACGAATTTTCC	59.801	20	CAGGATGTGGTCATCCTCAC	58.886	20
ACAAAAAGCAGCACAACGTG	59.951	20	TATGGGGGAGCTGAACAAAA	60.439	20
ACTGTCCTCTTAGACCGCCA	59.867	20	GACCGTTTTAACGGATTTGG	59.315	20
GGCACGATAAGGACACGAAC	60.526	20	GGATCAGTAAAATAATAGGCA	59.934	26
AATACCCCGAGATGGTAGGC	60.173	20	ATCCGTGCCCTATCAGGAAT	60.682	20
GTTGCCACCAATGTGTTTCA	60.413	20	CATCCTCAGCTCAGACAGCA	60.294	20
TTTTGCGTTTCCAATTTGTG	59.579	20	CGATCCTCCTCCTTCACATT	59.09	20
AAACAATGCAAGTGATATTCATC	60.258	24	AAGGACTCAAGCCCCTCAAT	60.074	20
GAGCTTGCACTCAGAGAGCTT	59.13	21	TGCATTTCACCAGAGAGCTG	60.136	20
GTGACCCTATGACGCCAAGT	59.997	20	GTGAAACGGAACAAGATTTGC	59.606	21
TCCCGCTTCATAGCAAATTC	60.175	20	CCCAGATTTGTTCCTACGCA	61.021	20
CGTGTTTATGATCCTCCGGT	59.813	20	CGTGTCAACTGTGACGAGAAA	59.93	21
AGTGCGTGCTTGTTTCAATG	59.911	20	CCCTAACCTGATGCCAGTTG	60.508	20
TTTGGCGTTTGATATTTGAGAA	59.603	22	GCTATGCATCAACGCACAAT	59.724	20
TTTCCACACCACGTCAGCTA	60.301	20	CGGCTGTTTTCCTTTCTTTG	59.855	20
CGACGGTTGTGATAACGATG	59.988	20	ATGGCTAACCATCAATTGCC	59.791	20
CGTGTTCTTCACTCATCCCA	59.676	20	TTATTGTTGCGAAGGGCCTA	60.58	20
AACGCCAAAAGATTTTTCCA	59.564	20	CTACTCCAAGTCCGACCCAA	60.103	20
ACTCCCCAAACCCACTATCA	59.259	20	CACAATATCAAGAACCCCCAA	59.671	21
TGAAGGAAACCAAAGATGGG	59.903	20	TTGCATCATCCAGGCATTTA	60.035	20
GCGATAGTGGTGAGGTCGAT	60.104	20	ATTTCAGCACCCCCAACA	59.893	18
GATGAACTCTCTTGGGTGGG	59.505	20	CTAGCCCACTAATCCCAAACC	59.843	21
AGAATGGCACAGACTCCAGAA	59.859	21	TGAACCTTCCATCTTCCACC	59.903	20

TTCCGACTTACCACCACACA	60.001	20	ACCCCCAATTCTTGATAGCC	60.152	20
AACCCAGAAGAAAGACAGCAA	58.969	21	TTGAGCTCCACATCAACACC	59.682	20
AGACTCATGCGGCTCTTGAT	59.981	20	TGCGTTTTGATGATATATAGGT	58.933	25
TCTGTCGATCAACACCACAA	58.618	20	GGCCGTATTAGCAGCGTAAA	60.246	20
CGAGTGAGCATTTTGGATGA	59.799	20	AGCCACGTGTGTTCATTGAG	59.751	20
CCTCCAAATCTAACCCCTCC	59.761	20	TCATCTGCCATAGCACCAAA	60.22	20
AAACACACACACCGTCTCCA	60.047	20	CCAGATAGTTTGGCCCGTTA	59.953	20
TTTCGTGCATTCCTACCCTA	58.241	20	TGAAAGCCTACCTTGCTTCC	59.452	20
TCTCATTCACGCTTTTCAGC	59.152	20	GTTGAGCTCGGATAAGCTGC	60.125	20
GGAGTCCTCTCAGTTTCATCAAC	59.244	23	CCTGACTTCGCTGTGGGTAT	60.134	20
CCTTGAAGACAATGAAATTTTGG	59.865	23	CCCACTCCTATTTCCTCTCATC	59.057	22
TGTTATCCTTTGTGAGCCCC	59.933	20	TCAATGCTCTTTTCAACCCTT	58.823	21
GTTCAAGTCCGGCTCTTCAG	59.989	20	GTGGTATGGTGTGGAGGACC	60.096	20
ATTTGCACCTTCCACGAATC	59.939	20	GGCATCAGAGCCAAGTTAGG	59.836	20
AGTGGGTTGGACTTCCACTG	60.002	20	AAATCGGGAAACCAGTTTGA	59.406	20
ACATTTTTCTTTTGGGCGAA	59.564	20	TGACAAAGGGTGTGTTGGAA	59.976	20
CATGAGAGAGAGGGCTGGAA	60.488	20	ACGAGGGGAGTGACACTTGA	60.713	20
CCCCCAAAGTTATGGTGAAA	59.657	20	TTGTGAGCGTGTAGCCATTT	59.347	20
AAAGTGCACGTCAGAGTTGG	58.932	20	CCATTGAGACTCGAACCCAT	59.927	20
CAATCAATCTCAGCCGTTTG	59.272	20	ATGCCTCTCACATGCAACAA	60.272	20
AAACATTTTACCACATGATTAAG	58.774	26	TCAAGTCTTCCCAAGGCAAC	60.232	20
ACCTTACATCCCCATCTCCC	60.015	20	GGTGTGGTAATTTGTTGGGG	59.948	20
CACCAAACTGATTAAAATCCCA	58.852	22	TACGACTCTTTCAAGGGGGA	59.665	20
GGTTTCACGTCGGAATATTGA	59.815	21	CATGCATTAACATAGTTGGGC	58.057	21
TCCGAATATGAAATCGGGTT	59.23	20	GAGTTGGACTGGTTGCCTGT	60.159	20
TCGAGAAGTTGTTTGTCTCAACA	59.944	23	AATCAAAACAAATACTAACAT	59.002	26
TTGTCATTTTGCTGTGGTCC	59.547	20	TTGAGAGGATTTGAGTTGGCT	58.923	21
CCCCGAGGAAGCTAGAAAAA	60.674	20	ACAATCAACCGATCACCGTT	60.24	20
TCCACTCCCACTTTCCGTAG	60.103	20	TGATTTCCTAGATACGGGGC	58.998	20
CCGGGCAGAGAGAGAGAAC	60.08	19	GCGAGAACTTAGTCAACGGG	59.875	20
GGGTGGGTTTGGAGAAGAGT	60.349	20	GAAGACACTTGGGCCTGAAA	60.232	20
TAATGACGGAGCTAGGGGG	60.037	19	CTCCTCTCTGCTGAGCCAGT	59.883	20
TAGGTCACGTCAGCAAACCA	60.301	20	GCCTAGCCTATTTGAACCCA	59.182	20
AGATAGGGGTTGGGGTGTTC	60.052	20	TTTTTAAGGTGGGGAGAATGT	57.596	21
CGTTGGACCTGAAAGAGCAC	60.833	20	CAACCCAAGTTTACATGTGAC	60.318	22
AACCTTAACAAAATGAATCATCA	58.144	25	AGGGGCTGTATAATGCGAAA	59.569	20
TTCCAACTCCATTTGCAATAC	57.62	21	ACCATCCCGTTTCAAACTCA	60.353	20
AAAGCCTACCTTGCTTCCGT	60.262	20	GAAATCCTTGAACCATTCCA	57.426	20
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ACAATAACAAATGGCCACGG	60.617	20	TATTCCGCCATAGAACCAGG	59.916	20
GGACAGGATGGCGATTATTG	60.296	20	CCGAAAGCTGCAAGTCCTAC	60.015	20
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TCAAGACCTACCGAGCTTCTG	59.624	21	TTCCCTTTTCGTACGATTGC	60.074	20
TCGAAGGGGATTTTATGTGG	59.756	20	GATCAAACACCAATCGCTCA	59.654	20
TAGAAATGGGATACGGACGG	59.778	20	TTAGATATGCAGCGCGGAC	59.952	19
TTTGACAGACAAATCGCTCG	59.988	20	GGTGGTTTTCAAACTCCCAA	59.807	20
CGCAGATCTAATGGTCCAGAT	59.164	21	TCATTCACCATATCCACCCC	60.404	20
GCACCACAAACATGTCACAA	58.978	20	TCAGAGCATCAGAGCGGTTA	59.697	20
GGAGAAAGATGACGACGAGG	59.803	20	GATAAAAATGGCACACGGCT	59.967	20
CTTCGTCGTACAACTCGTCAA	58.986	21	GAAATCCCACTGCCAACTTT	59.031	20
GTTTAGGCTCATGCCCATTC	59.533	20	TGCACATTGAGACGACAAAAG	59.896	21

CGCCTTTTCACCTCAAATTC	59.685	20	CTGTCCCGTTCTCTCTCTGC	60.135	20
GCTACTTCCGACTCTCTCGC	59.337	20	GCCGGTCTTCTTCTGACTTG	59.989	20
CTTCCACGATCTCCCATACA	58.515	20	TGAAGTTAGGAAATAAGGAGG	58.743	25
TGCTAATCAGAAACTTGGAGCA	60.018	22	CTCGGTTGAGCTCGGATAAG	59.971	20
ACCATGGTTTGAGACGGATT	59.263	20	GCTTTTATTGACTCAAGATCCG	59.75	23
GATATTGACGGTTGGTTGGC	60.199	20	CAACCCCACACATTCAACAC	59.701	20
CCACGTTTCACCCCTATCAT	59.67	20	TCTGTTGTGCTGCTGCTTCT	59.929	20
CCATGGGTGGTATGGTGTG	60.517	19	ACAATGGTCCAAGACCGAAG	59.966	20
GATCGGTGAGGAGATGAAGG	59.612	20	AACCACCGAGCACCATGTAT	60.263	20
ATTGCGAAGTTGGCTAGGTG	60.27	20	TGGTTGAATTTTGTCCCACA	59.792	20
TTACGTGTTAAGCCTTGGGA	58.293	20	TCTCACGATATCCTGCATCG	59.781	20
ATGCGTGTGTGTCTGCATGT	61.271	20	GCCTTTCATCATCTTCCTCAA	59.259	21
CTTCTCTTCCACATCCGGTA	57.739	20	AAAGTGGATAAACCCTGCGA	59.569	20
TTCGATGTTGTAACGGAGACA	59.184	21	CCTCATCATCGAACCACCTT	59.927	20
TGGCTCTCACACTCACTCTCA	59.747	21	AAACACACAAATTCCCACCC	59.55	20
TCGATCGATAATAACGCTTTCA	59.717	22	AGGGAAAGGAGATCGAGAGG	59.772	20
ATGTGTCCTATCCCGGTCAC	59.661	20	ATAATGGGGTTTCAGTCCGA	59.244	20
CTTCCCACATGTCGTTCCTT	59.966	20	AGCTCTCAAGGACTCCACCA	59.986	20
CATGGGAGAGGAACCTTGAA	60.042	20	AAGAATTCGAGGGGAAGGTG	60.434	20
GCTGCGAAGAACACAATCAA	59.995	20	CGACCACCTCGACGATTACT	60.134	20
TGCAGAGGTCTCCTTTGGTT	59.844	20	AGTGCCAGATAGGCCGTTTA	59.73	20
TCGAAACAGAAAATCCGAGG	60.184	20	CCGTTTTGAGACGTTGTTCA	59.734	20
GGGGCGTGACAATATCCTAA	59.784	20	AACCATTTGGGGACGATTTT	60.411	20
GTCGCTTGAATTGCGACATA	59.839	20	GCATACCCCGGTTTCATTTA	59.66	20
TGTGGTCCCAAACTCTCCA	60.071	19	GGAGAGTACGAGAGTGAGGA	59.505	22
TACAGATTATCAGCACGCGG	59.856	20	CTACCGTCAAATCCTGGCTC	59.694	20
CACTCACTCTCACTAGCCGC	58.78	20	AGAGCCGGGTTTAAAGCAAT	60.095	20
GATACGCATTCAAAGCTGAAGA	59.501	22	TCCCCGTTTTTACTCGTCTG	60.103	20
AGACTGGGGAATGGCTTCTT	60.074	20	TCCTCCAGAAATTGGGAGTG	60.042	20
TTGGGAATTCAAAATGATTCG	59.759	21	TGTTGGCGTCGAGTTAATGA	60.257	20
ACTCGCATTAATGAGCCGTC	60.243	20	CGTGTGTAAGTTTTGTGCGAG	59.444	21
TGTCAACTTCCCTCACCCTC	60.088	20	TCTCCACTCTCTCCCACGAT	59.792	20
CAGCACTGTGAGACTGAGGC	59.764	20	TAACCACCTCTTGGGTCCAC	59.82	20
GAAATAAGGCATCAAAGTTGTCG	60.017	23	TAGGCATTATTGGATTCCCG	59.751	20
CGAGGGCATTATGGGAAGTT	61.191	20	TAATCCCGCTGAAAATGAGG	60.031	20
AATGATAATCTTCGCCGTGG	59.923	20	ACCATCGTGCCTTTGTCTTC	60.119	20
GCAATAAATCCACGTACAGGAA	59.013	22	CACCGTACGTCGAACACTTT	58.701	20
CACCTCCTTAGGTGCAAACTC	58.851	21	CTTTAGGGCCCTTGATTTCC	59.903	20
TGGAAATGAAAGGCCAAGTC	60.051	20	TCGACCTTAACCACCTCGAC	60.111	20
CGAAGAACACACACTTTTGGG	60.568	21	ACAAAAGGACGATTGGGATG	59.79	20
ATCACCAACTGGCGAGAAAT	59.556	20	GACTCTCCGGCTGTTTAGGA	59.43	20
ACCCTATCTGCCCCAATACC	60.039	20	AGGGCTTTGAGTAACTGAGGT	59.81	22
ACAAATGGCCAAGAAAGTTTACA	59.926	23	ACATAACTCTCCGGCCAATG	59.955	20
GGGGACTTTTCACTTTTGGC	60.836	20	CTCGAAATGCAGTGGTTGAA	59.84	20
TGAAGAATTCCCTTGGGTTG	59.903	20	CGGAATATCGAGAAGGTTATT	58.231	25
TCATTTCTAACGATGATGGAAAA	59.851	24	CAACGGTGATGACGTCGTAG	60.175	20
TCAATGGTTTTGGTTTGTTCC	59.693	21	TATTGCAAAGCGATTCACCA	60.215	20
ATTTCACCTGCAGAAACGCT	59.882	20	TTCGTGCTTGGTCAGGGTAT	60.517	20
TTGGCCTTTCTTGATTGTCA	59.247	20	CCACCATTTTTCTCCTCCAC	59.381	20
TCCACTTAGGTTGGCTTTGC	60.249	20	TTCAAGACTAAAATTGGTAAA	58.241	27
TTCTCTTCACACGTTTGGATT	57.315	21	CGAGTGTGTACATGGGCATT	59.445	20
GCATCAGAGCCGAGGTTAGA	60.504	20	GCAACGGAATACCACTCGTT	60	20
CACTCTATAGCAAGATCTCACGC	58.327	23	CCATTTTCAATCCTGTGCCT	59.933	20
TTCGTCGGGTCTTCATTTTT	59.546	20	CAAGTTGATGCTAGTCCTCCG	59.883	21
TCCGCCCCTTGTATTAAAAA	59.429	20	CATTTAATGCACATCATATCAC	59.228	25
AAGTTGGGCTAAGTGGAGGG	60.488	20	CCCTTACTTAATGGGCGAAA	59.075	20
TGCAGAGTAGTTCCGGTCG	59.992	19	TGGGAATGAAAAAGCCATGT	60.309	20
TTAGGCCCATGTCGTTTTTC	59.938	20	GAACTCGCTTAGTTGCTCCG	60.154	20

TATGTTGGACCAAAAAGCCC	59.801	20	TTTCAATCCCAGCCATCAAT	60.274	20
CCTCACACCCTTTACGCATT	59.993	20	CCGGGTCAACAGATTGAACT	59.966	20
CATTTCATTTCAGGAGCTTCG	59.831	21	GGGGTACAACCTTTCACACG	60.269	20
TCACGTTAAAGCATGGTATCATTT	59.808	24	TGTTGATCTAAGGATTCAAATT	60.12	25
ATCTCCGCCTGTGACAAACT	59.727	20	TTGTGTGATCGAACTACGTTAA	57.469	23
TCATCACGTAAACGGGGATT	60.192	20	AGTTACAAGCCAACCCAACG	60.03	20
ACAGCTTACACCGTTGAGCA	59.515	20	GTCGCACTGCTGTTGGAAT	59.853	19
AGCAAGGAGAAGTTCGTGGA	59.989	20	CTTTGCCCCCTTTCTCTCTT	59.821	20
GGTGAACATTGGGAGCAAAT	59.797	20	GAATCAAAGCATGTCATTTCAA	57.752	22
ACCGATTGTTGCATTTTAAGTT	57.764	22	CCCCAATTTTTGTACCCGA	60.54	19
TGATTTGGAAGAAAACGATGG	59.924	21	TCGGGTACGACAAAACAACA	60.004	20
ACCCTACACTCTACACCTATTGTA	57.104	27	GGCTTCCATTACGAACCTCA	60.074	20
GGGTAACTTGGTTCTGTAACCG	59.799	22	CAACACCATTTCCACCTCCT	59.82	20
CCCACTAACCCTTCATCACC	59.259	20	CAACATGCAACCATCAAAACA	60.408	21
TGGATCGTATAGCTTTGCCC	60.06	20	TGCGACGGAATTTAAAAAGG	60.068	20
CTTAGCCGAGAAGAACCGTG	60.008	20	GACGGTGTAAATATGGGTTTTC	59.997	23
ACTCCAAATGATAAAATCGTGG	58	22	GAGTTTGTTCCATCATTCGGA	59.925	21
GAGAGTCTTCACAAGCGGGT	59.455	20	TTTTTATCCCATGTTTGTGCAT	59.234	22
TTTGAAGATATTAGTTCAATTTGT	57.193	27	TGCACACAAGACTTTGCCAT	60.31	20
TTCCCTAGGATGAAAACTTGC	58.315	21	AAGAAAAGGAGTTAGTGGCTA	59.4	24
ACGAACGGTTGGAATATCTAAA	57.713	22	GGATGATCACCATTCGAACC	60.143	20
CATACAGTGAACACGCACCC	60.032	20	ATCGAGTTCCCTTCCGTTTT	59.94	20
AAGTAGTTATGCGTATTGTTACCT	58.804	27	ACTGACAAAATTTCGGGACG	59.971	20
CTTTGCGACGTAATTCCCAT	59.96	20	TTTGAGATCGGAGTGGCTCT	59.95	20
AAATAATTGGCAACAAAGGGA	58.484	21	GGACACCAGGGTGAGAATTG	60.363	20
TTGTGCCTTTTATTTGAGTAAGAC	59.299	25	AAACATGATACGGCCGAAAA	60.323	20
TGATTCCGATGAGATCCTGA	59.117	20	CGCCGGTATTCGTGTAAGTT	60.018	20
GCTTGTAATTTTTGGCTGGC	59.726	20	CACGTGTCGACTTTTGATCG	60.301	20
CGGGTTATTACCTGATTGCG	60.335	20	ACAAAAACATGCCCCACTTC	59.836	20
CACCAACCCATCAAGAATCC	60.173	20	CCATGGTCGTCCAAATCTCT	59.927	20
CAAACGAAAAAGCCGAAACT	59.379	20	GCGTGTATCCGCCAAAAATA	60.831	20
TCAAGATGAGGAATGAAAAAGA	59.372	24	CCATTTACCCCAACCCACTA	59.541	20
GGAAATAAGGAGGTGTTATGAAA	60.434	25	AATATCGTCGGAAATGTCGC	59.929	20
GTGATGGTTGGTGTTGATGG	59.656	20	AACTCTCTCCCTCCTCTGCC	59.952	20
AGGGGGAAGAGGTTGAAGAC	59.534	20	AGGAACCAATTATCCCGAGC	60.286	20
TTTGATAGAGCCGGATTTGG	60.031	20	GCCCAATACCGTGACATACC	60.081	20
CGAAGTTTGCATTTTAAGATGAGT	58.926	24	AAACATGATTAACAATGATGG	59.553	25
TGTTTTGTCTTTGTGGTGCG	60.732	20	TGTGTATGGAATGAAAGGCTT	57.342	22
TGGTTACTGTTACGTATGCCAA	58.175	22	CACCAGATGTCATGGTTTTCC	60.225	21
TTAACCGTTGTTTTCCCCTC	58.925	20	TTCCATCTTTCAACCTCATCG	60.059	21
ACCATCAAGGTCAAACCTGC	59.973	20	AATTTGACGGTGGCAATCAT	60.199	20
ATTGCTGTTGTGTTGGCATT	59.054	20	CCGAAATGAAGAAATGAGTTC	59.945	22
TCTCAATGGGGACATCTGGT	60.326	20	TGACGGGATTTAGGTGTTTTG	59.847	21
GAGGGAGAAGATGAGGAGGG	60.149	20	TTGATGATGGAATGAAAATGA	59.291	23
AGGCGAGGGAGGAGATAGAC	59.801	20	CAAGCATAAGGATTTTCGGA	57.845	20
AAATATGTTTGTGCTGTGGGC	59.881	21	CCAGAAGGTGCAGTGGTATG	59.161	20
CGGATTTTCACAAGCTCGAT	60.214	20	CCCAAAAATAGCTACCGCAA	60.089	20
CCGTGTTACCCTTCCATCTG	60.366	20	TCACAAATAAGGAGGTGCCC	59.933	20
GGATTCTCCAAATCTGACGG	59.483	20	AATTGTGTGAATTCTAAATTTT	57.862	26
TTTTCCCCAAAACACCTCTG	59.942	20	CGTCGATCTGGTGAAATGAA	59.648	20
TCTTCTCCAACCCACAAACC	59.943	20	CAAGAAGGAATGCACATGGA	59.648	20
CCTAACAACAAAAGATAAAGTCA	59.181	27	TGATGCTCCTCAGAAAGCAC	59.116	20
ACCACCACCACCTCAACATT	60.135	20	TTCCCACAAAATCAACCCAT	60.029	20
TCTGCGGTACATCCAAATGA	60.073	20	GAAGTTGAAATGGGAGAGCG	59.813	20
TCACACTCACTCTCACTAGCTGC	59.871	23	ATTTGTTGCGTAGGGGCTAA	59.609	20
AGATGTTCCCAGAGTGGTGG	59.962	20	ATGCCACCTGGAATTGAAAA	60.309	20
ATTACCTCCACGCCGAGAG	60.225	19	CTTACCGAATTTTGTTCCCG	59.447	20
TTGGAAAATGGTGGAATGGT	60.029	20	CTTGCAACTGGTCGAAATCA	59.84	20

TGCACCCCAAGATGGTAAAC	60.755	20	TGCCTTCTTGCCTGTTTCTT	59.993	20
GCTTGCTGAGTTGGCATGTA	60.019	20	GATTACATGATGCAGTGCGG	60.104	20
ACACAGGGGCATATGTGTCA	59.837	20	GGGGATGGTTATGCATGG	59.534	18
AAAAATGTGCATGCAACTGA	57.761	20	TGGCCACAAATGTTTCCTAGT	59.485	21
TCTCTCTTTTTGGTTGGTGGA	59.697	21	GCGACATTTTGAGGGCTACT	59.34	20
TGAGGTTTTGGGAGAAGGAG	59.255	20	TTTATATCGCCGAAAATGCC	59.898	20
TCAGTGCTGAACGTGTCAAA	59.002	20	GCAAGCATCTAGAGCGGTTC	60.125	20
GTGATTTGTCAGGTCGTGGA	59.525	20	TGTGGATTAATATAGTGGTTCA	57.953	26
AGTGTTTTGACATGATTACTCGTC	57.373	24	CTTGTGAAATGAATGCACCG	60.111	20
AAATATCGGCCGTCAGATTG	59.923	20	TCCAACCCCGAGACAAATAA	60.301	20
ACTGCAGAAAAATTCACGCC	60.257	20	ACTCGGATTCGTCACCTTTG	60.111	20
GGCCACTAACACCAACCATC	60.24	20	TTTGTGGTGACCTTGAGGAA	59.109	20
GTTCTCGTTCAAACCCCTGA	60.088	20	TGTTTGATTCATTCCATTTCCA	60.167	22
TCTCACACACGCAGTTAGACA	58.053	21	CACGACTTGCAATCCGTTTA	59.729	20
ATTTAATGTCCCACCCCGA	59.999	19	CTCCCAATCCGGTTCTATCA	59.887	20
CAAATCTTTTTCACCGCCTC	59.685	20	ACATGATTACCAACCGGCAT	60.081	20
TTCTTGGCATCCAGTTCCTT	59.67	20	TGCCCCGTTTTTCTTGTAAT	59.451	20
AAGGGGGTTATTAGTGGATCA	57.425	21	GAAGATGAGTTCGTGGAGGC	59.81	20
AATTGGTGTTATGGATTGTGTGA	59.124	23	TTTGGAAACCCATGGGATATA	59.909	22
ACTATGTGCCCTCGCCAATA	60.49	20	GCTAGGTCCTCCTTTTTGCC	60.208	20
TTGCCTGCTTGAAATGTTTG	59.849	20	GCATCAGTAAATCCTGGCCT	59.154	20
TGTCCAGATAGCCTCACTGC	58.987	20	CTTCTTGGGGACTTGCCATA	60.066	20
GGGTATCGTCATTTATACAAAAA	58.388	25	CAGCGTAAGAAAATAATTGAT	59.557	24
ACCCCTCGTATGCACTCAAC	59.997	20	TCTTTCCGCACCTTCACTTA	58.501	20
CACCATCATCCTCAGAGCAA	59.787	20	TGGTGGTGTGGTGTGAAGTT	59.89	20
CGTGAATGAAAGTGATTGCG	60.257	20	CGTTTGGATCCGATTTGGTA	60.692	20
TAGATTTGGGCAGTGTGGTG	59.566	20	GACCGGGTACAGAGCAAAAA	60.11	20
GCGAATCGAACGAATCTGAA	61.258	20	CGATCATTGTGCGAATCAGT	59.679	20
ACACCTCCTTATTTCCTAACTTCA	57.525	24	TCGATTGGTTTGTGAATTGTG	59.43	21
TCTCCCTTTCCTCTCTCGTG	59.525	20	TTTCTCCCTTTCGGTCTCCT	60.183	20
TGTTCGTTGGTGGAGTTGAG	59.72	20	CACCACTCCTCTTTCTGCCT	59.45	20
CGGAAAAGCTTGGATGAAAC	59.685	20	TCGGTTTTACCGGTTTTGAC	59.839	20
TCTTTTGGTAGGTGAATGTATTG	59.016	25	GAGGAGTAGGGTAGTGGCCC	59.957	20
TCGTGTCAGAAATCGTCAGC	59.992	20	GGGATGAAGTTGAATTGTTGG	59.278	21
TCGCCTTGTTTAGGAGAGGA	59.948	20	TTGGTGTTTGCTGTTGGAGA	60.278	20
ATGGCAATGGGACCAAGATA	60.155	20	CGTGGTTCGATCGTAATTGA	59.542	20
AATTCATCAACATGCAGCCA	60.08	20	CCCAACCCTTGAGAACTTGA	60.081	20
GGTGCTTGGTGAAGGAAGTG	60.69	20	AGCCGTCGTATTCTAAACGC	59.388	20
TGCAGTTGAGATGTCCTTGC	59.992	20	CTGAATTCGAGCAGGTGGAT	60.218	20
ACATGGGCCAAATGAGAGAC	59.934	20	TGTGTAAAGTTGGTGGGGGT	60.126	20
CGTTCCTCACTCACTCTCCC	59.835	20	CCGGTGAAGTTGGATTATCG	60.323	20
ATGGATTATCACCGGATCGC	61.961	20	GCAAATTTGTGGAAAAACCG	60.335	20
TAAATGGCAGTGTGGGTTGA	59.964	20	CGTTGGTTAATCCAGCCATC	60.331	20
CAACAAAATTCTAAAATTGCAGG	57.955	23	GCTAAACTTTAAAGGTGATGC	59.692	23
CGGATTTAAGGGTTATTACCTGAT	58.81	24	ACATGGGAAGGGCATTTTC	59.741	19
GAACACGAGAGGAAGAACGC	59.997	20	TCCTTCAAGGCCAGATTGAG	60.331	20
CGGCGAATGATGTTTCTAGG	60.597	20	TTTCTCTCCAACCCACAACTC	59.173	21
CGCATTATGGTTATGCGAAA	59.562	20	GGAGGAGGTTTGAGCAGCTA	59.574	20
TTTAACGGTTTGAGCCTATTGA	58.806	22	TCAAAAACCGGTGAAAAACC	59.817	20
CTTGGAAGAAAAACCCCACA	59.942	20	TTGATCATTGTTTCTCTCGTGG	60.11	22
TATTCGAATGCGAGGGAAAG	60.167	20	AAGATTTGATCATGGGCGTC	59.9	20
TCATTCCAACCTCCTAATCAAG	58.188	22	TGGACATCCTATGCAATGTG	57.907	20
AATGTCGCCATCATATTTTGC	59.815	21	CAAATCTTCGTTATCCCATTTG	60.187	23
GCTCATTCTGCTTCTTCCGT	59.579	20	TGTCCAAGTGATCACGCAGT	60.319	20
TCGATCTGGAACCTCGAAAG	60.331	20	TCAAATGGTAACCAATCACTA	59.328	24
TCTTGACCGCAAGAAAGGTT	59.853	20	CACCTGAATCCACTCACCCT	59.962	20
CTTCGGGCTAAACGAGTCAA	60.378	20	CAGCATACCAAGGGCATTTT	59.96	20
ATCCTTCCTTATTTCGCCGT	59.93	20	CTGAGTCATCTACAGGTCAAT	58.732	23

GGATGTAAATACGGTCTGTGC	57.104	21	CCTTTCTGAATGTGGCTGCT	60.397	20
CGTTCATTCGTATTGGGCTT	59.96	20	GATTAAGGGAGAAGACGGGG	59.897	20
ACGACTCACGACCCTACCAA	60.567	20	TCATGTACGTTGCTTATGGCA	60.148	21
TGTATGGTCTCCTTCCCTTTG	59.038	21	TTCATATGGGAAGGGCATTT	59.23	20
CTCCAACACCTCCAACTTGC	60.69	20	GTTTGGATATCGAGATCGGG	59.344	20
TCTTTAGCCCAAGTTGTATCCAT	59.07	23	CCCAACCCAAACTCACACAC	61.266	20
AAAAATGGCGATGAAACCAG	59.938	20	GGCACTATCATCAAAACCCG	60.331	20
TGAGCTGTTATGCGTTTTGA	58.075	20	GCCCAGATTTGTTCTTACGC	59.713	20
ACACCGGATTTACGTGGTTC	59.717	20	ACTGACATTCACAGGCATTG	57.067	20
TAAGCAATGAGCGAAAAGCA	59.725	20	AAAAGTTGATGCCAAAATTAG	58.451	24
GTTAAGTAACCGGAGAGGCG	58.858	20	ATTCCCCCAATTTCTGCATT	60.511	20
TCAGAAATTGTAGTCGCCCA	59.272	20	CGTTTTCTACCTCAGGGCAA	60.241	20
TTTGGAACTTGAGCAACTGG	58.897	20	CCATCACCAGCTTTGTTGTG	60.152	20
TCTGGGGTTTCAGGTAGTCG	60.103	20	CGATCGACAAAGAGTTTCCC	59.67	20
CGCAGAAAATAAATCATGACCA	59.964	22	TCCTTCCAGTCATTATCGCC	60.036	20
AGAGGTAGAAGCACTTGTGTGG	58.532	22	TGAGGGTCAACCAGGAAGTT	59.549	20
ATCGATTAGGGCAACATTCG	59.923	20	TTCATGTTTCATCCCCCTTG	60.692	20
CGCACGTCGAGAATTGAATA	59.833	20	GTCACGCTCGAGAAAGAGGT	59.604	20
TCGGGTTTTAGTGGAGAACG	60.103	20	AATTTGGCCCCGTCTAAAAA	60.645	20
TTTCGAGAAGCAGTTGGTGA	59.566	20	TGTTGCTTGCCAAAATTTCA	60.229	20
CCTTGACCATCAGATCCCAC	60.326	20	TCTAAGAGATGATTGCACCTG	58.986	23
CTTACTCCCACCGATGTTCG	60.508	20	GGAATGTCCACTCGGTCAAA	60.903	20
CATGCATGCTCGTACTCACA	59.436	20	GGCCAAGAAATATTGCTCCA	60.038	20
TCCTTTTTGTCTTTCATTCGG	59.188	21	CCCCCATAACTCCTTTCCTG	60.674	20
GCCTTGCTGCTGCTAGTTTT	59.797	20	TTGAATCAACCCTTATCGCC	59.901	20
CAGCCGGAGAAACTCATCTC	59.95	20	CTGAAAGCCATGTTTCAGCA	59.988	20
TGATCTTGCAACTTCATGCC	59.805	20	CATCGACAAGCACAAGCAAT	59.871	20
ACACTCGACAATTTGGGAGG	59.966	20	TGATGAGTTTTGTGGGTCTTG	58.609	21
TGCTTTTCAACTTAGAATTCAATC	59.363	25	GCTCAAAACCAGGATTCCAA	60.051	20
GAGCTGAAGCGAGCTGATG	59.983	19	GGGTATATGCCACAGGATCG	60.177	20
AAACTATAGGTGTTTGGTAAACG	57.059	25	CGTTCGATTTGCCGTTTTAT	59.964	20
ACAATTACAATGTTTATCCAATCC	59.341	25	CCAGCCCAATAACTCAACCT	59.052	20
CAGGATCTCATCGGAACCAT	59.886	20	TGATCAGCGTGTGTAAACGA	58.863	20
TTTCCGATTCTCAATTCCCA	60.384	20	TCGTATGCTGTGGTTTTGGA	60.111	20
TTTGTGCATGCGGACTATGT	60.142	20	GGGCCGAGATTTGTTAGAGG	60.949	20
TTGCGGAAGAAAACTAACCG	60.236	20	ACCTTCTCCGATGTCTGCCT	61.192	20
AATCTCACAAACCCACACCC	59.679	20	GCCCCCTTTTGAGAAGAAAG	60.18	20
TTGGTCACTTACACAGCAATCA	59.245	22	ACCCAGTACCACCACCATTG	60.545	20
CCCCTTTGTCAACTTAGGCA	60.103	20	GCATCAGAGCCACGGTTAG	59.41	19
TGCAGTAGGTTGTAGGTACTAAA	57.062	27	AACGACGACGAAGAACGATT	59.74	20
TGAATTTGGGTCATGAATTTTGT	60.445	23	CATGGACCCCACATGTCATA	60.048	20
GGATTTTCTCGATTGCCAGA	60.155	20	TCCAACGGCCATAAGTTCTC	60.074	20
CGGGATTTTAGATGAGGTGG	59.382	20	TCCATTCCGAAAATCAAAGG	59.872	20
GGGCAGTAAGTTGAGTCCGA	60.255	20	TGATTTTGGTGTGTTGGCAT	59.823	20
CATGTTGATTGGTTGTTGGG	59.667	20	ACATGGTTGGTTGCTTGGTT	60.277	20
GAAGGCTTACCCCTGCACTT	60.63	20	CCAAGCTTTGTGAATTTTTGAA	59.272	22
TTCCAAATCGCACTAAAGCA	59.443	20	CATCCATACTATTATTTCTTCTC	58.339	27
TCCGGTCCAATTCCAATAAG	59.756	20	ACCTATGGTGGTATGGCGTG	60.657	20
AATGCCCCTATTTTTGGAGG	60.143	20	CGAACCCTCACACTTCTGGT	60.151	20
GCACCACCATCTTCTTCGAT	60.081	20	CATTCCCGCTGATTTCTTCT	59.269	20
TCAGCAACCTGAAAGCATGT	59.445	20	TTGGGTATCCAAAAACCAAAA	59.195	21
TTAAGGGGCGGTATCATTTG	59.789	20	CCAACCAAAACATACGTTGC	58.942	20
ATTTGGTGGATGGGACAAAA	60.029	20	GCGTGAAATTATTAAGCCGC	59.722	20
AGGGAAGAAACTCGACATGC	59.288	20	TGTTTGGCGTAAGAGACGTG	59.904	20
GCCACCTCAGAAGATGGAAG	59.803	20	GTCACACCCTCTCCCACACT	60.006	20
CAATTCATAAAATACATAGAAAG	57.131	27	ATTGAAGTCTGCTGTGCTGC	59.195	20
CCAAGTTTTACCCCATCAACA	59.71	21	ACTGTCACACACACCACCGT	59.96	20
CAAACCCCATCACCAACTCT	59.82	20	CACCAAATCAAGAACCCCC	60.157	19

TTCGGCCTTTTGAAACTTTTT	60.095	21	TCACCTCCGTCTAAATTGCC	60.074	20
TTCAGGCAATACCAGTTCCC	59.933	20	ACGTAAAATTCCGGTGCAAA	60.356	20
GAAGAACAATTACAATGTTTATCC	57.771	26	TAGAGGACACTTGGACCTGAA	59.797	23
TGTTTGCAATTATTTCGTGGT	58.084	21	ACATGCCCTAAAAACCGATG	59.823	20
TGCATCAAGTTCTCTTCTCTAATTT	59.092	26	CGCTTTCTGCCTGATACCTT	59.476	20
TGAACCGATGAAACTAAAATCAA	59.885	24	TTAATGAACGGTCCGGTTTC	59.801	20
TGCGAATGTTCAATCAGACC	59.654	20	GGTACCCCCACACAAACAAC	59.989	20
AGAATGGGGAAGCTCCAACT	60.074	20	CCATTTGCAATGGACAATATAC	59.616	23
AGTTGAACCTCGAACCGTTG	60.149	20	AATTCAAGGCGTTCTCAAGG	59.312	20
AATCATTGTGCGCATGTGTT	60.003	20	CTTTCATTGGATGTAGCCCC	59.387	20
CTAGGCCCAAGGTAGTGGTG	59.61	20	GCCACTGAACCAAATGACCT	59.973	20
ACGTGTTCAAGGTTGAAGGG	60.005	20	CCAGATATGGTTGTTTGCCC	60.192	20
AACCAAACGCCCCCTAGATA	60.683	20	GCGATCGTTCACACACAATC	60.128	20
TCGGCTGGGGTAGTAATTTG	59.953	20	CCGTCATCTATTAGCACCATCT	60	23
CCGAGATAGGAGCAAGCACT	59.598	20	GGGTTTGGGAGGGTATCCTAT	60.264	21
GGGAAGAAAAACGACGAGAG	58.909	20	TCAACTGAGTTCCCTACCCG	60.103	20
GTTTCCCAAAGCCACAAAAA	59.953	20	AATTCTTCATCGCTGCTGCT	60.125	20
AATGAGGAAATCCCTCGGAC	60.272	20	TACAAGTGCAAGAAGCGGTG	60.05	20
CTCCAACACCTCCAACTTGC	60.69	20	GCTGGTACCTTCGGAACTCA	60.255	20
ATTTCCTGCCCCAAATTACC	60.02	20	AAGATGTCGCCTCTGCATTC	60.37	20
TGAAACTCCATCAAAACCTCTT	57.841	22	AAAAGTTCACTAAAACTGCCTT	57.086	24
CACCGATGAATCAGGAATGA	59.451	20	CGATCTGGAGGGAATCAAAA	60.006	20
GAGATTGGAGCGAAGAGTGG	59.95	20	AATCGCCATAGCAAGAGAGC	59.579	20
TGTTTTGTAATTTCCCATGTTTG	58.816	23	CACCGAGCTTCTACACGTTG	59.51	20
GTCAATTTTCTCAAGAAACCTCC	58.31	23	ATGTTGGCTCCGATTGAAAC	59.939	20
AGAAACGCATCGTTTTCTGG	60.249	20	CCAAGTGGGAGATTGTTGGA	60.892	20
TGATGATCAACGTTACCGATAC	57.512	22	CCAACAATTCCACTTCCTCC	59.381	20
ATAACCCCACCATCCTAGCC	60.039	20	TGAAGCCTTGTTCCTTGCTT	59.993	20
GAGGCAACTTGGTGGAGAAG	59.844	20	TAAGGTGGTGACGATAGGGC	59.955	20
TAGAAGCAGTTTCCATGGGG	60.066	20	GACAGCTGTGATGAAGGCAA	59.992	20
AAACAAGCCAATAAAGGCCA	59.586	20	TGATGCAGAGGAGAGGAGGT	59.945	20
GTGGACCATAGCACAGCAGA	59.862	20	GAAGATTGTGGGGCGAGTAA	60.074	20
GCTCAGGAGGATGGTGATGT	60.08	20	CTCATGGATCAGGAATCTGGA	60.019	21
GGTATACACGGTCCGGTTTG	60.11	20	TTTGGTAAATACAACATAATTG	58.757	26
TGCGTGTGTATGCTGAGGTT	60.333	20	ATTGCATTGCATGTGTGGAC	60.409	20
CGGCCAAAAATCAATGTACC	60.188	20	AAGGAGGTGTTATGAAGGGAT	58.028	22
TGCATTCATGTACTCAGCCC	59.679	20	TCATACGCGACCACGAAGTA	60.28	20
GCCCATGGAGTCCAATCTAC	59.366	20	TGAGCAAAAGTAATAAGAGCA	58.341	24
TCATTGGTCAAAAGTGCAACA	60.142	21	TCTACAACCCAAACGCATGT	59.05	20
TTCTGTTCATCATCTTCGTCC	57.721	21	AATCCCAAAATCTATGGGGC	59.984	20
CAGCTTGCAAAAGAGAGGAAA	59.755	21	GCAGCCACTATCCTTTCACC	59.7	20
CACTCTCCCTCTTTCTCTCTCG	59.756	22	CACAATTTCAAGAACCCCCA	60.724	20
TCGAAATCGTAATAATCGGACA	59.455	22	AGAGTGCAGCAGCAAAAAGG	60.71	20
CCCTTCCCCTTCTACCTCAA	60.426	20	ATCTCTGCTCCATGGGATTG	60.034	20
TGTTCTCATTCGTTTGCTCTAA	57.719	22	TCCAATATGTGGGGCAAAAT	60.016	20
TTTGTTGTCTGCGGTAATGC	59.735	20	AGAAGACGCTCACACAGGCT	60.205	20
AAGCTTCAGCGAGGTTACGA	60.154	20	TCCATTTTCCTCACCCCATA	60.126	20
TGGAGTTGAGAGGAGTGAAGG	59.435	21	TGGTAGGTGGGTTTAGGTGG	59.705	20
GCCTTCAATTTTATACCCGAGA	59.483	22	TGTGGTCAATTCACAATCCG	60.367	20
CGAACAAGAGTCTTCCGAGG	59.982	20	TTTTGAATCTTTGTCCCCAA	58.039	20
GCCTAACGTGGCTCTGATGT	60.285	20	CTCACCTAAACCACTTTTGAAG	58.907	24
AGCCTTCTAGCATCTCTTGCTC	59.42	22	CGTGGTTCGATCGTAATTGAT	59.837	21
TCTCTGCCTGTGTCTGCAAT	59.577	20	GGTTCGAGTCTCAATGGGAA	60.05	20
CGACAAAATGGCGGAACTAT	59.96	20	TCAATTGTCACACGTGATTGAG	59.615	22
GTTCGCAAGAACAACGACAA	59.888	20	TCTGGACACATCCTTGTTTATCA	59.485	23
TTGATAAATAGTGCAATCCCAACT	58.988	24	TCTTTTGGGAATGGTTTGTTG	59.825	21
GATTGTCTAAAACGTAAAGCTTGA	58.527	26	TCACCTCATGGGGAAATTTTA	59.26	21
GGGACAAAAACCGAAGGAAT	60.166	20	CTCACTCACCCTCTGTTCCA	58.803	20

CGAAATTCCACCGACTCAAC	60.495	20	TTCTTGGAGGCTCTTGTTCG	60.508	20
TCTTGGGGAATGTGTGCAT	59.909	19	CTTTCCTCAACCGAGCTCAC	59.989	20
TCCGTAGACCTTCCAACCAC	59.966	20	GGAGAAAGCCACAAATCTTTC	57.916	21
TGGATATGTGGAAGCACGAG	59.673	20	AAATCAAAAGGCCCACAATG	59.801	20
TTGGGCCTGTCTTAATTTGG	59.931	20	TAGGGATCGCTCCAGAAAAA	59.778	20
TGAAAGAAAGAGAAAAGGAATTT	58.221	25	AAATGCGCAATTTTAAACCCT	59.864	21
CAGTGGATCGTTCTGCTTCA	59.984	20	CTCCCACCAACCTACCAAAA	59.824	20
TTGATTGCAATAAGCAAATTTTTA	58.045	24	CTCTCATTTACACCGCCTCA	58.874	20
CGCGGATATCAATTATCAACA	58.525	21	AGTTTTGACATGAAAATTGAAT	57.739	24
TCTGTAATCGAGTTCAAGAGAGA	58.861	25	TTCCTTCATTCCTAAATGATTA	58.94	26
GCAAGGTGAGGAAGGAAGAA	59.405	20	CCGAATCCATCATCACAACA	60.33	20
ACGAGGAATGAAATCGATGG	59.894	20	TGGAAAGGGCATTAAATGAAA	59.42	21
GCAAACCCGTGTTCTTCAAT	59.978	20	TCCGGATGAGGAAGTTATGG	59.887	20
GCCTGCAGACAGACAAACAA	60.032	20	CAAAGTGGAATTTGCTTCCC	59.546	20
TGCCATGGATATGATTGTTGA	59.76	21	TAAAAGCAGCACATGCAACC	59.879	20
GGCATAAATTCATCTGAACAAGG	59.857	23	CCTGGGACACATAAGCCTCA	61.055	20
GGATGAACGTCGGTCGTATT	59.82	20	CTGAAATGAAATCTTGGCCG	60.576	20
GAATGTCATTGTTCGGACCC	60.181	20	AACATGTGATGTGATCCCCA	59.611	20
AATTCTTGGGCACAAACGAC	59.978	20	TCGCATCATCAACCTTCTGA	60.353	20
AAAAGCAAAAGAGTCAGCCG	59.632	20	GCTAGCTCGGGAGAGAGGAT	60.081	20
CCGCATGTCATGTTATTGGA	60.343	20	ACTAGCACGTGACCGGATTC	60.142	20
CCAAAAATACCCCGAAAACC	60.393	20	CCAACCCAGAATTCGTCCTA	59.926	20
AATCTCCCACTTGGGCAAC	59.918	19	TGACGAAAACTGCTTAAATCCT	58.077	22
GAGCTTTCTTTCTTCCGGGT	59.827	20	CACATCGACGACGCTACCTA	59.888	20
ATGCCAGTCTTGAGCCAGAT	59.834	20	GCCCAATGGACTGTTTTCTT	59.031	20
AGGTCTTTTACTTTTCAGACAACG	59.765	25	GGAAATAAGGAGGTGTTATGA	59.323	24
GTCGAGCCGAGTAGTTGCAT	60.428	20	TGGACAAAATGAGTGGAGAGA	59.711	22
AACTATCGTCTCGTGCCGTC	60.285	20	CGTCGAGTCTCCTCCAACTC	59.986	20
TCAACAACGATCCACTTTGC	59.697	20	ATGGGTGTGGGTGTTAGTGG	60.545	20
GAGCGAGAGTAGAAGGAGCG	59.478	20	TTTGTCGGGTCATTGCTACA	60.111	20
CTTCCCAAAGTCATTTCCCA	59.903	20	ACGATGATGTGATGGTGGTG	60.255	20
CGAGGATCCGAGGATACAGA	60.173	20	GAGGGAATGAGGGATGGAAT	60.096	20
TTGCCATATGTGGAAACCTTC	59.815	21	AAATTCAGCAGGTCCACGAC	60.119	20
GTCACGCCCCGACTATCTTA	60.096	20	GGAGTTGGTTGATGAGGTGG	60.363	20
CCCAATTTGCCCTTATATGC	59.282	20	GTTAAATCTCTTGCGAGGCG	59.982	20
TCTGTTGTTGGCAGTTCTCG	60.025	20	ATCGCTGTCACCTTATTCCG	60.096	20
GGGGGTCTGTCAAAAATTCC	60.537	20	ATGGACAGGTGGCGTTAATC	59.82	20
CATCGATTTCGTGGAGATTG	59.075	20	CGTATACCCTCAAACATCCGA	59.831	21
TGTCAATTGGAGTGAAACGG	59.541	20	TGCATGGTTTGAGTTTTGTGA	60.142	21
CCAGGACTGTTAGCCAAAGC	59.875	20	ACGGTACCACCCCAATACAA	59.971	20
ATGGTTCGCCATAAAAATGC	59.801	20	ACCCCCATCAATCATGAAAA	59.991	20
GTGGGCTTGATAGTGGGTTG	60.375	20	CTCCTCTCCTATTCGCTCCC	60.306	20
CCCACTTTTGGGTTATTACCTG	59.641	22	TCCATTCCGAAAATCAAAGG	59.872	20
TACGTGGATTTGACAGTGGC	59.572	20	TCCATTTGTCTCCCTGCTCT	59.803	20
GGAGAGAGGAAGAGGGATGG	60.149	20	GAACCACCACACCAAATTCC	60.073	20
TTGTCCAAGCAAAATTGACG	59.706	20	CCATGCCCCAGTAATCATCT	59.773	20
AAAGCTCAAAATGAAGAGGGC	59.849	21	TGTCCCCATTGAACTTGTGA	59.935	20
CGCGACACCTCTAGAACACA	60.049	20	TGACCAAAAAGAAGCCAAGG	60.22	20
GGGAGGAAATTTTGAGGCTT	59.532	20	CGTCGCCTATTCTCGTTGTT	60.27	20
TCATAGTTTTCATTTGGACACCTC	59.415	24	TTCTGGATTATCCTGCGGTC	60.036	20
CATAAGCCTACGAGCCCAAA	60.223	20	TTAGGCAAAATGGAGATCGG	60.031	20
ATCTTGCACCCTTTGTTTGC	60.118	20	ACCGAACCGATTTTGTCCTA	59.429	20
TTTTGGAGAATTTTCTCTTGCTC	59.048	23	TAGTGGGCTTTGGCACAAGT	60.689	20
TGTTTGAGTTAGCAGCCAGG	59.072	20	CTTACATCTGAAAATTTGACGC	59.307	23
CAAATTTGCCCTCGTATGCT	60.096	20	GGGGTTATCACTGGATCACG	60.195	20
CTGCATGGAGACTTGCATCA	60.991	20	CAACCATCTTCGGAGAGAGC	59.95	20
AATGGCTCATTCCCTTGTTG	59.933	20	TCCATGACAGGAACCAAACA	59.935	20
CGCACCTGAGGAGGTGTTAT	60.134	20	TGTTGGACAAGTTTAGCCCC	59.971	20

CAATCCAATATCCCAATGTTTG	59.055	22	TGGCAGAAAGATTTTAGATATA	59.31	26
TTATCACCAAAAGGAGGGGTT	59.69	21	TTTCGAAGATCAACGAACGA	59.395	20
TTGGGCCTGAATGGACTTTA	60.439	20	GGTTTTAGACCGAAACCGTTC	59.864	21
GGAGGAGATGGAGACAGTCG	59.792	20	GACCACCAAGTCAGCACCTT	60.159	20
ACGTCGTCTCAAAGGGTGTC	60.159	20	AGAGCGGCAAGGAGAAAGAG	61.161	20
TGGGCTTGAATTCAGGTATTG	59.946	21	AACATGTAACCTGTAATCTGTA	57.047	27
AAATGCTCGCTCTCACACCT	60.02	20	AAATTCTCCCATGGCAGTTG	59.933	20
CGCGTCCCTTTTTACATGAT	59.96	20	TCAGTCGGCCTAAATATCCC	58.998	20
TCCAGACTCAACCGGGTACT	59.574	20	CGGGAGCATGAAATGAAACT	60.074	20
TCAGATCTGCGCTGAAAATAAA	59.985	22	ACCAATTTCGATTTCCTCCA	59.363	20
CACATGCACACACGTGATTC	59.575	20	TTGTGGGACGGTTGAAAAAT	60.206	20
ATGGAAACAATCACATCGCA	59.931	20	TGGATAGGCCACCGAATTTA	60.281	20
TTCTTGGCCAGCTCTAGGAA	60.088	20	CATACATTCACACGGGGGAG	61.176	20
TGCATGGTAGTTGGGTGGTA	59.84	20	GGTAAAGTAATGCAGCCCCA	59.96	20
ACACATTTTTCTTTTGGGCG	59.975	20	TGACTTGAGCACCAAGAATCC	60.248	21
GACTTCGTGGCGGTATTCTC	59.7	20	TTATGCAAGCCCAGCCTAAT	59.704	20
TGTCTCCATTTGTGTGTGTGT	57.381	21	CCTTCAAAATAGGCATAACCGA	60.317	22
ACCGACCTCCACTTCAACAC	60.009	20	TCCAAAGGCTCCATCTATGC	60.177	20
CGGATTCTCAAAAGGTGGAA	60.044	20	TGAATCGATTAGGCTTATCTTG	58.055	23
TTGCTAACCAACTACGTTGAGA	57.658	22	CAACGAAATGAAGAGGGTGG	60.486	20
TCGGAAGTCCAAAGATGACC	60.05	20	CGATGACCTTGAGGTTCGTT	60.111	20
ACACGCCTTTATCCGATGAG	60.096	20	GAAGCAGGATGTGATACCCG	60.483	20
ACAATTACAATGTTTGTGAAATCA	57.636	25	AGGACACGTTGGACCTGAAG	60.151	20
ACCCGTTCCCCGTAGATTAG	60.2	20	TGGTTGTATGTCATTTAGCGG	58.57	21
TCCATTCCACAACCCATTCT	60.173	20	GGCTTTCACATTAAGCCCTG	59.708	20
GGGTCCAGTCAATGAAACGA	60.903	20	AATGGTGGTATGGTGTGGG	58.918	19
AAGTCACGGGTTCGACTAAAA	58.754	21	ACCAAATAGGGTAAGCCGTG	58.973	20
CGTTTGAAAATGGGGAAAAA	59.783	20	ATCGGGCATTTCGACTACAG	60.096	20
AGAAACACGCAACGCAAGTA	59.536	20	GACAGCCCAAGATTGAGAGG	59.803	20
CACCATCCAGCGCTATAAAA	58.794	20	TCCAAGGCAAATTGAACTCC	60.051	20
TGTGCCATTTTGAGACCAGA	60.24	20	AGCGACAAAGTGTGATGACG	59.905	20
GGTTGTAATGAGGCTTTCGG	59.569	20	TTGGTGGAAAGATTTGAGAAG	59.165	23
AAGGGGAGTATCACTTGAATGC	59.487	22	AATGCTCATCGGATTCTTCG	60.177	20
ATGCAAAATCAGTCCCCTTG	59.933	20	CCCACCAACCCAGATCATAG	60.187	20
GTGGCCTGTTCTCCCAACTA	60.111	20	TGTGGTGTGAGGGCTGTAAA	60.152	20
TTTCGAAGATCAACGGATCA	59.2	20	CAGCACGCGCACTACATAAT	59.925	20
CACGGGTCTTCATCCATTTT	59.79	20	GGACCAATTGGCACTTTGAT	59.797	20
GCAAGAGAAAATTCTCCCAAA	58.43	21	TCTCCCTTTCCTCTCTCGTG	59.525	20
TGAAAGTGCCAACTTACGGA	59.317	20	GTTACCAAACACCCAAACCG	60.125	20
CAATTGTTTTTGCCCCAATC	60.167	20	CCCACCAGTAGTCTGCCACT	60.174	20
CCAACCTTGTCGGAACAGTC	60.545	20	TTGCGAATTAGCAGCTTTGA	59.725	20
TCTTCTAGCGTTGTCCAGCA	59.74	20	CCCAACCAACAAGAACCCTA	59.824	20
GCAGGTTAGCGACGTTTTGT	60.313	20	CCCAGTTGCTCACAATGACA	60.722	20
TTCTGTTCATCATCTTCGTCC	57.721	21	AATCCCAAAATCTATGGGGC	59.984	20
TTCTTTTCCAGCCTGCAACT	59.993	20	TGGTAGGGTGGTAAACCAGG	59.705	20
ACTCTGATGCGGAGAATCGT	59.834	20	CAATTCTCTCAACCAACCCC	59.381	20
CTCATCAACCGCCAGGAATA	60.992	20	CATCATGTAGTAGCGGGCTG	59.322	20
ATCCCAATTGTAGCCTGCAT	59.415	20	TCGTCGTCGTCAAACAAGAC	59.88	20
TGCTGAGACATAGCGGACAC	60.016	20	CTGGGTTTGGTGTTGAATCC	60.21	20
AAGAAGAACTAAAGCTTCGGAAA	58.004	23	TGGACCGTTGAAATACAGAAAA	59.492	22
TGTGAACACAGCCTCACCTT	59.31	20	GTTCGTCGAGGTCATCGTCT	60.269	20
CAGCCATGGATCAGCAGTAA	59.823	20	CTCATCTCTCTCGCCACTCC	60.096	20
TCAGAAAAGTTCGAGCGTGA	59.716	20	AGAAAGCCCACCTGATATGC	59.154	20
ATCACCAACTGGCGAGAAAT	59.556	20	CATTCGAACCAAAATGCGAT	60.837	20
TCTTCATGGACGTGGAACAA	60.088	20	TGACAAAATATGGAACCACAA	59.37	23
CAAGGTGTAGATCTGGCGGT	60.134	20	AGAGCAGCAACAGTGCAGAA	59.929	20
AAAAGTCAAACCGGCACAAT	59.476	20	GCGCGCAATCACTCTCTT	60.257	18
AAAAGGGGTTGATGATCGTTT	59.696	21	ATGCGGTTCAAAGGTAGGAA	59.569	20

CGTAACGACACGAACGGTTT	60.973	20	CATCCTCCTTTTCCCAATCA	59.864	20
TTGCACAAATTCGTTTAGGC	58.819	20	GGTTGACACACTCGAACCAA	59.571	20
ACTTGCGATCGTTTCTGTCA	59.445	20	GGTCCGAATGCTGGTATGTT	59.82	20
TTCTTTTGTCAATGGAGCATCT	58.836	22	GGGGATTTGATTGATGATCG	60.096	20
TGCAATAACAAATTTGGGAAA	58.074	21	GACTGCGGATCACCACACTA	59.707	20
AATGAGGCTGCTTTGCAAGT	60.022	20	TTTGTCCCCACAAATGTCCT	60.21	20
CCCATGTGTCCACAAAACAA	60.255	20	GAAGCAGAGCATTGATGGGT	60.226	20
AAAAGGAAGGAAATCTGGGG	59.393	20	GACGCCACATCATTCTCTCA	59.794	20
TGCCCATCCATTTCCTGTAT	60.155	20	TGACATGTCCTTTCACTCCAA	59.124	21
AAGCACAAGAGACGAAGAGTCA	59.281	22	AGCCTAACCGTGGCTCTGAT	61.173	20
TCGCCTACCTTCTGCTCTGT	60.156	20	TCATTAAACCCGAATCCGTC	59.762	20
ACCCTTGCATGCACAACATA	59.995	20	GGCACAGCTCCACTTTCTTC	59.997	20
GATGCATCAAGTCGACAATCA	59.67	21	AGCCTTATCTCTGGCCGTG	60.368	19
GTCCCCATTGAGACTCGAAC	59.511	20	CAGAAAGTGCTTGTTCAGCG	59.781	20
TAGAATCCGATGTATGGCCC	59.745	20	TTCTCTGCGACGTAATTCCC	60.214	20
CACCTGAAGGCGAAAAAGAG	59.986	20	AGAAAAACGTGTGAACCATCA	59.517	22
ACATACTCCACCAACTCGGC	59.997	20	TGGAAAAATGCCCATCTACC	59.762	20
CATATTTCCAAGTCACCTTCCA	58.949	22	CGTGTTGTTTTGCTTGTTTCA	59.801	21
CCAAAGGGGCTGCAATACTA	60.089	20	GGTCTTGGGGGTTCAATGTA	59.647	20
ACCATATTTAAGGGTTATCACCTG	57.552	24	GAAGGATTAGGCGAAGGAGG	60.166	20
ATCAGCACGAATCACACAGC	59.87	20	TGGCATTTCAGCTTTTGTAGC	60.391	21
ACATTTATGTGTCAGCCCCC	59.676	20	TTGGTTCACACAACCACTCC	59.415	20
ACTGAGCCCTGATTTGGAAG	59.284	20	CTCTCGCTTTCGCCTCTTTA	59.861	20
TCCTCTCGTGTTCTTCCTCG	60.523	20	GGCTCACTCTCTGGCTCATC	60.104	20
TCTTTCAACCTGAATTGCCC	60.051	20	TCTCGCCACACTACATGCTC	60.016	20
AGCTATCAAGCACCGGAAAA	59.845	20	CAAAAAGGGTGCGATTGTATG	60.362	21
GATTTACCCAAAGCGCACTC	59.713	20	GGTGAAATGGGAGGGCTAAC	60.693	20
TTTTATCAAGCGCAACCTCC	60.209	20	CGAGGAAAATGCACTTCTGG	60.766	20
TTTCGGACGATTTTGCTCTC	60.331	20	CACATGTCATGAATCGGTGT	57.712	20
ACGAAATTGCCCTTGTATGC	59.967	20	TGTCAAAATCTCCTTCATTTGA	59.038	24
CTGCAGCCTTCTTGTCTCCT	59.745	20	TGACGGGATTTAGGTGTTTTG	59.847	21
CCGCCTGATTTGTTTCTCAT	60.074	20	GGTATGCTGGAATTTTCGGA	59.901	20
CAAAGCATAAACATCCCAGC	58.241	20	TTCCATACGCAAAATTCGCT	60.588	20
GTGATGGCATTCATCGTCAG	60.08	20	TGCGTGTCTAAATGTGCCTC	59.871	20
CGCCCCAGATTGTTTCTTAT	59.043	20	AGCGTTGGATTTTTCAATGG	59.938	20
GGGGAGATGTTCCTTTAGTCG	59.948	21	TGATCTTTTCGCCATTAGAGA	57.592	21
ACTTATTTGCATTGGGCCAC	59.829	20	CTCCCAGTCTAAAAGTCCATG	60.13	22
TCGTACCCCAAACTTGCACT	60.55	20	TCTCTCCCGACACACACGTA	60.309	20
TCGACTGCCCCTTTTTACAC	60.11	20	TCAAGTCGCTACTCACCATCA	59.455	21
ATCACTCTGAGCCTCTCCCA	59.945	20	ACAATGGAACGAGATCCAGG	59.927	20
TCGTGCGGTCAATGATTTTA	60.073	20	TTTTCTTGCTTTTGCTGTGAAA	60.034	22
GGATTCAGTTGCTTCAAGAGC	59.069	21	TATAACCAGTGAGGGTCCCG	59.807	20
CAATATTACAATGGGCAAGAGAG	59.826	25	CAAGCTCAGTCTCAATGGGG	60.791	20
CCAAAAATGGATGGAATGCT	59.762	20	CTCTAGGGTTCAATTGGGCA	60.066	20
GATCGACGTCCCAGATTTGT	59.934	20	TTGCGATAGTTAACAGGCAGA	58.595	21
CTCGTCTCCTCCACTTCCTG	59.978	20	AACGCTGCCTCAAAAGCTAA	60.152	20
AAAGAACAAAATGACACGAAGA	58.783	24	TTTTGGTGTCTAATCCATTTGT	58.909	23
AATGGTTCGGTTCCAGTTTC	58.886	20	AAAGAGGTTGTTTCCGTTGC	59.218	20
TTTTGTGATTTCCCATGTTTGT	59.225	22	GAGAAACCGTAACCCAAGCA	60.11	20
TCTCAACACTTCAACGGGAG	58.852	20	GCTGCAGCAATAAAATTCCC	59.688	20
CCCGGCAACTTCTCAAATAA	60.067	20	TGAGTTGTTGTCTCCAACCG	59.72	20
CTGCAACAGCATAGTGGCAT	59.895	20	TGCACTCATCAGAGTTATCGGT	59.763	22
AGGAAATTGGGGGAAAATTG	59.992	20	TTCAAACACGAGTCGCAAAT	59.322	20
TCTTCCCATTTTCCCAACAG	59.903	20	CAGGAGGGTTCACACAACCT	60.002	20
TCTCTCTGCAGGGGAGTCAC	60.55	20	GTGGAATTTGGGGCTTGTAA	59.801	20
CGAAGGAGACTGGAACCGTA	60.246	20	TCTTCGTCAATCCACCATCA	60.048	20
GGGCCCCTAGTCTGTCTCTT	59.699	20	TGATATGGCACAGCAGCAAT	60.251	20
ACACCTAAACCCAAAACCCC	59.955	20	ATGCCAACACAAAAACACCA	59.864	20

TGTCAACATTCAATCACAGCC	59.562	21	ATTGATTACGAATCCTCGCC	59.001	20
TTCTTCCCACCACTGGTTTC	59.943	20	TTAGTGTGGCCGGTTTAATTG	59.876	21
TGAATCCCATCGATCCATTT	60.096	20	ACATATTTGTCCCCGGATTG	59.505	20
GGCTCTTCTCTGTCCGCTAA	59.717	20	ACCACGTACATCTTGTGTCCA	58.92	21
GGTCACAGAGGTCGTCCCTA	60.112	20	CAATCAGAGACGGTGAACGA	59.831	20
AAGCTTGGTTTGCAGTCTCC	59.478	20	TGCAATTTGTTTCTCTCCCA	59.247	20
TTCTGAACGTGCAACTCGTC	60.032	20	TGTGGATATGTAGATAATTTTT	58.476	27
AAGAGCTCACGTGCCTATTGA	60.03	21	TGGTAAAGGGACGGCATTAG	59.953	20
CAAAAGCAAGAAAATGTGATTTC	57.995	23	TCCTTCTTCACTTTTGCTCACA	60.03	22
CCACAAGCATTGCAGAGAGA	60.136	20	CAACTGCAACAGCCCAATTA	59.729	20
TGACGAAGGAGGGGTTAATG	59.926	20	GGCCCGAGCTAAAAACATTG	61.816	20
ATACCACTCGTTAATCCGGC	58.93	20	ACCCCATTTCAATCCTGTGA	60.173	20
GAGGGAGTTTCCGGAGAGAT	59.636	20	CCATGTCTCTGGACTGGGAT	59.92	20
TGGTTCAATGGGTTATTCGAC	59.677	21	TCTTTTATGTGCACAATGCGT	59.244	21
TGCATCAACTTATGCCAAAAT	58.174	21	CCCCAGAATGCAGTCAACTA	58.722	20
TGAAGTTAGGAAATAAGGAGGTG	58.743	25	TTCCACTTCCACTTCCATCA	59.059	20
ACGCGATTTCACTCACAACA	60.31	20	CCAGTAGATGCCCCTCCTAAC	59.969	21
ATGATGGGCACATGGATTTT	60.021	20	AACGTCAACTAGCTCGCCAT	59.904	20
GGTGTTGGATGGAAAATGCT	59.797	20	AACTTCCTCCAGCTCCGACT	60.393	20
CGCTTTGGGACAGCAATTAG	60.762	20	TTCGCATAATTTTTGTGAGAGG	60.017	23
TCGAACAATCAAACTCGTCG	59.84	20	CCCTCTCTCTCTCGGTGTTG	59.978	20
ATCCGCCATTGTTGAAACTC	59.939	20	AATCAAGATCCGAGCACACC	60.081	20
AACATGCTCTCCTTAGGCCA	59.836	20	TGTGACTGCTCTGGTTGAGG	60.022	20
TTTCCCTCTCCTCCTCCATT	60.008	20	TCATGGGAATTTGATCGTGA	59.859	20
GACCAATTCGGTTTGGTGAC	60.218	20	GAGTTGAACCCCCTCTCACA	60.088	20
CACGTGTCATCTTCTTCAGCA	60.04	21	GGGCCGATCCTATCAAAAAT	60.116	20
GATGCATTCCATTTGTGGTG	59.781	20	CATGCGCCTAGATAACGACA	59.856	20
TGGGCATGAATGACTGAAAA	60.049	20	CGCAGATATGCGTTTCTCAT	58.897	20
CTTGGACCAGATTGTCCCTC	59.505	20	GCAAACGAGCCTTATTGTCC	59.713	20
GCTGGAGCAGGTCTCTTGTC	60.143	20	AATGGAGAACTGCAACGCTT	59.882	20
GGGGAAGTGTGATGTTTGGT	59.679	20	TTCAGCAGAGCAGCCATATC	59.131	20
AGGGTTGGGGTGCATATTTA	59.158	20	CCTCAAATTGTTGAAAAACCG	59.478	21
ATATGGGTTGGGTACGGGTT	60.187	20	CCGTCCATCTCAAAAATGAA	58.546	20
TGAAAATAAAAATGGAGTGATGT	59.775	25	TTTGGCAAGCAGCAATTATG	59.842	20
TTTACGAGATGGAAGAAGCTGTT	59.445	23	TGAATTTCAGTCATGGATTCTC	59.136	24
GCGAAATTCATGTTGACCCT	59.939	20	TGCTATAAATGAAACCGGGG	59.789	20
GAAATGCAAGGATTTCCCAA	59.878	20	TCAAATCAAGGGCTAGGATGA	59.654	21
GCATTGCTAGAGCCATTGATT	59.337	21	GTGGACGCTCCAGATTGTTT	60.119	20
CCCTCGGATGCTAGTGTTTC	59.694	20	AATATTCAGACGAAGCCCGA	59.668	20
ACTCCCCTTCCCATGCTAAC	60.328	20	AACGGGATTTACTGTTTTGACA	58.539	22
AATCTCGCATCCCAATTCTG	60.036	20	AGCCCGTACCCGGTCTATAA	60.702	20
TGATGGGAATGGGAGGTATG	60.538	20	ATTTGGTGCATTGATTTCGC	60.847	20
AAAAGAGAGGGATGGGGAGA	60.008	20	CATCCCCGACAAATTTTCAC	60.17	20
TTTTGTGGCAGTCAGTGAGG	59.873	20	GACAAATCCAAGTGGGAGGA	59.903	20
GCCACATGAACATGAAATGC	59.939	20	ACCATTTTCATTTCGGGCTA	59.411	20
TGGGCTAATCATTCTCAGCA	59.375	20	ATGGGAAGAGGGGGTATGAG	60.147	20
CCTCTTTCTTCGCCTCCTCT	60.088	20	CAGTCGGGGGTAACACTCTT	59.062	20
AATGCCCACTGTTCTTCAGC	60.263	20	CCCTAGCTTTGCCCTCTTTC	60.332	20
CGCCTGATTTGTTCCTCATT	60.074	20	TAAACCCTAAAAACGCGTGC	60.13	20
GTCACTTCAGCCGTGTTCTG	59.467	20	TTCCCCTTTGCCCTCTATTT	59.903	20
TTGGTGCGATATTTTGTTCG	59.562	20	GCCGATTCTTAATGGCTGTT	59.186	20
CTCAATCTCAACCCAAACCC	59.381	20	AGCACTCTGCGAGTCTCCTT	59.355	20
AAGCTTGGCCATTCAACAAT	59.574	20	TTCGAGTGACACAAGGCAAG	60.025	20
AGCTATGATGCTGATGCGTG	60.003	20	CCCAAGATGACGAACAACAA	59.541	20
GTTTTTCCACCGAATCAAGC	59.551	20	TAAGGTGTCGCAATCTCCGT	60.657	20
TGCTGCTAATTATCCCTCCAA	59.69	21	ACTTTTTGCCTTTTGCTGGA	59.861	20
ATGATTGGCTAGACATCGCC	60.066	20	ATTGGAAGGTGACGAAATGG	59.79	20
TCATCCATTTTGCACCTGAA	60.049	20	CCCGACAGTGAATCGTACCT	59.989	20

CATTTTGATCCTTGTGGCCT	59.933	20	GCCGAAAACAAAGTCCAGTT	59.218	20
ATGACAGAAGAGGCGACGAT	59.834	20	CCTTATTTCCTATTCCCGCC	59.767	20
TGGATGGCTAAGACAACAACA	59.184	21	ATTCATATACACGTGCGTCTTTT	57.801	23
CACGAGAGAGGAAAGGGAGA	59.525	20	GGCTGTGCTTTCTGGTTCAT	60.263	20
CTACAGCTCTATCCCGTCGC	60	20	GGTAGCAGCGATGAAGGAAC	59.843	20
ATTTGCAAGTTCCAGCGATT	59.713	20	GACAAAACGGGAAAATGGAA	59.778	20
AACGTCGAGGCGTAAGTTTG	60.305	20	CCCCCAACACACTCAACA	58.839	18
AGCCAGGGCTTTTATCATGT	58.672	20	TGGACGAGATTTAACCCCAC	59.79	20
ATCAGGAGACAACGGAGTGG	60.112	20	AAGCTCCGGAAGAAGGAAAG	59.955	20
GCTTCATAGCATCTCTTGCTCA	59.758	22	TGTGAAAGAGTATGTGCTTCCA	59.799	23
GGTAAGCAGACTGCCAGGAC	59.874	20	TGATCACGAGTACCTCCACG	59.701	20
TGTGGCTGAATTTGACGATG	60.665	20	CGACTAATCACGCCGCTTA	59.984	19
GCACACAAGTTATTGGTTTCTATTT	60.209	26	TGTCGACGATAACAAGGCAA	60.257	20
TGATCTTACCGGGGCTAGTG	60.088	20	CCCACGTAGCAATTGACAAA	59.585	20
ATTTCGAAGATCAACGGACG	60.074	20	ATTACGTCGATCCAACGGTC	59.82	20
AATTGAGCCTTTACAAACTCTCTA	59.032	26	TGCTTTCCCTCTCCATCAAT	59.629	20
AGTTACCGCTTGCTCCTTGA	60.015	20	ATATTCGAGTCATCCGCAGC	60.207	20
TGCGATGTCTATGTGACGGT	60.144	20	TAACACCAACCACACAGCGT	60.072	20
AAGTCGGACTCTTGTTCGGA	59.844	20	CGAACGGATTCTTGATTCTTG	59.693	21
TTCATCCTCCCTCATTTTCG	60.006	20	CTTCGGCAAATACCACTCGT	60.132	20
GGTGTCTACACGGTCCTCCT	59.027	20	AAAACTCACCGGAATCCTGA	59.526	20
AAGGTGGGCATGAATTGGTA	60.192	20	GATGCGATCACTGCCCTATT	60.066	20
ACATCCATCTCAAAACAATATCAA	57.575	24	GGTGGCATGCTATCTACCCT	59.034	20
GCAGTTTGGCATCAGAGTCA	59.992	20	TACAGGGCTGCTTTGTCCTT	59.875	20
TGTGACAGAGCTGAAATGGG	59.831	20	GAACAAGACAGGGGTATAACCG	59.762	22
TGCGGATTGAACAAATCTGA	60.197	20	CCAGAAGGATTCTTCGGCTA	59.406	20
CGCATCTGTAAAGCAAAGCA	60.155	20	CCGGTCCTGAGTTTGTGTTT	60.005	20
TTGCTTCAATGCAAGCTGTC	60.142	20	GCGTAGAGTTACCAAACCCG	59.632	20
AAACGCCCCCTAACATTTTC	60.184	20	GATTTTGCCTTGCATGTTGA	59.67	20
CCCTCGTCAACTACTTCCCA	60.103	20	CGAGTGTGGAAAGGGAGAGA	60.377	20
AATTCATGCCAATTTCTGCC	59.907	20	TGATTGGCAGAACCAGAAGA	59.369	20
TTGTTTTCTCTTTTGCATAATCAAT	58.388	25	AGTCTTTCTTCCGTGCGTTG	60.431	20
CGTGCTTGGCTTGGAGTAGT	60.453	20	CTCCACGTCATTTGGCTACA	59.716	20
TATGAGCCCGCACATTATCA	60.058	20	AAACATGCCTCCACATCCTC	59.934	20
TTTTGTGCCTTCATTATGCC	58.627	20	ATTTTGAAGTGTTTCGGGGA	59.406	20
TTGGAAGGTATGTGAAATTTGGT	59.638	23	GAGGCCTTGAGGCAGACTTA	59.574	20
CTTGGCAAGGCTCTGAAATC	59.955	20	GGCTGGTATCACCATAACGC	60.361	20
CTGTTACTCTATCTGCATGCTCTG	58.388	24	AGGCTGTGAAAGCTCCATCT	59.043	20
AAAGGGAGTTGCAGTCAGGA	59.844	20	TTGTTATATGGCTGGGGCTAA	59.464	21
CCTCACTTCTCCCCCTCTCT	59.801	20	TGCAACACCAAGTAACCATCA	60.019	21
GCACGCATTTCCACACATAC	60.003	20	TTTTCCTTTTCCCTTCCTCC	59.505	20
TCGAAAGCCTACCTTGCTTC	59.592	20	ATTTCATTTCATGGGTTTCG	57.399	20
CCACGCCTCTTTTGATGTTT	60.11	20	CACGAGTGAGAAAGGGAGAGA	59.583	21
GACCGAACCGAAACTGGTAA	59.971	20	CCGAACCGAACCGAAATTAT	61.029	20
TGCAAGATCCAAGGGATGTA	59.075	20	GCCCAAAATTGCCCTTTAAT	60.148	20
CAAACATTTATCTTGCACTTGG	57.4	22	AAATTTCCCTGCTTTCCAGTT	59.123	21
ACAGCAGGGTGTTTGTGTGA	60.203	20	TGATGCAGGTTGGAATCAGA	60.201	20
ACTCGCGTCTCTCATCCATT	59.834	20	GTTTGGGTTTCTGGGTGTGT	59.721	20
GGGAGTATCACTGGAATGCG	60.483	20	CAGCACGGACGGTTAAGATT	60.132	20
CGACGCATAAAGAGGCAAAC	60.772	20	CGTTTTGCTTTAGGTTACAAGG	59.722	23
CAGTCGCTGTTTCACCATTG	60.301	20	CATCAACCACCAACATTGTTTC	60.132	22
ACCGCCATTAACTGCCATAG	59.982	20	TTTTCCCTCTTCTGGGATCA	59.6	20
AAGGTTCACCAAACTACGCAA	59.663	21	TGTTGAGGAAGAAGAGCGGT	59.989	20
CCTAGTCGCTCGTGGTTCAG	60.984	20	CATCATCCTCCTCTTCTCGG	59.755	20
AAGAAGCGCGCTAAATCAGA	60.251	20	TATTCCCTCAGACCACTCGC	60.218	20
GAACCAGAGGAGAAATAGGGAGA	60.082	23	GCTGGTTACCTTCGAGCAAG	60.015	20
TGATACCCTTGTCAGTTTTCCA	59.471	22	TCTTGTTTCAGGTTATCGTCTAA	57.253	24
TTCTTTTGAACCAGGCAACC	60.088	20	ATTTTTCGCTAAAGGGGGAA	59.909	20

CCAATCATGCTGGTTTTTCA	59.518	20	AAATGTTACCCCGCGTAGTG	59.883	20
ATGCAACCAGATTCAAAGGG	59.933	20	TTGGGTTGTCTTGATCCCAT	60.173	20
AAATTGCAAAACCCAACTAAGC	59.561	22	TAGGACTTTTATCCGCGCAC	60.23	20
AAGGTTTGGCTTGACCTTGA	59.711	20	TGAAAACCCAAAACACATGC	59.42	20
GGAAATGACACCCAAACCAC	60.073	20	TGATGGCTTATGGGGGACTA	60.288	20
TCTCCACTCTCTTCTCTCTCCC	59.175	22	TCAAGTCAACATAAACATAAA	60.083	27
ACCATATTTAAGGGTTATCACCTG	57.552	24	AAATTGTTCCGTTTTGGCTC	59.067	20
TAACTCAAAATCTTGCCCCG	60.067	20	ATCGTGATTCGCAACTCTGA	59.399	20
TGCACGCCCTTAATATTGCT	60.608	20	GTAATGTCAAATGCGCAACG	60.14	20
CAAGCCATGAGCCTTTGATT	60.214	20	TATGGGTTAGCGTGTGATCG	59.566	20
AAAAATGGGGGAAATTTGATT	58.593	21	TTCAAAAATCAAAAGGTCGAA	58.408	22
AAACCGTCCAAAATCGTATCC	60.068	21	TGACGGGATTTAGGTGTTCTG	59.978	21
CTAGTGGCCATTCTTCAGGC	59.836	20	CATATATTTCATTGGCCCCG	59.998	20
CGTTTCGCAAATTAATCGGT	59.964	20	GCACTACATAAAATGAACATT	59.095	26
GGGCTCAATCTTGCTGCTAA	60.49	20	GACACCTAGCCCACCCACTA	59.989	20
CAATGAAACCAAACCATCCA	59.222	20	ACGGCTCTGAAAAGTTGGAA	59.853	20
AAGAACAGGCTGTGCCATTT	59.74	20	TTTATCTTGCCCATGGAACG	60.827	20
TGCACTTTAAGAGGTGGTTGC	60.298	21	GTCCAGCTCTTCCAACCAAA	60.232	20
TCGAAAATCAAAGGCACACA	60.234	20	GGGTTTTAAATTGGGGATTTTG	60.588	22
ATCGGAACGCTCATCAAATC	60.043	20	TTTAGCCGATGAGAGGAGGA	59.91	20
TAGCATTTGTCCCGTATGGC	60.857	20	TCTTTTTCTTCGTCACGGGT	59.711	20
CCCTCTTGATGGATTTTTGA	57.584	20	TTTGTACGAAGGAGGCTTGG	60.241	20
TTGGCAGACTACTTTGTGGGT	59.648	21	AAACAATCAACCAAGGATGAC	59.336	22
CATTTATTTCTGCCCCTCCA	59.894	20	GAGCGTTGTTGGCAAAAGAT	60.257	20
CCAGCACGATAGATACAAATCC	58.606	22	CAAACGCAACAAACTGTTATC	60.082	23
TCGCTGGTTTTGTAGTCGTG	59.904	20	GAGTGAAGCAAGGGAACCAT	59.141	20
ATTCTGTCGGATAGGTGCGT	59.579	20	GAAAGCTCATCAACTTTGAAA	60.282	23
TTGCATTAATGAGCCGTCAG	59.833	20	CAATATTACAATGGGCAAGAG	57.725	23
GCGTTTTGACGATATATAGTGTTT	60.194	26	TCATGGCTGTCAGATCTCGT	59.372	20
TTTGAAACCGGCTTAATTTG	57.833	20	TGAGTTGCACCTTGCTATGC	60.019	20
CTCTAACAAATGCCAGCCGT	60.27	20	GAGAAGGAGAAACGTGGTCG	59.844	20
CCATTTAGTTCGCGGGTATG	60.335	20	TGCTTGTTGGCACCAGTAGA	60.449	20
GCTTCACTCACTCACGCAGA	60.343	20	ACGGTGCGTGTCTATGACTG	59.776	20
CACTGCTCTCTTTTCCTCGG	60.126	20	GCCTACAATTCTTTGAGGCG	59.845	20
ATTTCGATGGTTTTGGGTGA	60.17	20	CCATGCACTTCTTTCTTTGC	58.502	20
AGGCACACCTGTATACCCCA	60.255	20	TTCCTGTTATCTGCCCAGAAG	59.322	21
ATTGCATCTTTGGGGATGAG	59.894	20	GGCAAGGACCACTAGCAAAA	60.249	20
AAAATCGACCGCACATTTTAT	58.509	21	GGCACCGACATCAAGTTGTA	59.572	20
GGATAGGCCCTAACTCGACC	59.925	20	GGGTGGGTTTGGAAAAGAGT	60.204	20
CGTTGTCCTGAGCACGTTAG	59.51	20	TGCGTGTTCTTGGTGTTCTT	59.339	20
AGGGAGATCGTGGGAGAGAG	60.748	20	ACAAATTCGAGATCGAACGG	60.074	20
TCCATGATATTGTTCCTTCGG	59.77	21	AGCATCTGGAATGCAGGAAG	60.362	20
TGATGAAGTTGGGTGTTGGA	59.935	20	TTTGGGCTAATGGGATGAAG	59.894	20
CCTAAAATTGAACGAAACTCGAA	59.667	23	AAATAGGAGAATAGGGGCGT	59.472	21
TAGCCCCTTTGAGACCATTG	60.066	20	CCTTCAGATGGAACAGTTGGA	60.096	21
TCATCCAGTGTTGCTCTTGC	59.992	20	ATCCTCATCTTCACCATCGC	60.042	20
TTCCGATGGAATGCATTTTT	60.268	20	TCATAAGGATGCAAATCCGAG	60.045	21
GACACAGAAACACACGCAGG	60.357	20	CGAAACAATAAGATGCTGTGT	60.18	23
TCCCAGTTCAACTCTTTCTCG	59.458	21	ATGATGGAATTGGGTGTTGG	60.439	20
GTGTGGGTTCCTCTCGTGTT	60.009	20	GGTTCACACAACCACTCCAC	58.834	20
TTCCACTAGGGGTACCAAAATG	60.102	22	ACCCGTATGGGACAAAATCA	60.051	20
AAAGCCAATCGAGTCTTGGA	59.813	20	GTGGAGGATTTTCCTTTCCC	59.744	20
GGATGGGGCTGTGATTGTAG	60.34	20	GCGGATCCAACATGAAGAGT	60.081	20
CAATTCCGAACCGAATAAGC	59.547	20	CACGAACACACGCTCTCAAT	59.905	20
CGAATAGAGTGATGAGCCAAC	57.436	21	AATAAAAGCCCCGATTTCGT	59.808	20
GCAACGGAATACCACTCGTT	60	20	TTCGTGTCTATCCTCACCCC	59.927	20
CACACCATACCCAAAAGCCT	59.853	20	GCGGATAATCTGGAGATGGA	59.998	20
TCTCAATCATGCGATCCAAA	60.159	20	ATTCACCACAAACCACCACA	59.701	20

GGAAGCGCAATTAATACGGA	60.061	20	CCAAATTTGAGGGTTATTATTT	58.433	24
ACGATTTTGCCCTTGTATGC	59.967	20	GGGTATTTCTGGAAATCATTGA	59.962	24
CACGATAAGGGATGGATTCAC	59.259	21	ATGTGGTAATTTTCGCACCC	59.691	20
CGAGGGAGTGATCAAGTGGT	60.112	20	CGAAAAAGAAGAGGTGAGCG	60.125	20
TGTTCAAATGATTTTGGGGG	60.535	20	AAGGGCATAATCTATGATCGG	58.049	21
ACACGCACGCATTCTTCTTT	60.837	20	TGTGTTTTTCAGTGTGTGGGA	60.033	21
CGCGCCTTGCCTAATAATAA	60.202	20	TAATTGCACGGTAGTTTGCAC	58.762	21
GCTGGAGCGTCCATCTGTTA	61.348	20	CAGATGTGGACGGGTCACTA	59.545	20
AGCCATCGCTCAACCTACAC	60.285	20	TGGCATTTTCGATCTCTGTG	59.799	20
GGATCAGTTTCAATCCCATGA	59.741	21	AGGTTCAGACCCAGGCTTTT	60.11	20
CGACTGTGCTGCTGGAAAAT	61.375	20	GCAGGAAGTGATGAAGAGAA	59.478	22
CAAATGACCAAGGAGGAGTTACA	60.391	23	TGGTGGTTTTCAGATGCTCA	60.24	20
CTGGATTGTATGTGTCCCCA	59.215	20	TCTAATTGGGATCTCCACGC	60.036	20
TTACGTTATGTGGCCCGAAT	60.209	20	CGAAGCATTTTGATTTGCGT	61.131	20
CCCATGTTTGTAATTATTGTAGGG	60.228	25	GCCATTGTGAGGAAGGTTGT	59.973	20
CAGGGACGGGCATGTTACTA	60.904	20	GCAGCTTTACTTCAGCGTCC	60.162	20
GAGCTTGGCAGAACGAGAAC	60.142	20	ATCAGAGCATCAGAGCGGTT	59.981	20
CCTTATTTGATGCACGGACC	60.331	20	AGGGCTGCAAGTGTACATGA	59.318	20
AGAAGTCTGCGAAGGTCAGC	59.751	20	AAGATGCATGTGTTCCCCAT	60.203	20
GCCAACTATGAGACATGCGA	59.83	20	CCAAAAGCCCAATAAAACGA	59.937	20
GCGTGACGCACAGTTTCTTA	60.058	20	TATTACCCCTTCCCCGTTTG	60.892	20
ACTGATGTCAATTTCCATATCCA	58.316	23	CGGATTTAAGGGTTATTACCTG	58.81	24
GGCATATGCTTTGGCAAGTT	60.103	20	TAAATTGCACCCATCAACCA	59.786	20
AAAAAGGGGTTTGGTTGGAG	60.193	20	CCAAGTACACTCCTCCTCCTG	58.804	21
TTCGTCAAACCTCCCAAACT	59.569	20	TGATTTGAGTGTAAACACGTCC	58.688	23
GGCAACGGAATACCATTTGT	59.691	20	AACTTGGTGAGCGAGTGGTT	59.769	20
AGATGCTCCCTCTCCCATCT	60.179	20	AAAATGGCACATGGGTTGTT	60.096	20
TCCAAGGGAAAGTGTTCAAGA	59.697	21	TGGTAAAACCTCGTGCTTCC	60.11	20
AGGAGGGGCAAAGAAAAGAC	59.691	20	AGCCGACTCCATTTATTGCT	58.814	20
TCAAACACTAGCCTTTGCCTC	59.508	21	CCTGTGGCTCAAACCTGAAT	60.111	20
AAACACCTGGGACCACTGAT	59.279	20	GGCTCAAACATGTCAGCCTT	60.263	20
GTGAAGAGTACAACTTACACCCC	59.494	24	AGGGAGTGCTCTCACCTGAA	59.986	20
AGCTGAAGAGCGAGATTGGA	60.24	20	TTGCACACCCTCTCTCACAC	59.872	20
GACTACTGGTCGGGGAACAA	59.966	20	TCTAGCCTTCCATTTGCTTGA	59.967	21
CATGTGGCCTAACTTGACACA	59.624	21	GTTGGGAAACGATGGTTGTT	59.694	20
AAACGCTTTGTTTTCCGTTG	60.145	20	GAGAGGAAGGTGTGGAGCAA	60.386	20
CCGTATTCATTGTTTTCGGC	60.323	20	TGAAAATATCATCGGCCACA	59.891	20
CAATCTCAACCCAAACCCAT	59.647	20	GCACTCTGCGAGTCTCCTTG	61.3	20
GTTCTCACCGGAGTTGGTTC	59.555	20	TTCCTAACAGTTTGGCATCAGA	59.747	22
TCCCACTAAAATTTTCCCGT	58.417	20	TGCGTTTTGACAATATATAGGT	60.083	26
AGTTGATGCTGCAAGAAGCC	60.547	20	GGCCTGAATTCACATCCATT	59.756	20
GCATGCTAGTGCCTGTTGTG	60.481	20	CAAAATTACAAATGGCCAAGA	58.674	22
TTAAAAATGGAAGGTTGGCG	59.937	20	CCACTACATTCAGGGCCATT	59.813	20
AGGAAGGAGGCAGAGAGGAC	59.952	20	TTACGCATGACCCCTAGACC	59.955	20
TGAAATGGTGATTTGAGGGG	60.692	20	ATGAACGAATCAAGTTCCGC	60.081	20
AATGGATCTATAGAGCGCCG	59.301	20	TTCTGGCCACTTGTTTCTCC	60.232	20
GTGAGGAGTTCACGGAGGAG	59.835	20	CAACTCGCATACCCAAAAGA	58.771	20
CCACAACAAACCCTAGTGGA	58.468	20	CAAATTTCGCCGTTCTTTTT	59.231	20
CGACTACTCAATCATCCAACCA	59.993	22	TCCGTCTTATTGGTCCGTTTA	59.46	21
TCCAAGATTGAAGTCGCAGA	59.522	20	GCAGGTTCATGTTGCTTCAC	59.297	20
TCCGTGACATCAAACACTCC	59.525	20	AAAACCCATCGAATGCTGAG	60.074	20
AATTTTGATCGCCTTGTTCG	60.074	20	CGCTGTATAATGGGGATCTCA	59.93	21
GGGGAAAATTTGCAAGATGA	59.878	20	GATGGTTTGAAGATGGCGAC	60.47	20
TCCCCATGTGATTGATGATG	60.137	20	TTCGGACCATTCAAACTCGT	60.495	20
TCATCTGCTGAAAGGAGGGT	59.803	20	CGTGTTTATCCTCACCCGTT	59.853	20
ATCGGCGAATTTATCTGCAA	60.557	20	CCGTCCTCAACCTCTCAATC	59.655	20
AGAACGCTGACGTGGAAGAT	59.874	20	CATTAAATCCTGTCCACATACA	59.241	25
TAAGCAATTGATTGTCCGCA	60.215	20	TGGTTGCAAGAGAATGGTTG	59.691	20

ATGGCCACAAATGGTTCCTA	60.192	20	TGCAATGCATGGAGGAAATA	60.035	20
TAGAGCCAACCAAATGGTCC	59.933	20	TCCCTCTCTCTCTCAAGGCA	60.214	20
TTAGGGTTTAAAATCGCGCA	60.564	20	TTCATTCTTTTTAGGAATGCCA	58.739	22
CGTTGAGCCGAATGTGTTTA	59.729	20	TCTTTTCTTTTCCTTTTATGCTC	60.234	24
TTTCAATCCATTCACGTCCA	59.9	20	AGATTCTGGGGATTCTGCCT	60.037	20
CCTTTCCTAACAGTTTGGCATC	60.001	22	CATAGTTGACGCCCTTCGTC	60.657	20
CGCCATTCTCTCTCCACTCT	59.555	20	AGGATGTGGGTTGAAGGTGA	60.363	20
TGCGTGTTCTTGGTGTTCTT	59.339	20	CAAGCAAATTGTGGCTCTGA	59.988	20
AGTGCAATCGCAAATCACAC	59.728	20	TCGTTGTGAATTACCCAAGAA	59.492	22
TTGCTTCAATGCAAGCTGTC	60.142	20	GCGTAGAGTTACCAAACCCG	59.632	20
TGACTCGCCGTAGAATCCTT	59.836	20	AACCTCGTTGCCAATCTGAC	60.119	20
CCCACCTGGAAATCTCCTTC	60.822	20	ATCGTGTTCCTCAAGGTTGC	60.119	20
GATATTGACGGTTGGTTGGC	60.199	20	ACCCTCTCACTTCTCTCCCC	59.661	20
ATGAACCAAGTCATTGCAGC	58.726	20	TCAATGTCCCAACAAATCCA	59.75	20
GCCAAGCCAAAAGATACGTC	59.713	20	TGAGTGCTCAGGCACAGAAG	60.333	20
AGGTTGGAGGGAATGGAGAG	60.447	20	ATGGCATCACTTCAACCCTT	59.41	20
AAATACCATTTCATTTTGTAAACT	57.172	27	CACAATTTCTGCTCTAATAAAT	58.809	25
TGGTTAGAAAACTGGAGCCC	59.17	20	ACTTTGTTGGTGGAGCGAAC	60.156	20
CACGAGTGAAGAAAGGGAGA	58.001	20	CTTTATCCTTTGCGCGAGAC	59.982	20
TTGATTGATCGACAGCATCC	59.61	20	GGACCGACCGGAATTTTTAT	60.02	20
TGGGATTAATTTCCACCATGA	60.002	21	AGATTCGATCCGAAAGGTCA	59.629	20
TCAAATCATAGTCTTTCCTCGTTT	60.02	25	TTCGTTTTTCCGGTTGAACT	59.587	20
TGAAGTTAGGAAATAAGGAGGTG	58.743	25	ACGTCCTCCGTTGGATTGTA	60.375	20
GCCGACACTTCCTATCCAAA	60.074	20	TGCTCCCATTTAAACAACCC	59.801	20
GAAATTTCGCTAAGTCGAGAATA	58.255	24	TTTGGAAGAATCATAATCAAG	59.56	26
AGGGACAGCTGTGGACTCTG	60.458	20	GGCACCAAGGACAGTTTAGC	59.74	20
TTTGTGGTATCAGAGCCACG	59.716	20	AACCGTCCGCTTACTTCTGA	59.875	20
AGCATTTATGTGTCAGCCCC	59.962	20	TTCTCAACCTCGGCTCTGAT	59.95	20
TGGTGAACGTGTTTTGTTGC	60.596	20	TGTTATCATGCCAATCCACC	59.205	20
TCACCACCACCATCTTCAAA	59.935	20	TTTCCCATGTTGTAATTAATGT	58.388	25
TGTTCGTTGGTGGAGTTGAG	59.72	20	CACCACTCCTCTTTCTGCCT	59.45	20
CATCCTAAAGATAAGAATGGTAA	57.108	26	CATGGCCAAGTGTCAACAA	59.069	19
GGCAAACATGAATTCGTTCC	60.318	20	TGGTGACTCTTGTCCTCCCT	59.682	20
GAAAATGGGAGAAGTTGGTGA	59.017	21	TGAGTTGGTTGTTAGTCCGGT	59.506	21
CCTTTCTCCCCCGTAAATTC	59.772	20	GCCTTCTCGAATTTGTCTGC	59.962	20
GCCCTTGATTTCCAAGATCC	60.777	20	ACTCGTCTCCCTTCGCTTCT	60.532	20
GGTCCCTCCATCCTTACTCC	59.755	20	GAGCTGGAGTTGAGAAACGG	59.989	20
TGAGTTTTGAATTCGGACCC	59.91	20	ATTTGTTGGATATTTGCCCG	59.66	20
CCAAGATGACGAAGACAGCA	59.984	20	GTGTTAATCGCTTCCGCATT	60.103	20
GAAGGTAACGTCGCTGAAGG	59.875	20	ACCCCACAGTAACCCTTTCC	60.088	20
ACCGACTTCTGCACCATTTC	60.119	20	AATGCAGGAGGTCTCAGGAA	59.803	20
TCGGTTCTTGCTCCATTACC	60.074	20	GTTTTCAATCGCAGCCATCT	60.221	20
TTTTTCTTTCCACAAACCCC	58.901	20	GGATCGACACTTGCCTTGTT	60.119	20
TTTTCAGGAAGGGAAAAGCA	59.795	20	ATGACTCAACGGCTGGTTTC	60.119	20
TTGTAAAGGTAGGAAATTTTTGGC	59.804	24	CGGACATGGTACATTTTCTGC	60.38	21
GGGTTTGAAATTTTGAATGCTT	59.378	22	GTTGTGGCAGCTTTTGCTTT	60.428	20
CCTTGAAAATCTGAGCGTCC	59.813	20	TTTTCTGCATTGTCGAAGAGA	58.637	21
TTGGATTTGGCTAGGAATGG	59.894	20	GGAAAAAGCCGATCAAATCA	60.016	20
CGTCCGAACACATTGAAGAA	59.691	20	GAGAGGGTTGTCAAAGAGCG	59.989	20
GTCCTATCGGTACTCGGACG	59.574	20	CGTTACCTTCATCCCCTTCA	59.926	20
TAGGGCAGATTTATGCCAGG	60.053	20	CAGCATGTGTGTGAGTGTGTG	59.828	21
AGCCACGTCTCGTGTTTCTT	59.914	20	TTCGAGAGCTGTAACGGTGA	59.591	20
AGCGAGTGGTTGTGAGGTG	59.881	19	ATCTTTTGCACGAGATGCCT	59.843	20
GATTCGCACAAATGATAGCG	59.285	20	TCAGGGATAAGTGAGCTCGG	60.353	20
TGAACCACCTCTGCAAACAA	60.278	20	CATCCGGGTTTGATACCTGA	60.713	20
AACCCATTCCCCACCTTATG	60.797	20	AGACTTCAATGCCCCTCCTC	60.596	20
AGCAATATTGGTGGGACGAG	59.955	20	TCTCCGAAAGGGAACAAAGA	59.784	20
TCATCTCCATCCCCCAATAA	60.088	20	GAATGTCACGACCGACACTG	60.162	20

AAAAGCGAAGTGAAGCGAGA	60.27	20	CGAGGACATTTACTCATGGGA	59.94	21
GTGCAAATCTGGATCCTTCG	60.603	20	CTCGTCGTGAACTCCCTGAT	60.261	20
AAACTTGAGCAGTCAGTTCGATT	59.468	23	ATACCCACCTCCTCCCTCAC	60.194	20
AGCACCAGATTCTCCACCAG	60.261	20	TCAGAAACAACTTGCCCTCA	59.415	20
CTCCAACCTCCCTGTACTGC	59.721	20	TAATCGAGGAAGAGGGCAAA	59.778	20
TAGTTGGAGGGAATGCTTCG	60.206	20	TTTCTCTTTTGGTTGGTGAAGA	60.129	23
TTTGGCTCCTGAATCTCACA	59.369	20	GTGGGTTGGGGAAAAAGAAT	60.032	20
TGTTGCCCCTCTCCATTTTA	60.439	20	GACAGGGGTTGGGGTTAAGT	60.088	20
ATAAATATCAGGTGTTTTCTGAGT	57.122	26	AAGCTTGCGAGTGCATTTTT	60.025	20
CCCTTTTAGGCTCAAATCTCTTT	59.332	23	CCATGAGATTGGTGGTTGTG	59.806	20
TTTTCGCCTCCCACTAAAAA	59.693	20	AAATGCATGCACCTGATTACA	59.055	21
TTTTTGCCACCTATGCACAA	60.111	20	TTTGACAATATCGCGACCCT	60.469	20
TTCGGCCAGAGAGAAAAAGA	60.066	20	TTCGAAATTATGAGGCTCCAA	59.668	21
AGTGCGTTTGCAGAGCTTTT	60.197	20	TCGGGTTAGCAGATCAGGTC	60.218	20
TCATGATATTTTTCCTAAATTTTCC	58.916	27	CCAAATAATTTTGTTTCCACCA	58.76	22
CTCACCGTGGACGTAGATCA	59.701	20	CGGGCGGTTTTGTAGTTAAA	59.993	20
AGCGGCAGACGTTTCTAGTC	59.644	20	TCCTTCCACCCAACAAAAAG	59.942	20
CCGGAGATGAGGATGCTTAG	59.79	20	TACTGCATTGCGACCCTACA	60.28	20
CCACAAACCGAGCTCACCT	61.263	19	CCCCTTTTGTAAGTCCCCAT	60.046	20
TTCATGGATAGAGCGTGCAA	60.366	20	AAACATCGATCAGTCCCACC	59.786	20
CTCCGTCGGTGATTCAAGAG	60.791	20	AATGGCTGGATTTAGTCCCT	57.611	20
AATTCCCGGGCTGAGATAGT	59.925	20	TTTGGCTACAAATTGCTAGGG	59.262	21
AGGAACAAATGAGAATGTTAGTG	58.763	24	TTTTGGGAAATTCTTGCACC	59.916	20
GAGGGATTTGGGACGATTTT	60.131	20	ATTCCAAGATGGCAACTGCT	59.7	20
GTAACGCGCGAATGCTACTT	60.425	20	TATTCACAGCATTCAAGGGG	58.572	20
GGTGTTCTTGGCAACAGGTC	60.555	20	CAAATGAAAGGGGCTTCTGA	60.184	20
TCAGTTTCGAGTTATGAAGTTAGG	58.582	25	ATACTGGTGTTGCCTGCTCA	59.318	20
GTGGATTGAAGCATGAGCCT	60.226	20	TATCTCAACACGCATCCAGC	59.83	20
ATGGGGCTGTGGTTGTAGAG	59.989	20	CCATCTCTCCCTCACTCATCA	60.207	21
AGTGACTCACCTGAAACGCC	60.307	20	AAATCGGACTGGACCATTGA	60.317	20
CACCTGCAACAGAGGAGTCA	60.022	20	GACAACGGGGATAGCCAGTA	59.955	20
TCACATCAATTTTCACACCCA	59.808	21	TAAGGGTTGATTTTCGTCCC	58.879	20
TGCCTGCTGAGTGTAATTGG	59.864	20	TGTCTTGAGTTTGTATCTAAGA	59.365	27
TGCAAGCATCAAACAACACA	59.877	20	TCAACTCACCCTCACATTTCTC	59.187	22
GTCCGGGATTTGTGTAATGC	60.199	20	AAATATTTCTAGCACATGAAAT	57.859	25
ACCTTACCCAACCCACTTCC	60.088	20	GCTTGAAGAAGAGCAAAAATG	60.497	22
TTGGTTGTGCAGAATCGAAG	59.84	20	CGAAACGAAACAAAGTCCGT	60.147	20
ACGTCTTGATGTCGAAACCC	59.973	20	TGGGGATTGGGTTGTCTTTA	60.162	20
CTAGGGTTAGCATGCTTGGG	59.724	20	CCTTTGTCAACTTGGGCAGT	60.149	20
TCAACCGCCAGGATTATTTC	59.901	20	TAAAACACCATTAACGCCCC	59.699	20
TGATGGAATGGGGATTTGTC	60.526	20	AGTCGGCATTCAAGTAGTCG	57.98	20
ACCCCACCTTTCTTGGATTC	60.169	20	GAAGTTGTAGCATGGGCTTG	58.379	20
AACGTGAATCTCGGATCAGC	60.226	20	AATTGGAGCAAAATTGGCAG	60.074	20
GCGCGTGATTGTATGTCAGT	59.753	20	AAGCAGAATGCAAGCAAGGT	60.022	20
CATCCAGGTTCGGTTTCAAT	59.79	20	CAGCCTGATAAATGGGACAAA	59.946	21
ATTGACTTGGGCTTTGCATT	59.574	20	TAAGCGCACGCCAATACTTT	60.768	20
CTCTTGTAACAAAACCCCATGT	58.035	22	CTCTGTCCTTCTCCCACTCCT	59.856	21
AGTGGGCTAAGTGAGGTGGA	59.721	20	TCAAAACAACACCCAACCAA	59.834	20
CCAATGGAGAACCCTTTGTC	59.381	20	CACAACAGCCTTGTCTCTGC	59.622	20
CCAAGTCAATTCCTAGTGCG	58.379	20	TTCGGTAATTCCGGTTCTTG	59.931	20
TTGACTTGTGACCCTCTCCC	60.088	20	GAAATTTCCCAACATTCGCT	59.022	20
CGAAATATCGTTCGCACAAA	59.702	20	TGCAACTCGAGATGAGATGG	59.942	20
GTTTCAGTTCTCCTCTGCGG	59.989	20	CATCTCCTATCACTCCCCCA	59.879	20
TTAGCGATGCGAACTTGATG	59.976	20	TCCACCACCTCCAAGTTTTT	59.425	20
CAAATGGCCGAGAGAGAGTT	59.43	20	CTCCTCACCCTTTCCTTTCC	60.045	20
CCCCACAGATATCCCACCTA	59.623	20	TTTGAAAAAGTCGGCTGAAAA	59.855	21
TCATCATTCGACTTCCATGC	59.61	20	AATTGGGACAGGATATGGCA	60.155	20
AATCTCCATGTTCAGGACTTCA	58.646	22	GCAGTACCCGTGAAGGTGAC	60.577	20

TGTGACACCAATGTGATGGA	59.325	20	ACGTGCAAAAGTCAAGGCTC	60.44	20
GCAAAGTGTGCGGTCAAAT	59.713	19	TTGTCATAGCCAACCCAAAAC	59.853	21
GAAAGAGAGGAGCCCAGCTT	60.096	20	TCGTGCGACATAGTATGGGA	60.096	20
ATCTTCATAAGTGGAGGGGC	58.067	20	TCCTCCATTTCCAATCTGCT	59.629	20
ATGTGCCAAAACGTCCGTA	59.98	19	TGGAAAGATTGAGATGGGATT	58.44	21
TTGAAGATTTTCATGGTGGATTC	60.177	23	TAGTGAACGTTGGGGACACA	60.001	20
ATGTTTCAATGACACGTGGG	59.267	20	GGCCCGAGTTGTTGAGATAG	59.694	20
CCTTGACGAGGGCAAAATTA	60.067	20	TTTAAGCATTCTCTTGTAATCC	59.212	24
TTACATTTTTCTGGCTCCCAA	59.573	21	CTCCAGAGACCTACATGGGC	59.679	20
TCAGTTTCGAGTTATGAAGTTAGG	59.749	26	GCACATAAGATCGGACGGTT	59.962	20
GTGCTTTCCTTGGCTCTCAT	59.434	20	ATAGGGACAGGCACAGATGC	60.104	20
TGCATGCACACTTGTAACCA	59.746	20	AACAGGCGCCTTACCAGTTA	59.769	20
TAGCAGGAAGAATGCGTGTG	60.011	20	AATGAAATCCTTTGGGGTCC	59.996	20
TTCATGCTGAGGTGTTGTCG	60.873	20	TGGGGCTTGGTTTTCTACTG	60.103	20
GGCTGAACCATTCACCTGAT	59.934	20	TGACCCCAATTTCAACTGCT	60.495	20
TTATATTTGGTCGGTGGGGA	60.009	20	ATGTGGACGTCCCAGATTGT	60.246	20
TTAAACCATGCACGTAGGCA	60.133	20	CGAGTAGATCACAACGGCAA	59.864	20
ATTGGTGACGAGAGAGTGGG	60.112	20	GATCTTGGTTGTTGGGTTGTT	58.803	21
TTGCAATTAGTGCATACAATGATA	58.693	25	GCAAAGAACCAAATCTCTTCG	58.962	21
ATCGCAAATAAAACAACCGC	59.971	20	CAAAGGGCCGAGATTTGTTA	60.067	20
CTGCACCCAAATTGGTTCTT	59.971	20	TATATCAATGGCAGCCCACA	59.914	20
TCGCGAATTCAGCTAGAACA	59.712	20	GTCCGATACGAGCTAAAGCG	60.003	20
ACGTGTGTGTGATTGAGGGA	60.005	20	TCGAAAGAGTTGACGAATGTT	57.468	21
TGGTTATTACTCGAACGCGA	59.325	20	ACCAAAATGCCCTTGTATGC	59.829	20
GACCGTGTAGGAAGGCTGAG	59.867	20	ATCACAAAACCCTAGACGGC	59.056	20
TAGGCACAAAACCCACCTTC	59.971	20	ATAGGGATGGAAGGGTACGG	60.032	20
AATGGCAGATTTGAAGACGG	60.074	20	ACCTATCGTCTCCTCCCGAT	59.919	20
GCCAACATCAACTGCGAGTA	59.871	20	CTAATTCGCCCAATTTCCAA	59.901	20
AGTTCAAGAAAGCCGTGGAA	59.853	20	ATCGGGATTGGTGGAACATA	60.014	20
ACATCCTCATAACCCCCACA	60.05	20	GTTCTCGCAAACAATGCTCA	59.995	20
TTAAGACCCGATGCCTTTGT	59.569	20	CCCCGAAAATTAATCATTGC	59.259	20
CTCTATCAATCGGCTGGGAG	59.79	20	TCAACATTGGGCATTTTCAA	59.907	20
AAACCACCCCGTCTTTTCTT	59.842	20	TTTCCAGCCTTCCTTCTCCT	60.319	20
CTCCTTTCCATCTTCCCTCC	60.008	20	AGTGAACCGAAGGTCCATTG	59.966	20
AAATGAGACAAATGTGGGGG	59.647	20	CGAATTTACCAGAAACCCGA	59.931	20
GCACTGTGTGCCAAGAGAGA	60.187	20	GCCACAATGTCATGCTTCAG	60.272	20
TAGAGCTCGGAACATGGAGG	60.353	20	AAAACATACTCAGCCACCGC	60.14	20
TTTTCGTCCGTCCCATAAAC	59.801	20	ATGTAGGGTTCCTGTGGCTG	59.989	20
CCGTACAACTAACATCCTCCC	58.449	21	AAAAGACCCTAAGCACTCACA	58.061	22
GGCCTGATTTGCAATACTGTG	60.517	21	ATTCTTGTTGGTGTGTGGCA	60.008	20
ACCCTCAAGCATCAGCATTC	60.226	20	AGCTTGTGGGCATGAATCTC	60.226	20
ACAAAAGCCTGTGCGAGTCT	60.058	20	ATTAAACGGGTAACTCGGGC	60.204	20
GATTTTGCACGAAGCAATGA	59.816	20	ACGTGGTAGCACGAGAATTG	58.802	20
TGAAAATGGGTACCACACACA	59.725	21	CCTTCCTTCGTTTTTCTCCC	60.046	20
GCGCTACATGCTTTGTGAAT	58.948	20	CGGTTTGCTAGGTGATGGAT	59.955	20
GCAGGTTCGAAGTAGGGTGT	59.212	20	AAAGCTTTAAATGTGTTACAAA	59.182	26
ATCTTTTGCGATGCCTCAAG	60.352	20	TAGTGGCTACGGTTTCCCAC	59.993	20
TACGTCTGTTGAGGGTGCAA	60.301	20	CCCATTTTTCTAGGCACCTTT	59.489	21
CGATTGGGCCTATCCTATCA	59.878	20	CATTTCTAGCGAGCCGGTTA	60.356	20
TCGCTCTTCTTTCGTTTTGA	58.771	20	CATGAGCGAGTAAACCACCA	59.716	20
CGCAGAAACAATGATAGCGA	59.976	20	TGGCATCAAATCTAGCCATT	58.187	20
CTTTTTCGGGTTTGGACGTA	59.968	20	TGACACGTCACACATTGGACT	60.063	21
ACAATACAACTGTCGAGCTGAA	57.569	22	TTTCACGCATTTCCACACAT	59.972	20
GGCCCACGATGGTTATTAAA	59.66	20	CGAAAACACGGGAAAAACAT	59.839	20
GGCAGATGATGGTGGAGACT	60.08	20	GTCGGACCAGCTCTCTATCG	59.973	20
CCGTGTGTACAACAATAGCAA	57.242	21	AATCTGACGGCCGATATTTG	59.923	20
CCTCTCCTCTCAACTTGCTTG	59.218	21	TCTAGGTGACGGACACACCA	60.154	20
TAATTGGCCCTTGATCTCCA	60.405	20	CTCAACCGATATCCCCTCCT	60.285	20

GCATCTCTTGCTCTCTCGTTG	60.292	21	GAAGGTGGGAATTGTGGAAG	59.381	20
GCAGAAGGAACTGATGGCTC	59.957	20	ATCCCCATTTTTCAAAAGCA	59.388	20
GTCGACAAATTCAAAGGCGT	60.118	20	TGCTAAGAGAAAGCCCCTCA	60.088	20
CAGCAGAGCATACTGCCAAG	59.764	20	GGGAGACAGCAAAAGCTCAC	59.997	20
CTCTTGACTTCTGATCCGGC	59.95	20	AGCCACACATGTCACAAATGA	60.024	21
CCTTATGAAAAACGTTGGGG	59.311	20	GGATGATAGAACTCTGGCGG	59.653	20
AGCCTCGGATTTCCTGTTTC	60.578	20	TACCTTTTTGCCCTCGAATG	60.067	20
CTAGGGTTAGCATGCTTGGG	59.724	20	CATAGGAGTTGGTTCGCACA	59.716	20
TACGGATGCATTCGACATTT	58.994	20	CCGATTGGGCCTATCCTATC	60.623	20
TTGGGGTTGTTGGAAGAAAA	60.314	20	CCAAATGTGAGACCCTTAACC	58.423	21
GGATTGGGCTTTGAGAATGA	60.014	20	CAGAGACTGACGCACGTTGT	60.096	20
ACCGAAAATCCTTTCACCCT	59.805	20	TCAATCTAAAACCCGTGCAA	59.157	20
CAGAAATTGCCTTGGTTGTTC	59.601	21	TCAAGATTGTGCGAGCTGAT	59.552	20
TGCAAGTGTTGCACTTTGATT	59.381	21	ACCTGCACCAAAATGGAGAG	60.111	20
GGTCTTCTAGCCTCTCTCGC	58.378	20	CGTGGTTCGATCGTAATTGA	59.542	20
AATCGCATTGCTATCATCCA	59.094	20	AGGGTAGACATGGGTTTCCC	60.052	20
CGTCCCAAGTTTGTTTGCTT	60.147	20	GAGGCGGTAGGAAACCCTAA	60.443	20
TGAAACACTTTCACCTCCCC	59.943	20	CAGTTGGTCAGAGATGGCAA	59.831	20
TGGCAAACAGGTCCCTAAAC	59.971	20	GGCGTTGGACCAGTGTAGAT	59.997	20
ATGGGATAGCACTTTTGCCA	60.469	20	TGGATGACACGCATCAAAAT	59.931	20
CGGATTTAAGGGTTATTACCTGAT	58.81	24	TATGGGAAGGGCATTTTCAG	59.894	20
CGTGTGGTTATGACATCCGA	60.39	20	GCATTTCATCCTCTTCCCAA	60.014	20
CGTCGAAAGGGAAAGAAACA	60.22	20	ACTGCGAACCAACATCACTG	59.751	20
ACTTCTTCCTTGTCATGGCG	60.255	20	TTCTCAGCTCGGGTTCCTAA	59.948	20
CACAAAATGGATCGAAACGA	59.518	20	AATGCGCCTCCCACTTTAAT	60.821	20
AAAAGCGTTATGCGTCGAGT	59.911	20	TCCTCTACCACCCGAAAGAA	59.665	20
CCACAACTGCAATTTACTGTGA	58.75	22	TGATGATGACAATGATATCGTG	60.217	24
GGATTGGAAGCAGTGCCTAA	60.214	20	TTAGGCCATGTTTGTCTGCTT	59.761	21
GAGACACGTTGGGTCTGGTT	60.009	20	TGAGGCCTTCATTCAAAAGC	60.331	20
CACAACAGGAGGAGGCACTT	60.298	20	CAGCCGAAGTAACAAAGACGA	60.426	21
CCAAGATTGAGGTCCGTTTC	59.526	20	CGCAATTGTGACTTGTGTCC	60.16	20
ATCTGGGCACTCGGAGAATA	59.653	20	CGTCCACTTCATTGAATTTCTTT	59.531	23
GGACGCACCAGATTGTTTTT	59.978	20	AATTGCATTACATGCTCCCA	58.994	20
TTTTGACATCAACGGATGGA	59.9	20	GCACACCAAAGTGAAACCGT	60.996	20
GAAAGTGGCTTTGATGGAGA	57.864	20	TCAACAAAGCATTGCAAAGTG	59.903	21
TGCAATATGTTTATTTCGGGA	58.048	21	TCAAATACTAGCATATCGATGA	58.499	26
TTGCGATTTTCGTTTTCCTT	59.699	20	ATCCACCACAAAGCAGGAAC	59.973	20
GCCTGAATGTAATGCCGAAA	60.971	20	TCCACCCATATTGCACTCAA	59.924	20
TACCGTTGGTTAATCCTGCC	59.823	20	TGTGAGAACCATCTCGGTGA	60.246	20
CAGCTTTCGGCTTCTTCTTG	60.262	20	ATCAGCCACACCCAGATAGC	60.104	20
GGAAATCCCGTACGCTATCA	59.923	20	ACATTGTCAGAAAGTGCCGA	59.293	20
ATTTGGGAAAGGGGGAGTAA	59.639	20	TTTTCAAGAGCATTCACGGA	59.395	20
TGGTAACATTTGTCTTATTTGTTGC	59.404	25	TGTGCTTGTATTGGAAGCATAA	58.712	23
GGCCTCAGCAGCTTCTCTAC	59.337	20	CCCACACCTCCTAAAGGGAT	60.183	20
CGACCAAATGTGACTCGAAA	59.691	20	AATTTGTTTGATATTCAACCACT	59.243	27
TGTAGGCTTTGGTTTCCATTG	59.982	21	CTTTTAGGTTGCCTCGAACG	59.876	20
GAGGAGCCATGTTTTGGTGT	59.973	20	GCGTGGAAAGGCTGAATAAG	59.845	20
GAAGATGGAGTAGAGAGAGAGAT	59.94	27	CCCAACTAACCACCCCACTA	59.705	20
CATTTCAACCCACCATCTCC	60.173	20	TGTCCAGCTCTTCCAAACAA	59.415	20
AACCGGATTTAGAGCAATCAAA	59.97	22	CCAGCCCAATAACTTGACCT	59.052	20
TAGGAACAAATCTGGGCCAT	59.387	20	TATACACGGCATACATGGGG	59.136	20
GGTGTGGTGGGGACATTTTA	60.474	20	TTTATGGGTCCAAACAACCTTT	59.625	22
GACACCCATTGCTGTGTGAG	60.162	20	CGTGTTAATTCCCCTTCCAA	59.795	20
ATCCAACACCGCATCTTCTC	60.081	20	CAAATTTGATAGCGGTCTAATG	59.557	24
CAGACTAGAACGTAGACCTGGC	58.161	22	CTCAGGGACTAGTTGAGCGG	60.005	20
GGATGTCAATTTAGCCCGAA	59.901	20	TCATCACCGTGCCAATTACT	59.002	20
CACACACAGAACACGCACTG	59.976	20	ATTTTCCCTCCAGTTGACCC	60.169	20
TCAACAATCTCAAACTGCAACC	60.154	22	AAGCGCAAGCACCTAGAAAT	59.138	20

AACAACCTGGGTATCCCAAA	59.146	20	TGCACAGAAAATGAAAAGCG	59.992	20
ACGGAATTGAATTTGGGACA	60.17	20	AGCCATGTGAGAGGGAGAGA	59.945	20
TGGTGTGATCTCATCCCTTG	59.473	20	TCCAATGGATGTAATGAGTTAT	57.297	26
TTCAGCAGTGCTTGGTGAAG	60.175	20	AGCCGTCGTATTCTAAACGC	59.388	20
GACGGGAAGATGAAAGGACA	60.05	20	TCAAAGAGCTTTCTCTGTTTGC	58.906	22
GCGCAGATCTAATGGTCCAG	60.765	20	GTTGGGTGAAGATCATGGCT	59.934	20
CTACCGGAGAGTGGTGGTGT	60.026	20	GGAGCAATAAAGGGCAATCA	60.038	20
CCGAATGATGTGCATTTTTG	59.93	20	TATGGTATGCTGTCTGCGCT	59.474	20
TTACATTCAGGCCTTTTGAACA	59.625	22	TGCAGGACAATATCCATCACA	59.94	21
TCTAACTCCATTTGTAATAGTAAG	57.468	27	ATCTCGTTTCAAGCCCAAAA	59.685	20
GAGAAAGGAGATGGAGCGTG	59.95	20	TGATGACGATCTTTTGAAACCA	60.481	22
GGGTGATGAGGCTTGAAGAA	60.195	20	TTGGGCTAAAGTGGGATGAA	60.439	20
CTGAGGTCCCGAGCTGATTA	60.353	20	ATGCGCGTTTTTAGGGTTTA	59.624	20
TTGGGTGGAACTTCTTGCTT	59.711	20	CAGAGTCCTGGGAGCTCATT	59.405	20
GCAATGGGTTAGCGGTAAAA	59.964	20	TGTGCACAAGCTTGGAAAAAT	60.663	21
AGCTGGTAGCCATTCTCCTG	59.454	20	TCGCCTTTCATTTCATAGCC	60.175	20
TGCCTGAAAATGTCTGCAAG	59.988	20	ACCATGAGCACAGGATTTGA	59.09	20
CGTTCCCAAGCCTCCTATATC	59.938	21	GGGACGGATCACTCTTTTGA	60.05	20
GCTACGACTACGGCTATGGG	59.752	20	ATGGAGGTATGGTGTATGGG	57.047	20
AGCTGAGATTAAATCCCCCG	60.411	20	CGCCAACCTATAAATCACGG	60.335	20
TGGGATATCGTCTAACCAGCA	60.475	21	TGACGATATATAGTGTTTTGAC	57.754	26
GCAAATCCCAAAACCGAATA	59.773	20	CCATGGGTGGTATGGTGTG	60.517	19
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TAGTTGGGAAAGTTCACGGC	60.11	20	GCCTTTGCCCTTTTTCTCTC	60.32	20
CACCAACCCAACCCATTATC	59.91	20	TTCAAAAACGAATTTGGCGT	60.468	20
AGCATTCATTGCTACCTGCC	60.243	20	CTTGCCATGCATGTAAGGTG	60.134	20
TCTGCACTCTCCATGAGTCG	60.138	20	TCCTCTCGTGTTCATCCTCA	59.34	20
CAAGTGCAGGCAACAGTTTG	60.485	20	CGTCGATCTCAGTATCTTCGC	59.992	21
CTTCTCCACCACCACTTTGC	60.69	20	GGTAAATGGTTACCGGTTTGG	60.33	21
CCAGGTGAGCTAGCCCATAA	60.227	20	AATCACGTTGCAAAAATAGCG	60.143	21
TGGTGACTGCACAGAAGAGG	60.022	20	CTTTTTCCCAATCAAACCCA	59.772	20
AGGGACGAGTCCTAAAGGGA	60.067	20	GTGAGGCATCAAGATGGACA	59.637	20
ACGGCTGTCAATCATCACAA	60.12	20	AGCCACCTCCTAGCCATCTC	60.756	20
GGGATTTCAGCGACGATTTA	60.038	20	TCCCATGTTTGTAATTATTGTA	60.228	25
AGAGGAGGGCTTCAACATGA	59.803	20	TCTCTAAGTGCCCATGATTCTG	59.336	22
TTGGCTAACAGGTCCCTGAA	60.626	20	TTTTGTGATTTCCCATGTTTG	58.374	21
TAATGTGGAACCATAGGGGC	59.645	20	AAAGTGGTGTGTTCGAGGCT	59.769	20
ACCTATCGTCTCCTCCCGAT	59.919	20	CAGATTTGAAGGCCGGAATA	60.031	20
GCCTCTTCTCTGCTAAAAGCC	59.76	21	AGGGTGTGGTTATTCCAATCC	59.933	21
CAAAATGAAAAGATTTGAAAAAC	57.523	24	CACTCAGTGGACACATTGCC	60.162	20
TCCTTCTCTCCGAATTCCAC	59.213	20	ACTGACATTCACAGGCATTG	57.067	20
TAGGCATGGCCTCAACTACC	60.096	20	TGCAATGGAGGGACTTTCTC	60.195	20
GATGGAACGGGGATTTGTTA	59.622	20	CATGCATGATCAATGTTGTAAG	59.541	24
TCGAGCATAAACACATCCCC	60.864	20	TCATGATAATGCATGTCTCTGA	59.883	25
AGCTACACTCACCGTCTGAGAA	59.161	22	AAACAGTGGGTTTCGCGTAT	59.499	20
TCGATTGCTCTCCGATCTCT	60.057	20	GACTAGTTTTCTGCGACGGC	60.022	20
GCAAGACATGCAAGGCAGT	60.008	19	TTTCTGCTCTCCCCTCCAAC	61.67	20
CAAGAGCAAATGCAGCAAAA	60.133	20	TCAACGCATCTACAGGTTGC	59.871	20
TCAGCAAAGTGCTAAATGGTTC	59.406	22	TCCAATTGTTGTCTTCCATCTG	59.971	22
TTGGTGGTTTGTATGCTATCG	58.57	21	AGGTTTTGATGGTTGTGATTTG	58.858	22
CTATCGCCCCTCCTAGCAAT	60.562	20	AGTTGGCATCACAACCAACC	60.823	20
CCTCGGGGAAGTTACAATCA	59.926	20	TGACTCCTGGCTTACCCAAT	59.55	20
TTGGGATTAAGGCTTTGGTG	59.931	20	GCTTGACGTTTGTCGTGTGA	60.917	20
AAACAACGAATCCATTAAGTGAA	58.676	24	TGGTCGTGAGATAGAGTGCG	60.008	20
TTTCGGGACACGTTCTCTCT	59.844	20	TTGGCATCTTCTCTCAAATTCA	59.823	22
ATTGCCCCCTCATTTTCATT	60.511	20	TGTTTCGATGTGCATGGAGT	60.12	20
TTGTCATTGGTTGTGGCTGT	60.008	20	ACCTGTGAAAGCGATCGTG	59.846	19
ATGAAATGACGAAAATGCCC	59.768	20	AAAATCAAAGGCCCACAATG	59.801	20

TATTTGCATGGGTCATTGGA	59.745	20	TAAAAAGATGAGCCCACCCA	60.439	20
CACAATGGGGGTATTTGCTT	59.685	20	TGGAATGTTATCAAGGGTGG	58.27	20
GATAGGCCCTAACTCGACCC	59.925	20	GAGCTCTGGTTCCCACAGAC	59.841	20
CGAGTTTGTTTGCGAGATGA	59.988	20	CGAAAATGCCCTTTTATGCT	59.212	20
TGGCTCAAAAGACAAGTCCC	60.232	20	CATCAAGAGTCGGCTGTCAA	59.984	20
TAATTTGGTTGGCCCATTGT	60.053	20	AAGAGGAAGAAGGGGGTGAA	60.045	20
AACTCCATTTGCAATACTAAGGC	58.771	23	TCATCCCGTTTCAAACTCAA	59.097	20
TTTCAAGAAAAGGGTGCCAT	59.546	20	CCCTCAAACTCCCTTTTTCC	59.912	20
GACGTCGGTTTGGTTTAAAGG	60.736	21	CCACCAAGTATCGGTCCAGT	59.844	20
GACCCATTTAGAACCCACGTT	60.103	21	TGATGAAAAACAATTGACCAA	58.045	22
TGGAACAATTTTTGCCACAT	58.869	20	CCTCAAAATCTTTGAAGGCTCT	59.024	22
GAGAAAAACGACGTGAGGGA	60.232	20	CAACTGAGTCCCCTATCCGA	60.065	20
TTTTGGAGTATTCCGTGCCT	59.569	20	TGTTGCGATTTTCATTTTCCT	59.578	21
TCCACTTGACGAGGTCACTG	59.864	20	CCCTCATAACTCCTGACTGCTC	60.268	22
ATATTTCATTCATGCCACGC	58.458	20	TTCAACCATCAACTCCACCA	59.935	20
GTCGAGGAGTATACGGAGCG	59.859	20	AACCATCGATGCATTCACAA	59.931	20
ACGTAAAAACCCTTCCACCC	60.089	20	AAATCATGTTCCGTCCCAAG	59.79	20
ATGCATGCACGTGAATATGG	60.375	20	TCAGTTTCGAGTTATGAAGTTA	58.582	25
ACGGATATGCCCTTGTATGC	59.813	20	GCCGATTTGGAGATCTATGG	59.486	20
TGATGCTTACCTGAACAGCAC	58.94	21	TTAAATGGCCTCGGTATTCG	59.922	20
ACAAGGATTGCGAACTCAGC	60.406	20	GTTTGTTGGGCTCAGGTCAT	59.973	20
CCCCTCTCAACAACCACAAT	59.82	20	ACGGTGAGGGGGAAAAATAG	60.18	20
GAAATTGCCTGCTTCCAAAG	59.823	20	CATATGCATCCGCAATTCTG	60.058	20
AGAGCCGGGTTTAAAGCAAT	60.095	20	TGTTGTGTTCGTGTCCGATT	60.008	20
CCACTTCCTAGGCAAACACC	59.592	20	GGTTATCGTTGTTGGGGATG	60.051	20
GTTGGTCATGAGCTGGGACT	60.12	20	CGTCACGGTTATCCTTCGTT	59.993	20
TGGTGCAGTGGTAGAGCATC	59.862	20	TTTAGCAGAGTTGGTGAAATC	57.952	23
GACCACAATCAAACACCAAGG	60.262	21	CACCCTAACACGCACAAATG	60.027	20
CCAAATTGATTTCCCACCAC	60.029	20	GAGATTGGGGACTTGGTGAA	59.903	20
GGTGGTGTGGAGGAGAGAAG	59.682	20	ACACCCCTCCTCAATTTCCT	59.795	20
TTTTCCATTATTTTCGTTGGAGA	59.838	23	ATGCACCAAAAAATTGACACG	59.444	20
TTAATGCTTTGAAGGGGTGC	60.074	20	GTGATTGTATCGCCACCTCA	59.527	20
GGGGAAGATGTCGTGAAGAA	60.05	20	GACCGCTAAAAACCGTGAAA	60.11	20
TAATTCGTATTTCGGTCCGC	59.928	20	GGGCTTTGTCTTTTTGAAGG	58.809	20
GCCCAAAAATTTAACGACCC	60.528	20	GCCGTACATGAAAGACAAAAC	60.039	22
CCAACACAACACAGGTTCTCA	59.626	21	TGGGAAATTATGGATTGGGA	59.95	20
CCCATGTTGTTTGTAATTATTGTA	59.853	26	AGAACACGAGGAACTTGGGA	59.697	20
ATTTGGAAACCTCCCACTCC	60.169	20	TCAACTCAGAGCTCCATGCT	58.699	20
CTCTCGCTAGGCGACTTTGT	59.78	20	AAATGTGAATGAAACAAGCGG	59.989	21
GCAGCTAGGCTCCCTCCTAT	59.968	20	GATTTAGGCCAAGGCAATCA	60.038	20
GGGAGTGATTGAGGGAGTGA	60.048	20	TGCGAATCAATTATCCCAAA	58.958	20
TTTTGCAACAAAGAACCAACA	59.236	21	GGGTGTTTTGACAATATCACG	59.73	22
TCATGTCACGTCAAGCATCA	59.823	20	AAAGATCTCTGCAAGTCCGC	59.579	20
CGCTATGAGTCACGGGTACA	59.74	20	TGCTCTCAACCATACCTGGTC	60.126	21
GCCAAAAATGAAACAATGCC	60.31	20	AATTTTCGTTCATGCCCAAG	59.938	20
TGTACACGTGTGGCTAGCGT	60.393	20	TTGAGCTGTTATGCGTTTTGA	59.5	21
CGAAGAATTTTGTGCCATGA	59.664	20	TCACCAGGTACGTGCTCAAA	60.301	20
TTGTTGAACGCATAATTCGATA	58.25	22	AAGTTGGTGGGTTGAATGCT	59.454	20
CGTTCCTCAGAGTTTCCAGC	59.989	20	TGTGATATGAAGGGTCGCAA	60.073	20
CAAACTTTCTGGATTGACTTTGAA	59.682	24	TAACCCAAACCCACCCAATA	59.91	20
CTCAACACTCTGTTTTTCTCTCAC	60.007	25	ATATGCCCGGTAAAAGAGCA	59.569	20
CGTGTCCTCCTCAAACTGGT	60.151	20	CCGACCCATCTCTTGTGACT	60.112	20
TCTATTATATGTCATGTTTTGCATT	57.462	27	CGTCTTGGTGTGAGCGTTAG	59.51	20
ACCCATCCCTTAATCAACCC	59.881	20	ATCAACATGCAAGCATCCAA	60.08	20
GACGCGAGATTTACGTGGTT	60.14	20	GCTCTCATTGTAATCTCTCCCA	59.739	23
TTTCATGTTTAGCATTTGCGT	58.368	21	CAGCTCCAATCCATCTCCAT	60.034	20
GGGGTAGTATTGAGTCCGCA	59.955	20	TCTAGCACGGTTGCAATCAA	60.401	20
CTTTGCGACGTAATTCCCAT	59.96	20	TGCGAACTCAGTGCTACTCG	60.347	20

AAGCAGGAAGTCATGGTTGC	60.263	20	GTTCGACTGATGGGTGCTTT	60.119	20
ATTTAATCACGTGCAACGCA	60.14	20	ATTCAAAAATGAGTGGACCAG	58.554	22
CATCCAATAGCCGAACAAAAA	59.95	21	TGGCCTTCTTCTTCCAACTG	60.366	20
AACTGCGATGCTCCAAAAGT	59.882	20	TCCTAAATGTGGGAAGTGGG	59.784	20
TGCAGAGAAAGCAATTGTCG	60.134	20	TGTGGAAGCAAATGGTTAGC	58.773	20
AGCACAATACAAACATGTCCAC	57.538	22	CATGGGACCACAGGATAGGA	60.737	20
TTGTGTGTTATACGTGTGGGTG	59.29	22	CCTGCACCATCACCTTTTCT	60.111	20
TCAAGGTCTTCGCTGGTTCT	59.989	20	GTTTCGTGATGATTCGGGAT	59.756	20
TATATGATGTAGGCCGCGTG	59.567	20	CGAAATTGATGTGTTGGCAT	59.4	20
TGGACATGGCAATTATTCTTGA	60.323	22	GAACCCTGGTCTTCACCATT	58.842	20
ATGGGTTCCTTACCCCTTTG	60.046	20	CCTACACCACCCCTACTCCA	59.837	20
AGCAGGAGGACTGAGGTTGA	59.986	20	TGGTACCATACGCGAAATCC	60.721	20
TCCTTTCTCCAAGTCTCACCT	57.969	21	ATCAATCTTACGGACTGGCG	60.096	20
AGCAAGGGAAACTGATGGTG	60.111	20	AAGATCGTGCAAAATTTGAAA	59.672	23
GGATTTAGCGGTTATTACCTGA	57.387	22	GGATAGGCGGTTGAGATTTG	59.528	20
ATTCTCGCGTCTGACTCCTC	59.56	20	TCAGTTTGGTTTATGAGTAGGA	59.15	25
CAGTTGTGTTGTGGCAGCTT	59.946	20	ATGGCCTGATTTGTTTCTCG	60.074	20
TTTGAGATCGGAGTGGCTCT	59.95	20	CATCGGACCATTTTCTGACA	59.496	20
CCGACGGTTGTAGTGGAGTT	60.028	20	GCGCTTTTTGCCTGATATTT	59.349	20
TCAACCGTGCGTGTATGTTT	60.035	20	GAATGTGTACTGTGCAGGGC	59.169	20
GAAGATGATGGTGAAAGGGG	59.336	20	TAACTCCGTATTCTTGCGGG	60.089	20
CTCACTTAGGGATATATTTAGGG	57.128	26	AGGAGGAGCAAGAGAGGACC	59.952	20
AGACATGCATCGTTTGTACTCTTC	59.722	24	TATGGGTCAGAAAAGCCCAC	59.933	20
TTCAACAACTTTCAGCCCAA	59.293	20	GCGTTGCGTATGGAAGAATC	60.615	20
TCAACGCCCCATATTGTTTC	60.701	20	ATTTGGGGTGAGCTTCACAA	60.495	20
AGATATTTCAGGGTCCCCGT	59.651	20	GATGTTGATTGCTGCGAAGA	59.955	20
ATGTTGCGCTTTTCTCCTTC	59.457	20	CGTTAAATCTCTGTGTTGAATC	58.016	24
ACGGGCAGTACTCCAAAATC	59.056	20	CTTGTCACTTTCTCCCTCGC	59.989	20
AAATGAAGGGTTGAGCATCG	60.074	20	CCTGTTTCAGAGGGGATGAA	60.042	20
AGAACGTTGGGAGGGAAGTT	59.972	20	ATGGACCACCCACCAAAATA	59.91	20
CTGAACCTGAACCACCAACC	60.399	20	GGAACAAGAGCTCGAGCAAG	60.277	20
GTTGATAAATTACAAAAATTTAAG	58.406	27	TAAGCGGACCCCAACTACAG	60.125	20
ACACCAACCCATTTGCTCTC	59.973	20	GACATGGGCAAGACCAACTT	59.973	20
TGTGTATATCTGATAGCCGTAGC	58.876	24	TTTGCTGCTGATGTTTGTCC	59.847	20
AGGGGAGTTATCACTGGATCA	58.46	21	TGACTAAAACATGGAAATAAT	58.939	26
TTTCTTGGGGGAGCTAGGTT	60.068	20	GCAGTTTTGCTCCCACTCTC	59.997	20
GTCCCCAGCCTCAGATACAA	60.073	20	TGTTCCAGAAAGGAGGTTGAA	59.697	21
GACAACACCTGAGATGCCCT	60.12	20	GGTCGATACATCAGGCAACA	59.527	20
CCTCTGCCTTATTGATGGGA	60.029	20	TGCATGATGAGGTCTTCGAG	59.942	20
ACGTGTTACCCTCTCAATTTATCA	58.995	24	TTCGACTTAATCAATAAAGATA	57	27
ATTTAGGCATTCCCACCTTTG	60.19	21	CTCCAATCTCCAATCCATGC	60.426	20
GCATTCCCAGAAAATCCTCA	60.014	20	CGTGGTTCGATCGTAAATGA	59.542	20
TCGTCTGCAAGAAAATGGGT	60.636	20	CCGAAGGGATAGGATTGTTG	59.382	20
AGAGATTGTGGGGCTTGATG	60.073	20	AACTTGCTGTTTTGGATGGAA	59.601	21
CAACCCAAACCCACTTTCAT	59.688	20	CTTGGGAGAACTTGCTTTGA	58.077	20
GCATCTCTCTCTTGCTGTCATT	58.699	22	TGAATAAGAGTTCAATGAATTT	59.912	26
CCATTTTGACATGATCGACG	59.924	20	AAGGAGGTGTTATGAAGGGAT	58.028	22
ACGTGTCTACAAAACTTGCTGC	59.493	22	ACACGCTTGTCAAACATTTCT	57.402	21
CAAGGCATGGGAGGATAGAG	59.647	20	TGTGCAGAGGGACTTTAATGC	60.264	21
GGCAGACGAACCCAAAGTAA	60.11	20	TAAGTTGATGTGTGCAGGGG	59.566	20
ATTAAAGGTGGCTGGCATGT	59.457	20	ACAAACTAATCAAGTTCCGCA	57.439	21
CTTGTCTCCGTCCTATTGGC	59.694	20	TTATTATCTCGATCCAACCAAA	57.725	23
TTGCGCTTGGTTTGTAGACTT	59.934	21	GACATGATTACTCGTCCCCC	59.218	20
CTGTCTCCGGTCCATGAAAT	59.927	20	TTGAACAATGGTACCTCCTCCT	59.864	22
GCGAAAACAACAGACAGCAA	60.035	20	TTTGGGGTATGGAGAAGCAG	60.066	20
GAAAGGCTTGTGTGCATCTTC	59.874	21	TAGTTCACCAACTCCGGGAC	59.966	20
TATCACAGAGCCACGACGAC	59.862	20	TTCTCTCTTCTATTTCTTTCCTTT	58.425	27
GACATATTTTTCCCCTTTCCA	57.91	21	CGGACCGGGTGGTCTAAATA	61.972	20

ATCAAATAAGTCACGGCGCT	59.736	20	CATTTGGATCCTCAAGTGGG	60.309	20
CTCGCCATTTCCCTGTCTTA	60.206	20	GGGCCTGGTAATCCATTCTT	60.152	20
TCGTGATATTGGGAAACAATGA	60.188	22	TGTTGCCGTCAGTTCATGTC	60.733	20
AGCATTAAAATTGTTGGTCCC	57.987	21	TTGGGATATCCGTTTCTTGG	59.756	20
GGATACCCTCCCAAACCCTA	60.011	20	AAACTTCTTTCCAACCGGAAT	58.991	21
GCGGATTTTATTCTCGTTCAA	59.202	21	TTGGATCATGATTTGAGTTTGA	59.077	23
ATGGAAAAGGTAGGGACAAAA	57.596	21	AATGACCGATCTCTCTATCCCA	59.925	22
CAAGCAACAAGCCAATAGCA	60.014	20	GGCGATTACTCCGTACTCCA	60.096	20
AGTTATCAAGATGGCCACGG	59.955	20	AAGGAAACAAAAGCTCGGTT	57.983	20
TTTTACCCAAAACACCCCTG	59.696	20	ATTGGGGATGGAAAATTGGT	60.245	20
TTTTTGGGAAATCCTTGCAC	59.916	20	GGAATTGTCCCCTTCGTTTT	60.166	20
CCCAACCACTTTCACTGGAG	60.536	20	GCATGATCAGGGTAAAATCCA	59.776	21
CGAAAGTGAACTCAACCCGT	60.149	20	TCAGGGTTTTAGCCACAAGG	60.103	20
TGCTCCTAGTTAGCACACAACTT	58.288	23	GGGAATGAGAAACTTTGGAGC	60.067	21
TGAAGTTAGGAAATAAGGAGGTG	58.743	25	GAAGGGACAACGACTACGGA	60.111	20
GCCCCATTTTCTTAGGGTTT	59.311	20	CCATTTCCCTTCCTTTCTCC	59.875	20
CTTGGAGGCTCAGAGGTTTG	59.982	20	AATCGAACCCACGAGAGCTA	59.836	20
AAGGTTGGCATCACCTCTTC	59.141	20	AAAATGCTGACATTGGAGGC	60.081	20
GTGCTTTTAGCTTGGGCAAA	60.376	20	TGATTGAAGCAAAAGAACCAG	59.861	22
CACGAACGGCTGGAATATCT	60.096	20	TCATTCCACCCACGAACTTT	60.353	20
TAATAGGTGCGGGTTTGAGG	59.953	20	GCATGTTGTCACCCCTACCT	59.851	20
TGGAGGAATGAAGGTGAAGG	60.042	20	CCTCAACTACCCAAACCCAC	59.304	20
GGAGAGAGGGAGGGAGAAAA	59.749	20	CCGAACCACGTACATCCTCT	59.989	20
CCCTTGGTATTCTCCCTGTG	59.401	20	TAACAGGGTCGGCTCATTTT	59.569	20
TGCTGTGGCAATATGATGCT	60.251	20	GAGGGGAGGAGGAAGAGGAT	60.918	20
TGACATACATGGTTTGGGGA	59.623	20	CTCCCATTTCGCTTTCCTTT	60.553	20
GCTAATGCTTCAGCACCACA	60.019	20	ACCTCAATTCCCCATAACCC	59.881	20
TTGATCGTCAAGCTCGTGTC	59.992	20	GGCCAACATTTTTCAACTGG	60.344	20
TAAGGAGATGTGTGCATGGG	59.522	20	CAGTTTTCGAGTTATGAAGTTA	59.339	26
CCTCACTTTCAATGCTCGTG	59.44	20	ATACGAGCCCGAAGGCTTAT	60.082	20
CACCAAAACTCCACCTTCAAC	59.482	21	TCCTAAGAGATTTGATTGAAAA	59.651	25
GTTGGCAAACAGGTCCCTTA	59.971	20	ATTAAATGCGCCTCCCACTT	60.821	20
GGGGAAAAGAGTTATCACTTGAA	58.682	23	CCGAGCCCTCTCTCTTCTCT	60.23	20
TTGATTCATACAAGTCATCTTTAT	57.459	27	TTTAGAACGCAATGGTGCTG	59.872	20
AGGAAATAAGGAGGTGTTATGAT	58.113	26	ATGAACCTATTTCGTTGCCG	59.96	20
TTGTGACTGGATTGGCATGT	59.967	20	CGGGGTGTAACTTGCTTGAT	59.993	20
AAAAATGAACCGTAACCGGC	61.066	20	AGTTTCGCTTTGCTGATGGT	59.882	20
AGTGAGAGGAAGACAGGCGA	60.135	20	GTTATGCGTTTTGACGGGAT	59.829	20
ATGCAACTCAAAGGGAGGAA	59.67	20	GACACTGAAACCGAACCGAG	60.69	20
ATCAATGGCCACAAATGGTT	60.059	20	GAGCGTGACTATCCACCGTT	60.142	20
ATGATTTTGGTGTGTTGGCA	59.823	20	CACATGTACGCGCTCTTGAT	59.895	20
CATAAAACATACCTCGGCATCA	59.853	22	AATCCCAATTAATTTCGCCA	59.259	20
AATCACGTCAATTCCGAACC	59.797	20	CCTCAATCACTCACACGCAC	60.319	20
TGCCACTATAATTGTATGGTCTCG	60.27	24	CCTAGTTGGCACAAACTCCC	59.592	20
TACACCTTACCCACCCAACC	59.569	20	GGATGGTGTTTGTGGCTTGT	60.823	20
CACAAACACACTTGGGAGGA	59.565	20	CTTGGTGGGACAAGAACTCC	59.549	20
TTGGCCACATAGCTCTTTCTC	59.467	21	GTGGTAAACGAGACCCAGCA	61.096	20
GCAAGAACTTGGCACCATTT	60.118	20	TGTTCCCTGGCAGCTACTCT	60.012	20
ACGTTTTTGTAAACGTTGTCCT	57.794	22	GGTTCCTAAGCAGCCAGATG	59.836	20
GGACGCTCCAGATTGTTTCT	59.288	20	CAAAGGCCCACAATGGTTAT	59.685	20
AATGGTGCATGCAGTCAAAT	59.005	20	GGCAAGTGGGTTACCGATTA	59.823	20
CCCCAAACCCATTTCCTAAT	59.882	20	GGGATTTGTGGCAAGAAAAA	59.916	20
CATTTAGGATATTTTCTATTCTTGC	57.631	27	ACTCGTAAACGACACGAACG	58.851	20
AGGATACCGGAGTGTTCACG	59.989	20	AAGGAGTTTCATGCCCCTTT	59.94	20
CTCCGCCCAGTTGGATACTA	60.088	20	TCAATAAACCCTCCGAATGC	59.901	20
CATCCACCACCTGTCCACTC	61.434	20	TCTTGCTGGGTCCTTTCTTT	58.909	20
TTACTCACACGCACACCCAC	60.639	20	GAACAAGAGAGACAAGGCCG	59.989	20
TTGCTAGGGCCAAGGAGTTA	59.839	20	CGGAAATTATTTTTAACACCCG	59.633	22

TTCGAGTTCATATACACAATAAAT	58.52	26	CGTGCAATTAAATTCAAATCTT	59.476	24
CGTGATGCATGATGGGTATC	59.763	20	TGCGTTTTGATGATATATAGGT	60.054	26
GGTCTCCGGTCCATGAAATA	59.75	20	AGAATAAACAACAATGAAGTG	59.42	26
ATGTGAATAGCCGTTGAGGC	60.103	20	GAAAGCCAGCATTGAAACCT	59.316	20
TCACATATAAGAATGTCTCCGGT	57.647	23	TCGGGTTAAACAAACATAGAT	57.292	23
TATTTTCCCAACCTCCACCA	60.162	20	CATCCATGCAATGGAGATGA	60.444	20
TTGTGCGAACCATGAAAAAC	59.566	20	GTGAAATTTGGCCTTGGAAA	59.916	20
GCAAAGGTCGCGAAAGATAC	59.851	20	ATCATTTATTTCGGCAACGC	59.935	20
GGCATCATAATCAACCATCCA	60.547	21	GTTTTGAACGGTCTGGTTCG	60.529	20
CGACAGAAAGTAACCCCCAA	59.964	20	TGATATCTTTGAAGAACAATTA	57.905	27
TTGTTACCCCCACTTCATTCA	60.213	21	GTACGTTGGAACACGTGGC	60.024	19
CGTTTCCATTGTTTAGCCGT	59.996	20	CTGCTGACACCACCTCACAT	59.738	20
ATTGGTCGAGAGAAAGGGCT	60.212	20	TCGTAAGATTTTTAAAAGAATT	60.128	27
AAGTGATCTACGTCCACGGG	59.989	20	ACCGAATGGCGGTTACCTAT	60.582	20
GTATGTCCGGTGCAAGGAGT	59.997	20	TAGCACTTCTGCCTGGGTTT	59.875	20
GCACAAGTTTGGCCTTCATT	60.118	20	ATGGTGGCTGCATGTCATTA	59.955	20
GTTGGCAAACAGGTCCCTTA	59.971	20	AATGCGCCTCCCTCTTTAAT	60.061	20
ATTCAACACACGACATGGGA	59.812	20	AGAATTGAGTTTTTCAACTCTA	59.961	27
GCCACGACAGATAAACGTGA	59.722	20	CCCAAAAAGGGATAACATGC	59.273	20
AAGCATCTATTTTCGACCACTGA	60.143	23	CCCGCATCACTTGAACTCTT	60.255	20
CTGCTTAAAGCCCAGTCCAG	60.008	20	TCCACGGGAGAGAATGAGAG	60.34	20
ACCGCGGTTGAGGATAGATA	59.551	20	CAATTTGACGTGATTTAACGTG	58.978	23
TTTGCTGAGAAATCTAATGCG	58.2	21	TCTGCGACCCTTCACTCTTT	59.989	20
TCCAACCCATTATCAAAACCC	60.768	21	GGAGGAATTGGGATTTTTGG	60.482	20
CCACCTTGAGTTACATGCTCC	59.607	21	AAGAAGGGTTGTGGCTCAGA	59.844	20
TGACGAATTCTCAAGTTTGTCAC	59.276	23	TGAATGAGATGAGAGGAGGG	59.746	21
CGATATCTCTATTCCGGCGA	60.153	20	CCTCCATGTTCCTCATCGTC	60.475	20
GAGAGAGAGTCGGCAATTCG	60.096	20	CCGCCATGTTTCGATGAT	60.444	18
AGGACCATTCCAGCTTTCCT	60.074	20	TCCCCATTTTTGATCACCTC	59.727	20
TACGATGGGCTTTAAGCAGG	60.223	20	ACTCCGCCAATGATGAATTT	59.391	20
GTTTCTGCATTGTTGCATAGC	58.453	21	GGGGTTGTACTCGTGGGATA	59.67	20
TTCAGAAGGCCAAAGGTGAT	59.67	20	TTTTCCGGAGTTCACCTCAC	60.088	20
GTGAGTGCGCATTGATGTTC	60.281	20	GGACTTCACAAAGGCCAAAG	59.711	20
AATGGTCCGGGGTGATTT	59.987	18	ACCACACGTGTTGGCTAGG	59.606	19
TCACAGGCATTGTCAGTGTGT	60.219	21	TCGATATTCGGCTTGGTTTT	59.547	20
GCCAAGAACAACTCCTCTCC	58.868	20	ATCTTGCTGCTCCAAGGTGT	59.874	20
TAGGGATTGAGGGTGATTGG	59.744	20	GTGGGTAGGGGTGTTCAAAA	59.688	20
TGGATAGACTCATAGCCCGTG	60.103	21	TCATGCTGCATATATAAATGTC	57.652	27
TGACATTGCCTAGAAAGTGGG	60.118	21	GAACGCGGTCGAGAAAGAT	60.355	19
GCAGGGCTGAGTACACGAAT	60.285	20	TCGGAGCGATAAGGAATCTG	60.309	20
AAGAACACACAATTCATGTGGAA	59.392	23	AGGCGTCGCTGTAATAGTCC	59.364	20
TGGATGTCTTTGATTTGCGA	60.197	20	ATCACTCTCACCCATTTCCG	59.927	20
CTATAGCCCCCGATTCACAA	59.916	20	GGACTCCCTTCCTCAACTCC	60.05	20
ATTGGGAGAAAAGAGGGGAA	59.875	20	TCACCACTCACTTCCTCCGT	60.713	20
GAGGGTTGATGGGTGATTAAA	58.751	21	AGGGCATCACTAGAAAGCCA	59.836	20
TCCATTCCGAAAATCAAAGG	59.872	20	TCATTTTCCGCACCCATATT	60.153	20
AATGAAACATCAACAATCCAAA	57.018	22	CAAATTGATTATGAAGAAATT	58.222	25
TTAATTTCAGTCCGGGAACG	59.931	20	GACATGGCTTTGCCCATTAT	59.791	20
AAAATCAAAGGCCCACAATG	59.801	20	GCTAGGGTTTTTCTGGGGAG	60.068	20
TGTGTATGTGTGAGTGTTCGTGA	60.127	23	CACACACTCTATAAAATGCAC	57.108	24
GGAAATCCATGATCCGAAAA	59.699	20	ATTTGTGGGTGGTTCGTGAT	60.096	20
GCCGATCATTGATAGAGCGT	60.207	20	GAACGAGGAGAAGGACATGC	59.81	20
AACACAGAGACAAGCACCCC	60.159	20	GTCCACTTTGTTTCTGCTGC	58.498	20
TGTGAGTGACTGCGTGTGAG	59.624	20	ACCTCTCATCACCGTTCCAG	60.112	20
CACGGTCGAGAAAGAGTCGT	60.444	20	TGCATATCTTGGTGAGTGTATG	59.897	23
GGTCCTTGAACAGGACAGGA	60.088	20	TGGGGTTCTGCCTATCAGAC	60.073	20
CCCATCCTCATTTTTCTTTCA	59.006	21	CACATTCATCGAATCACATGC	59.947	21
TAAGGTGGCTGGGGTGATTA	60.323	20	GACGGTCAGCCACTCAATCT	60.269	20

CGCCATCTTGTTGGAATTTT	59.938	20	TTGGGAGAATTTTCAACTCTTG	58.352	22
TCCCATGTTGTAATTAATGTAGGG	59.089	24	CACAAAGGCAGCACTTGTTC	59.49	20
CCTTAAATCAATCCCAGCCA	59.894	20	ACATGCTTTTGCATACCACG	59.614	20
CTCCCACGCACACATACATC	59.992	20	TTTCCTTTCCCTCCAAAACA	59.518	20
TGGTTACTGTTCCTCAGCCC	60.111	20	TCTCTCTTGGTTGGTGAAGAAA	58.955	22
TTCTCAGTTCTCCCCTCAAA	57.424	20	CAACGGTCATGATTTCACCA	60.367	20
CTTCACGTGGACTGCTTTCA	60.025	20	ACACGAGTGTGGAAAGGGAG	60.151	20
TGCGAAGTACCCTTCAGAGG	60.388	20	TTCGAATTATCTTCAGGCCG	60.167	20
TAGAACCGGCATACTCAGGG	60.088	20	TTCCGGTCCAAACCAAATTA	60.16	20
GTCCACGGTGGTTTGAGAGT	60.009	20	TCCTTCGACACTCTTTTGGG	60.224	20
CCAAGTTTGGGACTTAAGCG	59.741	20	ATCGTCACCATCTCCACTCC	59.928	20
TATATTGTGGGGTGGATGGG	60.266	20	CTGGATTGGCCTTGTCTTGT	60.111	20
CCAGCATTGTTTCCCATTTC	60.309	20	GAGTCGAGGAAGATCGGTCA	60.349	20
AATATCCGATCCCTTGGAGC	60.252	20	AATTGGCAAATATGCGAGGA	60.424	20
GCAAAATAACCACATTTGAAGG	58.543	22	ATCGGTTATCACCGGATCG	60.697	19
CCAATCTAGGGTTCATCACCA	59.799	21	TCGAGTGAGACCGAAGTGAC	58.968	20
TCGAACGAATATGTTGCATCC	60.852	21	ATTCAAAGGGCATTTTCGTC	59.022	20
CTACGAGCATCATCATGTGTTT	57.783	22	TTTTTATACAAGGGGCGGAA	59.429	20
TTCCACTGCCAATGAAATGA	60.049	20	CTCTGCTGTGAGCATTCGAT	59.143	20
GATTGGATGAGAAGAACCGC	59.635	20	TGTAAGGCCCATAATCGCAT	60.31	20
TTTGTCGGGTCATTACTATTACGA	59.802	24	GTGATAACCTTGAGGAAACTT	59.19	23
GATCATCTCGGGTCCAAGG	60.423	19	GGGTGGGTTTGGAAAAGAGT	60.204	20
CACGGTCCGAGTTCATAGGT	59.989	20	AAATGCCAAATAAAGCTAAAT	57.912	23
ACCATGTTTCCATCGGTTGT	60.096	20	ACTATGCATGGGTTCCGTTC	59.82	20
TCTCTCTCAAACGCATGTGG	59.984	20	TTGTGCAGATTGTCAAACCC	59.547	20
TCTCTCTCTGACGCCATTCA	59.656	20	TTCGCCCCTTCTAGAGTCAA	59.948	20
TGAGTAAAACGTGTTTGTCAGAA	57.555	23	AAAACACGCACACACAAGGA	60.199	20
GGATCGAAAAGAGAGGGAGG	60.147	20	CCATGTTTGTAATTATTGTAGG	57.155	24
TCTGCTACACCCAAAATCCC	59.933	20	ACCTAGAACTGGCCTCACGA	59.867	20
AATGGATGAAAAGCTGCCAC	60.081	20	GGAGAGAGAGGCAGACATCG	60.096	20
AGAAATTTTGTCACACCCCG	59.83	20	GGCCCTATGCATGTGAAGTT	59.962	20
TGCAAATTCTTGACATTGGTG	59.576	21	TCACTCTCGAGCCTAACCGT	60.012	20
TGGAGTCCTAAACTAAACCTCTAA	57.014	25	ATGTTGGAAACCCTTCCCAT	60.422	20
ACATTTTTCCACACTCAGCG	58.775	20	GGATTCCTCCTCCTTCCTTG	60.008	20
ACCCTATTTTGGCGTAGCCT	59.987	20	GCTTCGACCTCCATTGTTGT	60.119	20
TCTTGATAGTACTTTTCATGGAACT	58.093	27	GGAATCGAACCTGGGTCTCT	60.456	20
GCCTCCATTGTTGCTTGAAT	60.081	20	GAATCACACCAACGCCTTTT	59.978	20
TTTGTGTGGTTTTGATTTAGTTATTT	59.682	27	GGTTTTGACATAACTTAGGTGT	59.358	26
AGAGATCGACGCCTTGACAT	59.834	20	AAGAGCTTCTGCGTCTTTCG	59.898	20
CATATCAGCCAAAGGGAGGA	60.029	20	GTGTGCACCACGTCATCTTC	60.171	20
AAATGCAGGGAAGATTGTGG	59.933	20	GTTAAGCCGAATGAAGGTGG	59.569	20
GGAACATGTGTGTGCTCCAG	60.162	20	TTGGCATTTGTGAAGCCATA	60.073	20
CCGAGATGGCTGCATTAAA	59.777	19	GGGTGGAACCCTAGATGACA	59.779	20
CGGATTAGCGTGTCGTGTAA	59.752	20	TTCTCACCAGTCTGTCAACCA	59.294	21
TTGCACAGTACATGCGTTCA	59.902	20	TCTTTGGCATTTTCCTGGTC	60.051	20
ATTCTGAGCTGGCGTGAAAG	60.538	20	ATGAGGGCTGCAAATTGAAA	60.585	20
TATCAATGGTGATGATGGCG	60.307	20	ATCCCCTCAACAACTTCAGC	59.141	20
TGAAAAACAGAAACCGAGATCA	59.724	22	TTGGCTACAATACAACGCCA	60.133	20
GGGATGCCATTCGTAAGTCC	61.606	20	AAAAATCGTCCCAAATCCCT	59.644	20
CGCTAAATTTGATCGTCTTCC	58.844	21	AGATCCGCACTCATCTTGCT	59.981	20
CACGTTGGACTTTGGATTGA	59.541	20	GGGTTTTGCTGTCTTTTCCA	60.088	20
AAGGCAGATGGACGGTAGAA	59.694	20	GGGGTTAAGATTTGGGGAAC	59.51	20
CTTCTTTGAATAGCGTGCCC	59.845	20	ATAGGCTTGGGAAAGCAGGT	60.096	20
CTCCCCCTCTTCGAACTTCT	59.811	20	CGATAAATGGTTGACGGCTT	59.96	20
CGATGATATTTCTGGGGTGC	60.296	20	CATTGATCGTACACGATGGC	59.955	20
CTCTTGTTGCCCTCCAACTC	59.844	20	CCTCTGCAGCTTCCAAAGAC	60.134	20
CTGATCTTGCCAAGTTTCCA	58.847	20	CGCATCATGTTGTTGGAAGT	59.572	20
ACGGTTGTGATCATTCGTCA	59.967	20	CCTTGCTTAGTTGCTTTGGG	59.876	20

GCACTCGCCACAATGTCAG	61.494	19	GTCACTTGCGGGTATTGGAC	60.384	20
GCCCTTCTTCAAAAAGTCCG	61.088	20	GCATAGTTCATTCAAAAATGTC	58.689	23
TTTGAGATTAGGCTATAAGGAATT	57.089	27	TTTAAACTGACGGCCGAGAT	59.708	20
AGTTTTCTCCCCTTCGTTGC	60.61	20	TTCCTCTCCAGCCAAAAAGA	59.926	20
TGGGTGGTCGTATCCACTTT	60.232	20	CCCAAAAATTGAACATATCGA	58.848	22
TGAGACACCCCCATCTCTTC	60.048	20	TTTGGTATTGGAGGAATCGC	59.901	20
CACGAGATTTACGTGGTTCG	59.195	20	GCCTTCTAGCATCTCTTGCTC	58.451	21
ATCGATGTCGGTAAAGGCAG	60.096	20	GATGATGATTGCCCCATTTT	59.587	20
TCTGTACGTGTGTGAATGGCT	59.228	21	GCATAATCACACGGAGGCTT	60.103	20
ATTTGGTGGGGTTACATTGG	59.406	20	GGTTAAAGATCAAACCAAACA	59.801	23
TATTACAGAATGCACCGCCA	60.096	20	AAAAATCCGCACACATGGAT	60.199	20
GATTGAAGGGGTGCTTGAAA	60.051	20	TTTGGATCCGAACATCCATT	60.133	20
AAACACGCAACACAAAGCAG	59.951	20	TAATTCATTCACGCGCAATC	59.668	20
CCATCCCACCAGCATTTAGT	59.813	20	ACGTTGATAAGCCATCCCAG	59.955	20
CTTCGAGCCTCTGCTATTGG	60.11	20	AACCTCATTGCTCTCCGCTA	59.978	20
CCCAGCCAATGGAGATTACA	60.853	20	ACGCCTTTATGTGACGTGGT	60.44	20
CTTCCTCATCATGCATCCCT	60.034	20	TAAGACTGGTGGGAGTTGGG	59.959	20
TGAACATGCTCCTATTTTAATACA	59.731	26	GGTGTTACAATTTCACCGGC	60.235	20
AAAATGCCCTTGTATGCTGC	60.103	20	TGCTATGTACCGTCCAACCTC	60.008	21
AATTTGGCAGAGGATGGAGA	59.629	20	TCCCAAAAGCAATAATGCAA	59.146	20
CCAACGCTACTTGGCCTTAC	59.769	20	TGTTGGACTTTTGGCCTTTG	61.029	20
TGCATTCTTGAAAGCTGGTG	59.988	20	CACGTCTCACACCCTTGGAT	60.987	20
TTAGGGGTGAGAATAGGCCA	59.523	20	TCGTGTTCTATATTCCCGTATC	60.226	23
GTCACTCACCAGTCCCCACT	60.006	20	TTGACCACAGCAGTACGACC	59.751	20
TGACATCTTTTGATTTGTTTTGC	59.156	23	TTGAACCTGGGACCTTTCAG	60.081	20
ATAGTGGTATGGTGTGGGGG	59.405	20	GGTCCAATATGAAGCCCAAA	59.762	20
CAGGGCAATACGTTTTTCGT	59.996	20	GGCGAGCCATATGTCATTTT	59.929	20
GCATGCTTCTGACCAATTCA	59.805	20	GGATCTTGGTTTGGTGTTTGA	59.822	21
ATTACAAATGGCCAAGAGGG	58.903	20	AATCTCCTCCTGCATAGCGA	59.939	20
AATAATCCACGCCAAACTGC	59.967	20	TATCCCCAACTGTTTCAGCC	59.933	20
GAGAAAGCATGTTCTGCACG	59.596	20	CATCGACGCCATATCTTTGA	59.646	20
CTAGTTGGGCTTAGTGGGGG	60.855	20	TGGAGAGGGTTGTTGGTGAT	60.363	20
CGTGTATGCCATCTGCAATC	60.104	20	GGGTATTTATGATATTTCCAAC	57.935	26
AGGGCTGAGAGCCTGAAACT	60.532	20	AATAAGCGGGTTAGGGTTGG	60.197	20
TGAGAATGGCCGAGAGTTTG	61.316	20	GGGCGAGTTAAGCTCGAATA	59.456	20
TATCCTCTCAACGCTTGGCT	59.978	20	GAACTCAAACTGGTTGGGGA	59.943	20
TCTTTGTCCGTTTTTCGTGA	59.293	20	GTTTATCCATGGCGCATTTT	59.801	20
TGAGGGGTGCCAAGACTTTA	60.626	20	CTTGATTTTCCTTCCTCCCC	59.875	20
AGTGCCGTAATAAATTGGATCA	58.521	22	CGGTCCAGTCTAAACCCAAA	59.964	20
CGTTAATGCACACAGCTTCAA	59.926	21	AATGGCGAAGAAAGCTACCA	59.845	20
GCAGCAATGGTGAGTGAAAG	59.445	20	TGTTTTCTAAAAATAGGACACA	59.056	25
CCAAAAACACACATTGGACA	57.837	20	GCCTATCAGGTCGTTGTGGT	59.997	20
GTCAACTTTGGCAACGGAAT	59.978	20	AATGCGCCTCCTTCACTTTA	59.845	20
TCCCATAGCATCTTTTGCTCT	58.941	21	GTGGATTGTTCTGCCCTTGT	59.973	20
TTTTGGGCAAAAATACCCCT	60.519	20	TTCCACTTGCAGCATTTAACA	59.359	21
ACCGCCATATTTGGTTGACT	59.316	20	TGGACAAAAGTACCAGGGCT	59.592	20
GGTGTGACTGAAGTGATTTGC	58.201	21	ATTTCGGTGAATGCAAGACC	59.939	20
TGGTACAAAATTTAGGGTTATTAC	58.558	27	CAATATCAGCTCGGACCACC	60.483	20
TGTCTGCAAACATGATGACG	59.248	20	TCATATGTCACGTTAAGACATG	59.406	24
CGCATACCACATATCATCGC	59.944	20	GGTGTTTGGGAAGGAAGTGA	59.943	20
TGGCTCCAACTTGTGTTTTG	59.734	20	CCATGTGTATGCTGCTGGTC	60.144	20
TACCAACCCAACCCACTCAT	60.088	20	TGTGAAGAACTCCCTTGGGT	59.549	20
CGATTCGAAGAAATGCATCA	59.769	20	AAATCCTAACAGTGGGGCCT	59.827	20
CAAATTCCGAAATTCTCCCA	59.872	20	GGGGGAAGGAGAAGTAGTGG	59.928	20
TCATTCTCAAGCCACTCCCT	59.803	20	CCGAGGTGGAGTAGTATCCG	59.569	20
GTGGGTGAGAAAGAGAGATAGA	58.175	24	GGAATACGATTCGGAGCATC	59.491	20
GCAAAAGTAATAAAGAGCGACA	59.861	24	CATCCCCAAACTCTCGTCTG	60.646	20
GGAAATTTTCTTTCTTCCTCACG	60.441	23	ACGTTTCTTTAACCGCCTCA	59.747	20

CTCCATTACTCACCCCCACA	60.769	20	CTCTGTCACCCCAGAAAACC	59.549	20
GCTCAGGACCGATGAATGAT	60.042	20	AAGGTGTCGAATGCTGAGAGA	60.005	21
TGTAGCCGGAATATGAGCCT	59.691	20	CTTAAAATGTCGCCGGAAAA	60.068	20
TGGACTGTGGGAATACTGGAC	59.835	21	CATGTGTCTTATGTTCGCAGG	59.209	21
TTCGATGATAACTATGGGTTTTGT	58.863	24	GCTACCCTTTTTGACCTACGG	60.008	21
TCGAAATTTGGCAAACAATCT	59.578	21	TGTTGTTCGGGTTGATTTGA	59.941	20
CCAACTTCTGCCTATCCGTT	59.195	20	GAGTTTGGGAGTTGAGCTGG	59.844	20
CCGGGCCATTTGTTTATTTA	59.669	20	AATTGCGGAGTTGCTGTTTC	60.257	20
CATTGTTTGTGTGTCGGAGG	60.001	20	GGGTCTCGCATAAAATGGAA	59.901	20
TCGGTTATTACCGGATCGC	60.812	19	CAAAGGCCCACAATGGTTAT	59.685	20
TGAATTAATGATGTCAGATATTGT	57.283	26	TTCCCCAGTGTCACACAGAC	59.55	20
AATTTTCTACAAAACAAGACCAAT	57.083	25	TATCAGTGACCACCCAACCA	59.806	20
TTGCTCTAAGCTTCATCCGC	60.626	20	CAAAATAGGGGGAAAAACGA	58.917	20
CCTCCGATTTCGTCTTCAAA	60.184	20	CTCTCATCTCTCTCACCTCACCT	59.115	23
TTCAAATCCGAAAATCGGTC	59.878	20	TCTTATGCCAACAAGACGAAAA	59.758	22
TGCTCTTATGCTTTGTTAAATTAGC	60.001	27	TATATGCTCGCGTTTCATGC	59.832	20
CAAGCTATTTCGAGGCAACAG	60.025	21	AGCAATGTTGTTGGGTGGTT	60.277	20
TGAAAGTAGCCGAGAGTTTACAA	58.273	23	ATCAATGCTTACCCGCAATC	59.929	20
TCGTTGCATCTGTGAGCTTT	59.596	20	AAATCGTGTTTCGTGCATCA	60.119	20
TCGAGAAATGCCACATGCTA	60.366	20	TTGCCTAACTCCTCCTCCCT	60.204	20
AAAATCACCGCGAAAAATTG	59.943	20	TCTTTGGGCAGAACCATTTC	60.051	20
ACCATATTTAAGGGTTATCACCTG	57.552	24	GAGAAAGGTTTCTTCGCACG	59.993	20
GAGGATTAATAGGCTGCCCC	59.894	20	GGTCTTTTGTGTTAACATCATGC	58.553	23
TGCCAAGTCTAAAGCCACTG	59.072	20	AGCTGTCCCTTTTCCCTGTT	60.11	20
CTTGTTCCCTCATTTGCTCA	58.847	20	GACGGAGGTGATTCTTTGGA	60.05	20
ACAATATTTAACGCAGCTAAACG	57.734	23	CACGTGACAGTCATACAAATAA	58.634	24
AGGCCTACCGATCCAAACTT	59.962	20	GGATGATGTGTAACCCCTCG	60.195	20
TCCCACTCGCCTGATACCTA	60.615	20	CCCGAGCTAGAGGAAGAGGA	60.988	20
GGATGGAAATGATGTTGGTAGAA	60.068	23	CCTTCCTTTTGCTTGTTGGA	60.22	20
AACCCTAAATTTTGTATCCGAATG	59.56	24	TCACCATAGGATTCTCTCAATC	59.615	24
TTTAGAAGTAAGTGGTGTTCGGTT	59.561	25	GGGTTCCCACGTCATAAAAA	59.662	20
ACATGCAGGAATTTTCACCA	58.976	20	TCTGCATTCTTGCATATCGG	59.792	20
GCATCTCTTGCTCTCTCATTG	57.78	21	TCAGCCTTATCTCTTGCCGT	59.978	20
ATTTCCTTTCAATGGGGGAC	59.996	20	GCAAAATGGCTGTGGAGAAT	60.081	20
GGCGGGGGAGATATAGAGAG	60.017	20	TACGGTTCCAAATTGCTCCT	59.569	20
GCATGCTCTATCTGTTACAGGGT	59.693	23	AAGCCTCCAGATTTAAGCCC	59.688	20
ATTGCCCAAGATCTACGGTT	58.53	20	ACGCCAGCCTCACTCAAA	60.557	18
CTGCAGATGTCCTCCTTTCC	59.803	20	TGTTCTTGTGTGTGTGCGTG	60.412	20
TGCCATCTCGAAAAACAATG	59.664	20	ATCGCCAAATTTACGTCACC	59.829	20
TGGAATCCGAGAAATTCAGG	60.006	20	TTTACGATATGTACCGTTCCCA	59.253	22
GACTTAAATTGCTGCAGACGC	60.039	21	AAAACCCGGAATGGGTAAAA	60.393	20
TGCACTAACCACCCTTGATTT	59.485	21	CGACCTCGTGCTAATGATGA	59.823	20
ATTAGGGTTGAGGTTGACCG	58.909	20	AAAAATGGATCGGATACGGA	59.23	20
GCATCCCAAGCCATACAAAC	60.339	20	GAGATCGGAGTGACTCTGGC	59.952	20
GAATGCTGGGCTGATAAGGA	60.177	20	GCAGTTGCGATCAGCAGTAA	60.165	20
CTCTCTGGTTGGCTGCTTTC	60.134	20	GCACAATTAAATGCGCGATA	59.705	20
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ACTTTGGCAACGGAATACCA	60.365	20	ATCAGAGCCGAGGTTGAGAA	59.95	20
ACAACCATCCAACCACAACA	59.701	20	CTACAAAATGCGCGAGATCA	59.976	20
AAACATGCTTGCTCTTGTCG	59.076	20	GGGGAACTTTAATTTTGTGCC	59.708	21
GCAACCTCAATGCTTCTCAA	59.002	20	CCGTTGAGCCGAATGTTTTA	60.989	20
TGAATCCGTATCCTTATTGTTGC	60.214	23	CTGCGACGAGGGTCTACCTA	60.41	20
TCAACATTTTGTGCATTGGA	58.519	20	ACGAAATTGCCCTTGTATGC	59.967	20
TGATTGGTCAGTTTGTCCGA	60.088	20	CTCCCCTTGCTGAAAAAGAA	59.424	20
GAATTTCCCCCAGCTCTCTC	60.154	20	TTTCGTGTGTGTTCCTCTCG	59.873	20
TATGGAGTGGAGCAAAACGG	61.021	20	AAGAATTCTGCCTCCTGCAA	59.955	20
TTTAAACCCTAAAACGCGCA	60.593	20	TGCTATCGATGTGTTGGCAT	60.104	20
TCACCTAATTGCATCCCCAT	60.155	20	CCACGTTCCGGTCTGTATTT	59.853	20

GAGACAGAGAGAGGCGATGC	60.255	20	TCTCAACCATCACGAAATGC	59.654	20
GACAAAACTAATTGGGGAGCA	59.077	21	TGAAATTTGGAAATAAGGAGG	59.382	23
CCGGCGTCTTTGTATTGAGT	60.132	20	TCTTTCAGCACAAATGCGAG	60.134	20
CATTCATCATCATCAATATCACAG	59.64	26	TCTGAAGGCCGATATTTGCT	59.807	20
CAATCTGACGGCCGATATTT	59.923	20	CATGTGGACCATCGATCTTG	59.918	20
TGCGCTGAAAATGTATCCTG	59.833	20	GTCAGACCAGCTCCCCTTC	59.783	19
GTGTGCATGCATGGTTTAGG	59.995	20	TGAAGCTTGGAAAGTGATGAA	58.488	21
TTAGCCCTTAATGGCCTGCT	61.066	20	TGGATTTCATCATCAAGTCTCC	59.954	23
CTGGTGACTTTGAGGAGGGA	60.229	20	ACGGCAGCTTCTCTCATGTT	60.02	20
AGTGAGGCCCCTTTTACGTT	59.998	20	CGGATGGCTAACCTTTTCTG	59.702	20
AATTGAAATAAAGGCGCCAG	59.212	20	TGTGAATGTGGTTTATTTGGC	58.4	21
AATCGTGGTTCAAAAATCGG	59.801	20	AAAATCTCAAACCGTGAGATG	58.695	22
TTCGGTTGCAATTTTAGTTGTTT	59.931	23	TTTCCGTTTGAACTTTTCATTTT	59.098	23
CAGGGGCATATGTGTCAAAA	59.395	20	ACGGATTTAAAGGTTATTACCT	58.84	26
TGGGAATTTGCCCAAATAAG	59.767	20	GCCTTTGCCCCTTTCTCTAT	59.688	20
AAACCGGACCGAACTGAAC	59.958	19	TTTCCGAATATGAAAACCGC	59.907	20
GGTCCATTGGTCTTTTGTATTG	58.353	22	TGGATATGGTTTTTGCAGGG	60.692	20
ATTACCTACCTGCTCGCACC	59.222	20	TCGTCCAACCAAATTGTTGAT	60.22	21
CTTCATGGGGCAATGGGATA	62.865	20	TGACAATGTTATCGATGGCG	60.488	20
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AAATAGGTCCATCCCTGCCT	59.789	20	TGTCGAGACAATCGTGGAGA	60.402	20
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TAAATAAGGCGGTGGGTGAA	60.315	20	AATTAAGATTTCGGGAAATTAG	57.21	25
AAAAGTAATGCATATGTTTTCCTA	57.308	27	CCAGTGCACATCAAAATTCC	58.976	20
CATGCACCTGAACATGCC	59.61	18	TGGAGGTACTTGTGGAATTCTT	60.391	23
ATGGTTGAATTTCGTACCCG	59.685	20	CGAACAAGGGAAAACAATGG	60.336	20
ACTAAACCAAACCCACCCCT	59.593	20	CAATCAACATGCAAGCATCA	59.232	20
ACACCCCCTTAGATTTTGGG	60.046	20	AAACAGCCGTTATCAGCCAC	60.14	20
TCGTTCCCTTCGTCTTGACT	59.844	20	CCTTGGCTATAAAAAGGGGC	59.93	20
ATAAATGTTCAAACCGGCCA	60.188	20	GCGGGTAAATATCAGTTTTTGA	59.101	23
TTAAACCATGCACGTAGGCA	60.133	20	TTTGTGATGCTCCATGCTTC	59.805	20
CAAAGAAGAGTGGGCTTTGG	59.846	20	CCATTCAAGGGTTAGGGCTT	60.312	20
GTCAATCCAACGTCCCAAAT	59.653	20	TTGAATGGCAAGGATTGGTT	60.309	20
CCTCTCGCATTTCTCTTGCT	59.717	20	AGATGCGCCATTTTAGTGGT	59.597	20
AATCACATCAACACCTCAGCC	59.989	21	TGGGTTCAAAGGGAATTCTG	59.903	20
CTCCCCTACTACACTCGCCA	60.269	20	AACCTCAGTGTTGCAGCAGA	59.622	20
AAAGCAAATCCTCCCCAAAT	59.777	20	CATGGTGGTGGAGAGGAGAT	59.92	20
TCATCGCCCTTGATCTCTCT	59.91	20	GTACGGTTGCTCATCAGCCT	60.285	20
TGGATTTCATCGTTCGTCAA	60.049	20	TTTCCCACCGAAAGCTACAG	60.241	20
AACCACATTAGGCCATGCAC	60.786	20	ACTCTGAGCTTGGGAAACCA	59.844	20
ACGTCGCTTTTAGGGTTGG	60.118	19	CCCAAGACCCCAATTTGATT	60.91	20
TATGCATTTGCACCTGAGGA	60.22	20	GGAGTGTAATCAAATGAGAGC	58.391	23
AGGGGTGTAGGCAAAAGACC	60.361	20	TGTGCTTTGTGTTGGTGGAT	60.008	20
TAGGGCAATTGGTAGGTTCG	59.953	20	TGTTTCATGTTTCATGTGTCCA	59.864	22
TTCCAGAGTCAATCCAGGCT	59.803	20	ATGAAACTGCGTTCCCACTC	60.119	20
GCTTCCAAAAGAAAGAGCCC	60.32	20	TCACAGGAGGGTTCACACAA	60.129	20
TGTTTCCCGTTTTATCAGCA	59.157	20	GCATAGGTTGTTTCATCATCTT	58.642	23
TCATTTATGAAGCAAGGGGG	59.894	20	GGAACCCGAGCTGGACTAAC	61.019	20
ATGCAAATTGATGAGGCCAT	60.304	20	AGTGGGGAGCCTTACCTTGT	59.994	20
CAACCCTACCTCCTTCTCCC	59.928	20	TGGGAATTTGCCCAAATAAG	59.767	20
CTGCAACACCATTGCAGAGT	59.905	20	AGGCCTAAAATGCAAGCTCA	59.982	20
TATAGGGCGGTGGTAGTTGC	59.982	20	CTACCTATGGCCTGCTTCCA	60.227	20
TGGTGAAGATGTGGGTTGAG	59.52	20	CATTCCAATTTCTTGCCTCC	59.505	20
AGCACGTAACATACATTGCCC	59.903	21	ACCTGGACTCATGTGGCTTC	60.12	20
GGCTCACTGCTTCTTTCTCG	60.277	20	TGTCTCCCACATTCATGGTTT	60.225	21
CAATTGGTAGCAAACCATGAA	58.544	21	TCGAAAGCCTACCTTGCTTC	59.592	20
CCCCATTTCGTCAGTTTCAT	59.79	20	TCTTACCGGAGCTTGGTTGT	59.734	20
CCCAAAAATGGGTTATTATTTGA	59.047	23	GGAAAATGTGGATGAAATTTG	60.4	22

CACCGTTGTCTTTAAGCCGT	60.168	20	CCAAAATCTATAGTTATCACAG	58.976	27
GCTGATCTCCATCTCCAAGC	59.917	20	AGGAGGAGCAGCAAGAACAA	60.134	20
TTGGGAAAAATAAAGAGGAAACC	59.731	23	GAACATCAGCGGGCATATCT	60.066	20
AAATCCCACCTACCCAAACC	59.919	20	GGAAAAGGGTGATGGATTGA	59.727	20
CAATCCCCACTGCATCTTAG	58.173	20	TTGTGTGTGTCCAGTAGGGC	59.597	20
TGCTTCCAATTCCTTCTTCC	59.244	20	TTAAACCCTAAAAACGCGCA	60.593	20
TCCTAATTTGGAAAGTACTGGGTT	59.36	24	TGCAGTGGATTTTTGGTGAT	58.976	20
AAATCCGGGTTGATTTGATG	59.622	20	CGGCCGTGTAGTTAACCATT	59.883	20
GTTGGCTGGATCTCCTGAAA	60.195	20	ACCCAGTAATCTCAGCCGTC	59.166	20
TCATTCCGAAAATCAAAGGC	60.016	20	ACGCGTTTTGGCATAAGAAT	59.614	20
GGGATGGGAAGAGCATTTAAG	59.917	21	TGACGTGGCATTTTCAGAGA	60.39	20
TCAATTGCACGTTTCAAAGC	59.856	20	TTCGTTTGGCATGTTTGTGT	60.011	20
CTCAGAATCCCATTAGAAGGGT	58.6	22	CATTGTACTACATGGATGAATG	60.03	26
TTGAAGGGATAAGAATTTCAAAA	57.986	24	TTGACGTTTCACCTAACCCA	59.021	20
ACCTGATTCCAGTTGGATGG	59.779	20	AGCAAGACCTCCACACACAA	59.31	20
CGAATAGGGATGGAATGAGC	59.486	20	CAAAAGGCCCTCAATGGTTA	59.931	20
AAATCCTATCCGGTCAACCC	60.017	20	CGTGGCTGGAAAAGTTTAGG	59.741	20
AGGGTGAAAGGAGAGGGAGA	60.186	20	TATTTCGAGAAATGGCACCC	59.901	20
TCGGGCTCGAATTTATCAAC	60.038	20	TGCGTTTTGACAATATATAGGT	60.083	26
GTCGCTCCCCATGTTGTAAT	59.82	20	CACCCTCTCCGAACAACATT	59.966	20
ATCTCGGCTACGAAGTGCAT	59.866	20	CGGAGTAGATCTCAACACGCT	59.511	21
GCTTGGTGAAGGAAGTGAGG	59.844	20	TATTCTAAACGCCGGTGAGG	60.089	20
GTCCTCCGAACTCATGGTGT	59.969	20	TTAAACTTCAGCCCGTACCC	59.087	20
TTACCCGGACAATAAATCCG	59.655	20	AATCGAAACACATCCCCAAA	60.17	20
GCTTCTTCAGCACGGAACTC	60.142	20	TCAACCTCGCAGATTGATTC	58.799	20
TCCCATTCAACCATTTTCAA	58.792	20	ACAAAAACCAATGGTGGAGC	59.836	20
CAACGCACGGGTAAAAGACT	60.168	20	CAAATGCTCGAGGGCTAAAA	60.335	20
AGAGCATTTTCATGCCATTTTT	59.976	22	TTGATCGATTGTTTTCTTGGC	60.067	21
GCACACAAGTTATTGGTTTCTATT	60.209	26	CAATAAGTGAGTGACTTCCCC	59.864	22
TACTGCCTTGTGTTGCGTGT	60.37	20	TGAAGTGTTATGCGTTTTGACA	59.274	22
AAATTGTGGAGTTGCCGTTT	59.476	20	TGAGTTATGAAGTGTTATGAAG	59.11	25
CCAATTTGATGAGGGTCCAC	60.173	20	AGTCGCTGCAATTTCCAGTT	59.882	20
TGGATTATCCTGCGGTCAGT	60.483	20	CACTCTCCTGCTCCAGCTCT	59.883	20
TGTGTCGGGGGTACAAAAGT	60.269	20	CGGTTAGTCCAGCCATCTCT	59.308	20
AAATTATATTCTCGCTTCTTCGC	58.222	23	ACCAATGGTGGTATGGTGTG	58.984	20
TCGAAAGCCTACCTTGCTTC	59.592	20	ATTTCATTTCATGGGTTTCG	57.399	20
TCAACACTTGGAGACAACGC	59.88	20	TGCGCTAACAAGGTCCCTAT	59.73	20
CGCGTTTTTGGGGTTAAATA	59.835	20	AATCATCAAACCCCGCATTA	60.153	20
TCATCAATTAGCAACTTCCCA	58.227	21	TTGTGTTGGCTTTGCATTGT	60.157	20
CGAAATTGAATGGCAAGGAT	59.901	20	ATGAAACGCCACTTCAAACC	59.978	20
ATCGAGGCGTGACATCTACC	60.104	20	GGGTTATTATTTGATCATCCTC	57.809	23
CGGAAGAATAAGAAACGGCA	60.202	20	ACGGATTTAAGGGTTATTACGT	58.461	23
TTCAAAAGTGCAACAAATCTGC	60.285	22	TGAAATTAGATTCGAAATTGCA	57.856	23
ACCTGAGTGGGTGTAGGTGC	60.033	20	ACCCAACACAAACCCAAAAG	59.728	20
TGAGCTCGGACCTCCAGTAT	59.827	20	TCAGACCTACGTCGCATTTG	59.864	20
TGCAACGAACAAATCTCATTG	59.72	21	ATTTCTGCTGCGTACTTGCC	60.416	20
CGTCAATCAATGATGCGATTA	59.534	21	CCCCTTGGTGATGAGAATGT	59.779	20
CGTTCCCTCCAATTTTCAGA	60.044	20	ACGGGAGAGGCATACAAATG	59.955	20
TCCAACACCCACCACATTTA	59.667	20	CGATCACACTCCAAATGCAC	60.12	20
GCACTCGGAACAACGAAAAT	60.118	20	TCGAGGAGCGTGGTTTTAAG	60.378	20
TGGCCATGATTCATTTTCTG	59.474	20	TGGAACCATGGGTAAAACAA	58.719	20
TTTTCCATTTCAGACCCAAAA	59.415	21	CCACACGACATACGATACACG	59.92	21
CGAAAATTGAAAATTTATTCCCC	59.921	23	TTAATGCAAACGGGATGTCA	59.93	20
TGGACCTCATATGTCATAACCA	57.821	22	TGTTACTTTTCATCGCACTCAA	58.489	22
ACTTGCGGGGTTGTTAAAGA	59.609	20	TGCGTGATTTACACCCGATA	59.953	20
AAAGTCTCTCACCCTTCGCA	59.989	20	GGTTTTCTCCGGTGATCGTA	59.933	20
TCGATGTTGTAATTCATCCGAG	59.96	22	GGAATGGGGATTTTTCAACC	60.358	20
CTATGCCCATGGAGGTATGG	60.17	20	ACTTGTCCACCCACATGACA	59.846	20

CAAACGCTTTATTGAACTTCTGG	60.166	23	CCCATAAACAATCCCCTCAA	59.617	20
CCCATGTGTCCACAAAACAA	60.255	20	ACCCAAGATTTTTGCCACAG	59.971	20
CTTGCTTTCCAATGTTCCGT	60.11	20	TCACTCGCGCTAGATTCTCA	59.847	20
ATTTACTAATTTATCCACCTCGATT	57.088	26	TTGATTCTGGAATATCCCGC	59.862	20
TCTATACGCGGGAACCACAT	60.352	20	TCGTTGTAAACCCGTAAGGC	59.996	20
TCCTTCTCTCCCCCATTTTC	60.38	20	CATCACACAAAACCAGTGGG	59.848	20
ACGTTTATCCATTTGCCGAC	59.829	20	CCCGGTATGCTGACGATAAC	60.352	20
ATAAAGTGCAGCAGACGGGA	60.796	20	CATCACCAAAGACAACCACG	60.001	20
GCTCTTCGAATTCTCCTCCC	60.293	20	TCACAACATGACAGCAACCC	60.58	20
AAAACCGTTCTCACCCCTTC	60.34	20	TCATGCCTTAAAATCCACGG	60.827	20
ATCTCGGCCCTTAGATCTGC	60.702	20	GAGATGGTTGCACCATAACG	59.002	20
TCACTTCAATTTTCGAGCCC	60.192	20	TTTGTGACGAGATCATGGCT	59.245	20
ACATGTTAAATAATCGTCAAGTTG	58.632	27	AAATATTTCTAGCACATGAAAT	57.859	25
TTTACCAAAACTGCCATCCA	59.013	20	GGTTTTGACCATATTTACTGTTT	59.631	26
AGTGATCTGGATGCTCCTGC	60.381	20	TCAACAACCAGTCCACTCCA	60.129	20
TTCGTGTCTATCCTCACCCC	59.927	20	ACTGTGGACTCCGGTTCATC	59.969	20
TGATCGTTCTTCACTCTCTTGC	59.621	22	TGAAAAGCTTTGAGTGTGCCT	60.045	21
CCAGATCGCGACCCTATAGAT	60.445	21	TCGTTATACAAATATCAGGCAA	59.061	25
AAAATCAAAGGCCCACAATG	59.801	20	TTCAGCATATTCTTTGGACGG	60.081	21
CATTAGCAGCTGGGGATTTT	59.182	20	ATCGCTCCACATGACACGTA	60.144	20
TCATAGTTGACGCCCTTCCT	59.694	20	GTTGGTCCATTTGCCATTGT	60.624	20
AAATTTGGGTCAAACCCCTT	59.549	20	TGAAATTGTCATCTCCCCCT	59.336	20
TCGTATGCTGCCCCTAAAAC	60.096	20	TTCTTTTACTTTGCATGCTACTTT	59.476	26
GAGCTGTTACCTCCGTGGAC	59.727	20	TGGAAAGATGGTGGCAAAA	60.034	19
AGACATGGCGATACGACGTT	60.547	20	GGGAGGGAGGAGAGAGAAGA	59.883	20
GTGTCCAACATCCCATTTCC	60.034	20	TCCTTATCGTGAGAGACCCG	60.21	20
GCATCTCTTGCTCTCTCATTG	57.78	21	ACCATCGTTACCGATTTCCA	60.192	20
TGGACGATTTTGCCCTTTTA	60.427	20	AAATTTAACATGGTCCGCCA	60.188	20
TTTGTTGTTTCCCAAGTTGC	58.649	20	AAAAACCCTGATGTGGATGC	59.797	20
TTTGCTTGATCCAATGGTGT	58.976	20	TTCCTTGGACCAAAATAGCC	59.019	20
TGCGTGATGCAGACATATTG	59.259	20	ATAATGCAGCCTCCCATTTG	59.923	20
GGACACCAGGGTGAATGAGT	59.817	20	CCAAGTCTTGCATTTGGTTG	59.17	20
CATAGTGATCGTCGGTGCAT	59.552	20	TCCCCAACTCAAGGACACTC	60.088	20
TTTGACCTTGCATTGCTGTC	59.847	20	GGAATCATGCTACTACACGTCC	59.66	22
GGAAATAAGGAGGTGTTATGAAG	59.323	24	CCCATTAATAGCGATATATGTA	58.562	27
AATTGATGGAAGAAGGCACG	60.074	20	GGACATGGACACCTAACCCA	60.634	20
CTCCATCGTCGAAGTCATCA	59.787	20	GAAGTCGAACCTTACCGCTG	59.875	20
TGCGTGTGTATGCTGAGGTT	60.333	20	GGATGGGTTATCACTTGAATAG	58.769	23
TGGCGCATTTTACTGATATTTG	59.989	22	TGAAGTTAGGAAATAAGGAGG	57.525	24
CGCAACGTTCTGAAACTGAA	60.027	20	TCCCTCCAAGGAATCTGATG	60.003	20
TCTTGCACTCGTCTCTGTCG	60.333	20	AGCGCAACTCCTATACACCG	60.292	20
AACTTCAGTCAACTAAGGCGCT	59.608	22	AGGAGAGAAAACCGAGAAGTA	57.808	23
TCGATAATGCACTTTATCAGAGTT	57.221	24	AGCCCTTGCAAGAATTGAGA	59.955	20
TTGGCATGTAAATCAGCCAC	59.548	20	GCTCCTTGTGCATCACTCAA	59.992	20
GATGATCACGATGAAGCCAA	59.61	20	AGAAGTCTCAAGTCAATGTATC	58.417	26
CATGCACGGAAAACTTGAAA	59.706	20	GAACGGAGAAAATATCACGAA	58.25	22
ACCCAATAACCGATGAGTCG	59.813	20	CGCTCCACAAAGATCTCACA	59.984	20
TTCATTGCGTTTTACAGCCA	60.251	20	TCTCAGCTTCCCCACCATTA	60.594	20
CGAATAGTAGAAGCTGCGGG	59.996	20	CCGTTGTGAGAATGGACGTA	59.566	20
TTGGTGTATACTTTTGTAGTGATCA	58.276	27	GGGTGGTACCTCACCTGTGT	59.732	20
GAAAATTCGGGTCTGGGATT	60.131	20	GCCTTGAGGGGGAGAATTAG	60.032	20
GAGAATAGATAGTTAGAGAGAGA	58.82	27	GTTGGGACTTCAACCCAAAA	59.807	20
CTTCTCACCGTCGACCAAAT	60.111	20	CATTTCACCACCTCCATTCC	60.173	20
TTCTCAGCATATGGGAAGGG	60.029	20	TCATCGGTCCACTAGCACAA	60.263	20
ACTGCCTTTTTCCTGCTGTG	60.431	20	TGTGGAAGGGTGTGTGATGT	59.846	20
TTTTGAGCCTATCTTGGAGCA	59.967	21	TGATCTTCACCTTAAATCTGCAT	57.9	23
TTCTTTGAATCATCTTCCACCTT	59.123	23	AAGTTTGGGGGAGGAGAAAA	59.912	20
CGGCTTCTCCAACCATAGTC	59.694	20	AAGGAGGTGTTATGAAGGGAT	58.028	22

AACAAAAATGGCCAAAATCG	59.81	20	GCCGGAGATTTTTCAAGGTT	60.431	20
CAACTCCACATGTTGCCATC	59.967	20	TTCTCCTCCCCTTAGCTTCC	59.783	20
CTTTTTAGCATGCGAGAGGAA	59.617	21	ACCTCAACAAACCACCCAAA	60.246	20
TCAACAACATGCAAGCATCA	59.833	20	AATCACTAACCCACCCCACC	60.862	20
GGATGAGAGACTCGGGTTCA	60.199	20	AATGGCCATCTCTTTCCCTT	59.903	20
GGGAATGTGCAAATAGCAAAG	59.6	21	TGTTGAGAATTGCCAAACCA	60.088	20
TCAGCCCAGCCCAATATTAC	59.923	20	ACCTATGGTGGTATGGTGTAGA	57.448	23
TCTCTCTCATCCGACCCCTA	59.755	20	GAAAGTGGTGGGGGTTTTTC	60.569	20
TGATCATCGAGGCAGAGAAA	59.476	20	AGGAAACCCATTGTGGTCAG	59.82	20
GGGCAAAACTTGAACAGCTC	59.859	20	TGTCCATGAGAAATGGGGTT	60.173	20
GATCGGAGTTGCCTAAGTGG	59.694	20	TGCACAATACAAGCACCCAT	59.995	20
GCACAACCACTCCACAAAGAT	60.028	21	CCCCAATTGGAGTGTCTGTT	59.82	20
ACCACAAGCAAGCATTTCCT	59.74	20	ATGGTGGTTTGGTGGAAGAA	60.21	20
CCGTTCATTTTCGGTTCAGT	59.971	20	ATTATGGCGCCGCTATTGTA	60.452	20
TCGAAGGTGAACTCGGTCTT	59.844	20	AACCGTCGAATTGTCTGGAG	60.111	20
GATAGGCCCTAACTCGACCC	59.925	20	TCCACGGTGATGCTAGAGTG	59.855	20
AGAGTTCACCAAGGTACTTTAATA	57.201	27	CCGTTTCGAACCTAAAACTGA	59.254	21
TGGGCACATTTGAATCTTGA	60.049	20	TGTTTTCAATCGCAACCATC	59.523	20
GAAAAGAACTTCAAAGGGGTCA	59.61	22	GGGCAGGGCTTTGTTTTAAT	60.312	20
AAATTGAGCTCCATAGCCGA	59.807	20	AGCTTCCATGGAGGTTGATG	60.073	20
CACACACTCACTCACTCCCA	58.154	20	GGAAGCACTTTTTGAACGGT	59.218	20
TTCGGGTATTCACCCTGTTG	60.745	20	TCAGCCGACTTTTTAATGGC	60.209	20
AAGGGTTATCACCTGATTTTCTC	57.73	23	TTTTAAATGGACGGTGATGATT	59.616	23
GCTGAAATCCATGGAGGAGA	60.158	20	GGTGTTTGTTGCTTCGCTTT	60.292	20
TTGACTGATTGGAGCAGTGG	59.831	20	CAAACAGCTGGAAATGGTGA	59.691	20
TCAAATCTTCAACATGCAAGC	58.909	21	AGCCTAAGGAATAAACACCTA	59.735	24
GGACGATGTCATGTGCCTAA	59.527	20	GGGATGAGTTATCACTTGAATA	59.765	25
CACGTGCGTCAACTCCTTTA	59.904	20	CCTATGGTGGTATGGTGTGGA	60.501	21
AAACACGCAACACAAAGCAG	59.951	20	CAAGGCTAAACAAAGCCCAA	60.236	20
CGAAGAGATGGAAGTAGCGG	59.971	20	CCTTATCAGGGGTGCTTCCT	60.455	20
GGGGTTATCACTGGATCGTG	60.195	20	CATGAAAATCATGTTCCGCA	60.466	20
GTTTTGGCTCCAGCGACTAA	60.386	20	CTCCAAAATGGTGCAGTCCT	60.111	20
ACACCAAATCTGTTAGTTTACCAA	58.2	25	ACACGAATCAAATCAATGGC	58.424	20
AGATGCCCATTTTGATCAGG	59.894	20	ACAAACAAGACCAAGTGGGG	59.861	20
ATGATCCCGATTATCGCAAG	59.885	20	GACTTGTGTGGGGAATGGAT	59.636	20
AAGCTGAGTGAGTGTGCGAA	59.776	20	ACCGACGTGGCCTAACATAG	60.015	20
CTTTGTGCTTTGCTGCTGTT	59.269	20	CAAATGTTGCACAATCATTGA	58.945	22
CCCATTCTCTCCATCCCTTT	60.264	20	GTTTGGATATCGAGATCGGG	59.344	20
CACGAGTGAAGAAAGGGAGA	58.001	20	ATCATAGTTGACGCCCTTCG	60.096	20
AATACTTTCCGTCACCGTCG	59.993	20	CCAAAACCATCGCACAATTA	59.42	20
CCCATTCACAAGACCTCCTC	59.505	20	GTTGACTGCTTTGGCTTGGT	60.299	20
GAGGAAGATAAATGTGGGACG	58.516	21	GCTCGAAACACAATCAAAACC	59.606	21
TCATTCCTTCGGCTGACTTT	59.813	20	TGTGGTTCGATATTTTGTTTGG	59.736	22
AAGGGGAAGTTCTGCATGTG	60.111	20	AGTTGGAGCCTGCAATTGAT	59.7	20
CGTCAGAAACCTCTCGCATT	60.397	20	TTCCTAACTTCATAACTCGAAG	59.436	26
GCCAACTTTTCTTGAGGCAC	59.859	20	ATTAACCGTGAAAATGGCGA	60.323	20
GGAGGAAGAACACGAGGGAT	60.456	20	GCAAACCATACACGAACACG	60.035	20
TGTGTTGTCTTTTAGATCAATGTTT	59.53	26	ACTCCGAGGACGATGAACAA	60.656	20
TCAAGGGTAATTTTTCAGGCA	59.573	21	TCGTAAAATAACAAGTGGATG	59.829	25
TAGTTAGCATGGGGGAATGC	59.923	20	GACCGTCTGCGCTGTAGATT	60.428	20
TTTAATTTGGCCGGATTGTC	59.773	20	GCCGGAGATTATCCATCATT	58.812	20
GAAAACTGATATGCGCGTTG	59.329	20	AAGGCCGAGATTTGTTAGAGG	59.733	21
GCCTCCAAGCACAGGTACAG	60.854	20	ATGGCTTGGAAAAGATGGTG	59.933	20
CCACTTAGGAATTTCATCAAATGA	60.339	27	AAATCCTGTCAATGAAAAAGCA	59.997	23
TTCTTGGACACAAGTATGGCTC	59.242	22	TGTGAATCATCAGCTTTGCC	59.805	20
TGATGCTGATGAAGAATCGG	59.756	20	TTGCAATGGACCTAAGCATTC	60.089	21
GAGGGGACAGACAGATGAGC	59.799	20	AGGTTGATCATTTCCATCGC	59.9	20
GTGAACAACAATCCCCACCT	59.679	20	GAGAATCCATGGCGGAAGTA	60.036	20

TCAAATCTTCAACATGCAAGC	58.909	21	CACCCATTCATTCCCTCATT	59.605	20
TGTAATGCTACAGTTCTTAATTTG	57.643	26	ATTGAGCGACGGAGTTTCTG	60.397	20
CCCAACGACCGGTTATATTTT	59.957	21	AGTTGGAGCCCAACAAATGA	60.495	20
AAGCCCGATCTCAAACTCCT	60.212	20	TCTTCCCCAAATTGGTTTCC	61.023	20
GCAAACTGATTGACCCGAAT	59.939	20	CTCTCATTTCCCCAAACGAA	60.044	20
GCTTAAACAAAATGGCATTAAAA	57.584	23	CATGGAATGGCTGTCAGATG	60.072	20
ACGGTTAAGATTCAGCACGC	60.278	20	TGAGGACGAATATGCCCTTG	60.992	20
CACGCACTCACATGTTCACTC	60.374	21	CAACGTTTGTTCGTGTTTGTG	60.096	21
ATTGGGCATTTTGACGGATA	60.153	20	ATGTGGGCTACGAGAAATGG	59.955	20
CAGTTATCACCGGATCACGA	59.522	20	CACGTGGCATGATAATAGCG	60.118	20
TGATCTCAACGGTATGCTCG	59.823	20	CCTCCCGTCTAATCTCCACA	60.065	20
GGGTAGTATGTAGCACCCCG	59.336	20	CGGAAATGACCCCATAATGA	60.523	20
TAGCTATGCTGCAGGTTCCA	59.59	20	GCAGCTACGTTTGTGTGCAT	59.942	20
GTTTTCTCTATTGGGGTGGC	58.504	20	AGATCCATGTTCATCTCCCC	58.741	20
ACAACCTATAAATAAGATCTCAA	57.587	27	GATGATCACGATGAAGCCAA	59.61	20
CCTGCTGGTTCTTGCTTCTC	60.134	20	AAGCCCGATGATGTCTTGTC	60.081	20
CATTTCGCACACAGAGATGC	60.423	20	TGTGTACCCACATCCTCCAA	59.806	20
CAAATTACCCCCGTATGCAG	60.202	20	TTTTTAGTCAATCAACGGTTAC	59.178	25
ACCAATAGGTCATGGGTTCG	59.67	20	CGAAACTCACCCCATTATGC	60.331	20
CAAACCCGAAAAATCGGTTA	59.805	20	CTGGTTTGCGTGGTTCTTTT	60.147	20
TTGTGGTTTTATCACACCCG	59.293	20	CTGTTGGCCGTTGTTTTACA	59.627	20
ACCCTTTTCGGGGCATAAAT	61.703	20	TTGACACGCGAAAAATGATG	60.644	20
TAAACCTTTGTGCGGTTGC	59.72	19	CCCTATTTAGCTTTCTTTGCGA	59.885	22
TCCAAACCCAATCTATTCCG	59.756	20	TATGGAATTCCGACGAGCAT	60.435	20
GATTGCCGCCTCTGATAAAC	59.674	20	TGTGCAACTTGTCTGGTCTCA	60.494	21
TATGATGGAAAAAGGCCGAG	60.031	20	AGTTCTGGCCGTGCATTG	60.84	18
TGTCATGAATGCCAGTGTAAAA	59.087	22	TGGAATCCGAGAAAATCAGG	60.006	20
CGAAGATGGTTTCGTGTAAGC	59.761	21	TCCGTATTTTGGGTAGCAGC	60.096	20
TTATGGGTTTTTGCCGTTTC	59.81	20	ATGTGCGCGTGTACTTATCG	59.782	20
GGGTGTGGAAAAGAACCTGA	59.943	20	TATTGGGGGAAGAAGCACTG	60.066	20
CAATCAGCACGTGTTCTTGC	60.459	20	TTGAATCCATTGGTGAAGCA	60.049	20
CAACATCACCAAAAACCCCT	59.688	20	TGAGAGAAACATTAATTCCTTC	59.9	25
GCACACTCAGATCACACAGGA	59.888	21	GGTGGTGGAAAGACCAGACA	60.966	20
ACCAAGATTTGATCATGGGC	59.756	20	ATCAAAATAGGGCAGGGGTT	59.666	20
ATGGAGGCAAGCTACTCGAT	58.914	20	TTTTGCTGTGGCTTGTGAAC	59.888	20
CGGGAAACATGATCCGAATA	60.66	20	CCGGTCATTTGTCTTTTTGG	60.336	20
ATATTGCAAATGGCCGAGAG	60.06	20	AATACAGCCGCTCTTGGAAC	59.34	20
GCCGAGTGATCCTCTCTCAT	59.364	20	AGACGATTGAAACCCTCCCT	59.935	20
ATCATGGCCACGTAGAGAGG	60.096	20	ATCCGCTTTCCCAAGTTTCT	60.074	20
TTTAATCCCCAAACTGCCCT	60.664	20	ACCATATTTAAGGGTTATCACC	57.552	24
TCCACCTCACTTTTCCCTTG	60.081	20	GAGAGCGGTGACGATTTCTC	59.957	20
ACAGCTCTTCAAACTGGACACA	59.953	22	GCGGATGTAATTTGGGTGAA	60.701	20
AACCGGTTAAAAATCGGACC	60.055	20	AAACCGAGAAAGAAACATTTC	59.926	24
ACAAACACCTGGGACCTCAA	60.399	20	TTGTTAGTGCGTGTTTTGGG	59.627	20
GAAGCCTCAAATCACAACCC	59.532	20	CGAACTTAGAAGGGCCACTG	59.869	20
GCTCAACTGTTCTGAATGCG	59.596	20	TCTCTTTTGGTTGGTGAAGGA	59.697	21
CTGGCAAAGATTCTTGGGAT	59.126	20	TTGTGTGATCAAGGGTCCTG	59.52	20
CATTGCCTAGAAAGTGGGAAA	59.211	21	GCTAATGGTGCCACAGTTGA	59.722	20
TGCCAATTAAGATTGCGATG	59.662	20	ATCAAAGGCCACAAATGGTT	59.292	20
TCATTCACATCGTCTCTGCAA	60.406	21	TCCAACTTCTTGCTGGTTGA	59.415	20
TCGAATGCACTCAAACTCCA	60.39	20	GGTTATCACCGGATCACGA	59.311	19
GTGGCCGCATTGTATGAAA	60.482	19	ACTCCCTTCCCCATCTCAAT	59.755	20
GGAGAACCGTCGACATGATT	59.934	20	ATGGGAAGGGGAGTTAGCAT	59.789	20
CCAAAACCGACACTCCCTTA	59.964	20	AGCTCACTAGGATGGCAAGC	59.603	20
CCATAGAAAATGTTGTTAGCAGG	59.577	24	AAAAATCATGCCACCGTACC	59.691	20
CAGATTTTGAAACCTGTAAGTGA	58.831	25	GTTTTAACGAATAAACATGTTC	58.53	25
TTCAATTCATAAATATGTCGAAGA	60.136	27	TGTTTTCACGAATAAACATGTT	59.448	26
CATCTTTTGCGAATTGTTGC	59.305	20	ATCCATCATCTTCCGTGAGC	60.042	20

GCTGCAAGCATGTATTTGTCA	59.894	21	GGTTTTCAACCCATGTTTTTG	59.211	21
CTTAAGACCCGATGCCTTTG	59.702	20	CAAATTTTCCGCTTTGTCGT	60.11	20
TTATCTCCACGATCCAAGGC	60.036	20	GGTTATTAGTTATTACGGATTTA	57.055	27
TTTCTGACGAAATTGCCCTT	59.685	20	CGGACTTCCTTTCTGCAAAC	59.853	20
TTCTTTGTCCCTCTCCTTGC	59.405	20	CTTCGAACATGCACACTCGT	59.905	20
ATACCGCCATATCGGACAAA	60.175	20	TTGACCGAGTGAAGTAAACCC	59.087	21
CGTCCAACGAATCAAGACAA	59.691	20	GGTTGACATGAGCGCATAAA	59.694	20
GGAGCCTCCGAACTTTGAA	60.324	19	AGCCCTCAACTCTCCCTCTC	59.952	20
TTGTGTACCAAGACATTTGTGTG	58.522	23	ACCGGATCAGCTCTCTTTCTC	59.972	21
CGACTATCTGCAGGAGGCAT	60.384	20	TCGTCTATCACCTTCCGTCTG	60.262	21
ACACCGGATTTACGTGGTTC	59.717	20	TTGATTCCTTTTGTTCCCTATTT	58.142	23
TGGATAAGTCTATCAAGATTTAAT	58.272	27	GGAGCTTCAGTCTTTCATCTCC	59.466	22
TTCCCCATGTCTTGATAGCC	59.894	20	TTTACGGGGGAGAATTGTTG	59.795	20
ACTTTTGTGGAAAAGTGGCG	60.147	20	TTTTCTCAACCGAGCTCACC	60.375	20
TGATCATAACTCTCTCTCGCGTT	60.407	23	TCTACGACCGAAATTCACTCC	59.184	21
TTGTGAGTCGTTTGTTCTTGGT	59.679	22	CGAACAAGGGAAAAACAATG	58.121	20
TGACCACCCAACCACACTAA	59.848	20	CCAAGGGGAGAGAGGTCAAT	60.447	20
TCCCCGGAATAATTGTTATTTCTA	59.945	24	GCCAAATCAACTTTTGACGG	60.481	20
GGTGTCCAAATGTTGGGTCT	59.679	20	AGGATCGGCATATCGAGAAA	59.628	20
TGTTCATTGAGGAAATTATAAAGC	59.13	25	TTTGCAAAACATTCTGACTTTG	58.007	22
TGTTGAGGGTTGTTTATTATGGG	59.991	23	GACTTTGATCAAGTGATAACAT	57.805	25
GTGGGGACATGCTTGAAAAT	59.797	20	TCGGATAATCTGAAAGCGAA	58.455	20
CCCAAACCCACTCAACCTTA	59.824	20	ATCCTCCCCTTCCTTGCTTA	60.032	20
AAAAACCCTTCCACCCATTT	59.549	20	ATGTCAAAAATGCCCCTTCA	60.309	20
GTGTGATGTGTGTGTGTCGTG	59.499	21	CCCTCCTCACCTCCTCTCTT	59.801	20
CTGCAAGCATTGAAGTTGAAA	59.097	21	CCAAAATGGAGAGGAATAATG	57.132	22
TCACCCACCAAAATCAAACA	59.792	20	GACGAAGGAACAGCTTCACC	59.851	20
CGGACGGTCGAATCAATTA	59.484	19	GTGTTTCGGAGTGTTTGGGT	59.867	20
TTCTCGTGTTTATCCTCGCC	60.214	20	ACCACTCCACAAAGATCTCACA	59.622	22
GGGAAACAATGGATACTCCTTC	58.826	22	ATCCCATACATGTCCGTCGT	60.081	20
AAATGCGGTGGAGATGTAGA	58.173	20	TGCAATGCTTCAATTCATCC	59.628	20
TTGCGTACCAAGTTTTTGGC	61.027	20	CATTTGCCATCCAATTTTCC	60.132	20
TTGGTAGCCTGGATAGCACC	60.096	20	GGAGGGGAGTTGTTGGGTAA	61.103	20
GGGAAGAAGTGAAGGAAGGG	60.045	20	TATGTTGGCGAACACAGGTC	59.572	20
ATGCAACTAGGGTTCGCTTG	60.27	20	AAATCCCTTTTCCTCTCCCA	59.875	20
TTGGGAACCGATTCTATCCA	60.266	20	TTGAATGGTTATCACCTGATCG	59.823	22
CGCCCAAAAATCTAACATTCC	60.659	21	GCGGAAATTACTTACAGCCA	57.926	20
TCCATTTCTGAGTTGAGGGG	60.042	20	GAATCCATGCAAACAGCAAA	59.67	20
TTTCCCCTGATCATGAACCT	59.336	20	ATGCGCGTTTTTAGGGTTTA	59.624	20
GACAACCTTCGGCTTGAAAA	60.227	20	CATGTTTGGTGACTTGGTCG	60.001	20
CTAGCTTCGGTACAAACCGC	59.904	20	ACATCCAGGAACCACTTTCG	59.966	20
GGATGAGCATCCATGTCAGA	59.591	20	AGCCCCCATTTTTCATTTTC	60.13	20
AACACCAGTGAAGCAAGCAA	59.49	20	TCTGCAGTCTCCGTTTTTCA	59.566	20
TAGCAGGCTGACCGTAGTGC	61.532	20	CTCCGAAAGCACCTAACCTG	59.869	20
CTGAAAACTCGCCGGAACTA	60.378	20	GGACCGGACCGTTAGGTAAT	60.074	20
GGTCCAATATGAAGCCCAAA	59.762	20	CCCACATTGGTTGGAGATTA	58.27	20
CCTCCTTCAGCCAAAAATGA	60.184	20	GAGGTTTTGACGAGATTTAGGT	59.187	23
TTTCTCGGAGGTTTCAGACG	60.366	20	ATGGTGGTATGGTGTGGAGG	60.51	20
CCTTCGTCAACTTTGGCAAT	60.11	20	AACTTGGTGAGCGAGTGGTT	59.769	20
CCCAACCAAGAACATTGAGG	60.345	20	CGAAAATGAGCTTCCACACC	60.636	20
TGGTAGCTTTGAGACACGATT	57.496	21	TTGATTCTTGAGTACACCATCG	57.757	22
TCGTGATTCGCAACTCTGAT	59.399	20	TGAGTTACCCTTGAATCACCC	58.898	21
TCGTGATCGAACCACGTAAA	60.111	20	CCATTTCATCTTCGGCATTT	59.901	20
TTGATGGTGAACAAACGGAA	59.941	20	TTCATGTTTTGGAGCATGATTT	59.456	22
GCGTGGAAGAAAAGATCCCT	60.578	20	TTCGTTCCTCTCTCTCTCGG	59.673	20
CCCATTTCTAACTACCCAAATCC	59.962	23	AGGCTTGAAGAATGATGAAGA	59.739	23
TGAAACATGGATTGCCACAT	59.781	20	ATCATTGTTTCGCAAGCAGA	59.425	20
CGAGTATGCTGACGGGAAAT	60.096	20	TTTCAACCATCTTGTTCTGTGG	60.008	22

TGTTAACCAAAAAGAAGAATCGT	57.104	23	TGAGAGAGATGGGATTTTAGA	58.779	24
ATGCCCTTCTATGCTGAGGA	59.797	20	TCTGTATCGTCCGCGATGTA	60.243	20
CGACCGGGCTGTATTTTAAC	59.474	20	CGGCCGGTTTGTAACCTT	60.883	18
TCCATTTGCAATACTATGGCTTT	59.884	23	TGCACCCTTTGACATCAGTT	59.139	20
AAAATGGGCGAGAGTTTTCA	59.685	20	TTTTTGTTTGTTCCCAGGTTG	59.862	21
GGTGTCCGAACTTTATATGGC	58.456	21	ATCCTAGCTTCCGCATCCTT	60.194	20
AGATGACAACCTTCGGCTTG	60.255	20	GCGGAAGGCATTTAAAACAG	59.72	20
TCTGCCTCGTCTGGCTAGTT	60.156	20	TGGTGTGTACTTTTGTAGCAAT	59.618	24
TAGAAGGAAAAACCACGGGA	59.541	20	CAAAAGAGCTGTGGGAGAGC	60.134	20
TGGTTTTGGGATTTTAACAATTA	57.59	23	GATGATGCATGTATACTATCAA	57.305	26
AAACTCGTAAAGTGTCGCGG	60.305	20	GATTAGGAATGAGGGGAGGG	59.722	20
GGAAAATATCAAGTCAACACAAA	58.257	25	TCACACTCACGCACTCACAA	60.07	20
TGTCATCGTCTCAACCCTTG	59.676	20	TTCGTAGCATGATTTAAATGGT	59.021	24
GGGACAATGGAGTTCACGTT	59.827	20	CCCAAGTGCACAAGTGTTTC	59.187	20
TGTTGGCAATTCTAGAGCCC	60.214	20	ATGATTGGGACACGTGTTTG	59.267	20
CCGACATTTTGGAGTATGCC	60.331	20	GTGCAGTAGGGGTTGTCGTT	60.035	20
TTGTCGCCATATACGATCACT	58.133	21	AAGGAGGTGTTATGAAGGGAT	58.028	22
CTGCTTCAGCTCAGTGTGGA	60.333	20	TTACAAACACCGATTCGCAC	59.59	20
GGTTATCACCGGATCACGAC	60.203	20	ACGAAGGGTATTTTGGGAAA	58.417	20
CCGAAAATTCAATCCTCGAT	58.974	20	CACCACCGTAAACCGTCAC	59.864	19
TCCCAACTAAAATATGCTGCAA	59.624	22	CTGATTCCGTCGACAAGCTC	60.945	20
CCTGACAGTTTGGCATCAGA	59.831	20	TGTATCACACAACGGTTCATC	59.888	22
TTGCAGAAAATGGAGAGGAGA	59.94	21	CACCAACCCAACCCATTAAC	59.948	20
AGTGTCGCGAACGGTATAGG	60.154	20	GGGTGGTTATGGTTTGTAGGT	60.385	22
TAATAGGCTGCCCTCCTCCT	60.187	20	TCCGCCTTGACTCCTTCTAC	59.43	20
GCAATTAGGGCTGAGCAAAA	60.343	20	TCGACCAAAATTTAAAAGTCCT	57.036	22
CAACACAACAATACCACACAGGT	59.733	23	TGTGGATATGTAGATGATTTTT	59.637	25
TGTAGATGGCCTAAGACGGTG	60.139	21	TAAAAATTTGTCCCCTTGCG	59.937	20
AGGCTCCAAATCAAAATCCC	60.265	20	CCATCACACTAACCTCCCTCA	59.974	21
TTTGTTCCTACTCACTCACATTAA	58.436	26	GGGAGAATCCAATGGTGAAA	59.727	20
TTGAATTAACTTCCCAAAACGTG	60.25	23	CAAACCTTGGCACTTGCATA	59.729	20
CAGACATTGAGGTTTGGATGG	60.36	21	ACTGCTTGTGGACAGTGCAT	59.341	20
ATTGAATTCGATCAAGTGCG	58.723	20	GCATGCAAATCTTGAGCTGT	59.031	20
GGAACCTATGTGACATCCAGC	59.425	21	ATTGGAATTGGAACCAGCTTT	59.828	21
ATACCCTACCCGTTTACCCG	59.96	20	TGAGAAGCTCAATGGAGACG	59.112	20
ATGCACATGTTTATCGCACG	60.554	20	TTGGAGTTGGAGCAACGTAA	59.317	20
TCGCTCATCCAAGTAAGTCG	59.024	20	TCCTCTATCCATGAATCTTTCA	59.966	24
GACGCATGCCAGCTAATAGG	60.762	20	TGGTATTGGTCCACCTGTGA	59.806	20
CTCTTTCCTTGCTCCCCTCT	59.95	20	AAAAGTCAGCCGAGAAATTCA	58.962	21
ACGGATATGCCCTTGTATGC	59.813	20	TTGACAATATTTAGTGTTTTGA	58.99	27
ATGTGCGCCTTTTAACCTTG	60.131	20	TTGTCAAAATCTCATTCATTTG	60.01	24
AATACGGTCCGTGCATGTTT	60.257	20	CCACACGAGCCTTCTTCTTC	59.989	20
AGAACAAGCTAAGGCACCCA	59.875	20	ACCTTGAGGACTTCTTGGGG	60.48	20
ACCTCCAAGTCTAAGCAGCC	58.551	20	GTCCTGGCACTTTGCTTGAC	60.844	20
GCACTTGCTTGGATTGTCAG	59.445	20	GTCCTCCGAACTCATGGTGT	59.969	20
TCGTTGATTGCATAGTGGGA	60.073	20	GGATACGCATCAACACACCA	60.399	20
TGGTGGTTGTTCTTTGGGAT	60.21	20	TGGGACTCAAGCTGTTGTTG	59.873	20
TCCTCTCGTGTTCTTCACCC	60.238	20	GTTTGACAGCCCGACAAGAT	60.119	20
GCCGTGAATCCACCATTAGT	59.82	20	AAATTTTCCTGTTTGCCACG	59.975	20
TTGGTGAGTGTATGGAGCCC	60.924	20	AGAAAGCCTACCTCGCTTCC	59.983	20
ATTTCGAAAATCAAAGGCCC	60.26	20	AACCGGTTAAAAACCGAACC	60.089	20
GAGTCACACAGTTTGGCACTT	57.845	21	GGGAGATCTTGCAGGATAGG	58.691	20
GCCTTAAAAGGTGGTGTGGA	59.971	20	ACCATTCACCGGATGAAAAA	60.17	20
ATGCAACACAACCAAAGCAA	60.157	20	GACGACCGATATTTGCTCCT	59.154	20
TTGCTGTGTTGGATGGAAAA	60.088	20	TTCATGAAATCAAGCAAACCA	59.982	22
ATGAGCCACAGTTCCAATCC	59.934	20	CAAGAGTGAGTGAGGAGGGG	59.828	20
GTCCGTGAAGTTTAGCGACC	59.74	20	CAAGACAACCGAGCAAGTGA	60.025	20
CCGAGTTCGTTCCTCGTAAG	59.869	20	CCAACCCATTCTTCACCAAC	60.21	20

AATGAATGCACCGGATTAGC	59.929	20	TTGGAAAATGAGGAATGGGA	60.244	20
GCATGGTTATCCTCGGTTGT	59.82	20	GGGTTCGTTGTTAGCTTTCG	59.747	20
ATTCGTCATCAAATTAAAGCCT	57.001	22	GCCCGTGATAATGACGAGAT	59.923	20
GGCGAGAATGGAGGAGAAA	60.288	19	TTGGATCCCAATGAAAATGAA	60.117	21
AGCCAGTCTCCACCTCAAGA	59.986	20	GGCCGTAGAGAGAGGGATTT	59.674	20
CGAATTCGGGATACCAGAGA	60.029	20	AGAGCGAGAGATGGACGATT	58.995	20
GGCCTAATAGGGTTGTGTGC	59.457	20	CAGAACTTGTCGTGGTGGTG	60.194	20
GAGACGAGAGAAAAGAGTGCG	59.367	21	TCTCACAAAGACGAAGGTGC	59.01	20
TGGCAAAAAGCTAATATTTTCAG	60.762	24	CTGTTCTTGCGCAAAATTATC	57.614	21
CACCGTTGTCTTTAAGCCGT	60.168	20	AAAGAGGTGTTATGAAGGGAC	59.817	24
GTGGTCGGTTTCAAGTTTGG	60.388	20	AAGCACACAATAACCAAAGTA	59.08	25
TCCTCGTATCCGTTCTCCAC	60.073	20	TCTCTCCCACTTGCTTGTTG	59.007	20
TGGGAGTCCTTTCCAACATT	59.381	20	CCAGCTTCGAACGTTGTATGT	60.183	21
ATACATGTCATGCCCGTTTG	59.276	20	CAAGGAGTTGTACCTGATAGC	60.539	23
GGTGGTTTTGTAAACGTGTTTCT	59.377	23	TTAGCAGCAGATGCAAAGGA	59.712	20
AACACCTGTGAAAGGGATCG	59.966	20	TCAGGCCATCTCCTCTTGTT	59.803	20
GTTGGCAAACAGGTCCCTAA	59.971	20	TGTGCTGCTGGAAAATTGAA	60.379	20
TTCGGAGTTATGAAGTTAGCACC	59.68	23	ATCACCAGCACCATCGTACA	59.992	20
ATTAGCAAATTTCGGGACGA	59.547	20	GAGGGGGAAAAGAGAGGATG	60.008	20
CGACCATAACAAAGAAAACACG	59.553	22	TTCAGCTGACATTGGGTTGA	60.24	20
GGACATGATTCATTTTCTGCG	60.463	21	TCGTAACTGAAAATCATCGGC	60.089	21
GGGAGGAGAGGAAATTGAGG	60.008	20	TTGGGAAAGCACTATGGACC	59.933	20
GGTGCTCAAAAATCCGAAAA	60.053	20	TCACTCATTCAAGAACATAGC	59.761	23
ATGAGATAAGGGGGTGTTTGC	60.201	21	TGACATGCTCTTAAGGATGGG	60.081	21
ACCCTCCTTCAGCCAAAAAT	59.94	20	TCATAGTCAAACACGATTGCTT	57.452	22
TCCCTATTTTTCGTCTCCCA	59.5	20	AACTGCACATGAAACATTTGT	58.606	22
CGAAGAGTGTGGAATCAAACC	59.583	21	AGAAGTGGGTGTGTGCTGAA	59.31	20
CACACAGATTTGACATCGAAAGA	60.161	23	TTCCAGGAAATCGGGAGAT	59.425	19
TGATTTAAGGGGGTGTTTGC	59.801	20	CACGCGCAGAGGAGATCTAT	60.526	20
TGATTAGTACCGATGAATCAACC	60.595	24	CACGTACTTAACCAAAATATG	60.177	24
ACCTATGGAAGCCCCAAACT	59.827	20	ACCCACTACCACATCCCTCA	60.238	20
GACTGCCCAAAGAACCAAAA	60.088	20	AGAAGGCGGATAAGGTTGGT	59.962	20
TCAACATGCAACCAACAAAAA	59.999	21	CCACTAACCCCTTCATCACC	59.259	20
CAGGAACCCTTTCTCTCATCC	60.059	21	TGAGGGAGTTGTTTAATTGTCG	59.131	22
TGCCAATGCTTGTCATAGGT	59.152	20	ATTTCCAAATCGGTACATGC	57.424	20
GCATCGTCTCAACCCTTGAT	60.081	20	AAACCCATTTATAACGGCGA	59.323	20
GTGGCTCTTGTCTTCCTGCT	59.604	20	GACTTACGTTCCGCCAACTC	59.74	20
CGTGTTCTTCATCCTTTCCC	59.526	20	GTCAACAGCTCGGTACAGCA	60.056	20
GCATGGTTTGTTCAATGCAG	60.119	20	CCATCTTCGTCCACCTCTTC	59.655	20
AACCTCGGCTCTGATACCAA	59.694	20	CTAGGGTTAGCATGCTTGGG	59.724	20
CCTTCCCATTTCCTCTCTCC	60.008	20	TCAGGTCTGCCCTTTACCTC	59.284	20
CATTGGCATTGTAAGCTTCG	59.325	20	AATTAATTGCTGGGTAAAACT	58.277	24
TTATCCTCCTCCCAATCGAA	59.458	20	TTTGCCTCTCCATCTCCATC	60.158	20
TTGATGATGGAGGACGACAA	60.048	20	GCAAAACTTAGGAACGAAGCA	59.527	21
GATCACTAACGGCCGGAATA	59.923	20	TTGAAATCCTTGAACCGTGTC	59.963	21
GGGGTGTTGTGTTGTGCTAA	59.465	20	ACCATCTCGGGTTGTAGTGC	59.997	20
GCTACGCCTAATTGCTTGCT	59.658	20	TGCTTTATGTTGTTGATCCGTC	60.003	22
GCATGCATATCGCAGAGAGA	60.088	20	TTGTTGCAGCAGATGCTTTC	60.142	20
TTGGAGCTGCTAGGATTCGT	59.978	20	CCGTCGTCGTTATGAAGAAAA	60.117	21
TCAACATCGTTTATCAGTTTTGTT	57.815	24	AGTGAAATTATTCGTTGATAAA	57.681	27
ACCACCACATGTCCCTTGAT	60.096	20	TGGTGGGTTGAATGCTATGA	59.924	20
GTTTTGACAATATTTAGGTGTTTT	57.818	26	ACATGGACGTCCCAGATTGT	60.246	20
ACGACTCCCAATCAGCAAAA	60.636	20	GGTAGGGTGGGGATGAGATT	60.015	20
TCTCTCTCGACGGTGAAGGT	59.986	20	GCGTGTACGTCCCCTAAGAA	60.132	20
AGTAAGGCTTTTCTAACTTATTGG	58.239	27	CCCTGCACCTCTTTCAAATC	59.67	20
CGGCCGGAATATCTAAAGTG	59.564	20	TCATTTCATTTCATGAGCTTCG	60.209	22
ATTTCGGTTCAATTTTGCCA	60.302	20	TAAAACAATAAGGTCGCCCG	59.958	20
TGGTGGCCATATATACGCAAT	60.075	21	GCAGTGACGGATGGTTTGTA	59.572	20

ACTTTGGCAACGGAATACCA	60.365	20	GCGAGCGAGTAGGTTGTGAG	61.136	20
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TCTATCTTCGGCCCCTTTCT	60.166	20	ATGGTTCGCCATAAAAATGC	59.801	20
GCGAAGCTTTTCCAACTCAC	60	20	CTTTACCCCATCTCCACCCT	60.183	20
TACACGAATAGCGGTTGCTG	59.895	20	TGCACACTTTCTGGGTTCAG	59.873	20
CCTTGGAGAAAAGGACGACA	60.224	20	GATGAAGGTGTTCGTTCACAT	59.459	22
AACTTTCGATCGCATCATCC	60.043	20	CGCGCCTCTACTTTTTAATTAC	60.473	23
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TAAAACTTCAAACCACGGGA	58.121	20	TATGCCATTTTCATCTGGGG	60.66	20
TCACAAGCATGCAAGATAAGGT	59.775	22	GCCATTTAAAAAGTCGGCTG	59.72	20
GGATGGACCGGATGTTAGAA	59.75	20	GGATGGTGGTGGAAACTCAA	60.758	20
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AATTTCGGCCTAGGATCTGG	60.411	20	ACGTGTCCGAGTGTGTTGAA	60.203	20
GTCTTTTGCAGTTGGGAAGG	59.711	20	ATGCAAGCTTTGTTTGGGAG	60.249	20
AAAATGCCCTTGTATGCTGC	60.103	20	GGTGTGTTGTTCTGCACTGG	60.203	20
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TTTCAGGAGCCATAGTTCGG	60.206	20	CAGTCACGACTTGCCAAAAA	59.881	20
CCTCCCCCTTGATTTAGCTC	60.032	20	TCGTATGAATTTTTGTATGGAC	58.927	23
TGAAGGGGATAGCATTTTGG	59.894	20	GTTTACCCATAGCGCACTCG	60.658	20
GACCCTTGGATCACATCAGAA	59.918	21	CCAACACTATTCGGTTTGGG	60.22	20
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AAATTGCTTGCCTCTGCCTA	59.982	20	AGCCAAATTTGCAACCTCAG	60.249	20
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CCCTTGTATGCAGCCATTTT	59.96	20	AGTACCGAACTGGAGACCCC	60.371	20
TTCGAGTCATACGGAGGAGG	60.21	20	AGCGAAGTGGCAAACTTGAT	59.882	20
GGGTTGGGCATCACAAATAG	60.192	20	TTATCATAGGATCACCCTCCC	57.807	21
TAAAAAGTTGAGCCCACCCA	60.472	20	CCCCTGTATGCAGTCCATTT	59.813	20
GTCCTTTCGTTTAACTCCTCCA	59.631	22	TCCAAATTACAATCGTCGCC	60.837	20
GTCAACTTTGGCAATGGGAT	59.797	20	ACGTTCGGCTCGAGAGTAAA	60.015	20
TATGCGGTGTTTTGGTTTGA	59.969	20	GTCGACCTCGATGCATTTG	60.217	19
CGAATCTTGACCGCTGATTT	60.214	20	CCCAAAATTGCGAATGCTAT	59.928	20
GGATCCCACTGAATTGTGCT	59.934	20	CGAACTTAGTCGACCTACATG	58.789	22
AAGAGGAATTGAACCCAGGA	58.568	20	TGGTATTACCCCTCAGGTCG	59.807	20
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AGGGGGTGAATAGCCTCACT	59.957	20	ATGGCTTCCATGGTGGTTTA	60.192	20
CTAGTCAGCCCATTTGAGCC	59.836	20	CAACCATCCCAAACTTCACA	59.389	20
TATGGGATCCTAGCCCTCCT	59.881	20	TTGTATGCTGAGGCTTGTGC	60.019	20
GGCTAATTTGATGCACGGAT	59.929	20	GCCACTAAGCCACCTTCAAA	60.249	20
AAAAATCACGCCACCATTAGT	58.504	21	CCAAATTTAAGGGTTATCACCT	58.849	23
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AAGCAGCCATTAAGAGTCGG	59.476	20	ATTCGGATGGGAAAACACAA	60.17	20
ACGCCTGAATATCGGTCATC	59.923	20	GCGGAATACGAAGAGTCACC	59.7	20
CCTAGATGACAACCTTCGGC	59.694	20	CGAAGTAATGCTCACACGGA	59.864	20
TGCCCTCAATCTCGAAAAAT	59.645	20	GATTCACATTGGCGGATACA	59.355	20
GCGGTTAGGCTTCCACCTAT	60.471	20	CTTGCTGGTGGAAACTCCTT	59.328	20
AAACTCCTCCAAACTTCCTCC	58.701	21	TTGGCATCCATCGTAACAGA	60.073	20

TCTCCTTACATAATTTGCCCTCA	59.977	23	TGAGAAGTGCTTGGCAAAAA	59.585	20
GGAAAAGGGCTCTTGGACAT	60.443	20	CACTTGTTCCTATTGCCAACG	60.54	21
CCACAACACCAGAGCAACTG	60.348	20	TTCACTCACCCTTTCGATCC	60.05	20
CCTCACACATTCAGCCCTCT	60.261	20	CTGAGATTTGTACTGCGCCA	60.011	20
TGATGTCCCTTCTCCTTGCT	59.803	20	GGAGTTGGGCTAAGTGGGAT	60.328	20
TGTTCACGGGAGCTTTGATA	59.272	20	CGCTTTGTTTTCGTGTTTGA	59.888	20
CGAGTGCATGAGCTTGAGAG	59.88	20	AAAATTAGGGGTAGGCACGG	60.197	20
TTGGTGATGGTGATGAATGTTT	60.096	22	ATGCGCGATTTTAAACCCTA	59.586	20
CCATGCATGCAAAATTGAAC	59.937	20	TGGTCTCAACGATATGCTCG	59.823	20
TCAGCTGAACAGGAATGTGTG	59.889	21	CAACACAAGGACATCCATCG	59.96	20
GTGTAGAAGTTGGCACGCAG	59.515	20	AAAGGGCGATGACACAAAAC	59.978	20
GTTCATGTACGGTCCGGTTC	60.24	20	ATCACGAGATGGGGACTCAG	60.072	20
TGATGCAGTATATAATCCTTAATC	57.536	27	TGTTAAATTTTGGAAGAGAAAT	57.381	27
ATGCTGTGAGATTCGCATGA	60.386	20	GCAGAAAACCTTTGTTGGGA	60.088	20
TTCAAGCTGAGATCGACGAA	59.673	20	CCCATCGTCGAGATCAAAAC	60.461	20
TGCATGCACCTGATTACAAA	58.703	20	TGGCTGCAAATTGAAAGTGA	60.379	20
GTCCATATCATTATCAAATGTTGA	58.746	27	AATTGAGAAGGGGGAGAGGA	60.008	20
CAGAATCACCATCAACACCG	59.96	20	CAATCCTTTCCTCTTTCCCC	59.875	20
GTAGGAGATGGAGTTGGGCA	60.073	20	TTTCGAGGATTGTGATTCCC	59.871	20
TCTCATGCAATGAAATCCGA	60.159	20	TTTCTTTGAGTGGGATGCAA	59.247	20
ATATCTGGAGGCGGGAACTT	59.925	20	TGCTTCTCAAACTTGATTAGGT	57.037	24
TACCCAAACCCACCAACCTA	60.081	20	AACGAAAAATTGGGGTTCAA	59.292	20
GCACCATCAGAGCAACAGTC	59.425	20	AAACCGTAGTGGGTTAAAATT	58.892	23
GTTAGGAGGATGCCACCAAG	59.55	20	TTGGGTGATGTGCTTGAAGA	60.24	20
CGACTCATGTTGTTCCATGC	60.12	20	ACCGGGTTCGTATCAACCTT	60.61	20
CCTCTAATGGCCGAAAATGA	60.031	20	TCTTCGTGTTCTTCGTCGTG	60.025	20
TAGATGGGCTAAGTGGGGTG	59.948	20	GGAGGAATGAAGGTGAAGGG	60.822	20
GGAAAGTCTCACTCGCAAGG	59.989	20	AGAAGAAATTCCAATAGAGTT	58.814	26
CATGCGGTATCATGGTGATG	60.779	20	TGCCTAATTTATAGATAATGGA	59.68	25
TGATCCAGTCACGTTTCACAA	60.144	21	AAATATGATCTTACTCCCACTG	58.89	25
TCTCGCCTCAACGAGAAGAT	60.096	20	GGGGTAACTTGTCATCCCCT	60.052	20
AAATCAAAAGCCCACAATGG	59.801	20	CTGAAATCCTGGGCGTAGAT	59.15	20
CTCATTGAGTTGACCCAGCA	59.831	20	CTTTGTCCAAACAAATGAAAA	59.062	23
TCACACCCTCTCCCACTCTC	60.243	20	GATGGGTTCTGTAATCCCGA	59.75	20
ATTTTTCCCCTTTTACCCCC	60.226	20	ATTGTGACATGGCCGAAATC	60.733	20
AATTTTCTGGCAGCCTTTGA	59.823	20	AAGAAGACCGAGAGACACAC	58.991	22
TGCAAGCACAATTCGATCA	59.931	19	GAGAAAAGACAATTCGGCCA	60.192	20
TCGAACCGCGAAAGAGTAAG	60.514	20	GCACACGAGCTCTCACTCAC	59.771	20
CAACGGTATGCTCGGATTTT	59.96	20	TAGCCGATAAAAATGGCACC	59.928	20
CGTTGTCTATGCACGCATTT	59.759	20	GACTCTCGCACCATCCATTT	60.081	20
TTTTGGCTTGTTGCTTGTTG	59.888	20	AATTTGTACACACGTCCACCA	58.813	21
AAATATACCCCCGCATGCTA	59.304	20	GTCTCAACCCTTGATTGCGT	60.119	20
TCAACATGCAACCATCAAAAA	59.961	21	CATGATCCAACCTTATTCCTCC	59.666	22
TCGCACAAATGATCGTGAAT	60.08	20	AGTCATGCGATCTGAACGTG	59.862	20
GCTTTCTTAACTTGTTGGAACCAT	59.945	24	GCATGCTCTGTTTTCTGCAA	60.142	20
CCGTTGGAGTTAGTTTGAGCA	60.29	21	TGCGAAAATTTCTGGAATCA	59.232	20
ATTAAAGGCTGGAATTGGGG	60.143	20	CAATTTTGTCTGCTGCATGG	60.257	20
ACAAGGGGCAGAAGGATTTT	59.94	20	TTGCAATATTCAACTACGAGC	58.52	22
TAAGAGATCCGAAGCCAAGG	59.406	20	AAAAAGTTTTCCGCTTTCGG	60.568	20
ACCCGTGGACGTAGATCATT	59.288	20	TTACGAAAATACACGTTCGGG	59.876	21
GCAAGGTAGGCTTTCGAACT	58.604	20	TCCCCAGTGTCACACAGACT	59.113	20
TGGAATCGAAATGATGAAGC	58.646	20	TCTGCACGCTGCAATAACTC	60.165	20
GGGGAGGGTGGTTAGGTTAG	59.685	20	TTAGGATCGGAATATCGAGAA	57.857	22
CATCGGAGCGATAAGGAGTC	59.797	20	ACTTTGGCAAATCACACAGAT	57.186	21
ATTTTTGGTGGGTTTCGTCA	60.206	20	ATGTTTTGTGAAAGTCCCGC	59.978	20
AAGGTGGGAAAGAATTTGGC	60.299	20	CATGGTAAAGAAACGGTGGAA	59.847	21
TGATGCCCAAACTTCCTACC	59.933	20	GATAATTAGTGGAGGCGGCA	60.06	20
TTTTGTTGTTTCCCAAGTTGC	60.004	21	GAGAAGAGGTCGGGAAGAGG	60.328	20

TGGTTGAATGCTATGGATGC	59.504	20	TCGTGTTTGGGCATTACTCA	60.111	20
GTCAAGGACTTACCGCTGGA	60.255	20	TACCGACGAATGGTTGTTCA	59.964	20
AAAAGGTTCCCCTCCAGAAA	59.912	20	ATTTCTCAGTCCCTGCCTCC	60.596	20
GCTCGAGCTGGATGAGAATG	61.058	20	TGTTCAATCTGCCACCAAAA	60.088	20
CCGGATAATTCAAACGTTGC	60.323	20	GTGTGGGGGATTGTTGAAAT	59.508	20
TCGCTTGAATTGCGACATAA	60.356	20	CACAATCCCAACAAAAAGAAA	59.007	22
TATGGGTTAGCGTGTGATCG	59.566	20	GTTGATAAAAATGGCACCCG	60.188	20
CAAAGAACCCCAGCATGAAT	59.933	20	AGTTGCTTAGCGACCCCATA	59.73	20
GGAAAATGTCTTGTGGTCCC	59.239	20	GTGGTTCGGGTATTCACGTT	59.717	20
TTCGGACTTATGAAGTTAGCACC	59.68	23	GGAGTTGCAGTTTTGGATGA	58.697	20
GGCTGTGAGATCTAGCGTGA	59.143	20	CTGTTCTGTCCTTTGCACGA	60.025	20
TGATCTATGGAAGCCCCAAA	60.405	20	AATGGAGACACCTAAGCCCA	59.55	20
TCCCATGTTGTAATTAATGTAGGG	59.089	24	CAAATTTCGGTTTGTTGGCT	59.975	20
CGAATTTGCAAAACCGAAAT	59.943	20	TTTCAAAAACCGAAAAACCG	59.951	20
TCCATGAAAGCTCACCCTCT	59.803	20	CTACCCAACCCACTAACCCA	59.705	20
ATGATGGAATTGGGTGTTGG	60.439	20	CCTAACCCCACTAATGACCC	58.24	20
CGCTTAGGCCACCAATACAT	59.982	20	TTCGTGATTATTGCTGCTGG	59.833	20
CGCTCAAATCACAAACCCTT	60.11	20	TTGACCTGAGGACGGATACC	59.927	20
CATCTGGTGAAGGTTTGCCT	60.111	20	TATTACAGGGGCCAGTCGTT	59.452	20
TCAGTTAATATCCCCCGCAG	59.916	20	CCTCACCTTCACCACCATCT	59.962	20
CTTGTTTGTACCGAATGCGA	59.729	20	GAAGCCTCAAATCACAACCC	59.532	20
CAACTGGAGAAGCTTGGACC	59.844	20	CAGTTGAAAAATTGCCAAAAC	60.014	22
GACAAATCAGGGGGTTTGGT	60.979	20	AGCCATTTAAAAGTCGGCTG	59.361	20
GCAAGTTTCCGTAGCTGGAG	60.015	20	CTGCTCTCTTGATTCATGGC	58.544	20
ACACAGATCATCTCGGGTCC	59.928	20	TTGAGGAGGCTTCAAAATCC	59.244	20
ATCGATCGGCTTATGAAACG	60.06	20	CCCCATGCATGTAAAACTGA	59.395	20
AAGAGATGGTTCCGCTCTGA	59.95	20	CTAGCTCCTTCCCCTTCACC	60.204	20
GGAGGTTCGACGTGGTTTC	60.504	19	ATAGGTTTCGTAGCCCACCC	60.208	20
CATCACACCACATCTCAAATGAC	60.292	23	GCATTATAACCACCGCAACA	59.448	20
CATGTCCTCTAGGTGTCGCC	60.678	20	GAGTAGGAGTCCGGAGCAAA	59.43	20
ACTCAGGCCTCACTCCCTTT	60.252	20	TGACCGGACGAAAATACTCC	59.933	20
GAATCACGGCCATTTTCAAG	60.448	20	TTGGCCTGTTACGACTCAAG	58.923	20
GATGTCCGAGATGATCCACC	60.297	20	TACAGTCGACCTCAGCTCCC	60.408	20
GGCGATGAGAGAAGGAAATG	59.773	20	TAAAACCGACATCCCCACTC	59.79	20
AAGTCTAATCGCCTGGCAAA	59.845	20	CATTTGGAAAATCAATGGATG	59.638	22
GTCCTCCCACCCTAGAAACC	59.795	20	TTCAATACTTTGAGGATAGATT	59.474	27
AATGTGAATGCCAGCTACCC	59.962	20	GTGTGTCACTCCCCGATCTT	59.969	20
ATTACCATATTTAAGGTTATCAT	57.31	27	GAGAGAAGTTTCGGTGGTGG	59.697	20
ATGCCAGCCAGACAATTTTT	59.574	20	TGTTGTCCGGTTCTCTCTCC	60.238	20
AAGGCGTCTCGAGTGAAAAA	59.993	20	GTTCCAATACCGCTTCCAAA	59.938	20
AAATACGACACCGAAAGGGA	59.429	20	AGCGGTTATTACCGGATCG	59.93	19
AGAGTCGGTGGAAATGGATG	59.927	20	TCTCACGCACTCACGATCTC	60.146	20
GCCGGCAGTTTATATAGGGA	59.058	20	ATTTTTACGGGTTGGGCCAT	62.456	20
TGACACCTAGCCCAAACCTC	60.111	20	TGAGGGAGGGAAAGAGAATT	57.863	21
TCTGAGACGACGGTGATACAA	59.303	21	AAGCTCGCAGAGTCACGAAT	60.164	20
CCTCGCACATTCAATTTCCT	60.074	20	GGATTGAAGGCTGTGTCGAT	60.081	20
GAAAAAGTCAGCCGAGAGAAAA	60.001	22	TCGCCCTTTCACAAATTAGG	60.067	20
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ACACTCACTCTCACTAGCCGC	59.685	21	ACGCTCCACCAAAAGGAGTA	59.734	20
AAATCGCACGGCTTATCCTA	59.704	20	GGAAATGTGATTTGATGGGC	60.141	20
TGGCTCAAATCCGATGATTC	60.953	20	CATTCCTTTTTATGTGTTTGTTT	59.38	25
AACCACGGAAATTACGGAAA	59.315	20	TGTGGGTTAGCATTTGATCG	59.542	20
TCTGCTAGGGTTGGGAGAGA	59.943	20	CGGTTGGATTGCTGAAAACT	60.11	20
TTTTGGACGATTTTTCCCTTT	59.81	21	GTTAAAAACCGGACTGCACC	59.476	20
TTTGCAAACATCCAACTACGA	59.216	21	CCACAATTTTAGGCAGTTTCG	59.634	21
CTTCGGAACTCTATCCACCG	59.688	20	ACCTCCACCTCCATTTCTCC	60.314	20
TAGCCCCCAATTTTGTACCC	60.902	20	AAAATCTTACACCTGGAGCCA	59.027	22
ATGTGGATGAAATTGGGCAT	60.021	20	TATGGTTTTTCGCCCCATTA	60.144	20

GACCTCCCCTAGTAGCACGA	59.308	20	TCCGAGTTGAAGTAGTGGCTT	58.994	21
TGAAAACTGAAACTAGGAACGAA	59.366	24	TGCGTTTTGATGATATATAGAT	58.21	26
TGCAAGGTGCTTTGAGAATG	59.988	20	TCCATCTTAATGCAGCAACG	59.833	20
TCCAGGAGATCGAACGAAAT	59.629	20	AGGAAAATGTGTCGAGAGGG	59.137	20
GTCAACTTTGGCAATGGGAT	59.797	20	CTCCCAACATTCGTGTGTGT	59.441	20
GACGCCTTTAAATCAGGTGC	59.713	20	TGAGGAGCGTTGATCTTGTG	59.984	20
CGCTACAGTTCACACGTTCG	60.507	20	ATCAGACGGTATTGCCCTTC	59.009	20
TCAAAATTTCCAAAAATCAAAGC	59.509	23	AGAAATCGAAGCTTGGAGCA	60.096	20
CAGGTTCCGACCTCAAACAC	60.545	20	TCTGCAAAAATGAACAAACTA	59.639	25
CAAGGCATTTATCTGGGCAT	59.923	20	CACGAGTGAAGAAAGGGAGA	59.072	21
TCGAATCTCAAACCCTAGCC	59.269	20	GCCGCGAAACAGACATAAAT	60.103	20
TTCCTTGGGACACAATCCAT	60.173	20	CGGTAACACAAAATTGCAGAA	59.685	22
GGGCTAGTCCTGCAACACAT	60.142	20	AACATGCTTCACCATATCCAA	57.957	21
CCCGATTTGTAAGGTTCCAT	58.762	20	ATATGGAAGGCAGTGGTTCG	59.955	20
GCTCTACAATATTACAATGGGCA	59.46	24	AATTGCAAGAAGCAAATCGG	60.209	20
TGTGATAGGATAGGGCCAGC	60.059	20	CTCAGGCAAGCAAAATGCTA	59.206	20
AGGACACGTTGGACCTGAAG	60.151	20	GGACCTTATCGCGAAGACAA	60.214	20
GCTTGAAAAGCCATGCAAAT	60.217	20	GGGGTCGAGAATGTATGAAGG	60.698	21
GTGAATCTCATCCGTCCGTT	59.934	20	TGCAAGAAAGTGGACTGCAA	60.574	20
TTGATTTCCAAGTGAAGGCTG	60.234	21	CTCTCAATGGACCAGCACCT	60.261	20
CTCACGTGATTTAGTTGTTCTCA	57.113	23	GCCCTTAGAACCTTGAATCTG	59.725	22
TCTTCCCGCAAGACGAATAC	60.214	20	TTTGTCTGCGTGGACAAGTT	59.339	20
AAGCACGGCTTGTGCTATCT	60.044	20	TAATGCATTCGCCAACTGAG	59.833	20
CCCCAGAAACACCAACTTGT	59.861	20	CCATCCCATCTCTTCCTACG	59.502	20
TATAACGACACGGCCATTGA	59.953	20	CCCTCGAATGCACTCAAACT	60.255	20
TGAAATCCTTGAACCATTCCAT	60.542	22	GGTGCCCCTACTTCTTTGGT	60.361	20
AGAATTCGTGCCCCTCATTA	59.528	20	GTTGGCATTCAAATCAACCA	59.375	20
CTCACGCAGTCTCTGGATCA	60.138	20	CGACGGATATTTGTTCTTGTG	58.161	21
ATGCTGACGATAACAAGGCA	59.301	20	TTCCCATCTAATCTCGTCCG	60.029	20
TGAGGTTGGAGTGTGTGGAA	60.129	20	GGGAGACAAACACACTCTCTT	58.843	22
GGGAGGGAGGGAGAGATAGG	61.291	20	CCACCCACACCTAAGGAAGA	59.959	20
GGAAGAATGATGGAATTGGG	59.175	20	CCCACTAACCCCCAACTAAC	58.292	20
TTGAACAATTGAACACCGGA	59.941	20	TCATTGTGATGTGTGGGAAAA	59.808	21
GACACGCATAAAGGGACCAC	60.384	20	CGACTTGTCGTTGTTCGGTA	59.758	20
TCACAATAGGGCATGGGACT	60.34	20	GGAGGGACAGCCTAGAACTTT	58.864	21
CACTCACACTTTGCACACTGAA	59.986	22	ATCTCGGCTACGAAGTGCAT	59.866	20
GGCAGATGCCTTTGAAGAAC	59.82	20	ACTCCCACCTGAAAAAGGGT	59.834	20
AAAACAAGAAAGCCCACCAT	58.554	20	CCCACACATTTGAGGGAAGA	60.892	20
CATCAAATCTCTAATTGCACCC	58.582	22	GGCAACTTGGGAGTTGAAAA	60.088	20
AGTTGAAAGAGCCATCAGCC	59.434	20	AAAATGACACGCAAAAAGGG	59.975	20
AAATGGGGAGATGATGAACG	59.75	20	CAATCTGACGGCCGATATTT	59.923	20
GTCCATTCAAGTCGTGGTCC	60.372	20	TTGTCACACATTTACACACACG	58.016	22
GAAAAACATTTTCTCTTGAACGG	59.194	23	TGGACTTAACTGGTAGCCCG	60.125	20
CACAACAATACCACGCAGGT	59.49	20	TGGATGTGTAGATGATTTTTGG	59.329	23
TTGTTGCCGTTAAAGTGTGG	59.627	20	GAAGCGATCCTTACAGGCAG	59.978	20
GAGGGAGAGAAGGGAGGAGA	59.883	20	ACACACACGATGGATCGAAA	59.967	20
CACGAGATTTACCTGGTTCG	58.228	20	CAAGGCAATATCTAGCAAGGG	58.865	21
CAGCTCACCATTTCATGTGG	60.112	20	CCATTTTTACATGCCGCAAT	60.7	20
TGCAAACACCACAACAATCA	59.563	20	CCTCACCAACTCAACCCACT	60.002	20
CACCCCTCCACTCTCTCATT	59.101	20	GGTGCTCAAAAATCCGAAAA	60.053	20
ACCACGCATGGTTGAGTACA	60.032	20	AGGTGCTGTGTGATGTTGGA	60.162	20
CACCAACATCATCGAACAGG	59.96	20	TTTTCACCGTCCAAAACACA	59.981	20
TTGTCACATACACGTTGGGAA	59.873	21	GAGCATGCAGAAGATGTGGA	59.95	20
CACCACAATGAAGTGGATGC	59.967	20	TGCAAGCTAACCGCTAGAAT	57.835	20
ACAACAATGTCGCGAAACAA	60.157	20	CACGTGTCAAAATTTGCTTG	57.823	20
CTCAATCTCTCGTGCTCACTG	58.765	21	GGATGGGAGTACATTGGTGG	60.05	20
TCAAAAGCAATCAAATATCCCA	59.433	22	TTAAGTTTGGGGGTGAGGTG	59.824	20
CAAAAGATCGGCTATTTGGTG	59.595	21	GCGTTTTGATGATATATAGGTG	57.758	25

TGGATGCCTTTCATTTAGGTG	59.946	21	TTGCATCGACTTTTGATTCG	59.809	20
CGGAAGCGCACATTAAGATT	60.23	20	TTTCACTTAGCTCATTGATTTTC	58.14	24
TTGGCAAAAAGCACAAAAAG	58.979	20	AGAACTAGGGCACTCCATCG	59.308	20
CCGTGGTCGCTATATCCATT	59.807	20	CGAACCACCACACCAAATTC	61.196	20
TCAATAGAAAATGAGTTTGAGTTT	60.059	26	TCAACAGTCAACAAGCACACA	58.908	21
GGTTTGGGTTCGGACTGTAG	59.449	20	TTTAAGGGTTATCACCTGATTT	57.757	24
GAATGATGAACCCCTTCCCT	60.133	20	GAGGAAACCAGCTGTCCAAG	59.844	20
TTCTTGCTTGCTGTCCCTCT	60.134	20	CATGCCTCAAACAACCTCAA	59.691	20
CAACAAGCTGTCAACCCAAA	59.734	20	CCATTCACACACACACTCAGA	58.078	21
GTCGGCAAACCAGAGCTAAC	59.882	20	AAGTGTTGCACCGACTTGTG	59.794	20
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CCAGGTTCAACTCTCTTCCG	59.837	20	CTAGGTGGCTGCTGTGTGAG	59.641	20
GGCTTTCTTAACTTGTTGGAACC	60.376	23	TTCCATTTATTTCATTTCATGGC	59.908	23
AGGAATAGGGCCGAGAAAAA	60.034	20	GGACACAATGCACACCTCAC	60.013	20
GCGTCCCTTTTACATGATCG	60.469	20	TCGGTCGTCAGATTGAGAAA	59.369	20
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GAGGGGTGGTCGAAAGAAAT	60.306	20	TTTACCCGTTGCATGTGTGT	59.888	20
TCGTCAAAAACTAATTAAGGCCA	60.013	23	GAGACGATCGAACAGCATGA	59.95	20
TGAATTACTTGAAGAATGATGAG	59.709	27	CATCAACCCAAACCCATTTC	60.029	20
TAACCAAACCCCCAATTTCA	60.024	20	GCTGCTGAAGAGACAAGGGA	60.678	20
GCAGGAAGCTTCAACTCCAG	60.134	20	CATTGCTGCTATGCCTGAAA	59.976	20
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TGTGTGCAATGTGTGTGTGTT	59.523	21	CAAATGCATTCAAAAGCCAC	59.161	20
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CGACTACAGGAACTGAGGGG	59.715	20	TGGGGTGACAGACCACAGTA	59.997	20
CACTTCTGCGGCTGAAAAAT	60.386	20	CCAATTAACGTTCCATTCACAA	59.736	22
GAATGCTGGGAGATCAAGGA	60.158	20	TTTCTACTCCCTTCCCCTGC	60.569	20
GACTTTGGGCGACTTTGAAC	59.717	20	GGTGGCTTCTCTCTTCGTTTT	59.878	21
TCTGTGCTCTCTTTCTCAGTCG	59.93	22	TCTTCGACCCAACACCATATTC	61.099	22
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TCGTGTGTGTGAGTGAACCA	59.737	20	TCTCTCACACCGAACACCCT	60.713	20
AAGGGAGGAATAGAGCCGAA	60.166	20	AACACACACGCACTCACACA	59.818	20
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ACTCTCGTGGATTTCAGCGT	59.874	20	GATGGTTTCCGAAAGTGGAA	59.91	20
CGGGAATTGATTCCTTCTTG	59.5	20	GGGCTCAGTAAACTGCTCTCA	59.63	21
CCAACACATGATTTGGAGCTT	59.985	21	CCCAAACATTTGAGGGTTGT	59.688	20
CTTCGCCAAAACCTTGATGT	60.11	20	TTTTATGTAAATTGTCGTGCGT	57.373	22
CCCCTGTTCTTCATACCCTG	59.401	20	GCTTGGTGAAGGAAGTGAGG	59.844	20
AAAAATATTAGTCCAAGTTGTGG	57.828	24	TTACCATCATTCTTGGCCATT	59.287	21
CGAACCCAACCCACAATAAA	60.587	20	TGACCCTTTGATGTTATACACG	59.393	23
CCACCGAGCACCAAGTAAAT	59.993	20	TGGAGGTCGGAGAGAGAGAA	60.064	20
AGTTGGGCTTAATGGTGTGG	59.853	20	TGGTGACTTGAAGAAATTTGG	57.715	21
AGGAGATGGAGAGAAAGTGTCG	59.878	22	GTGGGTTTAAGTGGGGTGTG	60.126	20
GAATCAACTCCAATCCGGTG	60.317	20	CCAGATTCAAACCCTACCCA	59.784	20
TTGACCGTCCAACTCTTCAA	59.262	20	AATGATTCCTTGGCACTTGG	59.933	20

CACGAATGGGACCTCCTTTA	59.926	20	GGATGCTGATGGAGGGAATA	59.854	20
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TACTGCTCTTGAACTCGCCA	59.74	20	CAAGGAACATGGACTTGCTG	59.288	20
TTACAATGGCCAAGAGGATT	57.155	20	GGGTGGTAGATGAAGAACCG	59.405	20
GAGTTGGTCATTTGAAGCGAG	59.867	21	ATTGAATCTACGTCCACGGG	59.813	20
TTTTGTTTGTTCCCAGGTTG	58.5	20	ATCGCTCGGGCTCATATCTA	59.791	20
TCTTCCTCTCCCTTCCGTTT	60.183	20	CGCTCCACAAAGATCTCACA	59.984	20
GATTTGAACTTGGAGGGCAG	59.67	20	TGCATGCAAAACTGAGCTTC	60.142	20
TGCATGGTTAATGTTGTAAGGG	59.758	22	GCCAATGATAGAACGCCAAT	59.929	20
TGTTCTGATTTTCTGCACCG	59.84	20	CTCTGCATGTACGCTACCTACC	58.954	22
GGCTGAGTACACGAATGCAC	59.323	20	TCGTGTAAGTTAGCCGGGAC	60.132	20
CTTTTCACACGAGGTCACGA	59.873	20	CCCTGCACCCTTTTAAATCA	59.931	20
CACGTTGGGATCTAGGCAAT	59.955	20	AAGGAATGGTTTGATGGGTG	59.647	20
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CCCTAACTGGCTTCGGTACA	60.125	20	AAATTGACAGCGATGGAAGC	60.221	20
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CGGAATACCGCTCGTAAGTC	59.73	20	CGAGCGAGTGGTTGTGTAAG	59.51	20
ATGATTTTGGTGTGTTGGCA	59.823	20	GCTCATGGTTCAGGGTTCAT	59.934	20
TCGACCCGGACAATCTCTAC	60.073	20	ATCCGCCTACATTGGATGAC	59.78	20
CATATGGCGCTCCACCTACT	60.118	20	GTTGCAGGTCTGCGAGAAAT	60.406	20
TGAAATCTCCCGTACTTCCG	60.066	20	GGGCACCTACTTGTTTGTGAA	60.023	21
TGCCCATACGGTTGTATGAA	59.809	20	ACCTCTGCCTCGTCTGGTTA	59.867	20
TTTTATCTGAATGCTAGATGTTTG	58.809	25	TGTCCGTGAAGTGAAAGACG	59.873	20
GAAAAATAGCATGCCTTCGC	59.822	20	CGCACAATATCATGCATTCAC	59.975	21
AAACGGAAATACGAATGCGA	60.456	20	TGGTGTAATAATTTGGTTTCAT	60.006	24
TGTGTACTTCCCTACTCATAAGCA	59.296	25	GTATCGCCGTCGTGTTCTTT	60.14	20
AGGTACAGCCATTCGTCCAC	59.997	20	GTTTACAACTCACAACGCGG	59.245	20
GTGGCTGCTTTTCATCCATT	60.081	20	CCATATTTAAGGGTTATCACAT	59.713	27
ATCAGCCAAATCAATCTCGG	60.036	20	TTCCTCCCTCGTTTTTCGAT	60.929	20
TATGATGGGAAGGGTGGGTA	60.006	20	CCCGTTTGTTCCAATGCTAT	59.823	20
TCCACTCACGAAAACACGAC	59.726	20	ATAACCCGGTCAACAAGCTG	59.993	20
GGTGGGAGCAGACAGAAAAG	59.844	20	CCAAAGACGGGCTAAAATGT	59.087	20
GAAGCGCAGTCATTTAAGGC	59.988	20	TTGTTGCAGTTGTGGGTGAT	60.008	20
ACTCATTGTAATCTCTCTCCAAAG	58.087	26	CATCAACTCCATCCCCATTC	60.135	20
CACCTTCATCTTCACCACCA	59.52	20	CCACAATAGCTTGGCACCTT	60.132	20
ACACTAAACCCGCGTATTGC	60.025	20	TGGTTGCGTAAGTTTTGGTG	59.627	20
GGATACCCTCCCAAACCCTA	60.011	20	CTTGATTGGTTGACGTCCCT	59.966	20
ACGAGCCTCGAGGTAGCTG	60.706	19	AGAGCTGCGGTTTTGATCTG	60.538	20
GTCCACGGTGGTTTGAGAGT	60.009	20	TTTGCTGTGGGGAGTAAACA	59.17	20
CGAATGGGAGAGAGTGGATG	60.612	20	TCTGCCTCACCACCAATGTA	60.112	20
AACAATTACAATGTTTATGAAAAT	59.12	27	CAGGCCCAATACCTTGACAT	59.813	20
ATCTTACCTCCGGTTCCGAC	60.328	20	CCTCCGAACTCATGGTGTTA	58.569	20
TCCTCACTCTCACTAGCCGC	60.7	20	CTTCCCTAAACCCCTGTGCT	60.488	20
ATATAGCCGTTGGGCTTGTG	59.982	20	CCTTTGTCAACTTGGGCAGT	60.149	20
TCAACTCACCCTCACATTTCTC	59.187	22	TGCAAGCATCAAACAACACA	59.877	20
TCCAAGAAACTACGCCAACA	59.317	20	CGTTTTAATTTTCGGGAAGC	58.739	20
TGGAGTTTAAATGTAGAGGCGAA	60.134	23	TGACTAAGGTCCCATCACGA	59.086	20
TTTAGTGTTTTGACATGATTACTC	57.557	25	TCAACCGCCAGGATTATTTC	59.901	20
GTATCGGTGTAGCGTGGCTT	60.162	20	AAATCTACCTCTGCCACCCC	60.328	20
GCATTAGCAAATCCCGAAAA	60.04	20	TTGTCATCTACAACACGACGC	59.779	21
ATGTTCGAAGCAGCCAAACT	59.882	20	TTTTGGATGACGGAAGGAAG	60.044	20
TGTTCCGGTCCGAGTTTATT	59.429	20	GGATGTTTCTGGAGCGATCT	59.243	20
TCCTTCTTAAAGGTCTTAATCGGA	59.658	24	TGATTTTCCGTCATCGTGAA	60.049	20
TTGGGGGTTTAGGGTTCTCT	59.799	20	TTTGGCAATGTCAGGATCAA	60.049	20
TACGGCAACTGTGGTTTCAA	60.149	20	TACATGGGACGATTCCGATT	60.155	20
GTGTTTGCAGAAATCGCCTT	60.257	20	TATTGAGTTCGGGGAGATGC	60.036	20
GACCCAACTACCAAACCCAC	59.162	20	GTGGAGAGGAGGGATGATGA	60.008	20

AACGATCCTACACAATGGCG	60.914	20	CCTGGATCACGGGTTTAATA	57.43	20
TGGGGACTGACCTTTGAGAG	60.229	20	GGGTGAAAAATGATTCAGAGG	60.299	22
TGGCAACAAACAAAGCTGAG	60.027	20	GATGCGAGGATCCTTTTTCA	60.155	20
TGATGGGTGATGATGGAAAA	59.707	20	TGCGTTTTGACAATATATAGGT	60.083	26
CCAAGGATCACAAGTGGATG	58.93	20	CCACTCTTCGATGGAACCAC	60.51	20
TTTTGTCGGCCATTTTCTTT	59.564	20	GCGGTTATTACCGGATCGTT	61.058	20
TGATTGATCTTAACTGCAAAAGA	59.465	25	TCTTTCCGAGTCTTCCGCT	60.081	19
TTCACGAATAAACATGTTCCAGA	59.505	23	GCAATATTCAACTACGAGCAT	59.292	23
TCGCCCACAATCCTGATATT	60.296	20	GTGGCGTTATTGGGTTCATT	59.691	20
CGCACCTATTAGGGTCGGAT	61.21	20	AGCCTAGTCGCGATTTTTGA	59.982	20
TAACGAGAAAATTCGGCCAC	60.074	20	ATGGAAGTGGGTTTCGAATG	59.79	20
GGATGTCCGAGGTGGAGTAG	59.53	20	AGCCACTCCCTCCAAAAGAT	60.074	20
CCTCATCCGAACAGAATTGAA	60.059	21	TATGCACGAAGCCAATTCAC	59.694	20
GGAGCAGATGGAAAGACCAG	59.803	20	TCGTCCCATCTTTTACCCTC	58.981	20
TTTTTCGCAAGCCACTAAAA	58.608	20	TTTGAACTCTCGGCCTCTTG	60.508	20
CAGGAAAGAAATGGGCTTCA	60.184	20	TTAACGGGCGTTTTTGTAGG	59.993	20
AAGCGAAACTGTTGTATGCTGT	58.978	22	AATAAAATGTACGGGCGCTG	59.985	20
CGAGCTGTTATGCGTTTTGA	60.014	20	CGAGTGTGAGGCTGTGAGAG	59.757	20
CCCGAGTTGAGGTCCTGATA	60.065	20	CACACGCACACACATCCATA	60.029	20
CCCCTACTCCAACCCTTCAT	60.183	20	TCTTACGGAATTCCACTGGG	59.926	20
GCAAATCTATCTCATACAAGGCG	60.128	23	CGTCATAGTCAAAGCAACCG	59.342	20
TGGTTTGGTTGTCACTTTCTTG	60.045	22	GGGCCTGGTCATTCCTTAGT	60.328	20
TTAGTTAGCAAGGGGGAGGG	60.435	20	TTCAAAGGGCATTTTTGTCC	59.916	20
CCCATACTTAATTCATAACCCAA	57.09	23	AACACTTGAGGAAGGATGATG	58.646	22
CTGCAGACATTTCTCGGTGA	59.984	20	GCTTTTTCGACTTTGATCCG	59.823	20
TTCGATGATAACTATGGGTTTTG	58.079	23	GTGACCCATTTTCGATCACC	60.181	20
CTCTCAATGGACCAGCACCT	60.261	20	GAAAATCAAAGGGCCACAAA	59.916	20
TGATGGAGAAGTTACGATGGC	60.088	21	ATCGGTTATTACCGGATCGC	61.031	20
GAGGTTTTGACATAACTTAGGTGT	59.398	27	ATGTTTGAAATATCGGGGCA	60.153	20
CCCAAGGGAACTTGACTGAA	60.081	20	TGGCACAATAGGAAAGCAAG	58.917	20
GGAGCCATTCGATCTTTGTG	60.603	20	ACAAACTTATGGACCGCTGG	59.993	20
TGCTCCGAGACCTTAGACTCA	60.141	21	CGTCACCCCACTTGGTAAAA	60.776	20
AGAATCCCGAGATTTCATGC	59.083	20	GAGGTTACGCCAAACATGC	59.141	19
GCTGGAAGATAAGATGTGAACG	58.861	22	TTATAACCGATCCCACCCCT	60.391	20
TGTAGATGGGGGTAGGATGG	59.623	20	CTGGCAGTTGGGGAATTAGA	60.066	20
TCCAAAATTGTGTTACGGGT	57.85	20	ATATGAAGTGGGGATGGACG	59.629	20
GAAGAGAAAGCGCGATCATT	59.556	20	CATCCACTTAAAGCAAGGCAA	60.25	21
GTGGGTTAGCACGTGATCG	60.128	19	GCTACGACATTGCCCTATGA	58.749	20
AAAAACTTGGGATTTAGGCCA	59.83	21	AAATTAAAATTATGGCAACTTT	57.89	25
CGGAAATACCTCGCCTCATA	60.053	20	GAGAACCACGGACAACCCTA	59.966	20
GCCATGATCTCATGATTCAAAA	59.907	22	GCACCGTCGATTTCTAGTGTT	59.256	21
TTCGGTTAATCCAAAGGTCAA	59.438	21	TTTTCCGACTCAAGGCATCT	59.813	20
TTGAATGGCAAGGATTGGTT	60.309	20	TCTTGCACATCTTGGTGAGTG	59.889	21
GTGTAATAGTACATACAATGCAG	58.539	26	ACCTGTAGAATCTCTTACTCTA	57.215	27
TAGAAGCCCCAAACTTTGCT	58.973	20	GATGGAGACACCTAAGCCCA	60.073	20
GAAAGGGCCGATCCTATCAT	60.252	20	ACTTTGCAAGTCACCGGTTC	60.156	20
CGCGCACAAAGAACTTTACA	60.052	20	GATAGAAGGCCGATTGACGA	60.177	20
CACTTGGACCTGAAAAGGGA	60.081	20	CCTTGAATCGAGTTTACATGTA	59.038	25
GCCTTTTGGCATGCAGTATT	60.103	20	CGAGCCTTCTCGTTGATTTC	59.955	20
CGTGCAAGCATGAATCACTC	60.423	20	TGTTGAAGTTTGGGTGTTGG	59.435	20
GGAATGCGAGATGGAAGAAA	60.155	20	CACTGTTGGAATCACATGCC	59.967	20
GGTATGTCTCGGTGTTCATGG	60.248	21	TTCATCAGGTCGTGGATTGA	60.048	20
GAAAATTGGTTGTTATCCACAAG	57.617	23	CGGTTGCTTATTTGTTCGTG	59.226	20
CAATACCGTGACATGCCTTG	59.988	20	TACGTCAACGGTGGTTTGAG	59.609	20
ACCCCAAACAAGAAAATCCC	60.032	20	ACTCACCGTGCTCTCCTCAT	59.866	20
GATGGGAATGGGAGGTATGA	59.563	20	TCCCGTTTTACCCTTGAATG	59.795	20
GCCACCACACGAGTATATCAAA	59.889	22	CCTCACTCTTTTACGCCTTCC	60.248	21
TCCTCTTTCTTTTTGCGAGC	59.708	20	TCACCGTGTGTTTCCTGTTC	59.571	20

TGTAGGCGCCTCTGATCTTT	59.978	20	ACATGCAAACATGGAACATTG	59.312	21
CTCGCGTTCGACTCCTTAAC	60.015	20	TTGATCAAGACCTTTTGGGG	59.903	20
TGCTCTCTTTGTAATCTCTCCCA	60.379	23	TTTTGGCTGCTCCTTTGACT	59.993	20
GTGCAGTTGTCAGCAGAGGA	60.187	20	GATGTTCCACAAAACCACCC	60.073	20
GCGAAATCAAAGAATCCGAA	60.153	20	GGACCGCGAACTTAGAGGAG	61.275	20
GGAAATCAATCACAGCCGTT	59.939	20	TGAAACAATGCCTGGAAACA	60.088	20
AGATGAGCCCACCCACTTTT	60.883	20	GATGATTGCACCATAACGCA	60.498	20
CCAAGTTATGATGGGAAGGG	59.24	20	TGTTGTCATAACAAAAATGACA	59.837	24
CGAAATGAAATCCTGGCTTC	59.645	20	TCGCCATATTCGATCACAAA	60.035	20
TCAGAAACTTGGAGCAGAAGAA	59.238	22	GGTTGAGCTCGGAATACCTG	59.694	20
CAAGCCCAAAAGCACAAAGT	60.284	20	GGAGTGAAAATGGGTGTTGG	60.21	20
TGATGGCGATAATTACATGGTG	60.588	22	TGTTGACTTACCAACAGTTCAC	58.255	23
CCCCAAACATCACACACAAG	59.848	20	GTCGGCATGACGTAGTTTGA	59.722	20
GAGTTCGTCAAACCTCCCAA	60.088	20	GGCCAAATATTTCCCTACCG	60.508	20
ACTTGCTCCCGAGCTCAATA	59.978	20	ACCATATTTAAGGGTTATCACC	57.552	24
CTGAGATTCCCCATCACCAT	59.737	20	CCCGTGACACAACAGATCAC	60.005	20
TTGACATGATTTGTTAACGGG	58.4	21	AGTCCCCATTAAAGATGTAAGT	57.81	25
GGCCTCCTGTCCAATTTTTA	59.019	20	TCATAAGTTAACATAAACCAAA	59.079	27
GAGGACACGTTGGACCTGAT	59.969	20	GGGTGGGTTTGGAGAAGAGT	60.349	20
ACTCACTCTCACTAGCCGCAG	59.824	21	AATACGACGGCGAAGAAAGA	59.845	20
CAATCATCTAGCCCTCTAACATCT	59.682	25	CTTGGACTATCGGGTTCCAA	59.926	20
ATCCTCGCCTCCTTCTTCTC	59.919	20	AAGGCCACACTCCAAGAAAA	59.711	20
GCCACGTTAGGCTCAAGAGT	59.501	20	CATCCCAGTTGTCTTGGGAG	60.501	20
TGCAAACCCATTTAAAACCC	59.677	20	ATTTCATGTCACACCCTCCC	59.636	20
GATATGGAAGAGTGGCACCG	60.483	20	CGGTACAGATTACAGCACGC	59.371	20
ACCGGCTACTTGTGAATTCCT	60.012	21	TTTTCGAGTTTCTTGTTCTCCA	58.994	22
ATGTCGATGAACACGGATGA	59.925	20	TCGAGAGCTGAGAGACAAAGA	59.112	22
CCCAATGACGGAGACAGAAT	59.927	20	ACCCTCCTTCAGCCAAAAAT	59.94	20
TGGTTGGAGGAAAATCTTGTG	59.956	21	ACACTTTTAACTCCAAACCAGG	59.098	23
CGTGTAATCACCATCATCGG	59.799	20	GTTGGCGATTTTCATACGGT	59.829	20
GGAGTCTCTCTCGCTGATGC	60.255	20	AGGGGAAGGAAAGAGAACGA	60.183	20
AGAGGGACAAAGCAAAACGA	59.853	20	AACGGTTATCACTGGATCGC	59.962	20
GGCATCAGAGCCACGTTAG	59.41	19	ATACCCGTCGGTGTTCTCTG	59.989	20
TGAACGGTTGAAATTTGCTC	58.747	20	ATTTGCTTAAAATGAATCAATG	57.325	23
CGAAAACCTTGAGAGCTCGTT	60.908	21	TTGTTTTCATTAACAAGACCATC	58.895	25
GGTCCTCTAGCCTGCATTTG	59.836	20	TCCGTCATCGACCACTATCA	60.072	20
GAGGGGAAAAGAAGAGTGGG	60.045	20	CGGCCGGTTTTTAATGTTTA	59.835	20
CCATTTGCATATTATTTTTGCAC	58.502	23	TGAGTGGAACGATCCATATAAA	60.427	25
TCAAGAGCCTCCGACTTTTC	59.55	20	GGACCCACACTCACACGATT	60.851	20
CGAGCGAGAGGAGAGAGAAA	59.966	20	AGACGAGGAAGAACAACGGA	59.844	20
CAAATGGCCAAGAGAGTTTACA	59.267	22	ATTAAATGCGCCTCCCACTT	60.821	20
GCCTGAATCGACGACAAACT	60.263	20	CTGCATTCGTCAGTAGTCCG	59.465	20
CGATTTGGATTCGAATTCTGT	59.033	21	TCTACAAGATCAACCGCCTG	58.874	20
GAAACAAAGAACGTGCACACA	59.797	21	CCCGTACCTCAATTAAAAGGG	59.719	21
GGAAGGATGTGAGATGGTGG	60.326	20	CCGAATTCCTCTACCGTCAA	60.066	20
ATGAGGTGAAGGTAAGGGGG	60.183	20	TGCACACTGTCACACTCCAA	59.905	20
TTTGAAATGGATGGTGGTGA	59.75	20	TATTGGAGCAGCTGGGAAAT	59.668	20
AGGGGCTTAAGATCCCAGAA	60.032	20	CCATTTCATCACCCTCACATC	60.188	21
CCGCCCTTCCCTACAAAA	60.961	18	ATAAGAGGTATTTTGACAGTAT	57.206	25
ATTCCCGTCGCCCTACTTAT	59.82	20	ATCGATGTGTTGGCATTCAA	59.931	20
GCGCACCGATATGATAGACC	60.465	20	CCACCCGTGTATGTCATGTG	60.722	20
CCCTAAGATAATGCCACCCA	59.778	20	TGACACGAAATTGACGGAAG	59.691	20
GGCCCTAACTTGACCCAGAT	60.328	20	AGCCGGATTTAGAGCAATCA	59.807	20
GAACAAAGCTTGTCACACGG	59.339	20	TCCCTGTGTTCCGAAGAACT	59.697	20
CCCAGACTCGATAACTGGCT	59.308	20	CGCGTCAATGTTTTCCATGT	61.866	20
TGGCTGTGGACTCAGTTGTT	59.31	20	TGGACTTCTCCAATCCATGC	61.016	20
CCAAAAGACGATCTGGGATG	60.452	20	CTGCAATTCCTTCTGAACCC	59.67	20
GAGGGTAGGGGTTCAAGTCC	59.795	20	CTCGTTCTCTTCTTCATCTAAAC	57.05	24

TGCGAGCCATCAACATGTAA	61.225	20	CCGAGGGGTTTAGGGAATTA	60.136	20
TCATGCACGAAACTCTTGGA	60.39	20	ATCATCAAATTGCCAGGGAC	59.756	20
TCCTTGAATATGAGAACTTGTTTA	57.989	27	CAACACTCAATTATAGGAAAA	59.318	27
ACCAAACATGGGGATATGAAA	59.009	21	GGGTAGTTGAAATGCAAGCC	59.574	20
AGCCCATTATTTTCCACCAA	59.273	20	GGGGAAGAGAATCAAGAGGG	60.008	20
GGATTTTGTGAATCACGGGT	59.653	20	CACTGATTCGCACAAGGATT	58.724	20
TTTTCTTGGCCATAGGCATC	60.038	20	ACATATTCCATGGTCCCCAA	59.871	20
GCATGCATCCACCACTCTAC	59.12	20	CAAATGTGGCCTTTCCATTT	59.801	20
ATCTGAATTTCGATGCCGAC	60.043	20	TGCATCACATTTGTTCATATCG	59.448	22
CCCCAAATTCACATGCTTTC	60.309	20	ATCTCCATCTCCTTCCTCCG	60.553	20
CACATCGCTATCGTCCATGA	60.653	20	TTTTTGCCCTTGTATGCTCC	60.074	20
TTTAAATGCACACCCCTTTCT	58.616	21	TTGGGTTTTTACGAAAGGCA	60.46	20
TTGATGCATGAAGACAGCAAG	60.003	21	CGTTCATTTCGTACCTTTAGAA	60.307	26
GAGAGAGTTGATTGTGGGGG	59.505	20	TGCCTTTAGTAGCCAGCACC	60.407	20
CCGTTGGAATCAGTAATGGC	60.331	20	GGAAGGCGTTGACATTTGAT	59.939	20
ATACAGTGCAGATGCGCGTT	61.799	20	GAATGTTGTCCCGGACTCCT	61.291	20
AAAGACAAACCAGCAGAGCA	58.65	20	TGGTAGTGAAATAAACATAAA	59.645	26
TAAATGTTTCAGCCCATAGAATTT	58.233	24	GGTTTTACGAACCACAATCCA	59.716	21
GAAAACGAGAGAGTGAGGCG	60.134	20	TACATTTCCCCAACCACTCC	59.647	20
CTCTTCTTCCCAAATTGCCC	60.929	20	AAAAATGGTTATTATTGGATCA	57.553	24
CATAATGAGAGGCGGTTGGT	59.955	20	AAAATGGAGGCGATTTTGTG	59.938	20
TGTATGCACCTGAACATGCC	60.549	20	TCCGTATGCTGTGGATGAAA	60.073	20
TCAAGAGTCCCCTTGGTCTG	60.229	20	ATGGCATATGAGGCTTGGTC	59.923	20
TACCCCCATATGCAGTGGA	59.741	19	GCCTATGCAGTCACAAATGC	59.306	20
TTGGCTTGTTTTTGCACCTA	59.344	20	ATCGCAATTCGATTAGGCAC	60.067	20
CCCAGCTATATTGCATTCACAA	59.985	22	CATGTTGCGTAATAGGCGAG	59.349	20
GAGGGGGCTTTTCTTTTCAC	60.053	20	ACGATTACAACGCAACATCG	59.614	20
GAGGAACCTCTTTAAATGCAGTG	59.317	23	TTTTACACCACCGAAAAATGC	59.861	21
CCGACGGTTGTAGTGGAGTT	60.028	20	AAAAATCCCCTCGAATGCTT	59.909	20
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TCGGCTGTCAAAGACAAAAA	59.439	20	GAAAGGACAGTAGGTGATCGG	58.658	21
TCTGGCCAATTGTGAAATGA	60.049	20	GGGTGAAATAGCATGCAAGG	60.469	20
GCCCCACCCTTCTATCTCTC	60.037	20	TGCCGCTGAACATATTGAAA	60.215	20
GGCTTTCTTAACTTGTTGGAACC	60.376	23	CCTCTGCACCCTTTGAAATC	59.67	20
GATGATGGAATTTGGGTGCT	59.756	20	GACCCTAATACCACTAACCCC	59.133	22
AACGGGGCCATTATCTTTTC	60.15	20	CCTTCAACAAATGGTTCATGC	60.359	21
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TCACTCTCACGCACCTTCAC	60.03	20	TTCAAACCTGGTTCTCGTCC	60.088	20
AGATTTAAACAGTGGCTGCG	58.054	20	CAACATCACCAAACACTCCG	60.001	20
AGTTCGAAAGCCTACCTCGC	60.894	20	TTCATCATTTCATTTTATAAGCT	59.91	26
GGTGTCTGGAACAAGGGAAA	59.943	20	TTGGTTGGTGGAAGAAATCA	58.947	20
TGGTTAGTATTGGAACGCGAC	60.011	21	TTTCCATGTTCCGTGTTTCA	59.941	20
GTTATGCGATCTGCTCGTGA	59.979	20	AGCACTGATTCGCACAAATG	59.871	20
TCTGATTCGGGAAAACATGA	59.049	20	TGTCCGATTTGCCGTTCTAT	60.469	20
GGTTTGCAGGTACGAGGTGT	60.035	20	TCCAGCATTTGTATGTCCCA	59.924	20
GTTGCTTTCGGTGTTTGTCC	60.538	20	CATGAACCTGAAACAGCGTG	60.301	20
AGGAAGCGAGGTAGGCTTTC	59.983	20	CCTCCCAACTCCAATATCACA	59.799	21
CCATACGATCTGTCCCTCGT	59.95	20	TTGAATCATTTGCGTTGCAT	60.081	20
CAATTTATTTACCGAGGGTTCG	59.743	22	GACCTGCCAAAAAGTCAAGG	59.711	20
AATTATCGTCCGTCCCCAAG	61.061	20	CGTTCGGAACTACTTCAGGG	59.728	20
GAAATATCCACCGAACGGAA	59.762	20	CTTAGGTGTTTTGACATGTTCA	59.164	25
TATGGGAAGAGGGGACTGAA	59.478	20	CCCACTTCCTCCAACCAGTA	59.959	20
GAATTGGTGGAATGATTAGAGAA	57.257	23	TGTTGTAATGAGGCTTTTGGAA	59.625	22
TTCGAGTTATGAAGTTTGCACC	59.271	22	AGCGCTTTTTGCCAGATATT	58.992	20
CCTCCGTGGACGTAGATCAT	59.95	20	TTTCCCCATCACCATCACTT	60.173	20
ATCTGGGCCATTAGATCGTG	59.917	20	CCGCCTGATTTGTTTCTCAT	60.074	20
TAAACTCCCCCTCAAACCAA	59.401	20	TCCGATGACTAAATGGAAGAC	59.569	22
AATCTTGGGACCTCCCTTGT	59.795	20	ACTTTCCGTATATGTCGCCG	59.982	20

TGCAGGTTTGTTGAATTTCG	59.706	20	ACACAATGCCAAACATGGG	60.232	19
CACGAGAGTTGAAAGGGAGC	59.989	20	TGGTCCTGGGAACCTAACAG	59.959	20
CAAATGGAGGTGAGAGGTTTG	59.578	21	ATGGCGGTGAAGATGGTAAC	59.82	20
TTCCCTCTCCTCCCTCTCTC	59.883	20	CCTTGGCGGTTCATATCAGT	59.955	20
TCCTGAGTGGCGATAAAGAAA	59.831	21	GAGAAGTTGTCGGTTTGGGA	60.088	20
ATAGAGCAGCAGACGCGATT	60.147	20	GGACCTTGTCCAGAAACCAA	59.943	20
GAGGCGGTTAAAGAAACGTG	59.747	20	GCATACTCTCACCAATCCCC	59.366	20
GGTGGCCTTACTCCACTGAA	60.111	20	TCCCAGCATTCTTGAACACA	60.24	20
GTCGTATACTGCCGCCACTT	60.162	20	AATCATGTTGCTACACGTTGCT	59.705	22
GGAGAGGAATCAAGTCGACAA	59.274	21	GACTCGGGTAGTCAAGTTTGC	58.854	21
GAGGGTGTTTAGGGTTGCAG	59.592	20	TGTACAAAAGCTTGTGGTGAA	59.836	23
TTTTTCGATCCTGTGCTGTG	59.84	20	GCAACGGAATACCACTCGTT	60	20
AGGCTAGCACAAGAATGGCT	59.104	20	GCACACTCGAAGAGTAGCGA	59.344	20
CAAATGGCCAAGAGAGTTTACA	59.267	22	AAAAATACCAAAGTCGATTAT	59.264	25
CAAACATAGAAACATGGACGCT	59.158	22	TATGGGTTATCACCGGATCG	60.544	20
ATTCATACCTTTCTGCCCCC	60.152	20	AAAAGCATTTCACACGTTCTG	57.947	21
AATGCATGCACCTGATTACAA	59.055	21	AAATAATTTCCGAAACCGCC	60.148	20
TTCTCAAGCTTGTCAACCCC	60.232	20	CACACGTTATATTTATAGTTTT	59.19	27
GAAGCGAGTTCCGAAATGAA	60.331	20	GCGAATTCAGCTAGAACAACA	59.541	22
TTCTGTCTTGGATGATGAGGC	60.211	21	TAGCTTATCACTATCACCCTCT	59.255	25
GGGCAATTATGTTGGAGGTG	60.192	20	ACGGTTCACATACTCCTGCC	59.997	20
CCTCACCTTCTCTCCACTCTCT	59.101	22	TGCAACCAACAAAAACAACA	58.626	20
ACGATGTCCTCTATCACCCG	59.95	20	TCCTTGGAACCTAGAAATGGTT	59.001	22
GAGTAATGCATCGCCTGGAT	60.066	20	GGGAGAATGCCTTGTTTCAA	60.051	20
TATCCTAGGGGAGACAGGGG	60.277	20	ATCCTTTTCGCCATCTTGAA	59.645	20
GGGGTTGAAGTAAATGAGGTG	58.423	21	ATGATGGAATTGGGTGTTGG	60.439	20
TGTCAAGATTGGTCTCGTTTT	57.315	21	TCTAATAGCAAGAGAGACCGG	59.871	22
CCGCAATTTTGTTCTTTGGT	59.975	20	TTTCAGCATTGAAACCAGCA	60.379	20
CCTAAGTGCCTACGTGTTGGA	60.175	21	GATTTCCCACCCTTCTTCTTG	59.926	21
TCCAGATGCCTTCATTTTTCA	60.57	21	TGCCTCTAATGCACACAAGAA	59.478	21
AGCTGACTGGTGGTCTTTGG	60.298	20	CGGAATCAACCCTCAAACTC	59.526	20
TCTGGCTCTTTTCCAGAGCA	61.196	20	GGGTGATTGTAGCCAGCTGTA	60.147	21
GAAGTTTTGATCAATTTTCACTCG	59.938	25	CTCGCTAACGGCACTAAACC	59.904	20
CACATGTTGCCATCTCCAAG	60.112	20	GGTATTGTCGGAACTTCGCT	59.198	20
CCATGAGTCCATGACCCTTC	60.326	20	AAAGCAGGCAGTAGAAGCCA	60.154	20
GGAGTCTCTCTCGCTGATGC	60.255	20	GACGATTGAGAGAAAGCGGA	60.483	20
GGCTGACCCAATACCTCAAA	59.933	20	AAATTTATTGTAATCTTCCCTCC	59.594	26
GGAGAAAAAGAGATTGAGAGGG	60.189	23	AACCCAACCCACTAACCCAT	60.34	20
TCAAACGTGAGGTGATGGTT	58.984	20	ATCAATGGTCCACATCGGTT	60.057	20
TTTTCAGTTCGGGCGATTTA	60.56	20	TTCCTCTTGTCGCCATTTTT	59.685	20
TACGTTGGACCTGAAAAGGG	59.964	20	AACAATTACAATGTTTATGAAA	57.992	26
TGCCTTCAGGGCATTTATCT	59.668	20	TGGTTGTGTGAACCAACTCTG	59.626	21
CCTTGAACCGAGAAAATGGA	60.044	20	CCAAGCTTTTCCAACTCACC	59.711	20
CCTTGGCGGATCATATCACT	59.917	20	CTGCTCAATCATCTCCGTCA	59.942	20
TTAATGGACGTCGTGACTGC	59.722	20	CAAGCTCATTTTGTGTCCCA	59.691	20
ATGAGTTATCACCGGATCGC	59.923	20	CTCAGCATACGGGAAGGGTA	60.088	20
TATGTGATAGGCTACGGCCC	59.945	20	CGTGAATGAAAGCGATCGTA	59.833	20
AGCTGTTAGGGTTGTATAGTGAG	57.436	27	TGGAAGCATCAACCACTCTG	59.831	20
CCCCAGTAGTTCCCATCAAA	59.784	20	TTCCCAACTCCATCATCACA	59.893	20
TACCCAACCCACTAACCCAA	60.081	20	GAATTTGGAGAGGGAGGGAG	60.008	20
AATGGCAGAAGCAAAGAGGA	59.955	20	AAAGGGATTCACCTGCCTTC	60.443	20
CAATGTTACAAAATGGGCGA	59.42	20	TTGGATTTCATTGATCCTGC	58.494	20
CATTTGATAGTTGTTTTTGTGGTG	60.185	25	AGACTCTTCACAACTTCTACAC	58.586	27
GTGACTTATGGGGGCTCAAA	59.933	20	GACACCCAATCCCATGAAAC	60.034	20
AGATTTGGGTGATGTGTGGC	60.79	20	ATTTGCGTCGCCTAATGAAC	60.103	20
TGGATTGATTATGCTTTGCC	58.577	20	TGCTGAGAGTGTGTTGGCAT	60.473	20
GATCCCAGACACCGTAAGGA	59.927	20	CCCTCAATCGATCCATGTCT	59.886	20
ATTCCGTTTTTAAGTCCGGC	60.312	20	CCTTTGTATCGATCCCGTGT	59.813	20

CTTTACCCTTTTGTAACATAAAAAT	57.251	27	TTTGGTTCAATGGGTTATTCG	59.685	21
AGTCCCAACCACTTTCACTG	57.611	20	GCATGATCAGGGTAAAATCCA	59.776	21
ACCCTCTCCCTCTCTTTGCT	59.439	20	AGATTTCGAGTTCGTCACCG	60.255	20
ATTGCCCACGAGAGAGATTG	60.218	20	AGAACGGGCAGCAGTCTAAA	60.015	20
TGATCAACAGAGAATGCAAGC	59.016	21	AGCATTTGAGATCGGAGTCG	60.362	20
ATATGCGGGCTGGAAGACTA	59.691	20	TGCTCACCTTCGATCTCTGA	59.656	20
GGAAACAACACAACCAAGGG	60.246	20	GGTGGGAGGGAATTTGAGAT	60.133	20
CTAGCAAGGCTTCCATCTGC	60.118	20	TGTGTTTTATCCCTCGCACA	60.111	20
CACCACCCTGCTTCTTTCTC	59.844	20	AGAACATGGTTTCCGAGCTG	60.255	20
TTCACACTACCGCCATTTCA	60.111	20	TCTCCCCCTCTTCCCTCTTA	60.139	20
CCTTGAAGACAATGAAATTTTGG	59.865	23	CACCTCACCTTCTCTCCACTC	58.885	21
CGTGGTTCGATCGTAATTGA	59.542	20	TGCCTCAAGGCTAAACAAGG	60.378	20
TCGGGAGTCTGTATTGAGCC	60.218	20	ACAGAAATTGCCTCTGTTGTTC	58.37	22
GGAGAAATCAAGAGGAGGGG	60.008	20	CCACAAGAAAGCATTCCTCC	59.67	20
TTGTGGTTCGATCGTAATTGA	59.027	21	CCTGCCTCAAGGCTAAACAA	60.378	20
GGTTCTCACAGGAGGGTTCA	60.088	20	CTCGTGTTTCTTCGTCCTCC	59.844	20
AGTGAGTGCGAGAGCAAGGT	60.205	20	TACACCGAAGGATATCCCCA	60.148	20
ACTCCCACCCTCTCTGGTTC	60.504	20	AACAAGTGTGTTTGTGAGTGG	59.969	22
TTTTTACGATTTTGCCCTCG	60.068	20	TTTTGTCCGAAACATCCCTC	59.91	20
GGACACGGTTTCTAATGTTTTG	58.539	22	AACTCTGCCGGAGAATGTGT	59.727	20
CCTTTCATGTTATTCTTTTCTCACC	59.472	25	TGGATTATCCTGCGGTCAGT	60.483	20
TGCCCTCGTATGCTATAAGTTG	59.298	22	GGTTAAATTTTGTCCCTAGTTA	59.109	25
GAACCAAAGTGAGCCCGATA	60.074	20	TTCTTGGCGTGGTGTTGTAG	59.758	20
GCAGTATGCTGACGAGGTGA	60.016	20	GAAGACACGGTTGGACAAAAA	60.001	21
TGGATCGTATCACAAGCCCT	60.483	20	TGTAGTGGTTCGTGGACTGC	59.751	20
GTTTAGCTGCTTGGTTGGGA	60.249	20	AGCTTCCATGGAGGTTGATG	60.073	20
CGATTCCCATACCATTCGAC	60.155	20	GGGCTCAAATATCGGACAAG	59.528	20
ATCCTTGACGACTGTTTGGC	60.119	20	ACTCCCCTGTTTGGGAATGT	60.607	20
GCCAATTTGATAGAAGCCCA	60.038	20	TCGTGGAGAAACTATCCAAGG	59.181	21
ATCGTGGAAATTCCTTTAATGTG	59.281	23	CCCCTACGTTGAAATTGTCG	60.357	20
TCAAAGTTAGCACCCGAACC	60.11	20	TTCGTTGATTTGAAACTCTAAA	59.028	24
CGGAGTGTATTGCGAACTCA	59.864	20	CATCGGACCATTTTCTGACA	59.496	20
TGTTCTCTCTCTCGCTGCAC	59.446	20	TACCTCATCACCATCCCCAT	60.011	20
GGTTTCCATGTTTCACCCAC	60.073	20	TCCCGTTGTTGCTTTCTCTC	60.375	20
ACCTCGAAGGATTTGGCTTT	60.074	20	TAGGAAAATCATGCACGTCG	59.688	20
GCAGGTGAGGGACAAGAATG	60.656	20	GGGTTATCACCTGAATGCAA	58.423	20
ACACCGTCAATCACAACACA	58.371	20	GAAGGTGGGCATAAGAGACG	59.694	20
ACTGCGGATGCCCTAATATG	59.945	20	ACGCGGAGATAGAGACAAGG	59.454	20
CAGCCTTTCCTGGGAACATA	60.066	20	CATTTATGAAGCAAGGGGGA	59.894	20
CACCCACACCAGACCAACAT	61.735	20	GAGTTCTTATCGCCTCCGGT	60.599	20
CACCTGAAAGGAAGGCAAAA	60.22	20	ACATAGCGCCGGAATACTTG	60.117	20
AATCCTTTAGGCCGACAACA	59.569	20	CATTTCCCCCAACTTCACAT	59.647	20
TTGGGCCGATCCTATCATTA	60.247	20	ACTTTCTCGCCTGGATTTTG	59.312	20
CTCCAAAGAAAGCCAAATGC	59.823	20	TAGAACATTAGCGGGATGGG	59.916	20
GTCGAGAGAAAGGGCTGAGA	59.679	20	GGATGAATTGATGGTTTTTGG	59.125	21
CCATGGGAAATGGTTAGTTGA	59.671	21	TCATGGAATTTGAAAGTTTGGA	59.429	22
TTGAATGGAAATACCCTCTTAGG	58.576	23	CAGGAGCAAACAAGTGGACA	59.873	20
GTGGTATGGAAAATGGGCAC	60.059	20	GGAGAGGGAAAAGTTGGGAG	60.045	20
TGTTTTGTAGGCCTGCCTTT	59.747	20	TCCGAGATCAGCGAATTTTT	59.784	20
CGTCCACGTCCTCTAGGTGT	60.174	20	GTGGAAGAGAAGATGCTCGG	59.95	20
GTCGACACAATTGGCTCCTT	60.119	20	CAGAGCGCTAGAGGTTTTCC	59.218	20
TACCGGCTTCAACAGCTTCT	60.015	20	TAAAACCCGACACCTGCAA	60.096	19
GAATCTTGTCACATTTACCAATGT	59.961	27	TGGGAAAGATTATTGGAACCTT	58.864	22
CGATACCCGAACCGTATCAC	60.214	20	GAATCCTTTCACGGATCGAA	60.014	20
GCACAAGTGCCAAAGAGTCA	60.032	20	TCTTGCAATGAAGAACGTCG	59.988	20
CAAGGGTACCATCCTGTGTG	58.852	20	GCAAGGCCAATGGAAATATG	60.289	20
ATGGTGGAGTTCTTCGATGC	60.081	20	TCATCTTCAACCCCCAACTC	59.903	20
GTGCTCTGGCTCATTCCCTA	60.362	20	TGCTGGTGTTGAATGGAAAA	60.088	20

CTGTAAGGGGAGCAATCGAA	60.206	20	AAACGCTCGTAGTGTCCCAG	60.312	20
TCACATTCTGCGATTGCTAA	58.017	20	TGCGTGGTTCAGATTGAGTTA	59.332	21
AAGGGTAGCTGGCATTCGTA	59.73	20	TCCTCATGTACGTTGTTTATGG	59.393	23
GACCGGTTAGACCGGATTTT	60.187	20	AGTGATTGAGGGTGATTGGTT	58.364	21
TCTCTCCCTTTCCACACTCG	60.377	20	CAGTCAACGTGCGCATTTAT	59.759	20
TGACGAATTCTCAAGTTCCTCAC	60.655	23	CACTGCACAATCAACCGTCT	59.751	20
AGAAGCTGCTCCTTTCCACA	60.134	20	AACTCCCCCACGAACTCC	59.896	18
TGGTCGGTGGAATGAATGTA	59.774	20	TTTTGATGATATATAGGTGTTTT	58.782	27
GGTATGGTAGCCCTTCACGA	59.955	20	CGACTTGTCGTGGTTCGATA	59.716	20
GAGAGAAAAGGTGGCAGGTG	59.844	20	GCCTCCTCTCTCTTTCACCA	59.53	20
CATAGGCCAAAGCCCAAATA	59.922	20	AATAGTGGTGGGAGGAGGCT	59.957	20
TGGCCTGGCTTAGTTGTATTG	60.138	21	TGAGGGATGCCATAAGGAGT	59.508	20
GTCTTCTCCGCCTTTGTGTG	60.833	20	GGATGGCTTGTTCACTCTCC	59.661	20
ACGTCAGCATCTACCCCAAC	59.997	20	GTTTCAGCCGTTTGGTTTTG	60.514	20
CAACACATTCAATACATTCTCCAA	60.154	25	CGTTTCCGACTACCCTTGAA	60.103	20
AATGTTTGATGCATTTCGCA	60.081	20	GCCACCCTCCCATATTATCA	59.605	20
CTCTCTCGCCTCGCTTTCTA	59.993	20	AAGTTTATCCCAGCTCCGCT	60.228	20
GACGAGATTGTCGAGTGCAA	59.992	20	TTATTTGCGTGAACAATGGTG	59.476	21
CGACGAGAAAGTCGTGTCAA	60.025	20	TCATGATAATGCATGTCTCCG	59.514	21
CATGTAAATTCTTGGTCATTCTCA	58.188	24	TCTGTTGGCAAACACAGGTC	59.726	20
CCCAAGCTATCACTCATCACC	59.565	21	GCGCACTCACACTTTCTGAC	59.628	20
TGTTTTCGCGTTTCCTCTCT	59.993	20	ACGGTACGAGCACAAACACA	60.222	20
GCAACGGAATACCACTCGTT	60	20	TGATCCTGTGTGCCTGTGTT	60.162	20
GAGAGAGAAGGGGGAGGAGA	59.883	20	TGGCAGAAGTGGGAGTCTTT	59.844	20
ATGCACGTAGGCATGTTCAA	60.142	20	TGTGAAAATTTGGTTGCAGAA	59.192	21
CATTCAAGGGGCATTTTTGT	59.801	20	CAAAGGCCCACAATGGTTAT	59.685	20
GGGCTCGAATTCAAAACTGA	60.192	20	GAAGAAAGAGGGGGAGATGC	60.154	20
GGAGGGTTTTAGCGTGATAGG	59.973	21	CCAACTATCCATGAGAAATGA	59.843	23
CCACCCAAACCCATTATCAC	59.91	20	GGAATCATCACCATGCAACA	60.339	20
GCATTTGGAGCAAGGCTAAG	59.982	20	CCTTCGGCTTGAAAACAAGA	60.357	20
TTTTGTAGTTTCCCATGTTGTCA	59.411	23	CCAATCTCAACAACACACGC	60.16	20
ATGCCCTCATGACTCTCACC	60.08	20	GGACGCCACAAATTGTTTCT	59.978	20
TCTGGACCATCAGATTTGGA	59.009	20	GCCATTCAAATAAAAATCAAG	60.833	23
AGAAAATGCATGCGAAGAGC	60.499	20	GTGGGGAAAGAGTTTGCGTA	60.11	20
AAAGGGAAAACAGTTGGAAGC	59.623	21	GTCGCTGCAATTTCCAGTTT	60.257	20
CAATATTACAATGGCCAAGAGAG	59.826	25	GCAGGCAGCTGATATGTTCA	59.979	20
CGGACCGAGAACTTAGAGGA	59.425	20	CCCTAGCCTTTGCCTCTTTC	60.332	20
TTGCCATATTTAAGCCGAGG	60.054	20	TCATGATATAGTTTTTCGTGGC	59.507	23
TGTGTTGTGTCTTTTCGTGTTG	59.7	22	ATGATCGACCAACCCTGTTC	59.786	20
CATGATTTTGCAACTTACCATTTC	59.788	24	GATGTCCCCATTGAGACTCG	60.475	20
CGTTGAACCCTAAATTGGACA	59.847	21	GCGACGTTACCCACTTTCAC	60.559	20
TTTCGGCCAAAAGAAAAGAA	59.805	20	TGGCAACAAGATACCCACAA	59.964	20
CCATCTCTCGTCAGTCGTCA	59.98	20	TTTCAATGGGAATCGGAAAC	59.739	20
AATGAGAAGCCCAATGGAGA	59.629	20	CAGTTGAACCAAACACCCCT	59.861	20
CCGTTGCCTCTTTTGAACTC	59.853	20	CAGGTGGATCCAGCAGTGTA	59.701	20
CGGAGGTTTGATATGGTTTCA	59.809	21	CAACGCCATGCATTTATCCT	60.857	20
GGAGGATTCTTTCCCCTGTC	59.874	20	TCTGTTGCTCCAAATCATTCA	59.262	21
GTGGCATGGGGAAGCTACTA	60.096	20	CCTAACCTTGGGCTCTGATG	59.688	20
CACTGTGTAGAAACATAAACTGC	58.944	24	CGTCAACACGAAATCACCAT	59.42	20
GAAGCCGTGGGACATAAGAG	59.694	20	GGGATGGGAAGAGCATTTAAG	59.917	21
GGGTTTTGCAGGATTGTGAT	59.797	20	GAAACATGTAGTCCGCCTCG	60.657	20
TTGTGTTACAATGATGGGGG	59.097	20	AATGAGCTCGCATAACACCC	60.103	20
GTTGGAGGTGCCAAAACTGT	60.012	20	TTTGAAGGAATTCGAGTGGG	60.044	20
GGGGTGTTTTGACCTAATCG	59.288	20	CGGTATCACCCTCCTTTTCA	59.926	20
CGAAATAGGGTTGGTGAAGC	59.569	20	TCTATTTGGAGTTGGGGCAC	59.933	20
CGGAACCCTCTCTCTTACCC	60.067	20	TCTCACACCCTTTTCAACTTCT	59.781	23
GGAAAACGACGAAGAAATGG	59.546	20	CCGACATGGGGAAATTGTAG	60.184	20
TATGCATCCCAAATTTCCGT	60.153	20	GGTTCGTTTTCGTCGTGATT	59.978	20

CCGAAATGGAGATCAGGTTG	60.452	20	CAGCAATTTCGATTTCAACG	59.301	20
GGGGCTTAGATCACCGAAGT	60.464	20	TAAAGGAGCCCAGAAAAGCA	59.953	20
CCAAACGCATCAAATTCTCA	59.664	20	CTCTGGTCCCCCTTTCTCTC	60.186	20
TCCATTTCACATCCGATGAA	59.859	20	TCATGAATCCAACGTACGCA	61.081	20
AAACAGTCTTCGGGACACCA	60.545	20	TTTCCTTATGCGGTTCTTGG	60.067	20
TCTACGTCCACGGAGAGGTT	59.721	20	TCTCTGTGCATCTCGGCTAA	59.697	20
CCGAACTTTTGGCCTTCATA	60.067	20	TGAAGTTAGGAAATAAGGAGG	57.525	24
AACTTCTCCTCCCAATCGCT	60.212	20	CCGCACGAGAATCCATACAT	60.884	20
CGATACCCTCCCAAACCCTA	61.05	20	CAAGCAAAGGCCAATATCGT	60.096	20
GTCTGCATGCAAGATAGTACGG	59.797	22	TCAATGCATGATACGCCCTA	60.058	20
ATTGCCATCACCTTCTCCAC	59.934	20	ATGCTCGACTTATGCGGTCT	59.866	20
AAAATCTTTGAAACGGGTGG	58.925	20	ACAAACCAAAGTTGCGATCC	59.978	20
TCGGATCTGGGTATTTGACTG	59.94	21	GATCGCTCATGCATCAAGAA	59.914	20
GATATTGGGCCGAAGAGTTG	59.528	20	ACCATATTTAAGGGTTATCACC	57.552	24
AGGGGTCCCAGAAAACTGAT	59.795	20	TGAAACATGAGGCCTTGCTA	59.42	20
CCAATACGAAGCCCAAATCA	60.827	20	TAGTGGTATGGAGTGGGGGA	60.187	20
GGGAAAGTTCGTTTTTGCCT	60.463	20	CGTGGATGCCCTAGATTGTT	59.955	20
ATCACCACGAAGTCTACAAAAACA	59.968	24	GGACCGGTTAGACCGAATTT	60.187	20
CGCGCCTACAATTCAAAGTA	58.982	20	ACCAAGGAGAGTGAGCCAAA	59.844	20
AATCCCCACTTTTTCGCTTT	59.945	20	CGACACGGATTGAATCACAC	59.967	20
CATAATGCCCTCGAATGCTAA	60.068	21	ACAAGGCATGCAATCAAATG	59.548	20
TGGTATATGGAGGAATGCCC	59.605	20	TGAAAAGGCCGGCATAAATA	60.405	20
GAGAATCTGGTTCTGGTGGC	59.661	20	CACCACAAATCATGATGAGCA	60.533	21
CACATCAACACACCCACACA	59.878	20	CCCTCTCTTCCTCAACACCA	60.229	20
GACCGATCGAAACACACTGA	59.682	20	CCATTGGCATTCTTCCATTT	59.762	20
TCCGTCACGTCTGGAAAAAT	60.495	20	CGAAAATCAATGGATGGGAT	59.581	20
GTCAACTTCGGCAATGGAAT	59.939	20	AGCTCGGTTGTGGAAAAATC	59.174	20
GGAAATTGATGGATTTGGGA	59.558	20	GTACGCAGTTGGGAGAGGAA	60.255	20
TTTGGTTCGGAAATAGGTGG	59.795	20	GAAAAGCTTGGCCATTCAAC	59.691	20
TCCCATGTTGTAATTAATGTAGGG	59.089	24	AGGGGCAAATGTTGATGAAA	60.309	20
ATTCTGACTTGAATTCGCGG	60.214	20	TTCCCCCTTTTCTCTCGTCT	60.183	20
CCCCTCCTAACTTTGCTGC	59.822	19	GTTGAAGGTGACGCTCAAAA	58.9	20
TTGACCCACCATTGTCAAGA	59.935	20	CGTAAAATTCCGGTGCAAAT	59.832	20
GTCCCACAAAAGCTCAGAGG	59.844	20	AACTGTGGAAAGGGAGCTGA	59.844	20
CTCAGCATTTGGGAAGGGTA	60.066	20	AAGCAAGTTCGATATATTAAAA	58.273	25
CGGAAGCAATTTTATCATAGAAGA	60.006	25	GCGATTCTCATTCCAATTCAA	60.031	21
TGATGTCCCTTCTCCTTGCT	59.803	20	CCCTAAGATAATGCCACCCA	59.778	20
ATCAACCACCACCTTCGTTC	59.827	20	AGGTCTTGACAGGTTGTGGG	60.002	20
TTCTGTGCCGCATTTATGAT	59.14	20	AGGATACAAGGCAAAAGGCA	59.708	20
TTTTCGAGTTATGAAGTTAGCACC	58.926	24	TTAATGCGTTCACACCCTCA	60.111	20
CCCAAGGTCAGTGGAACAAC	60.399	20	CCAAGAACACTCTCCACTCTCC	60.288	22
CACATAGCAATTTTCGGGGT	59.823	20	ACAAACTAATCAAGTTCCGCA	57.439	21
TTTCTTTCACACCGAAAACG	58.794	20	GTTATATCTATAGGGAGGGTTA	57.293	26
GCTACCCTTTTTGACCTACGG	60.008	21	AATTCGATGATAACTATGGGTT	58.407	24
TATGCTTCAATGGACCAGCA	60.22	20	TGGAAAGAAGGGAAAGTCAA	57.367	20
GCACGAAGAAAGGATTCACG	60.776	20	GTTTCCTTTGTTGAGCGAGC	60	20
TTGGTTCACACAACCACTCC	59.415	20	AGTTTACGGGGGAGAATTGG	60.18	20
TGAATGATTTAATAACCTATGGTG	58.467	25	CCGAGCTTGAGATGTACCAA	58.874	20
ACCAATTTTTCGTCGTGCTC	60.118	20	CACTTACACACGCACACACG	59.848	20
CAATGTGAAATGGGCAAGAG	59.123	20	TCTCTGAAAAGTTGAAGCCCA	59.978	21
GTTCGCACAACCTCTCCACT	60.307	20	CCTCCGACGTCATTCTTGTT	60.111	20
TGCAAGAAAATCCAGCTTCA	59.542	20	TCCTCCTCCTCACACTGCTT	59.986	20
CGTGCAATTCCAAGCTACAA	59.872	20	CTCTGACCTTGAGGGCTTTG	59.982	20
CAGCCGAAAAACCACAATCT	60.11	20	ATTTGCGATTTATGATGGCG	60.802	20
CCGTTTTTGTCCATGGAAGT	59.83	20	CGTGAGGAAAAACCGTGATT	59.971	20
ACACTCACTCTCACTAGCCGC	59.685	21	GCTCAGCCCAACTTCCTAAA	59.452	20
TGAGCAAAGCATTTTGGATG	59.809	20	AAATGCACGCGAGACAACTA	59.493	20
CCATTTGCAATACTAAGGCTTTC	59.224	23	TCTGTCCCGTCTTCTTCGTT	59.844	20

AGCAATAGCAGGTTCGGAGA	59.978	20	GGCCGATTGGAGTATAACGA	59.923	20
GCATATTGGCAAGAAACAACA	58.69	21	AAGCTTTCTGAATTTGTTTGCA	59.946	23
GTTTGGGGCTTGATTGATGT	59.797	20	TTTGCATGTGTTGCAAATGA	59.691	20
CAAGCAAACCACTCACTCTCC	59.899	21	AGATCCATGGCTCCAACATC	59.893	20
TGAGATTTCACATGGCAACA	58.62	20	AAGGAGGTGTTATGAAGGGAT	58.028	22
CTCCTCCGGGAGACTCCTAC	60.208	20	CTCCGATTTCTTGGTGTGGT	59.966	20
AATTCATTTCCCCTCGACCT	59.766	20	CCAGTCTCAACAAACGTGGA	59.72	20
GGTCCATTGGTCTTTTGTATTGA	60.102	23	ACAGCTCCTACCCGCAACTA	59.898	20
GATTGCATCACGTCTCCTCA	59.794	20	CGAAAAATTTAAAATCAAACG	60.521	25
CATGGACTCACGCTCTCTCA	60.138	20	GGGAATGAAGAAGTTTCGCA	60.192	20
TCCCAATTCAACGACAACAA	59.941	20	TTGGTGAGGTGGCATCATAA	59.924	20
ACATTCAATCCCAGCCATTC	59.756	20	TGCAGATTGACGAAGGAAGA	59.522	20
TCATTCTCTTCTCTATCTCTCTCGA	58.885	26	TGGGAGGAGGCTTAGGATCT	60.169	20
TAACTGCCATTTCCCGATTC	59.901	20	TAGGGGCAAGCCCTTAAAAT	59.93	20
TTCGTCCGAAATACTCCCAC	59.933	20	CACTTATAGATGGGTTAGCGT	59.972	24
GTGGCATGGGGAAGCTACTA	60.096	20	TTTCTGAGCCTAACCTTGGGT	60.116	21
TCTTACAGTAGGGTGGAAAACAA	59.138	24	AATTTTCGACTTTGCCGTGT	59.615	20
TGCATTTTCTTCTTTCTTTTTCA	58.236	23	TCCTGACCCTTTTTGAGATTGT	59.976	22
GGAGAAGAAAGAATGAGGAATG	58.837	23	GGGTACATGTTACGTGCCCT	59.74	20
GACAGATGGAGGGTGTGTGA	59.502	20	ACAGGTATCCGAAGGGATGA	59.361	20
CGTTTAGCCGCAAGTTTCTC	60.018	20	AACGGTAGCCATCACAATTTTT	59.778	22
CGAATTTTGTGTGGACCGTA	59.439	20	TGGGTTCATCGGAAGAGTTC	60.05	20
TAAAAGGCCAAGCAAGGAAA	59.826	20	GCCGATCATGTCCTCAAAGA	61.159	20
CTGGCTTCTCTTGCTCTCTCA	60.02	21	ACCACGCCAGTCAGGTAAAC	60.035	20
ATGCCGAGTCTTGTTGATGA	59.245	20	CCAATGACACGACACAAACA	58.974	20
ATTGAGTCAAGGGCGGATAC	59.009	20	GCTTCAATCCGTCACTCCTC	59.81	20
TTGTAATGTGGCATGCGTTT	59.999	20	GAAATGGTGTAAAAGGGGGT	57.759	20
GGTGGCACGCATCTGTAAC	60.136	19	TGGACACCCCAGATTGTTTT	60.21	20
TGATGTTTAAAGTCGTCGGC	58.773	20	TGCTTACTGTTGTATGGGGTG	58.566	21
GTTTCCACTGTTATGCTGCG	59.347	20	ATCGGATCTGCGATCTAACG	60.199	20
GATTTGCAAGCCTATGGTGG	60.469	20	GAGTTCGTCAAACCTCCCAA	60.088	20
CAGCCGAGAGAGATGAGGAG	60.238	20	TACGAGACCGAAAGGAAAAA	57.49	20
GGAGAAGGGTTCGGACTAGG	60.067	20	GCGCAGCAGCATGTTAAATA	60.009	20
GGAAAAGGGAAGAACAAGGC	60.053	20	ACCAATCCACTGCATGAACA	59.967	20
GAGGGGACCTTCCTTTTCTG	60.045	20	GTGGCCTTTGTGGGCTACTA	60.132	20
GATGCGAATACAGCACGAAA	59.839	20	TCCATTTGCATCCAGATTTGT	60.324	21
CTAGCCGTCGTTTTTGCATT	60.264	20	TGAATTGGTGACACACACGA	59.541	20
CTGACGTCTTGTGGGAGTGA	59.864	20	TGATCTGGAATCTGCGATGT	59.197	20
GCTATACCGATTTTCGTCGC	59.71	20	TTGAGGACATTTATTCGTCGG	59.946	21
CGGGTGCTTGAGAGAGTTGT	60.444	20	GCCCCTAAGCTCGTAGATCC	60.194	20
TATTTGCCTTCACCTTTGCC	60.074	20	TGCAACGCCAACTACAAAAG	59.911	20
CGGAATTCACTTCTTTGCTGA	60.372	21	TGCCTAACGTTAAATGGGCT	59.609	20
TGTTGGACTGTGTTGGGCTA	60.152	20	GGCTTCCAAAGCTTCCACTT	60.743	20
GGAGAAGAATTTGGAGAGGGA	59.637	21	CCACTAACCCAAACCCATCA	60.605	20
AACGGTATGCTCGGATTTTG	59.96	20	TGCTGTGAATTGTCCAGCTC	59.992	20
GCTCAAGCTTGCTGTTTTCC	60.14	20	AACATGGTTGGGCTAAGTGG	59.853	20
GGTTGTAATGAGGCTTTCGG	59.569	20	GAATTGGTGGAAAGATTAGAG	57.58	24
TTTTTCTACCTGCCCATTGC	60.074	20	TTCCTTCAATCCATGCAACA	60.049	20
TGTGGCTCTGTGGATTCTTG	59.831	20	TGCCAGCGTATTGTGAAGAG	60.011	20
TGTGAGATTGTGTGTGGCAA	59.705	20	AAGGCAAAGGCTGGTCTTCT	60.382	20
GCCGAGATTTGTTATGCGTT	60.103	20	GGCTTGCCCTTAACCCTATC	59.93	20
GAACAACACACTGCCCTGAA	59.726	20	CCCCAAGAACACTCAAGAACA	60.133	21
CCCACACCTCTTTGCTTTGT	60.149	20	CCCTTCAACCACCTTGTAGC	59.592	20
ACAGGTGGTCGTAAAGCCAA	60.55	20	CACTTTTCCAGTCTGCTCCC	59.844	20
GAAGAGGAAAATAAAATAATCCC	59.945	25	AATCGGACCGGATCGTTAAT	60.531	20
CTGTTGTTGGAGCTGTGCAT	59.905	20	TTAAACAAAGCGTGCAGACG	60.052	20
TTGTTGCCCGAGAGCTTTAT	59.845	20	TATCAAACGAAGATGTGGCG	59.688	20
CGATGTTGCTGGATTGTGAG	60.263	20	AGATTTCGATTTCCCCGAAC	60.265	20

AATGGCTGCAATTATCCCTG	59.923	20	CCCCAGTAACCAACGCATAC	60.249	20
ATCAACGCCCATGATCAAAT	60.163	20	GGGGTACCCAATATTCTCCG	60.391	20
CAAATGCCCAAGAGGGTTTA	59.931	20	CAGCACAAGCAGGGAGTTTT	60.431	20
TGGGCTGTACCATAAAAGCC	59.96	20	GGAGTGCTCATGATCCGTAGA	60.233	21
AGCGGACGATAGATACACCG	60.118	20	ACGAACAGAATCCTCATCCG	60.073	20
TTTGCCCAAACAAATGAAAA	59.026	20	TTTGACCGAACCGTTGTGTA	60.004	20
CGATCAATAAAGCTGCACACA	59.887	21	ATGATGCAAATCACCTTCGT	58.019	20
CGCACTACTAGGGTTTGGGA	60.125	20	GGACGGCCATAAGAAGTCCT	60.464	20
TCATTCTCAAGCCACTCCCT	59.803	20	TCGGGGTATCAGAAATCGAG	60.029	20
TGAAAAAGGACTCTTGGGCA	60.745	20	GTCTCTGGAGCTCTTTCCCC	60.336	20
AGAGGTAGCCATTTACGCGA	59.867	20	CTGTAGGCGCCATCTTTTTC	59.845	20
CGGTAAATCCTGCCATCTCT	59.15	20	AATTTTTCGATCATGTGGGC	59.768	20
ACACCACCACCTCACTGTCA	60.045	20	TCGTGTGTGTGAATTAAAATGA	58.136	23
AAATTCTTGATTCGCCACCA	60.448	20	TATATATGGGTTATCACCTGAT	57.071	24
AACCACAATGGTTGCTCTCC	59.973	20	CATTCTGTGTTCTCTGTTTTCGA	59.696	24
GACCTGGCTCGTTAGCTGAT	59.459	20	CATGGCGTTGTATTTGTGCT	59.614	20
TTCCAAAGCAACGTAACATGA	59.216	21	AATGTGCGTGCTTGCATAAG	59.902	20
GTGGTGAAAAAGGGTGGCT	59.958	19	CACCCTCTCTTCTGGTCAGC	59.986	20
TGCATGCTCTATGCAAGAATTT	59.881	22	ACCTGCACCAAAATGGAGAG	60.111	20
CAATGATTGTCAAAATTAGAGTTC	58.718	26	CCTCCCAGCTCACGTTCTAC	59.867	20
GGATACCCTCCCAAACCCTA	60.011	20	TTTCTTCCATTCCATGGTCC	59.727	20
TGCATGCATATTCCATACCA	58.371	20	AATAATGCCGAGTCTGGTGG	59.955	20
TGCACAGCATATGCCTTCAT	60.251	20	TTGACATGGAACTGCACCAG	60.722	20
GCTCCTCCTTGGTACTCACAA	59.343	21	GTTCGGGATCGATTTGTGTT	59.797	20
CGAGATGTCTTCAGGGCATT	60.218	20	CAACAGTTTGGCATCAGAGC	59.445	20
CCTCCTTCTATCTCCCCTGC	60.169	20	TGTGTGTGAGTGTGTGGGTG	60.088	20
ACGCTCTTGAAATATGCGCT	60.01	20	CTCTCACGTCAGGTTCACCA	59.864	20
TCTCACCTCCCCAAACCTCT	61.021	20	GAGAAGGGGAGAGGGACTGT	59.661	20
AAAAGGTTAGTGGGCTGAGGA	60.116	21	TCAACAGAGAATGCAAGCAAA	59.6	21
TTGAGCTAGCTTTTGTGGTGG	60.426	21	CGGATTAGCCACGGTCATAG	60.481	20
CACGCACAAGTACATCTCGG	60.324	20	TGGAAGAGAGATGGAGGGAA	59.731	20
GCCTTGGTCATGCCATTTAT	59.791	20	CCTTGTCCGTATTCATTCCG	60.323	20
CGACGATTGACCCAAAACTC	60.495	20	GGTAAGGGTAGGGTACGGGT	59.101	20
CTTCACCGTCCAATAAACCG	60.357	20	CCTTAACATGTCGGGTTCGT	59.853	20
GAAAATCAAAGGCCCACAAA	59.916	20	CCTTCCATTCCGAAAATCAA	59.872	20
AGAAGGCAATCTATCCCGTG	59.15	20	ACTTCCGCCTTGTTCTTTGA	59.853	20
TTCGTCGTTGTTACTGGCCT	60.689	20	GATTAACCTCGCATCCCTCA	60.036	20
TCTGATAAGGTTCGAATTCACG	59.225	22	ATCACCAACCAATACGGGAC	59.532	20
ATGGGCTTCGAGTTTGGATA	59.528	20	CAAAGGCCCACAATGGTTAT	59.685	20
GGCGACAGGGATAAGAATCA	60.036	20	GACATCTCCCTCTCCGACC	59.583	19
TGGTAGTGTTGAGTTGGCGA	60.301	20	CTCGCTCTCGCTCTCACTCT	60.182	20
GCATCGTGTCACTGAGTGCT	60.063	20	GACTGTGAGGAAACGTGCAA	59.88	20
ACAAGATTCGAAATCACATTCAA	59.884	24	GGGGAGAATGTAATATCCCGA	59.992	21
GTCCACGGTGGTGCTAGAGT	60.182	20	AGCCCTAACTCGACCCAGAT	60.096	20
ATTCTTCTTCAACCTCCGCC	60.578	20	ATATTTTTGATGACGCGGGA	60.289	20
AATGCAAGATCTTAGTGGGATAA	57.017	23	TGGAGGTGAAGAGAGGGAGA	59.913	20
TGCGAAAGTTGAGCTGAGAA	59.864	20	ACTATCAGCCGCCAAATGAT	59.556	20
TCATCTTGGCATGGTCAAAG	59.648	20	AATTCAAGGATTCAAGCCCA	59.505	20
TTCCTAGTTCCTACCGCGTG	60.262	20	GCCCAAAAAGAACACTCACC	59.574	20
ACTTGAGCGTAACCACGTCC	60.179	20	CTGCCAAAACTTGCACAAAA	59.888	20
CTGCTTAAAGCCCAGTCCAG	60.008	20	TGAAAGTGATTCCCCTTGATT	58.491	21
GGGCATTATTTTAACCCCGT	59.915	20	GGAAATAAGGAGGCGTTATGA	58.213	21
ATTGAATCTACGTCCACGGG	59.813	20	GTTGGACTCAAGTCATGCGA	59.837	20
AACTTAGAGTTTAGAGAGAGGAA	58.346	27	CCCCTTCATTCAACACCAAC	60.21	20
TTCGAAATCCCATCTACCCA	60.266	20	ATGTCTCAGCCGATCGATTT	59.658	20
TGACAACCATCACCTCGAAA	60.088	20	TGTCCGTTGCATGGTGTATT	59.847	20
TCCTGCCATCTCTCAATGTG	59.787	20	AATCGATCCTGGTGCAAATC	59.9	20
ACGGAGGTGTACGATGGAAG	59.989	20	CCGTACTAGCCGACGAACTC	59.898	20

GCCAACACTCCAAAGAAATGA	60.103	21	TCAGTAGCCACCATCTTCCC	60.073	20
TTCCTCCTCAATATTTTCAACACA	59.878	24	GGTGGTTTTGGATGATGGAT	59.464	20
TCAAGCCATGAAACAACACG	60.699	20	CACCTAAAGCCCATGCATTT	59.96	20
GCGTGTGGAAGAGGACAAAA	61.216	20	CCCCTTGAACTCCAGCAATA	60.066	20
CAGCATTCAAATGCGAACAG	60.401	20	CAGTGGCTACCGAGCATTTT	60.27	20
GCACTGCATACGGCTCAATA	59.862	20	TCCCCAAATGAAAGAATGGA	60.244	20
TCCGAAAATCAAAGGCTCAC	60.192	20	GAAAACGCCAAAAATCGTGT	59.982	20
TCTGGAAATGGGGAAAACAG	59.903	20	CGAATTCTCTCTCTGCAAACCT	60.019	22
ATCTTGACCGCTGATTTTGG	60.074	20	GGCGGCAGAGAGAGAGAATA	59.676	20
TCTGTTGTCTCTCCATCCCC	60.048	20	TGTCCGAAAAGGCAAAAATC	60.053	20
TCGGAAGACACCTATTTGCC	60.074	20	TCGATTTCTTAGTGCCGGAT	59.668	20
CCACCATCTCTCATCCCTCT	59.052	20	CACCCCGAACAGAGTCAAAT	59.966	20
GAACGCAAATGCGATATGAA	59.668	20	TGGAGGAAAGAGCTTGAATC	57.047	20
AAACCTTACTGTCACGCGCT	59.943	20	GGCACTCTTGTGTTTAGCCC	59.74	20
TAACCTCCAAATTATCGGCG	59.922	20	GTTAGCCACCAATGAGGCAT	59.962	20
TCTATATACAACTCGCATACCCA	59.051	25	TCTAGTGATGACGGGGAGGT	59.53	20
CATGATTTCAGAATCGTGCG	60.22	20	TTTGTTTTCCAAGCCCCATA	60.294	20
CTGAGCAGACCAGTCCAACA	60.022	20	TCTGGGAACTTGAACTTGGAA	59.697	21
TCTCGTCCCTTTGTGCTTGT	60.833	20	ACGTCTTTGTGTCGAAACCC	60.012	20
AAAGGTATGGGGAAAATGCC	60.02	20	TTCGATAAAACTTTACCAACAC	59.817	24
GCCCCACGTATGATTGTCTT	59.82	20	CGAGCAGAGCTTCCTTCAAC	60.277	20
TTCTCATGTTGTAATTAATGTAGG	59.318	27	GGACGTCTTTCTTGAGCAGC	60.142	20
GCCACTTTCCTTAAACCAAAA	58.286	21	GGTGTTGGTGATATGGACCC	59.91	20
TGTCCTCACTCGTTTCCTCT	57.416	20	ACGACGCAACATGATTTTTG	59.59	20
AGATGTGAACCAAGAACCCG	59.966	20	AGGTAGCGAGAGAGGGGAAA	60.34	20
CCTAACCTTGGGCTCTGATG	59.688	20	CTTTGTGAAGTAGTCGCCCC	59.734	20
GCATCAGAGCCCAAGGTTAG	59.836	20	CAACTTCGGCAACGGAATAC	60.502	20
TGAGGAATCGAACAAGGACA	59.215	20	TGACAATATTTAGTGTTTTGAC	57.78	26
GGAATTTGATCCCCACACAC	60.034	20	GCTCCGGTCTGGAACAATAA	60.074	20
CACCCATCACCTCCATTTTC	60.173	20	GAGGACGTTGTGGTGGTCTT	60.009	20
CTGTATCAAAACGACGTGCC	59.199	20	CTGCACTAACGCCATTCCTT	60.27	20
TTATAAACTGTTACTCCTGGGTGC	58.698	24	AAGGAGGTGTTATGAAGGGAT	58.028	22
TCGAACCATTCACATCCTGA	60.048	20	AAATGGGAAGACAGCGACAC	60.119	20
TGTGCCATAAAAATGGTTCAT	57.885	21	ATGTGGCTTGAGATCGTGTAT	57.152	21
GGTAACCGATGTATGACCCG	60.074	20	TCGACCGAAGAGCTATCCAT	59.797	20
AGCCTTCAATCCTTGCATGT	59.7	20	TTTTATGTAAATTGTCGTGCGT	57.373	22
TGTTGCGCGTGCTTTAAATA	60.401	20	CTGGGTTACACTGAGCGGAT	60.134	20
TATTATGATTCCGGGTTCCG	59.616	20	AGAGACTGCGGTGCAAGACT	60.205	20
CTTGTGCTTCCACCAAATCA	59.691	20	TTCAACCAGGCAAAGACCAC	61.075	20
GCTCTTTTGATCGATCTGCC	59.923	20	CCGGAATAGCATCAGTTGGT	59.955	20
CACGCATGAATTCTGTTGGA	60.665	20	GGCTGTCAGATGATGTAAGTT	59.256	23
AATGCATGGAGGTTTGTCGT	60.384	20	GCATTCGGTTGATTATGCAG	59.14	20
GCATTGAGGTTGCTTGGAAT	60.081	20	GATTGGCTCCATCCTCTTCA	60.158	20
GAAGGAGGAGAAGTTTGGGG	60.045	20	GTTTCCCTTTGGCCTTCATT	60.299	20
GAGAATGAGGGAGGGAGGAG	60.149	20	CTTTCTTCTTCATTTCGCCG	59.953	20
CAAACCATTCAACGGGAACT	59.83	20	TAGGTGTAGGTAGCCAGGGG	59.073	20
TGTTGTGTGGACTCTCCCAG	59.705	20	GCACTATCTCTCCCTCACCG	59.827	20
TCACAAATCGATGGTCTGGA	60.048	20	CAGTGGATTTGGTGGATGTG	59.806	20
CGAGTGCCATTCTGACAGTG	60.463	20	GCCTCAAATCACAAGCCCTA	60.214	20
GAACCAACTCTGTGAGAACCAA	59.232	22	GTTCGCTCGAGAATATCCCA	60.177	20
ATCGTGTTCTTCGCTCACCT	59.874	20	GTCAACTTTGGCAACGGAAT	59.978	20
CTCCTGCTTCCAACTTCGAC	59.989	20	CAAGAGCTGAAGATGTGATTG	60.022	22
CGGAACGCTTAATGCAAAAC	60.619	20	GTTCGAATGGATTTGTTGGG	60.17	20
GCACACCTCGTCTCTCACAA	60.03	20	TCTGCTCCTTCTTCCTCCAA	60.065	20
TCCACGGAGAGGTAAAAAGC	59.312	20	ACGACCCTGTAAGGTTCTTTGA	60.033	22
TATTCCTTTAACCCCCACCC	59.882	20	GCGAAGAAGAGGGGAAGAAT	59.789	20
GCGACTAACAACAAGTGGCA	59.911	20	TTCTACAGCGAATGATGCCC	61.141	20
AAATGCGCAATTTTAAACCCT	59.864	21	AATCATTCCATTCCCCGATT	60.345	20

CCGAAATCTGTAAATCCTAGCCT	60.001	23	AAGGAGGTGTTATGAAGGGAT	58.028	22
CATTAAATGCGCCTACACTTT	57.077	21	ATGTTGGCAAACACAGGTCA	60.008	20
TTTCTCCGATAACCGTGTGG	60.883	20	GGTCGTCGGATTTCATTTTG	60.309	20
TGCCAATGATCACCAAACC	60.322	19	AAAAAGCCCCTACCAAGCTG	60.603	20
TTCAAATGCACGTGTTGGAT	59.972	20	GTTGCTCGGAATTCATGCTT	60.221	20
GCTGATGCACCGAGCTAGTA	59.203	20	TATGCGGATGAGCAGAAATG	59.792	20
GTGCTGAAAGCCCCAATTTA	60.074	20	AAATACGGTCTGTGCATGTTT	57.167	21
GAGTTCTAGCCTCAAGCAACG	59.276	21	TTTGATGGTTATGGTATGGTGG	59.451	22
ATTCATTCTGCCACCTCTGG	60.073	20	TTGATGATGGGGAAGAGACC	59.862	20
CATTCAAGGGGCATTTTTGT	59.801	20	CAAAATAACCAAAATCAGCAT	59.788	24
CTGTCACCATCACCAACCAC	59.846	20	TATAACCCGTGTGTGGGTTT	57.729	20
TCTGTTGGCAAATAGGCACA	60.257	20	CAAGTGTCGAGAGGCAAGTG	59.616	20
TTTCTCTCGATGCACTCTCG	59.267	20	CGTTGTCATAACCCACCTCC	60.232	20
TTCGATGATAACTATGGGTTTGT	57.589	23	TGTGGAACTTGTGTTTGTACCC	59.797	22
TAGGCAAAAACTTCCGTCCA	60.608	20	GCGCAAGTACAACAACATGC	60.333	20
CAATGAAAATGCCACGTCTG	60.111	20	ACTTGTATCACTGGAAGAATTC	57.019	24
GGGGTGGAGAGAAAAAGAGG	60.045	20	CAATTTTCATTGCCCCTCAC	60.309	20
CCACATTTTTCCCGACTGTT	59.83	20	GAGAATGCCCCTGTATGCTT	59.154	20
TCACGCTCCATCTCCTTTCT	59.95	20	GTGGTGTAGCGATGGTGAGA	59.707	20
GGCATTTGTATACCCGTTGG	60.074	20	AGAGCCACGTTAGGCTCAAG	59.639	20
TGCGAACTCAGTGCTACTCG	60.347	20	TCAACAGAGAATGCAAGCAAA	59.6	21
CGAGTGAGAGAGTGAGTGCG	59.915	20	ATAGGGTTCTGAGACCGGGA	60.842	20
TCACACAGCACCTGATCACA	59.858	20	CGAGGTAGGCTTTCGAACAA	60.378	20
TACGATCCGAGTGCCTCTTT	59.836	20	TGATCTTAGTGATTTTTCTTCGT	60.02	25
TTCGAATACCCTAATAACCCGA	59.708	22	GACAACAGTCACGTGGCATC	60.171	20
AGTTTGATGAGGGCATCCAC	59.934	20	GTGTCAGCGTGTCTCTCACG	60.685	20
CCACAAAGATCTCGCACAGA	59.984	20	TGGTTCATGCCATTGTGAAT	59.781	20
TTGTTTTGTCCACACTTGGC	59.591	20	GAAATTTCACGAAACAACGAA	57.795	21
TTGTTTGGTTAAGACGGTTGC	60.025	21	TCTTCCAAGATGGGAATGGA	60.395	20
GTGGACGTCCCAGATTGTTT	59.827	20	ACCGTCTGGTCATCCCTTTT	60.746	20
CGCGAACTTAGATGGGCTAC	59.867	20	TTTCTCTCTTGGTTGGTGAAGA	58.955	22
CGAAAACTCAATTTAAAAGGCTT	60.47	24	TGAACCCTCTGAAACCTCGT	59.697	20
ACACTTGTCAAAATCTCCTTAATT	59.109	26	GCTCGAGCTCAGACATCAAGA	60.839	21
GCTCATCGTCATTCTCCACC	60.633	20	TTCCAAGCTTTAATTGCGGA	60.691	20
GGGGTCTTCTTTTGGGACTC	59.912	20	TATCCCGTGGGTCAAATACG	60.576	20
ATAAGCTGAAGATGGGGCCT	60.06	20	TGGATGCGAAACATGAAAAA	60.051	20
CACGCTATCTCGTTGCTCTC	58.777	20	TTTCACCACCGCCTTAATTC	59.938	20
AGGACAAGGGCAATCGTATG	59.955	20	TTGATATCCCCATCCTCCAA	60.088	20
TTTTGCGGTGTGCATTTAGA	60.251	20	CCTTTCAGGCATTTAAGTGGA	60.122	22
CCCAATCTCTAGTTGCAGGC	59.836	20	GGTTTCAAAGGGAGGGAGAC	59.912	20
ATCATGCACAAAATAAAAAGGGA	59.741	23	TCAGTTTCTGAGTTTTGAGGTT	59.835	24
TCTCACACACGTTTACACCCA	60.057	21	GTCTAAGCTTGTTAACCCCCG	60.008	21
CAAATTTCAGCCCAAAAAGC	59.699	20	TTTTCGACCAATAGGAACGG	59.931	20
TCGCACCCTCTGTTCTCTCT	60.135	20	GAGATGTGGTGGTGGTGATG	59.801	20
TAGCCATGTAGGTGCCTGTG	59.74	20	AAAGTCCAAATGTTGGCGAG	60.11	20
CCGTCCTCTCCATCACTCTC	59.792	20	TAAATCACAAAACCCACGCA	59.969	20
AAGACCAGTTTTTCAGGGGG	60.332	20	CCCAGCAACTGTTGGCTACT	60.312	20
TCGGATCGGATACCCAAATA	60.11	20	TTTTAGTAGGGTTTTCAAGTTC	58.424	25
TTTCCACGGAAGGAACTGAC	60.088	20	CATGCTTGAATGAAAACCACA	59.576	21
GGTCTGACAGGTTCAGAGGC	59.841	20	TTGTAGGGGCAATGATGTAAA	59.363	22
TCCTCTTTCAGGTCCAGGTG	60.229	20	CAGCCCAATAACTCAACCTAC	59.892	22
CCTTCTCCATCACCACCTTG	60.501	20	GGTAAATGGTTACCGGTTTGG	60.33	21
CTTGTCCACCCACCACTTCT	60.002	20	TCCACTGTCTTGTGCCTCAG	60.022	20
CCGGTCTAAACCCGGAATA	59.764	19	GAGCCGGAGTGAGATGATGT	60.231	20
AACACAAACGCTAAACCCGT	59.54	20	AAGAGTGGGAAAGAAAGGGC	59.691	20
TTGTAGTCATCCATGGGGGT	60.05	20	CTTTGAATTGCAGCTCGACA	60.134	20
TTTGAGATCCATTCCCTCAA	58.06	20	TTTCTTGTGTGTGTGCATGTG	59.203	21
GGGTTATCACCTGATTTTCTCC	58.826	22	TACGAATCTCAAGGGGCAAC	60.074	20

TGCCGAAGATTTACTCCTAATTAA	59.188	25	CGTAGTTTGTGGGGGAAATAA	60.102	22
GTGGCTAGATGCAAGCCTTT	59.481	20	TATGCAGATTGGTGTGTGGC	60.549	20
CAAATCTTCGAGTACAGAAATGG	59.667	24	CGTGCTGAGCTTATTCACCA	60.011	20
AGCAGCTGATGCACATATTCC	60.258	21	TGCGCAACCAATGTAATAGC	59.731	20
CTTCACTTGAATTGAGGGGG	59.521	20	TCGTGTCCGGTTTGTGTATT	58.9	20
GCCTGTTTTAGCGTTCTTCG	60.018	20	CACATTGTCACCCTCACCAC	59.846	20
ATGCGCGTTTTTAGGGTTTA	59.624	20	CTCGAAGGTGACTATCCCGA	60.21	20
GCTGAGCATTTTTAGCACCC	59.851	20	GCAGCATCCTTCACCATTTT	60.081	20
TTTTGTGAAACAATAATGACTTTG	57.874	25	TTTGCAGTAGGGTTGGAGATG	60.118	21
TTCCAGCTAATCTGGTCCGT	59.694	20	TGAAACAACATGGTCCGCTA	60.111	20
CCACTCTCTCACACGCAGAA	60.178	20	AAGACGACGCCCCTTTTAAT	59.966	20
GGCAAAAGGCAGCCTAAAG	59.967	19	CGTTTTGATGATATATAGGTGT	59.637	27
TTATGGGAAGAGGGGGAGAC	60.264	20	ACCCTTAATCTTTGTGGTTGTG	59.791	23
GTGGCATCGTGAGGAGTGTT	61.146	20	TTTGAGTTTGCATCTAAGAAGG	59.828	24
CACGCCCTACAAAACAATGA	59.585	20	TTTGGTTTTATCGAAGAGGCA	59.707	21
TTGGTGCATGCCTTTTGTTA	60.111	20	CCACCCCTAAGTGGATGAGA	59.92	20
AGCAACACTTGTCCCACGTT	60.611	20	CAGGAGCACTACAGTTCACGA	59.097	21
GAAAATCAAAAGGCCCACAA	59.916	20	CGGCCAAGATTTGTTAGAGG	59.702	20
CAACACACATCCTTCATGCAC	60.024	21	CATTCGGTTGAACCCTCAGT	59.966	20
TGATGGTGTTCCCCTTGTTT	60.21	20	GGATTGATGAATTTCCATTCG	59.221	21
CTGTGCATTCCACATTTCCA	60.517	20	CCATCATTCCAATTCAAGGAA	59.748	21
TCCCAGGTGTGAATAGCATTT	59.443	21	TTGACCAAGATACACCTTGCAT	59.499	22
AACCTTTGTTAGCCCGTTGA	59.609	20	GCTCTTTTATTTACCTTTTATGC	60.067	26
AGCGGTTATTACCGGATCG	59.93	19	ATGACGGTTGTGGGACTGTT	60.284	20
TGCCGTCCTTTCAATCTCTT	59.813	20	GAGAAATTTCGATGTTTCCACA	59.067	22
TGAATCTGGGGAGAGAGACG	60.34	20	TATGTTTCGGCCCGGTATTA	60.165	20
TGGGCAAACCAAGATACACA	59.964	20	GGTTCAATTTGGACGTTTGG	60.206	20
TCCTTAAACATAACGAGATCAAA	58.388	25	ATGAATCTCATGTTATTGAGTG	57.225	25
TTTTTACCAATTTGCCCTCG	59.937	20	CGTTTGCCATCCATCTCAAT	60.864	20
CTCTTTCTCTCTCCGCCCTT	60.088	20	AAATCTCCCTCGTTCGTCAA	59.67	20
ACAAATCCACCAGAAACCCA	60.21	20	CTTGTGAACTCCGATGGACA	59.676	20
ATCTCTTTTCCCCCACGAGT	59.935	20	TGAAGAGGCAATGCAATCTG	59.948	20
ATTACGGCCACGCTAAGTTG	60.152	20	GTAGAAGCGTCGGAGGAATG	59.836	20
CCCTCTCATTCAACACCCC	60.31	19	TCGGCAGAAAAGAAGAAGGA	60.066	20
ACCTACTGCCGTGTTCGATT	59.621	20	ATGGCCCAGATTTGTTTTGA	60.309	20
TTCATGAATGGATGTGTTTTGTT	59.238	23	GGCGAACATGATGAATGAAC	58.929	20
TTGACAATATTTAGTGTTTTGACAT	58.99	27	GAGAGAAGTAGCAAGCGCGA	60.955	20
ATTTGCTTGATCCAACGGTC	59.939	20	ACGAGCTCATTATTCTCCGC	59.439	20
ACCCTTCATTGTCATTCTCATT	57.52	22	ACACACAAGCCTCGCTCTTT	60.058	20
TGACCATTTTGCAACTCTCCT	59.726	21	AAACCGTTCAAGAAAAGGGA	58.669	20
TGGCCGTGAATGTATGAGAG	59.673	20	CGTGCGTAGGAGAGAAGAGG	60.149	20
AATGAAGAAAATAGGACTAATGA	59.438	27	CTTGTGGCTTGCAAACATCT	58.926	20
ATCGTGAGAAGCGTCGATCT	59.981	20	ATGCAGTGGGTTTTGAATGG	60.755	20
GCTTGCTCAGCTTCTCGTTT	59.904	20	GCATTTGAAAGGTTTTATATGA	60.438	27
TTTTCGGATCGGTAGAAGGA	59.64	20	ACTTACGGAATTCCACTGGG	58.909	20
CCAAATGCATGCAGCTTCTA	59.976	20	ACGTAACCTTGGTGTAGCCG	60.052	20
GCCAAATGTTGGATGAGCTT	60.081	20	ATGTATGGCAGGTGACCCAT	60.081	20
TTGGAAGCCATGCAAAATAA	59.146	20	AGTTGTCAATGGAGGTTGGG	59.82	20
AATTGGACACAGAATGCGCT	60.667	20	AGAGCGAAGAAAGCAGATGG	59.717	20
TTTCTTTTGTGACGCAATCG	59.849	20	ATGTGGAGCAACGTGAACAA	60.16	20
CATAGTGGAGGGATGTGGCT	59.95	20	AAAATTCTGGCATGCCTCTG	60.214	20
ACAAATGGCCAAGAGAGTTTACA	60.048	23	GCATTAAATGAGCCTCCCAC	59.533	20
TCAAAGATGGAGGTTGGAGG	60.042	20	ATGCTGGTAGAGGCAACGAT	59.723	20
AAACTTGTCTCACGCGGGTA	60.689	20	TGATACAGGTGTTCCAAACAAT	59.777	23
CGTTCGATTTGCCGTTTTAT	59.964	20	TCTGTTTCCAGTCGTCTCCA	59.388	20
CTCTCCTAGGGATGAGTCCG	58.84	20	GATGAAGCAACGAGGGTTGT	60.119	20
AAATCAGACGGGCAGTTGAG	60.255	20	AAATTCCGTTTTTGCCTTCC	60.292	20
TTAGGGTTTAAAATCGCGCA	60.564	20	CGGCAACCCTGATACTTAGC	59.73	20

GAGGACACTTGGACCTGAAAA	59.173	21	TAGTCGGGCAACTGGAGCTA	60.924	20
TCCTCGCAGGAGTTCAGAAT	59.95	20	TGCCACCCTAGATCCGTTAC	59.955	20
CCGTGATTTAAGGAGTCGGT	59.052	20	AAACAAAAATATAGCTAATGC	59.231	25
AGCTGTTAGGGTTGTATAGTGAG	57.436	27	TTGACGAGTCCATTGTGCAT	60.12	20
GTGATGTGGTGTTGGAACATT	58.172	21	GGGAGAGGATCAAGAGAGGA	59.763	21
TCACCAAGTCCAGCCTTCTT	59.844	20	GATGTATCGCCCAAAGGAGA	60.036	20
CTCACGTGGAGGATCGTTTT	60.111	20	CTGCCTTCCAACCATACACA	59.566	20
GAGTGTCGGTCTGAAGGTCC	59.688	20	AATGGGACTGGCGATTGTAG	59.955	20
GTTTTGTGAGAGGCGAGAGG	59.989	20	ACCGGTTGGACTGGTTGTAA	60.269	20
GCAAGCTTCTCTAACACGGC	60.162	20	TCCTACACTTCCTGCCAAGC	60.397	20
AAGCTCTTTTCGTGTCCCAA	59.853	20	TGGCAACAAATATGACTGCAT	59.055	21
TCTACCTGTTGCTGTGTGCC	59.905	20	TGCATGTGCATGGAAATTAGA	60.088	21
TCCTGTAATGCTATCTCAATGTTG	59.135	25	TCTTTGAATTCAGCACGCTA	57.257	20
CCAAATCATTGTATTTCATGTTTC	60	25	TTTGATGATATATAGGTGTTTT	57.624	26
ACACCAAATTTCATCATTTTCAA	58.397	23	GATGGTGGGTCTGAACGAAT	59.786	20
AGCTTTATGCGTTTGCAGGT	59.911	20	TCTTCAAGAATTCCGCCATC	60.155	20
TCAACATGCAACCAACAAAAA	59.999	21	CCCATTTCTAACTACCCAAATC	59.962	23
CATTATTATCAACGGCTGCAA	58.712	21	GGTTTGATGACGTGGCTTCT	60.119	20
TGCCAGTTGCCATATTTTCA	60.073	20	AAACAAAGCCTGTTTCCAGC	59.359	20
TGAGAGGAAGAAAGAAGATGGA	58.121	22	CCCACCCCACTACTCAAGAA	59.959	20
TCTAAAGAAAACAAAAGAAGTTC	57.236	26	GCTTTCCCATTTTGCTTTTTA	58.427	21
TGGAGCAACAAAGATGGAAA	59.247	20	TTGTGATTTGGTGTGTGTATGG	60.067	23
TAACAAAGAAAGGCGGATCG	60.202	20	AACGGCTTGGATTCTTTCCT	60.074	20
ATCCCTTTTGCTTTTGCTGA	59.823	20	GACGATATCCCTTGCACGAC	60.492	20
CCTTGCTCTCTTGCCTTGAC	60.134	20	TAGCCCATTATCTCCCACCA	60.288	20
AACGCAAGATGGGAAAAATG	59.938	20	GCCTCTGCTATTACATGCCA	58.897	20
CAAGCAGGTAAATATCAGTTTTC	59.271	24	ACATCGGCAGTGACTTTGTG	59.751	20
GGATCCCAAATCACCAACAA	60.56	20	TTGTGGCAGGTTATTCATGC	59.548	20
CCACCAACTCCGGTAAAGAA	59.964	20	TCCGCAATTCGTCTATCGTT	60.606	20
TAACCGACCACGACACCATA	59.84	20	CGGCTTCACCAGTTTCTTTT	59.355	20
GGTTATCACCGGATCACGAC	60.203	20	AGATGGTGGGTGAGATTTGG	59.779	20
GGCGGTAGGAGTTGATGATG	60.483	20	CACACGTTCTTCCCCAGATT	59.966	20
CGGAATGTGATCGAATAGCA	59.646	20	TCACCTGCGATATTCAACGA	60.22	20
GATTTGCCCTTTTTGCCAT	59.893	19	GATGATTGCACCATAATGCG	59.921	20
TGTCGAATGCAGGGTTGATA	60.073	20	CCGAGATTGTTGGGGTCTAA	59.926	20
CAAGAAACGCGCCATGTAT	59.703	19	CATCCATCTGAGCATTGGAA	59.604	20
TCAGGAAGATCATCTGCGG	59.884	19	CGTTCTGAGCTGCCTTTCTT	59.757	20
AGCAGCAATTTCCGAAAAGA	59.96	20	AGGGTCCCACCACCTAACAT	60.489	20
AACACTGCACGCATTTTGAG	59.911	20	AAATCACGTAACAAATTTCATT	58.93	25
GGAGACGGAGAAATCAGACG	59.803	20	AGATGCTGGAATCTTCGTGG	60.218	20
TCCAGTGTCTCCATCTCGTG	59.82	20	GTTGGCATTGCAGGCTAACT	60.278	20
CCACATTCTTGCTTCTGCTG	59.591	20	TCCATTAAGAATTTCCCATGC	58.888	21
CAACAAAGCAACAAAACATTGAA	60.062	23	CAGTGCGGACGGTTAAGATT	60.132	20
TGAGCATGTGGAGAGCAAAG	60.136	20	GAAGCTGGTGCAATTGTTTG	59.322	20
TTTTGAATGGCACAGATTGG	59.518	20	CTTTAATTTCTTGGTGGCGG	59.581	20
GAGAGATGCTGGTAGAGGCG	60.119	20	TGACGATGAGACGTGTAGGG	59.701	20
CCATAAACACCGTGTCCAAA	59.293	20	ACTTTCTTCACTACTGGAACTT	58.132	26
TTTGGCATCAATGCATCCTA	60.035	20	TAAGAACTCTGGCTCCAAGG	57.147	20
AGAAAATGGTGCACAAACCC	59.836	20	TCATGCACGTGTTTCACAAA	59.721	20
AACACATCGGCACAGGTACA	60.032	20	AAAAATCTCAGGGACGGGAC	60.306	20
GCAGCTGTCACGCACTTTTA	60.203	20	GTTTGCTTCCACGGCTAAAC	59.752	20
GAGGATGCAGACGAACCAGT	60.269	20	GTGTCGATTGTGTTCATGCC	59.975	20
TAAGCCTTGTAGTCGCGGAT	59.867	20	ATACTTTGGCCCAGTTCGTG	59.993	20
TGTGCTGTCCACAACCTGAT	60.162	20	TCGAGTGTTCGTTAGTTAGTGA	59.876	24
CCTCTCGCATTTCTCTTGCT	59.717	20	TTGTTCTTGTCCCACAGACG	59.72	20
ACCCAAAGTGCCCTTTTATG	58.949	20	ATTTCGAAGATCAACGGACG	60.074	20
GCCTTAAACTCGCGTATTGG	59.742	20	CCCATCGATTGAAACAAACA	59.371	20
GGATCTACGAGATTTGCTCCC	60.053	21	TTCGTTCTTAATTAGCGCCG	60.347	20

TGAAGCGTGAAAGTCAATCG	59.988	20	AGCGTCGATCTGGTGAAATC	60.226	20
TTGAAATTATACGAAGCCGGA	59.573	21	GCGATCGAGAGAGAGAGGTG	60.246	20
GATGCAGTGGGGTTTTGTTC	60.362	20	CCAAACAACGATCGACAATG	59.964	20
TCAAACGATTCCCAAAATGG	60.671	20	TGACGTTAAGAGAGTTTTCACT	59.855	24
ATTGCCACCCTTATCCACTG	59.813	20	TTTGGCAAGGGTTTGAAAAG	60.081	20
TTCCCTTCTCATTTCCATGC	60.014	20	AATTCCGAGGAATCGAGTGA	59.629	20
AAGGCAACATCTATCGAGGG	59.15	20	GAACGGGGATTTGTCAACTG	60.353	20
AGTACTGCAATTCTGCCCGT	59.763	20	CTTCCTCACACATTCAGCCC	60.656	20
GGTGGTTGGAGATCTTTGGA	59.903	20	ACCAACGTCCCTCATCTACG	59.989	20
TGGGTTTTAGGTGTCATTGC	58.476	20	GCAAACGGTATAGGATCGGA	59.923	20
CCGGATTTGGAGAAATCAAA	59.872	20	TGGCTCTCACACTCACTCTCA	59.747	21
AGCAGCGAAGGAAAAACTTG	59.632	20	TGGAGTTCGGCTTAATGGTC	60.074	20
TCTCCGACCACATTCCTCTC	60.199	20	TTGCAGAAGTCGAAATGGTG	59.84	20
CAACCAATGAGGCTCAGACA	59.831	20	AACACGTGGAGATGACACCA	60.005	20
TGGAACCATGTTCAATCCCT	60.173	20	TGGCTCCATTTGTAAATCACC	59.815	21
ACAAGGCAGTACCCGTGAAG	60.171	20	TCACACAGATTAAACACTGAA	60.128	26
AGCCCACCTGATTTTCTTCA	59.67	20	TGGAAATTTCGACACGCTTT	60.617	20
CGAAGTATGACTCGCCACCT	60.277	20	CGCGAAGTACCTGCGTTAT	58.956	19
AAGGGTTGGTATCATTTGAACA	58.353	22	CTGCTGGACCTCCACAACTT	60.298	20
ACCGGGTATCGGAAATTAGG	60.034	20	GGGGGAAAAAGAAAGGTTGA	60.271	20
GTGAAACCCCCAATTGTGTC	60.073	20	GAATCAATCACGTTTCGCAT	58.575	20
TGCGTTTAAACAACCCAAAA	59.094	20	TTTGGAGATGGTGATGGTGA	59.893	20
TTATTTTTCTCAAATGCTATGCAA	58.109	24	TAGTCTTTCTCCCGTGCGTT	59.875	20
TTTCAGCAATTCGAAGGTCC	60.192	20	CAGCAAGAAAAATACACCAGC	60.298	22
TGGGAGAATTTGTGGGAGAA	60.43	20	CCTTGGCCTTCTGACATCAT	60.073	20
TCTAAGCTTGTTAACCCCCG	59.221	20	TGACACTCACGCACACACAC	60.437	20
AGCATAACAGCTGGCAAACA	59.493	20	TAAAAAGGACCGTACCTGCG	60.124	20
GGTTCCGGTCATCTTAGTCG	59.55	20	AGCCCGAGCCTAAGCATATT	60.211	20
CAGATTACTGTGTGCGGCTG	60.472	20	CCCCCTTAACTACCACTTATGA	58.515	23
CAACTTCCGAATTCCAATTACC	59.716	22	AAATCCCGTTCTGGGAAACT	59.805	20
TGAGCTCATTCCGCATTAAA	59.401	20	GAGGGATTTGGGACGATTTT	60.131	20
CTTGCCCCTTCACTCTCATC	59.803	20	TTAGAAACGGAGGTTGGGTG	59.964	20
TGGAGTTGTCAGTTCCTTCCA	60.674	21	TGAGCCTATCTTGGAGCACA	59.547	20
TTGACCAAGGTGAGAATTTGAA	59.587	22	CTCTTCCCTCTCATCTCTCTCG	59.717	22
CTTTTTCCTATGTGTGACAAAGC	58.003	23	GTTCGGCGTTAGGAGAAATG	59.708	20
AGCATTTACCTGGGCATTTG	59.96	20	CCTCGCACATTTCATTTCCT	60.074	20
TGCTCCGAAACATGAAAAATC	60.067	21	ACGTTAAGGAGGGGATCCAT	59.651	20
GATCATGCTGGAAGCACGTA	59.83	20	CGTCCACGGAGAGGTTAGAG	59.861	20
CGCACTGATCCAACTTTTCA	59.84	20	TTACGAGCGCATAGCCTTTT	60.006	20
CCCTAAGTTTGCATCTCCCA	60.066	20	GACCTTAGTTGCGAAGACGG	59.875	20
CTCCACCCTCTCACTTCCAC	59.682	20	GGTTTCTTACTCGGGCTCCT	59.713	20
AAAATGTCGCCGAAAATCAG	60.074	20	GAAAAATCAAAGGCCCACAA	59.916	20
TGCTCCAGTAGGTTCCCAAC	60.111	20	GAGTTTATCAGCGGTCTCGC	59.985	20
TTCTGTCCCGTTTTCTTCGT	59.711	20	GGCTTTCTTAACTTGTTGGAAC	60.376	23
ATGTGGAGAAAGCTCTGCGT	60.02	20	CGTGATCGCTGCAACTCTAA	60.157	20
ATCGATGGCCAAGATTGCT	60.585	19	ATTCGGGAGATGTTCCAGTG	59.927	20
TCCTTTTCTTTTTCTGAGCACC	59.871	22	CATTGGGGACAATGTTGGTT	60.474	20
CATGCTGTGCAGCAGTAGGT	60.08	20	CATAATGTCCCCGTTGAACC	60.051	20
CTACCGGACCTTGGTCTGAA	60.103	20	TTTTCCTGGAACGTGAAAATC	59.054	21
TTTCCTACCAAATCTCCCCA	59.359	20	TGTACCTAAAAAGTTGTTCCCA	58.258	24
TGGATCTCGGAATATCCAGC	59.998	20	ACCACTCCCACCCATACAAA	60.088	20
CCGATTGACATCCCTACCTG	60.331	20	CGTCACAGCCTCTTCAACAA	60.025	20
CCAAGAAAACTATCGGCAGC	59.845	20	CTTGTTCCGGTAGGTAGCCA	60.125	20
ACGCAGACAACACACACACA	59.818	20	TGAGCCCGTAAATCACACAA	60.111	20
ACGTGAATGCCAAAGCTACC	60.14	20	TTCTTCCACGTCCTCTAGGTG	59.338	21
TGAATGAAGGGATTTCACCA	58.897	20	TCTCTCACGCACTCTCACAAA	59.76	21
GCGAAGCACCGAGACTACTG	61.136	20	TCGTCGTTCATTGCAGTTTT	59.322	20
GTCAAATCGCCTGAGAAGGA	60.34	20	AAGGAGGTGTTATGAAGGGAT	58.028	22

AATGCACTGACTTGGCATGA	60.272	20	TCTCGAAAATTGAATGACAAG	59.202	22
TTCCCCCTTTCAAAGAACAA	59.518	20	TTTGTCACATGCATTCCAGC	60.675	20
TTGGCCTAAAATCCCAACAC	59.801	20	TTTCTCATTGGCAGTCACCA	60.24	20
CGAACTCAATTTGATCCGAAA	60.06	21	TGATTCCTCCTCACTTGCCT	59.803	20
CCACTTTGGTGACTAACGCA	59.758	20	TTGAATTCGGACATGAGCAA	60.197	20
TATTTCCGGTTCAAACTCCG	59.931	20	TGTTTTCTTCCCCACACACA	59.976	20
TTACCCAACCCACTAACCCA	60.081	20	CTTGGAGCTTTGATCCTTGC	59.955	20
ACACACGAGCAAGCAAATGA	60.459	20	GGGGGCATTTTGCACTATTA	59.795	20
TATCCCGTTTCTTTGTTCCG	59.931	20	TGCCATCTCCTCATCACTTG	59.787	20
CGAATCCGTTTTCCAACAGT	59.971	20	CAAATTCAAGAATGCTGCCC	60.585	20
TGATTCAAAGGCTGATAATGGTT	59.857	23	TCACTGGAATGCTATGGTGC	59.679	20
TGTGATCGACGATTGGAAAG	59.648	20	ACGGATTTAAGGGTTATTACCT	57.667	23
GGAAATTATTGGGAGGGAATG	59.499	21	TTGCGCATAAATATTGGTTTCTT	59.89	23
CACGCACAAAGAAGATCTCTACA	59.571	23	GTATGCTCCTGGGTTGGAAA	59.933	20
CATTGTTTTCCTCTCCCCAA	59.903	20	TTAGTTATATGTATGGGGATGG	57.868	27
TTCAGCCTGTATGTTGGGGT	60.375	20	TCTTTTTCCTGAACGATGAGC	59.443	21
TTTCCTCCCAGCTTCTACCA	59.807	20	TTTCTTTCCTTTGAGCATACGAT	59.302	23
TCCCACTTTGTCTCCCAATC	59.903	20	CGCTGCTCTAACACAAACGA	60.195	20
CAGGAGAACTCGGCTGAATC	59.95	20	CCAGGCAAATAGCTACCGAG	59.861	20
CATTCAGTGAAAACATGGCG	60.111	20	GGAGTGATGAGAGAGGAGCG	60.096	20
TCTCACTAATGGGCCAAAGG	60.066	20	ACTCGGAGGTGAAGGTGAGA	59.835	20
AAGTTCGAATTCTCCCCACC	60.306	20	AGGATCTTAATTGGTTCGATTTT	59.762	24
TTGTTGTTTCACAAAATTTAAGCT	59.653	25	ATTTATGGTGGCTGCGGTTA	60.343	20
TGCTATGGACGAAATTGGTG	59.542	20	GCACATTGATATCGTGTCCAA	59.415	21
CACGTGCGTCAACTCCTTTA	59.904	20	CCTATGGTTGTATGGTTTGGA	57.354	21
AACAATTACAATGTTTATCCAATC	59.207	27	CCATCCATTTGCAACCATAA	59.232	20
TTCACGTACCCCTCATGTCA	59.96	20	CTGCAACTGGACCGAAAAAT	60.11	20
GATCCAGTTCAAGTGCCCAT	59.934	20	GTTGTTCAAAATTCGTCCAAAA	59.01	22
AATGCATGCACCTGATTACAA	59.055	21	CGGGGCGTGACATTAGTTAT	59.845	20
ACGCAACAGCTCATGACAAG	60.056	20	GAAGAGGTTATCCCTCGTCCA	60.449	21
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TCAACTGCATTGTTTCCCAG	59.691	20	CATTCGAACATCATCATCCG	59.883	20
TGATCTTACGCGCACATCTT	59.449	20	TTCCTTGGACCAAAATAGCCT	59.952	21
GGAAGAGACCAGAAGTCCCC	60.05	20	ATTGATCGCATTCAGGGAAA	60.414	20
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CCCCAAATGAGGAACTTTGA	59.903	20	CCATCCCACCAGCATTTAGT	59.813	20
CACACATGCGTTCATTCACA	60.164	20	GTTAAGGGCCATCAGGGATT	60.152	20
TAAAACCATGCACGTAGGCA	60.133	20	AACGAAGGTACGGTAAGCGA	59.769	20
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TCAATAAACCCTCCGAATGC	59.901	20	TAAATTGCTCCGTCTCCAGC	60.352	20
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TCGGAATTTTACGTGGTTTG	58.531	20	GGGTTGCCAGGTTGAATAAA	59.801	20
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TAGTGGGCTTTGGCACAAGT	60.689	20	TTTCTCCCAACGTAGCCAAC	60.11	20
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TCAAAAATCCAAGGGTGGAG	59.903	20	GGAAGGATGAAAGGGGGTAG	59.761	20
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CAGAAATGGCATTGGTTGTTC	60.359	21	ATTGAGTTTGGGAGAAGCGA	59.813	20
CGCATGATGTAACGTGAAGG	60.134	20	CCCAGAGAGCATACTTCCGA	60.353	20
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TCACATCCTCAGCACAAACC	59.682	20	TTGGTGAGGTGAGGTGAAAA	59.109	20
CATGGACTTTTGACGAGCCT	60.255	20	CGGTTTGTTTTCGTGTTTGA	59.603	20
CAGAATTAGCCTTACCAAGATGG	59.194	23	TACGCATCAAGACAACTCCG	59.864	20
ACAAGATCAACGCTCCTCGT	59.874	20	GAGCGAGGAGAGGAGAGACA	59.817	20

AAGAGTTATCACCGGATCGC	59.154	20	AAACCGGAAAAGTGGAAGAA	59.967	21
GGATGCAAGGTGAACTTGGT	59.973	20	GGTGGGCTTAGTTGAGGTGT	59.065	20
AGAAGAAGCAGAGACCGACG	59.745	20	TTCAATCAAACCAACGAAACA	59.048	21
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GCTCGACCTCGTGAGCTACT	59.775	20	TTCTCAGCATATGGGAAGGG	60.029	20
GCGGATTATCACATTGAGGAG	59.542	21	CACATTCTGAGGATGGAAATC	59.933	22
GAAAATACCCTTCGCATCCA	59.901	20	TGGCAGTAGATTCATTCTATCT	58.871	26
CGCCGGACTATTCTCTGAAG	59.971	20	GCTCCCAAGTTGTGAAGCTC	59.997	20
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ACCTGCTCTTATATCCATTTTAATT	57.552	26	CACAACTCCACCTGACATAAT	59.906	23
CCCGGACTATCGAATCAACT	59.006	20	GATTATGGCATACGTGTGGG	58.723	20
AAAGATTACTCATGTGATATTGC	57.463	24	CCATTATGTCGATATCCATCCA	59.507	22
TCCGGTCCAATTCCAATAAG	59.756	20	CCTATGGTTGTATGGTGTGGA	58.215	21
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TTTTCGTACACAATTCGAGGAA	59.625	22	GAAAAGCAAGGAAAAAGCCA	59.451	20
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TACGTGATCGGACACGAGAA	60.263	20	AATTTGTGTGGCCATTTGGT	60.096	20
ATCCTCCTTGCTTCCTCCAT	60.037	20	GAAGCAAATTCCAAGATGACG	59.699	21
TTCAATCATGGAATCGTTCG	59.474	20	CAACCCTACCTCCTTCTCCC	59.928	20
TCGTCAAAATGCAAGACGTG	60.844	20	ACGTGGCCTTTGATGGTAAA	60.365	20
AAATCAAACCTCAACCCGTC	58.886	20	AACACTATCACAAGGTTCCGA	60.047	23
GGTAGAGGAGCTGATGTGGC	59.834	20	TCCCCATTGTTCTACCCAAA	60.162	20
CCCCTTACTGCTAACACCGA	60.125	20	ACCTTCTTGGGATGTAGGGG	60.183	20
CAGTTTTGCAAGGATTGAGAGA	59.494	22	ATGTTGTGAAGCACATGGGA	59.967	20
GTGGTGGGAAACAAGAACCT	58.891	20	CAAATCCCTCTTTTCTTATTCTC	58.05	24
CGCTAAGGAGAGGCAAAATG	59.975	20	TCTCCATTCCACCATCATCA	59.85	20
TGCAGATGCTCTCCACTTTG	60.136	20	TGCATTTATCAGCTTTATCAGC	59.895	23
GCAAATGCTCCTGCACTTCT	60.547	20	GCCAAATTAAAGACCATATTTT	59.68	25
TTCATGTGTCAATTCCTGGG	59.343	20	TGCATCCATGATATGGCG	59.988	18
CACCAATTCCATCAGCCTCT	60.073	20	TCTGTAAACCGACCTCCCAC	59.966	20
TCGGTTGCAAGTTTGGAAAA	61.528	20	ATAGGCTCCCCCGATCATAA	60.623	20
TTACTAAAATACCCCCGCGA	59.45	20	GGGAGAAAAGGGGAAATAAG	60.173	22
TAGTTGGGCTTAATGGGGTG	59.817	20	GATGAACTCTCTTGGGTGGG	59.505	20
AAACGAAGGAGACGATCGAA	59.813	20	CTCTCATTCCGGTGTGGATT	59.927	20
TTGATTTTAAGAGGTGATATGATA	59.397	27	TCTCATTTCCCAAATGTCGTT	59.42	21
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GTTTTTGTACATCGGCGGAG	60.502	20	ATGGTGACGAGAGAGCGAGT	60.017	20
ACAAATGGCCAAGAGAGAGTT	57.922	21	TTCTTCGCATGCTTATTTGG	58.912	20
AGGAGGTGCGGTGTTAGAGA	59.867	20	ATAAAAATGGCAGACGGCAG	60.096	20
TTATCAAGCCCACCGTAAGTG	60.004	21	AACCGGGATAAAATAGGGCA	60.508	20
AACGAAAAGAGAAAGAGGGC	57.668	20	ATTATCATATTTAAGGGTTATC	57.31	27
TGAATTCATGTACACATTTGGAA	57.94	23	TTTCACTCTTCACGTTTGCACT	59.958	22
CCCTGGATATACGGTCGAGA	59.91	20	AAAACCCTAAACAACCAGTGA	57.717	22
TGCGTTTTGACAAGATTTGC	59.856	20	CACGTCTCCCCAAACCTAGA	60.103	20
TCGGAAGAAACAAACTAGAAAG	58.674	24	AACAATACAATCCCGTGCAA	58.895	20
GCGATGAAATGTACGTTAGAGA	57.104	22	TTGCAAAAGTCACACTCTGTC	59.534	22
CAGCCCCTTTCAATTTTCTG	59.679	20	TCTCCTACAACAACCCTCGG	60.103	20
GGAGGGATGATGAAGATGGA	59.821	20	AGACCCAACTACCAAACCCA	59.304	20
GCACCAGATGTCGTGGATTT	60.935	20	CACGTTGGGAGCACACTCTA	59.897	20
TGAATGGATTTTTGGCATGT	58.82	20	TTGTCCGTTTATTTTTCACACG	59.904	22
TGTTTTATTAACCTCAATTGTGAA	57.051	25	CCTTGCAACGGATCTGATTT	60.074	20
GTTGAAGATGGGAAACCCCT	60.169	20	GAATCGCAGAACCGATGATT	60.043	20
CCGAAATTTTACGTGGTTCG	60.348	20	CCTTATTGTTGGGTGTGGGA	60.605	20
GATGCATGCACGTGAATAAGA	59.709	21	AGATCTAAGGGCCGAGATTTG	59.696	21
TAGGGTTTCAAAACATCGCC	59.938	20	ACGGCTCAGAATGGAGAAAA	59.813	20
CTCTTTCGGGTTCTCAACCA	60.224	20	GTGGTACTTGCACGCACATT	59.646	20
GCGATTCTTCCGTATGCTGT	60.243	20	TAACATGTAGTCATGCGGGC	59.572	20
ATGGTGGTTTGGTGGAAGAA	60.21	20	TGTGAGGTGAAGTGTGGAGTG	59.766	21

TTTGCATACTGCATGGGCTA	60.237	20	GCTACGAGCCACAGCTACAG	58.854	20
GGCAACGGAATACCATTTGT	59.691	20	TCGATCCTGTGTGTGCATTT	60.12	20
AAACACAGCTACCAAAGCCG	60.305	20	TCCATTTATCGGAGTTACGGTT	59.737	22
GCTTAAAACAATTATTGAACCCG	59.009	23	CACCTCACGCACTCCACTAA	59.897	20
CCAGTTCGGCGATATATGGTA	59.824	21	AAATTGATGGAACGGGGATT	60.378	20
GAAGGGAAGGGAAAGAATGG	59.875	20	TTGTCACATTTTTGGTGTTTCA	58.964	22
TAATGGCTGCCTATCAACCC	59.923	20	GAACCAAAGCTTTCTTGCCA	60.365	20
CATGTGAGAAACGTCCCCTT	59.966	20	GATCCAAATTTCAACCCCGT	60.92	20
CAAAATTTAAGGTTATTATTGGA	59.806	27	GGCCTATAAATGCGTTTGGT	58.969	20
CCCCTCATTTTTCGTTTTCA	59.91	20	AGAGACGACAGCGAGAGGAG	59.883	20
CAGTTTCCACACGCCAATAA	59.585	20	CATGCAAGCAGCACTTCAAT	60.019	20
TCATCATGAAACACCCTAGAAAA	58.616	23	GAGGTAGCTGGGAGGAGGAG	60.349	20
TTGACCCACCTTTGACCAAT	60.21	20	TTGGCCGTGAATTTTTCTGT	60.481	20
ATCGTAGTGAAGTAGCCGCC	59.364	20	CATGAAATTGTTGGGGGTTT	59.523	20
CTTGTGAGTTGGTGAGGCAA	59.873	20	TCTTCACCTATTATTTCAACAA	57.674	26
GTGTTGCTGATGCAGACAGG	60.473	20	TCTTCGAGTACGCTCTGGGT	60.012	20
TGGAGTAGGGAGCCTCGTAA	59.83	20	TGCGTGACGGTTGGTATAAT	58.92	20
TGGTTATTACCTGATCACCATCC	59.959	23	TGGTTTTTCTCCCCAGTGAC	59.943	20
GTGCTCAGTGGACACATTGC	60.328	20	TAAAACCATGCACGTAGGCA	60.133	20
TTTAATGGACACCTCTGCGG	61.021	20	TCTTGCAGCCACATCTTGAG	60.136	20
ACGGTCACCATTTTTGTGGT	60.134	20	ACAAAGCTTACGCATCCAAA	58.439	20
AATACATCCAGTCATCCCGC	59.78	20	TCCATCGGCTACTTTGAAGG	60.206	20
CCACTCGTGCATCACTCAAG	60.463	20	TCTCGTGTTTGACCGTAATCAT	59.499	22
AAATTGGCATTACGGGTCAA	60.188	20	CAGAAATGCCACAGCAGAAA	59.988	20
CACTTCCGACTTCTTTTGCC	59.853	20	AAAATTTTTGGGCTTATCATGT	59.256	24
GGGGCTTTGAATCTACCAAA	59.019	20	CTTTCACGGGAGAAAGTTGC	59.853	20
ATCCATCTCATGTTGGGCAC	60.758	20	TTGTGTGGATCAATAACTGTCA	59.54	24
ATAGAGGGAGGGGAGGGTTT	60.144	20	TTAAGGTTGGCTTGGGTTTG	59.968	20
TGAACTAAGGAGGTGTTATGACA	59.249	25	CGCATGTTGTTGTAGTGGCT	59.788	20
AACAAACCGTGTTAACATCCC	58.732	21	TTTAAGAGATAGTACCGGATC	58.853	23
CTCATCTCTCGCTCTCCCTC	59.232	20	GAGGTCGGGTTCGTGTAGAG	59.721	20
CCCGTTCCATCACACTTCTT	59.966	20	ACCACTCTTTTGGGGCAATA	59.429	20
TGCTTGGAAAGACAATTGAATG	60.11	22	CACGCATGTTTCTGTCATCC	60.12	20
TCCATCACCAGATCATTTCG	59.451	20	GGAAACCACTCACCGTGTCT	60.009	20
CGAAGGTTGGGTGGTAGAGA	60.103	20	TAAAATGGCACACATCGGAA	59.93	20
CAATACAACTGCCGAGCTGA	60.011	20	TGTACCACACTTGCTCGGTG	60.779	20
TGCTTGATCCAACGGGTTAT	60.331	20	GCACTGCATAACAAGCGTACA	59.955	21
ACAATTCTTGGAAGCCCAAA	59.546	20	CGTATGAGCTCTGAGAGTGAGT	59.315	23
TTTCTCAACCGAGCTCACCT	59.989	20	CGTGTGTGAGTCCCCATGTA	60.44	20
TAATGGCCACCAAGCTTTTC	60.074	20	CTCCAACATCCAACCTCCAT	59.779	20
ACGACGGAAATATGGAGCAA	60.469	20	TGGTGGGGCTTAATTAGGTG	59.817	20
ACACTTGCCAAGGGCATAAC	60	20	TGGTAGAAGGCCGATTTGTC	60.074	20
TGATGGTTGTGATTTGTTAGAGG	59.007	23	AGCAGGATAAGGGGTGTTGTT	59.878	21
CGGCTGAGGACGAGAATTAG	59.971	20	TGGTTAACCGAAAACCGAAG	59.968	20
CGGGTTTGAACCCTCAATAA	59.795	20	TAGGGTTTGACAGCGCCTAC	60.27	20
ACTGCCCAACAATGGCTTAC	60	20	AAGCATTCCAAACACCATCC	59.797	20
TAAGGGCGGTATCACCTGAA	60.46	20	AAATAATCGAAGGTGACTGTC	59.885	23
CCAACACTCTGCTCTCTCCC	59.986	20	TCTCGTTCCAAATGGGATTC	59.871	20
AACGTAAACCCCTGGTCAAA	59.331	20	TGCTTCTTGAAAACTTTCTTCAT	59.84	25
TCCCAAATTATATCCTCTCCCA	59.637	22	GGCGACGTTGAATAGCTTGT	60.278	20
AAAATCAAGTTTAGGTGCGTCA	58.811	22	AATTGCTTCAATGTCACCCC	59.797	20
GAAAGGCCCACAATGGTTATT	60.068	21	GAAGGGATCATGCGTTTCTC	59.635	20
AATCCCTTACATGTCCGTCG	59.813	20	TGGAAAAGAATTCGTCCTCG	60.184	20
CCACTGATGTGAGCCAACTG	60.309	20	GAGTGACATCTTCGAGTGTTC	59.914	22
ATTCTTGCCGATGTTTACCG	59.96	20	ATGACGAGAAAATGGTTCGG	59.933	20
TGACTCTCAATGCCTTCTACCC	60.63	22	AGCCCCTTTGAGCTAAGGTA	58.098	20
TCAAAGAATCCACCATGCAA	60.049	20	GCTTGTTTAGGGAGAGCACG	60.015	20
AGCTGTTAGGGTTGTATAGTGAGT	57.436	27	AGTTCTCCCAGACTCCCGTT	60.111	20

AATTTCGACAAACAAACGGC	59.982	20	TGCAAAACGATTCCTTCCTT	59.685	20
GGCGGTGGTAGGAAGAAACT	60.496	20	CCGAATTTCTTTGCACAGGT	60.11	20
GAAAACATGCTTGGAAAGCC	59.691	20	TGAAATGAAGAAAAAGAAATT	57.512	23
TGGGACGGAGGGAGTATATG	59.767	20	TGGAGAAGGGACAAATGGAG	60.042	20
TGGAATTGAATGTGGGAGTG	59.343	20	ACCAATATCCAACGGCAAGA	60.331	20
GGTGGTAGCTTTCCGACAAA	60.11	20	TTTCAAAATTCCCCACAAGC	59.916	20
CAGTACCCCTCTTTGGACCC	60.736	20	TGAAGGTTGGAGGAATGGAG	60.042	20
AAAAATGCAGATTATGCTCCAC	58.275	22	TTCATACCAGCTTGAAGGGG	60.066	20
TCAATATCATCGCCATTTTGAA	60.282	22	TAGTGTGTCACGGGCAATGT	60.032	20
CTTCGGCCGGTTTAAGATTC	60.92	20	TATGGGTTATCACCGGATCG	60.544	20
CCGCATACGCGCTAAATAAT	60.102	20	TGAAGTTAGGAAATAAGGAGG	58.743	25
CTCCCGTGCTTCATCGTAGT	60.277	20	GGAAAATGGTTGCAAAAGGA	59.916	20
TGCACAATATGTTGGGAGGA	59.924	20	GCCGTTATAGTGTGGGATCTTT	59.398	22
GCCTAACTAATGGCACGGAC	59.597	20	TCATGCACGCAAAATAACCT	59.186	20
GTTATCATGGGAAGGGGAGG	60.517	20	TTTCGTCGGAAAAATTCACC	59.916	20
CAAACGAGGAGCAAAAATCAG	59.869	21	ACACTACCCTCCTCGTCCCT	59.991	20
TTTGTCCAAACAAATGAAAACA	58.097	22	GTAATGCTAGCCGGAAAACG	59.742	20
GTGACTGGTGAGGGATGGAC	60.383	20	AATCTTGCGAACCAAACACC	59.978	20
GCCTCTTGGGGTCTTAATCA	59.126	20	GATGTTGCGTTGTGCGTATT	59.62	20
AGCCACGATTCCTGATTTTG	60.074	20	AGGAAATAAGGAGGTGTTATG	58.113	26
AAACACGCAACACAAAGCAG	59.951	20	GAATCTGCAGCAAGTTTCCC	59.82	20
TGGAGTTGGTGGTGTCTTCA	60.129	20	CTGCAAAATTGGCTGAGTTG	59.464	20
TCATCGGGGTGTAACGAGAT	60.34	20	ACGTGTTGGATGGAATGCTA	59.002	20
CACTGCCAGCAGTCGATAAA	60.011	20	GCAGTTGGTGGTCGTGTAGA	59.751	20
AATGGATGGTTGTGATTGAGTT	58.293	22	TGAATGAAGTACGGCGATTT	58.241	20
GTCCACGTGCTTTCCTCTGT	60.307	20	TGAGTACAGGTGTGGCTTGC	59.905	20
AGTCGAAGGTCGCGTGTAAT	59.763	20	TTTCTATTCTTTATAATTGCCAT	58.633	27
GCTGGCAATCCTTTCTTCCT	60.713	20	ATTGCAGTTGCAGTTGGTGA	60.31	20
CATTCAAGGGGCATTTTTGT	59.801	20	AAGGGCACCGCTAATGTAGA	59.73	20
TTCTCTTGCATTGTCCCACA	60.24	20	GCTTTGTCGGTTTCTCCATC	59.676	20
CATTGTGTTTTCTCCATATTTTCA	58.116	24	CATCCCAAGTTACTCCCAGC	59.55	20
TTCTCAACCACGACCCCTAC	59.966	20	GCGTTGCCTCTCTCTCATCT	59.709	20
TGTTTGAGTGGTTTTTCCTTGA	59.626	22	AACCATAGATTGAAGGCCCA	59.387	20
CCTCTCACTCCCACTCCATC	59.638	20	CACAGCGAGGTTTGGAAAAT	60.11	20
CCTGAAACTCCAAATATTCTTCTT	60.267	26	TGACGGTCAAGATTTGCTCA	60.39	20
CTTGCCTTACATCAGCCCTC	59.836	20	TTCCATCCTTCTTTGCTGCT	59.955	20
TCCGGTGAACTTCTCCAACT	59.697	20	TTAACCTCCCGTGGACGTAG	59.986	20
GGACGGAGGGAGTACGTCTT	60.511	20	TTTTTGGCAATTTGTGACGA	60.088	20
TTGTTCGAAACCTAATGCCA	59.157	20	GGGGGTTATCATGGGATCAA	61.666	20
AAAAAGGAAGGAGGGAGCTAA	58.527	21	ACCTGCTTTTGTGCATAGGTT	58.781	21
AAAACATGTATGGGATTGAAGAA	57.563	23	AAATGATAGGGCACACAGCC	59.962	20
TGTGGTTGCGTCCTTATGAA	60.111	20	GCAGTGATGCCTGATGAAAA	59.805	20
AAACATGGAGGGGTCAAACA	60.21	20	AAACCTGGCTGGACTGATGT	59.579	20
GGGGTGAAATTGGGAGAGTT	60.169	20	AAGTGAAACTGCTGTATGCTG	57.719	22
TAGGATACCCTCCCAAACCC	60.011	20	ATTTGGGGATGAATCTGACG	59.75	20
TCTCATTCACGCTTTTCAGC	59.152	20	GTTGAGCTCGGATAAGCTGC	60.125	20
TTTTGAGCTTCCGCGAGTAT	59.982	20	CTAGCCTGGTCGTTTTGGAA	60.241	20
TGGACTTAAGTACCCTTTTACCAA	59.115	25	TCAACGGTTTTGATTTGTTCC	59.831	21
TGGGGTGGTTAAGTTGTGGT	60.126	20	GTGCATGGTAGGGCAAACTT	60	20
TTTTGCTAGGGACCGAAACC	61.327	20	TGCGTTTTGACAATATATAGGT	60.083	26
AAGTATGCTGACGCTGGGTT	59.763	20	ATGGCTGGGCTCTGAAATTA	59.668	20
CAACTTTCCCTCCACCTTCA	60.081	20	GCGAATTCAAACCCCTTGTA	59.938	20
GAGGACAGTCTGGGTGCAGT	60.315	20	TAACACCACCACCCACACAC	60.178	20
CAAATATTTTGTAGTTTCCCATGT	59.948	26	ACAAATGGCCAAGAGAGTTTA	57.433	22
TCGAGCTCTCCTTTTTGGAA	60.066	20	TTTTTGACAGCGAAAGTCCC	60.227	20
GCCCAAAATTAGTTGGGGTT	60.055	20	TTTCCCCTTTGCTCTCTATTTC	58.887	22
GGATTTTCGAAATTTTCTCGC	60.035	21	AAAATGCAAATGCCGAAGAT	59.552	20
CTGCATCGAGTATCGCTCAA	60.119	20	CAACTCCAACTGAAGAACACG	60.326	22

CGTGGTTCGATCGTAATTGA	59.542	20	GCAATCCATTCCGTACAAGG	60.331	20
TTCTTTAATCACCGCACCAA	59.157	20	GATCGACGCCTCAGATTTGT	60.226	20
TTCTGGTCGAGCTGGAAGAT	59.95	20	CCTCTAGCATCTCTTGCTCTCA	58.983	22
TTGTGATTTGTTCCCACAAGA	59.01	21	AGCAAGATTGATCCTCCTCG	59.386	20
TGTTACGCCGATTAGTGTCG	59.752	20	ACAGGGTACTCAGTGGACGC	60.182	20
AAAAGAAAAAGTGAAGGGCTCA	59.411	22	CCACGAAGCATCATCATACC	58.953	20
TCCTAAAAACGTTCCGCTGT	59.747	20	TTTCCAACTATCCAAACGGC	59.938	20
AAGAACAATTACAATGTTTATCC	58.084	27	CACACTATTAGGGTTTGGGAG	59.757	22
TGCAGAGCTCCATGACAGAA	60.711	20	CCCCGAAAAACCCTCTATCT	59.415	20
TCAACAGAGAATGCAAGCAA	58.129	20	CGAGCTCGGACCTTCAGTAT	59.454	20
ACATGATTTGATGGTGCCTC	58.36	20	AGGGCAAAAATAACCAACCC	60.055	20
TGCGTTTTGACAATATATAGGTGT	60.083	26	AGACGACCGAACAAAATGCT	59.74	20
ACTTCCCAGGATCGATTTGA	59.483	20	TCACATGGTGATGCCTTCTAA	59.138	21
AATGCAAAAATATGAGGCCG	59.928	20	TCAATGGTGGCTTCATTTCC	60.843	20
TTGGTGGAAAAAGGTTAACGA	59.478	21	CTCGTGTACAAAAGCCGTGA	59.904	20
TGACGAGAGAGAAAAGCGAA	58.874	20	TAAAACCATGCACGTAGGCA	60.133	20
AAGGGGGTTATTAGTGGATCA	57.425	21	TGGGGTCTTGGCGTACTAAC	59.993	20
TGTGCGTGTATGCAATGTGT	59.621	20	AGGGATGTTTGCACCTGAAT	59.41	20
ATGGAACGTTGATTGCCATT	60.199	20	TGAAGTTAGGAAATAAGGAGG	57.525	24
TCCTGCATCCTATCACATGG	59.476	20	AGAGTTTTCATCTTACCTTGAG	59.234	24
TCTCGACTAATTATTATGCCTACC	58.678	26	TTGTGGGGTTGTGGTGAATA	59.667	20
AATTAAAATTTGGGGAGGGG	59.034	20	TTAGGTATGGCTCGGTTTCG	60.089	20
CAGACCGTCGAATTTAGACCA	60.118	21	TTTTAAAGAGCTGGGGGCTT	60.197	20
TTTGGGACGATTTTCTCTCTATG	59.617	23	AGCGATTTTTAAACCCACCC	60.184	20
CTGCTGCAGAGAAGGTAGGG	60.149	20	TAATTGAATTCCTGGGTCCG	59.756	20
TCGTTTGTGTGTTCTTCGTG	58.305	20	TGGCTATTTTGGTTTCTACAAC	58.731	23
GGTTGTTTTAATTTGCTCCCA	58.976	21	TATCAGGCTTGATGATGGCA	60.182	20
CCTTTCCTTTACACCACAAGGA	60.377	22	AATGCGGAAATCTATGGCTG	60.06	20
TCAATGGCTCAAAAAGTTTCA	58.4	21	TGAAGCATCGTTTGTGTTTTC	58.81	21
AATGAAATAGAATTCGCGAGG	58.349	21	TGGTTTATATTTCGTTGATTTGC	58.141	23
ACACACACATTACATTAAACCGA	59.985	25	GGGTGTTCATGGTTCGATTC	60.181	20
CGCATGTTCGATCTTCAGTG	60.413	20	TCGAGTCCAATGTTGAAAGAA	59.724	22
CACATCCCACCCAACTCTCT	59.962	20	ATGATGATGACGAGCTCACG	59.819	20
TGGACGTAAATACCCTTTTACCA	59.667	23	CTCCTTTTTGTCATTCACCTTTG	60.022	23
GAGCCCAAACCTCAATCAAC	59.532	20	TGGACTGCGTTAGGGACTTT	59.734	20
GGGCATGAATTCCAAAACTC	59.368	20	CACCATACCGCATGAATTTG	59.809	20
TTCTCAGCTGTCAACGAATGA	59.581	21	ATTTGGAGGAGGATGGGTTT	59.629	20
ATCTCCGAGGGTGATGAGTG	60.072	20	CTTCCTTGGGCACAACATTT	59.971	20
CCCAATGCTATGGACAAACC	60.192	20	ACGTGAAAAACGGGAATGAA	60.344	20
CGTCTGAGCTCGGTAGAAGC	60.299	20	CTCACACAATTTCACTCTTCAC	58.044	24
GATCCGATGTCCCAAACACT	59.786	20	TGGACTTCGTCACAACCAAA	60.128	20
TTTACTTCGGAAGGCCATTG	60.067	20	GACGGAGCAGAAATGGAAAA	60.192	20
CATCCCAACCACTCATTTCG	61.296	20	GTGCGCATTCCTTACTCCTC	59.843	20
GTGTGGATTGATCTCTGGCA	59.637	20	AAAAACCGCCACATCAGAAG	60.11	20
GGTTAATCTCTCTATCTCTCTCAC	58.624	27	TTTGACCATGGTTTTGGGAT	60.029	20
CAGTGTAGTTAGGCGGTTTGG	59.679	21	TCAAACACGAGTAGAAAGGAT	57.147	23
TGTCGGTCATTGAATTGTGAA	59.956	21	TCTCCTTCACCCATTTGGAG	60.042	20
TTTTCATTTGATCACCTCCC	57.426	20	AAAATCAAATTTGGGCCCTT	59.659	20
TGCTTAGCCTCCTCCAACAT	59.836	20	TGAAGTTAGGAAATAAGGAGG	58.743	25
TTACGCGGACTCCTCAAAGT	59.875	20	TCTGATTCTGGGATTTTGGC	60.014	20
CTGGAACAACAGCTACGCTC	58.677	20	GACGTGAACTCTCATGCCCT	60.269	20
AAGTGCTCACAGATCCCACC	60.12	20	CATTATTTAAAGCACGCGCA	59.872	20
AAATAAGGAGGTGTTATGAAGGG	59.323	24	CAAAAATGGATGCAAATACGG	60.192	21
CCCCTGTATGCACCTCATTT	59.813	20	AATGGTTTCGCTCTCTGTGG	60.255	20
GTAGTGAAGGCAGCCCGTAG	59.898	20	TGCTCTTCACCTTTGTGTGC	60.032	20
TTGGCACTGAGTACCCATTTT	59.485	21	CGGCGGCATTCTAAATATGA	60.923	20
CCCAGGTCTCAATCTTTTTGG	60.831	21	GGGCCTCTTTTTGTCTGAAT	58.24	20
GGTGCTGCTATTGAAGCCAT	60.243	20	GTAGCTGCACATTGTCCGTC	59.323	20

GAAGGTGAACGTCGGTAGGA	60.111	20	CACCATCACCATCCTCACAT	59.184	20
TGATAGAAACACTTCGCGAGC	60.537	21	TCCCTTCAATGGTGTTTCCT	59.381	20
CACGCATCTCTCTCTTCCCT	59.555	20	ATAGGGGTCAGTGTGGGTTG	59.697	20
AATTGAGGCTCCAGATTTGC	59.273	20	ATGTACCCCGATGTGAGAGC	59.957	20
AGGAGGCCTACTTCCTGGAT	59.163	20	TGAACACGTTGCCAAAACAT	60.011	20
GGGTTTCTATTGCTGGGGTT	60.187	20	TTAAAAACTCGACCCGATGC	60.074	20
CGATGGTCTGAGTTATCCTCTG	58.815	22	GTCAAATCAGGAAAACCCCTT	59.316	21
TCGTGTGTAGGAAAAACATCG	58.687	21	GTTTTTGGAGGGAAAATGGC	60.653	20
CGATCACGTTTTCCAGTTCC	60.495	20	GCCTTATCAGTCTCCGAAACC	60.089	21
TCGTTTTGATGATGAGCTGG	59.799	20	CATGTTTTGTTTGGCTGTGG	60.004	20
GCGGTTTGAGCCTAATTTTG	59.72	20	CGGTTAGAAAATGGACCGTTA	58.997	21
GCATACACCGATAGCATTTTGA	59.992	22	AGAGCTTGGAGGATGGAGGT	60.216	20
GAGTGCTGCAGCGTATGTGT	60.088	20	CGTTTTGATTTGTGTTGGCA	60.535	20
CAATTGCTATAAATGAAACCGGA	60.203	23	TCTACCACTGCACCACGAGA	60.463	20
AAACTTGCTTCCGTTGGATG	60.11	20	GCGTGCTGAATCTTAACCGT	60.278	20
TCCTCAATTTCAGTGTGGAAAA	59.587	22	GCGAATCGAACAAATCGAAG	60.721	20
AATGTCATAAGGACCACGGG	59.67	20	TCAACAGAGAATGCAAGCAAA	59.6	21
AAATTAAGTGGGGGTGGAGG	60.046	20	CTCAGCATTCGGAAAGGGTA	60.206	20
TCCCAAATCTAGAAGCCACG	60.206	20	AGATGGCGGTAAACATGGAG	59.955	20
TTCGATACGAATTTTCATACCAT	57.615	23	ACCCTAATTGAGTAGAAAACC	58.212	24
CAAATGACCAAGGAGGTTACAA	58.994	22	TGCTGACTTGATTTTCGAGC	59.152	20
GGCGAGTGTCGCCTAGTGTA	61.394	20	TGATACGACCTTGGGGGTTA	60.184	20
TGAGCACGTATGGACACGAT	60.144	20	TCACCCAAAAAGGTTATTATTT	57.25	23
TCACAGCAAAGATCTCACCG	59.984	20	AATTTACTCGCCTCTTCCGC	60.711	20
TTGAATCCAGGATCTTGAGC	57.804	20	CACGCACATAATTCGCAGTT	59.759	20
GAGGGAGAGATGGATCGACA	60.16	20	TTGGTTATCGCTTGAACGAG	58.917	20
TTGCTAGAGGTTTTGACGAGA	57.771	21	GCGTTTTGACAGGATTTGCT	60.257	20
TGGATCTCGTGATGCCACT	60.222	19	TCTCAAAAGTCTCATTTTCACA	59.799	24
ATCGGGATCGGTTTATGGTT	60.399	20	ACACCTTGTCTCCCAAATGC	59.973	20
ATCCCGTCTGCGTTTATCAC	59.962	20	TATTCGCCTCGATCTCCATC	60.141	20
TTCAAACGTGGCACCAATTA	59.969	20	TGGATGTGGTTGGTGAGTTG	60.416	20
CACAAGATTTATGGGTTATCATTT	58.787	25	TTCGATTCTAGCTTCCGCAT	59.945	20
AAAAGGTTAAGGGTGGGGTG	60.082	20	ATATCATGGCCGAAACCATC	59.61	20
TTCCCATCAGTCAAGATCTACCT	59.114	23	TCTCTCCAACTCATTTCGCA	59.522	20
TTTTTCCCACTGGATTTTCG	59.91	20	CCCCTTAAGTGTGAACGCAT	59.993	20
GCAATGGTGTTGCATATGTGT	59.341	21	AGCTGGAATACAACTACCCC	59.892	22
GCTACGAAGACATCCACCAAA	60.125	21	GCAAGCTCGATGTCTTATGC	58.628	20
GCCTCCTTTTCTTTTTCTCG	58.188	20	CTTAAGTTTGGGGGTGCAGA	60.103	20
TGGGAGAATTTTCTGCTCTTG	59.438	21	AGCCGTTGAATGTGATATCTTG	59.114	22
CCTCCCAACCCCAAATTTAT	59.882	20	ACCGAGTAGAGAAGGGGTGG	60.502	20
ATCGGTTATTACCGGATCGC	61.031	20	TCGATATGTGTCCCTTCGTG	59.522	20
CACTTAAATCCACCGCCATT	59.823	20	TTTGTCACCCTCTCCCAGTT	59.549	20
TGAGGGACTTGGGTAGTTGC	60.111	20	TGCCTGAACAATGCTTTGAC	59.847	20
ACAGAAGAACGGGCTTTGAA	59.853	20	TCATGAGCAATGTTTCTGCC	59.805	20
TTTTTAATTCATCTTAACTGATGC	58.447	26	CGTTGATGGAATTCGAACCT	59.933	20
GCGCAAAAATACTCGCTTTC	59.992	20	GCCGGGAACTTAGGATTAGC	60.061	20
CGACAAATTTTCACACCCCT	59.83	20	GCAATGGAGTGGAGGAGAAG	59.803	20
GATCTTTCCACAAACCGAGC	59.676	20	TCGAAGGGAGAGAGGAAGAA	59.087	20
ACATTTTCGGCCATGACAAT	60.199	20	CCTTTGAGGATGGATTGATGA	59.879	21
AGCTCACGTTTTTCCCTCAA	59.853	20	GTCGCCTTGTCGGGATATTA	59.923	20
TCCAATTCGAAAACCGGTAA	60.294	20	TTTTTCCGAGCAAATGAAAA	58.394	20
AGGGCTAAGTGTTGAGATTGGA	60.13	22	ACCACCTAGCAATGGTTTCC	58.912	20
TGCGTTTGATCGTTAGCTGT	59.493	20	ACCGAGGACCACCTTGTATG	59.844	20
TGCACGTAGGCATGTTCAAT	60.142	20	AAGCGTTCGAAGTTTGGTGT	59.78	20
CCATCCATGCCTTGGTACTT	59.813	20	CTTCCATCTTGATCCCAAGC	59.629	20
TCGAGTGATCGTGAGACAGTG	60.038	21	ACCTTGACGAGGTGGTTGAC	60.009	20
GCGAAGAAACATTCAGGGAA	60.192	20	TTTCTCTCTTGGTTGGTGAAGA	58.955	22
ATCGAGTAAACTAGGCGCGA	60.003	20	AAGTGAGCCCCAAATCTCCT	60.074	20

ATGCATGTGTGCCAAGTGTC	60.614	20	AAAATTCCAACGAGGTGCC	59.925	19
ACAAAATGTCGAAAAATTCGC	59.114	21	ACCATGAAGCACATCACAGG	59.551	20
TATCCATGGAATGCCCAAAT	59.979	20	ATTTCTTCTTTTGCCACCGA	59.685	20
TGTTACATGGATGGATGGGTT	59.925	21	TTCCGTCTACCCCTTTTCCT	59.934	20
GCAAACCAAACATGTATCAAAA	57.628	22	GCCTCTCAACCTCCAAAATG	59.67	20
ATTTTGTGTTGGGCGAAAAT	59.32	20	AAAAATAGAGTTATCACAGGAT	58.199	26
CTGGACCTTTCGGTTCTTGA	60.224	20	CACCCCGGGCTAGATATTTT	60.164	20
AAGCAGGAGGTCCACAGTTG	60.298	20	AGGGCAAGGTAGAATTCGCT	60.228	20
GGTGCTCTCAAGGTTCTTGC	59.997	20	TATGGGTTATCACCGGATCG	60.544	20
GCTGGTGCATCCTCTTCCTA	60.362	20	TAATGCCCTCCAAAACCAAG	59.931	20
TTGCGTTGGATCAATTTGTG	60.501	20	CGCTGTAGATCTAACGGCTGA	60.549	21
ATCGCACGTGCTAGATCCTT	59.866	20	TGTCCGCCCTAATAAACCTG	59.953	20
TGCAATCCGGATCAAAAGTT	60.448	20	GAGGCAAATTATTCGGATTTTC	58.99	22
CAATCGGTTGTTTTCTCGGT	59.971	20	CCCCATCAACCTCCATACTG	60.187	20
TGAGCAAAAGTAATAAGAGCGAC	60.422	24	CCCAGACTCTCGTCTGATCC	59.792	20
TTGTAATTATTGTAGGGAATAAAA	57.858	27	CCAGCATGGGGAATGTTAAT	59.645	20
ATCTCAGTGCGTGTGAGTGC	60.063	20	CTGCTTTGTTTCCATCACGA	59.84	20
ACGCCCCAGACTGTTTCTTA	59.734	20	TCAGGTCCACGTATTTTCCC	59.79	20
AAGGGTTATCACCTGATTTTCTC	57.73	23	AATTTGCTTCTTTGCCGATG	60.209	20
CGTCGGTCAGAACCTTGATT	60.111	20	GGGTTATTACCTGATTACCTCC	59.052	23
CACTCACTCTCACTAGCCGC	58.78	20	AACGACCAGGCGCTCTAATA	59.867	20
CGGCTATAGCAAGGGTCAAC	59.73	20	GCTTCCACTGCCTACTTTGC	60.022	20
GCTATCCACGATGGACGATT	59.923	20	AATTTGGCAGCTTCTTGTGC	60.395	20
TGGCTGTGAATCATTGTTCG	60.665	20	TCGTCGATTGACTTTGTCCA	60.24	20
AAATGCGCAATTTTAAACCCT	59.864	21	TCCACCGTGGTTAGTTGACA	60.001	20
CGGCACCAATTTATTGTGAA	59.42	20	CAGCTCAGGGTGGAGAAAAT	59.284	20
AGGTTGGTCCACAAGATTTACA	58.486	22	CATCTGAGGAAGGCACATGA	59.787	20
CATACCTCCCCTTACCATCG	59.264	20	AAAGAACGAGTGGAGAGCGA	60.134	20
TCCGAAATTTAAGGAGTCGG	59.155	20	TCACAATATTTGAGGGTTATCA	60.337	26
ATCGTGGAGTAACTGCCTGG	60.134	20	TGTGCGTAGAACAGAGAGCG	60.347	20
TCTCAGGTGACAATAGGGGG	59.92	20	AGGACATCGCGGAGAGTCTA	59.973	20
TTTCTCACCCCATTTCATCC	59.727	20	CTCACCTCTTGGTGCCTCTC	59.986	20
CAGAAACGTTTTCCCTGAGC	59.853	20	TGAAAAGAAAAGAGGCACTCG	59.618	21
GATTGTCGGTCTCGTTACCC	59.41	20	GGTGAAGACGGCTTGTTGAT	60.119	20
TGCTATAAATGAAACCGGGG	59.789	20	ATTTCGAAGATCAACGGACG	60.074	20
CCCTTCGCATCTTACTGCAT	60.235	20	GCTGTAGATTCAAAGGCCGA	60.352	20
TTCTCACAAGCAAAGACCCA	59.415	20	CCAACAACCTAATCATCCAACC	60.463	22
GCGTAATATCAAATTTTTGGGTC	58.85	23	CCACCAACTTGTCCACTCCT	60.002	20
TTCGAAAATCAAAGAGCCTCA	59.946	21	GGCTTCACATTTCCCATCAC	60.326	20
TCTTAATTTGCATGTTCGTTATACA	57.939	25	TTTTTGCGAGGGAGAATGTC	60.192	20
GGTGCAAGTGTCAATAGAAGAGT	58.896	24	CGGAAGAATTAGAAACGGCA	60.202	20
AGAAACTTGACGTGTGCGTG	59.946	20	CTCCTGGTGAATGGCAAAGT	60.111	20
TCTGAAGTCCAGCAACAGGA	59.545	20	CGTGATGTGCAGTTCAAGGT	59.751	20
AGGCAAGAAACTGCCTGAAA	59.993	20	TATGGTGGTATGGTGTGGGG	61.296	20
TCATTCTCAAGCCACTCCCT	59.803	20	CTGGTGTCACAACGGATGTC	60.005	20
TTCCAGGTTTGCTGCTAGGT	59.875	20	TGCAAGAGCAGCAGGATATG	60.119	20
CGAGATTCGGGAAGACAGAG	59.943	20	CCGCCTACTCTCCCTCTTTT	59.842	20
TTTTGGTAAAGTTTTGAGATTCCA	59.107	24	ATGCGAGCATCATACACGAG	59.854	20
GGGGCATCCAGATAGTTCAA	59.894	20	CAGACGTCGCGATCAAAATA	59.833	20
TCCTTCAACCTTTTCCTTGTC	58.279	21	GGAGTTTGCTGTTGAGACCC	59.703	20
CCAATTTGATGAGGGACCAC	60.173	20	AGTCGCTGCAATTTCCAGTT	59.882	20
TGGTTGAAAATCATTGTGGG	59.222	20	AGCCTAAACACACACACCTCAC	59.186	22
AAAGGGAATTTTGTCAACTGGA	59.85	22	AGCAAGGGGCAAGTGTTATTT	60.014	21
TTATGTGGTGGTTGGAGCCT	60.375	20	ATCACATGCCATTCAGTCCA	59.925	20
CGCGAAGAACACAAGAGGAT	60.397	20	GCTATAGAGCCGTTGTGGGA	60.235	20
ACACGTGCCTCGTTTGAAAT	60.559	20	TCCATGCAATATGTATTAAATC	58.854	26
CAGCAGCAAAGCTTCGAAAT	60.658	20	CGCATTGGATCTCTGGTTTT	60.074	20
GGCCAACATATGGGATTTTG	60.016	20	TTATGTGTTCATCTGGGGCA	59.924	20

CCACCTGTACTTCCACCACC	60.275	20	GAAAGCCTACTTGGCGATCTT	59.87	21
CGACGTTGTCTTAACCTTGGA	60.154	21	AGTTCGAAAGCCTACCTCGC	60.894	20
TTAGTTAAACTCACGCACGGC	60.312	21	ATGGGAAGAGGGGGTATGAG	60.147	20
TTTTCCCTTCTTTTGGGAGG	60.395	20	GCAATTAAAACCCCCTCGAT	60.15	20
GACCATCGGAGTGTTGGAAT	59.786	20	TCTCTCTATCTTTTTGGTTGGTG	59.304	24
CACCCAAAATGGGTTATTATTTG	59.404	23	TCATTCTCAGCATACGGACG	59.823	20
GCACGTTTTTGGCCTGATA	59.679	19	TGGATCCCGGAGTATAAGCA	60.427	20
GCGGGGTTGTTGAAGAATTA	59.938	20	TGCGCGATTTTAAACCCTAA	60.564	20
TTACTGTTGCATGGACTGGG	59.566	20	CAATTACGAGGCCGAAAATC	59.547	20
GGTATTCGTGATCGTGATTCCT	60.215	22	TAAATCAAGTCCCCAAGCGT	59.569	20
CAGGGTTCGTAACCTAGGAGC	60.137	21	TCACTTCGAACCTTCTGCAA	59.566	20
CAAGCGGAACAAACAAACAA	59.746	20	CCAATTCATTCAAGCAGCAG	59.42	20
TTGGGACGAATATACCCTCG	59.778	20	CCAAAATTTATGGTTATCACAG	59.191	24
ATCAAGCCTGATATGTTTGACTC	57.388	23	TGTGGGGAGATATGATACGGA	60.163	21
GGCTGTTCAGCAATATGCAA	59.839	20	TGCAGGTGCTCTCTACACGA	60.767	20
ACGGATTTAAGGGTTATTACATG	58.008	24	TCGCATGCCACTAAAAATGA	60.215	20
CATTTTTCCACCTTGTGCCT	59.971	20	GGTGAAGTCGGATTGTGGAT	59.786	20
TGGGAAATGAAATGCGTGTA	59.93	20	AATAGAAAAACCACGCAGGG	59.087	20
ATCGTCGCCTCTAGCCACTA	60	20	GTCAATGGCGTCTGGTTTTT	59.978	20
GGTTTTACGAACCACAATCCA	59.716	21	AAATTTCACATATTTGATCGGA	57.59	23
TTTGCACCTGAGGAGGTGTT	60.69	20	GCCCCATTACCACTAAACCA	59.685	20
TTGCAGCTTGCACATTCAGT	60.606	20	CGGGGGTAAGAAAGTCAACA	59.964	20
TTCTCCTATCTTCCCCAGCC	60.537	20	GGGCTGCCAGAATAAAAAGG	60.92	20
GCATGCAAGCATCTGGTAAA	59.839	20	TGGTGATGCCAGAACAGAAG	59.831	20
AATCTCTCAATCGGCACACC	60.081	20	TTAGTGGTGCACAAAGCCAG	59.904	20
TTAGGGTTTAAAATCGCGCA	60.564	20	CAACGGTTTTGGTTTGTTCC	60.241	20
TCCCATTGGTTATGGGAAGA	60.126	20	TGGCTGGTGCAGAGATTGTA	60.413	20
TGATACACAGGAGTTTGCGG	59.716	20	GACTCACGGTTTTTCGGAAG	59.711	20
ACACCCACAAATCAACCACA	59.701	20	TCGGAAGATTGAACGTGTTG	59.691	20
TCAAACCAAGGTCGAGAGTTG	60.275	21	TCGGACCAAATTACCCTTCA	60.301	20
CTTCACGTGACTTGCTTCCA	60.025	20	TTGAACAATTGAACACCGGA	59.941	20
GGTGATTTGGCATTAAGGGT	58.765	20	CGCGACAGAGTGGTATCAGA	60.008	20
AAGCAATTTCAACATAGGTCGT	57.826	22	GGTGAATCTGTAAAAGGTCAT	59.885	23
CGGCTCGAAATCAGAAAATC	59.784	20	GAGAGCCATTTGTGGACGTT	60.119	20
CTCTGTAGTCGTGGTGGGCT	60.321	20	TTGTGGAGAACGAACTCGAA	59.415	20
TTCACAAACCCAGATATCATAAT	59.637	25	CAATTGGACGCGCTCTTACT	60.407	20
TAAAGAACCCTCCCCGAATC	60.258	20	AAAAACCGTTCCACATTCAAA	59.348	21
GAAGCACCGGTACTCGACAT	60.142	20	TCAAACAGAACACACCTTCCC	59.997	21
TGTGATGTTGTATTTTGGTACATG	59.22	25	CAACCGCATAGGCACAGTAGT	60.204	21
ACAAACGGTAATTCCCCTCC	60.053	20	TGCAAATTTCTTCGAGACCC	60.192	20
GCAACGGAATACCACTCGTT	60	20	CCTCCCAACTTGTGTGTGTG	60.039	20
TTGCTATTGCATGCTAAGAAGTG	59.588	23	TCAATTTGAATGGTTATCACCT	58.865	23
TGTGGAATGGGAGATAACAGA	58.005	21	TTAACGACTTGAACCCATTTTT	57.74	22
GTGTTGGACGCATCAGGTAT	58.444	20	CCTAGCTCCTTCCCCTTCAC	60.204	20
ACAACAATCCGGAGGTGAAG	59.966	20	GATTCCAACATGAAAGGCCA	60.843	20
CATGATCAAATCTTGGTGCG	60.073	20	TGTGATTTCTACCATTTATTCTT	59.708	26
TTACCTTTCTCGATCGGGTG	60.066	20	TTCTTGACGCACCATTTCAC	59.697	20
TCGCTTAATTGGTGATTGTGA	59.172	21	ATCCCACACAACGCTTGACT	60.577	20
TATTTTTCGGCGAGATTGCT	59.816	20	GAGAATGTGAGACATCATCAT	59.059	24
TCAATCAATTAGATTTTCGGCTC	59.601	23	AATTTCACAGAACACAACGAT	59.531	23
AACAGCAGGTGAGTTGGAGG	60.298	20	TGATGAAATGACATGGAAATG	58.82	22
TTTCACTGTTTCCACACATGC	59.606	21	AGGAGAACCAAACCGCATTA	59.569	20
AGAGCCATGTCTCCTTCACG	60.408	20	CCACTCCCCACTGCAATAAG	60.508	20
GTTGGATGGCTGGTTTCTGT	59.973	20	GACTCAACATAAATGGGGCG	60.331	20
TTCTTTTCTCTCCCTCCCCT	59.252	20	GTGTTCTCGTGAGAGTGCGT	59.051	20
AGCTTCTATCGCGCTCTCTC	59.083	20	TTCCAAACCTTTGTTCCGAG	60.081	20
TGTTCTTCGTGTTCTATATTTCTCG	58.935	25	GTTCTGTATGTCAACGGCCC	60.384	20
TGAAATGTGTTGGCTGGGTA	59.964	20	AATATCAGGGGGCGATTCTC	60.252	20

CATGTTCAGTTTTTGGGGCT	59.971	20	TGTCTGATCCCATCGGAAAT	60.281	20
TATCAAAACAACCCCCGGAC	61.84	20	ATCGAACAGCATGAAAACCC	59.939	20
GAGGAGAATTCATGGGGTGA	59.862	20	GGATGGTGATTATGGCTTGC	60.304	20
CAAGTCAAGCAAGGTGGACA	59.873	20	TTCGAACTCTTGCCAGTTGA	59.566	20
GCGACAAGTCTGCGTGTTAT	58.955	20	TAGGGGCACACCAAGAGAAC	60.111	20
CACATTCTCCGGTTTTTCGT	59.971	20	AGAACCCGGCAGAGAAAGAT	60.212	20
GGAAGGGGAGACCGAAATTA	60.258	20	ACGACAGTGGACAAGGGAAT	59.43	20
TGGCTAATCCCTGTTTTGAA	58.214	20	TCACTCCAAAGCATCAAGCC	61.329	20
TAAAGCCAATAAAGTGGGGC	59.078	20	TCTGTTTGCCTTTCGAATCC	60.192	20
AATGGTTGGGAAACAGGCTA	59.429	20	GCAGACTTTAAGGCAGCCAA	60.523	20
CAAAGAAGGCAATCTATCCCA	59.168	21	CACGAGATTTACGTGGTTCG	59.195	20
AATCCCAATTTCCCAACCTC	59.996	20	TGCTGTTGCTCTGCTTTGAT	59.746	20
ATGGACCCCACCTGTCATAA	60.05	20	TTTTGTGTCCGGTTTTCTCG	61.029	20
TCTCCATGCATGCAAACTTC	59.805	20	CTATCGTTTTCTCCGCCTTG	59.839	20
CACGCACTCACACACTCTGA	59.624	20	TAGGGGAAAAGGGGAAAGTG	60.284	20
TCGGTAAAATCAACGTGAAAAA	59.511	22	ACGCAGTCTAGAGATATATGTT	57.442	26
ATTGCTAGGGTAGCCTCCTT	57.088	20	TTTTTGATCGATCTCGGGTG	60.972	20
AAACGCCATGCAAAAATACG	60.859	20	CGCTTGGAGAAAGAAACGAG	60.125	20
GCTGCACGTGTTACACCTAAAA	60.228	22	TTGTCATTGGGCATCGATTA	59.891	20
AATAAAAGAGGAAGGCTGAGCTA	57.98	23	TTGTGGGAAGCATTTTCTCC	60.051	20
CCATTTTCCAATCTTTCCCA	59.733	20	ATTTAGCCGTTCCTCGGTTT	59.966	20
CAGTCACTCTCACTAGCCGC	58.78	20	GTCGACGCGATATTGTCCTT	60.103	20
TGAATGCTCGTTGTCTCCAC	59.837	20	AACTGGCTAACCCATCACCA	60.375	20
TACACACGCGCACACACTTA	59.968	20	TTCACAATTAACAAGAACAATT	59.077	26
TGGGTTCTCCTAGGCCTCTT	60.204	20	CAAGAGCAACAACACCATTCA	59.749	21
CCATTCTGCCCACAAAGATT	59.933	20	TGCTAACTCAAATTTCGGTGC	60.258	21
GCATCTCTTGCTCTCTCGTTG	60.292	21	CACGAGATTTACATGGTTCGAT	58.976	22
CATCCATCCTTTACTGCACG	59.148	20	GATTCCTCGTGGGATTGAAA	59.871	20
AGGTAAACAAACAATCAAGGGA	57.663	22	GATTGTAACGTTATTTGGCCG	59.376	21
TCCACCGTTGTCTTTAAGTCG	60.154	21	TTGAGGGAGAACTGCGGTAT	59.694	20
GAGAAAAACGACGTGAGGGA	60.232	20	AACTGAGTCCCCTACCCGAT	59.817	20
TGGTCAGTTTGATCGTTGGA	60.088	20	TTTGAGGCGAATCGAAATCT	59.784	20
AGCATCTCTTGCTCTCTCATTG	58.842	22	AACCATCGTTGCTGATTTCC	59.939	20
TCAAAACCCAAATCCGACTC	59.91	20	TTGTTAGTTTCCATTCCGCC	59.938	20
GCACCAAGACAATGCCCTAT	59.962	20	GTGGGCGATTTAGCAGAACT	59.34	20
CGTGTTTTACCGAAATGCG	60.118	19	CGGAAATTTTACCCGGATGT	60.902	20
CAATCCTTTGAGTATGGATTGATG	59.737	24	AATATCTCCCTTTTCGGCCA	60.764	20
CGATCCGTCGACTAAACCAT	59.955	20	GTCAAGTCAAACTTGCCAAAC	58.42	22
AATGCGAGAACGGAAAGAAA	59.823	20	GATCGCATCAGAGAGTCGGT	60.381	20
CCTATGCCGCTTACCTTTTT	58.409	20	TCTTCCCCAACTACTTTCCA	57.242	20
CCAACTACTGATGGTCCAAGC	59.607	21	TTACATCCCCGGAGATACCC	60.901	20
CCCACTCCACCTTCTCCTAAC	59.98	21	TTGCTTCAGAGGTGAAATCACT	59.031	23
CCGGGAGATGAAACTGTGTT	59.966	20	CCGCCATTCTCCGTTAACTA	60.089	20
TCGTGAATGGCATGACTGAT	60.08	20	ACAGAACCAAAAGGCAGTGG	60.149	20
GAGGTACGGTGATATCATGCTTA	59.843	25	GCCGTCAATCATTTAGGAACA	59.952	21
GATGGGGAGTTCAATGTCGT	59.786	20	CCATCTCCACCTCCATACTCA	59.935	21
CCACGAAACATCAGCATACG	60.134	20	CGCCCCAAGTTGTTTCTTAT	59.087	20
TTCAGTGCATATCTGACGGC	59.83	20	CATTTTGGACGGTCCTGTTC	60.353	20
ATGGACGCCCAATATTGTTT	59.162	20	GCATATACGAAGGGTATTTTG	59.289	23
TGTAGAGGAAGTTGGGGGTG	59.959	20	TCCCCTAACCGACAAAAATG	59.795	20
GTCAACTTGGGCAGTGGAAT	59.973	20	AATTAATGTGGCATGGGGAA	60.016	20
GGATCGCGTCGAATTAGTGT	60.103	20	AATCAGCTCCATTTCTTGCC	59.273	20
CATCTTTACCGCCACCATCT	59.955	20	CCGACAACGAAAGATGAAGA	58.847	20
CTATGGCACTATGCCGGATT	59.945	20	GAGCAGTAGTGCCCCTGAAG	60.012	20
ACGCACACTTACGCATTCAG	59.935	20	AAACACTCTGTGTTGTTGGGAA	59.538	22
TGAGCAACATGCTACAACCA	58.863	20	CGGGGCTTCACCTAGTCTAA	59.331	20
AATCATCTCCTCACTAATTCCATC	57.69	24	CTTTTGATTCCCCATTAAAAAG	58.925	24
CCAACCATGTGCTTCTTTCA	59.691	20	AAGGACAAAACCGCAACAAG	60.147	20

GACCGCAGGATAATCCAGAA	60.036	20	AGATTTGATCATGGGCGTTG	60.864	20
GTTGGACTTTTCGAAGAGCAT	58.45	21	AGCCGTGCCTTCAACATAAC	60.14	20
GCAGAGTGATGGGTGAACAA	59.682	20	GCTCCCTTAAACACGAATGTG	59.623	21
CAAGGAAGGCATCCACATCT	60.073	20	GCCCCTTAAAACTCTCCTTGA	59.712	21
TTAGCTCCAAGGGCCCTAAT	60.055	20	TTCGAACTCATGCATTCATTTT	59.592	22
CTTCTGTTGGGGCGAAATTA	60.067	20	GGTTTATTGGGCGTGTATGG	60.074	20
CCAATTGACTTCGTGGAGGT	59.966	20	ATGCAAGCTCAGCCTAATGAA	59.996	21
AGACCATGGTTCGGAGAGTG	60.112	20	ACTAAACCACCCGTGAAGCA	60.55	20
GGCATAAAACTCCCTGGACA	59.933	20	ACCGAATTCCTTCCAAGGTT	59.805	20
TCACGTTATGGGGAGAATCC	59.75	20	ACATGGAACAACATGAGCCA	59.967	20
CAACGATGGTTGTTGAAACG	60.004	20	GGTGATGTGCAACGCTATTG	60.142	20
TGCGTTTTGACAATATATAGGTGT	60.083	26	ACGAAAAATGTATTGGGGCA	60.188	20
TTCAGTGGAACATGGTTTGC	59.547	20	CTTTCCCCGTGGACGTAGAT	61.256	20
TTTTTGGAGTCGGAAAAACG	60.081	20	ATCGGTTATTACCGGATCGC	61.031	20
GCATGCATCAACTGCAAATC	60.237	20	TGGAACTGCAATGCTTCAAC	59.847	20
TGATGTGGCTTCTTTAGGGC	60.214	20	GCTTTCAATCCTCCAGCATC	59.78	20
GTTGCTTCCATCGTCACCTT	60.119	20	CACATTACACCACCCTTCCC	60.088	20
ATTTTGGCCTTTGATTTTCG	59.055	20	GAGGTTTCCAACTTGCTTCG	59.853	20
CTCTCGTCTCCCTTGTTTGC	59.989	20	TTGTGAGAACCAACTCGGTG	59.72	20
GGGTGCTTGAAGATAAACATGAG	60.014	23	GGTTGTTGCCGCTTCTACTT	59.383	20
CTAAATTCGCATGGGAAGGA	60.031	20	CGGCACGAAGTCTGGTAACT	60.312	20
AACGCGAAGAACACAAGAGG	60.431	20	ATTCAATTGCTGGTGGAAGG	59.933	20
CGCGAACTCAAATACCCTTC	59.708	20	TGGAGATAGAATGAGATAGAA	57.684	26
GTCTGCGAAGATTCAAGCGT	60.547	20	CAACCCTACCTCCTTCTCCC	59.928	20
TCCAAACAAGGCTCTATGGC	60.214	20	CAAGAGCTCTCATTCTCTCCC	58.214	21
ATTGTGTCACCGTCGTCTCA	60.162	20	AGCATCAAAATTCAAAAGCGA	59.846	21
TTCATGCCCGTTTTATTTGA	59.004	20	GATGAGAAGGGTGCACATGA	59.637	20
GGATATCCGATCCGGTTTTT	59.984	20	TCTCATGCCAACTAAGCCAA	59.42	20
TGCTCTCATTGTAATCTCTCTCAA	59.573	25	AATTGATGGAACGGGGATTT	60.378	20
ATGCTTAGGTGGATTTCCCA	59.387	20	GACAAAACTTCATGGGAGCG	60.636	20
CACCATAATTTGACACACACACA	59.28	23	TCATGATTCAAAAGCATCAAA	58.278	22
GCATATGATGTGCATATACGAAA	57.665	23	TTTCACATGCCATACACCAAA	59.841	21
GCTTATCCCTTCACCGTTCA	60.074	20	TCACCTTCGGTCAGAACCTT	59.697	20
CGAAATGTGAAGCGTTTGAA	59.849	20	GGGGTTGGAGGAAGAGAGAG	60.186	20
TTGAACTCACCACGTGAAGG	59.72	20	ATGGAAGGGACGAGTTTGAA	59.526	20
GGACAAAGGGTTTGCGATAA	59.938	20	CGGTTAAAAACCGAACTGGA	59.968	20
CAGGGGTAAAGTAGTCATTGTCG	59.935	23	TCTCCCTCTCAGTACTTTTCCTT	60.279	24
AGCGTACATGGAATCCCAAC	59.82	20	GAGATCGAAGGAGCTGATGG	59.91	20
GGGCGTGACAAAACTTACCA	60.924	20	TGATTACATCGATCCAACGG	59.35	20
GGTGGTGCGAGAGTGATTG	60.263	19	GGGTGGGTCGATTCAATATG	60.014	20
CTCACTAGCCGCAGCTCTCT	60.058	20	TGGAGCTCTTGTTCCTCACA	59.545	20
GTTTCTCACCCTTCACCCAA	59.943	20	GAATACCCCCTACTTTGCCC	59.666	20
CACGTTATATTTATAGTTTTGTGG	59.144	26	TCAACAACTTTGAACCTGCG	59.881	20
CGGTTGTATGAAACCGTTAGTTG	60.658	23	CTCTGCCTCGTCTGGCTAGT	59.769	20
TCGGAGCTAAAACGGAGAAA	59.953	20	GCTGGAGCTGAGAACATCGT	60.564	20
GAGATGCAAGAGGCAGATCG	61.058	20	AAAACATGCCTTTCGACCAC	59.978	20
CCTTCCAACAGAACAAACTCG	59.76	21	CCCCTCTTCTGCACGACTTA	60.388	20
ATGCGCGTTTTTAGGGTTTA	59.624	20	CATGCATGGCCATAACTCAC	59.955	20
TGCTCTTTGACCAGCTGTTTT	60.045	21	GGCAATTAATCAGGGCAAGA	60.038	20
TACTTGCCTTGACCCTGACG	61.224	20	ATATTACCTGCACAAGGCCG	59.982	20
TTGGGGGAATGGAGAGAAAT	60.632	20	GCATACACACCATCATTCTCG	59.016	21
CAATTAACGGTAGCCATCACAA	59.89	22	GAGATCGGAATCATGTGGGT	59.744	20
ACGACTGTCGATCCACACAA	60.162	20	CTGTTCGCATACAAACACGC	60.324	20
TCGAAACAGATCAAAACTGCC	60.242	21	TGTTAAGACCTCGTGGGGAA	60.486	20
GTCCCAACTTGCTCATTTCA	58.697	20	AAGATGGGCGAATAAGACCC	60.286	20
TTTCGATCTTCATCGCCTCT	59.917	20	TGTTGGGGTTGTTGTAGGGT	60.126	20
AAGTTGTCGAGCAGCTTACTTTG	60.122	23	ACAAAATTGTGCCCAAGGAG	59.971	20
AGCGAGTTTCGAAATGGAGA	59.955	20	TCGCGAATTCAGCTAGAACA	59.712	20

GATAGCGTCATTGTTTGGCA	59.694	20	TGCAATGCATGGAGGAATTA	60.035	20
GTTTCTTCTGCCAGCACCTC	59.997	20	TAAGGCAACGTCCCTCTCAC	60.255	20
TGTTTACGGCTGCAAATTCA	60.251	20	AGTTATCTGTGGCCGATGCT	59.723	20
CGTGGTTCGATCGTAATTGA	59.542	20	AACCACATGTTCCCCTTCAG	59.82	20
TGCACGTAGGCATGTTCAAT	60.142	20	AACGGACGAACAACGAAAAC	60.015	20
CATCTTTGTACTCAGCCCTGC	59.89	21	AAACGACATCCTGACGCAAC	61.107	20
GCCGAGTGTCACCCATATCT	59.957	20	TTTATCATTGCTCGTTTTGGG	59.95	21
CATTAAAGCTCGGTTCAATTTCA	60.464	23	GAACAAGGTTCCATTTCACAC	59.875	22
TCAATCCCCACCATTCATTT	59.991	20	TATTGTGGTTTAGGGCCACC	59.685	20
TTGATCCAAGGGTGTATAATGG	58.694	22	TGCATCATCAAGTCTCCTCAA	59.384	21
TCTCATGACTCCATCCTTCACTT	60.125	23	TTCGAAGTTACAAAAGGGCG	60.236	20
GTTGACAACTTGACATCAAATAC	57.197	25	ATCCTTGCACTCTTGCCCTA	59.836	20
TGACACGTTGGACCTGAAAG	59.72	20	GTTTGAATCCGAGTTTCCCA	59.91	20
TGTAGTCAATGCTTTTGAGATTAT	57.636	25	TTGAGCCATATTCATTTGCTTTT	59.986	23
TCGTGAAATGAAACCGCATA	60.073	20	TCTTGGGAGGGAAAATGACA	60.43	20
TTCAACCCGAACAACAATGA	59.941	20	AGGGTCAAGTCATGTTCCCA	60.363	20
TCTTTCAATTTTCAGCCCTCA	59.809	21	GGAGAGAGAGGCAGACATCG	60.096	20
TTGGTTTGCTTGCATTTGAA	60.229	20	TGAGGATGCAAGCCTCAATA	59.375	20
TGGTGTTCTTGGTGTTTTGG	59.435	20	GATAAGCCAGGGTATGGCAG	59.551	20
GTCACCTTATCAACGATCCGA	59.947	21	AAGCTGGTGGATTGAATGCT	59.7	20
TGGAAATTTTCGGGGAATAA	59.233	20	TCTCATACAATTCCCCACCC	59.605	20
GTGCCTATTGCCGACGTAGT	60.162	20	AGGGTAGGGGTCCCTGTATG	60.067	20
GATCCAACAAGCAACAGGGT	59.973	20	GAGCACGAGGGTGAAAGTGT	60.307	20
CGATTCGACGCTTTTTGAA	59.938	19	CCCAGCTGAATGCGAGTTA	59.956	19
CGCCCCATGGAGAAGTTTAT	61.191	20	CCATTCCTGAGACCAAAAGG	59.521	20
CGTGTCATAGGAAAACGAGC	58.379	20	AGTGTGGTGTTTGCATGAGC	59.758	20
CAGCATGGCCATTACAACAG	60.134	20	CCCATCATTTCGGCTACAAA	60.827	20
GGCGCAAGTTACGTGTTACC	60.564	20	AACGAATGTAACAATACGTAC	57.736	25
AAACGAGAAGAAAGCAGCCA	60.132	20	AGAGCACTCGTGGATTCTGG	60.408	20
TACAAAGTCCCACGACCGAT	60.375	20	TTACAAAAATGCCCTTTCGC	60.075	20
GCTTGACTTGCAACGATGAG	59.596	20	GGTACAGCCGAGTAGCGAAG	60.037	20
ACGCTTTGGATGTGCTTTG	59.856	19	CCTTCAAGGGGAAGAACACA	60.081	20
CGCCGAGTTGGTTCTCTCTA	60.529	20	ATCCTGTGTGCCTGTGTTTG	59.597	20
TTCCTAGAAAGATCGGGCAA	59.778	20	ATCAGTTCGTTGATTGGGCT	59.556	20
TTCAGGATAAATATCAGTTTCATG	58.52	25	ACGATTTGGAATCGATAAGCA	59.561	21
TGCAATCACACAATAACAAGCA	60.177	22	TACCTCTTCCACGGCCTCTA	59.83	20
CATGAATGGATGTGATTTGTTTG	60.103	23	GGCCAATGGAATGGAGATAC	59.204	20
ATCCGGAGTAAGTTCGAGGA	58.741	20	AATCTCACCAAGATGCCCAA	60.461	20
AATTGATCTACGTCCACGGG	59.813	20	TGTAATGGAGGGGGAATCTG	59.744	20
AAAGAAAAGGGAAAGGGCAG	59.698	20	ACAAACTTATGGACCGCTGG	59.993	20
ACCGAAACCGTGTTCTTCAG	60.149	20	GTGCACGAAATTGGAGGAAG	60.636	20
TATGACTCGCAATGAGCCAC	59.83	20	CCTATGGTGGTATGGTGTGGA	60.501	21
GTGACGCATTGTTTTTGTCG	60.157	20	GCGAAGGAACTGTGGAGAAC	59.851	20
TCTGGGGGTTAGGTTGGTTT	60.581	20	AAAAATCGACAAATTATCAGT	59.31	26
CCCTAAGTTAATGCCACCCA	59.817	20	CACCTTTGCAAAAGGGAGAA	60.22	20
CCTTTCTTGAGTTTCAACCCC	59.963	21	TTTGCAGCCTGAGTCAAGAA	59.716	20
ATTCACAAGCGGCACTTCTT	59.882	20	AGTGTACGGGGCATAACCAG	59.875	20
GCAGTTTTCAGAGCCGTCTT	59.621	20	GCGTGTTAAATTTGGATTCCC	60.541	21
TGGCATAGTTTGGTTGTGGA	59.964	20	GTGGCGAATATTTTGTTTTTGA	59.025	22
TATTGACGAATCCATCGGCT	60.435	20	TTGCCTAGAAAATCCACACAA	59.625	22
GGAGTATTGGTCTCGGTTGC	59.556	20	AATTCAATCCCCAAAAACCC	59.867	20
TGCAAGGAAGAAAAACAAACAA	59.774	22	GCCACTTTTGTCAAGGTGATG	60.544	21
GCTTGCTGTGTTTTCTGTCG	59.64	20	GGCTCTTCGGCAGTGAATAG	59.978	20
TTCCCATGTTGTAATTAATGTAAG	59.917	26	GAAAACGTCGAGTTTCAGGC	59.859	20
AGAATGGCCGAGAGTTTTCA	59.813	20	ATTGCCTTGTTGTTTGGGAC	59.836	20
CATGCAAACATCAGCCATTT	59.548	20	GGTCTATGGTCGATTGGGTG	60.195	20
TTGGGAAGAGGAAATGGACA	60.43	20	AAAACAGAAAAATTCCCCTTC	59.013	22
AGAATCAGGGGAGGGAGAGA	60.149	20	TCCGTTGTAAAAAGACCGTTG	60.018	21

TTCATACACACCCTTGCAGC	59.722	20	GTGGGGTTAGCATGGTGAAT	59.676	20
CTCCAGGAGTCGTGCTTGTC	61.009	20	TCACGCTAAAGAGGTGTTTGA	59.92	22
TTTATTATTTGGTCCCTCAACAAA	58.876	24	TCGTGCTCATTTGTGTTGGT	60.16	20
GGGTTCCTGTGCTTTCAATTT	60.346	21	GCCAGCCAGGAAAACACTAA	60.249	20
AGTCCCTGATTCTTCCCTCG	60.586	20	AATTCACGTGTTAGAGTTGATT	58.223	25
GCTTCAGCCATCGAGTTTTC	59.962	20	ATTCATCGACACCAACACGA	59.967	20
CCGAACTTATGGGCTAGGGT	60.332	20	ATCCCCTTCATTCAGCACAC	59.934	20
CGAAAAATGGTGGGAAAGAA	59.91	20	TTGCATGTGAGCCAACTCTC	59.992	20
TGAGTTTCATTTCCGGCTTC	60.192	20	ACTGACATTCACAGGCATTG	57.067	20
CTCATGTAGTGCTTTGGCGA	60.011	20	TTAAACCCTAAAAACGCGCA	60.593	20
AGTCCTAGAAGGCGACACCA	59.867	20	GGGATGGAGGAGGAAAGAAG	60.008	20
CTCACGAACACTCACGCACT	60.096	20	CCGAAAAGCTGAAAGAAACC	58.949	20
ATTGGTGACCAGATCAGGGA	60.326	20	CCTGTTGTGCCCATCAATTA	59.395	20
GGAACTTGGGACGATTTTCTC	59.933	21	TAGGATGATTGGCAACACGA	60.073	20
CATCGTCCTCCCAGAATAGC	59.653	20	TCCAATCAAGGCAAAGATCA	59.2	20
CCTGCATGGACAACAGAAAA	59.691	20	GGTGATGTGTGACGTTGGAG	60.005	20
TGGCAGGTTGGAGACACATA	60.112	20	GGGTTCACAGCGAATGAAAG	60.636	20
TAAATGATCTGCGAAAGCCC	60.175	20	TGTGGTTGATGAGTTGGCAT	59.967	20
TGTGCACTGTTTCTCTCTCTCA	58.804	22	GTCTTCCCCTTCCTCCTCAC	60.05	20
GTCGGTGGCTGAAAGAAAAC	59.717	20	AATTTGTTTTCCATCGTATTCCA	59.616	23
TGATTCAGATGTCAGCGAGC	60.104	20	ATACCCTTCCCTCGATGTCC	60.154	20
TTTGATGTCCAAAGTGGCTG	59.691	20	TGGAATTCGCCCATAAACAC	60.701	20
AGTCGATTGTGTAGTTGTGGGT	58.508	22	CTAGGCATGGAATCCGAGAA	60.17	20
TGGTTCTAAATTCATGTTTCTTGG	59.432	24	TTGTTTGATATGGCAGGGGT	60.192	20
TGTGAGAGGTGTGAAGCAGG	60.022	20	CAAACATGCAAGTGCATATCAA	59.631	22
TCACTCTCTTGCCTTCCTCC	59.53	20	TGCTGAGACATAGCGGACTG	60.16	20
ACTTAACCGACCCTCATCCC	60.19	20	GGTGGGTTCGACGACAATAG	60.375	20
CAAGAAACGGAGGGTGTTGT	60.005	20	TCAACTTCTTCAACAGGCCA	59.415	20
TTCTCTTTGCAAAACCCTCG	60.357	20	CAACCTAGAATGAGCATTGGC	59.722	21
TCACGTTAAAGGAGGGTATCATT	58.941	23	CACGGGTCTTTCTTCTTCCA	60.224	20
GACAGGAGGAAAGAATCGCA	60.34	20	AAGCCAGTGCTGGTTGACTT	59.914	20
GGCGCAGCATATATACACGA	59.714	20	GCGTGTATTTTGACGTTGGA	59.59	20
AATTGCCATCCCTCACACTC	59.934	20	AAAACCTCCACCAACAGCAG	60.149	20
TCGATCGGCCTATTTTTCTG	60.167	20	TGCGTGATCTTGGTGTTCTT	59.293	20
TCGACTCCATAGTAGCCGAGTT	60.282	22	AAAATTCGATGATTGGCTCG	60.038	20
TTCCATCCTTTCTTCCATGC	60.014	20	TCCTCCGTTTTTGGATTCTG	60.044	20
ATTTTGGTCGAAACCGAATG	59.801	20	TTGAAAACCAAAACCGAACC	59.817	20
TGTCTTATCCCCTGTCCTCG	60.065	20	TGGAGTCTTGAACAAGGGTTCT	60.146	22
TTGGCAGGTTGATCATAAATTG	59.832	22	GTCACAATCCCGAAGCTCAT	60.081	20
AGTGGCCTAATCCAAGCTGA	59.836	20	TTAGGGTTTAAAATCGCGCA	60.564	20
GAGGAGGTGCAAGAATTTCC	58.717	20	CAAGCCATGGGTCTTTGATT	59.933	20
CCCTTTTATGCTCACATCTCTTT	58.835	23	GAGATTGGTGGTTGTGGGAT	59.636	20
TTTACGTGCCTGGCTTAGGT	59.769	20	TGGAATAGGAAAGGTGCAGG	60.066	20
GGAGTAGGGCCTTGGATGAT	60.293	20	TCTTAATCCTTTGGCATTCAA	57.388	21
ATTTTAACATTGTTGGCGGC	59.838	20	GGAATTTTGGAAGGAGGGTG	60.663	20
TACTGGCGTGGATTTTCTCC	60.074	20	CGCGGATGGTTAAGATTCAG	60.597	20
TGTTTGGTTTCTGCGTGAAG	59.881	20	CAAAATCAGGCACCAGCTAA	58.917	20
CGATTTGCAAGTCTATGGCA	59.833	20	CCCCAAACAACGAAATGAAT	59.662	20
CATTGGTTAGCACTTGAATGAGA	59.28	23	TCCATTCCGAAAATCAAAGG	59.872	20
CTGCACCATAACAATATTCGACA	59.903	23	GCCTCAAATCCTATTCTATTTTC	59.549	24
CGAAACGAGTTGCTGCTGTA	60.195	20	AACCCTTCCAGTTCTGGTCA	59.549	20
AACACACAGCCGCTACTCCT	59.937	20	TACCACCGATCCCTCTGAAG	60.065	20
ATAGTGGTATGGTGTGGGGG	59.405	20	CACACAGACGAAACGTCACC	60.203	20
GCCCTCCTTGATACCACAAA	59.933	20	AACAAGTGCACCAGCACAAC	59.801	20
AAAGGACCCGACCTTTTCAT	59.805	20	GGGCAGATGCAACTACCTGT	60.142	20
CCTTGATGAACTGTGGGTGA	59.52	20	CAGCCCACAAATCCTTGACT	60.111	20
CAACGACGTGCATCATTTCT	59.722	20	ACTTGTTGAAATTCACCGGC	59.978	20
ACATTTCAGGCCAAATCCTG	59.933	20	TTGAGGCTCCCAACTTTCAC	60.232	20

CCTTCTTCTTGGCGTCAACT	59.473	20	CGTACGGCATGTTTTATGTTTC	59.429	22
GGCTAGATGATGTAGATGTGATG	60.02	24	CTTCTACCACCTCTGCCTCG	60.005	20
CTGTTCTCGACTCAGGGACC	59.835	20	ACTCCCCCTCGAAGTTTTGT	59.972	20
GCGCCACATCTTGTTGAATA	59.694	20	TTCATCAATTCTTTCTGCGCT	59.974	21
TGTGATCAGGTGCTGTGTGA	59.858	20	AATCTCCCGTAATTTGGCG	59.908	19
TTCTCAGCATATGGGAAGGG	60.029	20	TATGCGTTTTGACGGGATTT	60.323	20
ATGCATGTGTGCAGGTGTTT	60.04	20	TACCATATCTCCACCGCCTC	59.917	20
GATCGTTGACCGTATGGGAT	59.635	20	AGTAGAGAAGGGGAAGGGGG	60.797	20
CAAACAAAGTCTGCAACCCC	60.529	20	ATCGGTGAAGGTGTTCGTTC	59.973	20
TGTTTTGCGAGCTTTTATTGG	60.245	21	TGGTGTTGCAATGCTACTGAA	60.309	21
ACGGATTTAAGGGTTATTACCTG	57.667	23	TTGGATTGAGAAAGCGATCC	60.155	20
AGGCCAATTTGTGAGTGTCC	59.973	20	AGCCCACAGAGTTGGAAAAA	59.711	20
ATTTCTCACGCTGAAATGCC	60.221	20	TTCGCACTTGGACTTTCCTT	59.853	20
ACAATGGCCAAGAACGTAACT	58.641	21	TTCAAATGTTTTTGTAATTTCCC	59.653	24
TTTCCTTTTGCAGCTGGAGT	59.993	20	TCGCTCTCTAGCGGATCTTT	59.316	20
CCAATTTGAATGGTTATCACCTG	60.457	23	GAATGTAGGTATAAGACTGTG	58.156	27
CATGCACAATCAAACCTTGC	60.119	20	GGTTTGCCCCTGTATCTCAA	59.933	20
AACAATTGCACCTTTAATAGCAA	57.978	23	GGAACACGTGCAACATTGAT	59.425	20
TGTCTCTTCCTCCTCGCATT	59.95	20	TTCCTCTCGTGTTTCATCCC	60.05	20
CATGGTTTCTCGATGGCTTT	60.074	20	TTAGCCCATCAAAGTCCAGG	60.066	20
TGGCTTTTATCAATGCCCTC	60.038	20	GTTGCGTTCCACATAAGCCT	60.14	20
GTTATCACCGGATCGCAAC	58.941	19	ATGTCCTTCATCACGCAAAA	59.127	20
TGTTTATTTGAAGGGGCAGG	59.931	20	AACCTTATAGGATGTCCGGCT	58.994	21
TGGCGGCATTCTATATGACA	60.058	20	AGACATCTTTGGCACCGAGT	59.727	20
GAATTGTTGATGTTTTCCCCA	59.654	21	CGCGTCTATCGATACTGATCC	59.705	21
CCCATCTTCTGCAAAAATCC	59.505	20	CTAAAAAGGTCTGCCCTTGC	58.973	20
GGTTTGGGGTCAATTCTCAA	59.767	20	GGCTTCCGAGTTTTTCCTGT	60.61	20
GCACCCTTTTGGTGGTAGAA	59.971	20	CAGTCCACACATGAAGCCAC	60.162	20
TGTGTCATTCCTTCCACTGC	59.682	20	AAGGGGTTATCATGGGATCA	59.055	20
TCATTTAATATGGTCTGTGCGA	58.187	22	CGGTTAAAAACCGAATCGAA	59.937	20
TTAGGGTTTAAAATCGCGCA	60.564	20	CGAAGTTAGAAAATAAGGAGG	57.269	24
TGGGTTAGCCCAAAAATGAG	59.931	20	AAACCCTCAAATCCCAAAGC	60.299	20
TTGTATTAGATTGTGGCTCCG	57.795	21	CTTCTCGCGTCTGACTCCTC	60.284	20
CACTCACTCTCACTAGCCGC	58.78	20	GGGAATTGCCCAAATCACTA	59.762	20
AGCAATGGTGGTCTTCTCGT	59.727	20	TTTGTGTCGTCGGTGTGATT	60.008	20
ATCTAAAGCACACACGCACG	59.935	20	AAAAGGGGAGAAAAGAACGG	59.566	20
TCTGCCTGTCGATCTCACAC	59.988	20	CAGTGACCCTTTCGGAAAAA	60.081	20
GCATTGGTAAAACCGGGATA	59.66	20	TTCTCATTTCTCTCGTGCCA	59.522	20
TGGTTATTACCTGAATACTCCCA	57.591	23	TTGGTAAAACTCGAAGGATGG	59.074	21
GGTCGTCCAAATCTCCTTCA	60.05	20	TGTTGCACTTTTGAACAATGG	59.618	21
GGATATAACCACCTCACCCAAA	59.945	22	AGAGACGAAGGGGATGATGA	59.612	20
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TGTTGTCGATCTGGCACTCT	59.42	20	ACATAAAAGCCACCTGCCC	59.947	19
ATAGTAGCGACTGCGGGTTC	59.364	20	TAGCATCGTGAGTAGCGTCG	60.18	20
AGTCATTCGGGCCACATAAT	59.273	20	GGCATCACATGGTCTCTTGA	59.637	20
TGAGCACGTACAGATAAAAGGG	59.29	22	AGCCGATCGAGTTTTGGATA	59.668	20
CGTAGACACCACCATCTCCA	59.545	20	AGGCAGAAAAGAGGAGGGAG	59.95	20
GTGGCAGCATATCAACCCTT	59.962	20	TGAACACTATTCCCATCCCC	59.605	20
CGTGGCAGGCTAATATCCAT	59.945	20	AATAGACCCAGACACGGGCT	60.903	20
ATTGTTCGATGTCAGCTTCG	58.877	20	TTGCTCAATGAACTCCTTTGG	60.234	21
ATCGACATTCTTCTGCAGGC	60.37	20	CCCTTCGATAATCCTCAGCA	60.17	20
ACTCATTATTTCTCACTCACCAAG	58.405	25	GGGTGGGCTCCATTTTTAGT	60.187	20
TTCTGCTCTCTCTCGGTGGT	60.135	20	AAAAGAAAAGGACGGGAGGA	60.046	20
ACTTAGGACCAAAGCCCGAT	59.962	20	GCCGAGATTTGTTATGCGTT	60.103	20
TGGATTTTAGGGCTCATGCT	59.668	20	ATGTGTGCGTGTAAAGCTGG	59.788	20
CCAGTAAAGGACCATTCGGA	59.926	20	CTTGGGATGACGTGGAGATT	59.927	20
CCAAGTCACCCAAGAATTGC	60.495	20	TTGCCAAACACACATTTTCAA	59.999	21
AAAATCAAAGGCCCACAATG	59.801	20	TTGGTCTCAGGAAAGGTGCT	59.844	20

CCGTGTCCAGTCTGTGTTTG	60.194	20	ATCCATGGTTGGTTTGGAGA	60.173	20
GAATTACACAATCCTCGTGGG	59.302	21	TGCCTATTTTGAATTTTGGTG	57.705	21
AGCCTAATGTCATTGCCTGC	60.243	20	TATGGGTTATCACCGGATCG	60.544	20
CACATGTGCGACACATCAAC	59.575	20	TCGATCATAAGAGCATCCCC	59.998	20
ATAACCCAGTCACTGTGGGC	59.851	20	CGTCCCACAAAATATGTCCT	57.393	20
TCATGTTGGGTATTGTTGGC	59.251	20	CAGTTGGGTCAGTGACATGG	59.997	20
AGTTAGGCGAGAAGAGGGGA	60.34	20	CGCTTAAAAACCGGACCATA	59.958	20
ACGGATTTATTGGTTATTACATGA	58.262	26	GCCGAGATTTGTCAGAGGTT	59.288	20
CTTCGGAACTCTATCCGCC	59.782	19	CCCATTCTCTCCATCCCTTT	60.264	20
GCAGATCCAGATGCTCCAAT	60.189	20	CAACTCAAATCGCAGCTGAA	60.134	20
GCAACCCAATTCACCATTTT	59.668	20	CAAAATTCCCACCCAATCAG	60.162	20
TGCCTTCGTTCCAAGTTTTC	60.227	20	AAAATGCACCATTTCTTGCC	59.945	20
ATCCTAAGTTCGCCCCTGAT	59.925	20	TCGGAGTGAGAGGTTTTCGT	59.844	20
CGAAATTGAATGGCAAGGAT	59.901	20	CAAACGCTATGAGAGCGAGG	61.06	20
GCAGGTTAACTCTAATTAATCCGT	60.196	27	TCCGGCTACTTCGAACTTTCT	60.379	21
CTCTTCCCCCACATTCAAAA	59.903	20	AACATGGGCAAGAAACAACC	59.836	20
ACGGATGAAGAGAAATGGCA	60.603	20	CGGCATAGAATGTGTGGAAA	59.542	20
CCCCGGTTTCATTTATAGCA	59.789	20	TTAATCCCTGAAAGTCGCGT	59.708	20
CCGGTGAACTTCTCCAACTC	59.697	20	AGAACAACCAAGGCAATTTCA	59.601	21
ATGAGTTATCACCGGATCGC	59.923	20	CATTGTTCTGAATCGCGAAA	59.809	20
TCCCATGTTGTAATTAATGTAGGG	59.089	24	ACCATGATGAATGTGAGGCA	59.925	20
TGTCCCATTTTCTTCGTTCC	59.91	20	ATTGGAACAATACTATACAACC	57.118	26
TCAATCGCAACCATCAATTTT	60.316	21	TTCTTGATGTGTTGGCAAGC	59.847	20
GGCCGATATTTGCTCGTAGT	59.209	20	ATGGTCCATGGCCTGTTATG	60.603	20
AGCGGAGATTGACGAGAGAG	59.703	20	TTAGTGGGCTAAGTGGGGTG	59.986	20
AAGATCTACCTTTGGGTAACCGT	59.35	23	TTGCATCAAGTTTTAGAGCAGC	59.674	22
TTTTCCCGCAATAACCACTC	59.938	20	AATCAGCGCTCCAGATTTGT	59.843	20
ACAGAACAAGCATACGCACG	59.935	20	ACTTCCCTGCACAAAAGTCG	60.291	20
TCGTGCACTGGTGTTCTCTC	60.03	20	TCAAAGATGTCAAGGCGAAA	59.395	20
TGACCCTTTGTGGGAAGAAG	60.081	20	TACAGGTTCACCCTTCTGGG	59.959	20
GGACTGGTTTGACACCTTTGA	59.997	21	CGGTGAAAGAAGGAAGGAAA	59.284	20
CCCATTACTCCAAACCCAAA	59.657	20	TTCTTTTCTTTTCTTTCCATTTCA	58.53	24
CACGATCCATGAAAGCAAAC	59.127	20	GCCATCCTCTCCAAGCTACA	60.362	20
TGCTCAAACTTGAACTTGAATAAA	58.188	24	CGGCTATTTGAGACGACATT	57.849	20
GATGCCTTGGTCTTCCTCAT	59.094	20	CGACCCAGATTCAAACCCTA	59.926	20
TGATGAATGAAAGATGAAATGGA	59.402	23	ATGGTGGTGGGAGAAGAGAA	59.505	20
TCTTTCACCCGCTTTAGGTG	60.241	20	TCTTTCATCCCCCATTACCA	60.126	20
GAGGAGAAGAGGGAGGATCG	60.292	20	CGAACGGTATAGGATCGGAA	59.916	20
ACCGATTGCTGAGCATTTCT	59.843	20	ATTCCAAAAATCAAAGGCCC	60.13	20
TGGAAAACCAAAGCAAAACA	59.178	20	ATGAAGACATGCTGGTGCTG	59.862	20
CCTCCCTCATCTCTCCAATG	59.606	20	TGAGGCAAACTGAAAAACCA	59.293	20
CGAGCTGGCTTGAGCTACTT	59.92	20	GTCGATCCCACAGAGATTGG	60.475	20
TTCTCTCCTCCATTTCCCCT	60.008	20	CTGTGCATTTGCAGACCACT	59.905	20
TAATGGGTGTTTGTGCGAAG	59.585	20	AACAAGTTTGGGATTGCTCC	59.031	20
TCTTGGTTCCACCGGTAGTC	59.966	20	CACCCCTTATCTTCCACAGC	59.55	20
TGGGGTAAATATTTTGGGAGG	59.896	21	TACCTGCACGTTGCGTAGAC	59.935	20
TTCGCCCATTTTAAACAAGC	60.075	20	AAGGGGCAAGTTGGCTATTT	59.966	20
GCTTCCCCCTAGTGAACACA	60.111	20	CATCCTTTTGGACGAGCAAT	60.074	20
ATTTGTGCCAGTGTCCTTGC	61.107	20	TGATTGCATTATCAAGAACCAA	59.485	23
TTAGGGTTTAAAATCGCGCA	60.564	20	TGCTCCTAGTTGGCACAAAA	59.464	20
ATGGGTTCCTTTTACCTCGG	60.18	20	AAAACTTCCTAAGCCCCCAA	59.939	20
GCAACGGAATACCCCTCTTT	60.32	20	CCTGTGTGCCTGTGTTCCTA	59.745	20
GAGAATTCCAACGACCTTCG	59.67	20	CCACCTATCTGCATCCACCT	59.95	20
AATATTGAGCTCCATTGCCG	60.06	20	GGCGGTGAAACGATAAACAT	59.829	20
GACCAAAATTCAGTAAGGGTAAC	59.723	25	TTGACCCCAATGGATCGTAG	60.713	20
GTTATCACTTGATCATCCCCC	58.174	21	TTGGTGTTGGTGTTGTTGCT	60.049	20
TCGAGAAAATCGGAAGTTCG	60.323	20	ATTCGTTTTTCCTTCCCAGG	60.291	20
TGGTGGATTTTTGGAATGTC	58.243	20	AGGTTGAGTCGGACGAGTTG	60.298	20

TCGATCAGTCGGTAAGTCCC	60.073	20	AGCATCAATGGAGTATTGAAA	57.835	23
TGGGCTTTGATTCTTGCTTT	59.823	20	AATGTCGTGACACCTAGCCC	59.997	20
CAGAAATTGCCTTGGTTGTTC	59.601	21	CCAGAGAGAAGTGAGCTCGG	60.275	20
CGACTTGTCGTGGTTAGGGT	60.028	20	TGGTAAATCACTAGACCCAAG	59.879	23
AAAGAAACTGGAATACCTCGGA	59.133	22	TTGCGGATTCTAAGATTGGG	60.031	20
TGTGCAAGGTTGAACCAAGA	60.278	20	ATTCTGTGGGAAGAGCAAGC	59.434	20
CTTGCCATTGATTTTGGTGA	59.518	20	ATGCCCATTCAAACTTCAGC	60.081	20
AACGTTTTTGTGAATGTTGCC	59.897	21	TGATGGATGGATGGTCTTGA	59.85	20
CAAGGTGTAGATCTGGCGGT	60.134	20	TATGTATCGTCCGCGCTGTA	60.259	20
TGAGAATGGGGAGGTGAGAG	60.191	20	TAGTGCCGTATTGTTTCCCC	59.823	20
AACAGTTTCAATTCGCCACC	59.978	20	ACATCAGACTCCACCTTCCG	60.112	20
TTCCGAATGCTGAGCTTTTT	59.96	20	TGAAGTAGGAAATAAGGAGGT	57.525	24
GAGTTCGTCAAACCTCCCAA	60.088	20	CTTGAGCGTAAACACGTCCC	60.689	20
TTTGTTCCTACTCACTCACATTAA	58.512	26	ATTTTTGCTTGCAGCCTTCT	59.114	20
GAGGAGAGTTGATGGTGAGGA	59.243	21	CACCTAAACCCATAACCCCA	59.541	20
CAGGGGTTGCACAATATGTTA	58.426	21	GGAGTATCACTTGAATGCACC	60	22
GTTGGACCAAAAAGCCCTTA	59.064	20	AGGGGAGAGATGGAGGTGAT	59.889	20
CTACTCCGTGGTGTTCCCAG	60.557	20	AGCTGATCCTGCGACATTG	59.959	19
GAGGAGACGACGACGGTTT	60.253	19	CACTCCCCCGTAAAACAAGA	59.964	20
CAACCAGAAGCAGTGGGTTT	60.149	20	CCTCCGTGGACGTAGATCAT	59.95	20
CTCGGTGTTCTCGCTTCATT	60.397	20	CGGTTCATTCCCATCCTAAA	59.756	20
CGCCTTAAATATGCGTAGCC	59.738	20	GCCGTGTTAGCCAACGTAAT	60.025	20
GTTGTCACGGCGTGTGATAG	60.183	20	TCGTAGTGGAAGTGACAGCG	60.049	20
GTTGACCAAATTAGCCCCAA	59.801	20	ACCTTTTGCATTGTCAGCAA	59.322	20
TGAGTGGTTTGGTTGGAGAA	59.109	20	CTAAGCACCACAAGCAAGCA	60.195	20
TCTTTCGGCTGACTTTTTCTTT	59.539	22	GAGCTTCCGCATCGTTCTTA	60.49	20
GTGCCATTGATTTCTGAGGG	60.461	20	TGCATACGGAATTTCAGCAA	60.215	20
AGGGAGAATCTATGGCAGCA	59.797	20	TTCGAAAATGCTCGTGAAAT	58.361	20
GAATGCTTAATGGGAAGCCA	60.038	20	TTGGAACGCGATACACAAAA	60.111	20
TCAAGTTGAGCCTCCAAATC	57.864	20	ATCTCCAAAACCCGACAACA	60.353	20
TATGGGAAGGACATTTTCGG	59.756	20	TTGTTATGCATTTTGACGGG	59.42	20
TCGGCTGTAAGAGTGGAAGG	60.388	20	CACTTAAGGGGGTTATCATTG	59.604	22
AAATGTGATGTGGGTTGGGT	59.95	20	CATGAACGGTTTAGGATCGG	60.323	20
GCTCCTGTGCCACTGGTTAT	60.142	20	TGCTGTTAATGAAGGCATCG	59.833	20
CAAGCAAGCATTTCCTCCTC	59.955	20	CTTGCAAGGTGGTCGAAAAT	60.11	20
GATCGGACGTCGAACAAGAT	60.081	20	TGCCTCTTCAGATTTTTCGG	60.323	20
TGTGCTTCTTTTCTCCCCTC	59.405	20	AAAAATTGAAGCGCCAGAAA	59.832	20
TGGTTTAAACAAATCGTGTTCG	59.904	22	GTGTCCGTTAAGCAGTAAAGA	60.228	23
GATTCTTGGTTCCGTGTGGT	59.827	20	CCTACTCCACCCCTTCATCA	59.92	20
AGGTTGCTCTAAGGTGCCAA	59.875	20	GAACGATAACGCGTGTGAAA	59.735	20
TGGTTATTACTGGAACGCGAC	60.011	21	TGAATGAATCACAAAAGGGGA	60.294	21
GGGGTTATCACTGGATCACG	60.195	20	TTCAATTTCGTGTGCCAAAA	60.088	20
CCCTAACTCGACCCAGATCA	60.065	20	GGTTGAGGGTGTGTTTGGAG	60.399	20
TGGGAAGAGTGGGTATGAGG	59.92	20	CCTCCCGTTTTCTTGCATTA	60.067	20
CATGGAAGACTGATGGAGGC	60.622	20	TCCTTGTGGTTCTACAAAATAG	60.056	24
GACGAACATCACCATTCCCT	59.786	20	CACACCCACACGCACTTTAC	60.072	20
GCAGATTCCCAAATCCAAAA	59.878	20	ATGTACGCATGGAATGGACA	59.805	20
TCGAAATTCGTTGTTTTGTCC	59.967	21	CCGATCTTAATCTTCGCTGC	59.945	20
CCGTGTACTCTATTCGGGGA	59.948	20	GGAAATTGATGGATTTGGGA	59.558	20
TGATGCACGATGTATGTCGAT	59.971	21	CTCAGATCCAAACGCCTAGA	58.048	20
GAGAGAAAAGGGAAATCGGC	60.152	20	TTCGGGGCATACATGTGTTA	59.809	20
CCTGCATGGACAACAGAAAA	59.691	20	GAGTTGGGGGATGAACTGTG	60.363	20
CAAGGGTTATTGTGGTTGGG	60.081	20	GCTCCTAAAATATTGGTTTCTA	59.441	27
AAACTCATATTCCATCCAAAGG	57.132	22	CAGCATTGCTTGCACTTCTAA	59.264	21
CAATATTACAAATGGCCAAGAGA	59.11	24	TGTTTTGTAATTTCCCATGTTTG	58.816	23
GTGCTTTGGAAAACTCATGC	58.353	20	CGAGTATTGGTTCAATAGAATT	60.143	26
ATGGGAAGAAAACGCAACAC	59.978	20	TGTACCGCAGTTCAGAGGTG	59.897	20
CATTTGAGACGGACACATGC	60.12	20	ATCTACCTCGGCCATCTCCT	60.059	20

CGTGGTTCGATCGTAATTGA	59.542	20	TACCTCGAGACCGAACAAGG	60.246	20
TCACATGAATGGACCCCTATC	59.62	21	GTGAAAAGTCACACGAAAACG	60.19	22
GAGGGATTTGGGACGATTTT	60.131	20	TGGTTGTTGTGAGGGTTTCA	59.976	20
GTGTGAAAGCCGAGAGAAGG	59.989	20	TTCTCACTCACACTGCCGTC	60.03	20
ATCAAGGCGAGCCTCAATAA	59.807	20	GGGGTTATCATGGGATCAAG	59.055	20
TTCGAGATGATGGTTGGTGA	60.048	20	CCCAGACCAATCCTTCAAAC	59.381	20
TTAACAATCGCAATGCCAAG	59.702	20	ACCGGAACCGGAATTAGAAC	60.187	20
ACATCGATCAGTTATCATGGGA	59.273	22	TGTGTTTTGACAATATTTAGTGT	58.633	27
CAACCGAGTACCTAACCACAA	57.68	21	AGCCATCAACCCCTTAAACC	60.187	20
AGGATAGGGAATAGCGTCCC	59.402	20	GTTCAAATCGATCAATCCGC	60.423	20
TGAAACAGAGAGCCCCCTTA	59.807	20	GCAAATATTGGCCGTCAGAT	59.929	20
TATAGGCGTTCCACTCAGGG	60.088	20	ATGGTGGTATGGTGTGGAGG	60.51	20
TTGAACTTGAAAGCCCAACA	59.293	20	GGCTGCTTGTTCTGGGATTA	60.214	20
CCTTCTCCATCAACTGTGGG	60.501	20	GGGTCTACCCTTTTGCCCTA	60.312	20
TCCATTTTCAGGTCCTCACC	59.903	20	GACAGCCGTTGTCTGGAGTC	60.873	20
TAGCCGATAAAAATGGCACC	59.928	20	CGGGATTTAGGTGTTTTGACA	59.847	21
TTGTCATCACCCTAGCTCCC	60.073	20	AGAACGAGAGAAATCGACGG	59.43	20
CAAAAATCGGGAGAAGGTGA	60.044	20	CAGCCCCTTTTTCATTTTCA	60.046	20
CAGTGGGTTTTTGGTGATGA	59.389	20	GTGGACGTCCCAGATTGTTT	59.827	20
TAGGACCACATTTTGTCGCC	60.894	20	ACAGCACCCCACAAATAAGC	60	20
CAGATGGTGGTGTACGGTTG	59.873	20	CTGAAACCCTAAGTTCCCCC	59.799	20
TGCAGTGAGACCGAGTTGAC	60.03	20	TCGACCTACGAGAGTGAGGG	60.399	20
AAACTTTCATTCCACCCACG	59.83	20	CAACTTTTCCGGTCCGTTTA	59.968	20
AAAGATGAATTGGGGGAGGT	59.629	20	TGGGAAATAGAACTGGGTCG	59.926	20
TTGAGGGACAAAATCGACAA	59.097	20	TCTTCGATGAACTCTGAAATGC	59.457	22
CAGAACCGTTGTCTTTCAGC	58.497	20	CGAACCCTTTCATTCTCCAA	60.044	20
GATAGCAGGTGTGATTGGGAA	59.947	21	TTTTCTTCAAAATGCACAATAAT	58.319	25
GCATAGTTCGACGATGTAAGACA	59.307	23	CCATCGTCGCTATCACATTG	60.096	20
AGGCTGATATCACCATAACGC	59.084	21	GCAACAAATGGATGGTTGTG	59.823	20
TCACACACGTTTATTCGAGACAC	60.088	23	GGCATCAAAGTTGTCGATCAT	59.954	21
TATTCTCGCTTCTTCGCCAC	60.49	20	TCCCACATTGGTTGGAGATT	60.173	20
ATCGGAAGGAGCCTTGTTCT	60.212	20	TTGCAATTAACGAAGGTCCC	59.938	20
CACTTCCCAATCCCTTTGTG	60.345	20	TTCGGTCACATTCAATAAGGC	59.952	21
ATGTGGAATGAGGGTGAAGG	59.779	20	GTGCAAACCCATGATTGACA	60.376	20
AGTGACAGTTTCACCTGCGA	59.467	20	CAGGCTTGCAGCAACTAACA	60.195	20
TTCTGTGATCGCAAAAGGTG	59.84	20	ACAGCCCACTTCTAAAACGG	59.238	20
TGACAAATAAATGAAATACAAGA	57.062	26	GAGGGAGTTGGTAAGAGGGG	59.928	20
CTTTCATGGGTGATGGAAGC	60.461	20	AACGAAATCCTGCCAATCTG	60.074	20
CATATCAAGTTCCCGCCATC	60.296	20	AAATGCAAGGCACCCATTAG	59.96	20
GGTTGACTCTTTTACTTTAGCCGA	60.176	24	GAGGCCTCGATCTTCTGTCA	60.497	20
TTGAGCCAGTTTGTGTCCTT	58.342	20	TGGTTTGATTTTTGGTCGGT	60.206	20
GATCTAGGAGAAAAGTGACATTCT	58.94	26	CACTCTCAGCATATGCACGC	60.594	20
ATGCTGCACGTTACAACACC	59.646	20	CAATTTGAGAATGGGATGGG	60.126	20
CTTGCCGAATGTTTGTCTCC	60.636	20	TACCGCACTAAACCGTTCAA	59.226	20
CACATGGGGAATATGCATCC	60.953	20	AACATTGCGGACTTGGTACA	59.05	20
GCTTGGTCCGAAAATTTCAA	60.053	20	AACTGCTAAGGAAGATGAGAT	57.276	23
TTTCGCGTGCTAATTTCTCA	59.585	20	CGTGATGCAACGCATTCTTA	60.807	20
CGTCGCGTTGGATTAATTTT	59.964	20	TCCGAGAATCTGTTAGAGGAGA	58.148	22
TGCTTGTGGGTTTTGTTTTG	59.603	20	CAACCTTTTGCAAGCACTGA	60.027	20
GTCCGATTTGGGGAGAGATT	60.272	20	TTCCATGCAACAATCAATGC	60.476	20
TTCCAGAGGAGATGGGAATG	60.003	20	TTTTTATGCACAAGCCTCCC	60.074	20
GGACAAGCTGTCGGATAAGC	59.843	20	ATTTGAATGGCAAGGATTGG	59.762	20
GGGTGGATGTACAGTAAAGGC	58.45	21	GGCATTCTCATCTCCACCAT	59.893	20
TCCGATGATCAAGTCAGTGC	59.794	20	GCTAATGCAGATTGAGCGTG	59.596	20
CCATCAAAAATTCCTCCCCT	60.124	20	ATCTGGTTATTTGCCCGAAA	59.411	20
CAACGGACGCTATCGGTTAT	59.982	20	GATATGCGCGTTGGATTTTT	59.935	20
CTCAATCCCGTCACCTTCAT	59.927	20	TCAAAAATATCCTCGCTGCAT	59.696	21
GGGGGATGCCACTGTAGATA	59.773	20	CTATGCGCATGGGAGAGAGT	60.384	20

GGAGAATTCGAGAGATTGCG	59.917	20	CCGTCTCGACGAAAGCTAAC	60.015	20
TTTCGTACAGCCGTTTGATG	59.729	20	TGAGGCATGCAAAGATGAAG	59.948	20
CACGTCCAGAGGAGACCAAT	60.112	20	TTGCGTATGATAGGGTTAGCA	58.342	21
AGTTCTCCAACATCATCGCC	60.081	20	TGTGTTTCCACTCCCTCTCC	60.088	20
CTCGCAAGGCAATCATCATA	59.792	20	TTTCTTATTTCCCGGCTCCT	60.034	20
ACCATCTCTGCTCTTCCCCT	60.216	20	AAGACGGTGAGTTGAGGGTG	60.151	20
TTCAACCTGATTTTCCCCAC	59.767	20	GGCTGCTAGAATGGCAGAAG	60.118	20
TGCTGTGCGTAAATTAGCGT	59.537	20	GGGATGTTTGTACCTGAATGC	59.307	21
GCCGAGATTTGTTATGCGTT	60.103	20	ATAAAAATGGCACCTGGCTG	59.96	20
TAGAGCTGGAAGGCATCAGG	60.495	20	CAAGAGGCAATCACGTTGAA	59.84	20
TATTGGTTGGGTACGGGTTG	60.472	20	TCCTTGCGTGGCATTATTTT	60.456	20
TTTCTCATGTTGTAATTAATGTAG	59.318	27	TTCAAGAGCAAGCAAAGATCT	59.7	24
CGAAATCGAACCGGTAAAGA	60.067	20	TACTGACTTGTTGTGCGGGA	60.301	20
GGAACAAATGAGACTGTTTCTGC	60.165	23	ACCCGAAAACCGGTTAAAAA	60.549	20
AACATTCCCTTTCTTCCACG	59.028	20	CTGCTGTGATCAGCCATGTT	59.862	20
TTCTTCTATCTTTTGATTACCGTTT	59.171	27	CCCGCATGTCATAACCACTA	59.42	20
TTGCAACCGACATTTAGCAG	59.872	20	CCAATGGCGATATTTCCTGT	59.784	20
TGCAACAAATGATCCCAGAA	60.049	20	GTGGTGTCTATGTATGGGTGG	59.598	22
ACGTGAATTGGATGAGCCAC	60.935	20	TGGACATAAATTGTAGTGCCA	59.415	23
GTGTTGTGCCTTAGCCCATT	60	20	GTCCACGGGAGAGAGATGAG	59.792	20
TGATGATGCTTCATGCCCTA	60.182	20	CACCCTCCTTCCTCAAACAA	60.081	20
CAAGAAATTGACATGTTGGCA	59.576	21	AACAAAGGGGGTTGGAGAAT	59.668	20
GGGAAATTCTTGTACCTCCTCC	60.183	22	GTTCACGCGTGCTCCTAACT	60.462	20
AGCGTAAACACGTCCCCATA	60.386	20	GAGTTCGTCAAACCTCCCAA	60.088	20
CCGGAATCGCATCAATACTT	59.923	20	AAATAGCCAGCACCAAAACG	60.131	20
GTCTTCTGAAGTTGCGACCC	59.851	20	TCTCTCTCTTTTTGGTAGGTCA	60.165	25
ACTCCTATCTCCAATCCATGC	58.08	21	TAGAATGTTCCGAAATGGGC	59.901	20
ACCTTCATTTGGGCCTCTTT	59.94	20	TGTGAAGTGTTGCTGATGTGA	58.855	21
GGCCATGGACCATTACAAAT	59.51	20	TGAACTCCTGTGTGCATTGG	60.722	20
GCTGTAATTTCTTCCCCGCT	60.582	20	TGAAAATTAGAAACAGCACAT	60.051	25
GTATTTGGTGGTGGGAGTGG	60.088	20	TTTATCAGGGAAGGACGTGG	59.926	20
GGGTCGTATCATTCAGCCAT	59.78	20	GTCCGGACGGAAAGATTACA	59.933	20
AACATGGGGAGAATCGAGTG	59.927	20	CTGTTATGTCGTGTCCGGTG	60.025	20
CTCACTTCCCACACACATGG	59.997	20	TAATTCCGATTTGGCAAGGA	60.395	20
ACGGACAAAATGTACCCCAA	60.088	20	TGGCGCCTTCTATTCTCCTA	59.938	20
TATGGTGGACCGATACATGC	59.23	20	ACCCGTACAATATCAACCACA	59.134	22
ATGCAATGAACCATGCAAAT	58.849	20	GAAGTGTTATGCGTTTTGACAA	58.249	23
ACGTGATCTATGTGACCGCA	60.144	20	ATCTCACGATATCCCGCATC	59.884	20
AACCATTGCACATGAGACGA	60.12	20	AGAGGAATCTTCCCAATTCAC	59.94	22
AAAGGATTCGAACCCAGGAT	59.766	20	GACCAAGTGCACGAGCTACA	60.056	20
GCCATCCATTCTGAAGATCAA	60.029	21	CACATATGCAAGATTTCAGCC	58.254	21
GGGACTGTTAAGTTTCCGCA	60.11	20	ATGAGCACCAAATCTTTGCC	60.081	20
AATATGAAACCCAACGTCGC	59.829	20	TATGCCCTTGTATGCACAGC	59.718	20
TTTTACCCGCGGAAATAACTT	59.858	21	AATCCACACCCGAAATATGC	59.651	20
ACTGCAGACGCGTGAATTT	59.46	19	CAAATGGTTTGGGGTTTTTG	60.06	20
CACGTAAGTTCGCAACAACC	59.245	20	TCGGCATAGATGACTTAAAAG	58.544	22
AACCGAACTCGAGCTTCTCA	60.134	20	AGAATGGAGAGGGAGAAGGG	59.63	20
TTTTGAACCCTAAAAACTCGC	58.421	21	TCACACTGCAACCAACATCA	59.705	20
TTGTGTCTTAAAGTATAAAGGCAT	58.463	26	TCCTTGCTAGGCTTTATCCG	59.451	20
GGTTTTCGCAGAGACTTGGA	60.375	20	TTTAAGGGTTATCACCTGATTT	57.757	24
GTAACCCCTACACCACCCCT	59.972	20	GTTCGGTGAAGATTGGAGGA	60.05	20
ATTTTCGTTGGATTCGCAAG	60.074	20	AACCAAGATCAGGCTGCAAT	59.7	20
TTCGAAAAATTAAAGGCCCA	59.538	20	CTTAGGGGACACCCAAGTGA	59.959	20
ATAGGATTTGTGAAGGCCGA	59.528	20	GACTCGCAAAGACTTGAGGG	59.989	20
TCCATTCAACCAAATAGCCC	59.762	20	TGACGTGCTGGTTGTCCTAA	60.301	20
GCATCTCTCTCTTGCTCTTATTG	57.559	23	GACAATTGCAAATATGGCGA	59.525	20
TAACTTTATTCGCCCCAACG	59.958	20	GCTGCATCGATGTATTGTGG	60.104	20
AGAGATCGGGTTTGCTGAAA	59.813	20	AACCCTGACCATTTTCTCCC	60.169	20

ACCATTTTTCCTTGTCACCG	59.83	20	TCATTCTCGGGCAAAAATTC	60.016	20
TGAAGTTAGGAAATAAGGAGGTG	58.743	25	GTCGCTACAAGCAGTCACCA	60.056	20
GGTTATAGCTACGTGGGCGA	60.117	20	GGCGACTTTTCAGTTTCCAG	59.853	20
TGATGTCCCTGGAAGACCAT	60.326	20	ATTTGCAGATGCTGATGCTG	59.979	20
TCACACACACACTCGCATACAT	60.104	22	TGCGTGTGTCTGAGGATGTT	60.319	20
ACCTCAAGGAACACCACCAC	59.859	20	GCAAAATACCCTGAGTGGGA	59.933	20
GTGCAGTAGGTCACGGGTTC	60.577	20	TGGAGGTCGAACTCAATTATGA	59.569	22
TCTACGTCCACGGAGAAAGG	60.246	20	TCCAAGCCAACAGTCACTTG	59.873	20
TTTTTGGCCTGGTTTTTCTG	60.081	20	ATAGCCAAGGCAGCTCTCAA	60.118	20
CCATCCCTTTTTCGCTTTTT	60.412	20	ATGTGAACGAAGTACCCCGA	60.375	20
GGAAGCTAGGCGGTTTTGAT	60.582	20	AAACGCTAGGCGGATCTAGG	60.721	20
CTTCAGCCCCTCTAGGTTTG	58.931	20	TCTCACACTAGTGGCATCGC	60.016	20
TTGTATTGTAAAGCCGCAACA	59.269	21	AAAGCGCGATTTTAAACCCT	60.095	20
TTAATCCGTAAGAATAATCCATGC	58.535	24	TGGGACATTTTTAATTTTGCCT	59.728	22
ACGCGCGTTTTTGGATTTA	61.489	19	TTGGGCTAAAAAGGAACAAGA	58.862	21
GGCGGATGAATAAACCTCTG	59.528	20	ATATTCAGACCTCCGCCACC	61.242	20
GTCAAAACCCTGCCTTCAAA	60.088	20	GGAAGGGAAAGAACCTTTGG	59.912	20
TACTTGGTTGAGCTTGGCG	59.996	19	GTGTTGAATCACATGTCCCG	59.812	20
GCATTTTAAAACACGTGGCA	59.608	20	GCATGCATCTGTCGGATCTA	59.788	20
TTAACTTCGCCCCTGATCTC	59.269	20	GGAAATAAGGAGTTGTTATGAA	60.434	25
ATTTGCTCCAACAAACCTCC	59.031	20	TTATTTTCTCTGTTGCGGGC	60.209	20
GAGGTTGGCTTGCTGATTGT	60.263	20	TTTTACTTTGGCCGAATTGTC	59.111	21
GCCAATTCATATTTATTTGTGATCT	58.85	26	TTAAATTTTCGAACGCCTGC	60.205	20
AAAAATCTTGCTGCACCCAC	60.118	20	AGTTCGGATTTTTGGCATTG	59.938	20
TTGACATTCGCATTTTAAGAGTAG	59.668	26	AGCTCCAATAGTTGCTTCGG	59.476	20
ACTTGTGGCTATGCCTTTGG	60.132	20	CACTGCGCACACTTTGTTTT	59.951	20
CATGAAAATCATGTTCCGCA	60.466	20	AGCCGATTTCTTTCACTCCC	60.578	20
TGCAACCAAAACACACACAC	59.03	20	AAAATCAAAGGCCCACAATG	59.801	20
GGTTCCGCTCAATTCAGAAA	60.192	20	TGGCGTCTGGTAAATCAACA	60.111	20
ACCGGGCACTAAGGGATTAT	59.688	20	GCGAGAATTGGAGACGAGAC	59.957	20
ACCTTGACCTTCAGGCTTCA	59.844	20	CGTGGAATATTTGCATTGCC	61.218	20
TGCGCGTTTCAATGATATGT	60.103	20	ACCACGCAGTTGAATTGCTA	59.347	20
TGAAAATCTGACGAGCATGG	59.799	20	ATGGGAAACATGGCCTAGTG	59.813	20
TGTGAGAGTGAGAGAGGGGG	60.388	20	AAAAAGGGAGAAAGAGGCCA	60.18	20
CTGATTCGCACAAATGATCG	60.22	20	AGGCCGGTTAAAGGAGAAAA	60.068	20
CGGATTTAAGGGTTATTACCTGAT	58.81	24	GCGGAAATTAACCACAACCA	60.732	20
TTCCCCTCATCTTCAAGTGG	60.042	20	ATGCGTGTTCGATATTGGGT	60.221	20
TTGCGTGTCAGTGTTTTTCC	59.74	20	TTGACCTTCTCGAGCACTGA	59.701	20
CTTCATCCCTCAATCCCTCA	60.003	20	TCCCTCTACAAGATGGTGCC	60.073	20
CGCGAAATGAGGAGCTTAAC	59.982	20	TCTCTTTTGGTTGGTGAAGAAA	58.856	22
GGGAAACCCACAATCATCAC	60.034	20	GGACGCATCAGGTATAAAAGG	60.332	22
GATGTCTCGAGTTCATGGCA	59.794	20	CGCATCTGATTTTTGCAATC	59.261	20
CCCCCTTATTTTATCCCAACA	59.896	21	GAAGAAACCCCTTTTTCTTCTCT	58.513	23
CGTGGTTCGATCGTAAATGA	59.542	20	ATCATCACCACAACTCACCG	59.393	20
CTCAGAAATCAAGCCGAACC	59.813	20	GGATGGTTTATGGATGGTGG	59.871	20
CTTCTCTGGAAAGCCACCAG	59.982	20	TGTTCATACGCATTGGAAAAA	59.063	21
CAGTATTACAGCCGTGGCAA	59.752	20	TTGAACTCCCCTCTCTCTCG	59.525	20
TTCCCTTCCAGTTACACCGT	59.449	20	TAACGCCCCGTATTTTGAAT	59.323	20
GCCATTATCTTGGTTTCACAAA	58.989	22	GTTTGGCCTTGCATTTGATT	59.945	20
CACGAGCTCTTATTTGGCCT	59.476	20	TTTCTCCACCAAGCTTACACAA	59.785	22
TTAAGGGGTTTTGCAGGATG	59.931	20	GCGTTGTCGTTTCTTTGGAT	60.118	20
TTGGACAATTCAATAGAAAACCG	60.219	23	ATAGCCATTGGCCTAGCCTT	60.082	20
GGTTTGGTGAAAATGATGGC	60.177	20	TGCTTTTCCGAATCTGTGAA	59.395	20
GCTTCTTTCGCTTTCTCATTG	59.238	21	TCAGCATGTTTTGGCTGTTC	59.847	20
GTATTCCCGGGTTTCTCCAG	60.683	20	CCCCCTAAACCGTAAATCAA	58.805	20
GGACGTTTCCTCGTTTTTCA	60.088	20	TTGAAGTTGATCAAGCAAGGG	60.234	21
ACCCATGCATTCAAACAACA	59.823	20	AACATTAATGGCGTCGAAGG	59.96	20
AACCAGCTCGGTGATATATGGT	59.752	22	CGATCGTAATTGATCTACGTCC	61.213	23

TGACGGGATTTAGGTGTTTTG	59.847	21	GGTGCCAAAATTGCTCTTTC	59.691	20
ACTCATTTGGGGGATTGTTG	59.647	20	ATTACGAGCCACGGCTACAG	60.292	20
CACTGACATTTCCTCGCTCA	59.984	20	GCCAAAACAGACCAGAAAGG	59.711	20
TGGCCACCTCCATTTCTAAC	59.933	20	AGAAAAGCCGAATGCAGAAA	59.96	20
TGAAATTCCGATGAGCCTTT	59.645	20	CGGTTATCACCGAATCGC	60.033	18
GATATCACCGGCACTCCATC	60.312	20	GCGATAGAAAAGATGGCGAC	59.813	20
CACTCCACCAACTCGAACAC	59.152	20	TTTCCACAAGTGAAGCAACG	59.881	20
GGGGCTTTCAAAACATTTCA	59.916	20	AAGGCTATCGTTGCTTTCCC	60.582	20
AGAACACGAGGAACTTGGGA	59.697	20	TACAAGGCCCGACTTGAGTT	59.734	20
AGTCACCTTGTTCAAACGGG	60.005	20	CTCCTTTTGCACCTTTTTGC	59.861	20
GTGTGCGGTGTTGTCTGAGT	59.789	20	ACACCCTCACCTCCCCTC	59.888	18
GTGCAGGGGAGTGGTACATT	59.851	20	GGAACTCCCCATAACTGCAA	59.933	20
GCATATCGGTTCGGTCTCAC	60.492	20	TTACGTAAAAATGGGTTATTAT	57.717	27
CATCAGTCCAGCCTTCTTGG	60.791	20	CGTGACATGTTGCTGAGGTC	60.319	20
TGATGTTTGCATTTGAAGAGG	58.759	21	ATATGAGGATCCGATGTGGG	59.587	20
CGTTTTGACAATATATAGGTGTTT	58.178	26	ATTTCGAAGATCAACGGACG	60.074	20
AACGCCCATGATCAAATCTT	59.391	20	AAGGAGGTGTTATGAAGGGAT	58.028	22
TTTCTCAGCCAAGCTCACCT	60.134	20	CCATGTAAATAGCCGTTGGG	60.202	20
TCCCCTTTATCTCCTCATTCAA	59.903	22	TGATTTGTTGGGGCTTTAGG	59.931	20
AAACCCTCGCCTCTCACTCT	60.393	20	AAAACAAGAATTCGGCATCG	60.074	20
TGATTCCATTCCATGCTTCA	60.009	20	ACGAGTTCTGGAGCTAGCCA	60.156	20
TTTTCGTAATCCCCTTTTCA	57.23	20	TGAGTTTGCATCTAAGGAGGT	59.378	22
ACTGTTTCCTGTTCGGCTGT	59.769	20	TGAGGATACTCGATTTCACGG	60.081	21
AGACCACCGAAAAATGTTGG	59.83	20	AGAGAAGGGTTATCACTTGAA	58.38	25
AGGCTTGCAAGAAGCTGAAG	59.898	20	TGGGCTCTTTGGATTTCAAG	60.184	20
TCAGCGCCACGTATCCTAGT	60.817	20	TCGTTTAAGCCAATATCATTGT	59.44	24
TCATTTCGGGTTATTTTCGG	59.767	20	TTTTCAACCTCGCTATCGCT	59.982	20
ACAGGTCCCTGAAACAAACG	60.005	20	TGCGCATTTATGAGTCCATT	59.14	20
GCTCGGAATTTCCTTTCAGA	59.387	20	GAGGAAAACAGAGGCTGTTCA	59.463	21
AAAGGGATAAAGCCGTCGAT	59.93	20	CTTGATTTCTTTGTGGCGGT	60.11	20
CCTGCCATTTCTCTCGTGTT	60.255	20	CACGTTAGGCTCAGGAGTGA	59.034	20
ACAAAATGGCCAAGAGAGTTT	57.853	21	TTCGTATCGCTTCCATGTTG	59.688	20
AGGGCAAGAGAAAGGTTGGT	60.11	20	TTCTTGCCCAAATGAGCATC	61.121	20
CAGAACCCGAAGTGAAGAGG	59.837	20	TTGTTTTTCTTTTGGGGCAG	60.081	20
TCCACAGCAGAGTCTCCTCA	59.685	20	TTTGTTTAACTCCCACTAATGC	59.937	24
CAGAAAACTTTCATGCCGCT	60.386	20	TGTTTCCATTTCCATGGTACG	60.602	21
GGCGTGCTTCTTGAGAAATC	59.962	20	GATGATAGAAGGGGGCATGA	59.854	20
TCTCTGTGGGTATTCCTGGTG	59.974	21	AATCCAGCAATTTGCCTTGT	59.574	20
CTTTCTCTCCCGTGGACGTA	60.246	20	CAAAGTCCGGCGTAGAATGT	60.132	20
AGCAAGGTGATGCGAGACTT	60.02	20	CCTCTGTTTGTTTCCTTCCG	59.705	20
ACGGGTATACTTGGAGAAACACA	59.812	23	CATGGCATGCACATTTTAGC	60.103	20
TGCACATGTAAAACGATCCA	58.547	20	AAGGGTTCGAACTCGGATCT	60.074	20
GGACGGTTAAATTTTGTCCC	58.277	20	GGTGGGAGCCTATAGCAACA	60.096	20
GATTGGGGTGCAGAAGAGAA	60.195	20	GCATTGGGACACCTAAGCAT	59.962	20
TCATCGTCAATCGTCTGAGC	59.95	20	CAATATTACAATGGCCAAGAG	57.725	23
CATGGGCCTTGCATGTATAA	59.401	20	AAACTCCCTTGGGTGAGAGAA	60.096	21
TCTCGTTGCTATTCTTGCCA	59.566	20	AGGTTTGTTTTAGGCCCACG	61.242	20
GAAAGGATGAAAATCATTGGCT	59.446	22	CCATGTTAAAACGGGCACAT	60.617	20
CCAATGGTTATCATCCCACC	59.871	20	TTGAAACGGACAAACGATGA	60.088	20
TTGGATCTTCCTCCTCTCCA	59.731	20	AAAAGGGAAAAACCCTCAGC	59.571	20
TGGGGTATAAGGGCATACGA	60.167	20	AAAATACCCTTCCCCGAATG	60.013	20
GCAGAAAACGGAGGAAAAGA	59.429	20	AAGGGTGATGTCGCACTTCT	59.727	20
CACTGGAAAAATGGCACCTT	59.971	20	ACGACGAAGACGATGACACA	60.319	20
GAACGAGGGCCTTCTTCATT	60.578	20	GTTTCATCACCTCCACCGAT	59.786	20
GGTAAATCAATGTGAAATGATGG	59.956	24	CATGCTAGAGGTGACGTTTTGT	59.309	22
ATCTATGGACCCTTGCAGGA	59.508	20	TTTTGTCTTTTGGGATTCGG	59.91	20
GAAGAATCACCGGACTGAGC	59.81	20	AATCCAACCCATTTGTGGAA	60.029	20
CCACCTTCTTTCTCCTTCCC	60.045	20	CTAACATCGGAACTTGCCGT	60.132	20

CCAAAGCCAAGTCAAAGACA	58.897	20	TGGTGTACAGAGTGCATGTGA	58.719	21
CCCAAAGATTTATAGGTTTTATTT	58.199	26	GCGAATATAACCCGCTCTGA	60.196	20
AACCACAGCCCTACATCTCG	60.134	20	GACCTTGGGCGTTGATCTTA	60.074	20
CCAATTTGAATGGTTATCACCTG	60.457	23	GGGAGAGCGAGAGGAGAGAT	60.058	20
GATAATATGGCCGAGAGTTTGC	59.962	22	GTCCAAAGCCATTGCTTCAT	60.081	20
AGCCACACATGTCACAAATGA	60.024	21	CTGCGCAGATCTAATGGTCC	60.765	20
ACGGATTTAAGGGTTATTACCTG	57.667	23	AGGTGGCAACATAATCAGCC	59.962	20
TGGAGAGCTCGAGAGAGAGG	59.962	20	TCAATTTCGCACGCATTAAA	60.211	20
GCAAAAGCTTTCTCGACCAC	60	20	TGTGATGTTGGAGTTGGGAG	59.52	20
CTTCAAGCGGTCTTGATTCC	59.813	20	AATCAGTGGCTTCCACGTTC	60.119	20
TAGGGGGTGGTTGGTGTTTA	60.081	20	TTTGCTGCCTTTATTGGAGG	60.202	20
GATTTGATCCACTGGGGAGA	59.862	20	TTCCTTCACTCCCCCTCTCT	60.186	20
TCAATTAATGTTGTCATTATTCCA	58.498	26	TTCTTATTTCTCACTTTAAGAC	58.093	27
GAGACTTGCCAACGGTCAAT	60.119	20	AAAAACCCTTCTGAAACCCG	60.324	20
GACTCATGCTCGGCATACAA	59.83	20	TGTACTTCGCACTTCGGAGA	59.591	20
TTCAAGGCCGATAAGATGGA	60.544	20	ATGGGATTCACCTGCCTTCT	60.853	20
TGGACTAGGGGCTGAAGAAA	59.807	20	TAATTGTTTCGGGCTAACGG	59.958	20
TAAATATGCAGCAGACGCGA	60.517	20	AATAGGGGAAACCCACCAAC	59.919	20
CGGAAAGGAAAACCGTAAAA	59.094	20	GGGCGTTTTATTTCCCATCT	60.15	20
ATCGGCTGAATAGCCGTATG	60.081	20	GTCATTATACGGGCCCAAGA	59.784	20
ACCTCGTCGTCCAACTCACT	59.756	20	TCGCCTAACTTATGCAATGAA	58.458	21
CAGCTCCACTACTTCCTCCA	58.03	20	TTACATCGTCCACCCCATTT	60.051	20
GAAAGGGCTGAGGTATGGTG	59.55	20	CGTGTGGTTTTGAAGCAAGA	59.881	20
AAAATGGTTATTATTGGATCGC	57.149	22	ACCACCGGCTAAACCAGTC	59.981	19
CGTAGAGAATGTTGCCACGA	59.864	20	TCGGATGAACGAGCTACTGA	59.547	20
CCCCCTCCTTCGAACTACAT	60.319	20	CAATTTTCGGCAGCATTACA	59.702	20
ATGCGCGGGTGTAAAGTTAG	60.152	20	GGGTTATCACCTGATCGCAA	60.864	20
TCCTGTTCTCCGATCGTTTT	59.67	20	TAGAGTTCCAAGAGGGGGCT	60.204	20
GCCTTCGGATCTGGGTATTT	60.286	20	GAAAATCGCTCAAAACCAGG	59.685	20
TGCTTCAGTCATGTCGTTCC	59.837	20	CACTACTCATCATCCTCTCTTT	57.758	25
GCAACGAAGATGGGAAATTG	60.448	20	AGACGTTTCAAGGTGAACGG	60.149	20
CATCACACCACAAATGACTCTC	58.058	22	TCATTTATGAAGCAAGGGGG	59.894	20
CACGGCGTAACTACCATTCA	59.609	20	AAGCTTGGGCTTTCTTCTCC	59.962	20
TGTGGTTTGCTAGACATCGC	59.871	20	GCGAGATCTTCGTCCATTTT	59.273	20
GGACCTGAAAAAGGACTTTGG	59.963	21	CAGACACTTCGTGGTGAACG	60.348	20
ATGGCTGCTCCAATATCACC	59.923	20	ATGCCAACCCGTCTTATTTG	59.823	20
CATTCAGAAATGGCGATGAC	59.079	20	GGGTGGAGCAAAATCTGAAA	60.051	20
TAAAAGCCGATCGAGTTCGT	59.845	20	CAAGCAAATTGTGGCTCTGA	59.988	20
TCTCCACCCTCTCACTTCCA	60.795	20	GATCGGTGAAGATTGGAGGA	60.011	20
TCTACCACTGCACCACGAGA	60.463	20	GCGAAAGACATACGGGGTTA	59.96	20
TTGCGGAAACAATCCAGAGT	60.636	20	CAGAGCGCACTCGAAGAGTA	59.49	20
TCGATTCGACTGGATTCGTT	60.603	20	TCACGTGCACCGTCATCTAC	60.756	20
TCCTTTCGTTTAAGTTGCCG	60.236	20	CCACGAGATCAAGAATGGAA	58.643	20
TGGAGTTGGAGATGAAGGCT	59.803	20	CCCGTTTCGGAGTTTGTCTA	60.103	20
CTAGCGGATTTCTCTGGCTC	59.174	20	GGTTCTTTTCTTGCAGCACC	59.859	20
ATCGGTTATTACCGGATCGC	61.031	20	AACCCAACCCACGCAATAAT	61.339	20
GGTGATCAAGCGTTCGAATTA	60.089	21	TCCACGGAGAACCTGAATTG	61.034	20
TTCTTGCAAATGAATGTGAAATC	59.114	23	TCCATGGATCTGGATCATCA	59.806	20
ACACTCACTCTCTCTAGCCGC	58.86	21	TTGGGTTGCTGAAAATAGGC	60.074	20
CAATCTGGGGAGAGAGACGA	60.34	20	AGGCCCGAGCTAAAAACATT	60.095	20
TCCAATACCAATATCTCAGCACA	59.488	23	TGCCTAGGTGGCTACTATGTG	59.791	22
ATTCCACATTGATTCCTGGG	59.605	20	TTGTGATTCTGAAAAATAGATC	58.337	25
GAGTGCTTCTTGAAGCTGGG	60.134	20	ATCGAAAGACGAACACGCTT	59.882	20
CCCAATGATCTAGCCTCTCG	59.79	20	GAAGATACTTCATGCTTGTAAA	58.527	25
TTCCTTTCCCAAAAGGACAA	59.518	20	TGTGGGACAAGCAAATGAAA	60.088	20
ATTGTGCCAAGCTTCTGGAT	59.7	20	AACATGCACTTTCATTCGTGTT	59.545	22
TTTTCCTAACCGGACCACAT	59.288	20	AAAGGTAGCGGGGTCTTTGT	59.998	20
TCCCCATTGTTCTACCCAAA	60.162	20	CCGCACGTAAGTGCTGTAAA	59.934	20

TTTGTGTGAGGAATTGTTGAAGA	59.64	23	CCTAACCCCACTAATGACCCT	59.223	21
TTTTTGGGTTGAAAATAGCG	57.833	20	TTGACGTTGGATCTGCTTGA	60.39	20
CCAACCATTGCAGAATCCTT	59.933	20	CGACTCCTTTTCCCTTCACA	60.224	20
GCACACATTTTTCTCCCCAT	59.797	20	ATGTTCCGAATCTTCGTCCA	60.461	20
TTACTTTTCCGGCAACATCC	59.938	20	GTGGCCCGTTTCTTATTTCA	59.938	20
AACCATGATGGGCAACAAAT	60.059	20	CGCATATAGCTCGACTGCAA	60.14	20
CGTGTTAAATACCGGGATCG	60.202	20	AAACCCTTGAAACAAATAAAA	58.132	24
TGTTCTTGGTGTTCTTGGTGTT	59.538	22	TGAGTTGGTGGAGGGTTTTC	59.943	20
AATCCATCATGGGGTTTTCTT	59.523	21	TCGAATTGAAGTTAAAGCTTAG	58.353	25
ACAAATCAACGCGAATTCAA	59.161	20	GAAACGAGTTCCGAAATGGA	60.051	20
CTCTTCTTCAAACACCCCCA	60.081	20	TGAAGCCTTTAAATGGGCAC	60.074	20
GGTGATTGTGGCTTGCAAAT	60.905	20	CACCCATTCATTCCCTCATT	59.605	20
AGAGGAGCCCAAGATGTCAA	59.803	20	GGACACAACAGAGGGGAGAA	60.088	20
CAAGAATGCCCCTGTATGCT	60.096	20	GGCGAATGCTATGCATTTTT	60.068	20
ATCCACTGCCAACCTCATTC	59.934	20	AGGTAGCTGTCGTCGTGGTT	59.792	20
CAAGCCCAAAAGCACAAAGT	60.284	20	GGAGTGAAAATGGGTGTTGG	60.21	20
GGGACCTTATCTTTTGCCGT	60.32	20	TGCTCTCTCATTGTAATCTCTCT	59.688	25
GGATGCTTTTCCCCTTCTTC	60.017	20	ATTGTTGTGGTGCGTTTTCA	60.011	20
CTCCCTTTACCTCCCCAAAG	59.927	20	TTGGACGGAAGTCAGAATCC	60.05	20
ATATGGTTTGACGCCTTTGC	59.967	20	GCTATTCTTGTGAGGGGGTG	59.55	20
GAAGGAGGAGAAGTTTGGGG	60.045	20	GCAACACAAACCCTACAGCA	59.764	20
ACCCAATACTCTTTCCCAACC	59.204	21	TTGGGGGAGGGTTTAGGTAG	60.172	20
GTCATGAGGACGGTGAGGAT	59.928	20	AAAGAGAGCTGCAAATGGGA	59.955	20
CAATCCCGACTGATTTCGAT	59.894	20	ATTGGGGAGGATAAAGGACG	60.145	20
GAAAGCACAACTGCAGACCA	60.032	20	CCTGGAAACAAAGAAGCACC	59.711	20
CACTTTCTCTCTTCCGACCG	59.982	20	AACTTTGATCGCGATGGATT	59.533	20
GAATATTGTGCGTCCCCATC	60.163	20	TCCAGCAATTTCAGCTTCCT	59.955	20
GCGTGCGAATTTAATGATGA	59.668	20	CACTTAAGGGGGTTATTAGTGC	58.515	23
GCCGCATTTTAATCGAGAAG	59.816	20	GCTGCTGTATTAAACCGAACG	59.793	21
AAAACGGATCGGATACGGA	60.281	19	TAAGGGTTATCACCGGATCG	59.778	20
TGCTTTTCTAAATGGAGAGTTGG	59.78	23	GGCTTTGCTTTAATCCATACAA	58.332	22
TGCTGTAAATGAAACTGTTGTATG	60.454	25	CGCCTGCTTGAGAGATTTTG	61.041	20
GGATCATCAACGTTTGGCTT	59.939	20	TGAGGGCAGTCAAAAATTCG	61.137	20
TGGGTGAGGAATACCACTGT	57.84	20	TGGTTGAAACCAGATCGAAA	59.097	20
ACTTTTAAGGATCAAGGATATTCG	57.122	24	GATCTACGTCCACGGGAGAG	59.679	20
TCGAGTGTAAACACGTCCCT	58.215	20	CCCCAAACAACGAAATGAAT	59.662	20
TCCGGATACCTACTACTGCGA	59.738	21	GGAAAATAGGGCGAGGAAGA	60.522	20
TTGGTATACAACTTTGATTCCCC	59.154	23	GGCATTCTTGACCAAACCAT	59.797	20
TTTAACCATGCACACCGAGA	60.111	20	ACGGTTCCCATCAGCAATAC	59.82	20
TTCAACGGAGTGGAAGATCC	60.05	20	TCCCCTCCACCCTCTATTTC	60.264	20
TCACAGGTTCGAGCTTCCAT	60.801	20	TTGTAATCGGACCGGTTTTC	59.801	20
GCCTTTAATCAGCAATATAAGTCA	57.658	25	CACCTTCTGGACTCAGACGA	58.964	20
TTCACTCGCATAAAAGTCTCG	58.187	21	TGATTCCCGAAAGGAGTGAC	60.05	20
TATCGGTTATCATCGGATCG	58.404	20	AAATATCGGCCGTCAGATTG	59.923	20
GCACAACCACTCCACAAAGA	59.726	20	ATATAGCCGTTGGGCTTGTG	59.982	20
CGATGTTTGTTGGCTGTCTG	60.301	20	GCGTTTTGACGATATATAGTGT	60.194	26
TGGAACCAACTAATTGCCAAG	59.982	21	CCCAACTTTTCTCCCCAAAT	60.159	20
ACGTTCATACCTTTGTGGCA	59.05	20	CCAAAGCATGCGTAAATCAA	59.702	20
TTTCATTTCATCGATTTTTCCTC	59.454	23	AAGTAGTCCTTTCCTCGGGC	59.713	20
TTCAATTTCTTGGCTCAGGG	60.184	20	CCGAGAAGAACCTTGGAGTG	59.837	20
AGCGTGACAAACATCACAGC	59.912	20	TCCTGCCACATGTAATGGAA	59.924	20
TGCATTCCAGACGTGTGTGT	61.236	20	AGATTTCACTTTGCAACCGC	60.257	20
AATGGATGCTTCTGGAGGTG	60.073	20	AACAAACAAGCCCCCTCTTC	60.476	20
AGAATCACGGCCATTTTCAG	60.074	20	GTTGGCCTGTTACGAATCAA	58.625	20
GGAATCTTGTTGGCATGAGC	60.613	20	TTTGCATCTTAGCGAGTTGG	59.062	20
AAGGACGGAGAGAGAGAGCA	59.279	20	TCGTATTGAATGAGGGAGGG	59.887	20
CGCATTCATTAGCTACACCC	58.268	20	GCATAGCTATTGGAATTTGGTT	59.795	24
AAATGAATGTTGTGTTTGTTTGTA	57.687	25	GCCATGTGGAAAATTTGGAT	59.628	20

AATAAACCCACCTGCTGCAT	59.457	20	AATCTCCATCCAAGCACCAC	59.934	20
ATATCGTCGTCTCCCGATGA	60.448	20	GCGAGGAATACGAAGAGTCG	59.978	20
TCAAATCGTTTCTATCGTGCTT	58.901	22	CATCGAGCCCACTTAGTGCT	60.419	20
TGTGCAAGGTTGAACCAAGA	60.278	20	ATTCTGTGGGAAGAGCAAGC	59.434	20
GAAGAGGAGGAAAGAAAACGC	59.473	21	CGTATGCATGTCATGGAGGA	60.504	20
AATTGCGTTAGGGATTTGATT	57.647	21	AGGAAATAAGGAGGTGTTATG	58.113	26
GACTTGCCAACGGTCAATCT	60.119	20	GGGTTTTCTTGCCAAAAATG	59.429	20
ATGGAACCACTTGTTGACCG	60.812	20	CGATCCATATGGCAAGAGAA	58.671	20
CGAAGAACAATTACAATGTTTATC	60.478	26	CGAAAAGGGGGAAAGAAAAA	60.385	20
TGCACCTGATCATGAACCTA	57.608	20	TGCGAATATAAAAATGAGAAA	59.158	25
GTGACTCTCCCCTTCCATCA	60.048	20	ATCGGCGCTAGACGACATAC	60.265	20
TTTTTAGAAGGATACTCACTACTC	57.024	26	GCTGAGGAAAAAGGTGACGA	60.375	20
ATATTCCCCGGTATGCCAA	59.987	19	AAGGAGGTGTTATGAAGGGAT	58.028	22
ATCAAAGAAAACGGTGGTGG	59.83	20	TTTCCTCTCCCCTCTTGGTT	60.045	20
ATCTCCCACCAATGCACTTC	59.934	20	TCTTTTAATCTTGGCCGCTG	60.335	20
GCACATTTAATTCCAGGTCG	58.093	20	TCAATTACATTCCCGTGGGT	60.051	20
CGAGCTCTGAAAATTCTCCCT	59.969	21	TCAACAGCAATGAATTTGTGG	59.576	21
GGTGAATAGGCGGATAGCAA	60.06	20	TCAGCTGCGATGTCAATTTC	59.955	20
CAGCCTCCATTTTGTTACCG	60.493	20	GGTGACGGTTGAGAATGACG	61.527	20
AAAGAGAAAACGAGGGGTGC	60.61	20	AAATTGTGTGGGCGATTGAT	60.199	20
AGGACAACCCATAACCCACA	60.088	20	AGCGTATTTCTTGATTGCCG	60.23	20
AGTTTGGAGCACACGAGCTT	60.058	20	CGTTCCCTATTCCCACTCCT	60.319	20
TATTCAACTCCATCTCCCCG	59.887	20	GTGCGTCTCTCGACGTTACA	60.056	20
TTCAACGGTCCCACAAATTA	58.866	20	TTGTGACGTGGAAGAGAGAGA	60.028	22
TCAGATCTGCGCTGAAAATG	60.096	20	TCAGTGTTATCGAGCCTCTCAA	60.015	22
GCTGTTAATGGACGTCGTGA	59.722	20	CACTCAATCGGTTGTACCACAT	59.78	22
GTCCAATGTTTAGGCCCGTA	59.823	20	GAATGGAGGAGGATGCTTGA	60.158	20
GCAATAAAGAGGCTGGTGCT	59.481	20	GCCAAAACAAAACACACACG	60.05	20
AGCCCTCATTCCTCCCTTTA	60.032	20	TTGATGCTCGAAGAGGGACT	59.95	20
GGCAATATGCTGACAGACGA	59.83	20	CGAAAAAGCAAATTCCATCAC	59.578	21
GGAGTCTGGAAAAGAGAGAGTTG	58.658	23	GTAGCGAGTGGTTTGGGAAG	59.734	20
CATTCTTTCTCCTCCCCACA	60.042	20	GGGCCAGAAAAACCAAGATT	60.299	20
ACGACATCATGACGCAACAA	61.163	20	TGCTGGGATACACAGGGTTT	60.375	20
AAGGGTTATCACCTGATTTTCTC	57.73	23	GCCCTCATGACTCTCAGCAT	60.381	20
TCTAAATTGCGAGAATATGAGAGT	57.816	25	TTTCATGATCAAATCTTATGAA	59.741	25
TGCTTCAAGGTAGGTTTATTAGGC	60.047	24	TGGAAATAGGTTGGGTCGTC	59.79	20
TCGTATTGACGGGAGAAACC	59.933	20	TTGTTGGTGGATTGTGCATT	59.823	20
ATCTATTGTCCCCCTTGGCT	59.789	20	TTTAAGGGTTATCACCTGATTTT	57.757	24
CGAAGTTCCTTCAGAACCCA	60.224	20	CACCTCCCAAACACAAAGGT	59.861	20
AGAACTCCACTTGCACAGCA	59.622	20	TGACAGGTTGTGGGAACAAA	59.976	20
CGATGCTGATGGAAAATGAA	59.622	20	AGATGAGATCAATGCCCCAG	60.034	20
TGTTTGGTCAAAACGAACGA	60.127	20	CCAGTTCAAAAGCATCACCA	59.691	20
GCTATGGTGGCCAATGTCTT	59.962	20	ATCCAGCCCACAAAGAACAG	60.111	20
AACTCCCCTTTCCTTTGCAT	59.94	20	CTTGCCATGTTCTGCTTCTCT	59.63	21
GGCAAATGATTGATTGCCTT	59.907	20	AAGAAAAGAGACAATCCGGC	58.386	20
GACTTTCATGTAGCGTGGCA	59.871	20	GAACGAATGCATGGGTGTAA	59.4	20
TTTGCTGTGCGTCGTATTTC	59.879	20	AGCAGAACCCTCAAATCCCT	60.074	20
TGCCACTTATTTCAGGAGGT	57.268	20	AAGAAATGGGGTCGACATGA	60.317	20
AGCACCTGATTACTCCCGAT	58.622	20	CAACGAAGGATTTGGTGTTG	59.021	20
CCGTGGACGTAGATCCTTGT	59.989	20	TTGATTGGACTTGTTTCTCGG	60.096	21
TAGCTATTCACGTTGCACGC	60.044	20	TCTTCCAAGAATGGAGCAGC	60.483	20
GGGGGAGAATTGAATTGCAG	61.706	20	ATTCATTTGCCCCCGTATTT	60.389	20
AATGCAAATACGAATATCATTATT	59.205	27	CCACGAATCATGATCGAAAA	59.474	20
TTCAATCCAAAAAGACACATGC	59.982	22	AAAGATATATAATTCATTGAGC	57.631	27
CATTGTATCTTGTCTTGCCCTAAA	59.577	24	TGATTTCGAGAAGCAGTAGGT	59.517	22
ATTACCTTGATCGACGACGC	60.103	20	CCACCAGAACCGAAGTGATT	59.966	20
CCTCCTCTCAGCCCTAGCTT	60.11	20	GAGATGGAGTGGAGGCAGAG	59.945	20
GTTTAAATGGGCGGGAAAAT	60.022	20	TGCAGCACTGAACAATCACC	60.885	20

CATCCTCAATTTCAGCACCC	60.461	20	GAGAAGAGAGAGACGGTGGC	59.131	20
TGTGTCGATCCAACGGTCTA	60.112	20	CACCCGAAAATGAGTTATATT	60.438	25
CCTCTCCTCGTCTTGTGCTT	59.598	20	AGGCATTGCAGAGTTGAGAAA	60.008	21
AAATGAACGGTCGAGATTGG	59.933	20	TGCGTTTTGACGATATATAGTG	59.092	25
GGCTTGTTTGAACCATTTTGA	59.967	21	AAATAGCTTATTGAATTTGATT	58.677	26
CATGTCAATATCATCACGAGTTTG	60.183	25	GCCAGATGTGAATGGGTCA	60.489	19
AGGGAAAACCACTGCTCTCA	59.844	20	TCCCATTTCCATTTCCAAAC	59.599	20
AAAATCAAGGGCTGTGATGG	59.933	20	CCACCACGGAAGAGAGGTAG	59.715	20
TCCCGGATAATCCATTAACAA	59.134	21	TCCGATTAATGGGCTCTGAC	60.036	20
TGCTGAGCATATTTTTCACCC	60.089	21	TTTTTGCCTGATATTTGTATAAC	59.061	25
TGCATTGTTCGACGATGTAAC	59.605	21	GTTGGGGAGGCTACATTCTG	59.55	20
TTAACACCAAACCATCTAATTAGT	57.486	27	TTTCTGTCGAGCTTAGCCTCA	60.277	21
GTTACCGTCGTGGTTATGGC	60.257	20	TCTCTCCCTCTCTCTCTTCGG	60.215	21
TGGCAGAAAGATTTTAGATATAG	59.31	26	ATTGGACGCATAACCCGTAA	60.209	20
GCAGTCTGTAAGGCCTGGTC	59.874	20	GGAAGATCCGAGAACCACTG	59.655	20
GGAACCCAACCACCCTTTAT	59.919	20	TTGTTGAACCGTGTGCAAAT	60.011	20
ATTCCAAAAATCAAAGGCCC	60.13	20	GCTGACATGGCTTCGTATCA	59.83	20
GGCAAGTTGAAGGAACAAGG	59.711	20	ACAACTGCACCACACCGTT	60.063	19
TTCCTCTCGTGTTTCATCCC	60.05	20	CCTAGCAAGGCTTCCATCTG	59.971	20
AAACCACGCAGGGATGAGTA	60.517	20	TGTGTGCTTTATTGGAGCGA	60.401	20
CTAGCCATCCATTCCGAAAA	60.031	20	CCGTTGAAACACGAGATGTG	60.152	20
TGGCACAGAGAGTACATAGTTTC	60.575	25	GAACCGCCGGAAAAGAATTA	61.263	20
TCATGCACAAGGTGGAATGT	59.967	20	AAATTTTGGCTTTGTCGTCG	60.11	20
GGAGGGAGAAGAGGGAGAGA	59.883	20	AGCCTAAGTAATGGCGCAGA	60.003	20
TTTGTTGCAAATATCAGGTCTTTT	59.131	24	AGCCGGGTGTCAAATAAATG	59.823	20
TTTTCCGTATGCTGACCCTC	60.074	20	CAATGCCTAGTTTACCCCCA	59.817	20
AATAACAGTGGTGGCCGAAA	60.365	20	TCCGGCCAAATTAAAAGAAA	59.538	20
TCCGTTCTTCTTGTTCTGGG	60.224	20	ACCAACCTCCATTGAAGAGC	59.141	20
TTGCTTGGGATTTTATTTTGAA	58.652	22	GTGGCAGCCATATATCCGTT	59.813	20
TGTATGGGTCATTGGACGC	60.346	19	TTCCGTCTTTAGGCATGAGC	60.352	20
GGATTTGGGGGTGAGAAGAT	60.133	20	ACCCACGACCGTGTACTTTC	59.891	20
GGAGCAAATTGAGGCTGTCT	59.434	20	TGTTGCCGTAAACAATGGTC	59.444	20
TTGTATCGTTCGGAAACGTG	59.585	20	CAGATGTGGACGGGTCACTA	59.545	20
GCGCATTTTCTGCTGTTAGA	59.21	20	GGCAACGCAATTATCCATTT	59.801	20
GTTCGATGTTGTAAGGGAGGA	59.042	21	TGGTTCGATCGTAATTGATCT	57.168	21
TCCACCGCTAATGAATGACA	60.073	20	TTTCTTGGTGGGATTTGGAG	59.903	20
GAGGGAGACAAAAGGCATGT	59.141	20	GAGTTTGGCACTCTTGCACA	60.032	20
CATATTTCAAATGCATGCCG	59.92	20	ACCCCAGGTCTCTTCAACCT	59.968	20
CTAACACCAGCCTCTCTGCC	60.012	20	TGCAACCATTTTGTTGGAAA	59.946	20
CGGCTATATTAGCGATCCGT	59.216	20	TCGGATCGGATATCCAAAAA	60.225	20
TCGAGTTATGAAGTTAGGAAATA	58.22	27	CTTCGATGGAGTTCCCTCCT	60.586	20
TGATTCCAAACCCCAGTCAT	60.173	20	ATGGGGTGAGACAAAGCAAG	60.111	20
CAACTTCGGGACCACTCCTA	60.103	20	AAAAGAGCTTGGGCCTCTTC	59.962	20
TTTCAGAAATTGCCTTGGTTG	60.096	21	GTCCGACACAAGCTGAAGTG	59.467	20
CCAAGCAATCAAGGCATTTT	60.074	20	ACCCACTTTTCAAATCAGCG	60.11	20
TTCGGAGCATGATTTAAGTGG	60.081	21	GTGGGTGTGATCTTGACCCT	59.817	20
CCAATGCCAATCATCCTCTT	59.894	20	GTCCCAATCTTTTCCACCCT	60.169	20
GGAAAAACATGAGTTTAGGGGTT	59.657	23	AAATTCCCGAAGAGCCATCT	60.039	20
TGCTGTTGCATTTCGATGTT	60.265	20	TTCTCTGTTCTGGCAGTGGA	59.545	20
ATCCAGATCCTTGTGGTTGG	59.779	20	GTGGGCATGCCAAAAATATC	60.161	20
TTCCTATCTTCTGCGACGCT	60.118	20	CTGTGAAATTGCACGGCTTA	59.872	20
TTCCCTTCTCATTTCCATGC	60.014	20	TTCAAGTTTGGGGGTGTGAT	60.21	20
TCAACGATTTTGGTTTGTTCC	59.831	21	ATCAAGATTTAGGGGTTATCAT	58.8	25
TATTCTCCACCACCCCACAT	60.05	20	CTTTCCTTGGGGACTGTGAA	60.081	20
TGGAGAAGCTCTTACGGCAT	59.978	20	TTTTTGGCGGGAAAAATAGC	61.226	20
AATGGTTGTGGATCGCCTAA	60.331	20	TTGGAAGGAACGGATTTGAG	60.044	20
TCCGGTCCAATTCCAATAAG	59.756	20	CCTATGGTGGTATGGTGTGGA	60.501	21
TTGCAGTAAATATCGGTTTTCG	59.173	22	AAATGTCAATCCAACGGCTC	59.939	20

GCTGATTTGTGATGTTTGGAGA	60.118	22	GTATTGGGAGCAAGGCAAGA	60.214	20
GCCCTTCGAACAACAAAAAG	59.724	20	CACACATCCTCACACACTCAC	60.697	22
CCTCCACTGTTTTGTGCCAT	60.954	20	TCCAACACAAATGAACCTGG	59.389	20
CTCGTGAAGCGACGTGAATA	60.011	20	CCCACATCCCACTCTCTCTC	59.638	20
ATGGAATTGGGTGTTGGATG	60.439	20	CACGAACGGTATAACATCGG	58.917	20
AATGCTTTGATGTGTTGGCA	60.119	20	CCCTCGTATGCAATGAATCTG	60.475	21
CAAGATCGAACGGAACGAGT	60.255	20	GTGAGGGGGTGACAGAAATG	60.363	20
AGAAAATTCGAAAATTCCCCA	59.774	21	CTGATTCGCTAGCTTCCCAC	59.978	20
GGCAGTGGCCAATGAAATTA	60.837	20	GGAACCAAGTCTTCAGATGC	57.288	20
CTCAATCTGATGCACACTCAA	57.388	21	ACCGACAAAAGGTAGGCTCA	59.734	20
TTAATCTTGGCCGCTGATTT	59.682	20	GCATCGTGTGAAGCATTGAT	59.685	20
TAATTTTCGTCGGGATGGTT	59.273	20	TCTTAGCGCAATGTAAGCGA	59.748	20
GCAATCAACACGAAGCAGAC	59.45	20	GGATTCCATCAACACCAACC	60.034	20
TCAAATTTTGCGTAGCATCTCT	59.036	22	CTCATTGGAATTTTCCGGGT	61.042	20
TGAATCTGACTTCGATTATTTGTG	60.017	25	GCATTTGATGGAGGATCGAG	60.57	20
TCAATTGGTGCAAGAAGACG	59.84	20	CTGCCCATTTTACCCTTTTT	58.113	20
AAAATCCCAACAATTCGCAC	59.807	20	CATTTCCTTCAAGCACACCA	59.691	20
CCAGGCAAAAATGCGCTA	60.885	18	TCCCATTTCAGTATTTGCCG	60.827	20
CAAAAACCGGTGAAAAATCG	60.327	20	CGACGGTACACACTCCACAC	60.072	20
TTGGGGTTGGCAATAAAAAC	59.677	20	AAACCACCTCCGAAAACTTG	59.073	20
TCTTGGTAAATGTTTGGGCA	59.013	20	TCCCAATGATTGTTTGGTCA	59.75	20
GCTTGGTCTGAGCCTGCTAC	60.164	20	CACTCACAGCCAACAGGGTA	59.745	20
TATGGTTTTTGGCCACTTCC	59.801	20	TCCAATTGCGAAAAGATTTG	58.744	20
CATTCACATGGTCCCCTCTT	59.779	20	TAAAACTCCCAATGGATCGC	59.901	20
ATAGAGCCCCACGTTCACAG	60.134	20	GAATAAGGTGAGATGCGGGA	60.036	20
AGGGTGCCAAGATTAACACG	59.993	20	CAGAAACCATGGATCTGGAAA	59.918	21
ATATTCGAACGGCCTTGTTG	59.96	20	AAACGGCGAAGTGATACGAA	60.637	20
ACTCAAGCACACACACGCTC	60.104	20	TCCGGCAATCTCCTTAATTG	60.031	20
AGCATTTGATTAATCCCCCA	59.23	20	TCGACACGAATCCAAAACTG	59.691	20
AACAGCACGGACAGCTTCTT	60.058	20	TGCAAACATTTTGAAGGACAA	59.192	21
CGTAGCGAAGAAGCGAGAAT	59.752	20	AAATCGGAAGCTGGATGCT	59.788	19
CGAGGATGAGAGAGGAGACG	60.088	20	ACCACTGCATTCACTTTCCC	59.973	20
TTCTGATTGTAAATGAATTGAGTC	59.569	25	TTGCTCGCGAGATTTCTTTT	60.096	20
CAAAACAGGAACCGCTGATT	60.11	20	CATGCCAAGTGGTGTGATCT	59.551	20
AGGTGCTTTGACTTATGTAAAGTT	58.12	25	GGATGAGGTTGTATTGAAACT	59.891	23
TTCGGAGCAAAGAAAAGCTC	59.708	20	CCCTAGCCTTTGCCTCTTTC	60.332	20
GTTCTGGCGTCCCACTTTT	60.104	19	AGCGTTATTTTGCAAGGTCG	60.264	20
CGCGAGTTCATAACTCTCTCTCT	59.336	23	GGTGAGGAGGAACACGAAAA	60.088	20
CTCAGCATACAGCAGTTTCATTT	58.6	23	GGGTGGCCCTCAATTTTATT	60.02	20
GAATAATGGGGGTGATGTGC	60.021	20	CGGGGAAACATACGTCACTC	60.375	20
TGGTTTCAATTTGGGTGGAT	60.029	20	GGACAAATGTTTCATGGCCT	59.797	20
ATTCGGAGCGAGGCTAAGTT	60.36	20	TCTCTCTTGGTTGGTGAAGAAA	58.955	22
ATGCTCAATTTCCCAACTCG	60.074	20	GCACCTATATACGCACGCAC	59.238	20
TTCCATTTCACTTGAATGTTTGA	59.483	23	TTGACCGATCTCATTTGAAAAA	59.564	22
CAAGTTCGGCCTTTGGTTTA	60.103	20	CCAAAATCACAATCTATCAAT	60.076	24
ACAAGTGGTATAAACGGGCG	59.883	20	CGTATACTTGCGGGGTTGTT	59.883	20
TGGCGTTTGAGAGGAATCAT	60.603	20	TGAAATAGTAACCGCCGACC	59.96	20
GAATTAGCATACTGGCTCATTTAT	57.238	25	GAAGGATACAAAGGCTCGGA	59.269	20
CGTTGAAGAGATTACGCAACA	58.978	21	AACAGTTCAAGACCGTTTCG	57.856	20
CGAATTTGGTGTTGGAATTGA	60.717	21	AACCCACTACCCATTCCCTC	60.052	20
CGGCCATCAGATATGGAGAT	59.877	20	AAGGAGAGGAAGAAGCAGGG	59.95	20
CTAACCACTCAAGGCCGGTA	60.125	20	TTGAGCGAAAAGCCAAAGAT	59.96	20
ACAAACTAATCAAGTTCCGCA	57.439	21	TTCGGAAGCGTACATCAAGA	59.42	20
CTTTTCACACGAGGTCACGA	59.873	20	GTCCCGTTTTCCTTGTTTCA	59.948	20
CACAGGATGATGCAGAGGAA	59.787	20	ATGAACGAACATCGTTGCTG	59.722	20
CGCGATTTTAAACCCTAAAGAA	59.653	22	ATTGAGGACGCCCAATGATA	60.296	20
GAAATTTCATTATTTCGTCGTTATT	57.054	25	AACCAAACATGCTTCTCATGC	60.133	21
CCAAAGAAAAGTGCATTACAAAA	58.412	23	CCACCAGGTTCTGCTACGTT	60.171	20

TGGGAAAATTGAAGAACATTTG	58.963	22	TCTTAAGCATGCACGACTCC	59.028	20
CAAGCTGATTTCCCACCCTA	60.066	20	TCTTCCCCGTTTTGTTCATC	59.91	20
TGTTGATTGGTTCAGAAGCG	59.84	20	ATTCCTCCTTTTCAGCACCC	60.443	20
ATTTGATCAACAGGCGATCC	59.9	20	CGATAGAGTGGGGACGTCAT	59.95	20
CCAATGTGCACGCAAAATAC	59.999	20	CCACTCTCTCTCCTCTTTCTCTC	58.958	24
AGCTGGGAGGCTTGGTAAGT	60.268	20	GTCGCCTCTTGAAACTCTGC	60.142	20
CCCGCGTCATAAAAAGAAGA	60.202	20	TTCGCACGCTATAAAACAAGA	59.916	22
TGGAGAGGGCTAAACAGTCG	60.388	20	CCCTCCAGACGTGAAGAAAC	59.697	20
AGAAGCGAGAAGGGAGGAAC	59.957	20	TGCCTCATTTGTGTTAATTTGG	59.868	22
TATGCTCCTTTTGGTTTGGG	59.931	20	TCAATTGAATCTGGCCCTTT	59.505	20
GTCTTGGACGACTCTTGCCT	59.455	20	TTTAACCTGTAGGGCACCCA	60.357	20
CAACACATTGCCACACCAAC	60.895	20	TTGCGCCTAAGGAGGAGTTA	59.975	20
TGCGTTGACGTACACAGCTT	60.517	20	GGATAGGCTAGATGACGTAGA	57.085	23
AATATGTCTCCTCCGGCCTT	59.925	20	TGCATTGGAAAAAGTTGTGG	59.561	20
ATGATGTCAAGCCATCTCCC	59.893	20	GATGTCTGGTTTTGGCCATT	59.797	20
CAGCTGTCGAATCTGCTCTG	59.88	20	TGACAGCAAATCCCAGTCAG	59.831	20
GAGTGGTGTTGAGAAACGCA	59.88	20	CCGTTCCTCCCACCTTTAAC	60.714	20
TGAATTTTGTTGAAATTGGGA	57.978	21	TTGGAACGCCACTAGTTTCC	60.11	20
AACGCGATATGGATGAAACC	59.791	20	TGTGGTGTGTTAAATGCGTG	59.044	20
GATATGAAGTGTCACAATATAAG	57.063	27	CACCGTGCATTACAAGATGAC	59.065	21
CCCGTCTCAGAGAGGTTCAC	59.835	20	CAACCCTACCTCCTTCTCCC	59.928	20
ATTACATGAATGCCGAGCTG	58.749	20	TCTGAAGTTGTTCCCGAAATC	59.16	21
ATCCATATGGCAACCCTCAG	59.773	20	GAGGCGCGATACACTACACA	59.895	20
CGACGACTCAGTCAAACCAA	59.873	20	AATCCAAGCCATCCATTCTG	59.894	20
GGAACAAACCATCCTCAACC	59.239	20	ATGGGGGTGGTTCAGCTTAT	60.578	20
GCGAAGCACCGAGACTACTG	61.136	20	GAGGCATTTGAATTGACGGT	59.939	20
TGGACTTGGCTAAGAATGGC	60.214	20	CAGCAGCCATTAAAAGTCGG	60.762	20
TTTCATTTCGGATGGAAGGA	60.384	20	CCACATATTCATTTCCCCCA	60.384	20
CGTACTTTGGCAAATCACATAGA	59.197	23	CTGTGTGATGTTGGAGGTGG	59.997	20
CGGGTGATCAAAGGAAAGAA	60.044	20	GGCTGCAGAAGTGTTGATGA	59.992	20
CTCCTGGGGAGGTGTTATGA	59.92	20	TGTTCAGCTATGTTTGCCGA	60.401	20
TATATCACGGGGGACTCGAC	59.773	20	TTGGGGGTTGGGTTATCTCT	60.549	20
TTGCCTCAATCTCCATAAATCA	59.547	22	CCCAAACTTGGGGAAGAAAT	60.159	20
GCGTAGACGGAATAAAATTCG	58.775	21	GATAGCGATCGTGAGAGGGA	60.326	20
CCAGGGAATCTTTTGAGCAC	59.67	20	GTGGGTGCCTAGGTTTTCTG	59.592	20
GCAGTTGGTCAGTTCCCAGT	60.159	20	ATACGAACACTGCACCACCA	60.032	20
TGCATAATTGTAGATAATGGACC	60.114	24	CAAAATTAGTGTCAGCACCGA	58.833	21
GGCAGAGAAAGTTGTGCCTT	59.478	20	TGAAGTCTCTCCTCCGCAAT	59.95	20
ACGGTGGGCACTACAAGAAC	60.035	20	TCCATTCCATGTCACAAACG	60.367	20
AGCGGGATGAAGAATTGAGA	59.773	20	TCGACGACAAAACAACATCC	59.547	20
AAATATCGGCCGTCAGATTG	59.923	20	ACTCGGGTCATTGGATTGAG	59.927	20
GCTTGGTTGGCTTGAGTTTC	59.859	20	AAAAGGGAAGGGGAAGTGAA	59.912	20
GCGGTTGGATTTATTGCTGT	59.967	20	GAAAGGAAGAATGCGAGTGG	59.813	20
TTCTCTCTTGGTTGGTGAAGAA	58.955	22	TAAGTTGGAGTGGAGTCGCC	60.255	20
CCTCTTGATTTTCTCGCTCCT	59.969	21	GGTTCAAAAATCCGGGAAAT	59.999	20
TATGGTGATCGGGTTTGACA	59.774	20	TAGCCTTAGCCCCAAAACAA	59.715	20
CAAAACTTCACGAAGAAAACACA	59.34	23	CAGGGTTCCGTTTGTTAGGA	59.964	20
AGAAACTTGACGTGTGCGTG	59.946	20	CTTCTCCCAAAACCTCACCA	60.081	20
ATGCTTAAAAGAAAGCGGCA	59.985	20	CCCTAGTTAGCTCCTAGATATT	59.882	27
CGGTGGATGTCTTGGTCTTT	59.966	20	AGACAAAGTGGGAGGGCTTT	60.11	20
AAGATTTTCGGACATCGCAT	59.533	20	CAAGGATGAGATGAGGGCAT	60.034	20
GTTGCCGGATAATTCAAACG	60.323	20	ACCTATGGTGGTATGGTGTAG	57.076	23
TCCAGTATACAATTCCAACAGGA	59.433	24	CTTCACCCATTTCCACCAAC	60.21	20
TAGTTTGTTTCCCGCCAAAA	60.46	20	AGGGAAAATAGCTACTCCCAT	58.662	23
TTTCCTTCTTGGATTATGCGA	59.668	21	CTTGAAAACTCCAAGCCCAT	59.17	20
CCCACTAACCCAACCCATTA	59.541	20	TTGGGATTTTTGGTTTGGAA	60.138	20
TCCGAAATGTAACAGGGGAA	60.301	20	TTATTTGCACGCGCAGTAAT	59.379	20
TGTTTTGTAATTTCCCATGTTTGT	59.577	24	CGGCTTTCTCTATCAGCCAG	60.11	20

GGAGAGAGAGAAAGCATGTATTC	59.934	25	CCTCACCACCTCAAGCTTTC	59.844	20
CCGCTTTCTCATTTCTTCCA	60.323	20	GGTTTACACGTGCGAGGAGT	60.179	20
CCCTTAGATGTCTTCATCCCAA	60.312	22	CACCAACTGCTTTATTGCCA	59.729	20
AAATGGTCCACATGTTGTAAAAA	58.335	23	TGATGAACTCGTCAATTGGAA	59.112	21
TGAAAGGAAGCCAGAACTGAA	59.978	21	TGTTGGGTTGGTTTGACAGA	59.976	20
ATCGTATGCTGCCCCTAAAA	59.569	20	CACGTGTGGACATCCATATCA	60.256	21
TGTGCTATCCTAACCAAAAGC	57.092	21	TGCCGTGTAAATCCATCAAT	58.846	20
AAAATCAAAGGCCCACAATG	59.801	20	TCGGACCAAATTACCCTTCA	60.301	20
ATGAATTTTCTGCGAATGGG	59.901	20	GTGGTGCTTAAAGTAGGCGG	59.769	20
TTTGGGGTCTTCTGTCAAGG	60.081	20	TTTGCAAACCCTACTTCACTCA	59.785	22
ATTGCCCATGAATGTCACCT	60.203	20	CCTTCTCGAGATATTACTGGCG	60.237	22
CAATCGGCACACAAAAGCTA	59.872	20	GCCCTATCACAACTCCGAAA	60.074	20
CACAGAAGGAAAAGAGCGAGA	59.743	21	CTGATCCAGCGATTCTTTCC	59.773	20
ACTAGGCATGGAATCCGAGA	59.653	20	TCGAAATCAGCATATCAAAAC	59.616	23
CCCACAAAGTTCCAATCTTTTA	58.163	22	ATTGTGCCCCTATTCAACCA	60.192	20
CTTACGGCATTAGAGATAATGATT	58.452	27	TTTGTGTGCATGGAATTTTTG	59.453	21
TTCTAACAGAATAGAGCTTGGGG	59.705	24	CACAAATTTGGGTTGCCAG	59.949	19
ATATACGCCCACATGCGATT	60.203	20	AGGAGGTGGTGTACTGCTGC	60.329	20
TATGGCCAATTCCGAACTTT	59.411	20	GCAATGAATTAGCACCCACA	59.548	20
TTTGAGCAGTTCCAATCTCTTG	59.494	22	GGCCTCTCTCTGACTCGATG	60.096	20
TTCTCGTACACGTGTCCAGTTT	59.702	22	GCAAGATAAGGGAGTTGGCA	60.214	20
GGTGGTATTTCGTGTCGTGA	59.42	20	TTACATCAACCCGTCAACCC	60.615	20
GGGTCATCATGGGATCAAGT	59.593	20	CCAGCGCAGACAGAATACAAT	60.285	21
CTTAAGCCGAAAATTCCACG	59.715	20	TTTCCTGAGTCCACGAGTCC	60.238	20
GGTGATTGAAATGATTAGCAACA	60.239	24	TTCGTGTATTAAGGTCACGGC	60.011	21
CATCCGGGAGAAGGGTTAGT	60.319	20	AGCCAGAGACTCGGATTCAA	59.95	20
ACAGGAGCTCAGGGACTTCA	59.986	20	CACCAGGCAGCACTAAAAGA	59.072	20
CATGGCAAGCTTTCTCCTTC	59.955	20	CCAACCTCCATTAACAACCC	59.146	20
CAATTCCTCCCTTGGAGACA	60.042	20	TGAGGCTTTTAGATCGACCG	60.344	20
GGTGCTGGTAAAGACTTGGG	59.592	20	GGAGCTGCTCTTTGAGATCG	60.24	20
GCACCTGTAACACCCACACA	60.487	20	CCCGTATATTCACGACTCGTTT	60.257	22
TGTTGCTTGTTTCTTGCACC	59.888	20	AGCAAATTATTCACACCCGC	59.967	20
ATTAAAACCTCGCTCGGATG	59.182	20	GATCGACACATTCAGGCAAA	59.654	20
CAGAGACCGAAACCGGATAG	59.688	20	CCTAAAAATCACCGTCGGAA	59.931	20
TAGGGGCCTGCTAAAATTCA	59.677	20	CATTTTGTTGAGGGGTCGAT	59.79	20
TCGCTACATTTACGGATTGTG	58.713	21	TTTGCTTAAAATGGATCAATGG	58.98	22
GCGAGAACCACAAAGCTCTC	60.142	20	TGATGCGCATGAGATAGGAA	60.329	20
CAATTGTTGCAAACAACCAAA	59.495	21	GATTTCAGTTTGGAATCGGC	59.51	20
CGGTTGTTCCATCTCTAATCC	58.516	21	CCAAGCCACACATCTCTCAA	59.831	20
TGTTGGCGTTTTAATCTCCC	59.938	20	CCGCACCAAGATTTAACCAT	59.823	20
CATGTGTGTCGCTTTGATCC	60.12	20	TGCGTTTTGACGATATATAGTG	59.092	25
CCACATTTAAGGGTTATCACCTG	59.654	23	CTTTGATTTGCGTTGATTGG	59.157	20
GGGATTCAATCTAGTCGACAATC	58.974	23	TGCAGCCATATCTCTTGCAG	60.119	20
TGCTAGAGCCCTTGATTTCC	59.41	20	TGATTGAAATATGCCACCGA	59.891	20
GAAATTAAGAATGTGGAGTGCAA	58.311	23	GAGGCAGCATACCCATCACT	60.104	20
CCAAAGGTGAAAATCGCACT	60.11	20	TTCGCCTTTTGTTTGTGAAA	59.321	20
TGAATTCAATTTATTTATTGTCGAT	59.996	27	CAGACTGATGGTCAAACAGAG	59.762	22
ATGTGTGATGTATCCCCGCT	60.226	20	TGCCTATATTTTTCGCAGGC	60.192	20
GTTTTGCAGGATGGAACTCA	58.697	20	TGTTGCCGTTTGATTGAAAG	59.706	20
ATAACCCGGTCAACAAGCTG	59.993	20	CTTCTCCCTCTTGCTTCCCT	59.95	20
CCACGTGGAAGGACTGAAAG	60.68	20	CAACTTTTCCTCATGCGTCA	59.84	20
TTTGAGGGGTGGATTTGTTC	59.767	20	ACAGCATACAGCAGTTTCGTTT	58.978	22
ATCCGGAGTAAGTTCGAGGA	58.741	20	AATTTCACCAAGATGTCCAAG	58.554	22
GTTTGAGGCGGTACAAAGGA	60.11	20	AGTTTTGGTGAAGACCGCAC	60.156	20
CAAAGGATGAAAACGAGGGA	60.044	20	TTTTCCGATGCTTATCCGTT	59.547	20
GTTCATTGGCTGAGGCATTT	60.081	20	CGTTGCCGGTTAAAGCTAGT	59.424	20
AGCCGTAGAGCCCTGTATGA	59.859	20	GGTTTATCCATGACGCGTTT	59.829	20
TTCCTTCCTTTAGAGTCGTTGC	59.892	22	AAATTTTATGGGACGGAGGG	60.013	20

GATCTGGTCACGACAGCTTTT	59.347	21	GAATCCAGAAGGGCAGTTGA	60.195	20
TGTTATGATGGGAAGAGGGG	59.744	20	ACGCGCGTTTTTAGGGTTTA	61.796	20
TGATTTGGCAGTTTGAGAGG	58.847	20	CCTCGACTTGACAACTTTGC	58.497	20
AACGTAAATGAGAAACATGCAAC	58.249	23	AGGTTTTTCAAACGATTGCC	59.067	20
ATTTCGAGCCAGACACTGCT	60.02	20	GGAACTCCTCGATTGCTCTG	59.95	20
TTCCCTACAAAACGAGACCAA	59.595	21	CCAAACCCAAACAATTTTGC	60.202	20
TACGTAAAAACCCTTTCGCC	59.12	20	ACCATATTTAAGGGTTATCACC	57.552	24
TTCCATGATCAGAACGGATTC	59.886	21	ACCAATCTTGTTCGGGTTCTT	59.856	21
TCACATCGGAAATTCGTCCT	60.461	20	TGAAAGCGATTGTAAGCGTG	60.014	20
GTGGGCAAATCAAATGTTCC	60.177	20	TGCGTTTTGACGATATATAGTG	59.092	25
GCAGAAGCGGGAACTAACTG	60.015	20	TTTCCCTATCTCTCCCAGCA	59.767	20
GGTGACAGGCAGCTGAATCTA	60.412	21	CAAACTCCAAAGTCCAAACTC	60.012	22
TTGGGGTTTTCATTTTGAGG	59.772	20	TTTCCCTCTCCATCTCTAGCA	59.017	21
TTTTGACGGGGTAAAATAAAACA	59.66	23	AGAATCTGCTTTGCCCAGAA	59.955	20
AAAAACATCGCTCTCTCCCC	60.578	20	CCTTCGAAAACACCACCATC	60.353	20
TGGAACAGTTTGACACAACCA	60.033	21	CCGTTTTTCCTATTTCGTGC	59.586	20
TCGTAGTCCCCTTCAGATCG	60.21	20	GAGGTGGTGGAGTGGTGTG	59.984	19
ATGCTTGAAGCTATGGGTGC	60.243	20	CAAGAGAGAGGCCAGGAGAA	59.673	20
AGCTACTGCCTCAATTCCCA	59.836	20	TTTTGATGATATATAGGTGTTTTT	58.782	27
ATCCCTCTACCGCCTTAGGA	60.053	20	TGAAAACACGATAAGCGACG	59.872	20
TGCAAATTTCACCAAGAACG	59.706	20	GACATGTCGCTCATGTCACC	60.13	20
AATCGAAAATAACGTTGGCG	59.964	20	ACCTTTCTCACCTAATTACAAC	58.919	24
GCTATGCAGCCTCCATCTTC	59.946	20	TGCACGATTTGACTTGCCTA	60.401	20
ATCATAGCCACGCATGTCAC	59.558	20	TCTACGACCACAATTTGTCCC	59.845	21
CTTATTTCAAAACGACCCCG	59.447	20	CAGACGGAAGCTAATCGGAG	59.971	20
AGCCTCTGATTCACCCTTGA	59.803	20	CAAATATTAGGCCAAAAACGC	58.687	21
ACTCACACACCCATATGTCCC	59.57	21	TGAATTTCCATCGTTGATTTGA	60.302	22
TTTGCCCCTCAACCTAGAAA	59.679	20	TGGATGAAGGGGAGAGTGAG	60.191	20
AACACATATGGGGACACGCT	60.263	20	TTTTCATCATAATATTGATTTTT	59.604	27
ATGCGACGTATTGAGAAGCA	59.449	20	CAAACTAATAGCAATGGCCGA	60.102	21
ATGTTCTCTCAGGCCACCAC	60.12	20	TGGAGGGATTTGTTTTCCAG	59.903	20
TGGGTGAAAAGAAAAGGCAC	60.088	20	TGGCTCAAAAGACAAGTCCC	60.232	20
AAATGTTGGCTTCGTATCGC	60.103	20	GTGGGGATGGGAGGTTTATT	59.881	20
CAAGTCAACAAGCAAGCCAA	60.027	20	GATCGTAGGGATAGAGGGGC	59.888	20
CCATCTCGAAAAGATGGGAA	60.006	20	TTTGTTATTTCGGGGTCTGG	59.795	20
TGGCTAAAGATCGATGTGACTT	58.861	22	AATTTTGTGAATTTGGCCGT	59.32	20
TTGGGCGAAAATACCCCTAT	60.508	20	GGGCCATAGATCTTGTGGAA	59.894	20
TACAAGTGCAGCGGAAATGA	60.401	20	TCCTTGAATCCAGGTTGAGG	60.042	20
AGGTTATGGTTCTTGATGGGG	60.06	21	CCCAATTTCACCATCCTTCA	60.692	20
GCGGTGGTGGAGAGAAAATA	60.074	20	GAGGGGTGGTTGAAATGATG	60.173	20
GCATCGGGGCAATATTTAAG	59.415	20	CCAACGGGTAGATACCCAAG	59.308	20
CACACGCGCATATCAGTTTC	60.288	20	GGTGTTGGCTGGAATGAGTT	59.973	20
ATAAGGTGGCGATGAGTTGG	59.955	20	TCCATCAAATCCAGGTTGGT	60.173	20
GGACACGTTGGACCTGAAAG	60.545	20	GGTTCGGAAAAGGTTAGGCT	59.593	20
GTACCGCTGGATAATCCCCT	60.173	20	TTTGTGGTATCAGAGCCACG	59.716	20
GAAAACGGAGACGACGACAT	60.119	20	CGAGAAAAACAAAATTATACG	59.565	26
TGGTTGTCACATCTTCATGC	58.019	20	TCGTTTTTGCGTCGAGAACT	60.944	20
GTCAATGTGGGTGCTGTGTC	60.013	20	GGCATGTGAGGATGTTTGTG	59.967	20
TGCATGGTCTTCGAAGTAGGT	59.749	21	CAAGAGACGCATTAAGACGC	58.677	20
TCGCATGCAACGATAGTAGG	59.856	20	CATTCACACCAAGAAGGGGA	60.892	20
TCAACGCAAAGTCCCTATCC	60.074	20	ATTCCCCATCATCAAACCAA	59.991	20
ACTTCACCGCCAAAACTCTG	60.291	20	TGAGTGCGTGAAATCGAAAG	59.988	20
TGATACATAGTGTTATTCTTTGGC	59.504	25	TTTTAGTGTGGGGACATCCG	60.745	20
GGATCTATTACTAACCGCCCC	58.856	21	TCGGATATTTTTGCTCACCC	59.901	20
TTATCAGGCTGCCTACTCGG	60.365	20	CACAAGAAAATTATTGTCGCTC	59.307	23
GCAGGACAACTACCATACGGA	60.008	21	GGTATCCATCTCGCCCATAG	59.368	20
TTTGGGGTTTGTTGAGGAAG	59.942	20	AAGACCCCATTTCCCCTAAA	59.639	20
AGGCGTGTTTAGGCATCAAT	59.597	20	GGTCTCACGGGTGGTTTTTA	59.83	20

CTTTGAGGTGGGCCAAAATA	59.931	20	CACCGCGTCTTTTCACTACA	59.904	20
AACCCATGTTCTTCAGTTGGA	59.439	21	AATCATGGTGCACGAAATTG	59.4	20
GTGCTGTTAAGCATCCCCAT	59.962	20	GCCCTTTCCCCATATCAAAT	59.984	20
CTGAAATCTCGCATCCCAAT	60.036	20	CTCTTGACTTCTGATCCGGC	59.95	20
TGTCGATCGGTTAGCAATGA	60.22	20	CGAGATTCTCTCTCGCTCTCA	59.981	21
AATGCGCCTATCACTTTAATTC	57.518	22	GGCAAGCTTGGGTATGTGTT	60	20
CCCAAACTTGGTTGCTCTTC	59.711	20	CTATCGTTCGATTTGCGGTT	60.096	20
GCTATGAATGGCATCGAAGA	58.823	20	TGTTGGTGCTTGATGGTTGT	60.008	20
GCAACTTTTGTACTCAGCCCT	58.525	21	CCAAACGACATTATGACGCA	60.523	20
TTCCCAAAATAACCGTCAGC	59.938	20	AATGCTTCAATATCCGCCAG	60.06	20
ACTGACATTCACAGGCATTG	57.067	20	TGTGTCGCGAATTTTGAACA	61.233	20
GCCCCTTTGAGCCTAAGGTA	60.573	20	GCTCTTCTCAACCCTTTTATGC	59.398	22
TCCTCAGAAACTTCAACGCTT	59.111	21	GCTTTTGTGCCGCTTGTAAT	60.272	20
ACTATCGACGTCCGGAGCTA	59.859	20	ATGTCACCTGCTCATGTTGC	59.714	20
GTCGTTTACTCTTTCCGGCT	58.462	20	TCCGGTTGTATTTGTTGGGT	60.088	20
TGAAATGGATCACATGCAAAA	59.922	21	GGTTGATGACGGATTTGTGA	59.348	20
ATGACGAAAATTGCTTTGATCC	60.32	22	GAAACACATCGTTTCCTGGG	60.353	20
ACCCAAAACCTCCCATATCC	59.881	20	TCTTTCCATCGGACCAAGTC	60.05	20
AGATTGGGCTATTCGAGCCT	60.194	20	ATACACGTCGCCCTTCAATC	59.962	20
GGAAACAAGTGGATGACGGT	59.827	20	ACAAAAGCACAAATTGGGAAA	59.483	21
GCAGTTTTGTGTGTCCATGTG	60.064	21	TAACCTGCAACGGTCAAAAA	59.202	20
GGTTGGATAATACATGGCGG	60.038	20	CTCTAGAGTGTTTGCGGTGC	58.677	20
TCCTTTCGAATTTTTCCTCTTTT	59.631	23	ACGTGGAGTTCCAAATGCTC	60.119	20
TGATCCTTCCTAGGATAACCG	58.149	21	AGTATGCCGTTTTTCCTCCA	59.569	20
GTGCGTGTGTGTAACCGTGT	60.556	20	ACCTCCTCTCCGTCGCTAGT	60.414	20
ATCGAGGAGCTGTCATCCAA	60.769	20	TCTCTCCCTTTTCTCACGGA	59.92	20
GACTACGTCGATCCAACGGT	59.997	20	TGGTTATTACTGGAACGCGA	59.182	20
TAGGGGAGGATCGAAGGATT	59.859	20	TCTTCAAAGGAACCGACTGG	60.224	20
CACAATCCATCTTCAACCCA	59.343	20	ACCCGGGTTTTCTTTTTGTT	59.72	20
GGACCCAAATGATTGTACGG	60.051	20	CCCCAAATGGAGACGATAAA	59.756	20
CTTAAAGTGCGGCCAAACG	61.68	19	AAGGTGACAATTGTGATAGCCA	59.499	22
TTATCTGGTCGGTATGGCGT	60.352	20	ATTTGTACGGCGTTTCCTCA	60.502	20
TAAGTTGGGCCTCTCGATCA	60.734	20	TCTGCACACCAATCGTATCC	59.527	20
GAAACACGGAAAAAGCATGG	60.481	20	GTGGTGGTATTTGGTCCGAT	59.532	20
ACAATGATGATGCCAATCCA	59.738	20	AACGCTCCAGATTTCATGCT	59.843	20
CAAATGGCCGAGAGGATTTA	60.031	20	CTAAGCATGGCAGCCAAAAT	60.23	20
CGCAGCAAAGTAGCATACGA	60.177	20	GGCGAAAACAGGAAGGGTAT	60.32	20
TTTAGTGTTTTGACATGATTACTCC	57.557	25	CCTCATATTTCGCAGAACCC	59.528	20
GCGTGTGGGAGTTGGTAAAT	59.859	20	CCCAAATGCAAGCTGTACCT	60.132	20
TGAACTAATCAAGTTCCGCAT	57.379	21	AACCCGCTTATATCGTGTCG	59.982	20
TAGTAGGGTGCAGGGGATTG	59.948	20	CCACAGCTATGCCTAAGTGCT	59.553	21
TCCCGATAGGCTTGAAGGAT	60.92	20	GGCATTCAAATCAACCATTG	58.82	20
CTACATGGCCCTGCTCATTT	60.096	20	GGTCGGCTACATGAACCAAA	60.894	20
CGTGAAGTCCATCTCCCACT	60.112	20	AGTAGGAGGAGTGATCGGGG	60.468	20
ATTAATAAAATTTGGAATGATAGA	57.111	27	AACAACGGGAAAGTGAGCTG	60.291	20
AAACTACCCTTGATCGCACG	60.132	20	ATTGAGCAGTTATCACCGGA	58.173	20
CGACTCAGTCATGCACCATT	59.707	20	AAAAACGGGGCTAAGGATTG	60.305	20
TGAAGTTAGGAATTAAGGAGGTG	58.743	25	TGGAACTCACAAAGTATGGGG	59.838	21
TTCCTCACGAATAAACCAAGC	59.215	21	TGAGAAGGGATTCGAGTTGC	60.34	20
GAACGATTTGTTATCGAGGGA	59.033	21	AACCCCATGAAGCAGAGATG	60.073	20
TTTGACTATGTCTGCGTGCC	59.871	20	TGCACGTGAATGCTTTATTTA	57.051	21
CCTACAAAGCCACTCTAAGCG	59.187	21	AATGTTTTCGCCACGTGTTT	60.407	20
ATCGGCTTATGTGAGGAACG	60.096	20	TGGTGATGTGTACTTTTGGCA	60.019	21
AATATGATTTCACCGGGACG	59.645	20	AGGACTCACTGAAGGAGGCA	59.986	20
TCACAAGTGCAAGCACAATTC	59.903	21	CTTGCGTTTGATTCGTTGAG	59.464	20
TCGTCTCAAGAAGGTGCTTT	57.671	20	GGAGCAAGAACTTGAGGCAT	59.434	20
AGCGCTGAATGTCATTGGAT	60.634	20	ACCGATTTTGTTCCTTTTCAA	58.592	21
TGGGAAGGGTTGTTACTGGA	60.345	20	TGAGGGGAGTGTTGAGATGA	59.18	20

TGGCTGTGAATTGGAGATGA	60.201	20	GTGACATTTTTAGGCGGGAA	59.938	20
CCCTAGCTTTGCCCTCTTTC	60.332	20	CTCGTATGTACCGAATGCGA	59.712	20
CAAGTAAGCGAGATTTTCTACATT	58.649	25	AAGCCTAACAAGTGGATATTA	58.116	26
TGATATCTTTGAAGAACAATTACA	57.905	27	CCCTAACTCGACCCAGATCA	60.065	20
GCACCTCCAATTGCTTTCTC	59.82	20	CAGGTAAAACCTAAAATAGCG	60.36	23
ATTCATTTCGGGCTAATCCA	59.369	20	TGGTTATTACTGGAACGCGA	59.182	20
TGGATTGATGATGATGAGATTTT	58.381	23	AGGCATACTTGGTTGATCCG	59.955	20
CCTTCTCCGTCTGCAAACTC	59.989	20	CACACTAGGGCTTTGCTGCT	60.592	20
TTGCACAGCCCTAATGCTAC	58.945	20	AGCACTCCCTTTTACCACCA	59.592	20
AATGTCGTTTGGCTTGTGGT	60.419	20	TCTTCGATTGGAGTTCAGGC	60.34	20
GCTGGTTTGAGGGAGATGAG	59.803	20	TCAACTCCATTTGTATACTTCA	59.068	26
CCAATTTACTAATTCTTGATGAAT	59.314	27	CAGATCTGATGGCCCAGATT	60.034	20
GTGGTCTAGGATGGGAGCTG	59.679	20	TGATTCCTTCTCTGGCTGTTG	60.382	21
AGGGGGTGGGAATTAAACAC	59.919	20	TGAACTAATCAAGTTCCGCGT	59.761	21
CGCATCCGACTCCTCAATTA	61.129	20	GAATTTCACCCTGATTCCAATG	60.542	22
GTGAATGGGGATCAATTCCTT	60.01	21	TCTTCGCTGTCTCTCAGCAA	60.008	20
ATTAGTCTCCGCCCTCCACT	60.096	20	AAAGGGAACTTCCTGTTTTAGC	58.034	22
AGGGATCCCAAGGCACTACT	59.957	20	CTTATTGCATGGCTTGGCTT	60.23	20
TGGCTTATTTTGGGCTCTTG	60.202	20	ATCGGTTATTACCGGATCGC	61.031	20
CGGCGGAGATAGACAGAGAG	60.111	20	CTGGGCCCACACCTAATAAA	59.817	20
ACCATCAACCTCACCACCTG	60.84	20	CCTCTCTGCAACACCATTCA	59.831	20
TGGTGGTGGAGAAAACTGAG	58.695	20	ACCATCGAACCCCACAAATA	60.051	20
TGACATGCAGAGTTCAACAGC	60.048	21	GGGGTGGGGGTATGTTAGTT	59.805	20
ATCCAATCCACATCCACTCC	59.593	20	ATTTCTCCTCCATCATCCCC	60.096	20
GCAGCCCACAATTCAACATT	60.905	20	TGCGTCAGAAGGTGTCCTAA	59.44	20
CGGAAAATGGTTGGTGGTAG	60.22	20	GCAAATCAAACCCTTGTCAAA	59.967	21
CATGCCCATCTACCAAGACA	59.522	20	ACTTCCTCTGGCATCGCTTA	59.978	20
TCAACATTTTTCCCAGAATCG	59.924	21	GAGCAGTTGGAGAGGGTGAG	59.986	20
ATCATCAGTAGCGCCACCTT	59.723	20	TGTTGCACCTTGTGCAGATT	60.31	20
CGGACCGGACCGTAGATTA	60.858	19	GATTTCACGGTTTGGGCTTA	59.938	20
TCTGAAAATCAAAGGCCCAC	60.051	20	ATTCCGAAAATCAAAAGCCC	60.26	20
CATGTACGTTCTTCCCCGTT	59.853	20	CATGCACAGATTCCGTCACT	59.707	20
AAACCAGTGTTCTTGGTTGGA	59.482	21	CATGGTGCATGAAATTGGAG	59.924	20
CGAAACCCCTTTCTCTCTCC	60.183	20	CCTTTCGCAACTGGAAGAAC	59.853	20
TCTCCCTCGGTAATTCCCTT	59.897	20	GCGTGTGAGTGTTCGTGAAT	59.758	20
AGGGGTGTATTAAAATAGGAGCA	58.188	23	TCACATGAGATGATTAATTGG	59.343	24
CCTCCATCATGAAAACCGAG	60.452	20	CTGGAATAACCCAAGCCAAA	59.931	20
TCTCCTCTGCACCAACCTCT	59.986	20	TGATTCGGAGGAATACGAGG	60.029	20
ACACAAAACTCATACCCGTGC	59.912	21	AACAGCAAATCCGAGACACA	59.293	20
ACCAAAATAGATGGCATTCAAGA	59.857	23	CCATTTTCAGGTCCTCACCA	60.892	20
TGGAAGTTCTCTCCTCTCGC	59.679	20	TCGGAGATCAGCTACGGTCT	59.973	20
TATGAGAGTGGATCGTGGGC	61.037	20	TGAAACTGCTGTATGCTGAGTT	59.424	25
GGTTATGACTTGATCATGACCCT	59.231	23	TGGCAAGAAAACAACAGCAT	59.322	20
GCATATCAAATGGTGTTTGGG	60.067	21	TCACAAAGAAATCAGCACGAA	59.454	21
AAGGTGGCGTATGCTGAGAG	60.419	20	TCAACGGTTTAAAATTGTTCCT	57.74	22
CTCTCTTTCGTCCTTTTTCCC	59.335	21	TCCATCCACAGCAATGAAAA	60.049	20
TTCCCGAGTAAGATGGATGG	59.887	20	TCTTTCACTTCGATCCCACC	60.05	20
CACTCCTCTTCTGCGTGGTT	60.444	20	TGAGATTCTGGTTTCGGCTT	59.813	20
GAACACACGAAGATTGGGAGA	60.104	21	AGTATCGGCTTCGGAAACAA	59.708	20
ACGGAAAATCGGGGTAGAAT	59.666	20	CATTGGGTGGAAGTGTAAAGA	58.994	22
TGAAATCTTACTACTCCAAAAATC	58.36	27	TTTGAGGAGGAAGAGGAGGA	58.937	20
TCTTTCGGCTGACTTTTTCTTT	59.539	22	TGGTCAGTTTGTCCGAATCTT	59.583	21
AAGATCTACGTCCACGGGAG	59.162	20	GCTGAAATTAGTTGAGGCACG	59.897	21
CATGACTGCCCAAGAAATCA	59.648	20	TCATGTACCCCCACATGTCA	60.665	20
CCACGAACATTCATCGGATA	59.35	20	TTGGGTGTAAGACATAGAAGG	57.815	23
AACAGAAAGCCACACATGTCAC	60.081	22	GCGAAAAACTCGAAAAACCA	60.223	20
ACGGATTTAAGGGTTATTACCTG	57.667	23	TGGATGATGTGATGTTTTTAGA	60.237	24
CGCATTTCCATACATTTTTACG	59.407	22	CCTATGGAAACTCAAATCCGA	59.03	21

CCAGGTACCGAAGGCATAGA	60.088	20	CTCAACGGTATGCTCGGATT	60.096	20
TGGCTTCAGCAGACAATGAG	60.136	20	CTGGAAAACCTGGAGTCAGC	59.844	20
ACGAGATCGAAGGGAGACAA	59.803	20	GGAGAGAGGAGAACTGCGTG	60.135	20
TCACGATGCGTCACAAGTTT	60.31	20	TTCTCGCTTCTTCGCTATGG	60.617	20
TGTTTGGTAGCCCACACAAT	58.9	20	TGCCATTCTGTGCATCAACT	60.272	20
TAAGGCAAAGCACGTGAGTG	60.05	20	AAAGCCGATCGAGTTTTTCC	60.562	20
TCAGATGAGTTGAATGGAACAGA	59.726	23	TTGGTCAACCCCTTCTATCG	59.926	20
CACTCGCATAAGTATGCATGAAA	60.164	23	AATAGCGTGTGTTTTGCGTG	59.799	20
TGCACGTTCACTAGCACACA	60.096	20	CCCGGTTTTGACTCTTTGAC	59.569	20
CAAGAGCTTGAGCTCGGAGT	59.891	20	ATGCTGCGTGAACAAAAATG	59.735	20
TTTTCAAATTGCATCCTAGCAA	59.732	22	AACCGGTTAAAAATCGGACC	60.055	20
AGAGTGGAGGCCATTTCTGA	59.803	20	GCATGGCATGAAATTGTTGA	60.476	20
TCAACAACCAGTCCACTCCA	60.129	20	TTTTTCCGGTGATGGATGAG	60.832	20
TGCGTCAAAAGCTCTTCAAA	59.729	20	TTGTCTAGCAATCTTCGAGTTTT	57.519	24
TGGTCCAGATTTGTTCCTACG	59.978	21	TCGACAATGTTAAAAATCAAAT	60.026	27
GCACTCACATTTTCCCCAAT	59.797	20	TCAAGGAGTCACAACGTGAAA	59.324	21
CTCAAATTGGAATTGGGCTG	60.439	20	TGATGAACAAGCCGAACAAA	60.234	20
GGGAGAAGAGAGAGTTAGGGTG	58.483	22	ACGATCGTAAGGCGAAATTG	60.096	20
CTTGGAGCTTTGATCCTTGC	59.955	20	TTACCCAACCCACTAACCCA	60.081	20
AACCACCTTTACAAATGAGCTAGT	57.599	24	CGGACCTGCAGGAGATTATT	59.15	20
TCACTTCATTACGAAAAACACCA	59.544	23	GCAAATGCAATGACTGTTGG	60.119	20
TGTGTCATCTAGTCCGGTGG	59.545	20	GAGCGGTTATTACCGGATCG	61.686	20
TCCATTTCCTCCACCGTTAG	59.926	20	TACTGGATGGATACCCGAGC	59.917	20
ACGGTAATTCACCGACCAAA	60.227	20	CCAAGATCAATGGTTCCTAAGT	59.879	23
AAAAGTCATCCGCTATCTCGAA	60.224	22	ACAATGCGAGTGCATTTTTG	59.735	20
TTTTCATTCTTGACCCCTTCTC	59.571	22	GCAGTGTTTTGCAAGGAACA	59.888	20
AAGCTGCATGCATTTCAGAG	59.178	20	GGGCTCGAAAATTGAAGTGA	60.192	20
GCGCCGCCTATCACTTTA	59.937	18	CAGCTGAAAGGAGCCATCTC	60.096	20
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CCACATTTTTCCCGATTGTT	59.662	20	GCTCAAGGATTTTCGCAGAG	60.096	20
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CAAAAAGGGATGAGCGACAC	60.636	20	TCATAGGTAAAGCCGCAACC	60.096	20
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CCAAGATAATGCCACCCAAA	60.692	20	GGCTCAACAACACAATTCCA	59.547	20
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ATTTCCTTCACAAGCCATGC	60.081	20	TGCAGTTCATCTTTGCCTCA	60.539	20
AAACTCACGAACACACGCAC	59.801	20	AAGAAACAAACAGGGTACGA	59.56	22
GCATGCTAGCCTTGGCTTTA	60.497	20	TTGGTAGGGGTCAGCACAAT	60.375	20
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GGCGATCCTAAGAAATGCTG	59.807	20	AGGTATCGTTCGCGCTGTAG	60.428	20
GAAGTAAACGGCCAAAGTGC	59.752	20	AGCAAGAAGGTTGCAACTGA	58.65	20
CGAAATCTTACTTTGCGGCT	59.496	20	CATGTCAACTGTCGAAGGGA	59.676	20
CATCAAGTTTCCCAAGGCAT	59.933	20	CCGCTCACTCAATTCTTCGT	60.397	20
TTGGTTGGTGGAAGAAATCA	58.947	20	GTCCGGAACAAGGGAAAGTT	60.34	20
GACCGGGCTCACAGAATATG	60.483	20	TAGCCTAAGTCGGGACAGGA	59.83	20
TGCCCAAAAACATTTCAACA	59.946	20	AGAGGGCTTGCCTTTTGTTT	60.242	20
AGGGGTTATCACCTGAATGC	58.864	20	GAGAGAGATCGAGCGTGACA	59.239	20
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TACCACCTCCATGTTCGTCA	59.96	20	TCGACTTGTGCAATCAGTCC	59.837	20
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TTGGAAAATAACATGCATAGAAAA	57.857	24	TTTAAACGGCACGAGTTGGT	60.534	20
AAACCAGAATGAGAACCGGA	59.526	20	ACGACACTCGAATGGAGGAA	60.656	20
GCCGTAGTAACTCCAGCCAC	59.763	20	GTGTGTGCGTGAGTGAAACA	59.321	20
CTAGCAGGTCGACACGAACA	60.049	20	CTAGCCGTTGGTGGGAGTAA	60.125	20
TCATCTCAAATTTCATTGTGGA	58.066	22	CCACAACTATGTGGGGAAAAA	59.71	21
CCACATACCATGCCAACAGA	60.39	20	CACTCGAAAAAGGCATCCAT	60.074	20
CCGAATGAAATTATTTGTTTTCC	58.826	23	TCGTTTTAGTTGGCCATAATCT	57.848	22
CCAATCCTTGGACATTTTGG	60.162	20	TTTTTCAGCACCACTTCACA	57.867	20

GGCCAAGTTGGTGAAGTAGG	59.592	20	GGACAGGCCCTGGACTTTAT	60.328	20
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CGTCGTTTCGTGTTCTTTCA	59.881	20	GAAAGAGAGCCACGTGTGTG	59.467	20
TCATGGTTGGGTGTTTTTATCA	60.089	22	TTTTCAAAATCAGGCGCATA	59.286	20
TTGATCCAAGGGTGTATAATGG	58.694	22	CTCTAACAAATGCCAGCCGT	60.27	20
CGCTCAGGTTTGAATCTGTTT	59.369	21	TAAATGCCCTGCTGTAGGAA	58.387	20
CATGGTTGCAAAGGTGATTG	59.964	20	TGTTGTGCAGTGGAGGACAT	60.162	20
CCATATTTAAGCCCCAGCAA	59.922	20	ATGCTTAATGTGCATGTGCG	60.697	20
GGACCGCGTTTATGGTATTG	60.209	20	CGCTCACAATGATGGATACG	60.096	20
GAATGTCATGAGTTGAGGCG	59.245	20	GGGGTCAGGGGGTTAATAAG	59.527	20
AGTGCAAAATTGGGCTAGGA	59.708	20	TGAACAAATTACACAAACAAA	60.54	25
TCTGTTTGCGAAATTTGTTGA	59.335	21	CATCAAGCAAACAACCAGCA	60.844	20
TCCAACCTGTTTCGGACTAA	58.201	20	TCGTGGAGTGAGTGGAAGTG	59.864	20
AGATTGGGCTATTCGAGCCT	60.194	20	GGGAGCAATTTTTGCTTGAA	60.188	20
ACTTTTGCGTCCTTTGTCGT	59.78	20	GACGCCTGAATATCGGTCAT	59.923	20
ATGAGTTATCACCGGATCGC	59.923	20	AAATCAAAGGCCAACAATGG	59.801	20
TGTACAAATGCTGGAGGTCG	59.716	20	GATGTTCTCCAACGACCATGT	59.842	21
ATCGCCCACTTATTGAGCTG	60.235	20	GTGGTGACAGTTCGATGTGG	60.005	20
AGCTTGTAGAACGAGCCGAG	59.78	20	AGATAGCGAAGGGAATTGGG	60.411	20
TGGCTCAAAGCATGAACAAA	60.379	20	TGAGCCAACTGAAAACACACA	60.331	21
GGTTAATTGCTGGCAAATCG	60.456	20	CCATGGCCTAGCTTTGGATA	60.053	20
TGAAGCAATCAAAAACGGTG	59.706	20	TGCATCTTGGCTCATGTGAT	60.233	20
TGTGAAACGACGGTTCTTGA	60.278	20	TCCCTGTCCTTTTTCCCTTT	59.912	20
TTGATTGTAATTCTCTGCACCAG	59.28	23	TGCAAGCATCTTTTGTCTCG	60.134	20
AAAAACTGTAGTGGGTTAAAATT	57.487	25	TCAGGAGCGGTTTGAACAAT	60.636	20
TGTGACGAGCTTATGAAACTATA	59.767	25	CGTGAGGTGAGGGATGAAGT	60.112	20
TATTAACCCTTCATTGTTTTTAAAT	57.085	26	GGTTGTGGTTTGGTTTCTTCA	59.861	21
CAAATGAGCATGAGGGAGGT	60.073	20	CTATCATCTCGGGGTGCAAT	59.917	20
GCCGAGATTTGTTATGCGTT	60.103	20	CGGGGTATTACATAAATGATG	58.285	22
TTGATTCCTCCCCACAATTC	59.727	20	GCTTTGGGAGGTGGAGTTTT	60.476	20
AACAATGAATGAGGTTGGGG	59.647	20	ATTGAATCGGCAGGTCAAAC	59.939	20
AACAGAAGCAAGATTCGACCA	59.867	21	TTTTTGATGAGCTGGAGCCT	59.955	20
TTTCTCCCCATCGATAACCA	60.266	20	AGGGCCGAGATTTGTAGAGG	60.59	20
CTTGGGATGGGGGAGTATTT	60.011	20	AAAAGAAGTGTGTGGGGGTG	59.861	20
CCCAGTATCCCAAACTCGAA	59.926	20	TGGGGGCTTAACAAAGTCAC	59.971	20
TGCTTTTCCATGGTGACTGA	60.24	20	TCCAAAATCTAATGCGCGTC	61.105	20
TGAGAACCAAACACAAATGTCA	59.072	22	AAAAATGAAATGTGGGGTGC	59.668	20
AAAGCCAGATTCATTTTGCC	59.162	20	GGGTATCTCTCGCTGCTTTG	59.978	20
GGTATTGGCAAATGCAGGTT	59.829	20	GTAGCCAGCTTGTTTTGGGA	60.249	20
ACGCACCAATTTCCTTCAAA	60.481	20	TGGTGTCTGAACAGCAGAGG	60.022	20
TTTTGACATGATCACACCCC	59.193	20	TGACTTCGCCATTTTCCACT	60.636	20
CTGGGCCTATCCTATCATGG	59.363	20	TGTCCCAAAATCGTGTCTCA	60.088	20
GCCTTCTAGCTTCTCTTGCTTT	58.633	22	GGATAGGTTGAAACTGCCCA	59.933	20
AGATGCGTGCATAATTGCCT	60.636	20	TGCGCATCTAGCTTGAGAGA	59.995	20
TTGTTTAAATGCACACCCCTT	59.37	21	CCCCGATTCTTTTAGCCTTC	60.034	20
ATCGAACCGTTTTTCTGTCG	60.11	20	AGCCTTTGGGTCAAAATCTG	59.17	20
AGCCTTCTAGCATCTCTTGCTC	59.42	22	CGACCTGGTGGGTTGTTCTA	60.943	20
CACTCAATTCATTTCACCTCCA	59.971	22	ATGGAATAGCGTCCGAAGTG	60.096	20
TCTCTCCACCAAATGTCCAA	59.059	20	AAACATCAATGGCCTGATTTG	59.815	21
GCGGCACACGAGGTATAAAA	61.019	20	GCCCGGAACACAAATAGAGA	60.074	20
TGTGGTATCAGAGCCACGAC	59.707	20	ATGACACGCATAAAGGGACC	59.82	20
TCTTTTGCTATGTCCTCACTCG	59.517	22	CCCAATGACACGACACAAAC	59.855	20
AGGGAGGCAAAAAGAGGTTG	60.601	20	AACTGTGGCAAGATCCATCC	59.934	20
TGGGATATAGCGAGTTTGGTG	59.967	21	ATAACCGTTCCCGCTCTTCT	60.096	20
AGAATGCCCTTGTATGCTGC	60.243	20	CATAAAATGGACACGCACCT	58.502	20
GCGTGTGAGTGTGTGTCAGA	59.46	20	CACACACGCGCATATACAAA	59.211	20
TTATATCTCCCACCAACCGC	59.784	20	AAGTTAAGCGTGTTTGCGCT	60.082	20
TGGGATGAAAATAGGGGAAA	59.203	20	TCGGATTTTTATAGGCTTCTTC	59.997	24

TGACGGGATTTAGGTGTTTTG	59.847	21	TTCAATCATGAGCGTCCGTA	60.22	20
AAGGGGGATCAAATCTAGTCTTTT	59.766	24	TTGGCGAAAATAGCCAAGTC	60.209	20
CATTCAAGGGGCATTTTTGT	59.801	20	GCGCTTTCAGGGTTTAAAAT	58.386	20
CAAAAATAGTCGTGGAGGGC	59.569	20	TCATGATAGGATGGGGCTTC	59.854	20
TTCTCGCCATCTCTCCCTAA	59.91	20	TGGAAGGAGAAACGATGACC	60.05	20
GCATCTCTTGCTCTCTCGTT	57.35	20	CCACCTTTTCATTCCGACTC	59.526	20
CGTCTTCGTTCTCCGTCTTC	59.989	20	GCTCCCTCCATTTTTGTGTG	60.495	20
TCACTATAAGGTGGTGTTCCTACC	58.524	24	AACACAGCAGGTTTCGATCC	60.119	20
GAATACTTGCCTCAGCTCCG	59.978	20	AACTTCCCTTCATCAGCCCT	60.074	20
ATTGAATCTACGTCCACGGG	59.813	20	AGTCATGCGATCTGAACGTG	59.862	20
GCCAGCTTTTTCTTCTCCAA	59.569	20	AACAGAGAAGCCCACCTCCT	60.252	20
CCCTTTACCTCACTGGTGGA	59.959	20	GGTTCGATGTGGTGGAGAAC	60.372	20
TCACCCCCATCTTCTCTCAC	60.048	20	AGGTTGAATCGGTGAACTCG	60.111	20
CACAGGTTCTCATCGCTCTG	59.571	20	AATTTGTCGTTTGACCAGCC	59.978	20
CATGGTGATAGAGCCGGATT	59.917	20	CCTCCTTCGACACTTTTTCG	59.846	20
CTTCTCGTGTCCGACTCCTC	59.986	20	TGGAAATCCTCGTTTGATGA	59.049	20
AGGGCGAAGAGAAATGTGAA	59.813	20	CAAGCTTACCCGAGCTGAAC	60.015	20
AAAATATGGGGTTTTCCCAAA	59.428	21	CCGATCATTGCTATCCTCAA	58.671	20
ATTCTTGGGCTTTCATGACG	60.074	20	TTTTCTCGAGTTTCACGCCT	59.993	20
ACCCAAGACCTCAAGCTCAA	59.844	20	TTTTGGTTCAGGGGTGGATA	60.162	20
TGTTGAAATCTTGAACGGGTC	59.963	21	TTGTCGTATCCCTCCTCCAC	59.927	20
AAAAACGCGAATTTTTAGGGT	59.08	21	GAAAACAAGTGTTGCGGGAT	59.978	20
ATATTTGTGCGTGCACCTGA	60.142	20	TAACTGCCTCTTTGCACCTG	59.072	20
GAGCACTGAGCAGAAAAGGG	60.134	20	AATACCAGGCAAAAGAAGCG	59.361	20
ATCGGTTATTACCGGATCGC	61.031	20	TGAAACGGACGAACAATGAA	60.088	20
GCGTTGAGAAGAAGGGAGAA	59.55	20	CAGAACATTCTCATCCCGGT	59.927	20
TCCCCTAATTCCCTCATTCA	59.315	20	GCACAAAAACAAACGCAAAA	59.764	20
GGTGAAACTTGAACAACCCC	59.284	20	GGAGGATCACACCACGAATTA	59.805	21
ACGACGGTGTTGTTGATCTG	59.597	20	GCCTCTCTCTTTCTCCCGAT	59.919	20
TCGGAGATCAGCTACGGTCT	59.973	20	CTCTCGTACGCTGCCTCTCT	59.914	20
GTGGTAGAGCTCCCCTTGTG	59.721	20	CAAAACCACAGCCGACAATA	59.585	20
TCCATCAGACAGTTTCTTGCAT	59.74	22	CATGTGAGATTCCACGCTGT	59.707	20
TCCCTCCTCAAATTTACCCC	60.124	20	AAAATGACGAATGGGAGGG	59.735	19
CGGGATCTTCATCCAATTCA	60.801	20	AACTTGAGCAATGTTGGGCT	59.74	20
CTTGGAATAGGGTTTTCAGGG	59.816	21	TTCGTATCTTGCCCATGGAT	60.296	20
GAAAGGCACAAAGCGATAGG	59.845	20	TGGACAGTTTGTCCGAATCTT	59.583	21
GGTTGAACGATTCGGGTATG	60.192	20	AAGGAGGTGTTATGAAGGGAT	58.028	22
GCTCGTACGAAACCCTTGAG	59.875	20	GAAATCCATCAACCAAACGG	60.17	20
TTAATTTCCCGGTGGACTCA	60.301	20	CCGAAGCTAAGACACAACCA	58.923	20
TTTTTGCTCGAGGGTTTTGT	59.724	20	AAATTTTGTTTCCCACCAAATA	58.744	23
ATGCAACCCTCCCTTTCTCT	60.074	20	TTGATCACCACCCTCCATTT	60.173	20
GACCTACAGACCGATCATGAAA	59.056	22	TCCGGCTTCTGTAAATTTCG	60.202	20
TGCTCACATCTCTTTTTCTCTTTT	58.761	24	GATCACAGGCCATCTTTTCC	59.488	20
TGCCTTATAAGCTCGAGAAAA	57.021	21	CCGCATTTATGTGTGCAAAA	60.508	20
CGCTAAAGCAGGATGTGGTT	60.27	20	CAGCGAAGATGTGAGGATCA	59.942	20
TCGCATTGACACATAATCGAA	60.088	21	CGACGTGCTTTTGGTAATTG	59.226	20
TAGCCGTTTATGACCGTTGA	59.182	20	GAATTTTGTGATTGGGTGGG	60.029	20
GGTGGAGCAAACTTGGTCAG	60.69	20	TTTTCAGTTGATGCCTGATGA	59.262	21
TCTTGCCGATTCTCCTTGTT	59.813	20	CTTCCAGAAACCTGAGCAGC	60.134	20
CGATGCTTTAAAAGATGTCAACC	60.017	23	TGCCGTCTCACACATTAGAA	57.836	20
AAAGAAAGAAATAGAGCTGCTGG	60.045	24	CCCACCAATTTTGAGACGTT	59.83	20
CGTCCTGGTTGTTCCAAATAA	59.847	21	GTTTAACGAATGCTCCAGCG	60.772	20
CGACTTGGCTCCATGTTGT	59.692	19	CGCACTTGGCTCCTTTTTAG	60.011	20
TGCATCCAGTGGCGTATCTA	60.243	20	TTTAGTGTTTTGACATGATTACT	59.896	27
GAATTCGGATTCGAGTCATATAAT	57.681	24	CGATTTGGATTCGAATTTTG	58.082	20
TAGGCACCCAGGATGAAGAC	60.073	20	GGTTTGCGAGCATAAAAATGA	60.089	21
GAAGCTTCAATGGAGGTGATTC	60.081	22	AGAGAAACCTTGGCCCCTAA	60.068	20
TCGGAATTGGATTATGTTGC	58.43	20	AGCGCACTCAAACAATAGCC	60.416	20

TCGGTCACAAAATTCGAAAA	59.133	20	CAATGCCTAGTTTACCCCCA	59.817	20
AAATTTGGGTCAAACCCCTT	59.549	20	GACCGAAAATGGAGGTTCAA	59.91	20
CACATCTTGCAACCCACAGT	59.597	20	CACACACTCACGCACACATT	59.183	20
CCAATTTGAATGGTTATCACCTG	60.457	23	GGAAAATGTCACCGGAAAAA	59.778	20
GAGGCTTAAAGCTGTGCTGG	60.154	20	CCCCTCGTATGCAGTCAAAC	60.517	20
AGGATAAATGTGGCGAATGC	59.929	20	CTAGGCATGGAATCCGAGAA	60.17	20
TCCATCATCATAGGCGTCAC	59.482	20	AACCAACCTTGGCCACATAA	60.227	20
CCATCATCCTCTCTCCCAAA	60.003	20	CCAAAGAAAATGGCCAAAAA	59.916	20
AGGTGGCACTCTGAAATCAA	58.287	20	AGCGGTTATTACCGGATCG	59.93	19
TGATGCTACCCACTTGCTCTT	59.89	21	GTGGCGACATCCGAATAACT	59.962	20
GAGCGTATGGGTAGAGCGAG	60	20	CATAGCCGATAAAAATGGCG	60.424	20
GAAGAAGCCGACAATTTGCT	59.457	20	TTTCGAAATCCCCTTTTTCA	59.497	20
TTCTACCGCAACACAAGGTG	59.758	20	TACAGAGCCACCATTTTCCC	59.933	20
TGTAAGGGGGTGGGAATGTA	60.044	20	AGAATATTCATGGGGTCCGA	59.2	20
TATTTGCTCGAGCCCTTCAT	59.807	20	AACCCGGATCGGAAAAATAC	60.02	20
AGATCTTGGCAACTCCCTCA	59.803	20	TGAGTTGCACGTGTGTGAGA	60.07	20
ATGTCGAAGAATCCGAATGG	59.894	20	TTTGGGCACATTGCTCATTA	60.073	20
TGGACCGGTTAGATCGGATA	60.288	20	AAATAATGTTTGTCGGGCCT	58.443	20
TCCCCACCGTGGTATTTATC	59.505	20	TGATGTGTGATGCCTCCCTA	60.072	20
CGTTTGTGAAAAGAACGCAG	59.507	20	GTGAAGGGCCAATTTCTTGA	60.051	20
TCACTATAAATCATTTTTCTTGTAG	59.266	27	ATAAGTTGGGTCACGGGTTG	59.711	20
AGTCGTTCATCCCCTTTGTG	59.966	20	CTACGTAGCCCCCAAATCAA	59.953	20
GTTAGCCACTGTGACAACACAT	57.662	22	AGGGCAGTCAAGACCATCAT	59.535	20
GACTGTAATGCATGGCTGGA	59.679	20	GTGTGTTCATCACCAGTGGC	60.013	20
ATTTGGAGGGGGTTGAAAAA	60.514	20	CGAATATCCCCCAATTCAAA	59.593	20
TAGGGAAATTGGATCGTTGC	59.901	20	GCCTGCCTATTAAACTCCCC	59.93	20
TGGCCTAAAATAGGAAGCCC	60.4	20	TTTTGTTATGATAGGATAAAAC	58.996	26
AAACACCACCTCCCTCACTG	60.002	20	CCATGCTCAGGAATGCTACC	60.624	20
CACGGTTAGGCTCGAGAGAG	60.149	20	ATAGACCAACCGCCATTACG	59.845	20
TTTACGAAAATGCCACCACC	60.732	20	ATGCAGCTGTCCATTGTGAG	59.862	20
AGCATCTCTCCATCACTCTCA	57.528	21	TGAAACGGGGATTTGTCAAT	60.17	20
TTCGAACCTGGTTTTCGTTC	60.088	20	TCACCCACACACACACGAAT	60.928	20
ACCTTGATGTGGTGGTGCTA	59.01	20	ATGGAGAAAAGGTACGCACG	60.132	20
CAAAACTCCCAATTTCCACC	59.264	20	TGAATCGAGTGTTTCTTGCG	59.988	20
TTTCCCCTAGTCTAAGCCGA	58.925	20	CATGAAAGGAAACAAAATCGA	59.098	22
TGGGAGATGGTGGAGAGAGA	60.762	20	TTTGTTATGCGTTTTGACGA	57.846	20
TCGCTTTTGCTTTTGCTTTT	60.13	20	CCTTCTTCCACCGTTCTTCA	60.224	20
TCCAAAAAGTCTGGTTGCTG	58.897	20	ACAACCAAACAAGCCCGTAG	60.03	20
TCACCTTTTCCCTCTTCCCT	60.045	20	GACGTTGGTGGGATTTGAAC	60.218	20
AACTCCCATCCGAGGTCCTA	60.842	20	GGGCTGCACACGAATGATTA	61.98	20
TAGTCCGTGGGTTTACCGAG	59.986	20	AATGGGGAGGATAAACCGAG	60.145	20
GAAGCAGCAACAATGATGGA	59.805	20	TTCTCATCCACAGACCCCTC	60.048	20
AGCAAAGAAGGAATGCAACC	59.316	20	CTTCCAGCAAGAAAATCGGA	60.323	20
GCGCGATTATCGAAGAGAGA	60.594	20	TTTTGGTTGAATAGGGGTGA	57.917	20
AATTTGCATGAGAGCCAAGC	60.361	20	TGCAGGGCTGAGTATAGGGT	59.717	20
TGGCCCAGATTTGTTCCTAC	59.933	20	CAGCAAGGAACTGATGGACA	59.831	20
CGTGTTCCTAATCCCCATGT	59.67	20	CTCCCTAGGATGTGGGGGTA	61.084	20
TTTTACGGGCAACGTACTCC	59.996	20	ACCCAGAGCGTACTCGAAGA	60.012	20
AGCTATAAGATTGACTAGATCAA	57.118	26	TTTTTCAATCATACTTCCGGTTT	58.955	23
CTTCTCGCGTCAGACTCCTC	60.284	20	TTTTGACCAATCCTTTTGGG	59.772	20
TCAATGATGGCCGAAAACTT	60.448	20	GTAAAGAGACAATCCGGCCA	60.074	20
CCAGCCGTTGATCATTACCT	59.955	20	CCTCCATTCAAGCAGAAAGC	59.955	20
TGCCCTTTCTTTTAGGAGCA	59.953	20	CGAAATTGCGAGTCCCTTAG	59.839	20
AACGAACACGAGAGGTTTGG	60.149	20	AGAGCCGTTGTGTCGAATCT	59.874	20
TGCTACCTAGGAAGGCGATG	60.365	20	GCCGTAGATCTAACGACCGA	60.235	20
AAGGGACGACCGAACAAAAT	60.723	20	TTCTTGATGTGTTGGCAAGC	59.847	20
AACGGCGCGACAGTTATAGA	60.792	20	AGATTTGGGCAGTGTGGTGT	60.431	20
CATGAGCACTAATGAGCCGA	59.972	20	CAATATGAGAATGGCCGAAA	58.576	20

GGGACAAAAATGCCCTTGTA	59.801	20	GTGGACGTCCCAGATTGTTT	59.827	20
ATTGAAGAAGTGCCGTAGCC	59.34	20	CACGTGGCATTTAACTGGTG	60.027	20
TTTTGCCCTCGAATGCTATC	60.175	20	GGGGAAGTTATTATTTGATCAC	57.859	23
AACCGTGATGGTTGGGATTA	60.051	20	ACGGCGTACAAAAGGAAATG	59.996	20
TCCTCAACTCTGAGCCGAAT	59.95	20	GTCGTTGATGAAGCACCGTA	59.722	20
TTTAATGATGCGTTTTGGCA	60.074	20	GTTCCTACGCACTCACATTAAG	58.464	23
ATGGGATAGTACCGGAACGC	61.091	20	ATCCCGATTGAAGACGTTTG	59.933	20
CTCACACACACTCGCATTCA	59.431	20	CGATGACATTAACAATAACAA	60.095	26
AATGAGGCTTTTGGATCGAC	59.129	20	GCGTCTTTGAGGTTCTCCAC	59.851	20
AATGGCACACAGGTGAATGA	59.967	20	ACGGATTCACCAGAACAAGC	60.119	20
GGTCAACTTCGAACGAGGAG	59.844	20	TGTGTGGCTTTTCTGCAAAC	59.888	20
CGATTCGCAACAACAACAAC	60.157	20	CTTCTTCTTCCCCATCATGC	59.629	20
AGCATTCAGTCATGCACAGG	59.862	20	TCGTTCAAAAGATGGCTTGTC	60.242	21
CCCATCTGCAAATATTGCCT	59.923	20	TCTGTGGTTCCATTCCATCA	59.893	20
AACCAACTAAGGGGGTCAAA	58.41	20	CATTATCACAGGAGATTGGCA	58.586	21
AACTAACCCGCACCACAAAC	59.898	20	GCCTGAACCACCAACCTTGT	62.297	20
TCATTTCACCCATGAGCTTT	58.145	20	CGCCTCCGTAGATACATGCT	60.257	20
CCGTTTATCTTCCCCTCCAT	60.145	20	GCCGCAGTTGAGATCTAAGG	59.978	20
TCATACACGATGGGATCGAA	59.883	20	GGAGGTTCCATGTTGGAAAA	59.767	20
AACGTCAAGTATTCCGCCAC	60	20	CTTGCCTTTAGCTTTAGCCC	58.299	20
AATGATCAAAACGATTCGCC	59.907	20	GATTGCGAGAGACCAAAGGA	60.34	20
TGACATGGAAGGAAAAAGGG	59.903	20	TGCGCTTCTCTGTTACAAGC	59.371	20
TCTCCAAATTTGAGGGTTATCA	58.556	22	ACGACAAATTCAGGGGCATA	60.331	20
CAAATGGCCAAGAGAGTTACAA	59.267	22	GAGAGACGACGGATCGAAAC	59.81	20
CCCATTTTCGATCCTGTGAG	60.452	20	GCAACGGAATACCACTCGTT	60	20
AGCGGTTATTACCGGATCG	59.93	19	AAACAAAAGGCAACTGATTCG	59.257	21
CAAATGGCCAAGGGAGTTAC	59.429	20	AATTTCACATCCTCCCTCCC	60.133	20
GGGGAAGCGGTTATTTTTGT	60.184	20	TCATTTTCACCACGTGCAAT	59.972	20
AGAAATGACATCACCACGCA	60.12	20	AATTCTCAACAAGGGGCTGA	59.67	20
TCAAACAACTAGATTAGTCCATAT	57.069	26	CGTTTGTTGAGTTGCAATGG	60.149	20
AGCAGGTTTTTGGTGGAAGA	59.711	20	GCGTTGGGATCGTGTTAAGT	60	20
GAGAAGTGAAAGGGGCTCG	59.935	19	TGAGCTTCCAACGTAAGTTTCA	60.176	23
ACAATGGCAAGAGAGTTGCT	57.542	20	CAATGCTGCACATCAAGGTC	60.272	20
CGAATACCTACCCCGTGAGA	59.948	20	GGCATTTTGAGCATTGGATT	59.907	20
CCACCTCTCCACGTCAAACT	60.151	20	GTTGACGGCTGGAACCTTAG	59.734	20
TCTCTTCAATAAGGTAACAACCAA	58.381	25	ACCCTTACATTCCCGTTGTG	59.711	20
TTCACGAAGTCTGCATTTGG	59.84	20	TGCAAGTGGGAGGGAAGTAG	60.246	20
CAATTCAACATGATGGTGCC	59.781	20	TAATTTGGCAAACTCTGGGC	60.074	20
CAAAATTAAAAGTGTTCCATCCC	58.829	23	CCGTTTATATGCGGTCCAGT	59.845	20
GACCAGTTCAAGGGAGGTGA	60.088	20	CCACGTCTTGTTTTCCATCTC	59.583	21
ATGGCCACAAATGGTTCCTA	60.192	20	ACATTGTTTGGGAAAAACCTT	57.508	21
AACCCCTTGTAGGAACAGCA	59.592	20	TCGAAGGTCAATGGTTCACA	60.088	20
GATCTACGTCCACGGGAGAA	60.073	20	GCGCGGAGTTTAAGAAATGT	59.365	20
CGAGATTTGACACGCAAGAT	58.877	20	GCCATCAGATCTGCACTGAA	59.95	20
TACGCGACCCATTCTTGATT	60.469	20	CTCGTTTCTTGCTAGCTCGG	60.284	20
CCAGTATTTGAGAGATGGGCA	60.081	21	TGACGGGCAAGTGTTCATTA	60.111	20
TGTCTTTAGCTCTGGTGTGGC	60.447	21	AGGCCACCCTAATTTATGCC	60.171	20
ACTCCAGCCACCATCTTCAC	60.12	20	AGTGTGTGTATGCGCATGTGT	60.12	21
GGACGGAGGGAGTAGTTTCC	59.935	20	TGAGTCTGATGGACTGCCAC	59.827	20
CGCGGAAATACTCTCGAAAC	59.845	20	GATCTAACTAGGCCCGTCCC	59.925	20
GACCAAGCATGTGGTTCCTT	59.973	20	CAAGACTGGAAGCCCACAAT	60.111	20
CCGTTAAATTACATGATTTTCCCT	59.56	24	GCAAACCCGTGTTCTTCAGT	60.156	20
AACCACGTTTTGGCTAGTTCA	59.663	21	TGTCCATGAAAGATTGGGGT	60.173	20
GGAAAAGGGGAAGCAAAATC	59.888	20	GATCGCCGAAGGTTTTTGTA	60.074	20
TTCCTCGTGTTCCTCCTCAC	60.238	20	CACCCCGAGATAACTTTCCA	59.926	20
TTTTATGGGGCGAAAATGTC	59.773	20	TGTTCACCAAGTTCGCAAGA	60.427	20
GACAAGATCGTGCCAACAAA	59.697	20	TGATGCTCCACTTCCTACTCC	59.298	21
TCGATTCGAATTATGAGGGC	60.001	20	GAAGACATCTGGACGACGGT	60.12	20

ATGGCAAAAGGCATCAAAAG	60.074	20	TTGTGTAATTGTGTTGTGTCAT	59.278	25
ACGCGCTCAATAAACATTCC	60.103	20	AGGTTCGGACAAACAACAGC	60.156	20
CATGGTAAGCAGATTGGTTTTAAT	59.439	26	GCTATGAGCATGTCATCAACA	57.291	21
TCAGATTTGTTATGTGTTTTGACA	57.312	24	TCCATTCCGAAAATCAAAGG	59.872	20
GCCCAGATATGGCTCGTTTA	60.06	20	GGGATCTCAACGATTCACCA	60.871	20
CAACTTGGAACCCGATTCTC	59.526	20	CAGCACTAACACACACACGC	58.952	20
ATATTCGGAAGAGCGACCCT	60.06	20	GCTCTTTCTCCCTTTCCCAC	60.19	20
TTCGATTTATCTTCAGGCCG	60.167	20	TATCCAATCGAATTCCCAGC	59.862	20
ACAGGCCGTGTTCGTATTGT	60.44	20	AACCCGCGAGTTGCTACTAA	59.904	20
ACTCATGTCACGGCACACAT	60.038	20	GGTGTAGATCTGGCGGGTAG	59.574	20
AAAAGCTCCTCCACAATTTGA	58.823	21	TCCATTTGACTTAACAAACCCC	60.089	22
ATTCGCACAAATGAACACGA	60.119	20	AGCTGAAATTGAGTTCGGGA	59.813	20
TTGTCGATCAGCGGTTACAG	59.864	20	TGAAGTGCGGGGTATTACAA	59.037	20
TCTTACCCTGCGAAAAATGC	60.209	20	TTCTACGAATGTTGACGGAAA	59.625	22
CACGTGGCATGATAATAGCG	60.118	20	TTGAAAAAGCACACCTCCAA	59.293	20
CCACTATTGATCCTGACGCC	60.483	20	AAATATTTGAGGGGTGCGTG	59.823	20
TTGTTCGTATTTGGAAGTCGTG	60.032	22	GGTACAGAGCGAAAACGAGG	59.875	20
TCTCTATCTCTCTTGGTTGGTGAA	59.411	24	AAGCATGAGTTGTGTGCTGG	59.905	20
TCCACCGCTTTAAATTGCTT	59.72	20	TCTTACCGTCGGTCAAACCT	59.592	20
GCATGTCACGTGAGGAAGAA	59.837	20	GTGGATCATGAGCGACCTTC	60.633	20
TGCATTTTGCAGTTTGCATT	60.259	20	AGTGGTTATTACCGGATCGC	58.93	20
CTTTTTCCATCAACCAACCC	59.264	20	TGATGGTGAATACGATTGGC	59.355	20
TCACGGAATTACTAAGCCCC	59.043	20	TTTTAGGCCCGAATGAAATG	59.901	20
TCTTCCGATCTCAGTTTTTCAA	58.949	22	GCTCAACCCTTCACCTCATC	59.661	20
ACAACAAGCTGGGTTTCTGC	60.299	20	CCGGGGTAATCTCAAAACCT	60.18	20
GCCTGCAAGAAAGCAATCTC	60.103	20	CACTGGTGCACGAGCATATT	59.746	20
CATACTCACTCTCACTAGCCGC	59.173	22	TAGCCCATTCGTGATTTATGG	59.803	21
GTTGGAGGAATGGAGGGAAT	60.133	20	CGTCCATTCATCAAGATCCA	59.451	20
TCTTTTCACTCGAGCCCAAC	60.375	20	TTGATGCAGCCCAATGTATG	60.488	20
TTGCATTGCAGCAGTAGAGG	60.157	20	AGCGGGATTATCAGACGTGA	60.624	20
AAAAGGTTCCATCTTTCGCA	59.685	20	GGGAGAAACAACCACCATTG	60.21	20
CTTGCCTTCTCCTTCCTCCT	59.95	20	CATGAGCCTCCAAACCCTAA	60.066	20
ATGTTCCCATTTCACCTTGC	59.797	20	TCCGAAACTTTAGCACGAGAA	60.004	21
GCTGCCTACAACAGCAACAA	60.058	20	GCAAGAACTCACGCCTTTCT	59.621	20
TTACTATGTGGTTGCGGTGC	59.614	20	TATCCACATGGCAAAAAGCA	60.073	20
ATGATCAGGCCCATATTTCG	59.745	20	TTTGGGTAGGCCTGAGTCTG	60.246	20
TTTCCTAATTTTCGCCTCCC	60.381	20	AGCTTCAAACATTGATGGCA	59.276	20
GCCAAAATCCCAACAAAAAG	59.429	20	GCTTCGCAACGAAGGAATAC	59.851	20
ACCTGCCTACGCAAATACCA	60.523	20	CTCCAACCTGCCACAAAAAT	59.971	20
TTCGTGTTGTCCTGTCGTGT	60.203	20	GGGATGTGTGGGATTGATTC	59.995	20
AGATGGCAGTTTTTCCCAGA	59.67	20	TCACGCAATCACACAGATCA	59.823	20
ACGGCCATCAATATACACCAA	60.089	21	GGTGAACGTAGGGGTGAAAA	59.83	20
TCGGTTACCCTATAGCATTCG	59.111	21	TGCTATCGCGTAGAAATCCTT	59.002	21
AAGGAAAACCAAATGGGGAC	60.032	20	TGAAAGAAAACAAGAAAGAAT	60.499	26
CTACGAGCCACGGCTACAC	59.48	19	CGAGGGAATTAGGAGGAGGT	59.531	20
TATCGCCGTTAAGCTGCTCT	60.138	20	TGAAATAAAGGGGGAAAGGG	60.116	20
AAAGATGGGAAAATGGGACC	59.996	20	AAATAAACATGGTTCGGGCA	60.188	20
AGAAACTTGACGTGTGCGTG	59.946	20	TATCTGTCCTCTGGCCTTGA	58.387	20
AATGAGGTAAATTTGAGAATGAT	58.165	25	TGCGTTTTGATGATATATAGGT	58.933	25
CAAAGGCCCACAATGGTTAT	59.685	20	TTTTGGGGGATTATTTGCAG	59.767	20
GTGTTTGGTCTCCCCTCCTT	60.349	20	CCCATACCTGATGGGATCTG	60.15	20
GTGGTTCGATCAAGGTGAGC	60.667	20	TTTGGAGGATCGACGTTACC	59.933	20
GGGCATTTGTATACCCGTTG	60.074	20	GGTTGTGAGAACCAACTCTGT	59.664	22
AATTTGCCCTCTCCCTCTTC	59.651	20	CTGCTTATCGCCACTGTCAA	60.011	20
CAAAACAGTATACAACGGGCA	58.619	21	AAATCGCACCAAAATCAACC	59.807	20
TGCTATCGGCTAACGGTTTT	59.742	20	GAGGAGGAACCCATGGAGA	59.992	19
CACAATCGATCAATAAAGCTGC	59.748	22	CATGGTTGAATGGATATGGCT	59.659	21
GGCTTAGAGGGTGTTTTGACA	59.228	21	GGGGCGTGACAAGGATACTA	59.955	20

AGCCTTACCAAAGGGGAAAA	59.939	20	CTGTCAATTTCGGGAGCTGT	60.255	20
AGGAAGAATTGGAAACTCGTGA	60.11	22	CAGATGGGAGGAGAGAACGA	60.34	20
ATGATCTACGTCCACGGGAG	59.95	20	GGCAATATCAATCTCGGTGA	58.521	20
TGGAGCTAGGGTTACCGATG	60.088	20	GGGGAAGCACAGTCTAGGGT	60.511	20
AGCAAAAGCTTTCTCGACCA	60.132	20	GGTGTTGTGTGATGTCGGAG	60.005	20
TCGACATTGTAAAGGAGATGGA	59.569	22	GTTTAGTGATGGAACGGGGA	59.79	20
CCTTTGCCCCAAACAGACTA	60.103	20	CACGTGGCGCTAATTGAGTA	59.895	20
CATGCCATGGAGTCGTTCTA	59.673	20	CAGGCTCGTCGTGTTCAAG	60.6	19
GGCAACGGAATATCACTCGT	59.962	20	TTCACCTCCATTTTCGATCC	59.871	20
CACAACGCTTTCTGCTTCTG	59.781	20	AGCAAAAATGCCACGTATCC	59.967	20
CTCGTTGGAGGCCAATAAAA	60.067	20	ACCCCACCTTCCCAAGTTAG	60.218	20
GAAATAAGAAGGTGTTATGAAGG	59.022	25	CAACTTGCAGGTGCTAACCA	59.904	20
TCGCAGAAAATCAACTTCTCA	58.637	21	ACCCTCCTTCAGCCAAAAAT	59.94	20
TACACAGTGCCTGCTCCAAC	59.905	20	AGTGTCTCCAGTCTCCACCG	60.306	20
GGAGAAAATCAGGTGATAACCCT	60.885	24	GGGCTGAAAAGCCAATTAAAC	59.963	21
CACGATTGTCATGATAGTATGGG	59.238	23	GGCATTGGACATCAACATGA	60.339	20
TGGTGTTCTTGGGGTTTTGT	60.246	20	TTTCGGCTCCTCAGACACTT	59.989	20
TTTGAGATCGGAGTGGCTCT	59.95	20	GCCTTAACCACTTTGAGGCA	60.249	20
TCTTGGGAGTGAACATACATACA	57.171	23	AGTAGAGGCGGAGTGCTTTTT	59.556	21
ACAGCAAGCATCCAGAAAGC	60.547	20	GGCGTGTTCTTGTTGGGTAT	59.859	20
GAGTTGAAATCCTGGTTCCG	59.526	20	CAAACCGGACTGGACCATTA	60.745	20
ACAGAATATGCGTGATCGCC	61.034	20	CAAACCGGACTGGACCATTA	60.745	20
ACCACGGCTGAATAAATTGC	59.967	20	GCTTTGGCTTTGGTGCATAA	61.131	20
TCCGGTCCAATTCCAATAAG	59.756	20	CCTATGGTGGTATGGTGTGG	58.569	20
TATTGTGAGAGGGGACAGGG	59.92	20	CTCTGCATGTTTGTTGGGTG	60.152	20
CCTTGCGCCCTTTAAAACTA	59.381	20	TGGCGTATGCTGAGAGAATG	59.972	20
TTTGTCCAAACAAATGAAACATTC	60.128	24	AAAATCAAAGGCCCACAATG	59.801	20
CGAATGAGTGGATTTGGGAT	59.75	20	GGGAGTTATCATTGGATCAAG	59.805	22
CAATTTTGCCCTTGAATGCT	60.074	20	GGTCGACATTAAATCTTGGCA	59.952	21
TGCGTTTACATTCAAGCAGTG	59.926	21	TCACCAAAGAACTGATATCCT	58.707	23
CATCTCCTCCCACTCCTCAC	59.638	20	TTATCAAGGGCCCTACCTCC	60.278	20
GTGTGTGTGCATGAGTGTCG	59.772	20	CCACCACCATCTCACCTTCT	59.962	20
TGATTTTTAATGCCTTTCAGCTT	59.326	23	TGCCCTTTTTAATCCACCTG	59.931	20
TTCAAAAGGTTTGGGCTTTTT	59.971	21	ATAGTTGTTAGAGGCGCGGA	59.867	20
TGCACCTCCTCCTAATTAATCC	59.463	22	AGCTGAACGAGTAATTCTTGGT	59.833	23
TTTCTCTCTTTTGGTTGGTGAA	58.856	22	AAGATGCACGTAGGGAGGTG	60.134	20
TGCAGCTGAAATCAATGAAAA	59.434	21	AGAGAAAACCCGGCTCGTAT	60.096	20
GTAGTTTTGGGGCAAATGGA	59.801	20	TCAAAACTGCATTTCTGGGTT	59.601	21
CTTGATTCATCGAACGCAAA	59.809	20	CCTTTGAAAATTTTTGGGCA	59.916	20
TCATATGCGATGTTTTGCATT	59.046	21	AGAGCAAAACCCATCAGTGG	60.111	20
CCAAAGTTTATTTAACACGGAAGA	58.716	24	CAAATTCAAATGCCTCAGCA	59.809	20
TTTCTTTCAATCGACGCTCC	60.331	20	TGAGTGACAAGACCCTGCTG	60.022	20
TTGCTAAGCTCCAGCAACG	60.287	19	TCCCAATCACACCACTCTCA	60.088	20
CGAGTCATCTAGCATCTCTTGC	59.246	22	CGTGGTTCGATCGTAATTGA	59.542	20
ATCTGTTTCTTCTGCGGCTC	59.579	20	TTTGCTAACAATGATGGGCA	60.073	20
ATTGATGGCAAGAGCAGGAC	60.226	20	GTGGGCTGTGGCTTTTGTAT	60	20
CAGTGGGGTTGGTTTGAGTT	59.861	20	CCGAGACAGCACTCACGATA	60.008	20
TCCATACACACCAAATAAAAAGA	59.707	25	TTGATCTGATGCACGAAAGG	59.799	20
TTGGGGAAATAATGTCGATCT	58.381	21	AATGGCCCCCAAGAAAATAA	60.489	20
GCATAAAGCTCATCTTGCACA	59.08	21	AGCTGCATGCCTTCTCTTTC	59.723	20
CGGTGAAGATTGGAGGAGAG	59.797	20	CCATCCCATCACTACCCATC	60.011	20
CTTTGGAAAATTCGAGAGCG	59.953	20	TGTTTTCCCCAAATTGGTTC	59.64	20
ACGGCATAAAAATGGACTGC	59.967	20	ATCCTCATCTTTCCCCAACC	60.133	20
CCTTTGGTCTCGGTTGAAAT	59.028	20	GTCCGCATTGAAAATGGAAT	59.768	20
CATGAAAGACTCTATAGACAAGA	57.458	27	GCACTACCGGATAGGCTCAT	59.178	20
AGGGTGTGTGAGAGACCGAG	60.306	20	AACACCCACCACACCTCATC	60.701	20
TTGGATGCTTCAAATGTTGTTC	59.982	22	GCCAAATTAAGGGCATGAAA	59.907	20
GTTCGAAAGCCACAAATGGT	59.978	20	TCTCCTCCCCTTTTAATTCC	57.21	20

GCTAGGGCGATTGTATTGATG	59.583	21	GCAAGCATTAGGCGTCTCTC	60.125	20
TGATGTTGAAGAATCAGCGG	59.799	20	GGTGAACCAAGCGGATAAGA	60.074	20
CGTTGGTTAATCCTGCCATC	60.331	20	CGTTAGGCTCGAGAGTGAAGA	59.766	21
TTTCGAAAACATGCAATGGA	60.051	20	TTTGGGGTTGGAATAGGTCA	60.162	20
ATCACCCCTCACAAGAACCA	60.363	20	TTCCCGAATATCCCCCTAAC	59.978	20
CAGAAGGGCAATGAATTGGT	59.933	20	TCTTCAATCCTTCTTCCCCA	59.6	20
CAATGGTGAAATTGCGACTG	60.111	20	TTCGAAAATGGAGGGATGAG	60.006	20
AGCAAATGCCAATAAGGTGG	59.96	20	TGTAAATGGCCCTCGTCTTC	60.074	20
ATTGAGTCCCAATCTCGTGG	59.927	20	CGGTAAGCGGAAAAATTCAA	60.068	20
ACACTCTGCTAGGGTTGGGA	59.721	20	CAGTCCACTTTTGAATGGCA	59.691	20
GCAAGATCCATCCTCGCTAC	59.803	20	CAGGCACATGCAAAAAGAAA	59.849	20
TCGAATTTTATTATTGATTGAGCA	57.936	24	TCTTCATCCCATTGACCCAT	60.135	20
TGGCAATTTTAAGATCGAATCC	60.274	22	TTCCGATTGCAAGAAAAACA	59.277	20
CCGCGTTTTGGAAACTTTTA	60.102	20	TTCATCATCTTCCCTTTCTGC	59.259	21
TGTCACCTTGAAAGAATTACAAA	59.959	25	ATACTGCCAAAACGGAACCA	60.365	20
GAGTGACATCTTCGAGTGTTCG	59.914	22	ATGTCTCTTCCTGGGAGGGT	59.929	20
TTAGCAGCTTATACGTGTGAAAA	57.01	23	GGTCATTTTAGCTTGATCAACA	58.763	24
TCCTTCTAATCGATTCTTCCACA	60.082	23	TTGTTTCTCGATAGCCCGTT	59.708	20
TGAAGAAGACGTGGTCGAGA	59.545	20	ATCGTTTTGAGAACCGGAGA	59.67	20
CGTTAGAGCCATCCCTTCTG	59.83	20	AAGTTGCGGGTGCATCTAGT	59.763	20
GAAGCGACACGGGTTATTTTT	60.358	21	GGTCGGCTACATGAACCAAA	60.894	20
GGGACTCGGATAAAAAGGGA	60.258	20	AGCTGGCCATTTCTTGAGAG	59.574	20
TTCTTCCATGTCGTGGTCAA	60.088	20	GCGTGGTCTTGCCAATTTAT	59.967	20
TCACACTCACTCACAAACACACA	60.297	23	CTCAAGCTCGTCACCCTTTT	59.473	20
ATGTCCAAAATGGAAGCCTG	59.933	20	AAGGAGGTGTTATGAAGGGAT	58.028	22
TCCCTAGACTCCGTAATTGGA	58.657	21	TTGATTCTGGAATATCCCGC	59.862	20
TGTCCCACATTGGAAAATGA	59.75	20	TGAAGACCTAAGCCACTCGC	60.538	20
GCAAAAGGCAAAAGCAGAAG	60.131	20	AAGTTGTGGCTGCAAATTCC	60.118	20
ACATCATGTAGTCGCGTGCT	59.349	20	TTCTTTCTCATTCTCTCGGCTC	60.096	22
TTGAACAATTGAACACCGGA	59.941	20	TCCTCATTGTTTGTGTGGAAA	59.01	21
TTGTGTTCCTGCTTGCTGTC	60.032	20	ATGCCTCAAACAACCTCACC	59.973	20
TGCGTTTTGACAATATATAGGTGT	60.083	26	GGATGAGCTCCAATGTGTCA	59.637	20
GGCGGAGAGGAGAGAGAGAT	60.058	20	GACGCTCCACATGATGACAC	60.13	20
AGGTGCCAGATTCTCATTGG	60.073	20	AAAACTGCGAAATGAGGAAGA	58.962	21
AATTATGTGCAAGCTCATCCG	60.11	21	TACAAAACCAGTGGCACCAG	59.609	20
CGGGTGACATTGCCTAATTT	59.823	20	CGATGTTTATTTGAGGCGCT	60.23	20
TCACGTGTCATTGTAACCGC	60.584	20	GAACGTCGTCATTGTACTTGG	58.146	21
AATTGATTGCTGCTGCTGTG	60.019	20	CCACGTGGCACTTCATCTAA	59.716	20
CGTCAATTCATGGCTTCTGA	59.799	20	CCAGCAGACAAAAAGCATCA	59.988	20
ACGGAGAATTGATGTTCCCA	60.317	20	TTCCATTGGGTTTTGGGTTA	60.024	20
AAAACCCAGAAAAATGCAGC	59.205	20	TGCCCCTTCTGACTCTGTCT	59.986	20
TCGCCTTTCTCTTTCTAACCTC	59.155	22	ACTGCCCAACAATGGCTTAC	60	20
AATGATGAGCCATGCAACAG	59.679	20	CCATGATTTCCTTTAATTCGAT	59.7	23
TGTATTTTCGGAATTGCTTCA	58.291	21	TGTTTTGCCCGTACGTTGTA	60.029	20
CCACGAGATGGGGACATTTA	60.713	20	AGCTGGCAGAGACCTTTTCA	60.134	20
GGTTTCTTCTGCTTGTTGGC	59.859	20	TTAGGCCCCTCCCTACATCT	59.919	20
ACTACACATCCGAACTCGCC	60.142	20	CTCACCAGGCCAGGGTAGTA	60.126	20
TTTTTACGGTTCGGTTCCAG	59.968	20	TCCCAACAAAACGAAAAAGT	57.25	20
ACAATGGAAAACACGCAACA	60.011	20	CGCTCTCTCATTGTAATCTCTC	58.83	24
CGCTGAGGGATCTGGTATGT	60.096	20	CGATGGAGAACCCTTATTGG	59.382	20
ATGCTGGATTTTTGGCATTC	59.907	20	GCCCAGCTTATTTGGTGAAA	60.074	20
AAAATTTTCGGGTTTGGACC	60.034	20	TCCGTGAGTTTACCCAAAGC	60.11	20
GTTTCACTTTGGTACCCGGA	59.83	20	AGGACTGGAGGAGAGCGAG	59.673	19
AAAGTCGGCCAAGAAGAGAA	59.052	20	TTCAAACATGGCAACAATGG	60.357	20
CTAAGCGATGCCTAAGGCTG	60.131	20	ACACCCAAAATCCTTTGCAC	59.836	20
CTCTCACTAGCCGCAGCTCT	60.058	20	TTCTTGGCAATCATGTCCCT	60.461	20
GGAAAATATCAAGTCAACACAAA	57.333	24	TTCACGCCACATCACTCAAT	60.12	20
GTGATTAGCATCACAGCCCA	59.679	20	TTTGTACCAAAAAGTATATAAA	57.58	27

CAATCAACGCTAAAACATCTGA	57.98	22	TCGTTCAAGTCGGTCACATT	59.139	20
GATATGGATGCCCCAGATTG	60.118	20	CAGATTTGCGCAGAAAATGA	59.953	20
TGATTTTGGACGTTCTGCAC	59.697	20	AACTCAAAACGACACCCTCG	60.149	20
GGTTGTGGTGAAAAAGGGTG	60.246	20	AGTCACCGACAACTCCAACC	60.009	20
TTTTCCGAAGTACGAGCTGC	60.523	20	CATCCTGCTAACCACCCAAT	59.813	20
CGGATTAGAATTCGGAACACTC	59.966	22	TCGTGAGAGATAGATATGGAG	57.233	24
TCAAATGCACAAATTCAATGG	59.41	21	GGGGTCTGACATTGTAATAAA	58.812	23
AAGTAGGGGGCTTCAATCCA	60.817	20	AGTTCACGTTCGGGTTTGAT	59.454	20
ACATTTCGATTAGGTGTGACAA	57.154	22	AGGGTGTATGTGAACCAACCA	60.141	21
AATCGTGAGCAGCAGGTTTT	59.882	20	AATTTGGCTTGTTACAGCGG	60.131	20
TTTTCTTTGTCTTCAATGCCAG	59.379	22	CCTCCATTATCCACTCTCGC	59.653	20
CACAATAAGGGTTGGTATCATTT	59.556	24	AGCAGAAAGGGGGAAAATTG	60.423	20
AGGATAAAGTACGATGATTGACC	58.954	24	TTTTCCGGTTAACAAATCGC	59.943	20
CACCACTGGCTCGAACTGTA	59.897	20	TGTCGAAATGGGAGTCACAA	60.088	20
TTTTGCTTGCAGTGTCCATC	59.847	20	TCAGAACATGGGCAAATTCA	60.049	20
GATAGGTGTGGCCCAGTTTG	60.375	20	GGGACATCTTGGTGGGAATA	59.605	20
CGTTGGACCTGAAAGAGGAC	59.697	20	GGGAACATTCGAGCCATAAC	59.391	20
CATGGGTTATCACTTGAATGAGA	59.768	24	ATTGCGATGTGGAAGCTTTT	59.713	20
TACGTTTAGATGTGCAGCCG	59.895	20	CAGATGATGTCCCAGCAAAA	59.648	20
AAATTGAATTGTGAGTCCCG	57.517	20	ATCGTCCCCTCTCTTGCAG	60.356	19
GGGTTCTGAAACCGGGATAG	60.683	20	TTGTGTGATCGAACCACGTT	60.008	20
CCTAAAAGGAACTGTGGAGGC	60.116	21	TCGTCATCAACTTTTCCCCT	59.526	20
TTTGACCTTTTACCTTGCCC	59.064	20	GGATAGGAATCTCAAGAGTAT	60.007	25
ACTCAGGGTTCTTCACGGTC	59.153	20	TCTCTCTTTCTTGGTTGGTGAA	58.955	22
GAGGAGCAATACTGCTTGTGG	59.89	21	ATTCGGACATCGAGATTTGG	59.894	20
TTCTGGGATACACAAGGCGT	60.517	20	CGAATACTCCAAATGACACCA	59.861	22
TTGGGTAGAAGGCATTGAGA	58.298	20	TTGAATATGCAATCACCAAAG	59.485	23
AACATCAATCATAGTTCAACTTTA	57.122	26	GGTGCACCACCCCTATCTTC	61.684	20
GACTCCAAGCCCTGTTGTGT	60.159	20	GAAAACAGAGGTAGTGAATTG	57.489	24
TTATGTGGCCCGAATGACTA	58.991	20	TTTAACAACGTTTCGGAATTTT	59.027	23
ATATTCGATCCGGAAGGGTC	60.117	20	TTTCACCATGATTTCGATACAC	60.237	23
TCCAGTAATTTGGGAAGGCT	58.646	20	TTTCTCCTCGTATGCGTATTCA	59.742	22
CCTTTGGATATGGTGATTTGG	59.145	21	AGGGAAAACAGGGGTAGCTG	60.488	20
TGATGAATTGACCAAAGCCA	60.049	20	ATAAGCAACGAAGGGAGTGC	59.34	20
ACCGCACAAATCATTTCCTC	59.939	20	AATCCAATCTTCGCCCTTTT	59.909	20
TTCCAAACCTCTATCCCGTG	59.926	20	ATTTTATCCGACTGGCGTTG	59.96	20
CATGGCCCTTTCTTCACATT	59.933	20	ACAAAATCACCCCCTCACAA	60.21	20
CCATAAAAAGTTAGGCAAGTCTA	59.231	26	TTTCACTTTTTGCACTCCCC	60.088	20
ACAACATTCATCGTTCCCCT	59.263	20	TCACCATAACGCACCCCTAT	60.214	20
ACCCATGTTGTGTCCGTGTA	59.726	20	CCAGGTGGAGTTACACCCAT	59.697	20
GGCTGGCTCCAGTAGTTGTT	59.357	20	ATACCTGCAAGTGTCGGGAG	60.134	20
TCTGTGTGTTGAGAGATCAGTGA	59.566	24	TGAATCACTTTGCAAGCACC	59.847	20
CAAAAACAGAGTGAGGGGGA	60.081	20	ATCAGTGAGGAGGGATGTGC	60.08	20
TGTCCTTTTGGATCCAGTCC	59.903	20	TGAATCGCAAGCACATGAAT	60.228	20
TTGCTGCCCTATTTTCTTTGA	59.84	21	TAAGCTGTCCAGGATTTGGG	60.066	20
GCATACCATTATTGGCAGCA	59.549	20	GGGACTGTGAAACAGGGAAA	59.943	20
CGCTCATTTTCTCACACCAA	59.84	20	GTTTTGAACCCTAGAGGGGG	59.799	20
TATGCAAGAAACATGGCTGC	59.839	20	TTTTCCTGCCAAACCTATCG	60.067	20
TTAAACACTTCGCGCAGACA	60.578	20	CTCTTCAGCTGCTCTCCGTT	59.891	20
AACTCACATCAGATTCCCCAA	59.396	21	TGCATGTGTGAATATCCGCT	60.104	20
GCTTGGTTCGAGACTTGAGG	59.989	20	CCAAATAAGATCCGCCGTTA	59.922	20
TCAGCGGCTTAACATGTTTCT	59.897	21	GAATCCGAATCTTTCACCCA	59.871	20
TCCAAATGACCAACCAAACA	59.792	20	TGCTTTTACCAAGGTGAGGC	60.249	20
CGGCTGGATTTCATCCCTAT	61.165	20	GGTAGTTTCAAGGTGGCTGC	59.74	20
GCCCTGTTCGTTCATGTCTT	60.119	20	TGCAGATATTGCTGCCAAAG	59.976	20
TCCAATGGATGAGGATGGTT	60.135	20	TGATGCCAACTCACCCATAA	59.924	20
GATTTTGCCCCCATATGCTA	59.757	20	GAACCGTTTAAACAACCCGA	59.839	20
GGCTTTTGAGGGATGGAGAT	60.41	20	CATCTCTTTGTCTCCCCCAC	59.505	20

TGCAGAAGTTTCGAGGGAGT	59.989	20	AAAGAAGATTCCGGCGAAGT	60.208	20
TTCCTTGCTGCTGTCCATTA	59.42	20	TTACCGTGTGTGTGCATGTG	60.071	20
CCATGTTTGTAATTATTGTAGGGA	58.388	25	AGAACACGAGGAACTTGGGA	59.697	20
TCACTAGAATGCGCCCCTAT	59.691	20	GGGGAGCGATGATAGTTGTC	59.513	20
GTGAGACCCATTCTCCCCTT	60.314	20	TTTATGGGTACATCGGGGTG	60.439	20
GATTCTGATCGACCAGTGGG	60.475	20	AAGCAGGTTTTGATGGATGG	59.933	20
TCGATTGACCCCTCATCTTC	60.011	20	ATCGTTGTCGAAATCCTTGC	60.081	20
GTGGCTGGGAATTGCTGATA	61.003	20	ATGAATGGATTCCGGTCAAA	60.133	20
CCTCCCTTAGGGTTCCTCAC	59.928	20	TGTGTATACTCCACGGCGAA	60.134	20
AAAAGGAGAGCCGGTCAAGT	60.247	20	TGGGGCCTACGAGAAATATG	59.916	20
CTCGAGCAAGGAATAGACCG	59.971	20	GGATTTCCGTTGTTATTGCC	59.277	20
TGCAACGCACTCAAGAAGTT	59.64	20	TGGTTAGCACCAAATAGCCA	59.182	20
GTTTCCTCTTGGGTGGGTTC	60.725	20	GAAAGTTGGCTCAAGCTCGT	59.621	20
CGACCCTGAGAGATTCCTTG	59.797	20	CTGAGAGCTATACCGACGGC	60	20
TCTCAACATGCTGTCTTCGG	59.984	20	GGGAGTGGGGGACTGTTATT	60.052	20
TCACCATGAAGAAACCCACA	59.935	20	TTACCGTCGGTCAGAACCTT	59.592	20
GAACTGAGGATCTTGGGTGG	59.505	20	ATTTCCTTGGCCTTCTTCGT	60.074	20
TAGAGAAGCCGGATGCAGAT	59.939	20	CCATCTGTCTTGGGGGAGTA	59.92	20
ATGGTGGGGTTTTGTACCTG	59.569	20	GAAGTGCAGTTTCCCCTTCA	60.232	20
TTCGGTTTTTACTCCCACTATG	58.188	22	AATGGAGCAAACATTACCGA	58.093	20
CGTTGCTTTTAACCACCGTC	60.534	20	CCATGTCAAGGGTTCGAAGT	59.966	20
CCAGAATTTGCTGGGTTAGG	59.564	20	AGTTCATCAGCAAAGGTGCC	60.263	20
TCAAGCTTAATTAGAAGAAAAGA	58.427	27	AATGCAGTGAATGGAGGGAG	60.073	20
GAAAGCCTACCTCGCTTCCT	59.983	20	ACTTCCCCCATTCTTCATCC	60.133	20
TTCGTCCGAAATACTCCCAC	59.933	20	CCCTTAAACCCTTGAGCCAT	60.312	20
CTCAAATCTCTGCCCTCTGC	60.096	20	GGAAGAAATTCCCCCAAGAC	59.744	20
TGATTGCTGTGGTATGCTTTG	59.744	21	ATGTGTTTGGTTTTGGCTGC	60.934	20
TCCCGTATACAAATTCCAACAA	59.231	22	TGTGGTTGAAATCTAGCCCTTT	60.001	22
CAGAATCCCCGGTATCTTGA	59.887	20	GCACTGCTTTTTGGTGATGA	59.847	20
TGTCGTTGTTGAATGTCGGT	60.008	20	TGACACAGATTTGGTGCTTG	58.246	20
GGCTCCCCATTTCTCTCTCT	59.778	20	AGAGGTTAGGGTGTTGGGCT	59.994	20
ATTTTCTGTCGAATGGTCCG	59.933	20	TTCATGCCACCTCCAATTTT	60.309	20
CAAGAAACCTATCCACCCCA	59.784	20	GTCATCATCGTCTTCCCCAC	60.335	20
TTTAATAATAATTCCCTCCTCTCG	57.159	24	TGTGTTTTGACAATATTTAGTG	58.633	27
AATCCCCGTTCCATCATAAA	59.091	20	GTTAGGGATACCGCTAGGCA	59.205	20
TTTGATATACATGGTATTTAATTTT	57.034	27	CTTCGCAATGCTTTGATTGA	59.953	20
CCCTAGCTTTGCCCTCTTTC	60.332	20	GCGAGGATTCATTCTTGGAA	60.155	20
TCGATTTGGATTCGAATTTGT	59.402	21	AAAGAGCACCTCCTGCTTGA	60.134	20
GATGGAGATGGAGGGATTGA	59.821	20	CCTCCCGAATTTCTGTGTGT	59.966	20
TGGTGACGATTATAAAATCAAAA	57.729	24	TTAGTCAATGGAGGGTGGGA	60.309	20
ACTGGACTTCGACCTGGATG	60.112	20	CGTTGGATGTTAAGGATGCC	60.331	20
GAGGCTGACGGATTTCCAC	60.616	19	CTCAGCCAACAAAACCTTCC	59.711	20
CGGACTGAGCTGAGCTAAAA	58.405	20	TTGGTTGGGTTAGGTGTTGG	60.638	20
TATCATCACCAGCTTGCACC	59.679	20	TGCTTAAAATGGGTTTTCCG	59.937	20
GGCATTAAAATCCACCATTGA	59.652	21	TCAATGACCACACAACCACA	59.376	20
CCCACGTGCACTTCTTTTGT	61.124	20	CACTAAATAAATATTTTGGCAT	57.149	27
TCGAAAGCATTTCCGAGTTC	60.331	20	AAGCCTACAGGAAAGAAAGG	59.908	23
TCGAGCTTGCTCAAAAGTCA	59.864	20	TCAAACACAATGACTTCGCC	59.697	20
GATGAACACCCGAACCACTT	59.827	20	TTTTTGGGAAATCCTTGCAC	59.916	20
GGCAACGGTATACCACTCGT	59.882	20	CCTCCCAACATATTGTGCATT	59.699	21
GACATCTTCGAGTGCTCGTT	58.028	20	CTGAAATCTCGCATCCCAAT	60.036	20
CCCTCTTTCCCTCTCCAAAA	60.54	20	TAGTCACGTGCGATTTGGTC	59.722	20
GCAGCAGAAATGAAGGGAAG	59.955	20	GTGAACACCCAAGGTGGAAC	60.261	20
GATCTCCACCATTTACGGGA	59.75	20	TTATGCGGTTTATTGCGATG	59.562	20
TGCTAATCTACGAATTTGGGA	57.416	21	TCAGTTTTTAATCGTGGCCG	60.989	20
TAAGGGCGGTATCACCTGAA	60.46	20	AACCTTTTACGGGGAAGGAA	59.808	20
TCCACACAGAGACACTGGAAC	58.712	21	GGAGTGTTGGAGGAGGAGTG	59.682	20
TGTATCACATATGGCAATCGAGA	60.358	23	CGTGGTTCGATCGTAAATGA	59.542	20

TTCTTTATTCACAATGAACTCAGA	57.6	26	AACAAGTCAAGGAGGGCAGA	59.844	20
AGAGTGTTGTGGCCGAAATC	60.119	20	TGCATTTATCCGATTTATCAAA	58.561	23
AAATCAAACCGCCATCAAAC	59.807	20	GTCGTGGATATGGGCTGACT	59.957	20
CTTCTGAAAGGCTCAGCCAC	60.134	20	TCATGTTAATTGGTGGTATCAT	59.898	25
TCGAGCATTTGCAGACAATC	59.955	20	GTGGCAGCTTCATCCATTTT	60.081	20
GTCAAGGGCTTTTGTTAATTGTG	59.926	23	ACAGGGCTTGGGACAAACTA	59.592	20
ATCACGTTGAGGATTCGGAG	60.073	20	TATCCAGTTTTACCACCGCC	59.823	20
ACGCACTCACACACACGAA	59.922	19	GGGTATGTGGACAGAGTGGG	60.238	20
CAGCTCTCTATCATCCACGC	58.572	20	ATTTGTGCGAGTCTCGTGTG	59.905	20
GGTTGGTGGCATTTGAATTT	59.668	20	TATTATCACGGTTTTCCGGG	59.655	20
CCGTTAACAAAAATGATGGTGA	59.736	22	CATGTGTCTTCCACCATGAAG	58.995	21
AGTAATTGAACCTTGGGCTAAA	57.063	22	TCTTTCTTTCCCTTGCTCCA	59.926	20
TGACCACCACCTTGTTGAAA	59.976	20	CCAATGCATTACGAGTTGGTA	59.536	22
TTGACAAACTCACATGGGTCA	59.992	21	TCCTAGCCCTCAATCTCGAA	59.91	20
ACAAACATTTGAGGAAGGCG	60.11	20	GCACTCTCCAGCTCGATTTC	60.104	20
CAAGCTTGGCGTTATGAATG	59.325	20	ACTAGCAACGGAGATGCGTA	58.555	20
AACCCCTTGTTTGCCTTTCT	59.976	20	CACCCGACGTATTCGAGTTT	59.993	20
ATGACATGGCATCGTCTCAA	60.08	20	CTTCTTGCCGATGAAGATGAG	59.963	21
AGGTGGAATTTCGGGCTATT	59.799	20	TTCATCATCAGCTGCTGTCC	59.95	20
CGTGCAGCCTCTTCTAGCTT	59.92	20	TGCCACAGTTTCATCTTCCA	60.24	20
TTTTGCCCACGAATTAGCAT	60.456	20	CGGAGTTGAGGACTTAACGG	59.728	20
ACCCATCTCCTAACACGCAT	59.434	20	GGTTTGGAGCCATTTTGTGT	59.836	20
GGTCTGTTTTCCATGGCCTA	59.933	20	TGCACAACACAATACTAATGC	59.202	23
ACACGTGTCGCAATCAGAAT	59.169	20	TTGGGGGAGAATTGTTTGAG	59.903	20
CACAACACACACGGACATCA	60.044	20	TCTTGACGACTTCGAACCTG	59.007	20
CACGAGTGAAGAAAGGGAGA	58.001	20	ATCATAATTGACGCCCTTCG	59.923	20
GAACACGACACGATACGCAC	60.192	20	AATGGACCCTTGTTGGTTTG	59.688	20
GCATCTCTCCCTTGCTCTCTT	60.11	21	ATGGAAAATGGTGATTGGGA	59.991	20
TTGAAGACATGGTTGGACAAA	59.01	21	CCGCACACCCCTATCTTTTA	59.953	20
GTGAAACGGAGGGAGTACACA	60.02	21	ATTGCTTTGACACCACCACA	60.008	20
AAGGATGCTGACCTAACCCC	60.328	20	GACGAAAATTGCCCGTAAAA	59.943	20
TGGTTATGCCTTCTTCTTCCA	59.693	21	CCCGAATTTCCCATAACTCA	59.756	20
GAATGCGTTCCCAATAGCAT	59.929	20	GAACATCGACTCACTGTATTGT	57.373	24
CTGCAAAAGCATCACCAGAA	59.988	20	CAGCTTCTGCTTCACACAGC	59.929	20
ATCAATTTTTGAGTTATGATGTTT	57.321	26	CCCTCAAAACAGATTCCCAG	59.521	20
CATGTTACACGTGGACGCTC	60.183	20	TGTCCGAAATTCTCTCACCC	60.05	20
AGGGATTTTGGGACGATTTT	59.644	20	ACTGCAACCCATCCTTTGAG	60.111	20
TTGTGTGGTTGTGATTTAGTTATTT	59.328	26	TTTTTGGGAAATCCTTGCAC	59.916	20
AAGGAGGCCAGACTAAAGGC	59.848	20	AAGTTGGAACGAGCGAAAAA	59.861	20
GGGACGACGTTTTATGGTTG	60.227	20	CTCCATGCCTCTGCTCTTTT	59.574	20
ACGTCTCTTCATGCACCAAT	58.158	20	TGGGCCCAGTAGCATGAATA	61.382	20
CAACATACAGGCACGAAAATG	59.097	21	CGTAGTTGCTACATGTTAAAGA	57.052	25
TCCACCCTATTTCTTGCTGC	60.214	20	AAAATCAAAGGCCCACAATG	59.801	20
CCTCACATATATGCCCGTCC	60.177	20	CCCCCAGCAAAATAAAAAGG	60.637	20
ACACACACTCACGGCTTCAA	60.357	20	CCCCAAGAGAGGATTTCACA	60.042	20
CCGAAATCTCAAAATCCGAG	59.64	20	ATTGCATTGCAGTTTCACCA	60.119	20
TGGTCCCCTCAACACAAGAT	60.363	20	ATGAAAATGGGCGAGAGTTT	58.647	20
CCTAGCCTTTGCCCTCTTTT	59.85	20	TGGGATTGAGCCCAAATAAG	59.894	20
TCAAACATTCATCAATATACACA	58.864	25	CCAATGACACGTTATGCTCAA	59.6	21
GAAGCACGTGACAGCTAACG	59.664	20	GTTGTTTTTGTCGCGGATTT	59.982	20
CAGAGAAAAGTGAGCTCGGG	60.126	20	CAGAAATTTCCTTGGTTGCTC	58.823	21
CAGGTGGAGTTTCATCCACA	59.52	20	CGGGATTTAGGTGTTTTGAC	57.066	20
GCCGTTTCAGATACCAGCTC	59.843	20	ATCGATAATTCGCACCCAAG	59.923	20
AATGCTGCAAAGTGTCAACG	59.911	20	TCATCGAAAATCTGATCTGGG	60.021	21
TAATTCAACCCACACCCCAT	59.91	20	GGGAGATGAGGGGAAAAGAG	60.008	20
AAACCCATCACCCACGTTTA	60.088	20	GGCAATTTGTTAATTGTTTGAG	59.456	24
TTTGCGAGCAAATGAATAAGAG	59.516	22	CTTTGAATTGCAGCTCGACA	60.134	20
ACGAGGCCAAGAATGATGAG	60.218	20	TCGTCCGAAAATCCTTTCAC	60.051	20

TTTGGGCTATTTCCCAACAG	59.931	20	CAAATGATTTCCCTTTGATGG	59.26	21
TCATTCACATCATCCCATGC	60.3	20	CACTTTCTGCACCCCAAAAT	59.971	20
AGGCTTTATGATCCATTCTCAAA	59.135	23	ATACCGCTGACGACAACCAT	60.406	20
TGTTCCTCAAGCCGAAATCT	59.813	20	ATGTAGGGAAAGATGGCACG	59.955	20
CCAAACCAATTCAAAAGGGA	59.772	20	TTCTGGTTTGCAAAACTTTCTGT	60.188	23
CCCAGATGTTGAAATGGTGA	59.343	20	ATTGCTCTCCAACCCACAAC	59.973	20
AAAATCAAAGGCCCACAATG	59.801	20	ATTTCGAAAATCAACGGACG	59.938	20
CCCTAATTCCAATTCCCCTC	59.6	20	GCTGGTGTTGGGAGAGAGAT	59.258	20
TGCGTTTTGACAATATTTAGTGTTT	59.109	25	GGGTTGACATGGCTTCGTAT	59.82	20
TCGGTTATTACCGGATCGC	60.812	19	CCCAGTCGTATCACTTTGGC	60.517	20
CCACATAAAGGATTCCCGTG	60.184	20	CACAGGAACAAGAGCGAATG	59.44	20
TCAAAAACAGAGGAGAAGGGA	58.895	21	TGTGTGGGTGTGTTGATGTG	59.878	20
GAAGGCAATCTATCCCATGC	59.491	20	ACGGATTTGTCGATCGGTTA	60.331	20
GGCCAAGTCTGGCCTATTTA	59.182	20	TGGGTCTAATAGAGCGGCAT	59.691	20
TATCAGAGCCACGGTTAGGC	60.235	20	CTTCGGCAACGAAATACCAT	59.96	20
TGAAGAAAATCGAACCAGCA	59.395	20	TGTAGGGAGTGGGATGTGTG	59.388	20
TGCTTGCATCAACTCATTAGG	58.931	21	CCCACTTCTTGTCCTTCCTG	59.691	20
ACCAATGGTGGTATGGTGTG	58.984	20	GCCGGGTCTAGTCAATGAAA	60.074	20
TCGTATGATCCAACTTCGCA	60.22	20	TCACGTAGTGGGAAAAAGGG	59.964	20
GGAGATGTCTCACGGTTGGT	59.969	20	CTTATTGCCTCCATCGTCGT	60.096	20
TGGCAGAACAAAACTCATGC	59.847	20	CTTGATTCATGGCACACCAC	59.967	20
AGATGGGTGGCAATCTTGAG	60.073	20	AATTGGGGTGCAGTTCAAAG	59.971	20
CCATGCCACCTTCTATTGGT	59.813	20	ACACTTAGGGGGTTATTAGTGC	59.26	24
GGTGGTATGGTGTGGAGGAC	60.096	20	ATGCACACGTAACATCCACG	60.459	20
GCGAAAATTCCACCATAGTCA	59.952	21	AACAAATATGGCCTCCCAAA	59.273	20
CAACAAATTAGCTGAATGGCAG	59.779	22	ATGACAACCCACCAGAAAGC	59.973	20
GAGGGAGATCGACGTGAGAG	59.945	20	AGACCGAGCGCAATGAATTA	60.742	20
TGGGGCCTACGAGAAATATG	59.916	20	AGCGGTTTAGTGGGTTGTGT	59.52	20
GTCACCTCACACACCACTCG	60.207	20	CATTAAATGCCGGTCAAAGC	60.456	20
AACAATGCCCGAAGATTGAA	60.448	20	TAAGATCGAACGATCCAGCC	60.177	20
AGAAACGAAAGCACGACGAT	59.882	20	TGACCACCACGGAATTTGTA	59.816	20
TCTTATAGCATCAACCGCCA	59.281	20	AAAAGAGAAAGAGGGCCGAT	59.307	20
TGCAATCCAGTCGCATTTAG	59.833	20	AAAACACGAAACTTGATTGTGA	58.71	23
GGGGTTATCATGGGATCAAGT	59.895	21	CGGAATGAGCCACAGAATTT	60.074	20
ACTGCCCCTCTATTCCGATT	59.925	20	TGTTTGGTTGCTTGCTTGTT	59.366	20
ACACACACATGGATGGAGAGA	58.955	21	GGGGTCTTCTTTTGGGACTC	59.912	20
GAATCGTAACATGTAACACACAAA	59.332	26	TGTTCCCGACAAGAAAAAGAA	59.71	21
TCTGCCATGTGCTGAATTGT	60.272	20	CCAATTTGAATGGTTATTACCTG	59.191	24
ACCACTTCTCCCTCGATGTG	60.112	20	TGGATGACGAGGTCGAGATT	60.622	20
AAGCTTGGCCATTCAACAAT	59.574	20	TCGGAAATAGGTGGTTTTCG	59.931	20
TTGTAAAACATGTATGGGATTGAT	59.898	25	AGGAGCAATACTGCTTGTGGA	59.89	21
CCACTTTCCTTTCCCACTCA	60.081	20	CAACTTGGGCTAAGGATTTTG	58.751	21
TTAGATCCGAGATGGTTGGG	59.887	20	ACTGCCTTTCCAACACGTTC	60.156	20
AATAAGTTCACTTTATGCGAAAGA	57.806	25	TCCAATGGTAAAACAACGCTC	59.989	21
CACTCTTCCACTTGCCCATT	60.111	20	AACATGGCCGGAGAATACAG	59.955	20
CCCTTCCCCACTTCATTTTT	60.159	20	TCGAGACTTCGGTTGGTTTC	60.232	20
CGTGTCTGGTGTTTCAATGG	60.001	20	AATGGTGCTGATGGCAGAAT	60.492	20
AAGCCCACAAAGTTGCATTC	60.118	20	GAGATGTGTGTGTGCGTGTG	59.772	20
TGACGGGATTTAGGTGTTTTG	59.847	21	AATCATTCCCAGCCACACAT	60.203	20
ATGCTCTCACCAACTCGCTT	60.02	20	AACCGTCAGATTTCAAACCG	59.971	20
TTGCTTCATTGGTGGTAACG	59.585	20	ATTCACTCACCACCGTCCAT	60.246	20
AACCATGTCGAGGGTTTCAG	59.966	20	GAGGGAGAGAGAGCAGCAGA	59.969	20
AACGGTTGAAACGTGGGTAT	59.218	20	CGGATGAACACCCCTACTTG	60.366	20
CTGAAATGAAATCATGCCCC	60.274	20	TCAGCCTACTTTCGGCCTTA	59.975	20
CTGCTATTGAAACAACCCCG	60.493	20	AACGATGCTGCCATGATTTC	61.014	20
ATTCACAATGGCAAGGAACC	59.797	20	GGCACCAAAGAGATAGGCAG	59.836	20
GCTCGAGTTTTCTTCGCAAC	60.14	20	TTAACCGCCAAACTCAAACC	59.975	20
GGAATCAGCCGTTCTCACTT	59.288	20	TTAGATCATACACGTGGCCG	59.566	20

TGCTCCTTCTCACTCTTCCA	58.669	20	CAAGTTGAAGTTATGCCCCC	59.429	20
GCGGTTATCACCGGATCG	62.397	18	TCATGGAAACATGACGTGCT	60.12	20
AGTTGGGAATTGGGATAGGG	60.011	20	GCCAAGACTTGCTGGGTAAA	60.249	20
CAAACTGTGGGGTAAAATGACA	59.763	22	TATTTTGGGCCTGAATGGAC	59.762	20
TCTTCACTCTCACTAGCCGC	58.343	20	GTCCACGGTGGTGCTAGAGT	60.182	20
TTTTCTCCGCATCACATCAC	59.654	20	CAGTTTTCGTTGCACCCTTT	60.147	20
GCACTTAGGAGAGAGATTGTTGG	59.424	23	TGGTGAGGGCAACCTTTATC	59.933	20
GCTCGAGGCATGTAAGAAGC	60.125	20	AGTGGGGGACTTATCTGTTAGA	58.224	23
CAACATGTGCAGGTTGAGGT	59.597	20	TCCTATCATCGGTTGGTCGT	60.34	20
TCCGGTCCAATTCCAATAAG	59.756	20	GGTGGTATGGTGTAGAGGACC	58.242	21
CTACCCTTTCCGAACATCCC	60.683	20	CATTGGTATTGACAGCGTGC	60.142	20
GGACCGAAAGTAGCGAACAA	60.249	20	GCACTCTCACGAGCTCACAC	59.771	20
GCAGGCCTACTCTCCTGGAT	60.756	20	TCATGCCTAAATGTTTTGATGC	59.971	22
ATTCATTCTCCAACCATCGG	59.75	20	GAGAGCTTGCCGAGAGAAAG	59.454	20
CCTTGTGGTATAGCGGTTGG	60.378	20	TGTGCTTCTCCAAGGCTTTT	59.993	20
CCATCATTTCCCTCACCTCA	60.86	20	TGGAGGTTCAAAACTGACTGG	60.133	21
TTTTCCATCAATCCACTCCA	58.897	20	TTCAATTCTCTGCGTTGTGC	59.995	20
ATCAGAACATGCACACAGGC	59.714	20	AAATTACGGCCACAACAAGC	60.003	20
GGGTGAGTAACGGTGCAAGT	60.035	20	CTCCACTACCGTCGACAACA	59.745	20
TGAATTTGGGACTCAACGAA	59.097	20	TGTCTGTGAGAATGGCCAAG	59.831	20
GTGTGGAAAAGGGAGTGCAT	59.973	20	GTCCAAGTCCAAGTCCGAAG	59.697	20
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TCAAAGATGGAGGTTGGAGG	60.042	20	AAGGGATGATTGCACCTGAA	60.461	20
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CGAATCGGAGTGGATTTGAT	59.894	20	GTCAGAATGGATTGAGTGCG	59.245	20
ACCCCCAATTCCCATATGTT	60.131	20	TCCCTAACAAATCACACCGA	58.973	20
CGGATTTAGCGGTTATTACCTGA	61.448	23	TGTCCAAACAAATAAAAACATT	60.139	24
CTCTCGAGCCTAACTGTGGC	60.156	20	GCATGAGAAAATCCTCCCAAT	60.28	21
TTCCAATTTTGGGAAATACTATGA	58.836	24	TGGGTGGTGGAAAAGAAGTT	59.425	20
GGAGAGTTGTAGAGTCAAGTTGTA	57.416	26	ACGTCTTGGATCTCCGTTGT	59.579	20
AAAGAGCATCAAACATCATTTCC	59.498	23	TATTGGTTTCGGATCGTGCT	60.469	20
TCCCGTATACAAATTCCAACAA	59.231	22	TGTGGTTGAAATCTAGCCCTTT	60.001	22
GAACCACCAAAGCAATACCA	58.476	20	CGCATCACTCTTTTTAGCCA	59.062	20
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TCACTTAGCTCTTGATTTTCATCAC	59.864	26	GATTCGGAAGGTCGACAACT	59.141	20
CCTTAGAGCTCGGTTGCAGT	59.639	20	TCTGGATCTCACAGCTCACAC	58.983	21
CGACCGAATACTCACCCCTA	59.948	20	TTTTATCCCCAAAATGCCCT	60.489	20
CAAGGAAGGAACCTCCATTTT	59.447	21	AGCCATGATAAATCCACCACA	60.207	21
TCGATATGGCTCGGTAGGTC	60.059	20	AAAGCAATAATATTTGTGCCAT	59.783	24
ATCTAACGGCTGGCATTTGT	59.597	20	CGCGGACACATCATGTAAAC	59.995	20
ACATTCTAGGGGGAGGGCTA	59.919	20	TCACACATAATTGAGTTATCAT	59.685	26
AATTCACCAACCCTCATCCA	60.173	20	AGGTGAGGGAGACAATGTGG	59.962	20
TGCCTCAAATCAATAGCCCT	59.668	20	ACCGTGTCGGATACACATGA	59.837	20
AATTGCCACCTGTATCGGAG	59.955	20	AGAGAGCATTCCCACAAACA	58.287	20
TCGTGTGCTTGCTCGTTATC	60.019	20	GCAAGGACGAATTCCAAGAG	59.813	20
TGTGAATGAGGTGTGGGTGT	59.846	20	TCCCCTATCGGTATTTTCCC	59.978	20
ATTCCCAACTGATTGGCTTG	59.933	20	CTAATCTGGGCAGCTTCTGG	59.971	20
TGAGCAAGGGACAAATGTGA	60.24	20	ATTCTCCGCCACCTTTTCTT	60.074	20
GATTGAAACCATGCCCATTT	59.628	20	ACTTCACCCGTACGTTGCAC	61.016	20
CCAAATTTAAGGGTTATCACCTG	58.849	23	GGCTAATTGTTGGCCTTTGA	60.074	20
CCATGATCGAGTTCGGATGT	60.893	20	ATTAGGGGAGAGAGGGCTCA	60.169	20
TATGAAGCATAACCATGCCG	59.543	20	CCATCCGACGGACTTACCTA	59.948	20
TTTGGGAAACAACGGAAGAC	59.948	20	GTGCACATTTCCCTTTCACC	60.362	20
TTGAGCTGTTATGCGTTTTGA	59.5	21	CGTGCCCTATTCACATTTTT	57.635	20
TAGAGTTGGCATCGGGAAAA	60.576	20	GACCAACGTGGCCTAACCTA	59.993	20
GGCCAAGGGAAAGCTTTTAT	59.572	20	GACATTGCAGATTTTGATGAGC	59.719	22

TCGGCTTGAAAACGAGAAAT	59.823	20	TAAAAAGGAAACAGCCGTCG	60.236	20
GCAGGAAAATGAAAAGTGGG	59.546	20	TTGATCACACACGCACAAAA	59.721	20
TCTTCTCCTTGTCGTGCCTT	59.989	20	TCCAACTCATCTTTCGGACC	60.05	20
GTAAGCAACTCCGGTGGGT	59.981	19	CCCTAATTTATGAAAGAGTGG	58.576	23
AGAACCTGGTTGATTGGGTG	59.82	20	TTGTGTGGGTCGATTCTTGA	60.088	20
AATTTTGACGGCTCCAAGTG	60.11	20	AACACCAACCACGAACAACA	59.897	20
AGCATCTACTCTGGCTCTCATTG	60.054	23	TCCATCCTCCATAATCCTGC	59.854	20
TGGACCGGACGTGAACTATT	60.375	20	AGTCATCTCCAAATGCCTGC	60.226	20
AACATGTTGATCTAAATAACGCA	57.516	24	ATCGCCCAAAACATTACCC	59.636	19
CGTATTGCAGTGAAATTTTAGCA	59.352	23	GCATGCGACAACATGAATCT	59.685	20
CAGACATGTGTACCACCCCA	60.285	20	AGTGTGTTTAGCAGGGACCG	60.171	20
AAAACCGACAAAACCTCCCT	59.842	20	GTGTGGATGTGCGTGTTTTC	60.016	20
CACCTGATCGCGACCCTAT	61.041	19	GGCTAGACCATTGTAAGGGG	58.528	20
TTCTACACGCGCATGTCATT	60.288	20	TCCACGGATGTAAATTGTTCC	59.677	21
TTACCACAATTTCCCTTGTTTT	57.605	22	AGAAAGAATGTGGACGCCAT	59.556	20
AGTCTGTGGCGTTCGATTCT	59.874	20	ACATTTTTCCACACTCAGCG	58.775	20
TTTGCCCTTATTTAGCACGG	60.089	20	ATTTAGCATGGGAAGGGGAG	60.278	20
GACAATTGAAAGAGCACTCGC	60.015	21	TGTGACTCATACCATGGAGCA	60.128	21
GACAGTAATGGGGAGGGTGA	59.779	20	ACCATAGAACCACACGGCTC	59.997	20
ACCTGCCCAGATCTCTCTGA	59.945	20	ACCATAGAACCACACGGCTC	59.997	20
ATTTGCGGGGTTGTTAAAGA	59.451	20	TCGTCCGAAAGAAACCTTTG	60.22	20
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TCGAATTTCTAGCGTGATGG	58.869	20	GACAAGAGGATGAAGGCCAG	59.803	20
GCTTAATGCGTAGCTGGGAT	59.347	20	AGTGATGGGCAGCTCTGTTC	60.418	20
CAAACGTGAGTGGGAGATGT	58.566	20	CCGCTCCTCCTTTTTCTTTT	59.829	20
ATGGCGTTAGAATGCGAAAC	60.103	20	GGTGGCTTCATCGTGTGTTA	59.572	20
GTTTTCGTGGCCTCACATTC	60.504	20	GGCAGGCACAGAAGAGAAGA	60.678	20
GTGATAGCCAAAATTTACAACGT	59.842	24	TCATTGACCAAGTCTTGACGA	59.278	21
TGTGCTTATCCACCGACAAA	60.111	20	TCGAATAATGCAACCTACTCA	58.818	23
AAAACTACGATCTGCCACCG	60.132	20	CAAAGTTGATGCCCCAAATC	60.309	20
ATTCAAGTTCAATTGCGGCT	59.713	20	GCTTACTGATGCAGAAGCCC	59.985	20
GGTAGAAATTCGCCGCAGTA	60.23	20	ACCCCTCACATGCTCTTCAC	60.12	20
TAATTTTTGTTTGCTGCCGA	59.328	20	TTCGTTGACCCCATATGTCA	59.774	20
GATTACGTCGATCCAACGGT	59.82	20	CAGCACCAGAATTGCTCCTA	59.024	20
GATGGATGAAAAGGCTCACG	60.603	20	GATTGCCGACTGAACCTCAT	60.081	20
CACCAAATTTTATCATTTTTAATTC	57.837	27	CCCAATCATCCAACCACAAT	60.439	20
TTGGAGCTTCAAAACTTAGGCT	59.561	22	CCCAACACTCCATTCTTCGT	59.966	20
CACTTCACCATTCCACCATT	58.258	20	AACCAGAACGGCTTGAAAAA	59.724	20
GATTTCGGAGGTTTTGGACA	59.91	20	CGATCGGTCAATCGAATTTT	59.901	20
GCGACAATTCTGCGTGTTAT	58.801	20	GAAGCCTCAAATCACAACCC	59.532	20
GAGCATAATCTTGGGGCTCA	60.177	20	TGTCGTAGATCACACGGTGG	60.593	20
GCGGTTATCACCGGATCG	62.397	18	TCATGGAAACATGACGTGCT	60.12	20
TCGGAGCATGATTTAAGTGG	58.721	20	AACTCGATAACGGATGCTCG	60.235	20
TTTCCCCTTTGCCCTCTATT	59.903	20	CCTTCAGAGGCATGGTTTGT	60.111	20
ATCAGCGACGAGTCCAAGAC	60.418	20	ATCTACATCCACGGGAGGG	59.746	19
CCAACAAAAGGTGTGTGCAT	59.465	20	GGGCCAACAATATCATGAGG	60.155	20
GGCGACAGAAAAAGAACGAG	59.993	20	CGATCCCTCTCTCTCACGTC	59.945	20
GGGTTGAAAATGGTGTCAGC	60.362	20	CTGAATGGATCGGAAGCAAT	60.036	20
TAATTCCATTCAAGCCCCAC	59.762	20	AAATCCTTTCCCCAATAAACG	59.216	21
CGAGGCTTAATGGGGACATA	59.916	20	TGACACCGTTACGCAGACTC	59.905	20
CCCTTTATTTTCACCCACGA	59.795	20	TCCCCTAATTCACGTGTTGA	58.973	20
TTGGAATTGCCAAAGACGAT	60.448	20	GCCGATTCCTCCTTTCTCTC	60.293	20
ACCGCTCGAATCCGTACTCT	61.173	20	TCGTCGATGATCGTATAGCAA	59.295	21
GTGCGTGTGTATGCTGAGGT	59.783	20	AACACGCGTTTTTAGGGTTT	58.676	20
TCTTGGTTGGTGGAAGAACA	59.109	20	CCCCACCAAAAGTCCAACTA	59.824	20
AGGATTGTGGAGGATGGTGT	59.232	20	GAAATGGGTTCTCTCTCCCC	59.874	20
CAATTTTCAATCACAAGTTATAGT	58.222	26	ACGTGTGAGACTTCGTGTCG	59.94	20
AATTATTTCGGGCTAACGGG	60.161	20	CTGCTGGACCTCCACAACTT	60.298	20

GATGGAACCAACCTTGCACT	59.973	20	TGCCCCACCCAAGTATTTT	60.177	19
TCCCTTGCTTTCTAACCCCT	60.068	20	ATGGGAAGGGTATTTCTGGA	58.307	20
TTCCTTTGTCATTCCAACCA	58.947	20	CACGCCTCTCTCTTCCTCAC	60.135	20
ATAAGTTTGTGCCTCCCGTG	59.993	20	CCTTTCCCTTCTCCCTTTTG	60.04	20
ATGGTGAATATGTGGGCTGG	60.603	20	CACACAAGCAACTTCCCTCA	59.873	20
TCCTAAGCTTTTCCTGCTGC	59.73	20	GGCTTTTGCTTGCATTTGTT	60.251	20
GCCTTTCATGTTTGATGGCT	60.081	20	CAACGAGCCTTCCTTTTGTC	59.853	20
TCGAAGTGTTGATTGAATTGC	58.761	21	TGAAGAAGGAAGCTAAAATGC	60.03	23
TCGAATCAATCTCACCCAATC	59.886	21	GCATTTGTTAGAGGTTTTGACC	60.389	23
ACTATTGAAACAACCCCGGA	59.288	20	GGAGATCGACCAATTTGGAA	59.871	20
GCAGTTACCTATCCCCACGA	59.955	20	ATCGAGGAATGATAGAGCCG	59.249	20
ATGGAGAGTGGAGGTTGACG	60.112	20	CATCTCTCCTTCTCTTTCTCGG	59.593	22
GAAATGCACGAAACACGAGA	59.847	20	AAAAATGAAAACGTTACTTCT	59.949	24
TCTTCGGTCCGACCTTGTAT	59.55	20	ATTGTGGACTCTTGGGGTTG	59.82	20
GCTGGAACCCATGAATTTGT	59.797	20	CCCTTTTCTCCTTCTCGCTT	59.955	20
TCTCTCACCTCACCTCTCCA	58.446	20	GGTCTCGATGGTGTGATCG	60.063	19
GAAGAACGATTACAAAGTTTATC	59.101	26	CATATATGGGGAGCGTACCG	60.188	20
GAACACAGAACATAATTCCGCA	60.003	22	GCCGAAAATACCCCCAACTA	61.029	20
GGGGTGGACTATTTCTTGCT	58.121	20	TGCTTGCCCAGACTTTCAAT	60.776	20
CCAGGGCATATACCCATTTG	60.031	20	ATTTCCTGGCCATTTTTGTG	59.801	20
GTACCTGGCTGTAGGATGCC	59.579	20	AAGTCCACACAGGTGACTCGT	59.664	21
CTCGGGATGCAGTGATTAAA	58.721	20	GATTGGCGAGGGGAGAGT	60.16	18
TTGTGATGGTGATTGGATGG	60.177	20	TCAGCTCCAGCTCCTTGATT	60.096	20
ACAAACTAATCAAGTTCCGCA	57.439	21	TTCGGAAGCGTACATCAAGA	59.42	20
ACGGTGGGCCGAGTATATTA	59.32	20	CTCACGCATTCCCAGAAAAT	60.074	20
AGTGAAGGTGACGAAATGGG	59.966	20	GATTCTCCCTACTCCACCCC	59.755	20
TGCTCTAGGTAAACCCACGG	60.125	20	CAGCAAGGAAAGCCTTTGAC	59.993	20
ATTCCTGCAAACCATCTTGG	59.933	20	AGAGCAAACTCCGATGGCTA	59.978	20
CTTCTTGGCGTGGTGTTGTA	59.758	20	AAGACACCTAGTTGCCCCCT	59.994	20
ATGAGCTTCGTGTCTGCCTT	60.02	20	AATTAGCCGAAATCCCCATC	60.116	20
TTTCAAATGGAATTCATATAGCCA	59.724	24	CTGTAGGTGCAGGGTTCGAT	60.134	20
CCCCATCAGATCATCTCCTC	59.415	20	GAAGCCTCATCTCGGGTTC	59.753	19
ACGAGACTGTCGGTCAACAA	59.31	20	ACGCACACTCACTTCACGTC	59.948	20
ATTGCAATGACTTGGCATGA	60.08	20	GGAACCGTGCAGCACTATTTA	60.145	21
GGATCGAAAAGAGAGGGAGG	60.147	20	TGCCAGTGAGGACAAAACAC	59.726	20
CGTTTCAAATCGGACAAACC	60.344	20	CGGTTATTAGTTATCACCCGAA	59.322	23
TTCATCAATTTTCAGGCCAA	59.087	20	GCGTTTTAACTCGTCGTGGT	60.176	20
TTATAGCACCCTCCACCTGC	60.096	20	GAGCTGAAGCACTTTGACCC	59.997	20
TGGTGAGAGAAAATGGAGGG	60.042	20	TGGGAAGACAATTGGTGTGA	59.935	20
ATCCGCCGAAAAGACAAATA	59.547	20	GAACCTGAAATGCAAGGAGC	59.82	20
CTCCAACTCCATCACCATCAT	59.794	21	GAACTAGGCGAGAACGATGC	59.985	20
TTGCAAAGTCAGACGTCATTG	59.896	21	ATGTTGGTAGCTGTTTGGGG	59.853	20
CCTCAGTTAGGATTCACTGATCAT	60.155	27	GAACGTAAAAGGAAATGCATG	59.124	22
ATAACCCCACCAACCCAACT	60.34	20	CCTTGTTCTCCTGCCTTGAC	59.844	20
TCATTTGATCACAAACCCCC	60.56	20	TCGGTAATTCACACGCACAT	59.995	20
TGTGCAGAAAACAGAGCTGG	60.175	20	GTTGGCCCTTGATTGTTGTT	59.836	20
CAGCTGACTGACAGAATGGG	59.415	20	AACTAAAGGGGAAGCTCTGCT	58.683	21
ATCCAAGCATGATACCCCAA	60.155	20	CTGGGTACGGCTAGAAGGAA	59.331	20
CGGATTCAAGCTGTGAGAAAC	59.867	21	AGGGTCGTTCATGGATTACA	57.864	20
GGATGTTGAGATCAGAACCACA	59.973	22	GATTTGGACAGACCACCACC	60.223	20
TTGGGAACTGGATACAAGGC	59.933	20	ACTCCACCCGTGGTAGACAG	60.026	20
TGAGAAGGAAATTAATGTGTTTTA	60.157	27	GAGGCCTAAGCCAGATAGCC	60.327	20
TGTCATGTAATAGCCGTGCAA	60.148	21	CCGAATTCTATTCCGTCTGC	59.668	20
CAGCACTCTGCATTTCCCTT	60.397	20	GCCTTTTTGCTTTGCTCATC	59.967	20
CTTGAAGGATGAAGGTTGGG	59.521	20	TGTAACTTGATTGCTAAGAAAT	58.849	25
ACTGCGAGTTGTTTCATGCC	61.248	20	GCATATCCAGCACGCTAACA	59.862	20
GCTCAAAAGCACATCTGCAA	60.142	20	GGTTCATGTCTGTGTGCCAG	60.162	20
AATGGCATTTTCCCACGTTA	60.188	20	TTTGCATGGGTCAAAGTGAG	59.691	20

CATTTGGTGAGGAGGGAGAA	60.042	20	TCAAGTCCACATTTTGCAGC	59.847	20
CATGTTTTTGCGCAATTTCT	58.819	20	AGAGTGGTATCAGAGCGGGA	59.827	20
TTCTCAGCATATGGGAAGGG	60.029	20	ACTTACACGTGTCGCCATCA	60.183	20
GAGAGTGGAGAGAGAGAGGGAA	59.175	22	TTGGGATATGAAAATGACACC	57.261	21
CCCTTTATTTGGTTGATCTAATGG	59.973	24	AAAATGCCCTTGTATGCTGC	60.103	20
TGTGCGAGTCGGTAATTCTG	59.864	20	CCCATCTGAAACACACAGGA	59.52	20
GCAAAAGGAACACGTGTGAA	59.74	20	CCCCTCACCAATGTCTCACT	59.962	20
AGAATTGGTATGCAAACGTGG	59.875	21	AAGAATTGATCATGCGCGTT	60.615	20
TTTAATCGCAGTCGTTTTCG	58.958	20	TCTAATCGGTCAAGGATGGC	60.036	20
ACGTGGCATGATAATAGCGG	60.876	20	ATTCCCACAACAAAATGCAA	58.869	20
CCTCACCCATTCACACACAC	59.846	20	CAACAAGCTGTCAACCCAAA	59.734	20
GCCTACATCCACTGGGTTTG	60.375	20	CAGCTGAACCATCAAGAGTCA	59.022	21
TCCAATGGATGAGGATGGTT	60.135	20	ATGGAAACAAGGGAAAGTCAA	58.54	21
ACAAGGAGGTAGCATCTGGC	59.313	20	TTAAGAGGGAGGGAAAAGGC	59.661	20
TAAGAAATGCATGCACCTGA	57.86	20	CGACGTGTAATCACCCTCAA	59.566	20
CTGCTCGTTAATGCGAGTGA	60.157	20	ACGAGTCGGAGACAACCAAC	60.159	20
CAAAAATCTAACGGCCCAGA	60.067	20	CCATAACCGTGTAAAAATGCA	59.769	22
ATTGTGTGACGGGAAAAACC	59.694	20	GATGTGAATGCACCTGAATAC	60.395	22
CGCTCTATCTTCTTTCTCTTCAGG	60.159	24	GGCCTCTTCTTCCACAAAAA	59.288	20
AAATAGCAAATGTTTAGCATGCA	59.621	24	GTGATTCACGCTAAAGCACAA	58.981	21
CCTGGTTTTGGTCCAACTGT	59.861	20	TTCGTCGACTACTCATGCAA	57.997	20
CATTTTCAATGACCCGAACA	59.371	20	CAAATCCCACCATTTAGCAC	57.944	20
AACCCGTGACCTTTTGGTCT	60.776	20	AAAGACCCGCAACGTACAAC	60.037	20
CTCTTTGCTGCCTGATCCTC	60.096	20	TCAACAGAAACGCACACACA	59.912	20
AGAGGACATTTGGACCTGAAAA	59.976	22	ACGGTGGTGCAAGAGTGATT	60.577	20
AAAATTGCAGTGCCATCACC	60.905	20	GGGGATCCCTCGTATCTTTC	59.728	20
GTCGCAATTCAAGCGACATA	59.839	20	GCATCATTTTGGCCTTTGAT	59.907	20
TGAGAAATGCAAAAAGCATGA	59.434	21	TTTCGACTTTCAGTATTGCGA	58.57	21
GAGATATACCGGAAGGGGGA	60.11	20	ATTCGAACACCACCGACTTC	59.973	20
CACTACTAGGGTTTGGGAGGG	59.866	21	CACATATTTCAACGAGTGCCA	59.6	21
TGTCACCCAAGTCTCATGCT	59.261	20	CTTGCATGCATTGCTTAAGTCT	59.563	22
CCCTCGAATGCTAAGCAAAA	60.335	20	CATGGGGAGAGGAGTTAGCA	60.21	20
ACCGATTGTGAGCATGAAAA	59.127	20	CCAATATGGCGAACCACTCT	59.955	20
GGCGACGAAATTAGAGAGGA	59.41	20	TTGATGGGGTGAAAATTCTTG	59.787	21
TGCCCCATCTCCATCTATTC	59.854	20	CTTTGTTTGGGAGTCGAAGC	59.853	20
TCCTCGGAATACACCTTCGT	59.55	20	AAGCATTGATGTCTGAATTTGA	58.755	23
GTCATCTTGGGCAGTGGAAT	59.934	20	CAACAGTTTGGCATCAGAGC	59.445	20
CAATCTAACGAAATCTGCGG	58.387	20	TGTTGCCAGAAAAAATTGTCG	59.706	20
GTTGTGGTTGAGTGAGTGCG	60.357	20	CGTGTATGCTGCATGTTTGA	59.307	20
ACTATTATGGCCGACCGTTG	59.845	20	CCTATGATGGTATGGTGTGGA	59.195	22
GGATATCCGAAACATCCGATT	59.998	21	GGGGTGTTCAAAAAATATCCG	59.135	20
CTGCACCATCTTTCCCGTAT	59.955	20	GAATGAGCAGACGCGTTTTT	60.395	20
AAACCCTTCTGCCCCTTCTA	60.068	20	ACATTTGGCCATTATGGAGC	59.791	20
AAGATGGAACGACCCTGTGA	60.51	20	CGATAAATCATGCTGATATCGT	60.247	25
AACCACCACCATTGAAAGGA	60.21	20	ATGGGGCCTATTTTAGCGTT	59.829	20
TCCAACACATCCCTACAACTTTT	59.791	23	AATCCCTCCCCAAGTGTTTT	59.668	20
TGGCTGATGTTGTTGTTGGT	60.008	20	TTACATTGGTGCGTGCACTT	60.18	20
CCAAAAATATGGCCGTGAAC	60.188	20	CGTTTTGACAATATTTAGTGTTT	59.39	27
GTTAGGAAACGAAAGGGGGA	60.291	20	TCTCATATGACCACAACCCG	59.369	20
TGGCTGAGGATGAATGAACA	60.201	20	CTCAATAATGCTGCTGCCTG	59.59	20
TGCATGCATTTATTTGACAGC	59.722	21	AGGCTCACCCAAATATGGAA	59.387	20
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TTAAGGTGGTGTTTGCATGG	59.439	20	TCCATTCCGAAAATCAAAGG	59.872	20
GGGCGAATAAGAATGCGTAA	60.061	20	CCCATCTCCACGACGTTATC	60.34	20
TAAAAACAGGGGCAAAGGTG	59.968	20	ACTCACTTACACACGCACGC	59.977	20
AACTCGAATTGCAACGAAAA	58.413	20	GATCCATATTGGGTCAAACG	57.735	20
GTGCTGAATGGAGTTGCTGA	59.992	20	TACCAAAGAGCAGGGAGGAA	59.807	20
CCCAAAACATGCAAACACAG	60.004	20	GATCAGTATGGCAGTTGGGG	60.34	20

GCGTTTTGACGATATATAGTGTTT	60.194	26	CTGATCTGGGTTGGGAATTG	60.309	20
TATGCGGAGAAAACTGCACA	60.401	20	ATATGTGCTGGAGCCTTGCT	59.866	20
GAAGCACATTGCAGCAAAAA	59.999	20	AGTCGCTCATCACTGTGTCG	60.055	20
TTGTGCTGAAAATCTCCTCAGA	59.993	22	ACACGCAAGTGTACGTGGTC	59.673	20
AGCAAGTCAATTGGGGAATG	59.933	20	CATGCAAGTTTGCTCCTACTG	58.592	21
AAGAAAGAGGGAAGTGGGGA	60.045	20	TTTTTCGAGGTCCATTTTCG	60.046	20
CGGTTATCACCGGATCGC	62.397	18	AAAGTATTGGTCGATCGGTTTT	60.12	23
TTGCACTCTGTGGAGCAATC	59.992	20	AGAGGGTGGTTTTCCCAAGT	59.834	20
GATTTGATTCCTTTTGTCCCC	59.636	21	GTACCATTTGTCGCGGATTT	59.829	20
TGCTTGTGATCTCATGCTCA	59.061	20	ACTCAAGTTTATTTGCCGGG	59.087	20
AGCAATTGATTGAAATGCCC	59.907	20	CGGATTTATTGGTTATTACCTG	57.222	23
AGAGGCGGCCTTTTTATTCT	59.355	20	GGGAAGTGTTTATCAGGCCA	59.933	20
TCCTCTTTCAGGTCCAAGTGT	58.78	21	GGTAGTTGATGAAAGCCGGA	60.074	20
GATCAAGCTTCAGACCGGAG	59.95	20	TCACACTTTACACACACTGAAA	59.163	25
GTGGGCTATGGCTCAAGTGT	60.142	20	TCAGAGCCCACGGTTAGTCT	59.867	20
GCGGCTAGACTCAACCTCAG	60.156	20	GGGTTGTGTGCCCTATCATT	59.676	20
CAAGAAACCATGGAGAATGGA	59.918	21	TTTCTTTGTGGGTTTGGGAC	59.807	20
TCCTCTATCCATGAATCTTTCACA	59.966	24	TCGCTCAACCAAGTAAGTCG	59.072	20
TCTCTCTCTCTTTTTGGTTGGTG	59.908	23	TTGGGAGGAGAGATTGTTGG	60.042	20
TTTCCCAAATTATGCTCACTCA	59.586	22	TCACCTGATGCCCTCTCTTC	60.349	20
GTGATCTCGCCGCTTTAGAC	59.985	20	TGCTAACACCACGCCACTAC	59.788	20
CACTCTCTCGAGCCTAACCG	60.149	20	AGCAGTTATTGTGATGTGGGT	59.92	22
GGTGCATAGAAATTGCTGCC	60.615	20	GTTGCCTCATCTTGGTTGCT	60.263	20
AGCTGCTGGACGAAGAAAAA	60.132	20	TTGTGAACTTGTGGTGGTGG	60.454	20
ATTCACTTCGGCAAAATTGG	59.938	20	CTTTGACGATTTTCACAGAATA	57.899	24
GACGTGTAAACCATCACCCC	60.096	20	TGTGGAGAGGATTTTGGGAC	59.903	20
AATCCCTTTCTCCTCTCCCA	60.008	20	TCCCCAATTTACCAAACCCT	60.403	20
TTTCAAAATTTGGCACTTAGCA	59.769	22	CAAGAGGGCGATCTGGTATC	59.653	20
TCTTCCTCGCAATCACTTTC	58.019	20	ATTTTTGGATGAGGCAGTGG	59.933	20
TGCTGGCGACATTATCAAGA	60.366	20	TTTTCTGACCAACACCACCA	59.976	20
AGAGGGTTATCATGGGATCAA	58.32	21	AAGGAGGAAGTGAGGGGAGA	60.186	20
TCATATGCGTTCGTCATTCC	59.504	20	TGACAATATTTAGTGTTTTGAC	57.78	26
CTCTTCCCTCCCTCATTTCC	60.008	20	CCTTTCTCTTGGCCTCCTCT	59.95	20
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TGTCATGCAAACAAACATGG	58.966	20	ATGCAACTCCCAAACGAACT	59.598	20
TGATCGGCCTTGTATCACAC	59.527	20	AACAGCAGCAAACATGCAAC	59.918	20
CCACCCGATCATTTGAATTT	59.622	20	TCACCACATTTAAGGGTTATCA	57.051	22
GATTTGGACACCTAACCCCA	59.647	20	TTTGGGGTGTTTGGAGTTGT	60.246	20
CCTCCGTTAAAGACTGTTCATCA	60.519	23	GGTGGGCTTGGTGTACTAACA	60.172	22
TCCCAACTTTTTCTTCAAAATCA	59.971	23	TGTAATAGGCCCACACCACC	60.636	20
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CGACACATTCAGACATTGGG	59.96	20	TGTGAGGCCCATCATACTTG	59.522	20
CCGAGCTGAAAATCCACAAT	60.074	20	ACCGATTCTGCCTCACTCAT	59.685	20
GCACGCAAATAATGGTTTCTT	59.137	21	GTACGAGGAGAGACCGCAAG	60.012	20
AGGATAAATGTGGCGAATGC	59.929	20	TGTTTTGACAATATCACGACCC	59.73	22
ACAGTGCTGTATTGCAACGG	59.788	20	GCAGATGCCACAAAAGGATT	60.081	20
TGAAGGGGATTGGACACTCT	59.505	20	GGCCGTGAGTCCATTGTAGT	59.997	20
TGTATGCAAACAAGGGGAGA	59.123	20	AAACAGCTGGCATCTACGGT	59.763	20
TGCGGATCTGTGAAAAATGT	59.127	20	ACTACATCAACCGCCAGCAT	60.547	20
TGAAGTTAGGAAATAAGGAGGTG	60.026	24	CTGCTACACTCGACAGTCCG	59.641	20
GTTGAGTAGGGCAGAAACGG	59.734	20	GGAGGGATCGGATAGAAAGG	59.859	20
CTCTGGATATTGCTCGTCGG	60.755	20	ACCAATACTGGTCGGGCATA	60.214	20
GATAAGTGCCAGGCTGGATG	60.624	20	AACAACGTTATCTGCGACAAG	59.813	22
GAATAAAACGGCGCCTACAA	60.095	20	GAGTGGCCCACAGTCTCATT	60.12	20
TTTATTTTGGCGTTTCGTGC	60.969	20	GAATTTCTTGGCCTACACCG	59.569	20
CCACCGAGGAACATACAAGG	60.366	20	TATGCACTCTGCAACCAACC	59.722	20
TATAAGCCAACCATCTCCCG	59.916	20	TTTAGGTGCTCCAAGGGATG	60.066	20
TGGTCATTTCTGTTTATTTCGATT	58.967	24	CGATCCATCCCGTTAGTACG	60.344	20

ACTGTCCTTGAGCTCGCAGT	60.205	20	TGGTGTCTGCAAAAGCATTC	59.847	20
ACCAGACCCACACGTTTCTC	60.009	20	GAACAAGAGGAGGGGTCCAT	60.314	20
ACTTTGCCACCTCATATGCC	59.962	20	GGAGATGCTTCTAACGCAGG	59.978	20
ACCCGGTCTGATGAGTTGAG	60.112	20	GGCGCACTGAATTGTTGTTA	59.735	20
TCATCTACAGGTCAATGGTGACA	60.425	23	AAGGGTCACGAATCCTTCCT	59.935	20
TGGGTTATCACCGGATCG	60.282	18	AAAATGCCCTTGTATGCTGC	60.103	20
GAAAAATCAAAGGCCCACAA	59.916	20	GGTAGGATTTGAACCTGCGA	60.074	20
ATGGCATTCCCCATACACAC	60.47	20	GGAAGAAATTGACTTCTGCTG	60.381	22
TTAAATGCACACCCCTTTCA	59.013	20	CCGTCGATTTTCAGGTTTTG	60.472	20
AAACCAGACCATGAACACCC	59.679	20	CGGAGAGGACTTACCGGATT	60.455	20
TATTCTTGATGGAACGGGGA	60.266	20	TTCATTCAAGCTACCCACTCTT	59.317	23
TGGCCATGTTGGTAGATTCA	59.924	20	CGTTGGCCATGTTGGTAGAT	60.776	20
TTGCCTACATCATCCCACAA	59.924	20	TTCACCACTCAATCTGCGAG	59.984	20
TGGTTGCACCATAACACACC	60.287	20	CGAAACGTAAATCAGCAGTGA	59.941	22
GGTGGTATGGTGTGGAGGAC	60.096	20	ATGTCCACTTGTGTCACGGA	60.005	20
CACCCCCAGATGAGCTAAAG	59.688	20	CTTCGAACGATAGCTCCCAC	59.836	20
CGCTCACCGAGATAGGTTCT	59.454	20	TCATCATTTCGATCCTGTGG	59.451	20
CTCACCGCCTTAATATGCGT	60.117	20	ACCCTCGAAATGGGTTTTTC	60.166	20
TTCTAATCAAATCAAGCGACCA	59.72	22	GGCAATTTGTCTTTCAATCCA	59.93	21
CACCACCACATTACTGCCAC	59.88	20	AGCATCTCCAATGCCAGGTA	60.624	20
CGTGCGACGACTTAACTGAG	59.658	20	GATCGGTTCCGTCAGACAAT	59.934	20
CCAATCCTTGGACATTTTGG	60.162	20	CAGCACTTTTCATGTTGTTGC	59.381	21
GTTGCCACGAACTCACCTTT	60.156	20	GATATGATTTTGCGCGGAGT	60.067	20
AAGAAGCCTGTGTTAGGGCA	59.875	20	CAGCAACGATTGGAGCATTA	59.833	20
TTTCATCTGGTTCCCTTTGG	59.903	20	TTTTGTCGATGATATGGTTGTG	59.261	23
CTCTGGATAGCCCTGAATCG	59.79	20	TGTAACAAATAAATTAACGTA	57.577	27
AAATGTCAGGCAAATCAGGC	60.081	20	GCGTGTTCTAGGTGTTCTTGG	59.788	21
TTACATTTGATGGAACGGGG	60.555	20	CTCATTGTAATCTCTCCCAAAG	57.927	24
TGTGATGTTGGAGTTGGGAG	59.52	20	CATGCATGATGTGATGTCAGT	59.999	22
TGATGGTTTATGCTCGTAAGG	57.795	21	CCATTTACTAAGAACGACATG	60.404	24
TGTTGCACTGTGGTGTTTCA	59.751	20	TTTTCGGATCGAAATTAGGTT	57.759	21
TCCACTTGAAACTATCAGTCCA	57.331	22	TTTTTCTTTTGCACGACTGC	59.087	20
CGGCACGAATCCAGTTTTT	61.016	19	CGGAAGGAATGAGATGCTGT	60.218	20
ACCCTATTCCACCCCTTCAT	59.513	20	GCACAACCATGGTGAGAAAA	59.547	20
TCTTATAGCATCAACCGCCA	59.281	20	CACACGAAGGGTATTTTCGG	60.357	20
CCCATCATCTCAATCCAACTAT	57.875	22	CCATTGGCTCGTTTATTTTAGA	58.331	22
AAATGAGTGGCTGGATTTCG	60.074	20	CAGATCGGGTCTTGAGGGTA	60.065	20
GGAGAGAGGAAGGGAGATGG	60.149	20	AGTATGCTTCTCCGAGTCCG	59.454	20
CCGTGAATTCATGCCTGTC	60.064	19	TGCATACAAAGGTAAGGAGGC	59.238	21
TCATCCCCAAAATACCCTCA	60.126	20	ATGGGAGAAAGACACGTGGA	60.51	20
AATTTCTCTGGCCGACACTG	60.255	20	TGGCAACATAGTTTATGCATCC	59.859	22
TTGCCCTCAAATGCTATCAA	59.257	20	ATTGTGAACCGGTGGTTCTT	59.308	20
ATCGATTCAACTCATGGGGA	60.281	20	GCATGATCAGGGTAAAATCCA	59.776	21
GAAGAAGGTGATGTCATGGGA	59.918	21	CACCTTACACCTCACACCCC	60.275	20
TGCGTGCATGTATATGCTGA	59.85	20	TTTTCCTTCATTCCCATTATGTC	60.076	24
CCATAACCGTCGCATAACTCA	60.891	21	AACGGCCAAATCTAACGAAA	59.586	20
AGGAGGAGAGAGAGTGTTGGG	59.856	21	ATTTCAAAAAGTGGGGTCCA	59.264	20
GAAAAAGAAAAAGGGGTGGG	59.787	20	GAAAGAAGAAGAGAGATAGA	58.05	27
CCGATGATGACGAACCTTCT	60.073	20	TGAAGAGAGTCCCATCGTCC	60.199	20
GGGGTGACAACTATCAACCAA	59.703	21	CACAAACACAAAAACGCCTG	60.187	20
CGGCCATTCTCTTTTCCTTT	60.553	20	GTCCAAACTTGACGCGCTAT	60.278	20
AAAGGTGAACTTGGGGCTTT	59.976	20	TTGGGCCTAAATGAGGTGTC	59.933	20
AAGCTCCACCATCTCTTCCA	59.803	20	TCTCCTTGTTTCCGTGGACT	59.697	20
TTTTTACAAACCTGCCACCC	59.839	20	GATTTGATTCTTCGCGTTGG	60.585	20
595	595	595	595	595	595
ACTTACCCAATCTTGGTGAACA	58.486	22	GGATGGACCTTCCCAAACTT	60.169	20
ATTTCTCTCAGTCGGTGCGT	59.874	20	CTTTTCCGTTCCCCTTCATT	60.291	20
CGGAGGGAATACAATGCTTTT	60.318	21	TCCCAGTACGCAGACTTTTC	57.951	20

TTGGTTTGGTAGCCCTTTTG	59.968	20	TTGCACAGCACTGTCCTACC	59.905	20
GCATAGGAATATTAGCGGTGG	58.62	21	CGGCTTCTCCCTATCAAATG	59.662	20
TGGGCACTTTGGCTACTTTT	59.747	20	AAAAACCCCGACTCAAACTT	57.697	20
CTGCGCAGATCTAATGGTCC	60.765	20	GTGGACACCTTGTCAAAGCA	59.726	20
GACCTTTTTACTCCCAGCCC	59.94	20	TGACAATATTTAGTGTTTTGAC	57.78	26
AGCAATTTGATTCCGTGCTA	58.388	20	TAAATTTGAACTTTGCCCCG	59.937	20
TCCGCATCATTTGATTGACT	59.079	20	GTTGCCCACAAGTTCGAGTT	60.156	20
CAAGTTCTCCACAGCAAGCA	60.175	20	TGCAAAATGGGGATTTGATT	60.132	20
AAGAACAATTACAATGTTTATCCA	58.084	27	CACTTGGACCAGAAAAGGGA	60.081	20
ATTCGTTCAAAAACGGCAAG	60.11	20	CAGACGTTGCATGTGCTTCT	60.056	20
TGCACACCTTATTTTTCCTTCA	59.625	22	GGGTGGCAGAGTTTGATGAT	59.934	20
GCAAGTGGGAGGATGAGAGA	60.349	20	GGATCCGAACCAGAAAACCT	60.306	20
TGCATCCTTCCAACAAGTAGC	60.264	21	GAACCAAGGGATTGAGTGGA	59.903	20
GCTTCGATTCTCAATGTTCCA	60.207	21	GTTTGTTGAAGCAACTCGCA	60.035	20
CTTCGATTCTCAGTGTTCCAGA	59.473	22	GCTGATTCTGAAGGCATGGT	60.226	20
CGAGAAACTTTCAAGGACGC	59.993	20	CCAGAACCGTGAAATTCGAT	59.933	20
ACGATGAACTAGGGGCTGAA	59.694	20	CCAACCATAATTGTTTCGGG	60.046	20
CGTCCCAAGTTTGTTTGCTT	60.147	20	CGTCATAAACAGCCGGAAAT	59.96	20
AAAGCGCAGAAATCCAAAAA	59.832	20	CCCATAACCATGACAAACAAT	59.975	22
AAGGGTTATCACCTGATTTTCTC	57.73	23	GATATTCAGTCTGCTGGCCG	60.765	20
TTCAATACTTCCAGCCACCA	59.123	20	GTGGGAAAAGTGGTTTTTGC	59.452	20
TTGAGTCGTTTGGAATTTGTTG	60.011	22	AAAATCACTAGCATGCACGG	58.799	20
CCCCGGGTGCCTATATTAGT	60.055	20	TTCATAGTCGGCTCAATCCC	60.036	20
GAGGGGATGTTGGAGTGTGT	59.817	20	CCTTGCTAGATGGCCAAAAA	60.202	20
GCCCATTTGAGCCAATCTAA	60.038	20	TCCACCTCATATCATTCCCAA	60.14	21
GGAGCACCTCATAAATCCCA	59.894	20	ATCCTTGTCCTCCTGTCCCT	59.929	20
GCGGTCATGTGATGATTTTG	59.931	20	CCATTGCATGCGTCAGTATC	60.104	20
CATGCAGGGCTGAGTACAAC	59.318	20	TGCAGAGATGGTGATGGTGT	60.121	20
AAAATTTTCCTCACTGCACG	57.878	20	TCCAAACCGCTGTAAACTCC	60.11	20
TTTTGTGCTTCTTGCTGGTG	60.027	20	ATGAGCTTTGTATGCCCCAC	59.962	20
CAGTTATCACCGGATCGC	57.543	18	AACAAACGCCATCAACATCA	59.972	20
GGTTGTTCACAACTCCCCAC	60.261	20	AATGATTGAAGCTTCCCCCT	59.903	20
TGGCCCATGTACACTGCTTA	60.134	20	TGGATGCCTTTGATCTGTGA	60.201	20
GACCTCGACGACAGGAAAAG	59.844	20	CGAGTTGCTTCTATCGTCACC	59.89	21
AAACTTCATGGGGGAAAACA	59.264	20	TTGGCATGTAATGCGAGTTT	59.186	20
CCCATGATTCCATGATCTCC	60.096	20	AACAAGACGGACAAGTTGGG	60.005	20
CCAAGAGACGTTTTTGTTGAAA	59.286	22	TTTGGAAGCAATTGCATGAT	59.115	20
GCCGGCCCTCTATCAATTA	60.009	19	CACGTCAGCTTCATCTCCAA	59.984	20
GAAGCACATGCAAGGATTGA	59.805	20	ATGCGCTGTGTTCTTCATTG	59.871	20
TCTCTCTCGTTCTTCCTCTCTC	57.062	22	AGCACCGACTGAAAATGAGG	60.255	20
GGATCGTACCTTTTGCTTGC	59.713	20	CTGTGCTGCTTCAATTCGTT	59.076	20
AAAAGCCTGTTGGCAGGTAA	59.747	20	AACCCATCCTCTCATCGAAA	59.483	20
CCCAAAAATCTAACGGCCTA	59.075	20	CTTGCATACATGGCATCGTC	60.104	20
GTTATTCGGTTCCGCCATTA	59.795	20	AGCGATTTCATGGAGATTGG	60.036	20
CACATCATTCAAGGGGCATT	60.723	20	GCACACAAATAATGGTTTCTTC	59.771	23
GCATATCGCTCGATCAAAAA	58.867	20	GCTGTATTTGCACAGTGCCT	58.955	20
GGTTTCTGAATTTGATCCGC	59.51	20	TTTTAAATGGATCGGCCTCTT	59.922	21
GAAGAGGTGGATGCATGGTT	59.934	20	AAACGGGTGAGCAAGACAAC	60.156	20
GTTATCACCGGATCGCAAC	58.941	19	CATTTCGAACGGTCCAGTTT	59.971	20
AGTGGTGGTAAGCAACGGAC	60.035	20	CATGTTTTTGGATTTTGGGG	60.024	20
CCGTTGCACAAGTCACAGAG	60.5	20	TCGAACCACTTTCAAGCCTC	60.375	20
TATGATAGGCCACCGGTTTG	60.712	20	GGCTTGGTTGTTGTAGATTCTG	60.528	23
CCCATCGAAAAATTAATGCAA	59.791	21	TTGGGAAGATCTCTCCATTCTG	60.569	22
ATGTGAGAGACCCAGGTTCG	60.112	20	GGGTTATCACCTGAATGCAA	58.423	20
TTCAAATACGGTAGACTTCCCA	58.628	22	CGAATTAATCCGTCCAATGAA	59.781	21
TGATTCACACGAGAGTGCAG	58.509	20	TGAATCACTTTGCAAGCACC	59.847	20
GGGGTTATCACTGGATCACG	60.195	20	ATGCAACCGAAAATTAGGGA	59.411	20
TTCCCTTCATTTTCGTTTTATTTT	59.348	24	TTTCTCATGCATATTTGTACAC	59.962	26

ATTACCCCACCGAAAGGAAG	60.18	20	TTTGTTATGCGTTTTGACGA	57.846	20
CATTACCCACACACACACTTCA	59.385	22	AAATTTCACCACGTGCAACC	60.796	20
GAAGTTAGCACGTCAAGGGA	57.951	20	GCTTCCTCTGAATGCCAAAG	59.955	20
GTGGACGCTCCAGATTGTTT	60.119	20	TCACGTTAAAGGGCGGTATC	59.96	20
GGGCCCATTATTTCATCTCA	59.722	20	AGGCGTCGGTCACAATAAAG	60.132	20
TCATGTATTTTTCCTATGGACCG	60.082	23	TAGCCATGATCTCCCGATTC	59.998	20
ATCCGATGACTGGATGCTCT	59.642	20	GAGGGCTATGCTGATTTGTTCT	59.752	22
TTTTCTTGATAAGCTCGAAGCA	59.275	22	GTGCGTGCCATTTGTCTTTA	59.735	20
TCATCATCACACGCTGCTTT	60.423	20	GACCAGAGGAATTGTAGCCG	59.694	20
CAGCAGAGAATGCAAGCAAA	60.28	20	TCGGGGTATCAGAAATCGAG	60.029	20
CCGTTCTTCATGCTCACGTA	59.864	20	CCATATAACGATGCCATCCC	60.001	20
GCTCAAGGTCACACAAGCAA	60.032	20	GCAGAGGATAGACGGTTGGA	60.218	20
TTTCTCTTGGTGGAAAACTCTT	57.152	22	GGATAACCCCCACCAAAACT	59.919	20
TGTAGATTGTTGTGAGGCGG	59.716	20	CCATCCCCCTCTCTTTCTCT	59.63	20
TGGAGTTGAGATAATTTGCTGG	59.225	22	TTTCGCTTCCAGTTTTGTCC	60.227	20
TGCGTTTTGACAATATATAGGTGT	60.083	26	CAACAACAACAACGTCGTCC	60.049	20
GTGCACAAGCAGGGGAAA	60.818	18	ACCGACAATTCATCTTTTTCTC	59.994	23
CTACGTTCCTCAGGCTGCTC	60.156	20	GGCCGGATTGCTGATATAGA	60.023	20
GGTTAAGCAAAGGTGCAAGG	59.747	20	CAAGCCTAACACCACAAGCA	59.904	20
TCTCTCGTTAACGTCCCATTT	58.707	21	GAGCATGTCCGCAATTCTTT	60.221	20
CATAAACTAAGGTGGAGATTGTT	58.21	27	TTCTTGCTTCCTGGTTTCTGA	59.978	21
CTTGTTATGTTTCCATGAGCAGA	59.28	23	TACATTCATTGGGGTGTGGA	59.623	20
GGATCTTATAGCATCAACCGC	58.686	21	TGGCAGATTTAATATTTACGTT	57.88	24
CCGTTTTTACACCCCCTACA	59.719	20	GATTGTTGGGTGGCTTTCAC	60.362	20
TGCGAGTCGCTGATTTCATA	60.51	20	GACCTGACACAACCCTCCAT	59.817	20
GGAATAAAACCGTTTCACCG	59.315	20	CATGTTACACGTGGACGCTC	60.183	20
TCTCACACTTTGCACACTGAA	58.023	21	GGATCATGCTGGAAGCAGTT	60.226	20
TGGCCACTTAGGCAAATAAAA	59.611	21	TGATACAAGTGTTGAAGCCAA	58.346	22
TGAATACGCGAGAACCACTG	59.864	20	GGCATGTTGACACCCCTACT	59.851	20
TTGAGCTTCGATCTCACGAA	59.673	20	CGGTGATAACTAGGAACAAAT	58.941	23
AAATCTTGTGGATGTTAGTGGTTA	58.577	26	CCCGGTATGCTGACGATAAT	59.807	20
ATCTGAAGAGCTCCACGCTT	59.191	20	ATGGTTGCTTGATGGAGAGG	60.073	20
TCGTTCGTCCTCTTCCTGTT	59.844	20	TTTCAGCAATTCGAAGGTCC	60.192	20
TCCACGGTCTTTACGAATGG	60.883	20	TGGGTCCAAGAAAACCAAAG	59.942	20
AAGAGCAGTAGCTATCGCCG	59.775	20	ACACGGAGGTGATGCCTATC	59.957	20
AGTTATGATGGGAAGATGGGG	60.025	21	TGCGTTTTGACGATATATAGTG	60.194	26
GACGATTTGCAAGCCTATGG	60.606	20	ATGAGTTCGTCAAACCACCC	59.827	20
GGGGATACACACCTACCGTC	59.141	20	TGTAATCGAGGGAATCGGAG	60.029	20
TCCAAAATGGAAATGGGAAA	60.103	20	AAGGCGATGAATTCTGATGC	60.185	20
ACTCCCCAAAAATCCAAACC	60.032	20	CCCTTTTGTCATTTCCGTTG	60.336	20
CATGAGCAGGCTGTTTTTGA	59.988	20	TTCATGGATGGGGACTTGAT	60.135	20
AGTTATGATGGCAGGATGGG	59.773	20	TGACTGCAACTCGTCAACTCA	60.645	21
CCAGACCTGGACCTACCAAA	59.959	20	GCGAAATGAATGTACCGGAT	59.791	20
CGACAATCATCTAGTCCTCTAGC	59.934	24	TCGACCTGGTGGATTGTTCT	60.51	20
GGCATGCATGTATCCGTATG	59.799	20	ACTCCAGATTTTTCGCCAAC	59.174	20
ACGACTGTCGATCCACACAA	60.162	20	TCTCCCAACACTTCCCTCTG	60.229	20
GGTGTCCCTCCATCCAAAGT	61.152	20	TGAAGCAAGAAAAGGGGCT	59.94	19
AGCTTCTCTTGCTCTCTCATTG	58.109	22	CAACATGAGACGCAAACACC	60.16	20
GAGCCTTGAATCGCATCATT	60.185	20	CGCGTTACGAATCCAAGTTT	60.131	20
TGAGAAATAAGAAACAATCTGGG	60.667	24	AACCGAAAAATTAATCATCAC	58.037	23
TGGTTGTGTGAACCAACTCTG	59.626	21	TAGGCAATGGAATACCTCCG	59.916	20
TCCATGACTCTCAATGCCTTC	60.211	21	CATGAGATTGGTGGTTGCAG	60.112	20
CTCCCTCTCCTCTCGCACTA	59.697	20	CGTGTATGTGTGTGAGTGTATA	59.332	26
TGGATCAAACGTCGTCTCAC	59.682	20	AAAGTAGCGATGTCGGCAAT	59.736	20
TCTCCGAATTTCAAGAGGGA	59.744	20	AAAATCGAGAATTTTCCGGG	60.252	20
TTTCGTCCATTGTAAGCAGTTC	59.271	22	TCAAGAAAGTTGTGGGGTTG	58.594	20
GGCTCTCAGCATATGGGCTA	60.339	20	GCAACATCTAATGGTTGTGGG	60.242	21
GCATATGTGCGTTTTATTCTTTC	57.929	23	GGATATGCACGGGAACAAAC	60.199	20

CATGGCACAGAAATCTTAAATGA	59.133	23	GTTCAAACATCGCATCCTCA	59.654	20
CGGTTGTGCTCTTATGATGG	59.148	20	GCAAGACCAAATCACTCTTTC	60.117	22
AAAAGCAATTAATGCGTTCACA	59.666	22	TGATTTTTCATGTTTCGGAGC	60.067	21
CATTGCTACTGAATATTGTTCTTG	59.566	27	GCAAAGATGACACGGAGGTT	60.119	20
TCCGTGAAAGGAGCCTAAGA	59.948	20	CGCAAGCATGTTAATTTTATTC	59.213	23
TGGGGCTGCTTTACTGTTTT	59.747	20	GAATGCATTTCCGGTGACTT	59.939	20
TCCCATTTGTGTTTTCTTCG	58.597	20	AGTGAGAGAGAGGGCTGCTG	59.883	20
TAGAGCCCTTCTCCTCTCCC	59.912	20	TCTTCATCGTTGTAACCCTCG	60.118	21
ACAATTTTGTACCCGCCAAG	59.861	20	TGCAAAACGGATGAAAAACA	60.088	20
AAGAGGAAAATCCATCGGCT	60.039	20	TGGAAAAGCCATGCAAGTAA	59.301	20
TGCTCAAAGTCATCATCCCA	60.201	20	CAACACTTCACAGCTTCTCCC	59.899	21
TTGTTGAATTGGTCCTGCAA	60.088	20	AAAATGGATGGGGGTTAAGG	59.882	20
CCAATAAAAATGGCACCCTG	60.181	20	AACAAAGGGGCAATATGCTG	59.96	20
CACACACTTCCATCACCCAA	60.416	20	AAGGAGGTGTTATGAAGGGAT	58.028	22
TGCATCACTACCTCCTTGTTG	58.787	21	GGTTCAACGTCAACCAGTGC	61.566	20
TTGGTTGGATTGGATTTTGG	60.535	20	AAAAAGAGACAAAAGGCAGC	59.144	21
CCAAATCGGACTAATGCTGAA	60.081	21	ATTGGGATTGGTCGTTTCAA	60.17	20
ACTCGATAACGGATGCTCGT	59.723	20	TGGCTTCTGTACGATCCCAT	60.483	20
ATCCCAGCCACACATTTCTT	59.41	20	CCAATGCTGCCCTTAGTGAT	60.096	20
CACGAGTCCAGGCTACATCA	59.855	20	CAATTCCTTCCAACACCGAA	60.863	20
TTCTTTCCCAAACCAACACC	59.807	20	CGTGTGTGTAACGTGTGTGTG	59.591	21
GGTGTTGGTGAGGCTGTTCT	60.159	20	AAGAAAATAACCACGTGCCCT	59.885	21
GCGTGACAACAACAATTTCG	60.157	20	TCGGGAGTCTGTATTGAGCC	60.218	20
GCACACGACCGTGTATGAAC	60.04	20	ATCGGAGTTGATTTGATGCC	59.9	20
CTATCCAACCACACGCACAC	60.032	20	TGCTTTTTATAACTCGCCCG	60.218	20
GAGGATTCGACATTGGGAGA	60.011	20	CAAGGTTGGCTCGACTTTGT	60.291	20
TACACAGCCCGTGTTCATTC	59.572	20	CTTTCCATGGCTATGCTTCTC	58.941	21
TTCCTCAGATTTCTGCACACT	57.528	21	CATGGGTTCTTTCCTCACAAA	59.956	21
CTGCTTTGTGTTGCGTGTTT	59.951	20	GGTAGCAGCTGATATTCCCG	59.691	20
ATCTTTTCACGCGGTTTCAT	59.574	20	TGGATGTTGGTTTTGAGCTG	59.691	20
TGAAAGATGGGTGTGTTCTTG	58.609	21	TGCCTAAAGAACGTTACACGG	60.172	21
CCCTACCCATTTACCCGTTT	59.939	20	GAGGAGAGACTCGAGATGCA	59.694	21
GGCATGAGATTCTGTTGGGT	59.934	20	AACGAGGTAGCAAGTTGGACA	59.788	21
TGGGCCCCACACTAATTTT	60.177	19	TGAGCGAGAAATTTTGTCCA	59.395	20
TTGCCTTGAAAATGGGAAAA	60.407	20	GGCCGGATCTCACTAAATCA	60.036	20
CTCAAGATCGGATGCGAAA	59.892	19	AGTTATTATCATCTACAGGGGT	57.754	27
GGAGAGAGCGAGAGGAGAGA	58.95	20	GCGTTTTGATGATATATAGGTG	58.907	26
CTTCATTTTCGCGTTGGTTT	60.11	20	ATCGAAGTGACGATGGAAGC	60.226	20
GTGAAGCGCTGATCTTGTGA	60.144	20	GGCATGTAAATCAGCCATCC	60.304	20
AACGAGAGTGGTTGAGGCAG	60.444	20	AAGGTGACAACCGATCAAAA	58.048	20
CGGGTAATGTCGAGAGTGGT	59.989	20	AGTAGGAACCTTGATCCCCC	59.256	20
AAACCAAAGACGATGTTGCC	59.978	20	CCGTGTACCGTGTATTGCTG	60.05	20
TCCCAATCGTTTCAAAATTCA	60.288	21	TGGCTGAAAGAAATAGCAGGA	59.967	21
TAGACCTGGCATCTTGTGGG	61.055	20	TGTTCTTCACGGTTCAATGC	59.697	20
TTGAAATGTAACACAAAAGGAGA	57.925	24	AGGAGAGAGAGGGAGGGAGA	59.489	20
TGATTTGTCATTGTTGGGGTT	60.081	21	CGACTCAGATGCTTCACAGC	59.733	20
AACGAGAGAACTTTCGACGC	59.621	20	GAGGATCGAGAGAGACGTGA	59.142	21
AAGAGCTTCTGCGTCTTTCG	59.898	20	TCGGAGGAATACGGAGTGTT	59.55	20
CATGCAAGGGTTTCGCTAGT	60.27	20	CACTTCCCACACGTTCCATA	59.415	20
ATTAACGATTTCCCTTCGGG	60.143	20	GGCCTCATGAACTCTTGAATG	59.685	21
CATGCTCCTATTTTAATACACCCC	59.997	24	GTTTGGTATGGTGCCGTTTC	60.235	20
AATCGAGCTTACACCCCAAA	59.569	20	CACACTTCCACACGAACACA	59.15	20
AGAAGACGACGAGAGGGTGA	59.986	20	CCAACTGAGTCCACTACCCG	60.557	20
TTGTCGTCGGATCAATGAGA	60.201	20	GGTTATCACCGGATCGCT	58.462	18
CACCAAATTTCATCATTTTTAATT	58.035	25	TCCACACCATCTCAATCCAA	59.893	20
TCGGTTTTTCTTGGGAGAGA	59.784	20	AACTCTATCTCTCTCACACAAT	57.487	27
CATAACATGATTTTGCCCCC	60.016	20	GGAAATAAGGAGGTGTTATGA	59.323	24
ACTTGCAAAATGATCCCCAA	60.309	20	AGCTCATGGATGTTTGACCC	59.934	20

GGCAAACACAGGATCGATTT	59.939	20	CAACATTGCAAGCTGTGGAT	59.722	20
CCAAGGACTGAGGCTTGTTC	59.844	20	TTCCTAAGTCGTGTTGCGTG	59.904	20
TCCCCTCGGAAAATCCTAGT	59.897	20	GTAGGAGCCCACAGTCCTTG	59.721	20
TTTCCCTTCCAATTTTGTCG	59.91	20	TTTTTCTGCACATCCCAACA	60.088	20
GTTCAAATCTAACGGCCCAG	59.569	20	AGATATGCGAGATGGATGCC	60.028	20
TCTAAGGGCCGAGATTTGTT	58.787	20	TTCTCAGCATATGGGAAGGG	60.029	20
CACTGTTGCTCCGACTAGCA	60.199	20	TTTTTGTTATGATAGGATCAAA	58.947	26
CTCACAGGGTCGTTCCATCT	60.112	20	CGTGTGGGAAAGATATGCCT	59.955	20
CGAAATTGAAATCGGACCAT	59.762	20	TCATCGATTACGTTGAGATGAA	58.595	23
AAGAAGGATGGCGGAGAGTT	60.212	20	TCACCCACTCTCGTCACTTG	59.864	20
TGTGAAAAACAGTGGCAGGA	60.278	20	GCCTTCAAATTGCGACTTTC	59.829	20
CAGCAATTGGTTTTGAGGGT	59.971	20	ATGAATGCGACAACATTCCA	59.931	20
ATGAGTTTGGTGTGTTGGCA	60.008	20	CCTTATTTTTAACCCTAAAAAC	58.713	24
CGCGGAGGAAATTATTTTTG	59.56	20	GCAATTCAGTGGGAAAGGAA	60.051	20
GAATGAAATGAATGGCAGGG	60.274	20	TTACGAGCTTGCGAGATTGA	59.712	20
GGATATGCTCAGTCCGGGTA	59.917	20	ATCAGTGACCACCCAACCAC	60.701	20
AGAAACACGTTTTGCTTTTGA	57.616	21	GACTGAAAGAGAAGCAGCCG	60.277	20
CACAATGCGTGTATTGACAGTG	60.096	22	GGCAACAAGCCGACAACTAT	60.14	20
GGCATGAATTCTTGGATTGC	60.423	20	AATGGGATATTCGGGGAAAA	60.329	20
TATTTAGAGCAAGGACCGGC	59.32	20	TCTTTCATGCAATCGCTTTG	59.953	20
TGAATTAACAGCGAGCATGG	59.833	20	GGGGAATTCTTGCAAATTGA	59.878	20
TGGTTTCCCGTAGTCCTGAG	60.103	20	TCCTCAATCTGGTGCTTGTG	59.831	20
GCGTCCGACACCTCAATTAT	59.962	20	TGGTTTCCGTTTATATGACGAA	59.637	23
ACGCGAGATTTACGTGGTTC	60.14	20	TTTCGTGGAAGGATACCGAC	59.933	20
TTGCGATGCTTCTGCTAATG	60.118	20	GGCATCACGATGAGAGATGA	59.75	20
CCCCATCCATGTTGTTTTTC	60.029	20	GCAGGATAAGGGAGTTAGCA	57.062	20
ACCTTCATCGAGCGAGAACT	59.043	20	ATTCTGCAATAATCCCGTGC	59.929	20
TGCTCTCTTTTTGGCTGGAT	59.955	20	CTTGTGGGAGGAAGAAACCA	60.081	20
GTCCCTTTTTACCCCTCAAA	58.02	20	TGTCAAAACACCTAAATCCCG	59.847	21
AGGAAATAAGGAGGTGTTATGAT	58.113	26	ATCGAGAGGAAAGTGGAGCA	59.95	20
GCAGTAACCCTCTCATCGGA	60.218	20	TTTTCCATATTTCTCACGTTCTC	60.004	24
TGGAACCAGCTCCGATTAAC	60.074	20	TGCGACGATGATGATACGAT	60.065	20
TTGGAAAAATCCTAGCCACAA	59.573	21	TTTGGACTGTATCGGTCTACCA	59.494	22
GACCGAATGTAATGAACCCG	60.192	20	GTCATGAACTAATCAAGTTCCA	58.175	24
AAGAGCGGGAACAAAAGTGA	59.853	20	ATCTTGGTGGGACTACGTGC	59.997	20
TGCATGCACCTGATTACACA	59.701	20	CTCTCCCTAACGTGCTAACTTC	59.955	23
GGCAGCTAGGGTTGAAAGAA	59.452	20	CACTTGGGACCTTTGGATTG	60.345	20
GCACATCAACCCACTCAATG	59.967	20	GGAGCCCATTGTTTTTCTGA	60.051	20
CATTTGCCTGACCTACCCAC	60.375	20	AAGCTGTGCATGAAGCAGTG	60.207	20
AAGTGGATGGCAGCTTCTCT	59.043	20	TTGGAATTTCTGGGAGTGGT	59.381	20
TGGGGCCAATTTACTCTCTG	60.066	20	CTTGTCGATTTTGATGGGCT	60.074	20
GGGAGCAAAGTGATTGTTCG	60.636	20	CCGAATGTAGTGGATACGGC	60.352	20
AGATTTTGAGTTCATGGGCG	60.074	20	CATGAACAAATGATGGCTGG	59.924	20
GAACTATCTACAGGCCAGGGG	59.969	21	TGATAGGGCACACAACCCTT	60.375	20
TCGCTTTTGTATGGACGACA	60.257	20	GACGGCACCAGCTTCTTTAG	60.015	20
TTTCCAAACACGTTTGCTACC	60.025	21	TCAATGTGGCGCAATTAAAA	60.074	20
TGTCCTTCCATTTCATGCAG	59.648	20	CCTCTTCAAACAGAGAGCCG	60.126	20
GCATCTCTCTCGCTCTCATTG	60.256	21	TTATTTTATGGTCTTCCAACATT	58.49	26
TCCCATTCAAAATCTTTCCA	57.983	20	TGGAGGACTGGTGCTCTTAG	58.03	20
GGTGTGTGCGTGTGATGTTT	60.497	20	GCCTTGCCTTGTCCATATTC	59.533	20
AACCGATCCCCATATAACCG	60.764	20	GTAAAGGGTGAGTGGTGGGA	59.82	20
CTGAATGACCTGCCTCCATT	60.073	20	TTGGATGGCGGATTCTCTAC	60.036	20
TCTCTTTGTAATCTCCCCCAAA	59.939	22	TGATGGTCCGGTTAATACTCG	59.831	21
CCCTCTTCATCCTCCCTCTC	60.149	20	GACTTGAGCTTGTTCGGAGG	59.989	20
CTGGGTTTCCTTCCTCTTCC	60.045	20	GACAGAACTGCTGGACCAT	60.12	20
CCTTCCCTAAAGCCCCACTA	60.435	20	TTCCAAACAGTGCACGAGAG	60.025	20
CCCAGCACTGCTTCTAGGAT	59.454	20	GGGACGACAAAAAGTTCCAA	59.948	20
CAAGGGCTTGAGTAGCTTGG	60.008	20	CGTCCATTGTAAACAGTTCCA	58.54	21

ACGCGTCACACGTAATTCAG	59.788	20	CTCAGCCGTACAGAAAAGGG	59.869	20
GTGCCATAGCCACCTGATCT	60.104	20	GAGTTGACAGTGGTGGCTGA	59.872	20
ACGATTCAAGGTGATTTGGG	59.79	20	GATGGATAAATGATTGCGGC	60.262	20
TGGGTGAGACAAGATGAGGG	61.071	20	CTCTCAAACTCACGGCCTTC	59.989	20
CCTTGACCAATCGATTTCTTG	59.555	21	GACCGAGCCCATTCTTACAG	59.694	20
CACTCGCTACGAGCCACA	59.705	18	ATGAGTTTGATGGAGCGAGG	60.218	20
CCATCACCGCATTTTCTTCT	60.074	20	TTTCATGTGGCATCAAGGTG	60.517	20
CACCCACAAACTTTTCAACTTC	58.65	22	GCACTCACTCTGGAACCCTT	59.305	20
TGCAGACCTGATCAACCTCA	60.402	20	TGGCAGCTCATAATCAGTGG	59.823	20
TGCAAACGGATGGTCTGATA	60.073	20	AGCAGCAGTGCAACTGAAAA	59.788	20
AAAATAATCCCAAAACCAATGA	57.444	22	ATGATCCTTCCAGCACTTGG	60.073	20
AACGCACAACAAAATACAAAAGA	58.777	23	GCATTGAATGGACTTAGCCCT	60.465	21
GGGTGAGTTGGCATCATTTT	59.797	20	ATGCACCCTCACCCTTTATG	59.813	20
ACCCTGCCCAAAACTCTCTT	60.11	20	CTTTCTTCTTCTCCTCCGCC	60.455	20
CCCATTTCCATGCTTCAACT	59.933	20	GACCCACTCCAACTCTTCCA	60.088	20
GCGGGTAAATATCAATTTCGAG	59.837	22	GCACCTGAGGAGGTGTTATGA	60.126	21
AATTGTGGCCTCACCTTCAG	60.111	20	CCCTTTCATGCATTTGCTTC	60.585	20
TGTGGGTTAGCACTTGATCG	59.716	20	GAAACAGAGGGAGGGAAAGG	60.045	20
TTCAAACTACATTTGGGGGA	57.917	20	TTCAACAACTCATCCACATCAA	59.024	22
TCGATTCGAATTTTCATACACA	58.161	22	AAAAGGTTCCCCTTTCTCCTC	59.934	21
TGGTATGACAATTGCAAGCAT	59.055	21	AAAGAAAAAGTCGCTGCCAA	59.996	20
CAGCCAACTCGATCTCATCA	59.942	20	GATCAGGTGTCTGGGACGAT	59.928	20
TTTGTGCATTCTTCCCTTCA	59.247	20	GAGCAATTGTTGGACCGAGT	60.119	20
TGCTTCTCCAAATCCATCTTC	59.259	21	GCACCCCAGACCATTACAAC	60.24	20
GAAGTGTGCCCAACACCTTT	60.012	20	ACCGACCAAAAATCAAACCA	60.206	20
ACACTTGACGAAGCCCAACT	59.769	20	TGGATCGACAATTAGCTGGA	59.226	20
CACTCACTCTCACTAGCCGC	58.78	20	CTACGTCAACGGTGGTGCTA	59.781	20
CAATACCGTGACATGCCTTG	59.988	20	GGACTTGGCTGGTTCTCAAA	60.232	20
ATGGCTGTTGATGTGGACAA	59.967	20	TTAATCTTGGCCGCTGATTT	59.682	20
TGGTTGCTGCTGCAAAATAG	60.014	20	TGAAAATTTGAGGCTGCACA	60.379	20
TCGAACTCCAATAGCAGCAA	59.566	20	TCCTGATTTCACTTGGGAGG	60.042	20
ATTTGTGCAAAAGTTTGGGG	59.839	20	CCTTCAATGGAGGTTCAGGA	60.042	20
ATTGGTGAACCTCTCCCAAA	59.381	20	ACCGATTTTCCCCCATTTTA	60.361	20
TGGACAAGACAAGGCTAGGG	60.246	20	GATTTGGTGAAAGCCCAAAC	59.41	20
TATGGCACACCATACCAGGA	59.799	20	GAGGCTTGATGATGCACAGA	59.95	20
GCCCTTTTCATTGCTGTCAT	60.081	20	TTTGAAGTGGCAACAATTCG	59.706	20
AACGGTGACGAATGGTTCTC	59.973	20	AACCGACATAATACACCGCC	59.713	20
AATTGGAAACATGGCGAGAC	59.939	20	CCTTATGGTGGCTTGTTTGG	60.357	20
GGTCCAAACAACGAACCAAC	60.255	20	AAACTTCCCGGACAGCATTA	59.569	20
TTTTCAACACCCTCACACCC	60.791	20	GCGGCAGAATGAAGAAGAAA	60.469	20
GGGGTTAGAGAGGGTGCATT	60.328	20	TCCATGCAAGTCCATTCTGT	59.09	20
TTCAACCCACTGCAGTACCA	60.152	20	ATCGGTTATCACCGGATCG	60.697	19
AGGAAAGGAAACCACCCATT	59.668	20	CCGTGTCCGTGTACATTTG	58.394	19
CCAATTGGTTTCGAGATGGA	60.832	20	TCAACCATTTTTGTGCTCCTT	59.601	21
CACCCACATTACATTAAACCGA	59.625	22	GCGCGCGCTGTATATCTAAC	60.898	20
TGTGCCACATCAGCTTCTTC	59.992	20	TTTTAGAGCATCCCCAGTGTG	60.118	21
TCGCTGCCATATTCTTGACA	60.366	20	ATTAATTATGGTGCAGCGGG	59.816	20
GGACAGCAGCCATTAAAAAGA	59.352	21	ACAAACTTATGGACCGCTGG	59.993	20
ATACAATTCCACGCACCCTC	59.82	20	TTTTGGTGTTTTGCGTGTGT	60.05	20
CCTTGACCAATCGATTTCTTG	59.555	21	CGAACCCATTCTTACAGGCA	61.021	20
ATCCACGAGGATGATGAAGC	60.042	20	GCTGGCTGGTGAACTTTCTT	59.478	20
TTTTCATTTGATTAGAAGTTCTGGA	58.439	25	TTCATTCTGGGATAAGGAGCA	59.654	21
CAGCAAACTGAAGAACAAGGAA	59.534	22	GGGTTTGGAATGTTAGCTGG	59.429	20
TAGCCAACTCGCTTAGCCTC	59.752	20	CGTTTTGAGGGTGGATGACT	59.966	20
GTCTGGTAATGGCCGGACTA	59.955	20	TTTGCAGATCTTCATCCAACA	59.262	21
TTGGCAATGAGATACCGATG	59.499	20	CATCCTCAATTCGATCCTGG	60.417	20
TGAAATTTGAAGTCCATGCG	59.664	20	TTCAGAAAGCCGAGAATTGC	60.469	20
CCACACGAACTCATTTGACG	60.152	20	CAATTTGTTTCGAATTTTGCTG	59.64	22

TTTGAGAAAGTGGACCTCGG	60.224	20	CCCTGCTTCTGAAACCCTAGT	59.759	21
AGCGTAACATTATGAAGGCGA	59.756	21	TCTTGGGAACCCTTGAGATG	60.042	20
AAAGCGCTCGTACATTTTATG	57.218	21	GGATAAGGGAGTTTGCACCA	59.933	20
AATAAATTCAGCGCAAACCG	60.095	20	TGCATAGCCTCTACGAGTGAA	60.039	22
GTATGAATTCCGTGTTGGGG	60.051	20	AGGAAGGGTCTCGTGTGTATG	59.076	21
TCTTTTTGACATTTGGGTTCA	58.107	21	AGGATCTCAAGCCATTTCATGT	59.968	22
GTGGGTTGTTCTGATCTGGG	60.363	20	TTGATCGACAGCATCCTAGC	58.979	20
AATTCGCATGGTGACATCAG	59.527	20	TTCTTGAGTCGGGGGAATTT	60.797	20
GATGCGTTAATGTACACAACTTCC	59.839	24	GGGAGATCTAGCAGGATACGC	60.209	21
GTTGGGAACGAATTGGAGAA	59.91	20	CGCCTAGAATTCGTCAAAGC	59.982	20
CTTGGTGCGGAACATGACTT	61.096	20	TGTGCAGATCTAATGGCACAG	59.879	21
AAATCACGTTTGCAGCATGT	59.203	20	ACGCACGCACTCAGTTACAC	59.977	20
GTGTTACGATAGAATCACGCC	57.255	21	GACGCCAATGGAACCTTTTA	59.938	20
CTTGCCTCCACCATCTTCTC	59.803	20	AAAATGGGTTTCCTTACCCG	60.048	20
CGCTTAGAGGGTGTTTTGACA	60.29	21	AAATTGAGCTCCATAGCCGA	59.807	20
TTTTGACAATATATAGGTGTTTTG	58.82	27	CAAAAATGCCCTTGAATGCT	60.074	20
AAATGGCATTGCTCCTCAAC	60.081	20	GCAAAACCGTCTTTCCACTC	59.717	20
CGCGGTGTTTTAACTTGCTT	60.298	20	TCGAAACCCATTGACCTCAT	60.317	20
CTCGATTAAATGGGACCGAA	59.894	20	ACCGAATGCACTCACACAAA	60.16	20
CCTCACGACGACTCCAAAAC	60.69	20	TGCACCGGAGAAGAACTACC	60.255	20
TCGTGTTCTTCCTCCCTCTC	59.38	20	TTTCTCAACCGAGCTCACC	58.945	19
CTGAAAGGCAGGTGAAGTCC	59.844	20	ATCCGCCCCTTATCTCTGTT	59.925	20
AATGCGCGTTTTTAGGGTTA	59.624	20	TTTCCCTCGATTCTCGTGTC	60.195	20
TTTGAGTTGGGAGAGGGATG	60.042	20	AGGTGTGCTGCTTTTCTTCG	60.571	20
TCAGTGGCTACAAATCCCCT	59.55	20	TCTAACTTGACCTCACCGCC	60.255	20
TTGTTCCCTGTGGGATTAGG	59.784	20	TCCGATATTAAACGAGCGGT	59.569	20
CTGACGGTTGGATTTTGTCC	60.353	20	AAAATGCCCTTGTATGCTGC	60.103	20
CCAGGCTTGAGTTTCCTCAC	59.844	20	CAAATTCCAATGAAAGGGGA	59.733	20
AAAATGCCCTCGAATGCTAA	59.682	20	ATTTACGTCGATCTGCGTCC	60.103	20
TAAAGACATATCGCGACCCC	59.923	20	TGCACCGTGTGCAGTTATTT	60.18	20
GTCACATCTCGATCTTCGCA	59.95	20	ACCAGCTGCACCTGTAACAA	59.365	20
ACAGTCTGCAGGCCAAAACT	59.914	20	TCAGAGAGTCAGGATTGGGG	60.191	20
GCAGGGGTTACGCATTCTAC	59.597	20	AAATGATCTACGTCCACGGG	59.813	20
AAACGCGTCATGGATAAACC	59.829	20	ACCGTTCATAAATGGTCCGA	60.192	20
ATGGGAAGAGGGGTATGAGG	60.147	20	AGGCGCATCTGATCTTAAAAA	58.979	21
GGGACGATTCTGAAAGGTGA	60.05	20	GAACGGCTGTGGTTTCAAAT	59.978	20
TGCAATGCATGGAGGAAATA	60.035	20	CCAAACAATGCCAACAATGA	60.357	20
CAATTTGCAGCCCTCATTTT	60.074	20	AGAACATGGATCGGATGAGC	60.042	20
ATACCCACCCACCCTCTCTC	60.194	20	AATTCTCGCGCCATTACAAC	60.103	20
CTCGAATTCGGTTCCAGAAA	60.184	20	ATGGTAGCCATTTGAGTCGC	60.103	20
ATCTCCTCCTCCACCGTGA	60.627	19	TCCGCGGTTCTAATCTCCTA	59.801	20
ATCTCCTCCTCCACCGTGA	60.627	19	ATCAAGAGCCTCCTCGAACA	59.95	20
TGAGGGTTCTTTGCCATAGG	60.066	20	CGATCGAAGACTCCATCCAT	60.034	20
TTTTTATAACAGTGGGCGGC	59.964	20	TTGCTCTAACAATTCTGAAACG	59.065	23
CACGGGAAGCGTGATAATTT	59.96	20	CGCCAGGGGAATTGTATTTA	59.789	20
CGATCTTGCTCTACGTCTGGT	59.511	21	GCAGCCATGGTATGGACTCT	60.104	20
TCTCGCTCTACACTTTCGGTC	59.63	21	GTGGTTTGGTCCGGTTAATG	60.088	20
AAGCGAATCCAGGTAAGGCT	60.228	20	GTGGATTTGGGGATGATGAC	59.995	20
CTCTCGACTAGTTGGCGCAT	60.559	20	CGTGGAGTCGACGACAATTA	59.716	20
CGGCGGCTCTATAAAATTGA	60.185	20	ATTCCACACACGCAACCATA	59.847	20
TCATGGATCGACACGACAAT	59.925	20	GCCAAATGCCTACAAATTGC	60.465	20
TCCAGGGCTACTGGAGGTAA	59.688	20	TTTGGCTTGTCGAGCTCTTT	60.132	20
TGACTTGGGGTCCATCTCTC	60.048	20	ATGATGGAAATGGCAAAAGC	59.907	20
TGCATCAAGGAAAAACGAAA	59.277	20	TTTTTGGCTCGTTGAGCTTT	59.996	20
CATTGCATTTTATGCAGAGCA	59.856	21	ATGCAAAGCATACTAAAGATG	59.73	24
ACTCAGGTGGTTCAAATCGG	59.966	20	CGGCCCAATTATTGTCTCAT	59.784	20
GTTGTGTTGCCTGCAGTTTG	60.347	20	ACGACCCATTCAAGGTGAAA	60.353	20
ATCACCCAAAGCCATTTCAC	59.797	20	TCGGTCTCCTTTGTCCAACT	59.697	20

AGTTTGAAGAAGACCGCACG	60.431	20	CGACTCCGTATTGCATCGT	59.688	19
ATTTGGAGGTTTTGGCAGTG	59.971	20	CAAGCCCTAGTTCTTTCCCC	60.068	20
AGTGCTCGAATATCTCCCCC	60.431	20	CATTGAATATGCATCACGCC	59.921	20
ATTGATGTCCGAATGCAACA	59.931	20	ACACGACAGGATGACACGAA	60.162	20
CACACCTTCAGAAATGCAATG	59.184	21	TTCACTACCAAGGGGTCTGC	60.111	20
CCTAGCTTTGCCCTCCTTCT	59.976	20	AATAGTTGGGAGCGGTTGAA	59.569	20
CCATTGCATCACCATCAATC	59.738	20	CCGGATATACAAACTACAGGG	59.758	22
AAACCACATCCTTCGCAGAG	60.255	20	GGGATGAATTTCCACCATGA	60.526	20
TGTAATCTCTCTCGAAGTTATAGT	57.16	27	AAACACGCAACACAAAGCAG	59.951	20
ACGAGATTTACGTGGTTCGG	59.993	20	GCATCTCTCTCTTGCTCTCATT	60.665	23
TATTAGAGCCACAGCGGCAT	60.762	20	ATCGGTTATTACCGGATCGC	61.031	20
AACTCATTAAATGTGCCGCC	59.967	20	ATGTTCGGATTTTGAAACGG	59.801	20
ATTTCGAAGATCAAAGGCCC	60.399	20	AGCCGTCGGATTTAACATTG	59.96	20
CATGCCCACAAACACTCAAG	60.152	20	TGCAGCTGATAGCACACTCC	60.168	20
TGACATTTACGCAGTTTGTCG	59.784	21	GACGGAATTTCGGTGTTTTG	60.344	20
TGAGCTTGGTTGGGAAAATC	60.051	20	CAGTTGGTTTTGCATCATCG	60.111	20
GGCTCCCACAATGAACAACT	59.973	20	CCTCGCCTACAAAACAAGGA	60.241	20
CGAAGACACGATGTTGAACG	60.301	20	CTTGAGGGATGACGGGAGTA	60.065	20
CCCAGAATTGTAAAGCGCAC	60.637	20	TGATAGGATCAATCCCCACAA	60.14	21
GCACCGAAACAGAGCTGATA	59.028	20	TGTGTGTGCTATCTGCGTGA	60.054	20
GAGAATGAGGGAGGGAGGAG	60.149	20	CTTTCTTCTTCATTTCGCCG	59.953	20
TTCCTTTCCTCCTGCATCAC	60.195	20	AGGACATGCTCAATGTCTGCT	59.889	21
TCTGCAGCTGAGGAAGTTCA	59.855	20	CACAGAGAATCAAACCAACAC	60.06	23
GTGTGGTTGGGAAGGAGAAA	59.943	20	AATGGACCAGCCACTACAGG	59.989	20
TGAACTCTGCATCATCTCCG	59.942	20	AACATCATCCAAATCCCAGC	59.756	20
GAGGCTTTTCGCTTTCCTTT	59.966	20	AACTGTCCCTACCTGCCCTT	59.994	20
TTTTATCCCATGTTTGTGCAT	57.885	21	ACCACTCCTCGCTCTCTCCT	60.548	20
CAGCGAATGTAACCGGATCT	60.096	20	GAGCGGCGAAACAAATAAAA	60.205	20
GTTAGGTGACCCACCTTCCA	59.82	20	TTAACAGCCATAAGCACAAGC	58.136	21
TCTTTCGAGTCAGGGCATCT	59.95	20	GAGTCAAACATGCGATCCTT	57.735	20
ATGCCCATCTTTTTCCCTTT	59.777	20	GAGTGGAGGATTCGGTGAAA	60.05	20
TGCGTTTTGATGATATATAGGTGTT	58.933	25	ATGCCAATGGCCCAATAAT	59.994	19
GATGCTGAGGTGGAGTTGTG	59.261	20	GCAAGTGGTCACGTGAAATG	60.16	20
GGGCACGTAAGCCTAATGAA	60.096	20	CCCTAATTTGTGAAAATGGGTT	59.141	22
TCCTTGTTACGGGGAAAGTG	59.964	20	GGTTCTCTGGTTGCACCATT	59.973	20
AACTCCGCGAGAGAAATTGA	59.955	20	CGAAAACCCTTTCGCAAGTA	60.236	20
TTTTTGCACCATTGGTATTG	57.023	20	GGTTCGAATCCTCTCTTCCC	60.015	20
TGACGAATGATACCATTTAAGCA	59.507	23	GGGTAGCCTTTCATTCCCTC	59.903	20
AACTAAAAACGATGAAATTTGGT	58.595	24	TAAAGCAATTTTGCCCAAGG	60.068	20
CATTCAAGGGGCATTTTTGT	59.801	20	CTTGTCTCCATTCCATTGGC	60.461	20
ACGTCAGTCCGTGGGTTTAC	59.891	20	AGGCTATAAAGGAGCGAGAGT	57.926	22
TGTTTTCACGAATATACATGTTCC	60.501	25	ACATATTTATACGCATATAGCA	57.577	27
TGCCCTAACGCCTTATCTTG	60.223	20	CAGAGATTTCGCTCGATTCC	59.917	20
TGGCCTAACTTCTGGTGACA	59.288	20	ATCTTCAACCTCATCACCCG	59.927	20
GAGAGGAGTGAGATTGAGCGA	59.694	21	GTGCGAGTGTTAACCGTTTCT	59.299	21
CCCTACCCATTTACCCGTTT	59.939	20	TCGACAATTTTAGAGACAACGT	59.322	23
TTCTTCCCCACTGCTCATCT	59.803	20	AGGGAAGGAAGGTTTAGGCA	60.068	20
TCTGCTCCATTTTCACAACTG	58.912	21	TGTAGCCCGGTGCTAGAGTT	59.898	20
TTGGCCGTGAGTTCATTGTA	60.111	20	CGTTGGACCTGAAAGAGGAC	59.697	20
TGAGCCGTCAGTGCATTAAA	60.401	20	AATGGCCAAGAGTCTCGCTA	59.978	20
GTCACAGATGCGTGACACCT	59.744	20	CTTGTGAAATCAATGCACCG	60.111	20
ATGCATACATGACTCGAGCG	59.854	20	TTCGTCAAACCTCCCAAACT	59.569	20
CGGGCCGTGTACTTTACAAT	59.883	20	TCAAACCCTAGCCCATGAAC	59.933	20
CGCGTTACGAATCCAAGTTT	60.131	20	GGCACGAACCTCTTTCTCAT	59.288	20
TTTTTAGGGTTTAAAATCGCGT	59.118	22	CGGTTAAAGGTGGTGCTAGG	59.626	20
ATGATGGACAAGGCATCCTC	59.893	20	TTGGTTGGGTAGCTTTGGAG	60.103	20
AAGGCCCACAATGGTTATTAGTT	60.02	23	ACAATCGTCGGATTTTAGCG	60.096	20
AGAGAGGGGCGAGAGGTAGA	60.489	20	CGGATGGACCGGATGTATTA	60.544	20

TTGTGACGGTGACTAGAGCC	58.882	20	AGCTCGGTATGCGAGAGAGA	60.263	20
ACCATATTTAAGGGTTATCACCTG	57.552	24	GCAGTAAAATACGGCTGCGT	60.293	20
GGCTACTGTTCCCGACTCAG	59.867	20	CCCTAGCCTTTGCCTCTTTC	60.332	20
TGTCGTTTCCCATGTTGCT	60.104	19	GGCTTGTCTGGAGTTTGCTC	59.997	20
GATTCTCCCAATCTGACGGA	60.011	20	GCGTACCAAATCATGTCGAA	59.548	20
GTTTGGTTGTTTGAGATTGTGG	59.378	22	CACATGGAATTGCCTGAAGA	59.648	20
TTGCCTTTCTTTCCCCTCTT	60.18	20	CCATGAACACATTGATTGGC	59.781	20
TGGATGGAGAGAATGAACCC	59.862	20	CACCCGAAAACCGAATAAGA	59.931	20
TTCTCACATAACTTAGCTGTTCTCA	57.502	25	ACGGCCTGAATGACAGAAAT	59.556	20
GTTATGATGGGAATGGTGGG	59.871	20	CGGAGTGGGCTCATAAATGT	59.955	20
TGGCTAATTTGGCAGCTTCT	59.982	20	ATCCCAAGCCATACGAACTG	59.955	20
AACCGGTTAAAACCCAGACC	60.089	20	TTGGTCCTTTGTTCCTTTGG	59.942	20
GGTTATCACCGGATCACGAC	60.203	20	ACACGGTCTCATGGCATAAA	59.002	20
GCCAAGATTTCAGAATTCGC	59.791	20	GTTTCCTCCACAACGCTCTC	59.851	20
GTGTGTGCATGCATTTGTTG	59.595	20	TTTGCAATAACAAAACTCGGG	59.986	21
TGCAAAGCATTTCACTTTGG	59.849	20	TTCCTACTGGCTGTCCTTCG	60.388	20
GAAGCATGAAGCAGCAATGA	60.104	20	TTCAGATGCTCCACCTGTTG	59.831	20
TCAATGTTGTAGAGGGGATTCA	59.429	22	CAATAAGAAACACGCAACACA	60.082	23
GTCAACCAATGCAGATGCTC	59.25	20	CCGATCAACAATTTATGCCC	60.153	20
CCTCACCAGCACCTTCTCTC	59.986	20	TGTGCGCTTGAGTGTGTGTA	60.096	20
CAATTTCAACCTTGTTGCCA	59.561	20	TGACGTTCTTGCTGCTATGG	60.011	20
TTAGAAACGGCATACCCAGG	59.953	20	GACACATGTCACGAATCGGT	59.399	20
AGACAGCGATGGTGAAGAGG	60.408	20	TAAACAACCATGTCGGCGTA	59.992	20
AGGTTCCCTCTTCTCTAACGC	59.001	21	GATCGACCAATTGTGTGACG	59.967	20
ACTCGAGATCGGTCCACCT	59.654	19	ACGTCCATGGGAGAATGTGT	60.246	20
ACCCAAAGGTCTCATTTCCA	59.381	20	AGGGCCACATGATGATAACC	59.635	20
AAAAGCACCAGCAATGTGAA	59.322	20	GCCCGTCTCTTGGATATGAA	60.036	20
ACGGTCGCAGAAAAAGCTAA	60.018	20	ATTTCTCTCGTCACACGCCT	59.874	20
TTCCACAGACAACCTCACCA	60.129	20	TCTTCGAATAAACCCCCACA	60.301	20
GGATCGAAAAGAGAGGGAGG	60.147	20	TGGAGGAAGAAGACAAGATGC	59.42	21
ATGATGGGCGATTGAACACT	60.348	20	GGAGTGGCTTGCGAACTTAG	60.015	20
GGACTGCTGGATAATCCCCT	60.293	20	TGCGTGTTTGTCGTGATTTC	60.709	20
ACGATCACTCCCTGTTACGG	59.989	20	TAGATCACATTTGGCACGGA	60.073	20
TCGGTAAGTCGTTAATGGAGG	59.098	21	GTCTTTGCGGGTGAAAAGTT	59.218	20
ACGATGCTGCTGTGAACAAA	60.459	20	TCCAAACCAACAACACCTGA	59.976	20
AACGGGAATGGTGTGTTGAT	60.096	20	TCCGTTATGGGCCGTTAATA	60.165	20
TGTGGCAACACCAATCACTT	60.008	20	GGGACATTTTCTGCTTGCTG	60.776	20
ACTCCAGCTACCGAAGCAGA	60.156	20	ACATCTCCCTCACCCTCTCC	60.469	20
TAGCGATGAAGACGACGATG	59.972	20	CATGCCATCAAATCAACAGC	60.08	20
AAGAGATGACATTTTCGGCG	60.214	20	GATACTCCGGCCAACTGAAA	60.074	20
TTTCGATTTGGGGTGTAACAA	60.209	21	TTGAACCTAGCCGGAGAAGA	59.948	20
TTCCGGCGAGGATATATGAG	60.016	20	GCTTGCCACGTCAACATAAA	59.735	20
CAAAAAGGGAAGAGCGACAC	59.853	20	TGACCGTTTCACCACAGGTA	60.001	20
GGGATCCGACGTCCAATATAC	60.413	21	AGATGTAGCAACCTATTTCTAA	57.349	27
AGTTTCGCGATCTCAACCAG	60.397	20	TCTTGGACCAGATTGTCCCT	59.505	20
AAAAATGATGCCAATCCAGC	59.907	20	TGCATAGAAAAATATGTAAAAT	58.929	27
TGATTCTTTTGTTTGGTTTGC	57.795	21	TCATGAGATCAGTTTGGGCA	60.201	20
GGTGTTTTTGGATTGGTTGG	60.066	20	GCATCAGTGTTTGCCGAATA	59.694	20
CCGCAATAATCCATACCTCA	58.455	20	TCCCAATTTAAGGGTTATTACCT	59.555	24
GGTGATTCGAGATGATCCGT	59.893	20	GCTAATTGCATTCTCCCGAA	60.175	20
CAGAAACTCACCATTTGCCA	59.691	20	AACCAGCTGTCAGAAGTGGG	60.298	20
TGACGTGGTGTTGTGGTTTT	59.897	20	TCCATGAGCAGAAAATGTGG	59.648	20
GTGAATCACACTCCCCCATC	60.184	20	TGGCCTGTAGACCAATACCC	59.813	20
AGAGCTGCCCAAGAAGGATT	60.349	20	TGACTGCCACAGTTTCCTCA	60.44	20
CGAACTGGGAAAGGAGAAAA	59.284	20	CGGTATTTGGGGCATGTAAT	59.547	20
GACACTCTTCTTCACCCCCA	60.088	20	GATTGTTGGAAAGCTGGGAA	60.051	20
TCTTGAACCGAACCACGTAA	59.17	20	AAGGACCAATGAGATGGGTG	59.779	20
CTGCTGCCCAAAAACTTAGC	60.018	20	TGGTGAATGAAGGTGACGAG	59.676	20

GGATGCCATTTGTAAGTCCG	60.331	20	GGTGTGTGAGGTGTGTGAGG	60.045	20
GGGACCTTATCTTTTGCCGT	60.32	20	TGCTCTCTCATTGTAATCTCTCT	59.688	25
GCTTCTCGTTCCCTGTTGAA	60.375	20	CACACTGGACATCCCTTGAA	59.52	20
AGGTCACCTCCTGCAAGAAA	59.844	20	TGCTGCTGAACTTCTTGTGA	58.276	20
TGAATGCTTACCGATGCGT	60.235	19	TGCATATCTTCGTGTGTGCAT	60.158	21
TCACCCTTTCTTTGATGGGT	59.381	20	TCTCGAGTTCAAGCGTTGTG	60.175	20
TGTCATGAATCGGTGCATTT	59.931	20	GCCGAGATTTGTTATGCGTT	60.103	20
TTTCGAGAACTCGGGATGAG	60.331	20	CAAGATCCAAGGGCTGTGA	59.771	19
TCCTTTTCCATTATCCATGTTTT	58.787	23	CGATCCGGTCTGATCCAA	60.582	18
TCGGGTGCATAGGTTAAAGG	59.953	20	GCAGCCCATTCTATGCAAAT	60.067	20
TGGATTGCATACCAACCAGAT	60.207	21	ACGAAAAAGGGCATGAAAAA	59.564	20
TGGCTTACACATGCAGATCC	59.679	20	TTCACACGAGAGTGCAGATTG	60.04	21
TGAAGGCTTTGATTCATCTCTCT	59.496	23	GCCAGAAATAGTGGATTTTGC	58.709	21
CTTCCGCCCATTCTACAAAA	60.067	20	ACCATATTTAAGGGTTATCACC	57.552	24
TGGAATTCGCAATATCCAAAG	59.914	21	TTTTTAAAAGGAGACATTGCTG	58.494	24
CCTTTGAACATCATGCGTTG	60.111	20	TGTTGCAAGTAGTAAAGTAAA	59.475	25
CCAGCAGTTGGCTTCATTTT	60.249	20	AGAAGGTTATCACCGGATCG	59.006	20
GGCGGACATCAAAGGAATTA	59.901	20	TGTAACCGCTGTTATCCCTCA	60.508	21
ATCACGGACCCCACATACAT	59.934	20	CAAAATTTCTGCCCTTTCCA	60.046	20
ATTTGCAATGGACTGCCTCT	59.7	20	GAGATATCTTGCGGCAGCTT	59.579	20
TCGTGCGAACAATGACATTAC	59.605	21	AGAGGGTATTTCGGGAAAGC	59.554	20
ATGAGGATTGTCCCGTCAAG	59.927	20	GGCTGGGATGTCATTCATTT	59.756	20
TGAGCAAGCGCATTGTTTAT	59.472	20	TGGAAAAGGAACAACCAACA	58.995	20
TCTACTTCCCAACACCACCC	59.82	20	TCTTCTGTCTGTCCCTGGCT	59.986	20
TCCTTCCTTTCTGCATTTGG	60.184	20	ACAGCTTCACCGGTTTGTTC	60.156	20
ACAGGGCTGGTGTGTGTTTT	60.466	20	ATGGCTGTTTTCCAATGAGC	60.081	20
CATCTGATCCCAGCAAATGA	59.604	20	GCCCACATTTCAACCAGTTT	59.836	20
TCCATAAACAGGGAAGATGTGA	59.429	22	AATTCAAATCTTAACCGCCG	59.078	20
AAAATTCTGAAACCCCCAGG	60.159	20	CCTTCCGTTTTCGACATCAC	60.495	20
TGGGAACCTAGGAGAGCCTT	60.204	20	CAACAGTTTGGCATCAGAGC	59.445	20
AGATTTGGGGTGATGGGTTT	60.422	20	GCCAACCACACAGTGAACAA	60.616	20
CCGAAATGCAACGATAAACTC	59.6	21	GTACAGTGGTGGTGTGCTCG	60.227	20
TGGATGTGGTTGGTGAGTTG	60.416	20	GGCTAATTGTTGGCCTTTGA	60.074	20
CGAAGTAGCTCGAGCCGTAG	60.305	20	TAGGAGCAAGCGAGGATGAT	59.939	20
ATTCCAAAATTGAACAGCCG	59.938	20	TTCGTGGATGCTATGCTCAC	59.83	20
CAATCTCGAAAATGGATGGC	60.414	20	GCACAACTAATGCTTCCTGC	58.53	20
GGGGAAAAGGGTGATGTTTT	60.032	20	CATCCTTCGGCTTTTTACCA	60.067	20
GCGCGTCACACTTTTATCCT	60.278	20	AGGTGATTGTGGTGGGTCC	60.649	19
GGGACAACGCCATTTATAGG	59.297	20	GCCAATGCCTCATCCTAAAG	59.668	20
CCAGTGTGTGAAAATTTTGTTCC	60.647	23	AAAAGTTTGGCGTCATCACC	59.978	20
TTTCAACGTCGGACAAGACA	60.278	20	TCGAGCTGGCTGAAGAATTT	60.096	20
GCAGACAGGGGAATCTTAGG	58.741	20	ACGTAGGATATCACTAAATTGA	57.146	27
TCCTCTAGCATCTCTTGCTCTC	58.055	22	GGTGCAGCCTTATCTCTTGC	59.985	20
TTTTACCGATAGAAGCCCACA	59.595	21	TGGGTAGCATATGTCGATGG	59.375	20
TATGCAGTGAGTTGCCCAAA	60.257	20	GCGTTTTGATGATATATAGGTG	58.907	26
TCCCCGCGTATAGAAATCAC	59.923	20	TCGTGCACAAAGTGGAATGT	60.16	20
CAAGATGATGAAGGTCAAACGA	60.11	22	CCCTTGAAGAACTCATCCCT	58.173	20
GAGAAGGGTTATCACTTGAATAG	59.113	25	TCGTGAGAAGCGTTGATCTG	60.136	20
ATAGGCACCCCTGGAAAAAG	60.312	20	TAATGGAAACCAACAGCGTG	59.585	20
GGTGAACCGCGTAAATCTGT	60	20	TCGAACTGGAACCACACTTG	59.72	20
CTTGCATTATCCGGTCGATT	59.923	20	AGTTTTGTGGTCGAAGGTGC	60.156	20
GGCACCATACTGCCGATATT	59.813	20	TCATTGACAAACCATGTCCA	58.292	20
CAACGGATAAACCGATTGCT	59.96	20	GCAAACCCGTGTTCTTCAGT	60.156	20
GCGATGGATTGATTCACGTA	59.504	20	CCACCGAAACTCGAACTTGT	60.149	20
TTCACCCATTGTTTGCGATA	59.93	20	TTTGGCTGAGACGAATCAAA	59.395	20
TCGACATTCTAGCCACTGGA	59.394	20	ATCTCCATCGTCTTCCATCG	60.034	20
GCCACACGTATACCACGTCA	60.459	20	ATCGGTTATTATCGGATCGC	58.88	20
TGTGCACGAGAATACATCCAG	59.731	21	AAGGGTTCTGCTGAGAACGA	59.989	20

GACATGGACGGGAAGAGAGA	60.199	20	GTTAGCATGGGAAGGGAAGG	60.817	20
CGTACATTGTCCATGCCTGA	60.539	20	TAGGAATCACACGTGGTGGG	61.777	20
GACAATTGCTCGCAAAGGAT	60.221	20	TAATTCAAGCCACAAACCCC	59.801	20
TTCTCATTTGCAACCGATGT	59.127	20	ACCAACTCAAGCTCGAAAGC	59.621	20
GCTGTTTCTCAGATCCTCGG	59.95	20	TCCATAAACCATGCAAACCA	59.786	20
ACATGACCCACCAAACATGA	59.656	20	CACAAATGGAGGTGATGTGG	59.806	20
TCTCTCTTGGTTGGTGAAGAAA	58.955	22	GAACTCAGGATGCCCACTGT	60.12	20
TGTTGGCTATTTGTTGCTCA	57.919	20	CCATCGTGAAGAACAGACCA	59.676	20
TGGTACTTGCAATGTTGGGA	59.964	20	GCCATTTTCTTGCTTGCAGT	60.395	20
CCTTTGGTGTTTGAAGAGGA	57.77	20	CCCCACTTCACCACTTCACT	60.002	20
GGATGGGAGTCAATCCAGAA	59.862	20	ATTGCTCTCGCTCTGTCCTC	59.709	20
CAACGAGATACGCTGCAAGA	60.157	20	ATAGGAGCCCCGGTAAGAAA	59.924	20
TGTACATCTAGCTCTGTTGAATCT	59.079	26	GGACAGGATGATAAAGGCCA	59.894	20
TGTTGGAGATGTGAAACATGC	59.562	21	TCGAGATGAAAACATTGGCA	60.197	20
TCGGTTTGGCCAATATTTCT	59.411	20	TTCCACCCATATTGCACTCA	59.924	20
GATATTTGATTTTGCGGGGA	59.735	20	CATGGTGAGGTGACTGGGTT	60.84	20
TGCTTTGGTGACTGAATGATG	59.707	21	GCTCTAATCATGGCAGGTCC	59.658	20
TGGTGGTATGGTATGGGGAC	60.317	20	GGGGAGTAAAACGACCGAAT	60.187	20
TCACGTCAACTTATTCCCCC	59.79	20	AAGAACCGTGGTTTTTGTCG	60.008	20
GAGAGGAAATTAGGAGGGGG	58.986	20	TCCAAAATGAGACCAATCTTG	59.546	22
TCAAACAAAACCCTACACCCA	60.248	21	ACCATGCACCAATTCCTTTC	59.797	20
TTCGATCTACTGGGCCACAT	60.483	20	GTCTGATTGCCATGCTGAGA	59.95	20
ACAGATGGACTCGCTGGTCT	59.866	20	ATGATTTTTGCAGCGAAACC	60.081	20
GGCAAAATTAAAAATGCCACT	58.188	21	CAACAATGCCTTTGGTCTCA	59.691	20
TTTGCCTTAGGGAAGTGTGG	60.103	20	TCCCAAGTCGAATATCTGCTG	60.22	21
TGCCTACCAAACACTAGGGG	59.986	20	GAGCGAGGTGAGAAGAGGG	60.08	19
TGGTGCCGTACCGATAATTT	60.209	20	CATCCTGATCCACACAGTGC	60.121	20
CATGGCTGGGAAGAGGACTA	60.21	20	CCAACTGCAGAGTAACGCAG	59.658	20
CTGCCATAACCCGAAAAAGA	60.067	20	AGAAGTTAAAATAACGTACGT	59.214	26
TGCCGTGTTATTGTGAGTCC	59.572	20	AGGTTCGTGTCGTTTTCAGG	60.149	20
CTTTTCAATCGACCTTTGCC	59.685	20	ATGCCATCACAAGGAAGAGC	60.226	20
TTTTGCTGGGTTTTCTGGAC	60.088	20	CCCGAATATTCTGTGCCAGT	59.955	20
TGGAATCGCGATGAGATTTA	59.212	20	TTTGTCAGGAGAGGCGTTCT	59.989	20
CTTGAGGAAACGATCCCAGA	60.187	20	CCGCTGATGAAATGATCTGA	59.756	20
ACAAGTGTCGGCACAAACAA	60.199	20	CTGGAGCCATTTTTGTGGAT	59.933	20
AGAACCAAATGTGCAGGCTT	59.74	20	AAAACACTTCGTCCAATGCC	59.978	20
GTGCATTGGGTCAAAGAGGT	59.973	20	TCGATTACTCCACCCTCACC	59.927	20
AACATCGATCATCGTGCTCA	60.233	20	TTGCAAGTCAAGGGGAAGTC	60.232	20
TTGATCGAAAGGGAATCGAC	60.014	20	TTACGTCCCGATCCCAATAA	60.146	20
TCTCTTCTCCCCCTCTCCTC	59.883	20	TTTCACAGCAGAGGGAAACC	60.232	20
TGAACGGTTTATTCGGGTTC	59.801	20	TGAAGTATCGACGCATTCACA	60.272	21
CACGTGACATAAAATGCATCG	60.006	21	AACATTTTCAAAAACGCCAA	58.187	20
TGAAACCAGGGGAAAAAGG	59.888	19	ACCACCACCGTTAAATTCCA	60.088	20
CGGCACAAAATTTTCCACTT	59.975	20	CGGGAGTGGAGATAGCAGAA	60.353	20
TTTGCTGCGGTACTTTCATTT	59.772	21	GGGTTGATAGATCGGGTTGA	59.75	20
GACCGAAATACCCCCAAACT	60.053	20	GCGTGCTGAATCTTATCCGT	60.243	20
TTCACAGTTTTCATTTGATCACC	58.986	23	AGCATGATTTGGCTGGACTT	59.7	20
GCTATAGAGCCGTTGAATGTGA	59.388	22	GCAAATGCTTCTTACCCATCA	60.089	21
ACGGGACCCTCATCTTCTCT	60.073	20	CGGTAAAAACAATTCGCACA	59.603	20
CATCTTATCCCCAATTCTGTGA	58.903	22	GAGAGAGAGTGTGGAGAGAG	59.828	25
AGCGGTATGTTCGGATTTTG	59.96	20	TTATACCACCGCCACCCTTA	60.202	20
CGAGCCACAATACTTCGGAC	60.657	20	CTGCCACTTTACGACCATCC	60.517	20
GGATTTAGCGGTTATTACCTGA	57.387	22	TTCTTGATGTGTTGGCAAGC	59.847	20
AGAAGATGCCGAAGGATGAA	59.773	20	AAATGTTCGTGCGAATGTGA	60.119	20
AGGGAGTGCTCTCACCTGAA	59.986	20	CATTCAAAAATTGATCACCCA	58.321	21
AGGAGACGAAAGCTTCCCAT	60.212	20	ATGCGTAAATGGATCCCTGA	60.296	20
GGGTTCTCGTGATAAGCTCG	59.836	20	AACGATGTATGGGATTGATGA	57.748	21
GAGGGTTATCATGGGATCAAG	58.32	21	AACAATCGTGCTGAAACGTG	59.764	20

GGGATTTATGACCGTTTGCT	58.906	20	CCCATAGACAAAAAGGCCAA	59.931	20
AGGAGGCCTCTGAACCATTT	60.074	20	CAAGTTGTATTCGGGTTGGG	60.22	20
TGTGATGTTGGAGTTGGGAG	59.52	20	ACCCTGTGTATCCCAGCAAA	60.375	20
ATCGCGAGAAATTGAGAAGG	59.41	20	AAAACACCAACACTTCTTGCAT	58.677	22
TGTTAAGCCTTGGGATGAATG	59.946	21	CCGTTGTACATAAGCGGGTT	59.883	20
CGTTGATTTGAGGCAGGTTC	60.636	20	TGGTAGTTTGCCTTTTTCCG	60.103	20
GGTGTCCGAGTTGTAGGCAT	59.997	20	CACTGCATCACTCTCAAGCC	59.577	20
TGCCAGTTTACTCCGAAAGG	60.241	20	ACTCCGGTGTTCCATTGTTC	59.827	20
AGCTTCAAGTTTCCTCCTTTTG	59.066	22	AGACTATCAACAAGCCCCGA	59.694	20
CAGAGGAAAGCTGAGATGGC	60.096	20	GCCACCTGATCTAGCGATGT	60.249	20
GTTTTCTCGATCTCACGCCT	59.434	20	CCAGGTGTTATGACCCGAAC	60.232	20
CATGGACCAATGGGACCTAC	60.05	20	TCTTCGTCACAAACATCCCA	60.088	20
TTTGTTTCTGGTCCAGTCCC	59.943	20	TGCCACTTAGAAAAGTAAAAA	57.794	23
AACTCCATGCAAATCACACG	59.572	20	GGTGAATCGTCAAACGTCAC	58.987	20
GCGGGTAGGGTAGGGACTAT	59.33	20	TGGTGCCGTACCGATAATTT	60.209	20
GGTCGCTTCGAGTTGTTTTC	59.859	20	GAAATTCTGCAGTTCGGAGC	59.962	20
GGAAATGGGAATGGGTTCTT	59.996	20	TGGGGTCAGCTCTTGATTTC	60.195	20
TGCAAATCTTACAGAATCAGCAA	60.652	24	GTGCAGGGGATTGGTTAGAA	59.933	20
CTCCACTCCCTGAGTATCCC	58.538	20	CCGCTTTGCCTAGAAACATC	59.845	20
CCATCCCAATTATACGGTCC	58.974	20	AGCTCCTCTTTCCCTTTTGC	59.962	20
CAATCCAGTGGCTCATGTTG	60.112	20	AGTCACAGGATCCAAGAGCC	59.258	20
GGAAATGGATCAACCAAACG	60.17	20	CATTCCCAACTCCCAAAATTA	58.794	21
ATAAGCACGCCACAAAACCT	59.637	20	AGAAGGAAGAAAGGGGGACA	60.045	20
ACGGCCGTGTACTCTGTTTC	60.179	20	ATGAAGCATGCAATTCGACA	60.228	20
CACAGCATGGACTTTGTTGG	60.152	20	TTCCACCCGAGCTTTAGTTTT	60.116	21
CAAAGCAACCCTTAAGAGCG	60.011	20	TCTTGTCTTGCCAGATCCTGT	59.859	21
GTTTTGAGATGGGTGGTTGG	60.21	20	TTTGATGTTCGAAAATACCCC	58.796	21
ACGATTAGCATCGCCACTGT	60.688	20	ACATGCATGCTCGCAAATTA	60.245	20
TAGCCGGGTCGTGACATAAT	60.352	20	GCAGCGTCAAATCAATAACC	58.241	20
ATGGGAAGAAAACGCAACAC	59.978	20	CGTGTGCAATGCATCTGGTA	61.713	20
CCACATGCTATGCCTCAAACT	60.147	21	ATGGTTCTGGCTTATGTGGC	59.962	20
TGTAATTATCTACAAAACGAGAC	58.343	26	ACCCAACCCAACCACAATAA	59.948	20
TTCTATCCGCCAGTGCTCTT	59.978	20	ATGGCCGAGATTTGTTATGC	59.929	20
TGGCATTACAAACTTCAAACCA	60.389	22	TGTTTGCTTGTAGATGTTGGG	58.687	21
CAACACTGCATCAGTCCCAT	59.551	20	TTTGGCCGACTTTAGAGCTG	60.514	20
ACCTTGAGCTCTGATGCCAC	60.418	20	TGGCATGGGGAAGCTACTAT	59.551	20
AAGACTTCGCATCTCGGAAA	59.955	20	TTCTCCCCAAAAGCTAATCGT	60.082	21
GAGTTGGTCATTCTCAAGATGG	58.646	22	GGACTTATGCCGGAAAACAA	59.938	20
GCGGAACTTTCACTTCGCT	60.532	19	ACTTTGAATCTGGCAACGTG	58.775	20
GGAGCTCTCCCTTCCTGAAT	59.778	20	TTGTGTAATTGTGTTGTGTCGT	59.468	23
CACCAGCCATCCAAAGGTAT	59.813	20	AGGAGCTTTCTGCGTGGATA	59.978	20
GGCCCATGTGTTAAATCAAGA	59.815	21	TTTCCCTTTACGCATTCCTG	60.067	20
AAGGAGGTGTTTGCATGTGA	59.139	20	TCAGTTTTTGAGTTATGAATTT	57.598	24
AGCGCCTAGCGATTTCTACA	60.138	20	AGCTGGTGTGAGTTGTACGC	58.962	20
GCCGCACATTGATCTTACCT	60.103	20	CCAAATTTAAGGGTTATCACCT	58.849	23
GGCTGTTGTCGTCTATGCCT	60.285	20	TTTCGACCGACAAAAAGGAG	60.22	20
TAAGATACGGGCAGCGAAAC	60.23	20	TCCCCCAAAAGAAAATCTCC	60.237	20
CTTCCCCTGTTCTTGCATGT	60.111	20	AGCATCGAGCTTAACGGTCT	59.104	20
GCGGAGCATTGTTCATACAAC	60.526	21	AAAAATGCAACCAGCATTAAA	58.72	22
CGTGTACTCTGCCTCACAGC	59.648	20	TACCCATTTGAAAATCCCCA	59.988	20
TTTTTGTCTATATCGCTCAGTCAAT	58.484	25	ATGAGGAGCGTCAATCAGGT	59.685	20
TGGCGAAAAATGTTGACAGA	60.234	20	GCCTGTTATGGCAACCAAAT	59.829	20
ACCTCTGCACTCTCCAGGAA	59.986	20	CGATCCTGTGTGGCCTAAAT	59.955	20
GGAGTCCCTTCTTCCCAGTC	60.05	20	CTGCGCCGATATACTCACCT	60.257	20
TCTGCAATGAACGAAAATGC	59.816	20	GACACTTAGAGGGTGTTTTGA	59.97	24
TGAATGAGGGTTGTGGGACT	60.363	20	TTCCAGATCCAAAATATCCAC	60.02	22
GGCTAACGGGCTACACAATTA	59.156	21	TGGATCATGTAAGGAACAATG	59.738	23
TGAATCCACCATGGAAGAGA	59.009	20	TCGCAATGATACATGACCAGA	60.088	21

TCCAAAGGTGGCCAAAATAC	59.801	20	GAAGAAAAGACATTCCGGCT	58.386	20
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TGGGCATAAAAACGTGCATA	59.958	20	CCCCAAAGAGTTTCATTCCA	59.903	20
TCATCAACAGCGAAGCAAGT	59.596	20	GATTGAAGATCCCGGTGAAA	59.871	20
GGCAGCACCAGAATTACTCC	59.7	20	ATGCGCGATTTTAAACCCTA	59.586	20
AAATTGTTGAAGTCGGTGGC	59.978	20	CCCCCTAATCCCTAAATCCC	60.678	20
GTAAAACAGCGCCCGTACAT	60.025	20	TCTTGTTCATATGGGGAGCC	59.894	20
GCCTACAATAGCGACAAGGC	59.873	20	ACGCAACCGTAAAGAACCTG	60.168	20
ATGAACGTCGGTAGGAATGG	59.813	20	GCACCACTTCACCTCCACTT	60.159	20
AGGGACCACTAGACATTCGC	59.166	20	TGGTATCAGAGCCATGACGA	60.225	20
ACCTGGTTCTCGTTCCAAAA	59.569	20	GCACGAAGAAGGTTAAAAGG	60.116	21
CATTGCGAGAAAAGCAGTCA	60.134	20	CCAGCTCCGGAATGAAAATA	60.031	20
TTTACCCAAAGCGAAGAAGC	59.474	20	CTCGATAGGAAAGGATGCAA	57.916	20
CTTAGTTAGCATGGGGGAAGG	59.967	21	CAATCTTTGGGCGTGAGAGT	60.255	20
CCGCTCAAATCACTCACTCA	59.984	20	GTGCGTTGACCAGCATTT	58.186	18
CCCCACATTTGTGGCATATAA	60.442	21	AAGGACGTAACGGCTCTCAA	59.875	20
GATCTCAACGCATCAACCGT	61.078	20	TTTTGGAGATCTATGGCTGTCA	59.708	22
TAAATACTTGCTGCCCGAGG	60.223	20	TCCACATTGTCTTGCAGTCC	59.682	20
GTAGGTGTGAGCCCAACGAA	61.096	20	AAAGTGGGAGTTAGGGCACA	59.592	20
TTCGATTCGCAACAATTGAG	59.809	20	AGTTTTCCGGTAGCTGCCTT	60.262	20
AGCACCCTTATTGTGGCTTG	60.132	20	ATGGTGAACTGCCTTTGCTC	60.263	20
GATGGGTTATTATTGGAACGAGA	59.242	23	CGTTGAGCGGATTTAATCGT	60.096	20
TTGTACGTCCAATATGTAAATTAT	57.296	27	GACTGGAATTCTTTGCCGAG	59.813	20
TTGCATGTGCATAACGGTTT	59.999	20	CGGTTATTAGTTATCACCCGAA	58.092	22
CCTTTCGGACTCCTTCTTCC	60.183	20	CATCATCACCTCGTCCCTCT	60.072	20
AAGCAGGACGGTATTTTCCC	60.32	20	CAAACCATCCAACCACAACA	60.255	20
ATGAATCCAGGTGCCTCAGT	59.535	20	TCCTTCAATCTCAGCCTTTCA	59.94	21
ACCTAAGGGGGTGTTTGCAT	60.61	20	CTACAATTTCGGCTGCCACT	60.27	20
CGGAACCAACTTTCAGCTCT	59.473	20	CATATGGGCACAGACACTGG	59.984	20
CGGAACCAACTTTCAGCTCT	59.473	20	CATATGGGCACAGACACTGG	59.984	20
AGGGGCTGATTGTTGATGAG	60.073	20	AAAGGAGCTTCTTGCACTGG	59.615	20
GGTGATAGAAGGCTACGGCA	60.235	20	CGTCAAGCATGAGCAACACT	60.056	20
TCAAATCCTTCCATTCCCAA	60.244	20	AGGGTTTTGAGGGTTTGCTT	59.976	20
TTTTTGCGATGGAACATGAA	60.051	20	CAAATCCCAACAAATGACCC	60.029	20
GGGTACGGGTTGAGACAAAA	59.83	20	ATGCAGACGAATAAGCGAGG	60.374	20
CGACGACTTGTTGGAAATGA	59.691	20	GCATCCACCACCATCACATA	60.21	20
TATTCTTTTACGCATGCCCC	59.928	20	TACAAATGGGGTCCTGATCG	60.713	20
TCTATAGGGAAGTTATCACTGGAT	59.464	26	GAAAGCTAAAATTTGCAATCAA	58.619	24
CAACGGATTTGGTTTGTTCC	60.206	20	AAAATCAAAGGCCCACAATG	59.801	20
TTTCAGAAACGAGGGCATTT	59.685	20	GACAAAGCAGGCACACAACT	58.935	20
TGGTGTTTGATTTAGCGACG	59.729	20	TTGAACGGAATCATGGACAA	59.9	20
TTGATATTCAGTGAACGTGACAG	57.827	23	TTTGTCTACCAGTTGCCCCT	59.592	20
CATCCTTCACCTGACCCATT	59.779	20	GGCATGATTCTGCTGGTTTT	60.081	20
TGGGGTGTCATGATAAGTGG	59.215	20	GCACCAAGATTTGACCATGA	59.502	20
CGGATTTAAGGGTTATTACCTGAT	58.81	24	AAATGGTCCCCTCATGAACA	60.173	20
CCATCGATCTTGCAGAGTCA	59.942	20	CAACCAGCAAACAAAAGCAA	59.888	20
AAATTACACCTTTGTCATTTTTCA	57.864	25	TATTTTAGGAAGGATCGGGG	58.011	20
TTCGTTAAAGGGAATGCACA	59.157	20	AAGCCTTCCATTCCGAAAAT	59.909	20
TTATTGTTGGAGGGAGTGGG	59.784	20	TTTTACACGGGACCGTCAAT	60.227	20
TTGCAATCCGATATCAACCA	59.891	20	ACCCCAGTTTCAGATGTTGG	59.82	20
AAACAAACTTGGTTCCACGC	60.015	20	AATCCTCCTGCTGTGGTGAC	60.12	20
TTGAAGCATGACCTGCAAAT	59.276	20	TTCTTTAACAACCCCGCAAG	60.103	20
GATGCCGTTCACCTTCAACT	60.119	20	TCTTCTTCCACTCGCATCGT	60.945	20
AGGGATAAGATTGGTGGTGATG	60.074	22	AAGCGCACGTTTGAGTTTTT	59.926	20
GTCAAGCAATGAGAGGGGTC	59.661	20	CAAATTGTTTGGGCTCGATT	59.938	20
TTTTTCTCCCAAAATTGCC	57.656	19	TTCCAATGATGCATGGTTATG	59.247	21
CGGTCATTATGTGGCGTATG	59.833	20	TGTGTGTGTGCTCAGCAGTG	60.758	20
CACATCACCCCTTCGTTTTT	59.83	20	GCAGGTAAATATCAATTTTCGA	59.075	25

GCTGGGCACTTGAAACCTAA	60.249	20	TGCCAGCAGAGAGGAGGTAT	59.973	20
CTCTTTCCAGTTGTGTCCTGG	59.748	21	GTTTACGCACGATGTTGGTG	60.035	20
ATGCGAAGATAGGCATACCG	60.081	20	AATTAACATCACGGCCATCC	59.651	20
CTTCCTCCCACCTTCGTCTT	60.619	20	AACCGTTGGAATTTTAGAGTTA	59.847	24
AACGGAGATATCGGTTGTCG	59.955	20	GTGGGCTTCGACTCTCAGAC	59.993	20
GATGTGCAATTGTCTTTGCC	59.131	20	GCGCGTTGATCTACCAAAAT	60.103	20
ATCTTCCCGCCATTCTTTCT	60.039	20	AGGTGCTGAGGCGTTTCTT	60.005	19
CCATTTCCCTATCTATACCAATCA	58.361	24	TGTTCGGATTTGGCGATTAT	60.289	20
AAGGAGAGGAAGGTTGGCAT	60.074	20	TCCTCACCCCACTCCAATTA	60.309	20
CGAGTTGGAACTTGGAAGGA	60.224	20	TGGACTCCGTGTGTATGACTG	59.606	21
ACGTTCGCTATCCAAGTCAA	58.379	20	GCACCTTTCATGTGCAATACC	60.388	21
TATAACATCAACCGCCAGCA	60.096	20	CATGATTTGCAAGATGCCAG	60.22	20
ATTCCCAAGATAATCTCAATCG	57.214	22	CCGGCTCTGATACCATTGTT	59.955	20
GCTCCCGTAGAACTTTCCCT	59.713	20	GGTCTTACATCTCCCAGGCA	60.073	20
TGAGGAGCGTTGATCTTGTG	59.984	20	ACACGGTAACAAAATATATTG	57.382	26
GCAACAAGATGGTGCTCTCA	59.992	20	TCGGTTTCACCAATGGAAAT	60.17	20
AAGGCCGAGATTTGTTAGAGG	59.733	21	TCTTTTGTCAAGGGCGAATC	60.192	20
TGAAGTTCGGAAATAAGGAGG	58.315	21	TCGTGCATCTTGCTACTTCG	60.157	20
TCTTATCCATTTCGCCATCC	59.862	20	AGGATTGTGCACTCAATGAAT	59.059	22
GGAGGGCTGTTTCTTCATCA	60.195	20	TTCCTCCTTTCCTCTTATGGG	59.536	21
GAGGTGGGAAATCATCCCTT	60.133	20	TCCCCGAATATTCCAACTCA	60.266	20
GGACCAAGTTGCTCTTCTCG	59.989	20	TTGGTGAAAGGAGACGAAGG	60.224	20
CTCTGATTTCTCACGCCCTC	59.95	20	TGAGTGAACATGTGTGTGCG	60.373	20
AATGAGCCGTCAGTGCATTA	59.301	20	ATCCAACTCCTGCATTTTGC	60.081	20
CACTACATAAATTTGGCAAAGAG	59.966	26	CGGTTAAAAATCGGACAGGA	59.931	20
CCGGGAATTTTGAATGAACA	60.671	20	GCACCATATAATCGGGACGA	60.69	20
ATCTTCCCCAAGAGCTCACA	59.803	20	AAAGTGGCCGACAAAAACC	59.963	19
CTTGCCCCTTCACTCTCATC	59.803	20	GGATCGTTGATCGGGTTAGA	59.894	20
TTGACGTGGGTGTTGGAATA	59.816	20	GATCTTTTCACTCGAGCCCA	60.34	20
TCGAGATTTGCTCATGTTGG	59.799	20	CGACTGGCAAATACAAAAGTT	57.007	21
GCCGAAAGCTGATCACAAAT	60.221	20	ATGGCTCCATTCTTCCTCCT	60.037	20
CAAGCCATCTGTGGTTGAGA	59.831	20	TCCCACCTGAAAATGGAAAA	60.28	20
TGGTGGTTGAAGGAGGCTTA	60.626	20	TATTTTCGGCCACCACTCTC	60.074	20
ACCCTGAGGTGCTTTGTTCA	60.69	20	TGCCTCATCCTCACTCATTTC	60.211	21
TGTGGGTTCACTGGATACGA	59.96	20	GCGATGGGAACTCGTTAGAC	59.7	20
AGGACAAATTTGGAATTTTAGGG	59.631	23	AATTGTTGAAACCGGTCCAG	59.83	20
GGAAGGCCATGGTAGTTTGA	59.933	20	AATCACTAGCCCTCGCAAGA	59.978	20
TAATGTCTTCCCATCCAGCC	59.894	20	GCAAAGCCTGCATTTGACTT	60.395	20
TGGCCGGTTTTGAATCTATC	59.901	20	GGGAATTAGGGTTAGGGCAA	60.143	20
GGGTTTCATTTTGATTCCCA	59.599	20	AGATGTGGAAAAGCCCAGAA	59.67	20
CTTTCTTGCGAGAACCCTTG	59.986	20	TTCCGCTGAGCTTCTACTCC	59.717	20
TTTTGACCAAATCAATCCCA	58.792	20	CCACCAAGCAGTGTTTATAGT	59.308	24
CTCGTCCTATGCAAGCAACA	60.011	20	ATCCCCTCATGCATTCCTTT	60.662	20
GGATTCAGCATTGTAAGGGG	59.387	20	TTGGACCATTTGTCCTTCAA	58.947	20
TCTGAGAAAGCAGCTGGTGA	59.855	20	TGGTCAATACCAGAAAAATCC	59.315	22
AAAGAGTTGGGAAAAGTTATGAG	58.402	25	CCCCTTATTTGTGGTTCCAA	59.657	20
CGCTATGAGTCACGGCTACA	60.035	20	GATTGATCCCAACCAGAGGA	59.862	20
CCATAACCGTCGCATAACTCA	60.891	21	AAGCCCTAAATGCACTCGAA	59.845	20
TTCAATTACAAGCCGCAGTG	59.872	20	TTCCACGAATTTGACACGAA	60.088	20
TTTGCTAGAGGATTTTGTTAATAT	58.427	27	TGAATTTTGTTTCCCACCAA	58.841	20
CGAAAGTTTTGGAATTTGAAGG	59.978	22	TTCAAAGAATTTGTGGTAGAAT	59.119	25
TGCACCATCTTCTCAACACC	59.682	20	TGCTCCAGTTTCCTTTTGCT	59.993	20
GAAAAGGCACTCGAATTTCC	58.765	20	GTGGCACTGCACAAGTATGG	60.183	20
TTTTACGCTAACGAAACGGG	60.123	20	TTCCTAAATCATTGGGGCAG	59.894	20
ACACCCAAACCCTCAAACAC	59.721	20	TTGGGAAGGATGAAGTTTGG	59.903	20
TAGAGCAGGAAGAGCCGTGT	60.156	20	GGTGCCGGTCCATAAAATAA	59.66	20
CCACACTTTTAAATATTTTAGCTG	60.573	26	TGCTTGCATGAGAGATGGAG	60.096	20
GCTAGAGCTCACTTCACGAGC	59.54	21	TTGAAAAGAGCGCTGAACG	60.264	19

TGCATGCCAACCTATAACGA	60.096	20	AGATGGAGGCCGAGAGTTTT	60.212	20
GATACGCGTCACACATGCTC	60.304	20	TTCTACAACCACCCAAAGGG	59.824	20
ATCCGATCCGAAGTATCCGT	60.682	20	GGATATCCAAAATATCCGAAA	57.071	22
AGATGCCAATCTTCCATTGT	57.043	20	CGATCATATCCAATTTCGTTTC	59.369	23
GAACCCCAGCAACATCAACT	59.973	20	CTTCATTACACCGGCAAGGT	59.993	20
CACTTGAAAATGCGATGAGC	59.425	20	GGATCTGCGAGATAAGCGAC	59.946	20
TGAGGGGTGAAGACTTTTGG	60.081	20	ACACCCTTGCAAATTATCGC	59.967	20
TCTTAAAGCCCCTTGGTCCT	60.068	20	TTGCAATATGTCCTTGCACC	59.548	20
TTCTACTGGAACTGACGCCC	60.255	20	AAAAACATGAGCGCACCAAC	61.071	20
CACCCAAAAAGGAGTTATTATTT	59.696	25	TGACAGGAGATGGGACACAG	59.659	20
AGAGGAGAGAAGAGCGGACC	60.096	20	GGCTAATGTGTGGCAGGTTT	60	20
TTTTGCTTTGTTTTTGCTGG	58.979	20	CATCTCAAACATTCAAAGAGA	57.689	24
AAAAATCAGCGAGGCAGAAA	59.96	20	TACTGCCTTGCATTGGATCA	60.22	20
GGTTGTTTAAATGCCCCCTT	60.055	20	AGGACTTATTACCAATCATCCC	58.769	23
TTTTCGCAAATTCTGTGTGG	59.706	20	TCTCAGCTTTCTTGATGGGAA	59.94	21
CCAGAATGACACTCGACGAA	59.831	20	CCCCCAAATTTTACAAGCCT	60.177	20
GAGAGAGGGGAGGAGATTGG	60.149	20	TTGCCTTGGCCCATTTAATA	60.275	20
CTCTCCCTTTCCACACTCGT	59.3	20	TTGTCCATTCAATCCTGTGG	59.343	20
GAAAGCCGTCGATGTAGCTT	59.481	20	CAATTAACAATAGACTGACGC	60.404	24
CAAAACCACCTGCATTACCA	59.439	20	GGAAAGAGTGTGTGTTTGCG	59.339	20
CATCAAAAATGTTTTCCCCC	59.111	20	CCGTCGTATTTTCCCAACAC	60.227	20
CTCTCAATGCCTTCTACCCAA	59.322	21	TGTAGCCCCTTTGAGCCTAA	59.839	20
TGGCCCACCCATTTTTACTA	60.181	20	TTTTCTTTCCACAACCCCC	59.752	19
TGATTGCACCATAATGCACC	60.352	20	AACCATTGATTTGGTTGATTGA	59.182	22
CCAGTTATCCATCCATTCCA	58.215	20	TGACATTGCTAGCACCGAAC	59.871	20
TTCAGATCCACTAGACATTTGAGC	59.789	24	AAATGTAACAACTTTTGATCCC	58.549	24
CTGCGCAGATCTAATGGTCA	59.972	20	TGATGTGGCAGCTTTTCAAC	59.847	20
CCCTCCAATCAATTTTCCAA	59.733	20	ACGCCAGATTTATCACCCAG	59.955	20
TCCCAAAAGAGTTGGGAATG	59.903	20	ATCGGAGTTGATTTGATGCC	59.9	20
CGAAACAAGTGGCTGCATAA	59.872	20	TGCGAAATAAATGCACCAGA	60.215	20
TTATGGGCCAATTATGCTCC	59.757	20	ATGCGTTTTGATGATATATAGG	59.202	26
GGAGAGTTCGCGAAATAACAT	58.341	21	AACAATGAAATTTGGAACAAA	59.68	24
CTGGACTGCCTTCATCTTCC	59.803	20	GCTATCAGCAACAAAACCCC	59.574	20
TAGGTGTGGGGAAATGGTGT	60.088	20	CACCCTAAAAATACGCCAACA	59.876	21
ATGCATCGATGGAGGGAATA	60.26	20	TCAAATGTAAAGCACTAGAGC	59.088	23
CTTGCTGGCAACAAAAACAA	59.888	20	TTGACATTGCCTAGAAAGTGG	59.747	22
AGCTGTTGCAGAAGCCATTT	60.022	20	GTCGTGAGCTCTGTTGTGGA	60.03	20
GTGCATGTTTCCATCGTGAA	60.526	20	GGCTTTTGTCCTCATGCACT	60.263	20
GGGGATTGTAACATGTGGGT	59.386	20	ATTCCATCCCTTGGCTCTTT	59.903	20
CTGCAACACCATTGCAGAGT	59.905	20	GATGAGTGGCAGTCGGTCTC	60.84	20
TGCACATATCGGCTAAAGGA	59.281	20	ATGTAATAGGGTTTGGGAAGG	57.006	21
AGACCCTTCACCCCCATAAC	60.052	20	CCCGAAGAAGCCATCAAGTA	60.206	20
GGCTGGCTTTCACTTCTCAT	59.434	20	CATGACCACTCTTTCCTCCAC	59.564	21
GAGAATTTTAATTCGTTCATCTTG	59.576	25	TGATGGTGGAGCCTAGAAGG	60.21	20
TGGTGGTATGGTGTGGAGAA	59.806	20	ATGGATACAAGCAAGGGCAC	59.962	20
GTAGGGGTGTACATGGTCCG	60.111	20	TGCTTAATGGTTTCGTGCTG	59.872	20
CGTGCGTTGTAGTCGTGATT	59.788	20	ACCGCTGGATAATCCCCTTA	60.653	20
GGCCACAGCAGCTCAATAAT	60.243	20	CGGTGTTGGATTGGTGAGTA	59.415	20
CATCCAAAACTCGAACCCAT	59.79	20	ACGACGATGATGGGATTGTT	60.203	20
CCCGTGCTTCAATATCCTGT	59.955	20	CACTCCTTCACTCCCAGCTC	59.986	20
TGAGTTTCCAGCGCAAAGTA	59.609	20	GGCAGCTCATCAAGTTCACA	59.992	20
ATGATTGTGCTCAATGGCAG	59.679	20	CATGATCCATGTACCCATGC	59.61	20
TGCCCCACTTCTTCGTTAAA	60.608	20	TCTTCACCAACTGTACGCCA	60.301	20
TGTTCAACTAAATAATGCAGCG	58.075	22	CAATTCAATTTGTTTCAGAACC	59.745	23
TCAATAAACCCTCCGAATGC	59.901	20	AAATGCATGCACCTGATTACA	59.055	21
TGCATGATCAATGTTGTAAGGA	59.041	22	GCCGTAGCTTGTGAACGAGT	60.462	20
AGGGGTTATTAGTGGAGTAAGCC	59.011	23	CATTTCCTTTTCCACCAACG	60.336	20
AGGTGGTTTCTTGCCTGAAG	59.328	20	ATCATATTCCGCCATCTCCA	60.26	20

TCGGGAGGAAGAAGAAGAAAG	59.941	21	TTTTGATTTTATTGGGATTTGTT	58.024	24
CACAGCTAGCGATGAAGACG	59.764	20	CGAGCCAAATCTTCCTTTTG	59.817	20
TGACTTGAGGATTGTGTGCC	59.682	20	GCGGTTATCACCGGATCG	62.397	18
GCAGGATCGCCATAAGGATA	60.023	20	GCCTTGGACTTTGAATTTGC	59.691	20
TTGACAATATTTAGTGTTTTGACA	58.99	27	ATCCAATTTGGGCCATTTTA	59.124	20
CTCGGAGGCTCCAACATCTA	60.353	20	ACTTTTCCGATGGTGTCGTC	59.973	20
CCAGTTCGGTGACATATGGTAAT	60.014	23	CGTGGTTCGATCGTAATTGA	59.542	20
TTGCTCCTTGCAACTTGATG	59.988	20	GCCTCCATTTCTTGCTTCAG	59.955	20
TATGGTGGTATGGTGTGGGG	61.296	20	GAACTGGATTGGAGACGGAA	60.05	20
TATCAGGCCTGTGCAGTCAC	59.862	20	TTTGAAAACATGCAAAGGCA	60.229	20
TTCGGGTTGCTTTTTGACTT	59.724	20	AGGGGTTATCACCTGAATGC	58.864	20
CACGTGGCATCGTAAGGAAC	61.494	20	GTGGACGTCCCAGATTGTTT	59.827	20
TGGCGGTGGAAATAGTAAGG	59.953	20	TCGAATTTGTTTAGGTGTGGC	59.989	21
TCACATGCTGAATGACCAAC	58.019	20	TGAGCCATGAACACCAACTC	59.682	20
ATCGGTTATTACCGGATCGC	61.031	20	TCTTGTGGCTCAAATTCCATC	60.066	21
GGCGAGGACTGAAATTGGTA	60.074	20	TGTTCCGAAAAGGAAAATGAG	59.188	21
TTTTTGCCCCTTCTTTCCTT	60.048	20	CGCATTATGTTGCCTTTGAA	59.702	20
ATCGGTTATTACCGGATCGC	61.031	20	GAAAAAGCCAAATGAATGGG	59.388	20
CGTATCCATGGTTGAGGTCC	60.195	20	GATCTTGCAAGCCCATGTTT	60.081	20
TACACTGAGAGCGACATCGG	60.008	20	TGGAGCGTGTAATTTGCGTA	60.273	20
TTGGACGAAAATGGTCCTGT	60.353	20	TGATAACCATGACCTCACGA	57.442	20
CCACGGCTCTGATACCAAAC	60.517	20	TGAGAAACATTAAATGCGGC	58.771	20
TGGATTTGGCTAAGAATGGC	60.038	20	AACAGCCATTAAAAGTCGGC	59.229	20
AAAGCAAAAGAGGCGATTGA	59.96	20	GTACCAGGGAGTCTCGGTCA	60.112	20
GGAGATCACTTGCGGAGAAG	59.95	20	CGATATTGTTGTTGCCGTGT	59.469	20
AACTGTAATTCAGGCACCTACG	58.338	22	CCAACTTGGATATTGGTGGC	60.192	20
CATTTTTCGATGAACCACCA	59.371	20	CCGCCGTAAAGAAATCAATG	60.448	20
CAATTTGCTCGATTTCTCCC	59.645	20	CGGCTTAGCTGTTCGTTGTT	60.44	20
TCGAAAATTCCGCCACTATC	60.038	20	GGTGCTGATGACGATTCTTG	59.245	20
TGGTGCTCTTGTTTCGTCAC	59.88	20	CGAGCTCGAGTTTGAATTTGT	59.508	21
GTGGCAGATCTGAAAAACGG	60.636	20	CGCCCTCTCCACCTATCTCT	60.746	20
GCATTTTGCTACGTGGTTCA	59.735	20	TGGCAAAGAGCAAGTCAAAT	58.502	20
TGCACACAGCAGTTGTCAAA	60.071	20	CATTCAACTGGGATGCATGT	59.374	20
TGATCATGCTCAACATGCAA	59.789	20	TGCCATCCACTACACCAAAG	59.566	20
AGACAAAAAGTTTGAGGCCG	59.355	20	AAATGTTCGAAATACCGGGG	60.902	20
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TTTATTTCATCCCTTGTCATGC	58.946	22	CAGAAACTACATCGCGCAAG	59.632	20
TCCTGTTTTCTCAAGGCTCC	59.405	20	GGGGTTATCATGGGATCAAA	59.439	20
CAAAAATGGGTAGCCGAAAA	59.937	20	GCATGCTGATAGGCAACAAA	59.839	20
CTCTCTCTCAATTGCCACCC	59.803	20	AGTTGGAGGTGATGATGGTG	58.349	20
TGGTGTTTATGCTACTTTGAACG	59.238	23	CATAAGGTTATGGCGGGTGT	59.708	20
TGGAACACGTACCTTCTGATTC	59.101	22	TCCAATTTTCTGCGATGAAG	58.843	20
GATTCTTCGGCTCTTGTGCT	59.579	20	TCTGGTTTGGAAGGGAACAA	60.465	20
TTTGTACCTGAATGCACCCTT	59.485	21	TGTCAAACGTGGTGAATGAA	58.514	20
CGTTGGACCTGAAAGAGGAC	59.697	20	GTCCACGGTGGTTTGAGAGT	60.009	20
GCCTGAAAATGAACACCGTA	58.625	20	ATTGGACCTGCCACCAATTA	60.192	20
TGTGAATTTGCATCGTGGTT	59.972	20	AGCAATATCGATCTCGCAAA	58.483	20
CCGGTCAAAACCAAATTACG	60.215	20	ATGGATCAGTTAATCGGGCA	60.296	20
TTCGAAAATTTAAAGGCCCA	59.538	20	AAAATCAAAGGCCCACAATG	59.801	20
CCATGACCGATAAAAATGGC	60.153	20	ATCTCAACGATATGGCTCGG	60.059	20
GGCAACGACTATCGATCCAC	60.492	20	TTCACAAACTCACGCACACA	59.912	20
CCCCTCTTCTCTCTACCCGT	59.694	20	TGAAGAGAGAGCTTCTGTCGG	59.876	21
GCAACCGAAGTTTCATTTCA	58.747	20	GTGTTCGATACCGGGTTCTT	58.912	20
CTCACCGTCGATCAAATCCT	60.073	20	ACCCCACCTCATTTTCAACA	60.21	20
CATGCAAGACCCGAAGAACT	60.255	20	GATGGAACCACTTGCATGTTT	59.851	21
CACACATTTCCTTCCTACCAAAG	59.914	23	TGCAAATACGGAAAATTTGAC	60.347	22
TGTCGGTACCTTCGGAACTC	60.111	20	TTCTTCCTCACACCTCAGCC	60.386	20

TATGCGATCTGCACGTGATT	60.251	20	TGAACAATTGAAACACCGGA	59.941	20
TGACTGTGGCTTGCAAAGAG	60.175	20	TGATCCATTCCGACTTCCTC	60.011	20
TGTATTCATGTGTCAGCGCA	59.859	20	CTCCTCCATCAAACCATTGTC	59.396	21
ACTCCTGGAGGTCAATGCAC	60.12	20	TTGAGCTATAGTTGGAGGGTA	58.986	23
ACACCCAATAGCTTGCTTGC	60.278	20	ACATCTGTGGAGCTGCTGTG	60.055	20
CCCTCGAATGCACTCAAACT	60.255	20	TCTTTAGGTGCATCTCTTGACG	59.517	22
GTTTCAATCCGGGTCTCTCA	60.05	20	GTGATTCATGGCCGAGGTA	59.466	19
TTAATAAATTGTCGCGAACGG	59.975	21	TAATTTAAGCCCCATCCCCT	59.637	20
AAATACTCAGTAAACCAGATGAT	57.497	26	CAATTACCCTCAAGACCCGA	59.926	20
AAGGGGAGTATCACTTGAATGC	59.487	22	GAGAAAACCGAGAAGCGAAA	59.569	20
CCTAACCTTGGGCTCTGATG	59.688	20	AACACCTGTAATCGGGATCG	59.813	20
CCACACTCAATACAATATGAACG	58.945	24	CAGATCGAGATCGATTGAAGC	59.931	21
TTTTCGCCTCCGACTAAAAA	59.826	20	CGCGTCAGATTTGTTATGTG	57.792	20
GCATCAACGGCGTGTATTATT	59.873	21	ACCTGGTGTGTTGGCATTCT	60.431	20
CATGCAATAGGTTGTGCAGC	60.288	20	GCGTCAATTACGTTCCATGA	59.548	20
CAGCATATGCAAGCTCAAATTC	59.881	22	AGGGGTCAAACCTCCACTCT	59.968	20
GATGAGTTCCTGAACCAGCAG	59.859	21	TGCCAAAAATTGTCATCCAC	59.375	20
TGTCGCACAGAATGGTTGAA	61.277	20	AACTGGGCCATGATAGGTTG	59.813	20
GTTCGGTGGTCATCTCACCT	59.969	20	GGACTCCCTTCCTCAACTCC	60.05	20
TAACGGGCAGCCTAAGTACG	60.277	20	GGTGTTTGGGCTACTGGAGA	60.111	20
TTTTGAAAATTTCCCGCATC	59.886	20	TTTTGGGAAATGGGGTATGA	59.988	20
CGTTCACGTTCTGCGATTTA	59.872	20	CATACCTAATCTCCCGCCCT	60.299	20
CACTTTTGGGACCCCTTTTT	60.193	20	GAAACGATCGGAGGAGATGA	60.158	20
GCAGGTGTGAATGGAGGAAT	59.934	20	CAGAAGCAGTGGAGGGAGAA	60.523	20
TGTTGCATACGATGTGTAGCAG	59.822	22	TTGTTGGAGGATCTTCTTGAGA	59.743	23
TATGGGCCAACTAAAGCGAC	60.096	20	TGATTGAGAGATGGGGGTTC	59.862	20
GGGCGTGACATAGTGGATTG	61.329	20	TGCATCTTGGAGGTGAGTAGG	60.262	21
ATCTGCCCTATTGCTACCCC	60.307	20	TGGTACCTCCAACAAGAGGG	59.959	20
TTTCATGGGCATTTGCTTTT	60.436	20	CTGCTGACTGAAGCGGGTAT	60.419	20
CAAAAATTCGATCTTGGGGT	58.879	20	CACCCCTTTCCTTTACCCAT	60.046	20
GAGGTGCTGTAAGGGTTGGA	60.111	20	GTTGTAGGCAAAAGGGCGTA	60.131	20
ACGCTAGTGTGTTTGCTTGC	59.151	20	CTGTATATTGTCATCCACGCA	57.113	21
TTTATTTCTTTCCCGCCTCC	60.381	20	TGGGATAGGGCAACAATCAT	60.155	20
AAAATGAACTTTATCGGATCTATC	57.463	25	TTGTCATGTCCACCTCATTCA	59.951	21
TGCTGACGAAGTACACTGGG	59.897	20	CATCCAAGACATGATCGCAC	60.08	20
GTGTGCGTCTGAGTTCGTGT	59.948	20	TTTAAACCCCAACACCTTCG	59.833	20
AAAGCCCATGTTTTGTCTGG	59.971	20	TGCAGGCTGACCAGTTCTAA	59.591	20
CCCAACTGAAAACTTCCCCT	60.332	20	AAGGATTTGCAGGTTGAGGA	59.67	20
CAATCAATCCATCGTCTCCC	60.281	20	GAAAGGGACTGGGATTGAGA	59.065	20
GCACGTGACATCTAACGGAA	59.722	20	TCAACACTCTGTTTTTCACTCA	59.858	24
TAACCCCACCACACCCTAGA	60.224	20	CCCTTTGAATTTTGCCTCTG	59.679	20
TCCGTCAAGGAGATCTTGAAA	59.799	21	CTGGGAGATTGCTTGAGACC	59.803	20
GGGTGGCTTGATTTTGTTCA	60.874	20	AGAATTCAGCAACAAACTTCA	58.941	23
CGGATCGCGACCCTATACAT	62.112	20	CATGGATCCGAAACATGAAA	59.325	20
TTTAAAGCCTGCCCTTTTTG	59.359	20	AGGCACAATAGCCACGAATC	60.103	20
CAATCCCTTTAAAATAGGTAATTG	59.127	26	ACGAACTTGACACGAACACG	59.794	20
CCTATCTTTGCCATACCCGA	59.916	20	AAGAGGGATATTCGGAGGGA	59.859	20
TTACAACCAAACATGCCCCT	60.227	20	TTTGGGGCTACGTGTTCTTC	60.11	20
AGGAAGAAGATTGTGCCACG	60.255	20	AGAGAAACTGGAACCCCCAC	60.349	20
TGCCTACATCATTTACCCCA	58.843	20	GCGGTTATCACCGGATCG	62.397	18
GCCAAATCCTAGCCACACAT	59.962	20	ATAGCGCATTTTTGCCTGAT	59.71	20
GCACTATCCAATTTGCAACAA	58.69	21	GCTCGTGCTTATTTGTGGGT	60.14	20
CTCACGTTTTTAGCCCAAGC	59.883	20	GGGGTGTGTTAATGATGGGA	60.439	20
TCTTTTATGTGGGGGTGACA	58.821	20	GAATTTCCCAGTTCCAACCA	59.767	20
GTCTCCTTTGCGTGGACAAG	60.833	20	GCAAGATCCAATGGTTGTGA	59.502	20
TGGGGTGTGTGTTCTTGAAA	59.976	20	CTTGTTGACTTTGCAGGGGT	60.149	20
AGCAAAGAAATGCAGAAGGC	59.597	20	TTGCCATCCTCCTCCAATAG	60.029	20
TCTCGCATTTGTGGTTCTCA	60.39	20	CAAGCAACAAATCGAGCATC	59.425	20

TCGTTCTTTCTTGCTTCCGT	59.993	20	TGTTGATTTTGGACGATGGA	59.9	20
GCATTTTGGGTTTATGTTTGG	59.221	21	AGTTTTGAATGGCTTGGTGG	59.971	20
TCCATCGAGTCAAGCTCAAG	59.112	20	AGGGAGGTGGTTGATCAGAA	59.505	20
TTGGAAGGGGAAATGAGAAA	59.476	20	ACGGCTGTGTAGTGTGTTCG	59.819	20
ACATCCACTGGCCAAGAATC	59.934	20	AGCAAAAGCTGAGGTGTCAAA	60.045	21
CGAAAAACCAAAAACCCTCA	59.947	20	GGCACGTGGAGCAATAAGTT	60.14	20
GGCCAGTAACACAAAGGCAT	60	20	TGAAAATCACCTTCAAGCCC	60.051	20
ACCATTGTCCTGACGACTCC	59.969	20	TAGTCGGCCGATAAGTTTGG	60.089	20
TGAGAGATCAGTGAGCACGAG	59.299	21	TCCTTCGAGCTCCTCACATT	59.95	20
AGTAACCACCAATAACCGCC	58.836	20	CGTGGAATTTCATGGTTTGA	59.371	20
TGTTGATCTTATGAGTGTGAAAAC	58.734	25	GTTTCAATCATGTCCGTCCA	59.348	20
CAAAGGAACAAGGGGTTTGA	59.942	20	CCCTCCCCTCTCACTTTCTC	60.186	20
GGCGATCACTGTGCAATAAC	59.156	20	CTACCCTGCTGATGAAACCC	59.55	20
CTGGAGAATTGGGAGGCATA	60.029	20	ATCAAAATCCATCCCATCCA	59.952	20
TGGGAATTTTGTGGAGAAGC	60.051	20	ACAGCCAGCTAGTCGGTTTG	60.453	20
CATCTGAACAGTGTCAATTTTGC	59.668	23	GAACCCTCACCCCTTCAAAT	60.169	20
TCGAACCAAAGCAACACAAG	59.881	20	TGCATGTGAGTTGCACTTGA	60.029	20
GCCCTCAACTTTGTACGTGA	58.775	20	TTTTGATGCAGCAACCATAAG	58.83	21
TTGATTCGGAGGCTTGTTTT	59.685	20	CATTGATTGATTCACAGCCC	58.926	20
CCCCAAATGGAATTCAACAG	60.162	20	GAAAGTATGGCTGCTCCTCG	59.978	20
CACCCCTCGAGTTTCGTAAG	59.728	20	TTTGGGTGTTCTGTACACGG	59.46	20
CTTTGCTTTGCTGCACACTG	60.775	20	GGGTCTCGCATAAAGTGGAA	60.074	20
ACGCAGATGCCAACAAAAG	59.856	19	TGATCTTGCTTGGTTGCTTG	59.988	20
CCAGAGGATTTTGCTGCTGT	60.397	20	CACATGTGGAGAGCTTGTGC	60.473	20
TGGCTGATGTGAAATCTGGA	60.201	20	GATGTCACCATCGTTGTTCG	59.967	20
TTCACCACGTTCTACGCTCA	60.449	20	CCAACTTTGTGTTCTTGGCA	59.734	20
TCACAGGATTTAGCTGTTCTCA	57.635	22	TTGTTAAAGGTTTCGACGGG	59.968	20
CCTCTCATGTTTTCCCCAAA	59.903	20	GCCAAGACTAGAGGCTGTGAA	59.63	21
TTCTTTCACCCCTCCCATAA	59.359	20	CAACCCACTTACCGGAGCTA	60.125	20
TCCCAAAATCTCAATCCCAA	60.244	20	ATGCGCGATTTTAAACCCTA	59.586	20
CCCGTGACATGGAAACTCTT	59.966	20	CTCAGAGTTGACGGATCGCT	60.555	20
AGTAGCAGCTGTGGATTCCC	59.313	20	AGGAAGATGGAGAGACGGTG	59.254	20
GTTTTGCTGCCCACCTTTTA	60.11	20	TGCCAATGGAATAGTGATCG	59.499	20
CGAGAGTGGTGAGAATGTCG	59.415	20	CCCACACTCACATGTACAAAC	59.385	22
GGGGGAGGAATGGTAGAGAG	59.89	20	TTTTCTACCCCAGCCATCTG	60.066	20
ACTATTGTCGGACACTGGGA	58	20	CGAACATGTAGTGGTCAAACT	60.081	23
TCGCCTTTAATTCTAGCAACA	57.757	21	TGATTGAACAATGAGATCCAC	58.976	22
TCGAGAACTTGCTTGGTGACT	60.043	21	TTTTTACCTTCTCCAGGGCA	59.679	20
GGTGCACTCGGATTTTTGAT	59.939	20	ATGTCACTGCCTTGCCTCTT	59.874	20
GCAAACATATGGTGGCATTT	58.362	20	GGTCACACCGATGATGAATG	59.769	20
TCAACAATTGGAGACAACGC	59.697	20	GTTTTGCCTTAGATCCACCG	59.569	20
TCCCCCAAATTCTCTCCTCT	60.008	20	ACCCGAATTACCACCCCTAC	59.94	20
CCCATTAAAATCTTCCGAGC	58.647	20	ACACACGAACACTCACCCAA	60.047	20
CCTTGTGGGGTACAAGTGCT	60.028	20	TTCGGCTACCCGATTCATTA	60.415	20
ACTTCAAGCACTGGAATGAGA	57.528	21	TTGCCTTTTGATTTTCGGTC	60.053	20
TTCCCCAGAAATCGAACAAC	59.91	20	GCAACCAAGTTGTCAACCAGT	60.066	21
GGAACTGACGTCCTCCTGTG	60.713	20	TTGACTGAACTTCACCCATTT	57.16	21
GAACAAGGGCAACTCGAAAG	59.853	20	AAGAGCTCTCCTCCTCACGA	59.279	20
TTTGTGTGGGCATGTTCAAG	60.552	20	AGACCGGAGTAGATGACCTTC	57.321	21
TTTTGGAGCATCTCCCATTT	59.505	20	TTTTGACATCAAGATAAGGCA	57.459	22
TTCCGAAGCTCTTCAAGCTC	59.836	20	AAAAATCCAGCAGGCAAAGA	59.823	20
TCCTTCCCAACAGAGGAAAG	59.255	20	TTGTCCTCAACTGAAAGAATG	59.359	22
TTACCCTAAGGGCATCCACA	60.323	20	CCACAGCTTTCAACATCACG	60.301	20
GGCCACTAAAACAGGGATCA	59.933	20	AGATCGGAGCTGAGAAAGCA	60.24	20
GGGTTTACCTATCCCGTGCT	60.208	20	TCTCGCCATTCTCTCTCTAACC	59.983	22
CCTTTGCATAGAGTGCGACA	60.011	20	TGACCTTGAAACCCCTTGAA	60.465	20
ACTTGTCGAAGGAGACGCAT	59.874	20	AGCTTGTCGAATGCATCAAA	59.425	20
TTTGGCTCGTATGCAGTCAG	60.011	20	GTAGATCCAAGGGCCGAGAT	60.431	20

AAGAAAAATGAACATGGCCG	59.938	20	TCCATTCCGAAAATCAAAGG	59.872	20
TCGTCACCCTTATCCTACCG	59.948	20	TTGGCTCCGGGTTGTAGTAG	60.125	20
GCTTGGAACTTAGCCCACAA	60.249	20	CATCGGTTCATGTCACTTGG	59.96	20
CTCATGTACGTTACGATGGCA	59.623	21	CATTCCTCCGAAGGCATTTA	60.031	20
TGGTAGCTTGAATACACGTATGA	57.44	23	TGATAGGATACGGCCCATTC	59.745	20
TTGATATCAGAGCCACTGCG	59.972	20	TTCTAAATGGTGGCCGAAAA	60.427	20
CAAGGAGTGGAGGTCGGTAA	60.103	20	CCAACGGCTATTTACATGGG	60.202	20
TAACGCTTTTCTTTCGACCC	59.338	20	TGCATGCTATACGGCACTGT	60.31	20
TTGACGATATATAGTGTTTTGACA	58.972	27	ACTAATAGCAGGCAAAATGCG	59.42	21
AAGGAGGTGTTATGAAGGGATT	58.028	22	CCAAACTCGGATCCAATGTAC	60.242	22
TCAAGGTAAATGGGTCTAGCAAA	60.01	23	TTCTCCGATAATTAAACGGATT	59.662	25
TTTTGGGTAATTGGTGAACCT	58.34	21	CAAAATTTGGGGCAAAAA	57.057	18
GAAATCGGGTCCTCATCATC	59.296	20	TCTTAGAAGGGGCCAAAGGT	60.068	20
AAACAACCCAAGAAAAATACGG	59.307	22	ACTCCCAGAGGAAAATGGGT	59.795	20
AGGGGACTAGGGTTGAAGGA	59.928	20	TCAGAGGCACCTCATCCTCT	59.945	20
ACTGTAGAATCCGGCGAGTG	60.277	20	TCAAAATCAAGTCTTCCTCCG	59.298	21
CCTAGAAAGAGAAGAAACAGAG	59.255	24	GACCTCGCGAAAGAGACAAT	59.434	20
CACCATCAGCAGAGAAAGCA	60.136	20	GGCAAGACATGGTGTTGTTT	58.47	20
GCCCTCATATTTTGCTTTGC	59.688	20	TGTAGGGGACTCGCTTCAAC	60.255	20
GGACGCTCCAGATTGTTTCT	59.288	20	GGGTTCCAGCGTCATAAAAA	59.938	20
CCTCCAAAAATATGGGCATT	58.761	20	TGGGTGATCTGAGAGGAAAAA	59.656	21
CGTGATAAGAACACTCATGTCCA	60.045	23	CCTCATCTGTTGTAACCACTAT	59.484	25
GTACTTCTCACCATCCCCCA	59.779	20	CGGTGGAAGCTTTGTCTGTT	60.291	20
ATGGCGTACCTTGCAGAGAG	60.419	20	TCACGCTAAGGGGTGGTATC	59.955	20
CCGCCAACTTGATCACCTAT	59.955	20	TCCGTGCATGAGAGAGAGAA	59.656	20
ATGGATCCTAAACGGCTCG	60.044	19	TGCAATGTCATCCTTTTCCA	60.049	20
AACCATTGAGCAAAAACAATG	57.677	21	GCAGGTTGATCGAGGATGTT	60.081	20
AGAGCCGGGTTTAAAGCAAT	60.095	20	GAGGACACTTGGACCTGGAA	60.088	20
GTTCTTGAGCAGCTTCAGGG	60.134	20	GCTTCGTGTCTCTGTGGTCA	60.03	20
GCAAGCCCATAAAGAGCAAA	60.343	20	AATTGAGGGAAATGTCAGCG	60.074	20
TTTGACTTGCAGCCACTCTG	60.175	20	CCTTTTCTGTATTGGGGCTG	59.564	20
GGGAAGGTTTGAACCGAAGT	60.34	20	GGTGGAGGAGGGTATTAAGAT	58.847	22
TCGTGGCTTTGTTGAAACTG	59.881	20	CCTCTGGACCGACCATTTTA	59.926	20
TAAGGGAGTGCTCCCACATT	59.55	20	CGCAGAATCATGAGACACAAA	59.856	21
TTCTTTTTCCACATTTGAAGTTCT	58.422	24	GCTGCTGTGTTTGTCTTGGA	60.032	20
TCGCAGCGAAACGTGAAC	62.18	18	TTGGGTGAGAGAAAGATAGAT	57.943	23
AGCCATCAACAAATGCAATG	59.548	20	CAGCAGGCAGATCACAGGTA	60.008	20
TGAGGAAAGGAATCAGAGCG	60.474	20	TTGGTCCACCAATCTTGTGA	59.935	20
ATGGGAAGAGGGGGTATGAG	60.147	20	CCCAAAAATCTAACGACCCA	59.795	20
GTCCAAACAAACCGGCATAC	60.235	20	TGAGGAGCGTTGATCTTGTG	59.984	20
GCACACGTATTAGGACCTCCC	60.758	21	AATGATTTCAAAACCCGCTG	59.938	20
CACCCTGTGACAGATACAGCA	59.76	21	ACATAATGCCTTCCCGTGAC	59.82	20
TATTATTTGCGCATGCACCT	59.197	20	AACAATGATGGACACATGGC	59.223	20
TACCAACAATCAGCAGTGGC	59.722	20	GAAATGATTGGAGAAGGGCA	60.014	20
TGATCAGCGCAGTCCAGTAG	60.16	20	TCCTTGCACCTCCTCTTGAT	59.803	20
TGTAGAGCACTGCCAGATCAA	59.606	21	CCACTGCTGTCAGCTCAGTC	59.764	20
GGGAAAGTCGATGGTTTCAA	59.91	20	TGCACAACAATCTGCAATCTC	59.862	21
CCTTTGAGGATGGATTGATGA	59.879	21	CGCGTCCGACTCCTTAACTA	60.399	20
GGTTGAACCCTTACGTTGCT	59.101	20	TGAAGTTTGGCAAGGAAACC	60.088	20
GCCTTGCAAGCCAGTTTATT	59.365	20	TTGGTAGGCCAGAGCTTGAT	59.836	20
GGCCCTCAACGTTGGTATCT	61.268	20	ATGCAATTTTTGTGGGCAAT	60.196	20
TTGCATGCATAACCCACAAT	59.816	20	TCAGCATGATATTGCGGAGA	60.329	20
AGGCTTGAGTTTCCTCACGA	59.989	20	CCAACAAATTCCAATGAAAGG	59.302	21
TCCAAAAACACCCCAATTTC	59.64	20	TCTGGCTTTGATTTTGGTCC	60.051	20
CCGAAAAAGGGTATTGGGTT	60.048	20	ATCGCCTGTTTTTACTTGCG	60.264	20
TCCTCCGCAGTTAATTTTGC	60.209	20	TATGTCGAGGAGGACGCTCT	59.973	20
GCAACAGTTGTGGTTGATGG	60.008	20	TGGCTTGAGTGAAGTTGCAG	60.175	20
TCGAAGCTTTGCTACTGGCT	60.292	20	CAGCAATGGAACCAAATTGA	59.518	20

CAAGATAACCCTTCGATTTAGGA	59.875	24	CGTTCAAATAAGTCTCGGGC	59.708	20
GCCCAATAACCTTCCTTGGT	60.187	20	TGGGAACATTATGATGGGAAA	60.002	21
CGTAAGGCCTACTCGAGCC	59.985	19	ACCATGTACTGGACTGGCGT	60.453	20
TTGGTGGCGGTAGGTAACTC	59.993	20	CACCGGGTACTGAGGGATTA	59.807	20
GTACGACATTGTTTGCGCTC	59.351	20	CACGTGTAATTAATTCGGTTAC	60.057	24
CCTTTGCCCCTTTTCTCTCT	59.821	20	GGGAATTGGCCCAAATAAGT	60.02	20
GGAAGTTTTCCCACACTTGG	59.425	20	CATCAGTCTACAGCCAGGCA	60.008	20
TGAAATTCACTTGATCCGCA	60.197	20	GAAAGATGAACCGGAAAGCA	60.192	20
TCGAAATATCGGGGCATTAC	59.757	20	ACTTTTGATGCCGAAGTACAA	57.439	21
TTCCTTGGACCAAAATAGCCT	59.952	21	ACACATGTCGCCTTCTGGTT	60.577	20
TGTGGTAACCGATTGGGATT	60.051	20	CGAGGAATTTGAAGAACACTT	58.88	22
TCAAAGCGATGGAACATAACA	59.172	21	TAAGCCCTGAACCTGTGACC	60.111	20
TGAGAGAGGACCGATTGGAG	60.34	20	TTGAACTCACGATCTCACGC	59.992	20
GCTGATGTGGGAAAATCTGG	60.461	20	GCATAAATTGTGTTCCCCGA	60.701	20
GGATTCCCCCTCGAAGTTT	60.257	19	GTTGGGAATGAGCCCAATAA	59.762	20
AGGGGGTTATCACTGGATCG	61.095	20	CACTCGAAGGGAGGAAACAA	60.224	20
AACCTTCAATTTTATAACCGAAAC	59.299	25	ATGGGAAGAGGGGGTATGAG	60.147	20
AAGGAGGTGTTATGATGGGATT	58.714	22	GAGTGTGTCGGGAGTGAGGT	60.161	20
CTCTTTCCAATCTGGCCTTG	59.807	20	ACAGGGTCAAATCGAGATGC	60.081	20
AGAGAGAGAGAAACGCGAGG	58.917	20	AGAGGAAGAAAGAAGGGGCA	60.319	20
AAGGTTTCAGCGAACCAGAA	59.853	20	GAATGCTGCTGTTGTGCATT	59.878	20
GCGTCGAGTACCACTTTTCC	59.74	20	GCTTGGAGCATCACAAAGGT	60.263	20
TTTTCTCTGGATCACACCCC	59.903	20	AATGAAAGGGACACGTGGAA	60.353	20
GCGTGGCTCAAGATATCAGC	60.915	20	GGAATGGTGTGGGGAATATG	59.871	20
TGCAAAAGTTTTTGTTGGGT	58.174	20	GCCCGTAAAAGAAGTCGTTG	59.747	20
TCTCTCTCCCACTCTTCCCA	59.913	20	TCACCATCACTGACTCTGCC	59.827	20
AATCCAAGCGTTTGCTGTTT	59.752	20	GGCCCCTCTACTCCTGTGAT	60.477	20
CTCTCCATTCTCTCGCTGCT	59.851	20	ACGAACCACCACCACTGTTT	60.321	20
CCTCCTTTAACCAAAAATCCG	59.825	21	CATGATTGATTAATTCGTTTGTT	60.03	26
GATTGAACTCCGAAAAGGCA	60.192	20	TCCATGAAGGAAAAAGTCGG	60.044	20
GTGGCGGTCAACAGAAAACT	60.156	20	CTCCATTTCTTCTTCCTGCG	59.948	20
GGCCAATTTTGAAGCAGAAA	60.188	20	AGCTGGCTCAACTACTCCCA	60.012	20
GGGAACTGTGCCCAAAGATA	59.933	20	CCTAGCTCTTGCCCCTTTCT	59.976	20
TGGACTGCTGTTCAGAGACG	60.178	20	CGCTCCTCGAGTTTCGTAAG	60.147	20
TCTGTAGGTCTGTGCCCACTT	59.777	21	TGTAAAGTGAACAATGGAAGC	59.677	23
CTGCAGATCTAAGGGCCAAG	59.971	20	TCTTCGGTATGCTGACGATG	59.823	20
AAGCAGCGACCAAATCAATC	60.221	20	CCAATTTGAATGGTTATCACCT	60.457	23
TAGGTTTTAGGTTTGGGGGC	60.177	20	ACAGTGGCGAATGTATGCAA	60.142	20
TGCAAGTTCAGACAAACCCA	60.278	20	AGTTTTCGTTGTTTCCAGCC	59.218	20
TGGTTCAACCTCCCAGATTC	59.903	20	TCTGCTTAGCTTTTGGACGTT	59.167	21
CCAAAGAACTGATTTCCTCACC	59.976	22	GTGAAGTGGGGTAGAAGGCA	60.111	20
TCATATCCAGAAATCCCCCA	60.088	20	AACATGCACACAAGCACACA	59.785	20
GCATCACCTCAACCCTTGAT	59.934	20	TATATCGTGGCACCATTGCT	59.019	20
AAGTTGCACAATCCTAATGATTTA	57.046	24	ATGTTTGCATTGCAGTTGGA	60.119	20
TGATGGCTGACTCACAGCTT	59.577	20	GCTTCAGCAAGGAAGATGCT	59.723	20
GGTGCCAATTGAATGGAGTC	60.326	20	GAAACCCGTGAACTAAACGC	59.615	20
TTGTGGGGAAATGATCCAAT	59.991	20	TGTGAACCTTTTTCAGCCGT	60.668	20
CGTGGTTCGATCGTAAATGA	59.542	20	TCCAACGTTGTAACACACACA	59.435	22
TCTCCTTCCTTCTTTCGTGG	59.401	20	TGAAGCACAACACCAAGCTC	60.032	20
ATAACCATACCCACACCCCC	60.558	20	TGGAATGTGTGGGAAAATGA	59.75	20
GCTGCTGTAGTCGGAAGTTG	58.677	20	GGCAACTTTTGATTCTTCTCG	58.962	21
GAGTCCTACGCTGATCTCGG	59.973	20	CCCAATAACTCGCAATAGTTTG	58.698	22
TGACCATAATGCCCCTATCA	58.794	20	CACAATATTTGAGGGTTATCAT	58.787	25
CCCACGACATCAACTGGATA	59.369	20	TTCCAATAACTCACAAAACTTT	58.364	26
CAAACCTAACTGAAATAGGAATG	59.802	25	CAAAATCAGCAATCGGACAA	59.664	20
GGAAATTGATGGATTTGGGA	59.558	20	GCACTGAGGCAGAGTACACG	59.648	20
TCAAACTTGCCAATCCAAAA	59.133	20	TTATCCCTCGACTTTCCCCT	59.897	20
AAATAAGGATGTGTTATGAAGGG	58.049	24	TGTTCCCAATTAAATAAATGTT	57.601	24

TCCACCCGAATTGGATAATG	60.523	20	AAAGAAGGACCTCCCGTGAA	60.988	20
ATGTGTCGGCCTGAATATGG	60.744	20	ATGCTCTGGTTTTTGCTGGT	59.74	20
AACGTCATTTTATCCGCGTT	59.479	20	TTGATGGTGGTGGATATTGG	59.049	20
TGGTGGGTTGAATGCTATGA	59.924	20	TCAGTTTCGAGTTTTGAAGTTA	59.033	24
TCACAAGCTTGAAAGCAACAA	59.641	21	GAACTGGTGGCAACTGGATT	59.973	20
ACGCACTCTCAAGCACACAC	60.104	20	GATAGGGCCGAAAACAACAA	59.938	20
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CTAGCCTTTGCCCCTTTTCT	59.85	20	GTTTGGAGAACAGGTAGCGG	59.734	20
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TGATTTAACTTGCATTCTTTTTCA	58.072	24	GCCCACCATTTATCTAAACCTG	59.737	22
GAAGAAGGCGAAGTGGCTTA	59.592	20	TTTCATTTCCACCTTCCACC	59.767	20
CTAGCTCCTTCCCCTTCACC	60.204	20	CGACATTAAACACACGGTCG	60.027	20
ACAAAGTGGTGAGCATTCCC	59.973	20	AACCCACACATGCAAGACAA	60.008	20
AGACCAAAAGGTCACGGGTT	60.776	20	GATCATGAACCTCCAGGGAA	59.862	20
CCCAAGATTTCCCATAAGCA	59.894	20	CCAACACCTACACCAGGACA	59.435	20
TTGACGATATATAGTGTTTTGACA	58.972	27	AACGATTCGATCCTGTGAGC	60.226	20
CAGATTTTAGGATTTCAGCTCAC	57.228	23	CCCAAATTCAGGCTGTTCAT	59.933	20
CTCGGTCCGGATCTTTCAT	60.019	19	GTTCCAATCCTCCCCGTATC	60.526	20
TTGAAGATATGCTACCCGGC	60.06	20	GACTTGATGCATGCTGCTGT	60.024	20
AACCCCTGTGACCATCTGTC	59.817	20	CAAAATGAAGGCAATGAGCA	59.809	20
TTGGAAATCAAGTAGAACTGAAA	57.228	24	AAGCTATCCGCTGAAAAGCA	60.117	20
GCCAAACGCCAAAGAAAAAT	61.298	20	TGTCCACGGCTCCTAAAAGT	59.734	20
CGAAATAGTTGGACATCGGC	60.469	20	TGGAACAACACTTCAACAACG	59.643	21
AAAATTTGTTTCCCACCAAATAA	58.744	23	TGCTAGAGGGTTTTGTTAATAT	57.964	25
TCTGACGTCTTGTGGGAGTG	59.864	20	TTGGTGGGAGATTGCTAGAG	57.894	20
CGAATCGAGTATTGCTTCGC	60.876	20	TGTTTAATCAGGTAGAAAGTTG	58.854	25
GAATTGCTCACTCCTGCACA	59.992	20	ATGCGGCGCCTTTTTAAT	60.557	18
GGATTTGACTGGTTGGGAGA	59.903	20	TTCTTCCCCAATCCTCCTCT	60.008	20
GTGTAGATCGCCATGGTGTG	59.992	20	GAATGCTTGGATGGGAAGAA	60.014	20
CTCCTTTCCCCTCCAAGTTC	60.045	20	TTTCCCAAGGATCAGACGAC	60.05	20
CACCCTCAACAAAAGGTCGT	60.005	20	CTTGCTCGTTTTATCCCTCG	59.839	20
CAAAGGCCCACAATGGTTAT	59.685	20	TCCTGACGAGCAAGGATAGC	60.504	20
ACGAATCTTTTCGTGGAGCA	60.776	20	TTGGACACATAGTTCATGCCT	58.09	21
TATTTGTCCGGTTCACCCAT	60.051	20	AATTAGGCTTGTTGCGAACG	60.264	20
TCTAATTACACATACACGTGGGC	58.958	23	TCCCGAACTCTTTCAGCACT	59.989	20
AGGCTAGGCTGGATAAGTTTCA	59.415	22	CATCTTCTCATCTCAACTCCCA	59.284	22
GCCATAATTCCTTTCAAATTGC	59.822	22	AGTGGCGTCTACGGAATTGT	59.621	20
CCCATGCATCCATATGAGAGA	60.838	21	GAATTCGTTTGATCGGGAAA	59.878	20
AACATTGTTCTCCCCCACAA	60.21	20	ATGTTGAAGAAGCACAGGCA	59.445	20
CGAACGCTCCAAATTAGGTC	59.708	20	TGCAAATTAAATCAACGGGG	60.671	20
GACGTTAACAGAGGGGTGGA	59.966	20	CCGGCATCATCTGCTTTTAT	60.06	20
GTACTCTCATGCGCTCAGCA	60.319	20	CCCGAATTCGATACAACAAAC	59.329	21
TGCTTTTGACGGAGTGTGAG	60.025	20	TTTTGAGGGAAAGTTGTGGA	58.173	20
AATTAAATGAATGGGTGGCG	59.66	20	TTTTGTGGACGGTGAAATGA	59.941	20
GCAAGGCAATATCCTTGTGA	58.723	20	GATCGTGAATGATCTACGTCC	59.962	22
GTCACGGGTTCGAGTTTCAA	61.075	20	AATTCCCCATGACCCACAT	59.854	19
CTAATGGCGAAGTGGATCGT	60.096	20	ATGGAAGAACACCCCATACG	59.67	20
CATTTTACCGGCATGGTGTT	60.617	20	TCCACCTTCCTCACTTCACC	60.088	20
AACCCACATGCAAGTTTCGT	60.419	20	TTGGCTGATTGAATTTATGGA	58.096	21
TCCATCTCCACGTACGACTG	59.701	20	ATCGATTACTCCCGCCTTTT	59.93	20
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TTTGTCGATTCAGTTTCCCC	59.91	20	GAAGTGAGGATCGTGGAAGG	59.655	20
TGAATTCGGTCAAGCATCTG	59.799	20	TTCTGCACACGAGCTCAATC	60.144	20
TGGTGTTGGGAAGAATCACA	59.935	20	CACAGCAAGCTGAAACCAAA	60.027	20
TGCCTTTCGTCACAAACATC	59.697	20	AAAGCAATGGCGGATACAAG	60.096	20
AGAAATTCAAACCCGGAACC	60.166	20	GCCCTTGTGGATTGATTCAT	59.756	20
TTCTGCCTATCAGGTCGTCA	59.394	20	GTTTGGGCTTTTAGCCTTCA	59.338	20

TCATTTTACTTTTGGGGCGA	60.427	20	GGGATTTATTTTGGGGGTACA	59.774	21
GCAATGATGGCTTTGGATTT	59.907	20	CCATCTTCCGTTGTCGATTT	59.933	20
TGCGTTTTGACGATATATAGTGTT	59.092	25	TGAAGTTTGATTTCCCAGCA	59.247	20
TGGCTTTGCACATAATTTCG	59.702	20	TGGAAGAAAAGGTTGCTGCT	59.993	20
TCTTCTCTCTCCCCGTTCAA	59.92	20	GCGGTCCAGATCTGCTACTCT	60.938	21
CACCCCACTTCCTTTCTTGA	60.081	20	TCTTCTTCCTCCCTGGGATT	60.008	20
GACATGGGCACCTTATTGGT	59.676	20	TGTTTGGTTATGGAGTGCCA	59.964	20
ACATGAGCAGCATCGAAATG	59.83	20	ATTCTTCAATCAAGGCGTGG	60.074	20
AAGGAGGTGTTATGAAGGGATT	58.028	22	AAGGCTCTGCATGCTCTTTT	59.222	20
ATGAATGGCCCATATTGGTT	58.977	20	GGGGGAAATGGTCTTTCAAT	59.996	20
TTTACGATTTCGATAGCCCG	60.054	20	AAAATGGTTATTACTGGAACG	57.304	22
TTGGGGTTACCTCGAATCAA	60.301	20	TATGTGTGATTTTGGCTGGG	59.395	20
AGAGTAGCACGACCCGAAGA	60.012	20	AACCACAGGATCGAAAAATGA	59.42	21
TGAGATAAGGGGGTGTTTGC	59.933	20	CGATAAGGGCCTAGAAAAACA	59.64	22
TGGTCTACTTCTATGGCGGG	60.088	20	CTTTTGTGAGGACTGAGGGC	59.844	20
TTTGGTTTGCTTGGGATTGT	60.344	20	TGGGTTTGATTCCCAAATGT	60.029	20
TCCCTTTGATTCCCTTCTCA	59.6	20	GCTGCGACTTTCAACCAAAT	60.257	20
GGCTACCCCTCTCGCTCTAC	60.37	20	CAGCTTCGATTTAGGGTTCG	59.839	20
GCTGATGTCGATTTTCCAGAT	59.143	21	CGCTTCCGGAGTGGATAATA	60.053	20
AATTACAATGTTTTTCCAATCCC	58.246	23	ATAGCGGACACTTGGACCTG	60.134	20
CGCATCAAGTTCCCTCATCT	60.218	20	TCTTTCCGATAGGTGTTGGG	59.926	20
TCCCGTATACCTCCAATTTACA	58.385	22	TCGGTCAAATTCAAACTCGT	58.201	20
TCACATGTGGCGTCTTTTTC	59.697	20	TTGTTGTTGGGTTGTTGGTG	60.292	20
CTGTGGTGGAAGGGTTGTCT	60.002	20	AGGTCTAGGCCCCTCAAATC	59.536	20
AACAACTATCTCCAGCCCCA	59.55	20	AATCGAACTCTTGCGTTGCT	60.022	20
AGCTCTGGACTCTGCGTTTC	59.751	20	ACGTAATTTGGCGGTCTCAG	60.132	20
CAAAGAAACTTGGGACGGAG	59.705	20	CAAGACATGCGAATTGATGG	60.073	20
AATTCTTCCTCCGGAACACC	60.306	20	GCCTTCAACCAGACCACATT	59.973	20
CTTCACGGGGTTGTCCTTTA	59.964	20	ACTTTGGCGTTGCTTGTTTC	60.292	20
AATCCGTGAACCATTCCATC	59.611	20	CTTTTCACACGAGGTCACGA	59.873	20
CCTAGGAGGTTCTCGCATTG	59.83	20	TGCAATCCAGTGAAAACTCTG	58.912	21
GGTTTGGTTTGATTTGTTTGG	59.211	21	TCATGTTGCATATTATTTGGCA	59.256	23
GGCGAGAGCTATGTGGAGAC	59.981	20	ATTTCCCACCAAACAGCAAA	60.344	20
CAAGATAAGGGAGCTGGCAC	59.836	20	GGCACACATCTGTGACATCC	59.97	20
TTGAGATTGCGAATTCAACG	59.809	20	CGTGCTCACCATGAAACCTA	59.716	20
GGGTTGGATCAACCACATTT	59.508	20	AGTTGGCACCAGATCACTCC	60.12	20
CATCCACACAAGCACACACA	60.209	20	TCGTCACTATCTCGTCGTGG	59.855	20
TGCACGTAGGCATGTTCAAT	60.142	20	AGCGGTTATTACCGGATCG	59.93	19
CCAACTCAGTGTGTGAGTGGTT	60.111	22	CCCTTTATCAACTTCGGCAA	60.067	20
AGGATCGAATGAACAAACACG	59.985	21	CAAGGCTTGAAGCTGGTAGG	60.008	20
TGTTCTGCCTGTTCTGCTTG	60.175	20	AACAACGGTATCACCTGAACG	59.906	21
GGTTATTAGTTATTACGGATTTAA	58.826	27	TTCGCGTGTCAGAGTTTTTG	60.027	20
TAGGCAATGGAATACCTCCG	59.916	20	CACGGTTAGGCTCGAGAGAG	60.149	20
CAATAAATTGGGGTCGGCTA	59.789	20	TGTGAAGGTTGAGTTGGCAG	59.873	20
GACTAGAGTTGGTTTCTTAAATGA	57.439	27	TGCGAACTTGGGTACACTTG	59.758	20
AAGAAAATGGGCAGAAACGA	59.685	20	CGGCTGGGTACCAACTACAC	60.431	20
TCATATATAAACGCCGGGGA	60.13	20	GTGAAGGATGGATGCAGGAT	59.893	20
CGAAAACATTTACATACGATGCC	60.593	23	GAATCGGTGAACAGTTCGGT	59.973	20
AAAAACGAGCATTTTAGGGTTA	57.155	22	CACCAAATTTCATCATTTTTAA	58.865	26
GTGAAACCAGACGACTGCAA	59.88	20	TTTCTGTTCCCGATCTGAGC	60.34	20
TAGGTGTCGGATTTGGGAGA	60.452	20	TGGGAGAATCGAGATTTGTTTT	59.945	22
AAGGTCCGCCTCTTCCTTTA	60.2	20	AAATTTGAGGGGGTTCATCC	59.996	20
TAATTGAATGAACCTGCCCC	59.762	20	AGTCCCTTTTTGTTGCCTGA	59.711	20
GGCTTCTAAGCTGCCGATAA	59.592	20	CATGAAGCGCTGATTGTTGT	59.871	20
CTTGTGGAATGAAAGGGTGG	60.345	20	TGCATGCAAAACTGAGCTTC	60.142	20
GGAGGTGAAGATTGGGTGAA	59.903	20	ACGCTAACTTCCAAAATGCC	59.229	20
TCCTTCCTTGCTCCTTTTCC	60.683	20	CCGTGTGCATCACTACTTTGA	59.773	21
AGCGCTTTTTGCCTGATATT	58.992	20	GCACCAAATAATTCGACTTGC	59.605	21

ACCGCTTACATTCCGATTTG	59.96	20	CTTAGCGAGCTTCAGGCATT	59.752	20
AGCAATACTGTTTCCACCGC	60.14	20	GCATTGATGGGATTCCACTT	59.756	20
TTCAGCACTCCATCAGCAAG	60.136	20	ACCTTCCATTTTCTCTGCGA	59.813	20
TGGCCAAAACATCAACTCAA	60.088	20	TACCAGTTCAAAAGGGTGGG	59.824	20
GAGGTCTTTTGATCCCCACA	59.903	20	GGGTTTGGAGGGGTATCCTA	60.011	20
GGTGACGATGGTGATTGATG	59.769	20	TGCATGCAAACTAAGCTCCA	60.545	20
GTAGTGAGTAGTTCCGCCCG	59.757	20	GATTTGCGTGGTCCATTGAT	60.733	20
GTGACTTTTTCTGGGACGGA	60.088	20	TCAGCCTCCATCAATTATCAAA	59.547	22
ATAGGGATCGGTGACAAAGG	58.861	20	AGGGGTGACTTCATGGAATG	59.779	20
GATGCAGCTTGGTCTCCTTC	59.957	20	GAGACAGGCCTGGAAAAGAA	59.405	20
CAGCACCAGAATTGCTCCTA	59.024	20	CATGCTGCCGGAAGTAATTT	60.096	20
TTGTCCAAATAATTCATCACCAA	59.221	23	TGGACATATGGAGGGAAGGA	60.272	20
CAACTCTTCGCCATCTGGTT	60.255	20	TCCCTCTTGAGTGAGCTTTGA	60.119	21
GGGACTGCACAATATGCCTC	60.492	20	GCATTTTGGGTACACCTGCT	60	20
TTGCTGCCACTACCTGTGAA	60.449	20	ACAACAAGAACCAGGCATCA	59.139	20
ATGGGCTGTCTCTTGGATCA	60.622	20	ATGGACTCCGAGGATGATGA	60.439	20
TTCCATCCGAAATCCGAATA	60.225	20	AGGGTTTCAAGAATCCACCC	60.169	20
TTATACAAATGGGCGCATCA	59.92	20	TTTTTGACGATTTTGCCCTC	60.053	20
CCTGCATTTTCGCAATCATA	59.662	20	CCGACCTCGGTAAATGCTTA	60.089	20
CCTTTTCACAACTGGCATCA	59.691	20	GCATTGTGATGTTGTTTGCC	59.979	20
TTGGTTACGGGAATTGCATA	58.887	20	TCCAATCGAAGATTCGGAAC	60.014	20
AAATTCAATGACAATTGGAGGAA	59.708	23	TTTGTTAGAGATCTTGACGGGA	58.834	22
TGGCATTAAATATTAGCCCCC	60.018	21	TGTGTATGAGAGCCGCAAAA	60.401	20
GCCAATAATTTTTAGCAAGCAA	58.513	22	AGCTCTTGCAACTCCTTTGG	59.615	20
AGGGACGAAGACCTTTGGTT	59.972	20	CTGGCACATCTGCAGTTCAT	59.862	20
CATGATCCCGTGAGATACCA	59.322	20	AGCTGTGGGAGATGGAGTGT	59.713	20
CACCACCATCACCTTCCTCT	59.962	20	GTGGATGGTCCTCAGCTGTT	60.12	20
AAGGTATGTCAATTTGCCGC	59.967	20	TGTGGAAATTATGGTTCGCC	60.701	20
CGAATATGCAATCACCAAAGAA	59.964	22	CGAGAGGAAGAGAAAAATGG	60.186	21
CACGAGATTTACGTGGTTCG	59.195	20	GGCTTCTCTTGCCCTCTCAT	60.873	20
CTGCATGCACCTGATTACAA	58.288	20	GCGTTCACACCTTCAGCATA	59.871	20
TCACCTTCACTTCCTGCTCA	59.545	20	CGCCCTCAGATATGTCTCCA	61.168	20
CATTTGTTGTCGTTTTCTTGGA	60.011	22	CCCCATTAGCTTCATCCTCA	60.029	20
ACACACACCGTGGACGTAGA	60.072	20	CTTCAAATTTTGTGCCCCAT	59.801	20
CGTTAGACCTGTGGAGGGAA	60.103	20	CAATACAACTGCCGAGCTGA	60.011	20
AAAGTGCACAGAAAAATGACTTT	59.744	24	TCCGATTTTAAACCCGAAAA	59.407	20
CCAGCTCCTCTTACACTCGC	60.156	20	GCAACCAGGTACTCATTGGC	60.526	20
AAAAGTGAAGCCCACACACC	60.012	20	AAACCCCAACGGACAGATTT	60.59	20
ACAAACACGGAGATTTCAACAA	59.517	22	TTCCACCTGATCCTGGTTTC	59.903	20
GCGCTGTAGATCTAACGGATG	59.881	21	ATTGCATCCACGGCTTACAT	60.361	20
ATTTGGGTGTAGAGAGGGGG	60.183	20	ACTTGGTACGCAGTTGGGAG	60.171	20
CGCCAACAAAAATCTCCACT	60.11	20	GATAAAACAGGGGAAAGGGC	59.777	20
TTGTTGAAGGGTGGTTGTGA	59.976	20	GGGCATTTGTATACCCGTTG	60.074	20
GTTGCTTAGGGTCTGTTGGC	59.74	20	GAAAGTATGGCTGCTCCTCG	59.978	20
TTGCTTAGGGTCTGTTTGGC	60.249	20	TGCTCCTCGTGCCTAATCTT	59.978	20
ATTTTTACCCCAAGTCCCCA	60.403	20	TCGACGATCACAATTTGTCC	59.502	20
TCGTTTGGCACGTTTTGTAG	59.769	20	CCCAAATTTTGACCATTTCC	59.111	20
CCTTGATTTCAACTGTCTCCG	59.72	21	AAAACACATATGGTGACACGG	58.269	21
TTAAAACCGACACCCACTCC	59.83	20	TCGGTGGCTGGAGAAAGTAG	60.388	20
AGTTTCGATAGTTTTCATTTCATTT	57.978	26	CCCATAACTCCAAACCCAAA	59.657	20
CAAGCGATGTGTGGTGAAAC	60.16	20	TCACATGGAAACATGTGGCT	59.967	20
AGATGCAACATAGGGGAAGC	59.154	20	GGAATTTAATTTCTGGCCCC	59.621	20
GAAAGCATCGTTTTTGGCTC	59.829	20	CCAAAAAGCTGGGTGAACTC	59.711	20
ACAATATGGTGTTGGGTATTAAGA	57.055	25	TCTTAAAAGGGAGGGGCTAAT	58.295	21
TCAGTTTTTGAGTTATGACGTTTGT	59.192	25	CGGTTTAGGTATTTTGATGTTTT	58.937	24
GAAATATGCATTTGTCGTCACC	59.347	22	TTATTTTGCAATTTTCCCGC	59.913	20
CACAATTCAAAAATGAGTGAACC	58.528	23	TGGTTACAAGCAGTGGCGTA	60.316	20
TCTCTACACATAGAGACCAATTTT	58.467	26	ACATGGATTGTGCATTCGAC	59.379	20

CACGGACGGGAAGAGATAAA	60.066	20	AGGGGAGTGATCTCATGTGG	59.92	20
CTGCCTCTTTCCACACCATT	60.111	20	AGTAGCCGAGAAGGGTGGTT	60.132	20
GCGACAATAACTGTCTGCGA	60.019	20	TGCAGCAATTCAGTTCAGATG	60.003	21
GCCTCCATAACGAGCTCATAG	58.965	21	CCAATCCCACGATTTTTGAA	60.671	20
AGGTGAGGGGTGCATGTTAG	59.989	20	GTATGTGTGGCTGTGGATGC	59.999	20
GCACAACGGCTATCTGGTTT	60.14	20	CCTATGGTGGTATGGTGTGGA	60.501	21
TGGCTCATTCATGACCAAAA	60.049	20	TCACCACCTTCACTGTCGTC	59.712	20
CTACTTGCGTGCTGGAACTG	59.658	20	TCTTTTCGTTGGCGATTTCT	59.823	20
GGCCATTCAAATTTCAAATCA	59.765	21	TGGTACCTCCTCCTAATTTCC	57.165	21
TTGTCTATTCCTCCGATGGC	60.036	20	ATGATGGGAAGGGTGGGTAT	60.272	20
CAAAGGATCGAAAGGGTGAG	59.665	20	AGCGAATGTTGTGAGAAGCA	59.596	20
CCATCTTGATGCAGGTGACA	60.688	20	ACTCGACACAAATCTGCACAA	59.354	21
CGGTGGAAATGGCTGAGTAT	59.955	20	CGGTTTTCGGTTTTCACAAT	59.839	20
CGATCCCAATCCCCTATTCT	60.11	20	AGGGCTACAACTCTCAGCCA	60.012	20
AATTCAAGCATTTTCCGCTG	60.209	20	ACCCGAAGCTACGTAAGCAA	59.904	20
GCTGTCCACCATCTCCTCTC	59.799	20	GCTTGAGTGCGTGTGTGAGT	60.104	20
CCATAGTCCAAGATGTGGTGC	60.39	21	ATTGGGAAGGGAATGTGTCA	60.173	20
TGGATGGATGGATTAGCAGA	59.027	20	CTAAACGACACCAGTGGCAG	59.36	20
CCTCACCTTCTCCTCTTCCC	60.186	20	TGCGGAAATTATGCCATTAAG	59.941	21
ATGGGAAGAGGGGGTATGAG	60.147	20	TTTCTTTGGACGAAAATGGC	60.053	20
TTTTAAAAGGATTTATGGCATGAT	58.122	24	CATTTCAGGCAGTGGCATTA	59.688	20
GGAAGAATGGACCCTAATTCAA	59.311	22	AACATTTTCGGTTCATTGGG	59.662	20
CGCTTTCACCAGAATCTTCC	59.813	20	CCATTTTCCCTCCTCCATCT	60.264	20
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CGCCAATTAATCATAGCCGT	59.95	20	AGCATGAAATCTGGAGCGTT	59.843	20
AGGCCATGTGTTCGAGTTTC	60.119	20	CCATTTCCTTTTTCGATTCC	58.483	20
AAGGGTTATCACCTGATTTTCTC	57.73	23	GGTGTATGTAGGTCCGCCAC	60.263	20
GATGGTGGACAAGAGAGGGA	60.048	20	GAATTGACGGCCCTAAACAA	59.938	20
GAAGTGTTATGCGTTTTGACAAT	58.249	23	CTATTGTTTCCTCCGCCTTG	59.702	20
ACTGTCGGCAGAAAAGCAAG	60.571	20	TGTGAATCAAGTACCCCGAA	58.973	20
AAGAAAGGGGGAAACAACTGA	59.963	21	TCGAACCTGCCCTCATTATC	60.036	20
AGTGTGTGTTTGTGCGTGTG	59.234	20	CCACCAATCACCTCCTTCTC	59.505	20
GGTCTTCCCCTTACCAAACC	59.668	20	GGTGAGAGGAGCAGGAGTTTT	59.87	21
TCCGACCGGTTTTTAAATCA	60.294	20	AGTCGGATGCACGCTACTGT	60.886	20
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AACAACACAAAACCCTACAGCA	59.58	22	CAGCATTACAGCCGTGAGAA	60.011	20
CCAAATTTCACGTAGACCCAA	59.847	21	ATGCAACTGACCTTCGTTCC	60.119	20
TGCAGGGTATGCATGTTTGT	59.995	20	GCAAATAGGCTTGTGGCTTC	59.851	20
ACTCCCTATCCAACTGCGAA	59.694	20	CGTGTTTTTCCCCCTTTTTC	60.674	20
TGTGGCTTCTGCTGTTATGG	59.864	20	TGTGTATCCATTGTCACGGG	60.24	20
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ATCGCCTTTACTCCATTCCA	59.528	20	TCCACAACCAGGGGTAGAAC	59.82	20
TTCGTGGAAGGGAGAGATTG	60.187	20	CCTCGACGTTTTCCTTCTTG	59.846	20
AAGGCCCTTGGATTTGAGAT	59.903	20	ATTTGTCTGCATACGGGCTC	60.103	20
TTGTCCGTCAATATTAGGGATTT	58.809	23	TTGGATGTTCCAAATACAGGC	59.815	21
CGCCCCAAGATTTGATAATG	60.281	20	TGTTGGACGAAAATGTCCCT	60.353	20
TCACACAACTCTGCGTCTCC	60.03	20	ATCCCATTTCCCTCCTTGAC	60.133	20
ACCAATGCACATTTCCTGCT	60.526	20	GGATTTTCTGAATTGTGGGTG	59.278	21
GATTTCCAGGCATGAGGTGT	59.934	20	CATGCAACAAAACCACCTTC	59.024	20
TGCTTTCGGGAAAAGCATAA	60.691	20	AGACCGAGGCTAGCAAGAAA	59.218	20
TCAAAGCTCCACAAGCTCCT	60.134	20	ATGCATCCGTTAGATCAGGG	59.917	20
TCCCACCTCCATCTCATCTC	60.008	20	TCCAGCTGACGAGCATACTG	60.16	20
TTAGACCAATCCCAGATCCC	58.787	20	TCTGAATCTGATTGCGTTGC	59.955	20
TGGGAATTGGGTTTTGAATG	60.535	20	CCGAGGACACATAAGCCTCA	61.196	20
TGTCGTAGCATTTTTGTATGTTTT	57.909	24	TCCATTCCGAAAATCGAAAG	60.009	20
TGACGCCTAGAATCATCGAA	59.375	20	GTAGGGTTTAAAATCGCGCA	60.095	20
TGCATTGGCAAAGAAAGATG	59.809	20	TCCGGTGAAACATTGACAAA	59.941	20
GTGCAACGCACGTGTAAAAT	59.662	20	GATTAAAGTTCTTAAGTCCTGG	59.716	24

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CAGCCGTTTGTCCGATTTAT	59.96	20	GGCACCAATTCTCATAATACAC	58.891	23
GGAAAAAGAAGATTGCACCTG	58.823	21	TGGTCGCCGTGTCTGTAATA	60.134	20
TCATGGGAAAACATGACAACA	59.808	21	CGACAGGTGGGAGAGTCATT	60.112	20
ATGCAAGGCATGTGCAATTA	60.103	20	CACCGTTGTCTTTAAGCCGT	60.168	20
GGGATTTTAGAGAGTATTGTGACC	59.919	25	ATACGGATCTCTGCCTCTCG	59.41	20
CCCCCTTTCTCTCCCTACAC	59.928	20	GAGGTTTGCTTTTGGTTGGA	60.088	20
GGCCCACTTCTTGGTAAACA	59.971	20	GTGAAATCCCATCCACAACC	60.034	20
TCGACTTTAACCGTGGGTTC	59.971	20	AAACACGAGCAAAACGACAA	59.366	20
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GGGTTGACATGGCTTCGTAT	59.82	20	GAAATAAGGAGGTGTTATGAA	59.323	24
TCCCATTTCTGTGTTCTTCG	58.695	20	GATGTTTTCCGGCTCAGTGT	60.119	20
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CCACCCTACATAAAGCGGAA	59.953	20	CATCAGATCCATACTCGGCA	59.629	20
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GCATGTATGCATATCCCTGG	58.823	20	TGGGTATGTGATGTGGATGA	58.095	20
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AGCAATCAGCTCCTGCAAAT	59.985	20	CAAGCACGCCTCTCTTCTTC	60.277	20
TACCAATCGGCAGAAGTTTG	58.771	20	GGTTGTTTCATGACATTTGAGG	59.336	22
CGAATGAGCTCGATTTGGTT	60.214	20	GCGAAGCACGTTTCAGTTCT	60.581	20
ACACGGGAGACATTGCCATA	61.329	20	CCGTTGCAAGAGTAATGGCT	60.27	20
TTTAACCGAACGAAAATGCC	59.943	20	ATCAGCAGGCGAGGTGTTAC	60.285	20
AGATCCGACTGCCATGAAAC	60.081	20	TTGATTAGTTCGTGCAACGC	59.879	20
TATGAATTTTGGCCCTTGGA	60.26	20	GCCATATTCACCTCCACCAT	59.635	20
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AACAATGTTTCCCCAATCCA	60.029	20	TGGGTTGGTTTGCTTACCTT	59.471	20
TGACGACCTTGTCATCCAAC	59.525	20	TTTACGGGTCAAAAGAAACCA	59.478	21
GCATCTCTTGCTCTCTCATTG	57.78	21	TGGCTTGTGAACGTGTAACC	59.615	20
GGAGATGCACTTCACCCAAT	59.934	20	TAAACGAAACCCCGGATCTA	59.406	20
AGAGGCATTTTGTTTGGAGC	59.316	20	ACTTGGAAAGTGCAGGGATG	60.111	20
CAAAACCCGTTACATATCTTTGG	59.667	23	TACCATCATTCTTGGCCATT	57.887	20
GAAGAAGTGGTGGCGGATTA	60.074	20	CAAAATTGCGTCTCCAGTCA	59.84	20
CATTCGGAATTCATTTGGGT	59.622	20	TATCGGTTATCATCGGATCG	58.404	20
GGGAGGAAGAAGAAGAAAAGG	58.451	21	GGAATTTCCTTGATACACATAC	59.918	26
TTGGTGCTCCACTATATTGCC	59.974	21	AATGGGATCTACATGCTGGG	59.773	20
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TCGAGATTGTGTTTGGGTGA	60.088	20	AGTTGATGAAGCAGTGGCCT	59.874	20
GTAACCGTCATGTTCCGGTC	60.24	20	CCTCAAGACGCCACTCTCTC	60.135	20
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AACGGTGAGTTATGGCAAGC	60.14	20	CATGGAGATCGTACGTTTCGT	60.008	21
TGTTAGAAACAAACGCGGCT	60.802	20	CGATCTCCGAAGCTCAAAAC	59.955	20
GCTTCAATTGAGCAGAAGCC	60.103	20	TTCCACAGTTTTGTACCCACTTT	59.827	23
ACAATTACTCGAGCATCGCC	60.243	20	TACACGCATATTCGCACACA	59.741	20
ACAACGTGATACGCTGCAAG	59.935	20	GATCGGAAGGATAAGAGCCC	60.003	20
GTGTGCGTTAGAGAGAGGGC	60.02	20	CGAGCTTAAAACTGTTCGGC	60.018	20
ACCATATTTAAGGGTTATCACCTG	57.552	24	TGGCGTTAGATCATGGAGAA	59.226	20
CTAAACCTTATCCCCCACCG	60.545	20	ACATTCGGATTTTGAAACGG	59.801	20
CAAAATTTGGAACCTGTCTTCA	59.108	22	TGCGCTGTGAATGGAAAATA	60.215	20
CCAAGAAAATCCCAGAAGCA	60.184	20	CTTCTGCTCCATCCTTTTGC	59.955	20
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CTCTTCATTCCCTCATCCCA	60.003	20	TTTACGATCTTAATCCGCCG	60.054	20

TTCGAAACTGCATGAAAATCA	59.291	21	TTTTGAATTTCGTAACGGGG	59.805	20
CACGTGTAAGGGTTGAAGAAGT	58.304	22	TCGGGACGAAATTTTTGTATG	59.818	21
CTGAAGAGCTGATGGCTTGA	59.267	20	GGCAACGGAACAACAACTTT	60.015	20
TGAACTGGCTACTGGCTGTC	59.037	20	GTTCAAATCCCACCAACACC	60.073	20
GTGTAGATCGCCATGGTGTG	59.992	20	GAATGCTTGGATGGGAAGAA	60.014	20
GCGTCGTGGATCAAGGTAAT	59.962	20	CCGAATAACCGAACCAAATC	59.273	20
ACGGTTACGGGCTGGTATTT	60.612	20	TTCCAATAAACCGTTGGCTC	59.938	20
GGACAGATCAGAAGCAAGGC	59.957	20	CTTTCCTCATCTGCACCTCC	59.803	20
AGAGCCACAAATTTTTCTTCAT	57.073	22	CCTTCTGCTGGTAGAGCACC	60.012	20
TGTGTGTGTGGTTCTATGTTGTG	59.445	23	ACACTTACCGCATTGGGATT	59.316	20
GTTTTCCGGGCAGGTAACTT	60.352	20	TCGGAACGTTCTACACGAGTT	59.788	21
TGCAGATCAATAAAATGGCG	59.662	20	ACGACGATTCCAAGGTTTTG	59.971	20
CAGGTAAGCCCTTCCTCTGA	59.425	20	CAACAGTTTGGTTTGGCTGA	59.734	20
CACTCTGCTAGGGTTGGGAG	59.861	20	AAATGATCTACGTCCACGGG	59.813	20
TCTCAAGTTCAAATGCCAAGC	60.38	21	GCTTCAGGGGGTGTGAAGTA	60.111	20
AGCAATGTCAATCCCTCAGC	60.226	20	CTCTCGCCCCAAACTTAGAA	59.448	20
CTGCGATCCTTTATCGCTGT	60.374	20	TTACCTCCTCCACCATCGAC	59.927	20
CGCTGCACCTTCAAGTAACA	60.05	20	GTTTCTTGTCTATTGGGCCG	59.569	20
TCACGAACTGCATCAAAGGA	60.39	20	GAAAAGAAATGAACACCGGC	59.551	20
GGTACAGCAGATGCCTCGTT	60.285	20	AACTTTGCTGAGTTCGGGTG	60.291	20
TTCTTATACCAAAACCTCCACTCA	59.098	24	CACCGACATTTTTGTCCCTT	59.83	20
TTGTTGGACCCCCTAACTCA	60.345	20	TCCGTGAATATTTAACCCGC	59.795	20
CCGTAAGCCTCATTACAGCC	59.73	20	TGCAATCACCAAAGAACTGA	57.806	20
GGATGCGTCCCAATCTAAAA	59.901	20	TGTCCCCTATTTGGACGAAG	59.926	20
AGAGGAAACCACCACCGTTA	59.449	20	GAAATAAAGGCCCAGCTCCT	59.688	20
TGTGGCATATTGATGATGGTG	60.213	21	TCTGATGGCCCAGATTTGTT	60.461	20
TTTTCATTTGATCACGCCTC	58.697	20	TATTGAGAATCCAAAGGGCG	60.031	20
TTCCCCCAGAGAAGTTGTTG	60.081	20	AGAGGGTTATCATGGGATCAA	58.32	21
AATGTTATCGCCCCAAAGTG	59.823	20	CAAGCTTGTGGAGTACATGAG	58.036	22
GTGACAAGCATTCCTCCACC	60.52	20	GGTCGCATGTTACGTGTTTG	60.035	20
CAAGGCCTTCCTTGGTAGTG	59.728	20	AATTGCCAAGTTTGCGAGAT	59.713	20
TTGACACATAGCCCGATGAA	60.073	20	ATTGGCTGAAATGGAGTTGG	59.933	20
AAGCTGAAAAGTCGAGAAAATG	57.828	22	GGAGATCCGTCGTGAAAAGA	60.195	20
TCGATGAAATAGGGTCGAGG	60.029	20	TAGATGCCCGGTTACCCTCT	60.836	20
GGAGAAGGAGATTGGGAGGA	60.532	20	GTCTGGGACAGACAACCGAT	59.969	20
ACAGAGCTGAGGAGAGCGAG	60.033	20	TCAATCCTTTGGAAACACTCCT	59.976	22
AAATGGACCCACGAGATTTG	59.79	20	TGCGTTCACACCTTCATATTT	58.161	21
TTTTTGAGGGAACAATTTGAGAA	59.971	23	TTTGGTGGGACCTTTCAGTC	59.943	20
TGCAATCACCAATGAACTGA	58.62	20	TTTCAGGAAAACAGAAGGGG	59.143	20
TTCAATCAGCCAATGGACAA	60.049	20	CAAACCAGTTGCACTGATCG	60.301	20
GAAAATCGGACGTCGAAGAG	59.813	20	CCACCATCATCGACAATCAC	59.769	20
AAACTTCGACTCTCGTTGGC	59.478	20	ATTTAAGCTGCACTTTTATTCA	57.118	25
GGTTATCACCGGATCGCTAC	59.415	20	TTCCACGTTTCATGTTTCCA	59.941	20
TGCATTAGTCTTTGGCATTCA	59.315	21	CTTGCGCCGCCTAAATAATA	60.202	20
AAGGGAGGCTCTGCATCATA	59.797	20	CTCCCACTTCCCTTGAAACA	60.081	20
ATCCAAACCATCCATTCCAA	59.991	20	CCCTCGGATGCTATGCTAAA	60.188	20
GCCCACAACTCTGGTTTCTC	59.703	20	CGTCCCAATTTGTCGTCTCT	60.111	20
TGAACTTATGGGAAGGAGAACC	59.46	22	AAGTTGGGGATCGTGCATAC	59.82	20
CATAGCGAGGAAGTCCCAAG	59.83	20	CCCCTATATCCCCATGACTC	58.133	20
CCTCAAGAATGATCCCAAGC	59.629	20	GTTGGATTCGAGCAGCTCAT	60.37	20
ATCATTACTGACCGCGAACC	59.962	20	CAGCCACCAAATCAAATCAA	59.518	20
GTCCAATACGAAGCCCAAAT	58.906	20	AGTGGTATGATGTGGGGGAC	59.511	20
AAAAAGGGATGAAAAGGGGA	59.75	20	CGGTGATTTGAAAAGAGGGA	60.044	20
CAGAGGGCCGAGATTTGTTA	60.206	20	AACTCTTCCGCCCCTTCTAC	59.713	20
GAAATGCTTCCAGGGACAGA	60.195	20	AGGAATCCTGCCCCAAGTAA	60.817	20
GCACACAGGTGAAGACGATT	58.727	20	TGATTGGTGTGGTGAATTGG	60.216	20
CTCCCTCCGTCCCATAAACT	60.319	20	TCCGTCCCAAGAAATGTGAT	60.317	20
GCATTTTCTCCATGTGGGAT	59.756	20	CCTCGTTGGAATTTTTCGAG	59.679	20

TGTCCACAGCCACAAGTCTC	59.872	20	CAATGTAAGGGGGAGCAGAA	60.066	20
CCCGAGGATAGTCTCAATGC	59.653	20	AACATGTTTGCTGGTGCTTG	59.764	20
ACTTCGGCAAAGGAATACCA	59.569	20	GGCAAGCGAGTAGGTTGTGT	60.321	20
TGGGGCGCGTATTTAGATTA	60.424	20	GGTTGTTAAAATGTCCACCCC	60.326	21
CCCACACTCTGCTTTCCATT	60.111	20	AAACCTTGGCAACAGTCGTC	60.156	20
ATGCATGGCATGAGTGTGAC	60.578	20	ATGTTTCATCAACGGACACG	59.42	20
ACCGGAGTGTGAAGACGAAC	60.159	20	AAACAGGTTCGGAGAAGACG	59.328	20
AATCTGACACGTCGGGAACT	59.579	20	ATGAACATGCTCCTATTTTAATA	57.053	26
ATCAGCAATGAGTTGCTCCA	59.399	20	CCCAGTGAGGTTGTGGAGAT	59.962	20
CTGTGGTTGTCGTCTCTTGC	59.467	20	ATGTGGCGACAAATTTAGGG	59.823	20
ATGTTCGGATTTTGAAACGG	59.801	20	TGCAATGCATGGAGGAAATA	60.035	20
ACCTTACTCGAACAGCCCAA	59.734	20	CCCCCTCTCTACACATTGACA	59.974	21
GCGTTTTGACAATATTTAGTGTTTT	60.205	26	AGATTCTGCATCAGGCCTTC	59.39	20
TTTCACCACCACACCACATC	60.27	20	TGCGTGAACCAGAGAAGAGA	59.701	20
TGAGAGAGAGGTTGTGGCCT	59.986	20	ACCGGTTGACCCCGAATTAT	62.535	20
AAGAGTGTGTGTGTGGGTGTG	59.527	21	TTCCCCTCTCTCCTCCTCTC	59.883	20
CCAAGCCCAAGACTCTGTTC	59.844	20	CTTGAATTATCGGCGGTGTT	59.96	20
CAATACAACTGCCGAGCTGA	60.011	20	CACGTTAGACCTGGAGGAGG	59.715	20
TGGATTTTCCCAAATTCAATC	58.726	21	CGGTGTGTTGGCATTGTTAG	60.027	20
GTTTTGTTTTCGTTCCCTCG	59.587	20	TATTTTTGAGCAGCCCCAAG	60.202	20
GACGGCAACAGGAGTTACATT	59.115	21	GCGATTTCAATTCCGACTTT	59.162	20
AGGTGGCAACATAATCAGCC	59.962	20	TATGGGTCAGAAAAGCCCAC	59.933	20
GCTCTGCATTAGCAGCTTCC	60.265	20	GCGCAAGTGTATTGTACCAGG	60.569	21
GGATTTGGTTGGTCAAGTGG	60.21	20	CAACGCCATAGGGAAGTGTT	59.993	20
TCACATTCACACCTAACGCAA	60.165	21	GATAGTGGTGGGATCGGAAA	59.75	20
TGAGACCTCTCAGTCCCAGG	60.388	20	CTCATCGGGTTAATTGGGTG	60.184	20
TAAAGGCCGCATCCTATCAC	60.06	20	CGAGACTCACAAGGAGGAGG	59.978	20
GCGGTTATCACCGGATCG	62.397	18	TCCGAAAATCAAAGGTCCAC	59.91	20
CCAAGAATCAGTTAAGCCCG	59.702	20	TATCAAACGCAGCGATTACG	59.864	20
AGGCCAAAAATGAACCACAC	59.836	20	AGCGACCATCAGACCAATGT	60.542	20
CTAGGAAGCTGAGGAAGCCA	59.711	20	TCATTGAACTCCCCATCACA	59.893	20
CGAGTCGGCAGACCTAAGAC	60.012	20	CCTATGGTGGTATGGTGTGGA	60.501	21
GCCAGTGTCCATCCATTTCT	59.934	20	CTCACGAAGCATTGCCACTA	60.011	20
GTTTCAGGTGAGGCACAGGT	60.159	20	CATATCGGGTCAAAGCAACC	60.331	20
AGTAGAAGCATTTCGTCGGG	59.336	20	GTTAAAATCTCCACTTGGGAAA	57.302	22
TGAAATGACACTGGTTGATTTTG	59.89	23	AACATTTTGGGTCTTTGTCG	57.578	20
GTGATTGGCTGGAAGAGCAC	60.812	20	CATTTAATGCCCCAGCAAAG	60.448	20
CTGACGGAACACGTCAGATTT	60.164	21	TGAACAGGTTGCATTTTAGATG	59.639	23
CATACTTCCACCGCCTTCAT	59.955	20	AACGGTACGTTCGGATTTTG	59.861	20
CCACTCACGCACACCACTAC	60.227	20	CGACAAGAGAAAGAGGGTCG	59.982	20
TTCAGGGAATCTTCGAATAAAAA	59.14	23	AGGGAATTAGAGCGTGGGAT	59.925	20
TTGAGGCTTGTGGTTCAGGT	60.69	20	TGGAGACGGCTGTTTTCTTT	59.853	20
ATCGCGGAAGGTTTAGCATA	59.704	20	AGCAAGTGGTGGTGGATAGC	60.142	20
TGCAAGCGGTTCAGACAATA	60.401	20	GGCATTACCACATGCTCACA	60.549	20
AAGAGCTCTCGACGCAAAAC	59.763	20	GAGATATTCTGTCGGATAGGTC	59.13	23
CCCCGGTAAACAGAATTGAC	59.288	20	CACCGTTAATCGCAACAAAA	59.603	20
ATGTATGGCCCAGATTGGTT	59.129	20	ACTGTGAGGAGCGTCGATTT	59.874	20
TCCGGTCCAAATCCAATAAG	59.756	20	CCTATGGTGGTATGGTGTGG	58.569	20
TGTTGGGATGAAATGTGAGG	59.343	20	CACCAGTTACCCGACTTCGT	60.028	20
AGCCATGGATATGAAGTGGG	59.773	20	TCTTCCTTTTCTCGTTCACATAT	58.4	24
ATGCCACCAAAATCAAATCC	59.628	20	TATGGGTTATCACCGGATCG	60.544	20
TCAAACCCTGTCATTCACCA	59.935	20	ATACGCAGTTGCTCGGAAGT	59.904	20
CCCAATTTGCCCTTATATGC	59.282	20	TTTCGAAGTTGTGATGTGGC	59.697	20
TCTGGGTGAAAATCGAATGA	59.049	20	CTCAATCGTCGCCGATATTT	60.06	20
TGCTGCAAGCTTAAGAAACAA	58.901	21	ACACCATGTGACGAAGGTTG	59.441	20
TCTTTTTCGAACCGAACCAC	60.088	20	TTGTTAATCCACCAATTTGCC	59.69	21
ATTTTTCTGATAAGCCGGGG	60.272	20	GGAGGCATTCGATCTTTGTG	60.603	20
CATCAGTAGCGATCCGGTTT	60.096	20	ATGCCAAATTGTGTTGGGTT	60.096	20

ATCGAAACCAGAACAGACCG	60.111	20	GATTGAAGATGTTGGGCGTT	59.939	20
AACACCAACATGCTGACGAA	60.16	20	TTCGAAGATCAACGGACGAT	60.603	20
AACCTCTCGTGCTCCAACAT	59.727	20	TTGGATTTTTGAAACGTGGA	58.987	20
AGAATCGTCCCAAATTCCCT	59.766	20	AAGCTTGCATTTTATCGGGA	59.682	20
GTTTGGCCTCACTGGTGATT	59.973	20	AGCAACAAAACAAATATTGGA	59.788	24
CGTACGAATTCTTGCCAGGT	60.132	20	GTGCTGTTTTGGTTGGTGTG	60.049	20
TCACAACCAAAATCTTGCTCA	59.307	21	CCTGCCAGGACGAACTTGTA	61.224	20
CCATTCAACGCAACCATTTT	60.732	20	ACGTTGTAGTTGAGGCCCTG	60.171	20
ATGCTGCTGTTTTCCATTCC	60.081	20	TCACGAATTCTTCTTTCCTTTCT	59.786	24
AAATCATTGCTTGAGCTTGAAAT	59.306	23	TCAACTCAATAGGTTTTCGAGT	59.732	25
CAATCCAAACTCTATTTTATCCGA	59.778	25	ATTTGGCACCATTCTTCACC	59.797	20
AGACCTGTCACCGTTTTGCT	59.769	20	GTGTCAGACGTCCTCCTGGT	60.161	20
ATTTTAGTTATCACAGGATCACCC	57.577	24	CCGCGCTGTAGATTCAAAGT	60.407	20
ACTTGGCCCACAAGAACAAG	60.149	20	GGTAGTGGGAACTTGCGAGA	60.255	20
ACGGCCAATATTTGCTCCTA	59.569	20	GGCGCAATTGGAGATCTAAG	59.807	20
TCAATCGTGACACCAAGGAG	59.676	20	AGGCTGAGATCTTTCCAACG	59.43	20
CACCGATGTTGAGGCCTACT	60.134	20	CGTCGAGAGAAACTCAACGG	60.964	20
TAGCCTCCGTATGCAGTGAA	59.444	20	GCCACATATGCAAAATATCAG	59.486	22
GTTTGCTGCTGCTGTTGTGT	60.104	20	TCGCTTTATGAAGTGGCTCC	60.352	20
CCATGCGCGGTCTAAATAAT	59.95	20	CTCCCAGGAAAAGCATCATC	59.629	20
TTTAGTGTTTTGACATGATTACTC	57.557	25	ACGTGACGAAAGTGGGAATC	59.973	20
GGACCTCTGGACAATCCCTT	60.314	20	CGGCATTCGATCTTTGTGTA	59.688	20
AACAGTGTACAACCCCGGAA	60.269	20	GTGGGGTGGGATTGAACTTA	59.647	20
ACTACAACATCATGCAAATCAAT	57.395	25	AATAGATGCATGAAACATTTT	57.786	24
ACCAGTTGCAGTCTCTTGGC	60.453	20	AAGGAACAACTGGTGGATGC	59.973	20
GGGTCAAGGTGTCGGAAATA	59.79	20	TGTTGCGCGTGCTTTAAATA	60.401	20
CAGCTCCAAGACATTCCACA	59.831	20	AAATTGCAAAGCGGTGTCTT	59.752	20
ACAAATGTGGCGTATGCTGA	60.142	20	TCCTAGCCCTCAATCTCGAA	59.91	20
CCTTTCCCATCTTCATTCCA	59.864	20	AGATCCACCACTGCTTGGAG	60.261	20
AGGTCATGGGGTATGTTTGC	59.676	20	TTGATTGTCTTTGCGTTGGA	60.234	20
TCGGAGCATGAATTAAGTGG	58.721	20	ACGCGGACGGTACAGATTAC	60.022	20
TGGCATATGTCCCCAAGAGT	60.34	20	GTAAAACGCTAGAAGGCCCC	60.095	20
TGACCCAGCCTTTTTAGGATT	59.952	21	CCCAACTTCCCATTCACTGT	59.82	20
CACTTTGCAAGCCCATTTCT	60.249	20	GGACAAGGATTGGAAAGCAA	60.051	20
TTGCAAAAGAAATTGCTTAGCTT	59.604	23	TGGGTGTGATCTTGACCCTT	60.363	20
GCCTCTCTGCTCACCAGGTA	60.555	20	CAAGCAAATCCCCTTCTCTG	59.807	20
GCAGCACTCTGGACTCTCAA	59.288	20	CATGTTGCTTTTGCATGTGA	59.28	20
CAACCTTTGAAGACTCCGTCA	60.275	21	GATGGGGATTTGCTTCATTC	59.324	20
TGGATGGAGTCAAAGCCAAT	60.461	20	CGACAGCGTAATTGAAGCAA	60.014	20
CGAAAATTCGGATCGGCTAT	61.256	20	TCCGAAATATCCGGTTTTTATT	58.843	23
AGGTTAGGAATGCATTAAATACC	59.283	25	AAGGGAGGGTTTCATTCTCA	58.568	20
TACCATACGTAACGCCCAAA	58.958	20	CTGGCTCCCTATAGTGCTGG	59.853	20
TGCATTCATCAATTTTTGGAG	58.613	21	ACGTGCCATGTGTTTGTCAT	59.887	20
CACTCTCTCACCTTCCATCCA	60.245	21	TTTGCTGTAGGCCTTTTGCT	60.018	20
AGCCTCCCTCTCTTGCTCTC	60.238	20	TGGGCAGCTGTAAAACCTTC	60.249	20
CGAAGAGCACACACTTTTGG	59.485	20	TGAACTGGCCCAAGATCAAT	60.461	20
TCTCGAGCTCAAATCCCAAG	60.474	20	GAACGATTAGTGTAGGTTGGG	59.898	22
AAAGTTTTCCGCATGAATGG	59.938	20	TGAGCAGCCTAGATCAGCAA	59.847	20
TATTTCACAGCAGCGACAGC	60.165	20	TGTTGATTTATGGCGGATTG	59.377	20
CCATTTCTGTTTCCCCACAC	60.21	20	TTTCTCATTGGCAGTCACCA	60.24	20
AGTGGGTCGTAGCCTGACTG	60.321	20	ACGGAAATCTAGGGAGCTGG	60.59	20
GTCGTCAAAGAACTCGGAGG	59.844	20	GTGGGTCCCTCTCTCACAAA	60.088	20
AAAGGAGATTCCAGCGATCA	59.773	20	TTTTTGTGCCTAAAATGCCC	59.943	20
GATCGACGGTCCGAAATTAG	59.528	20	TGTTGTCGCTTTAGCTCCCT	60.015	20
TTCAGAGTGGCCATAGCAGA	59.547	20	GGGTTAAAAGAAACCCCCAA	60.027	20
CCGAAAATCTAAAGCCCACA	60.067	20	TACTTGGGATGCTCTCCACC	60.073	20
GTTCGATGGACCTCGATCAT	59.893	20	GAATGGAATTCACTCCTAAAG	59.622	23
AGCAGAATGCAGTTGTTGGA	59.445	20	GAAGAAGCCAGGCAGAGAGA	59.827	20

GGAAATAAGGAGGTGTTATGATG	60.02	25	AGAAGATTTCTGGGGTGGGT	59.795	20
TCTCGAATGAATCCAAACCC	59.871	20	AGGGCCTTTTTGCAATTTGT	60.83	20
TAGGCCGGTCTTTTAGCCTT	60.217	20	CGACTCGGGTTTCGAGTTAG	59.869	20
TTCAGCATTGTAAGGGGGAC	59.933	20	CGTGGTTCGATCGTAATTGA	59.542	20
CTTGCACCAATAAAATTTGGC	59.485	21	TCAATCGAGCTACAAACGTG	57.506	20
GGGGATTGGTAATGCAAGAA	59.762	20	AGGAAAGAGAAGTGAGCCCC	59.817	20
CCATTCCGAATATCAAAGGC	59.369	20	TTGTTGCATGTCATTGGTCA	59.516	20
GTCACACAAGCTTGACTCGG	59.467	20	TGCGCATTTCTGATATCGTC	59.799	20
CGTAAATTGTTGCAACCGAG	59.226	20	TTCGTGAATTATCCAAACTTTT	59.885	24
GTTTACGCCTTGTTTTCGGA	60.11	20	GCGTTGGAGATGGTCTTACAA	60.125	21
TAGAGCCCTTCAATGGACAA	58.298	20	CCAATGCGGATGCTCTTAAT	60.06	20
CAACGGTACGTTCGGATTTT	59.861	20	ACCGCCCTCCTATTTCGTAG	60.463	20
GCCCAACTTATTTGGATATTTGA	59.268	23	AGAGGGAGGAAAGACTGGGA	60.186	20
CCAGTTAAGAGCGTTGGAGG	59.869	20	CCCTACCCCATGATCTCAAA	59.744	20
CACTTCTCGGAACGAACAAA	58.897	20	GGGGGTTATCACCTGATCG	60.142	19
TTGCTCGTTTTTAACCCGAT	59.586	20	TTTGATTTCTCCCCTACCCC	60.124	20
ATTGGGCTCTATGGATGTGG	59.773	20	CCACCCGTTGATTTTTCACT	59.83	20
CGTGTCATCCAAACAAATGC	59.972	20	CAGATCTATGGGCCGAGATT	59.105	20
ACCAGAGTCCACCACCACTC	60.006	20	TGCTGGAAAGGAAAAGGAGA	59.926	20
GGTCTGATCTGTCCTACCCTTG	59.994	22	GGCCGATATTTGCTCCTAGTT	59.606	21
CCTCTTGGACCTTCCTTTCC	60.045	20	AACACCTGGGTGAAACCAAA	60.246	20
TCCCAAATTTAGCCGATTGT	59.411	20	CACCTAAAATATTGGTTTCTAT	57.121	26
GCCACACATGTCAGAAATGAA	59.562	21	TCACGTGGCATCATGAGAAG	60.84	20
ATTTCTGCTCACTGCCTCGT	60.02	20	AGCAAACAAGAAACATGCCC	60.118	20
CCAAATTAAGGTCATATTGCACA	58.927	23	ACAGTGGGCTTGCAGGTATT	59.621	20
GCGAAGTCAAACCACCAGAT	60.119	20	CAAATAATGGCCCTTAGCCA	59.922	20
CTTCGCCCTTGGATGAAATA	60.031	20	ACCCCGGATCTACCATTTTT	59.532	20
CGAATAGTAGCTTCTGCGGG	59.996	20	AAAAAGAAAAGAAAAGAAAG	57.998	27
ACTTTTGCGCACACAGTCAC	59.953	20	ATGATGGAACATGAAAGCCC	59.756	20
CGTCATCTTGGTCTGAGCCT	60.408	20	GCCTTCTCCGAGGAAAGATT	59.789	20
ACGCCCCAGATTGTTTCTTA	59.569	20	GATTTTCATGTTTCGCGATTT	59.071	21
CACTGGTCCGAGTTCTCCAT	60.112	20	TTGAAACGCTGCAGAAAGAA	59.729	20
TGAGGAAGTTGATTTGTTGGG	59.956	21	ACGTCATTGGAAAATAATGCG	59.846	21
AACGTCACCTTGAAACACCG	60.984	20	GGAAAGAACTCAATGTCGGC	59.676	20
CGAACTAAAGAAATAGGGACGC	59.311	22	ACAGTTCATCTCCCGTCTCC	59.105	20
CTGATAGGCCAACTGTGCAA	59.864	20	TCTCCATTGCTGTTGGGAAT	60.461	20
TCATGGGGAATTCAAAGAGG	59.864	20	GCGGAAAGGAAACATCAAAA	60.053	20
ACACGTGTGCTGACTTGTCC	59.789	20	CCTATAGTGGTATGGTGTGGG	60.365	22
TCGACAAAGAAATCATCGGA	59.2	20	GAAGAAGGTGAAATCGACGC	59.82	20
GGTTATCACCTGATTTTCTCCC	58.826	22	GGCTAGCCTTTGAAGCAATG	59.982	20
GCAAATATGATATGCCTGCAA	58.667	21	CGTTGCTTCCTTCCTACTCCT	59.893	21
CAAGGGTAATCCCAAACCTT	57.904	20	GGGGAAGTGACAACCTCAAA	59.943	20
AACCACAAAAAGGATAAGTGGG	59.282	22	AGAGGGGGTATGAGTGGAAA	59.813	21
CGAAGCTTTGATGGTGTGAA	59.84	20	TGCGTTTTGACAATATTTAGTG	59.109	25
TGTTGCTCTTGCTCCAACAC	60.032	20	TGCATATTTCTCGATCCCGT	60.435	20
CTCTCCACTCCCTTCACTGG	59.828	20	TGAGCAAAACTGGTTCCCTT	59.711	20
GCTGGCAGCTTCAACAGATA	59.178	20	TGTATGGCTTTCCCTTGCTT	59.708	20
GGTTTTGATGGTTGTGATTTG	57.836	21	TGAACACCCCTACTTGAGCC	60.111	20
AACCTTGGAGTCCCTTCTCC	59.534	20	TGGAGGTGGTGAGTTTGGAT	60.363	20
TGGACCCCCGATTTATAGGT	60.391	20	AGTTCCACGATAGGAGGGTG	59.014	20
TATTAACGGTCCGGTTCCTG	59.817	20	GCCATGTTTACGATGAAATGC	60.345	21
AACGTCAGATATGGCTGTTGG	60.008	21	CAACAAGATTCGATAGAAGCC	59.361	22
GGAGCTTTACACTCCCCTCC	60.074	20	GATCTGCTGGCGGTCTTTAT	59.297	20
CGCGTTTAGAAAAGGGAAGA	59.469	20	CAAAGGCTCCTTGGATTCAT	59.126	20
TTTATCGTGGTGCATGTTTTT	58.084	21	CTGTAAGGCTTCATACCGGC	59.73	20
CAAGTTTGCGTTTGAATGGA	59.706	20	GAGACGCGAATGTTGAGACA	59.992	20
TGTGAATTTTCAGATTGTGGTTTT	59.793	24	TTTGAGCTGATCTTGAAATGC	58.106	21
AAAGGGTTAATATTGGGCCG	60.036	20	CTCCCTCTCTAAAGGGACGC	60.34	20

ACATTAAATGCAGCCGCTCT	59.873	20	CCAGTCTCTTTGGATCCTGC	59.803	20
TGGTTCACATGGTTGATGGT	59.656	20	TGGTATCCATAGCAAAGCGA	59.281	20
AATAATTTCCAAAACCGCCA	59.3	20	GATTGACGGGATCACAGGTT	59.786	20
CAGTTTTGCTATCGTTTATCTTCG	59.392	24	TCTTACTGCCACACAAAATCAA	58.346	22
ATTATTTTGCGGTTCCAACG	59.832	20	TGGTAAAAGTGCTCAAGACGA	59.424	22
GTCCAGCCCTAATATTGCACA	59.974	21	TATTCCGCCGTGGTCTAAAG	60.089	20
AAACAGGGGTACAAGGGTGA	59.304	20	CACTCACACACGCACTCTCA	59.624	20
ACAATGCTGCACTCCCTTG	59.846	19	CAAACTCGCTCAAAAAGACAC	60.453	22
TGGTTTTGAAAGTGTGATCTGG	60.008	22	CCAAATAATGCTGCGTGATG	60.096	20
GGGAGAATCGTGTCATCGTT	59.934	20	AGCCCGATAAGTTCGCAGTA	59.867	20
GATTCTGGATTATCCTGCGG	59.486	20	CGGAACCAGACCGAATATGA	60.853	20
CCTCAAGATTGTGCAACCAA	59.691	20	AGTCCGAAAATCCCAACAAT	58.36	20
GGCCATCTATCCCTATCCGT	60.138	20	AACATTAAAAATCGCCCGTG	59.832	20
AAGGGAAAGAAACGGGCTTA	60.068	20	ATCTTCTAATCACCGCCCCT	59.925	20
TCCTCCTTTCCTCTGCATTG	60.331	20	TGAGTTGAGGAAGAATGGGG	60.042	20
GTCAATGATAAATCGCGGGT	59.791	20	TTTGGAGGATCGACGTTACC	59.933	20
CGGTGTAAAGGAGGGGTGTA	59.846	20	TCATTCAAGGAATTTCACCAAG	59.064	22
CACTTCTTCCCAAGGCACTC	59.844	20	CGAATTCAAACTCTCCCGAA	60.184	20
TGAATCAATTTAACATCATGCAAT	58.44	24	AGCTTCACAACAGGTTTCGC	60.44	20
ATGCAACACACGCACATACA	59.621	20	ATGACTGCAAGCAACCTGTG	59.905	20
TCCTTGCACTGGGAAAAAGT	59.711	20	CTCCACCCTGGTTCTAATGC	59.55	20
AACATCAACCGTTCACCACA	59.855	20	AATACCGGGAAGAATTTGGC	60.15	20
GTAGAGGGAGTTGGGGGTGT	60.23	20	TTATGGGACACGTTGGTGAA	59.816	20
TTATTGAGCGCCATTGATGA	60.179	20	CCGCTATCGAAAATATAATCCC	59.732	23
ACTTTTAAGGATCAAGGATATTCG	57.122	24	ATCCACGGGAGAGAATGAGA	59.612	20
GTCTAAATTGCCCCGTATGC	59.438	20	AAAAAGAGGGAGGGATACACC	58.452	21
GGAAAAATAACAGGGGAGGG	59.639	20	TTCTTCACCCAACAACCACA	59.976	20
ATGGGCGAGAAATAGCAGTG	60.235	20	GGAAAAGCAATCAAGATCCG	59.645	20
TGACCAATAGGATGTTGCCA	59.924	20	CTGGTTCTCTACGACCAGCC	59.867	20
CCATGAATGGAAAATGGAGG	60.126	20	AAACAAAATGTGGGTGCCAT	60.096	20
TAAAAGTCACGCTTGAACCA	57.008	20	ACGGGTTATTACCTGATCGC	58.93	20
CCAATGGGTGACCAGTCTTT	59.82	20	TGCAGTGAAGCATACACCGT	60.333	20
GTTCGAACCGAACCATGAAC	60.362	20	CAACCTTTTCACACCACCTTC	59.482	21
AATTGCCATTACCATTCCCA	60.016	20	TACCCTTCATCTTCAACGCC	60.074	20
GATTTTTGGAGGGTTCTTGC	58.622	20	AGGAGCAAAGCTGGAACTCA	60.134	20
CAGGAGACGCTCATTCATCA	59.942	20	TGAGGAGTACATGTGCAGGG	59.701	20
CATCCACTCTGAAGTTTGAACA	57.856	22	GGGTGGAGTTATGGCTGAAA	59.933	20
GGACCAGGATTAGCCCAACT	60.328	20	ACCATTTCAAGAATGCAGGG	59.933	20
CATAAGGCCCACTTCAACCT	59.052	20	CGGTTCAACCCTTTTGTAGG	59.466	20
GGAGGGGTTTCCCTTACCTT	60.528	20	CAACACAAGAACTCACCTCCC	59.607	21
TTTTCGGGAATCTTTCATGC	60.016	20	TATGGAGAGTTCCAGCTGCC	60.362	20
AAGGTCCCAGGTTCAAATCC	60.169	20	TCTCGATCACTACAATCTTTGA	59.445	25
GAGGGTTGTTGTGGGACTGT	59.859	20	TGCCGTAACCTGTCATACCA	59.988	20
AAATGAACGTAGCAAAGGGG	59.087	20	TGCCCCAATTCAATCATTTT	60.132	20
TCTCTATCTTTTTGGTTGGTGAAA	59.203	24	GAAGGAACGCTTACACGGAG	59.875	20
CGGACCGTGAAAGCTCTAAG	60.008	20	TTATCATTTCGTCCCCAAGG	59.756	20
ACTAATGGATATGCGGCGAG	60.081	20	TGAACATCTGTCACGTCTTCG	59.889	21
GAGATTTGGGCGTTTACGTG	60.502	20	CCTGGAACTGTCATCACCCT	59.962	20
GCCGGATTTTGTCCCTATTT	60.15	20	ATGGAGATTGGTTGGAATGG	59.605	20
TTGTGTCCCTGAAAGAGGTG	58.695	20	AGAAAGCCGGCAAACTGTAA	59.883	20
CACGACAAGAATCCAGCTCA	59.984	20	GATCGAATCACCACTGCAAA	59.654	20
TGCCGAGAAGAGGAAGTGTT	59.989	20	AACTGCCCAATCTGGATGTC	59.934	20
AGATTACGAGAAGGAGGCGG	60.723	20	CAATTAGGTCATCTCCAACGC	59.583	21
GACACGTGGCGTAATCTTCA	59.722	20	ACTTTTGGGGGACAAATCCT	59.668	20
GAAGACACTTGGGCCTGAAA	60.232	20	GTCCATTGTAGCGGTTGGAT	59.82	20
CGTTAGAGAGCGTCGGGATA	60.365	20	TCAACCATATCCACCCGAAT	60.014	20
GAAAGGCTGCATGAGAGAGG	60.096	20	TAGTCGCGTGCGATAATTTG	59.864	20
TCATCTATCCCCCGGTGTAA	60.148	20	CCTCGGGACGGTTTACTACA	59.986	20

TCACTTTGCTCGAAAGTTGC	59.199	20	CTAAGGTCGGCGATAGCTTG	59.996	20
TCCAGCCCATTCTTATTTGG	59.894	20	TGGGTCCATCACTCCTCAAT	60.326	20
CGTTGAAAGGAGAGCGACAT	60.397	20	TGCACGTGTGTAGGGTTTGT	60.072	20
CACGAAAAGATCAGCAAGCA	60.134	20	GGAGGGCTGTGTGATATTGG	60.34	20
AAGGAGGTGTTATGAAGGGAGT	58.15	22	TGTTGCGCGTGCTTTAAATA	60.401	20
TTCTCCCACGCACTTTCTCT	59.989	20	GGAACGAACCAAAAGTCCAA	59.948	20
ATGTAACTTCCACATCCCGC	59.82	20	ATGCAAGAAAACAAGTGGGG	59.971	20
TTCTCCCTCATCCCTCCTTT	60.008	20	TATGGTCCTCACACCAACGA	59.96	20
GGGTTCCCACGTCATAAAAA	59.662	20	GCATCATCTTGTTGTATTCGTT	59.532	23
TGCAACTCATTGCACCTACA	58.863	20	CCTCCCATTGACGAAAGAAT	58.981	20
CCTTTCTTCCGACTGCAAAA	60.357	20	TTTGTCCCCTTGCTACCATC	59.933	20
CCACCACTCGAAATATGGCT	59.955	20	TATTGTGGAAGGACGGGAGA	60.452	20
ACCGTGGCATCGAAGATTAG	60.096	20	TGCAAATAACCATCACCCAA	59.786	20
AAACCAATGCGAGGTAGGTG	59.993	20	GGCAAACATGTGGGGTTTAG	60.227	20
TTTTTAAGTTATCGGTGATGACAC	59.829	25	GTCCGTGGTTTTACCCAGTG	60.269	20
ACGAGAAGCGCGAGTAATGT	60.044	20	GCCTACGATCCAAATCCTGA	60.036	20
TGGGTTCCATGAGAGAGAGG	60.191	20	AGCCCCACATAATCCCACTT	60.578	20
TGCGTTTTGATGATATATATGTGT	59.956	27	TGTACCGCACCAAGATTTGA	60.111	20
TGTATCGCTGCAAAAAGCAC	60.021	20	TTGCAAGAAAAGCCACACAC	59.888	20
TTCCACCCAAAAACCGAATA	60.16	20	AAAAATTTAGTATGAGGTCAC	59.925	26
CTTTGTGAATGAAATGGTTGCT	59.134	22	AAAGGGAGTTCTCCCAAATCA	59.926	21
CACCCTCCCACACATCAAAT	60.634	20	ACATAAAGCCACCCCAACAA	60.227	20
GACAACCCTTCGGTGCTAAA	60.11	20	AAGGGAGCCCAATTGAAAAT	59.777	20
CCTCGGGACGGTTTACTACA	59.986	20	GAAAAGCTTGGCCATTCAAC	59.691	20
CATTCGATGGAGACGCATTA	59.646	20	TCCCATTTGTGTGTTCTTCG	59.541	20
GACTTTGTTGTGGTGGACCC	60.261	20	GGTAGGTGCTCTGACTTGCC	59.874	20
AGAAACGTTGAAGGACGTGG	60.149	20	GGAGGAGAAGGAACAAACCC	59.912	20
TGGGTTTTGTAATTTGACCCA	60.074	21	AACTCGCTACGGGTTAGTCG	59.401	20
TCGATTTTTGTCAAATCCCC	59.739	20	TGAGATTTGGACGGTTATGATT	59.729	23
CAGCTCAGGGTGGAGAAAAT	59.284	20	GCGAACTCGGCTAGAACAAA	60.523	20
CATAAACCCTCACTCCGAGC	59.694	20	GACGCCCAATGATCAAAGAC	60.47	20
CCCAATCTTGATTCCCAGAA	59.864	20	CTGCAAGGGACAGCAAAATA	58.917	20
AAAATGCCCTTGTATGCTGC	60.103	20	TTGCAGAGGCGGAGAAGTAT	59.978	20
ATAATGTTGGGTGAGGCCAA	60.192	20	TTTCTGGTTGCATTTTGCTG	59.849	20
GGGAGGAGAAAGAAAAGCGA	60.817	20	TTCTTTGAATCATCTTCCACCTT	59.123	23
GAACCCCCTAGCACCATGTA	59.813	20	GGTGTGCTCGGATTTTTGAT	59.939	20
GCAACCAATTTTCTCTCTGCT	58.592	21	CTATTTTCGCTGGCTTGGTG	60.762	20
GCAATAGCATTCCAGTAACGG	59.622	21	CACTGCTGTCCCTGCATCTA	60.008	20
ACCCTTATAAATGCGCTTGAA	58.775	21	AAGGCGGTTTTTGATACGTG	59.996	20
CGGTGCATTTACTTGCAGAA	59.872	20	TGTCTCAGAAACTGTAACCCT	58.898	23
AATGCCTTTTGTTTGCATCC	59.945	20	GAAAGGCAGATTTCCCAACA	60.051	20
GTCCTGCCCTCTCATAGCTG	59.973	20	AAGATGAAGATGACCACGGC	60.081	20
TTCTAGTCCACCCGACCAAG	60.103	20	TCCATCGTACGGTTGCATAA	59.953	20
CGTCCACAGTGGTTTGAGAG	59.305	20	AGGACACGTTGGACCTGAAA	60.545	20
GTCGATACGGCATGACACAC	59.999	20	TTCGAAGATCAACGGACGAT	60.603	20
ATGCAGCCCATTTGTTTCTC	60.081	20	ATAAAAGCAAAAGACGGGGG	60.305	20
ATCGGTCGTGGGATTTTTATC	60.034	21	TGCCAGTAATTCACAACCCA	59.964	20
CGGGTCGAGAGAGGAGAAAT	60.725	20	CAATCAAGGGCTATGCAAAT	57.725	20
TATGGGTTATCACCGGATCG	60.544	20	TGGCAATTCTATGACCCTTGA	60.454	21
ACGAAAAGAGAGCCTTGCAC	59.621	20	CCGTTTTCCCCGTGAATAG	60.308	19
TGGCATCCCACATGAGTTTA	59.924	20	TCTCTGTGTGTGAACCTGCC	59.872	20
TAAACAATGGTGCGTGAAGG	59.585	20	ACCATATTTAAGGGTTATCACC	57.552	24
TCTATAGCAAGATCTCACGCAG	57.452	22	TTGTGCATCGTGTTCTTGTG	59.298	20
TCAAAAATCCAAGGGTGGAG	59.903	20	GGGAAGGATGAAAGGGGTTA	60.124	20
TCATCCAACACCCATCCATA	59.579	20	TTGATGGTGACGTAGAACATTT	59.912	23
CGCACACACTCTCTGATTCAC	59.482	21	AAAGTGCGTGTGTGTGGTGT	60.121	20
GCGTGGAATTCACCTCAAAT	59.939	20	AACCTCCCCCTCCATCTCTA	59.89	20
TCCGGATTCGAATACTCACC	59.894	20	AGTGAAACCAAACCCAGTCAA	59.482	21

GTACGGATTGATGGAACGGT	59.676	20	TCATCTAGCATCTCTTGCTTTCA	59.261	23
CACACTTACGCCCTCTCCAT	60.134	20	GTGGAAGATTTCTTGGCAGC	59.82	20
CGTAATGTTTTGGTGGGAAGA	59.847	21	ACGACCACAAAATGGGAGAA	60.353	20
ACACAACTTAGGTGTTCTCATTTG	57.432	24	AACGGCGTTAACTAACCTGG	59.154	20
CTTTCGTCAAACCCTGCTTC	59.853	20	ATATCGTTGACCATTCCCGA	60.155	20
TTGTGAGCGCTATCATGGAG	59.972	20	GTCCCACCCAATCACATTTC	60.034	20
ATGATTGCACCTGAATAAGCC	59.06	21	TATGTCGTTAGACGATGGCG	59.712	20
TTGGATTATAGATGCACGAGGA	59.569	22	TAATGGGAATGGCTTGGCTA	60.415	20
GACAAACTTAGGGACCGCTG	59.734	20	CGACTTGTCGTGGTTCGATA	59.716	20
GGAAATACTTTTCCCGGAGG	59.772	20	ACCCCCACCAGATTTTCATT	60.422	20
CATGGACGAAAATAGCCTCAG	59.716	21	TTTCCTATGGACCGAAATGC	59.901	20
CATGACTGCTTTGGTTCATGT	58.637	21	CGATTTGACCTCGGATAATCA	59.908	21
CCCCCAAGATATTGCAACTG	60.323	20	CTCCCACGGGAAACCATATT	60.929	20
GAGCACTCGTGTGGGATTTT	60.119	20	CACACCTCCTCCAAAGCACT	60.298	20
AGGCAATCTAGGCGACAATC	59.297	20	GGGAGGGAGAGGGAGTATTTC	60.27	21
TCGTGTTCTTCACTCATTCCA	59.278	21	ACGATACTTCCCGGCTCTCT	60.233	20
GTGAACGCTCTGTTCACCAA	59.88	20	CGTCAATCGGCTTTGAAACT	60.249	20
ACACCGATCCGTTCCTACAC	59.851	20	AGTGCATATGCGAGGTGATG	59.704	20
CCTCCAGTGCCCACTCTAAA	60.246	20	TGGTGGAGAAGAGAGGGAGA	59.913	20
GGCAAGCAGTGGTGAAAGAT	60.263	20	AACCCGTTTGAGGTTGAACA	60.388	20
GAAGGAGAACCGGGAGTGAT	60.456	20	TGTCTGAGGTGTGCTTCCTG	60.022	20
TAAGGCAAGCAGTAAACGCC	60.397	20	CAATTCCGGCCAAATTAAAA	59.778	20
GCAAGGAATCTAACCTGCGA	60.352	20	AAAATGAAGGGTTGAGATGGG	60.173	21
TGTTGGCATTCAAATCAACC	59.375	20	TCATTTTACCTTTCTGTTTTTGGA	59.107	24
TACAGCACAAGCAAAATCGC	60.021	20	ATTCCTTCCCACTGGATGGT	60.575	20
TCACAATGGCAACTCAAAGC	59.847	20	TGTCAACCCTGTTGAGCCTA	59.288	20
CTTGTGGGACTCTCTCTCCC	58.819	20	TCATGCAGGAAAAACCATCA	60.049	20
GCCTTTCTTCATGCTTTCCA	60.331	20	TGCATTTTATTTACGTGGTTACT	57.087	24
ATTCGTGAATGACTACCCACG	59.867	21	AATTTCGAAAATTTAAAGGTCC	58.2	23
GCACAACGTATATTCCCACTTTC	59.791	23	GTCATCGCATTCTCGATTCA	59.763	20
GCCAACTCAAAAGGGAGAAA	59.288	20	CACTGGCCAAGAATCAATCA	59.648	20
TCCATCCCCTGAAATAGCTG	60.029	20	CCGTTGGATTTATCTTCTCCAT	59.333	22
TGCACATTTAGGCTCTGACG	60.011	20	TTGCTCGAATTCATATTTTTATG	57.083	24
TCAACGTTGCTGCGTATGAT	60.288	20	GTAGCCCGAGTCAGATCGTC	59.834	20
TACCGTGATTTCCTTCCACC	59.79	20	TCCACCACACACAGGGTTAT	58.697	20
ATTCTATCTCCTCTCCGCCC	59.634	20	AGGGATGTGTTTGGACGGT	60.23	19
CATCAACAACACCATCACCC	59.656	20	TCTCCATTCCATTGACCCAT	60.135	20
GACAGCATACGCGCTCATTA	60.006	20	GATGAAAACGTGAGGCTGAAA	60.242	21
GTTCGAACTGTTGCATGTGG	60.16	20	TTGGTTTTGGGGGTTAATGA	60.024	20
TTCCTTTGGACAAAAATGCC	59.916	20	GTGGCAGTAAAATTGTGGGC	60.374	20
GGTGTGCTCGAATTTTTGGT	59.978	20	CTAGTGTGCCCCCTAGTTGC	59.757	20
GACAGCCGATATTTGCTCCT	59.297	20	TTTCGAACTCGGACGAAGAT	59.813	20
TGTTCTCTACTATATGTCATGTTTT	58.033	27	GCAGTGTTATCGATGGCGTA	59.718	20
GAAGAAAACGGCTGAGCAAG	60.132	20	ACTCTCCATTCCATCAACGC	60.081	20
AAAGAGCTTCCTCCCACACA	59.844	20	CCGAAAAATCAAAGGTCCAC	59.406	20
ACCTTAACTTGCATGCACCC	60	20	GCATGCCTTGTACGGTTGAT	60.925	20
GGGACTTGATTCCATGATAACC	59.537	22	CAACTTGGTCACCTCCTTGG	60.536	20
GTGCATGCAAGGAAAATGAA	59.67	20	CCCTGGATTTTGATTGAGGA	59.864	20
AAAACCCCATATCTGTGGCA	60.192	20	GAGTTGTGCAGCCAGGATCT	60.418	20
GAACCTCGAACCGTTGAGAC	59.703	20	CGGGATTTAGGTGTTTTGACA	59.847	21
TACAGTCGGGCAAGTCTCCT	59.867	20	TTGTTTCGGTGTTGCTTCAG	59.881	20
CCATCCCGCATCATAACAG	59.892	19	TTGGGACACATTCACGAAAA	59.941	20
GCATGTGGTCCCTAACTCAA	58.57	20	TGAGTTGGCCAAGAGAGTGA	59.545	20
CGTGTGCGTGTATCCATGA	60.13	19	GGAAAAATCAAACAAAAACAC	60.238	23
CATCCCAGTTATGTCAAGCG	59.148	20	CTTTGGGTTGAGCTTTTCCA	60.22	20
CCTTGGATTTTGACGCCTTA	60.067	20	CAACTGAATGCGATGTGAGG	60.263	20
TTGGTTATCGCTTGAATGAGA	58.374	21	CGAAGGTTCGGTGATGATTT	59.933	20
AGCTCCTGCTGACTGAGAGC	60.041	20	CTTTCACCAAAATGTGGCCT	59.971	20

GATTGCAGCTCATCCTTGGT	60.226	20	TGTGCCATTTCTTGCACTTC	59.847	20
TGTCCTTGTTTTCGGATGTTC	59.963	21	TTCTTCAACCGATCAATGAAA	58.201	21
TTCAGATGCTTGTTTTAGGTTCC	59.659	23	TCATGAGATCCTGGGTAGTGG	59.935	21
AATGGCCGACACTGCTTTAC	60.14	20	TCAAAATCTTATGAAATCCGCC	60.274	22
TGTAAAAACTTCCTATACATAACG	59.5	27	GGGATTGGGATGAGAAGAGA	59.016	20
GTCCCGGGAATGAAGAAGTT	60.306	20	ACAGACTCACGCCCTCTCAC	60.467	20
TCAAATGTTGATCCAGCAGC	59.805	20	CGCAAACTGGTCGGAGTTAG	60.817	20
CCCTCCATTTCTCAAACCCT	60.298	20	CTTGAAAGTGACGTTGCTGG	59.485	20
ACAAATATCAGTAAAAATGCGCT	57.188	23	GGTGTTAAAAGATGCCCTCG	59.569	20
AGACAACCCACAAATCCGAC	59.827	20	CCCTCTTCTCCATCATCACC	59.46	20
CTAACAGTCCGGTTCACGGT	60.028	20	CGATCGATTTTAGGGTTTTCC	59.795	21
AACACAAGGAACTTGGGACG	60.005	20	CTTTCCGCCTCTTTCCTTCT	59.955	20
CCCAATTCTCCATCATTATTATTC	57.89	24	ATCAAGATCCAAGGGCTGTG	60.073	20
CCACTCCATCACCATCACTG	59.954	20	TTACAGAAAATCGGATCGGG	59.894	20
TCCGAATCTCGAGCCTTAAC	59.41	20	TTTCAACAAACACACACGCA	59.765	20
GTTGAGATTTGGACGGGAGA	60.05	20	GACAACCAAGCACAATCGAA	59.697	20
ACAGCCCCTACTTCCTCGTT	60.132	20	TCACCCTTCGAGCTTAAAACA	59.869	21
GCAAGATTTCAAAATCGCAT	57.843	20	CTTGTCTCCGTTCTGCTTCC	59.989	20
TTTGAGGCAAGAAAAGGTTTG	59.366	21	ACTTGCACTCCCTGTCACCT	59.756	20
GTCGGCCAAGAAGAGAGAAA	59.55	20	TGGAAACAAATCAATTGACCA	58.855	21
TCACATACTCATGCAAGCACA	58.878	21	CACAGCAGTAGGGTCCAAAA	58.773	20
TGTCCATCGTGAAAAACCTTC	59.963	21	CCCACCCCCAATATCAAAA	60.369	19
GAAGCATGCGAGACATTTCA	59.955	20	CCACTTCAAGATTGGGGAGA	60.042	20
ACGCAATCGATCTTCCATTC	60.043	20	AACAGGATTTGCTCGCCTTA	59.845	20
TCATGGTTACGAACCTCCAA	58.973	20	TCTATCTCATCCCCTCACCG	60.027	20
CAAGGGCCGAGATTTGTTAG	59.702	20	TTATGGTGCTACTCCCACCC	59.813	20
CATTCAGATCTCGTCCGTCA	59.787	20	CCACACACTGCTCACCTGAT	59.738	20
CCGCCTCCTTTTCTCTTTCT	59.955	20	CGGAAGTCACTTAGGGTGGA	60.103	20
CGGGCTAAACGGGTCTATTT	60.324	20	TGCAGTGGGTTTGATTGTGT	60.008	20
TCATTCCAACTTTGTAATCAAGAA	59.119	25	TTTTCAGTTAATGAGGTAATGC	58.849	25
GTGATGATAATAGGCGGCGT	59.951	20	CAGAAATTTTGGAGGCTGGA	60.184	20
CCCAAGACCCCAATTTGATT	60.91	20	ATTGATAAATGCCGCAGACA	59.14	20
TAGGCAGTGCAACGCATAAC	59.902	20	TTGATTTGTATATAAAGAGGCT	58.367	25
CGTGTGTGTGAGTTCGTGTG	59.811	20	TTCTTTCCACCGAAAACTGC	60.227	20
ACGATGCCTATGATTCTCCG	60.059	20	TCTTCTAAGGTGCCCATCTG	57.894	20
AATCAGGGACCCAACAACAA	60.21	20	GCATTGGATTCCTTTTATCCG	60.63	21
TGTCATGGCAACAAACCCTA	59.964	20	ACGCAGCCGGAGTAGTTTTA	59.904	20
TACCGTACCCTTCGCACC	59.522	18	TTTATGCCTATGTGGCTGCTT	59.756	21
GACTCCCTTGAGCAAAGTGG	59.844	20	TGTTAGGTGGTGGGGTTGAT	60.088	20
CTGAAGGCAACTTGAGGAGG	59.982	20	AGATCACCAAACCAACCAGG	59.82	20
AAAATCCAACCATTCACACG	58.325	20	TTGGTTTAAAAGTCGTTGTTGA	58.405	23
AGAGTTGGTGAGGGACATCG	60.112	20	AATCTAACTAATGGCGCGGA	59.704	20
TGGAGGAATTCTTCTGCCAT	59.629	20	TCCAGCAGTTTCAATCACCA	60.24	20
TTGATTGAACTACATTACAACAAG	57.557	27	TTTTACAATTCCTGGGGCAG	59.931	20
CGGCATGCATGAGAGATTTA	59.792	20	CCTGCTCAAAGGGAGACAAG	59.982	20
TGATCCATTTTGTTGGCAGA	60.049	20	CAGCACCAAGAATGCAACAT	59.722	20
GTCTTCCGGAGTACGAGCTG	60.012	20	TCAAATCGGAGGAGAAATGG	60.006	20
AATCCTCGTAGCTCCCGTTT	60.096	20	AACAGTGCTTTTGTGATTCCA	58.269	21
TTCGAATGCGGTTTATCACC	60.837	20	CACCGTGTGCAGATTTGTTG	61.18	20
CCGAATACTTTCTTTTGTAGGC	57.198	22	TGGGATAAATCTTCAACACCG	59.809	21
CAATGCAGAGATGGACGAAA	59.799	20	TATTCGCAGTAGCCGTGATG	59.856	20
TGTTGCGTGGGCTTTTTATT	60.488	20	TTCACAGTTTTCATTTGATCACC	58.986	23
TTGATCATCCTGGAGTAAGATTG	58.2	23	AGTGTTTTGACATGATTACTCG	57.373	24
AAATCAGTCTCCATCCGTGC	60.081	20	GCAACGAAATCCGTAGCTGT	60.278	20
ACCCTTGGTCGAATTCCATA	59.244	20	ATTAATCAATATAAGGTTGCAC	57.338	25
TGCAAATGAGGATGAACACG	60.665	20	GGTTCGAATCCTCCACTACAA	59.042	21
GATGATGATCGGTGGAGGTC	60.297	20	TATTGCTTCAACCTGCTGCC	61.304	20
TCCCAATCACCATTCAAGTG	59.343	20	CCTTGTTCGTGTCGTCACAT	59.597	20

CCAGGATCGAATGGAGGATA	59.848	20	TGGTTCCAAGAAAGTAGCCG	60.241	20
ATTTTCGTTGGAGGAGGGTT	59.805	20	ATCGTTTTCGACTGATTCGG	60.074	20
CTATGACTCCACCCTGTGGG	60.377	20	TGCATTGTCAAAGTAGTTAACT	59.027	26
GCGATGGGAAGATGGTAGAA	60.036	20	ATTCGTGCCAAGTTTATGCC	59.967	20
AATTCAGCAAGAATGATAAATCG	57.507	23	GAGTGATTTGAAATAAAATTTG	59.694	26
CCAAAAATTAAAGGCCCACA	59.805	20	AGGATGGCGTGATAGGTGAG	60.096	20
CAAACTGTTGAAGATTGTTTACGG	59.966	24	CGAGTAAACCAAACACGTGAA	59.71	22
AAAAGGGCACAAACAGCAAT	59.615	20	AATGGCATGCAACTGTTTGA	60.119	20
GTTCGCGCAAACAATGTTAC	59.234	20	GTTAAAATCGAACCGAACCA	57.607	20
TGGGTGTGGTGCTTTGAATA	59.964	20	ATTTCAACCTTTGCCAACGA	60.481	20
CAAATTGATCCAACGACACG	59.964	20	CTTCTCCCCTTTCTCTCGCT	60.088	20
GTGTTCATCTCCGCCTTTGT	60.119	20	TCCTCACCACTGTACCCCTC	59.962	20
AAACCATTTTCAGACACGGG	59.83	20	CGAGATGGGGACAGTTGTTT	59.966	20
ATCCATCAAGTTTGCACGGT	60.384	20	GACAGCCAGCTGAAGAAACC	59.997	20
ATGCATGGGTATCAGGCTTC	59.923	20	ATAGGCAAATTCGGAGGCTT	60.061	20
ACCTAATCATGTTTTGGGCG	59.823	20	AGAAATTTTGCAGCGAAACG	60.376	20
CACCCACCCTTCCCTTTATT	60.046	20	GGCGTTTGAGGTAGGAGATG	59.694	20
ATGGGCCAGGGAAATGTTAT	60.399	20	TTATTTGGAAGTGCAACCCA	59.013	20
AATGATGGTGGAGCTGACCT	59.535	20	CACTCCAACTTTGCAAGAACAC	59.819	22
TGGGAAGATCTCTCCGTCAT	59.612	20	ACTCCCCCACTTTCCTTGTC	60.349	20
GGACAAGTGGCAATGTGTGA	60.58	20	GGAGGGAGACCATGTGAGTG	60.527	20
GGTTCCCCAATATTTTCACG	59.135	20	TTACCACAGGCTTTTGGAGG	60.103	20
GTTTTCTGCCGAAGCAAGAG	60.132	20	AAATATGGGTGAGGTGGCTG	59.813	20
GTGGAAGTGTTTTGTGGGGT	59.721	20	GTTTAAAGGTCCCTCACCCG	60.714	20
TTGCCGCCTTTGATTACTCT	59.845	20	AAATACACAATTGAACCAACA	59.589	25
AGCTGACGTGAAACCGAAAC	60.299	20	CGCCAAACTCATTCCTTCAT	60.074	20
GTGAGGGATAGTGAGACGGC	59.685	20	CCCTCTCCTCACCACACTTC	59.682	20
TGAAGCATGTATCACTCTGCAT	58.407	22	GGGCGAGCAATCTGTAAGTC	59.843	20
TATGGGTTATCACCGGATCG	60.544	20	AAATCAAAGGCCAACAATGG	59.801	20
CGTCTCACGACAAGAACGTG	60.5	20	ATTGCATGTGCGAAAAGGAT	60.478	20
TCATGATGATTACATTTGTGTTGA	57.953	24	GTGTGCAGGGTTGAATCTGA	59.682	20
CATGTGGATTCTATTCCGGC	60.296	20	AACAAAACCAGGCACACACA	60.049	20
GAATGACACACGCACACACA	60.218	20	CTTCAGACGAAGCGATCACA	60.136	20
GCCATCAAAACCAACGAAAT	59.807	20	GGGCAGGTGGCTAATCACTA	60.096	20
CTTCTGCGGTGTTCCAAGTT	60.291	20	TGCATGCTCACGCAAAGTAT	60.432	20
CCAAAATCAACGTCCCAGAT	59.79	20	GGTCAAAATTGGGGAAATGA	59.599	20
CTATGTTCCCTGCTTCACCC	59.55	20	CCACGTGCTCCATACTTCCT	60.134	20
TTTCATGGCTTTCTGGGTCT	59.67	20	AAAGCCGACAGACAACAAGG	60.291	20
TGTATGCTGTAAATGAAACTGCTG	59.381	24	ATCCGAAACAAAAGGGACAA	59.406	20
TCAGATATAACGGAGGAATCCAA	59.816	23	CTCCATCCTCTTGCTTCGAG	60.088	20
TGAGGCTAGGGAAGGAATGA	59.767	20	ATGTGAAGAAGCTGCTGGCT	60.164	20
GGGCCTTAGTCCATGTCCTT	60.328	20	GCCTACCTGCAATTGGACAC	60.526	20
TGACCAACTCCATGTTTCCA	59.935	20	AAAATAGGCCCTTTTGCGTT	59.97	20
CAATCAATTATGCTAACAATTACG	59.083	25	AAAAATGAGTGGTTCATATTGG	57.968	24
GTTTCTGCATTTTGGGAAGC	59.691	20	TCCCTTGTCCCATTTACCTTT	59.69	21
GATTCAGTAGCACAACCACCC	59.468	21	CCCTTTGAAAGTTGATGGTTT	58.085	21
TGCTATTTTCAGCCCAAACC	60.074	20	TTTTTCGAGCAACATCTTGTG	58.953	21
CTTTCTGCATACTTTCCCCG	59.702	20	TGAGATCACGAGGTCACGAG	59.98	20
ATGGGATATGAGGGGAATGC	60.882	20	TGTTTTCAATCACAGCCACC	59.547	20
CGGTAATTTGAAGTCAAGGGA	59.074	21	CCAATTGTCCATATTTCGCC	60.153	20
GCGGATGCTCTTAGTTACGC	60.01	20	TGTGAAAAAATTTCGAGCACA	57.891	20
CTCCCCAATCAATCCAGGTA	59.744	20	AGAGCATATCCAATGCCAGG	60.059	20
TCTTTTCCGTGTCCATTTCC	59.91	20	TGGAAAACAATGCCTAACAGC	60.124	21
TTATCATGCAAATGAACGGG	59.377	20	CTCCTACATTATTTGGGGATTA	59.567	25
AAAGATGGCCAAAACTGTGC	60.118	20	ACGGGCAGTTGTCCATTATC	59.82	20
ACGTTGCAAGGTCTACCACC	60.035	20	CAGTCCCCGACTCAAAAATG	60.486	20
TGCGTTTTGACGATATATAGTGTT	59.092	25	GTGCAGTCGATATTTGCTCCT	59.354	21
AGGTTGCGTACATCTGACCC	59.997	20	TCACAGCATACGAGGGACAA	60.263	20

AAGTCGATCGAGCAGAGTAACA	59.149	22	TCTCGCGGTTTTCAGTTTCT	59.993	20
AAGGGCCGAGATTTGTTAGA	58.787	20	TGGCCTTCCTCAATCTATGG	60.029	20
TATGACTTCGGCATTACCGC	60.991	20	TCTTGCAATTGAGACCGCTA	59.566	20
CGTGTCAAAAATCTGTTCATTTG	59.544	23	CATGGTTTGCTTCCATCAGA	59.648	20
TTCAACTGGATATCAAACGCA	59.172	21	TCGATCACACAGAAAACACGA	60.294	21
CATCCCTCCACATTTGCTCT	60.073	20	ATATTTTGGCATTTGGAGCG	59.928	20
TTTGAATACAATGCTTCATCCA	58.161	22	CCAATTACACAAATCAACCTG	59.244	22
CTGATGTGGCTGAAATCCAA	59.648	20	TGCGTTTTGACAATATATAGGT	60.083	26
CTTGAACATGGCCATCACAC	59.967	20	GCATGTGTGGGAGAAGAAAG	60.248	21
AATTAATGGGCATTCGAGCA	60.424	20	TGCCAGGGTTATCTTGATCC	59.894	20
ATTATTTGCATTGCTTGCCC	59.935	20	GAGGACAAGAGGTTGGGACA	60.088	20
ATGTGTTGTGATGGGGGATT	59.91	20	TGAACTTTGGCGTTCTTGTG	59.881	20
ATGGATTGCAGAAAGATGGC	60.043	20	TTGTTTGGGGGTGTTGAGTT	60.246	20
GACGGCTGATATTTGCTCCT	59.297	20	TTTGCACCTGAGGAGGTGTT	60.69	20
TGTTATGCCTATCCCTATCAAGTA	57.02	24	TCCATACTCAACACAAGTCGA	58.283	22
TTTCTCCTTGAGCCTCTTCAA	59.181	21	TTGTCCAGCTGCTCTCACAC	60.187	20
ATATCGCGGGCTAAGAACCT	60.082	20	ACAAAAGCGATTTCGTCCAC	60.118	20
TCCGGAGAAAATGAAGAAGA	57.459	20	ATAATGATATTTTGGAACGCAT	57.16	23
TGGGAACTCGAGAGGAAAGA	59.92	20	CGTTCACGAGTGGTGACAAA	60.757	20
TGATTTTGATCCATTGCCCT	60.274	20	AAGGGTTTGGGCAGTCATAA	59.429	20
ATCACGCTGATATCGCACAG	59.854	20	CCATCAAGGAAAGACGCATT	60.074	20
CTCTGGGCTGATCAATTCAA	58.797	20	TCTGCCCTAAGATGAAACGG	60.206	20
GGCTGAAATCTGGTCTTCCA	60.195	20	TGAATCAATCTTGTGCGTTGA	60.25	21
TGAGTGCTAGACTATTGTAAAAA	57.09	25	CGCCATAATTGACTGCAAAA	59.702	20
TGTGAAGGGGTGTTCAAGTG	59.565	20	TGTTTGGCTTTCGATTGTGA	60.234	20
TTTTGAAACATGATGGCGTC	59.523	20	CACGTGGCATGATAATAGCG	60.118	20
TCATTGATTTCATTGCATAATCTG	59.005	24	GATGATCGGAACGTGAAGCTA	60.228	21
AATCCACGAAACGGTTTGAA	60.344	20	TCATCTTCTCCACCAAAGGA	58.201	20
AAACAGCCCATGTGAGAACC	59.973	20	CAAGTGTCGCAGTAGACGGA	60.049	20
AAACCAATTGGCAACGAGAG	60.11	20	CCAGGCGTACAGTCAAAGGT	60.171	20
CCGAATTTGGCTCTTTTCCT	60.553	20	CGAGCAGAAAATCTGTGCAA	60.134	20
ATCTGCTCCTCTCCTAGCCC	59.942	20	ATTAGAAAAATGCGCGATCC	59.174	20
AGGATTTCTTCCCCCAAAAA	59.75	20	CAGCTGCAGAGATGGAATCA	60.096	20
TATCGCATCATTCCCCTCTT	59.486	20	CGCGTTACGAATCCAAGTTT	60.131	20
CTCGGTCTCTGGGACCTTTA	59.28	20	CTCCATGGTGCATTTCACAC	59.967	20
GTTGGGCGATTTGAAGCTAA	60.209	20	TGGGTCACTCCTGTTTAGTGA	58.201	21
GGCAATGGTTTGGTTTCAGT	59.836	20	TTGGCCATGTGAAAATCAGA	60.049	20
CTTGAGGCCCACACAAGAAG	60.822	20	CAATAGGTAGCTCGGATATGT	59.891	23
TATGCACGTGACTTGCTTCC	59.871	20	TGCGGATTGAACAAATCTGA	60.197	20
ATCCCGGAAATAGTTCCAAA	58.368	20	GGCCTAGGCACCAAATCTTA	59.182	20
GTTGCATAAACCCTAGGCCA	59.96	20	CAAAACCCACACCCTGTACC	60.126	20
CCTAGGTCAGTTCCAACCCA	59.959	20	CACCATACAAGCATTCAGCG	60.28	20
AAGGTTTCAAGTGGCAAACG	60.147	20	CTTTCAATCGTTGATGGGGT	59.79	20
CCCTAACCCTAAAGTAAGGACCA	59.788	23	TCAAACCAAGAACCGACTGA	59.262	20
CAATGCACCAGAGTAAGTTGGA	60.168	22	TGGTTTTATGTTTCTCTTTGGG	59.865	23
GTGGATGAAGATCCTGGACG	60.475	20	AGAGATGCCGGGGAAGTAAT	59.925	20
TATCGAGCACCACCAAATGA	60.073	20	TCTGTGAATCAAGCTCAAGCA	59.731	21
TGATCCGAGCTTGGAATAGC	60.318	20	TTTCTCTCTTTTGGTGGAAGAA	58.098	22
GGTCTCCCTCCCTTTCTCTC	59.226	20	ACTGTGAAAGAGACCTCCGC	59.455	20
CATGGAATTGAAACTTTCGGA	59.924	21	AGGTCGAGGATTGTCGTCTG	60.261	20
TCGAACACCAAACCAATTCA	59.941	20	GCCGATGCTGAACTGTGATA	59.83	20
TGATGGCAACCAAGAACTCA	60.24	20	TCACCCTCATAATGTGTGGC	59.374	20
TTGCATTTGGATGCATGATT	59.898	20	GGAATCTAGAACAGACCAATC	60.196	23
TGTAACTTTACGGCTTTTCTGGA	60.166	23	TGAGTCCATGACCCAACTTTT	59.439	21
TTTCTTCCATTGGCTTCACC	60.051	20	CACATCAAATTGAGGACGATG	58.987	21
GGACATGGGATTGGAGAAGA	59.862	20	AGGCGGCTAAATCAATCAAA	59.682	20
TCGAAAACCGGTTAAAGACC	59.064	20	TGAGAGTCTTCTTCCTTGCACA	60.171	22
TGAGAAACGAATGCACATGA	58.782	20	GTTTCCCCAAGCTTCCTACA	59.17	20

GGGCCAAAAGAACAACAAAA	59.953	20	ATTGTTTCCACGCACTCACA	60.16	20
TTGTTGTACCATTGTGGAAAGAG	59.051	23	GTGCGTTGTGTTGACGTTG	59.768	19
ACCCAGAGAGCACTCGAAGA	60.135	20	TTAGCATTTGACTACACTCCTC	58.151	24
ATTTGAGTGGCTGACCCAAG	60.111	20	TGCTGGAGCAGTCATTTTTG	59.988	20
AGAGAGAAAATTGCATCGGG	59.269	20	TTCCCGAAAATAAAAAGAAAA	59.552	24
CGCATTAAATTCGGAACAGA	58.769	20	GATAACATGCCATCACACGC	59.963	20
TCGTCGATCGGTTAAGAAATG	60.081	21	AATTTCATCTTCACTGCCCG	60.074	20
TGGGGTAATATAAAGGTTCATCC	58.223	23	GAGTGGGGATCAGTCATGGT	59.774	20
CCGATTCAGATACTCCCCAA	59.887	20	AACACCTTCCACGCAAACTC	60.156	20
TCGTGCGCAAAAATTATGAA	60.211	20	TGTGATTTCATCCATTCGGA	59.859	20
TTCTCAACTCGTCAACCCGT	60.69	20	CACACAATTGAGCACACACG	59.778	20
TGGAGAGAGAGAAGATCGGC	59.636	20	CAACACACCACGCATTCTTC	60.16	20
ACAATTGGATTAGTGACATGGCT	59.781	23	ATGCGCAGATCTAATGGTCC	60.066	20
CACCAAAGGAAAATTGAATGG	59.302	21	TACAGGGGTTTGCCTTTAGC	59.225	20
CCCTCCTCATTTCCAACATC	59.336	20	TGGCCCTTTTGTACACTTCA	59.17	20
TGGTGTTGGGGTTAATTTCG	60.587	20	GTGCAGCACTAGGTCCATTG	59.318	20
TCATTGTTTGAAGAGTGGGAAA	59.587	22	AATGAATCTACGTCCACGGG	59.813	20
ATTTTCTTGGCCCAACCTTT	59.814	20	CACGCCGCATTTCTTCTAAC	60.772	20
CCAACCTGTATCGCTCTTTCT	58.474	21	ATTTGCATGGCTCTGGGTAG	60.096	20
AGTGACCGACTCAAAATGGG	59.966	20	GGGGCGTATAGACGCAAATA	59.95	20
TGCAAAGATGACAGAAACAAGA	59.912	23	CGGATGGATGCTTCAAAGTT	60.074	20
CGATATGCTTTGTTGGGGAC	60.331	20	TGGGGTTATTAGTGGATCAAG	60.204	22
AAACCCTCTCAAGAACTCCAAA	59.255	22	TGCACCTCCTCTTCAACAAC	58.854	20
CATGTTAAGGAGGGGATCCAT	60.025	21	ATAATGTTGCGCGTGCTTTA	59.379	20
TGGCTGGCGGTTTTAAATAAT	60.659	21	AGAGCAAAGTGTTGAACTCTC	58.794	22
TCGGGTCTCAACACATTCAC	59.525	20	AGAGAGAAAGTGGCAGTGGG	59.45	20
ACGAACCGAGACTGACTGCT	60.057	20	TCGCCGTGTTTGTATTCTTG	59.729	20
TCGAAGTCCCACTTCAGCTT	59.989	20	AACGCGCATTTTTAGGATTT	58.764	20
TCCCTCTTTTGTATCTCGCC	59.269	20	TCAGCTCGGGAAGAAAACTC	59.55	20
ATGGGCACGGTACTTCATGT	60.263	20	CGCTATGTGACCATCTGTGG	60.136	20
TGTTGTGTATAAGGAAGTTTTTCG	57.546	24	GTGTTATACCCGTGCGTTCC	60.257	20
TGAAACCTAAGTGGCCTGTCA	60.674	21	GATTGAATTGGTGGGTTTCG	60.17	20
CCTTGCTGGTTTTTGAAGGA	60.22	20	TTTCTTCTCCCTCCCTCCAT	60.008	20
TCGATCAAAGTTATGAATTGGAA	59.851	24	TAGGGCAATCAAGCAAGGAG	60.344	20
CTCCAGACCACCGCTACTTC	59.867	20	GGGCAAAACTGTAATTGCTCA	60.124	21
GCATCTCTTGCTCTCTCGTTG	60.292	21	ACACGAGATTTACGTGGTTCG	60.045	21
CAGGTCGAGGATTGTCGTCT	60.261	20	CATGGAATTGAAACTTTCGGA	59.924	21
GGTGCCACGTGTCATACTCA	60.604	20	ACCTAAAACCCGACCCGAT	60.564	19
TTTTTGGGAAATCCTTGCAC	59.916	20	CGAACCATCGTCTCGTATCA	59.673	20
GGATTGGACCTATAATATTGACC	59.848	24	TTGGGGAATGGAAGAATGAG	59.864	20
TGCAGAATCATAAAGTGCAAAC	57.98	22	TTGGCAAATTTTCTTGCACA	60.229	20
AGAGGAGAACGCCATTGTTG	60.255	20	TATTGAACTGCCTTTCGCCT	59.845	20
CATGGCGGATTTACAACTGA	59.542	20	CGATGCAGCAGAAAGACAAA	60.134	20
TGCCCTCTTGTGATACCCTC	60.073	20	AAGGGCTTTGTTGGTTTGTG	60.008	20
TCCGACAAACACAAGAACCA	60.128	20	TTCATTCTTTGCATCCCTCC	60.014	20
CTGTTAGCAAGTTCCACGCA	60.05	20	GGAGTGGTCGGAGAGTTGAG	59.835	20
AGCGAAATTGATCTCTGCGT	59.985	20	GAGCTGCAAAAACCATCACA	59.847	20
CTGGGAAACCAATCTTGTCG	60.486	20	TGCTTCCGCATTTTCTTTTT	59.832	20
CAAAGGCCCACAGTGGTTAT	59.853	20	AACCTGACACGAACACGACA	60.203	20
ATGATTGCACCATAACGCAC	59.43	20	CTGAGGATAAAGGTGGCGAA	60.206	20
GAGACCCTCAACCTCACCCT	60.504	20	CCGGAAAACACCATCAATCT	59.79	20
GCCTTTCGAATTGGTGTTTG	60.481	20	CTCTCAGGGGCAGATACAGG	59.82	20
GGCAGGAATGAGACACCAAT	59.934	20	TTTTGAACGTTTGCAGTTGG	59.746	20
TGGACAAACAAGCCTCACTC	58.854	20	TGTTCTCGTATGATTACGCTCC	59.252	22
CTCGTAGAAGGGCAGTGGAG	60.005	20	ACCATGCACGTAAATCCCAT	60.081	20
GGAACCATCATGCCGTTATT	59.651	20	TTGTTATTGAGAGGGCAGGC	60.214	20
TGAATTCAATTGTGTTTTGGG	58.374	21	GATTGATGAGGGTTCCAAGC	59.488	20
ATCCAAGGGTCAATAATGGTT	57.278	21	TGACTTGTCACATTTTGGGC	59.547	20

TGGAGGAGTTCTTCCAGGAG	59.375	20	ACACACCTAGTGTGCTATCATC	60.002	25
CGAGTATCCTCCCACTCCAA	60.065	20	TTTCCCGGAGAGGAGAAAAT	60.011	20
ATCGTGAGGAGCGTTGATCT	59.834	20	CCAAATTGCCCTTCTGTGTT	59.971	20
AGGAGAGATTGTAACGACCCA	58.658	21	ACCAAGATTTGATCATGGCG	60.864	20
CATTATTTAATGTAGGGTGGGTGA	59.089	24	TAACATAATGGTTGGCGGCT	60.343	20
TGCTTCCCTCAATGGTTTTC	60.051	20	CATTGCATCTTCCCTTTTGG	60.439	20
ACTGGCTGCTCTACGCTCTC	59.921	20	GTATTCGCTCTGCCACAACA	59.871	20
CATTGAAGATCCCGGACAGT	59.927	20	TACTCCTGCTCAACCTGGTG	58.879	20
AAAAGGCCAGCCAGCTAAAT	60.224	20	CCACACCCTCTTCCTCTGAA	60.229	20
TTTGGATCACTAGGGCTTGG	60.066	20	AACCAGCCTAGGGTTGAGGT	59.994	20
TCACGTGAGATGCTGAGTAGG	59.049	21	TGTAAATCTGCCCGAAAACC	59.938	20
GCTCTTTCCCCTTTGTCCTC	60.19	20	GGTTAACATTTCAGCGAGGC	59.713	20
AGCGGTTATTACCGGATCG	59.93	19	AATGAACGCAACCCAAAACT	59.476	20
CGCTACTCTTCGAGTGCGTT	60.73	20	CGCGGGGTTTAAGTAATGTT	59.01	20
CAATACACCGGTTCCAAGTG	58.897	20	TGGTGTACAGTAAGAGGCAAA	59.724	23
GGAAGGGGAGTTAGCGTATG	58.671	20	ATCCTGCAATCATCACCCA	59.866	19
ATCCGATGGATGAAAAGCTG	60.036	20	AATGAGGAAATCGACGATGG	59.894	20
AGGAAAGAGCAAGCAACGTC	59.621	20	ACCCGGACAATGAGCAATAA	60.331	20
AGCCTTTAAGACACGCCAAA	59.883	20	CTCCCCTCTTCGAATATCCC	59.859	20
ACGCGTGGGTGATATGCTA	60.112	19	TGAACCAAACACCCGTGATA	59.816	20
TCCAAAGTCACACTTGCTGC	60.032	20	TTGCCACCGATATCAAACAC	59.4	20
AGTGATGGCGGATCTTATCG	60.059	20	CAAATCATGTGCGCTGAAAT	59.694	20
TTTGGCCCAGACATTAAAGC	60.074	20	AGTTTGGTTCTGGCTCATGG	60.111	20
AAATCCTTTGCACAACCCAC	59.836	20	GTCAAGTCGACCACCCTTGT	60.009	20
CAAGAATTCCAAGCTTGCCT	59.452	20	TGGAACGAGGAGAAGGAAAA	59.784	20
CTCATGGCGCTACATCACTT	58.903	20	CCAATTTGAATGGTTATCACCT	60.457	23
CGAAGAAAACACCCGGACTA	60.103	20	GAAGCCATTGATAATCACCGA	59.915	21
AGAAAAGGGAGCTCCTCAGC	60.096	20	TCCTTCCCTGCATTTCATTC	60.014	20
TGAGTGAGTTGGCGAGAATC	58.96	20	TCATTTCAAAAATCAATGGATG	59.291	23
CTTATCCCTACACCGCCTCA	60.088	20	GTTTTGTAGCTCTCGTCGGC	60.022	20
AAGAATCGAACGGGAGGAAG	60.569	20	TTCTTGGTTAGCTGGTCTGGA	59.861	21
TTGGGATTAAGGCTTTGGTG	59.931	20	TTTTGAACAATGATACCTTCTC	58.271	24
TTGTCAATTCCTCCCTTAGACA	58.694	22	TCATGGTGCTTGAAATTGGA	60.049	20
GCATCTCTTGCTCTCTCGTTG	60.292	21	GTGGTAACATAAAGGGCCGA	59.823	20
AAGGGGAGATGAAGGGTGAT	59.755	20	GCTACGAACTACGGGGTGAA	60.132	20
GTCTATGTGCGTTTTTGGCA	59.735	20	GATGGGCTAGGAAGCGAAA	60.303	19
CGGCGTTAGCCAAATCTAAG	59.868	20	CTTACCACCATTCACCACCC	60.088	20
CAATAATGCCCCCTTCATGT	59.645	20	AAAAACGAGGGCCAAAATCT	59.945	20
GCGTCTCCAAACAGGAGAGA	60.533	20	CTAAAACCACGCATTCCTGC	60.637	20
CGTCGTTCTTGATTCTTCCA	58.847	20	CAGCTCTCATTATTTCCGGC	59.807	20
TACCGTTTCAAGGTGCAATG	59.585	20	AGTGGAACTCGTCTTCCTCAG	58.533	21
TGCGCTACAAAAACGAGTTC	59.111	20	TCACGATCGAACCACGTAAA	60.111	20
AGTAGTTAGCATGGAAGGGGA	57.827	21	ATGGGGCTGTAGCGATGAT	60.464	19
CGGGACCAAGTGACTTATTTTG	60.741	22	TAAAGTAGGGTGCAGGAGCG	60.399	20
ATCGCATTGCCTCACTTTTT	59.713	20	AAGGCAGAGTTTTGCACGTT	59.92	20
TTGGTACATGGATGGGGATT	59.871	20	ACCTGGTCTCCAAGTGATGG	59.962	20
CTGATTTTCTCGGTAGCCCA	60.206	20	GGGAATCAAAACCATTCCCT	59.996	20
AGTGGGACATCCAGGAAAGT	58.44	20	GCCTGCCTTGGAAACTATTG	59.708	20
CATGAGAGCGGTGATTTTGA	59.799	20	AAACTTGCGGGAATGAGTTG	60.11	20
TGACAATTTTGCCCTTTTCC	59.916	20	GCTGCAGATCTAACGACCAA	59.028	20
AGTCCTAGCCCCACATCTCA	59.679	20	CGATTAACGGTCCGGTCTTA	59.953	20
AATGCGGGCATAAGACCATA	60.31	20	TTAGACGTGAATTGCAAGCG	60.014	20
TATGTTAACGGGGTTGGGAA	60.046	20	AGGCCCATCATACCACAGTC	59.81	20
AGTCATTGCTGATATCGCCC	60.066	20	CATTTTGTGGCCTGTGTTTG	60.004	20
GTCTCCCCATTTGATGCACT	59.934	20	GAGCTCACCGGTTCTTTTGA	60.375	20
CGCCATTACCGTGGATTTAC	60.209	20	CAACGATGTGCTAGTTGTGGA	59.773	21
CTGCACACATTGATGAAGGG	60.112	20	AACACAAAAGGGCTCATTCC	59.031	20
CATCATTTTCTTCGACGGGT	59.933	20	AGAAGAGAGAGGGAGGGTCG	59.945	20

TGCGCTTTTGTCAGTGTACC	59.911	20	TTACGGCAATTTGCATCAGA	60.215	20
TTTGATGCCGGGAATGTAAT	60.153	20	ACTTTTCACGGACTGCCAAC	60.156	20
CACGCTGATATCGCACAACT	59.895	20	AGATGGAACGACCCTGTGAG	60.112	20
ATCCCAGAATGCCTACACCA	60.34	20	TTTTGTCCTTTTGGGAACCA	60.314	20
TTAAATGCACAGCACAGCTC	57.662	20	TAGGAAACCCGCCATACAAC	59.823	20
TCAACTTATATTTCAGCGACGA	57.628	22	AGAAACTTACCGCCAAGTCG	59.378	20
CCTGGATCAACAACAGCAGA	59.831	20	TGAAAAATGACGCCAAAATG	59.538	20
AACGACACTCATCCGCTCTT	59.874	20	GTCGAGTGGGACCAAAAGAA	60.088	20
CTTTCACGGGTTTGAAGCTC	59.853	20	TCCAGTTTTGCTGGAAAAGG	60.22	20
TTCATATATCACGTTAAGACATGG	58.031	26	ACCAAGTCATACATCATGTTAT	58.868	27
TAACCCTTGTTAGCCCGTTG	59.99	20	TCTCACAGGATTTAGGTGTTCC	58.174	22
TCAGCCAAATGCAGAGATGA	60.504	20	TCGATGAGGAATGGGAAGAA	60.538	20
CTATAAGGTTGCACCCACGC	60.523	20	TTTGTGTGATTTTGACCCCA	59.792	20
TCAATTTCTCTAACCTGTAAAATG	58.065	25	TTGAAATGGGAATGCAGGTT	60.309	20
CCCATTCTCTTCATCCCTCA	60.003	20	TGCTGGTACCTTCGGAACTC	60.255	20
AATACACCCCAAAGTGGAACC	59.969	21	TAAAAACCGAACCAGGTCGT	59.471	20
CCAAATGTTAGGGTTATCACAGG	59.654	23	TGGACATTCACTTTGTGGGA	59.935	20
AGATGATCTTGGCATCACCC	59.893	20	GTTGCTTCTTTAACGCTGGC	60.025	20
AGCTTTGAAATGACATGGGC	60.081	20	TGCATACAACACGCAAATGA	59.716	20
TGCATCATACGGCATACATTT	58.928	21	TTCGGAATTTATAATATGGGCA	58.4	22
TTGATCCTTTTTATGATAACCCAA	58.836	24	TTTGCTCGTGTGTTACAGGG	59.758	20
TCAAAGAAAGAGAGTTTAGATCA	58.804	27	AAATATGCCACCTATTGCCG	59.816	20
TTGAAATATACTTTTCATTTCAGC	57.253	25	CTGTTTGGCTACGGAAGAGC	60.015	20
CAATTCGAAGCCCAAATCAT	59.901	20	GGCCCTTTCTCTTGAGTTGA	59.405	20
AATGGGTGGGTTATAATGGGA	60.137	21	ATACCATGGCGTGCAAGAGT	60.547	20
ACAATGTTTCACGTGGTTCG	59.465	20	AATTAGTTGAGGCACGTGGG	59.993	20
GCACTTTGCCTATTCTTGGG	59.708	20	TTTGCATCAAACATGGCTTC	59.67	20
TCCAACCGCTATTTGAATCC	59.901	20	GTTGCGACTCAACACCAGAA	59.88	20
TTTAGTGTTTTGACATGATTACTC	57.557	25	TCGATCTTCTTTCCTTTCCAA	58.89	21
TGCTTTAGGTCTTTGCCTGC	60.523	20	GTACAGGGTTCTCCAACCGA	59.966	20
TCCTGCACTGTGTGTGTTCA	59.905	20	GGTGGCCATTGATAGGAGAA	59.894	20
GAATGCAGCTTTGGTTTCTTG	59.875	21	AAAAAGGGATTATCACGGGG	60.013	20
GGGGAGAGAGAAGGGAAGAG	59.367	20	GCGTTTTGGTGGATGAATTT	59.807	20
AAGAAAAGGGGGAAAGGTGA	59.912	20	ACTCTGGCAGTGCAACTTGA	59.622	20
TTATTGAATTTTCGCCCCAG	59.901	20	GGATTTTGATGTATGAGTTTGC	59.297	24
TCCCCTTTTACTTTATTCTTTCAA	57.604	24	TAACCTGAAAAGGGTTCCCC	60.159	20
TGGACTAGGGGCTGAAGAAA	59.807	20	GGGTCGGGCTAATAGGCTAC	59.951	20
CAAGGGGTATTTTTGTCCGA	59.795	20	TCATATGGGTTGGTGTTGTCA	59.682	21
CCTGTGACTGTCGATGAAGTAAA	59.295	23	TGTGTTTTCAAAAGCCTAGACA	57.63	22
CGAACGATGACATGCTCCTA	59.823	20	CTAGATCGCGGGCAAGTAGT	59.499	20
ACTTGCAAAAGACTCCAGGC	59.478	20	AACCAAGCCTCAGCAAAATG	60.249	20
ATTCACACCATTTGCCATCC	60.591	20	TCTTTTCTCACACACCACGC	59.88	20
AATCCCCGCCTATCTAAGGA	59.888	20	TTCAAGGAGGAAACACGAGG	60.224	20
TGGATACATGGGTGGATAATATG	58.461	23	TTTGTAATAACCCTTATTTTCGT	59.73	25
GCGAGGAAATTAAAGCAGCA	60.476	20	AGAGGGGAGCTCGTACCATT	60.096	20
AATCTCGCAGTGCAAAATCG	61.304	20	TCAAACCTCTTCCATCACCC	59.903	20
TCAACTATTGCCCCTTGGAC	59.933	20	TTGCCAAATGGTGTAATGTCA	59.841	21
CAAGACCACGAGCCGTTAAT	60.132	20	ACTCACACACCTTCACACGC	59.789	20
TCTCATACAGCCAAAACTTAGGA	58.089	23	TCAAGGTGTTGATGCTTGGA	60.24	20
GTAATCTGGGATAACGGGGG	60.391	20	TGTGAGAGACGTCGTGTGTG	59.454	20
GTAAGCATCGCCCTCCATAA	60.06	20	TGCAAGAGCTTAGAACGGGT	60.015	20
CGTCAAAGGAAGATTCGGAG	59.807	20	GTACGGCTGAGCCTGATTG	59.41	19
TGTCTAGGCATCAAGGAGCA	59.547	20	CTGTCCGATATCTAGGCCAAA	59.192	21
AGGGGTTCGAGTGGAAAATC	60.306	20	CGTGTATAATCGGAATCGCC	60.31	20
AGAATTGGAACCCCAAAACC	60.032	20	GCATTCAGTTGGGGTTGAGT	59.973	20
GCCCCAAATCACAAACAACT	59.836	20	ATTAATCCGATGGCCCTCAT	60.499	20
CCCCTCGTATGCAGTCATTT	59.955	20	TACGATTGCCCCGTATTCTT	59.433	20
ACCTTGACGCCATATGCAA	60.088	19	TGTTTTCTTTTACCTGTATTCAA	58.442	27

TGCTCCTCCTCTTCCTTTCA	60.065	20	GCCATAGCTTCTTGGTCTCG	59.978	20
AATATGGGAGGGCTGGTTTC	60.152	20	CCACCTCATTTCCTCACACC	60.363	20
TAACCCACCAAATGCTGTGA	59.964	20	ATCAACATACAATGTGCGGC	59.43	20
AGCGTGAGAGATAGCCGAGA	60.263	20	TGAAAGAATATGAGTTTGAAC	60.004	24
TTTCACCTACCAATTCCAGCA	60.487	21	CCAACCAAATCCGGTTACTG	60.22	20
CACGCGATACCATTCAGTTT	58.651	20	AGGCCTTGCTCTCTCTGTTG	59.745	20
TTAGCTGCTGGGATTTTGCT	59.982	20	TGAGGAGAGGAGGAGATGGA	59.871	20
CTAGCAATGGGGTGCTTGTT	60.132	20	ATCGAAAATGCCTCTCACCA	60.603	20
TGTTTGCTGTCATCGCTAGG	60.011	20	AATGAGTTGGTGTGTTGGCA	60.008	20
AAGAATGGATTGGGTTGGGT	60.422	20	CGGTTGACAGCCGATTTTAT	59.96	20
TTGGATAAATGGGAGGCTTG	59.894	20	TGGCTGGATAGTTTTGGCTC	60.214	20
ATTGAATACGCGAGACCCAC	59.962	20	GATGCAGTGAATGGGAACCT	59.934	20
GGTCAACCTACAGCACCGAT	59.997	20	AATTCTCCACGCTCAAGGAA	59.813	20
CATGGGGAATGGAAAAAGAA	59.733	20	GGTAGCCTGCTGATGCAAAT	60.243	20
GCCTCCTACCCCACTTCACT	60.511	20	CATGTCAAAATATGGGCATCC	60.031	21
GATCTCTGTCGCCATCGAAT	60.189	20	GAAAGTTTGGGGTGGGTTTT	60.068	20
ACGCGCGTTTTTAGAGTTTA	57.824	20	TTTCATATATCACGTTAAGACA	59.191	27
TATTTTGGGCACCCACCTAA	60.181	20	CCAAACGTATATGCCCTGGT	59.708	20
TTTCCGAAACTTCCAATCAAGT	59.98	22	GCGTCGTTTCTTGAATTAGGG	60.962	21
GTCGGTCCCTAAACCCAAAT	60.053	20	ACAATACACGCCACACAAGC	59.646	20
TTTGGAGGTGCACACAACAT	60.008	20	AGCATTAATGGTGCCCAAAT	59.301	20
GGAAACCTTATGCGATTGGA	59.901	20	TGCGTTTTGATGATATATATGT	59.956	27
TGCTTGAGAGTGGGAGGAGT	59.986	20	GGGCAACCTCGAATCAATAG	59.528	20
GCGAATACGTACGGGTGTG	60.003	19	TGAGAAAAGGTTGTACATGGC	60.534	22
ATGCCTTTGCAATTTCTGCT	59.851	20	GGACACGAACTTGAGGAAGC	59.851	20
TGTAGTGCATAAACTCGCCG	59.895	20	ATGCATGCACGTGAATATGG	60.375	20
CTATCAGCGCTTCTTTCCGA	60.617	20	CAAATATTGGTTTCTTCCCGA	58.93	21
TCGTCCTCGTTTCTTTGCAT	60.776	20	TCCCACCATTCACATCTTGA	59.893	20
TAAATAGTGGCGGATCCAGG	59.916	20	ATGGCATTCAAGATTCTGCC	60.043	20
CGCCAAGCACTCACAAACTA	60.05	20	GGGTTATCACCTGATTTCCTCC	60.901	22
AAGGGGGTTATTAGTGGATCA	57.425	21	CCCCCAATTCACCTCTTTTT	60.159	20
AGGCTGGTATTTTGGCCTTC	60.451	20	CCGGGTTTCGAAGTAGACCT	60.488	20
TGATAATGCACTTCAATACAAGC	59.688	24	CCTTGCCAACAAGATAGTGC	58.379	20
CATCTCTTCTCCACCAACCG	60.646	20	TTAGCACAACTGCACAAGCA	59.226	20
ATCAAGAAATTCACCAGGCG	60.074	20	CGAAGGATGTGTTCATTGTGA	59.556	21
TACGATTTTTCGGTTTTCGG	59.937	20	GTTGGGACGGAGGGAGTATT	60.19	20
CGAAAGAGTGCAGTGAGCAG	59.922	20	GCACCATAAAGTTCAACGAAC	60.039	22
GTTGTGTACGCGAGAAACCA	59.764	20	CAACAGGTCTCACCAATCCA	59.52	20
CCCCCTTCTACTTTGGTCAGA	60.473	21	TGACGAGTTAGAATGGCAAAG	59.883	22
AACGAGAAAAGACTGCTGCC	59.621	20	GGATCCAAGCTGACCAGTGT	60.12	20
ATCGGTTATTACCGGATCGC	61.031	20	ATTTCGAAGATCAACAGGCG	60.214	20
CAGGTGCGCCTTATCTCTCT	59.598	20	TGCATATATTAGGGGAAAAAT	57.826	26
TGCATGATTTCTTCAATCTTCG	60.209	22	TCCTTTAACAAATTGGTGTAGT	59.768	26
AAATCTGTCGGTTGCTTTGG	60.11	20	AGAAATTTGTGAATCGCCCA	60.448	20
TGTTTTGTTCGACAACGACTC	58.813	21	TGAGAGGTCTAGGGTTCGGA	59.797	20
TTTTTGTCTCACTAGTGTCGTTTTG	59.786	25	CCGCGCATGTATAAATTCCT	59.95	20
AGTTTTAGCGTGTCAGGCGT	59.943	20	TCTTACCCAAACCCATCACC	59.647	20
AGGACACGTTGGACCTGAAG	60.151	20	GATAGACGTCCACGGTGGTT	59.851	20
TCACGATATCCACATTTAGCAT	57.162	22	TGTATGACATTTGGCTCCGA	60.073	20
CATTGCAGAGAGGCAGTTCA	60.136	20	AATTCCAGCCATGTAGGTGC	59.962	20
TCCACCCCTAGATATCGATGTAA	59.708	23	GCAGGCAGCAGCTGTAAAA	60.295	19
TTGCGAACTAGTTGTCGTCG	60.05	20	CTGCCCACTAATCTGTAAAGG	60.015	22
TCCCACTGCCCAAACTTATT	59.429	20	TGGCGGTAGGTAGCTCTTGT	59.898	20
AGCATGAGAATCGGATGGAG	60.181	20	TCCGTGAACCGTTCTTCTTC	60.232	20
CGATAAAAATGGCACCCAGT	59.823	20	AATGAGGCTGGGTGTGAGAG	60.261	20
CGCTGCTTTCGTGTTTAGTTA	58.327	21	TCCGTTCATTCAACGAGGTT	60.495	20
ATGCTTGTTCCAGCTTGAGG	60.397	20	AATTCGGGTACCATCGACAG	59.813	20
ACAGCGGCTTACTAGCTTCG	59.813	20	TCGGAAAAACTCCTGAGTGAA	59.838	21

AATTTCCCCCAAATCATTCA	59.067	20	TGTGGTGTTGACGGTGATTC	60.426	20
CCCAAGTGGGATATTGTTGG	60.044	20	ACCTGTAGCCATGTGATTGTTG	59.92	22
TTATCACATAAATAATGGTTTCTT	57.797	27	GGGAACATGCTTCCTGAAAA	60.051	20
GTAATGTTCTCATGCGCAGC	59.454	20	CGTTCTTTCTGATTCGCCTC	59.955	20
TTCTCTTGTAATCGCCCCC	60.021	19	AAACCACATTTTACGTGCCA	58.942	20
GGAGAGGCTCTTGGTTTTCC	60.19	20	GAAGAGCAGGGGTGTCTTTG	59.844	20
TGGGCTTCATTTCTGTCAAA	59.247	20	TCGTCCCTTTTCGAATCATC	60.014	20
CCCCCGTTAAATCAAATCAA	59.633	20	TCATTCCCGAGAATCCTTCA	60.538	20
ATCCACCAACCAAACATTCC	59.508	20	GCAAAAGGTTTGAAGTCCTGA	59.345	21
ACCCATTTCATGTCACCTCC	59.636	20	TGCTGTTTTGCTTGCTTGTT	59.656	20
GCCACTGCGTTTGTTAGAGA	59.076	20	CATTAAATCTCATACCCTCAGT	57.435	25
CATACACTTTTCCTCCCCCA	59.784	20	ATCAAGAGCACGGTGGTTTC	60.119	20
CCGTCTTTGTTGTGGCTTTT	60.147	20	TCACTCCATCTTCACACCCA	60.088	20
CCTCTGCAGCCTAAAACCAC	59.875	20	TTAGAATGGCGCCGATAGAC	60.196	20
CCTCCACACCCAATCTTCAC	60.363	20	GCGGGGAAAAATAGGAAGAA	60.381	20
GCAAGAAAGCAGTGCACCTA	59.224	20	TCCTCAATTTCTTCCACCCTT	59.926	21
TTGGCGTAGATTCCACTTGA	59.272	20	CTTTCCAAGCATCCAACCAC	60.495	20
TCACTCATTTGAGGATGGATTG	59.933	22	TACTTTTCGCATCCGACTCC	60.214	20
TCCACGAATCGTAGTTGACG	59.716	20	TCTCGGTGAGCGAGTAGGTT	60.012	20
AGTTGCCATCGTGTGTTTCA	60.16	20	GGTTTTGACCATATTTACTGTTT	59.631	26
GCTGCCACAAAATCATTTCC	60.457	20	TTAGTTAGTACCGATTTCAGGG	57.499	24
ACGTCCTCTAGGTGTCGTCC	59.179	20	TTCAAATGCACGTGTTGGAT	59.972	20
GATTCGTTGCAGAAATCCGT	60.081	20	CATTGGGCCTTTGACCTTTA	59.931	20
GTATTCCTTGGTCGGTCCCT	60.19	20	TTGTTCTTTGGTTGCAGGAA	59.293	20
TCGCTGATTTTGGTGAATTG	59.664	20	TGCCAGTGTCTCAATCCTCA	60.402	20
TCTTTCCCATGGAGTTCAGG	60.042	20	CCAAAACGTCCATTTTCCAA	60.702	20
GCTTAATTGTAAACCGTTGTCAT	57.369	23	TTGGATTGAATGGATGTTTGG	60.55	21
TGGCACTCAGTTAAGGGTCC	60.111	20	CCAAAATGTCACAAATACCCC	59.054	21
TTTATGCGTCGTGGATCAAG	59.688	20	TGTCATGGCATTTTTGTATGTTT	59.288	23
TGAATCCTTCCTTGCTAGTCAC	58.462	22	CATCGCTAAAGTTGGTGCAA	59.872	20
CAATGTATCCAAACATGATGACG	60.124	23	CATGAAAATCATGTTCCGCA	60.466	20
ATCAGGCAAAAACGTGCATT	60.511	20	GGGCCGATATTTGTTAGAGG	58.533	20
CAAAGCGGGTAAAGGAACAA	60.103	20	TAAAGCTTATGGGCTGCCTC	59.456	20
CGTGTGATTCTGTGGTGGAT	59.393	20	TTATATGACCCCCTCCCCTC	59.974	20
CCACTCACATGGGAATTGTT	58.258	20	TTAAGGCACACTGCACCAAG	59.904	20
CACTAGCCGGACACATCAGA	59.855	20	GTTTGGAGGAGCAAGTGGAG	59.844	20
TTTTGAATTGGCAAACATGC	59.543	20	CATCATTTCATTCCCAACCC	59.991	20
GGGCATGTCCGAGTTCTTAG	59.694	20	GCCCCAAACGACTTACGAT	59.947	19
TTCCATACGACATTGCAAGC	59.694	20	ACAACACCCTCAAATGGCTC	59.973	20
CCAGAACCCAGCTTCTTCAG	59.982	20	CTTAACAAAAGCAAACCGCC	59.758	20
TCAACGTACCTATTTTGTTCCTAG	58.736	26	TTTCGAATGATTTTGCCCTC	60.016	20
CACACACAAGATTTGGGAGG	58.98	20	CGGTGCGATCCAGTAAAAAT	59.96	20
TTGGTGAAACCAAGGTGTTG	59.435	20	ATTTTCCCCAAATTTGTCCC	59.867	20
GGGGATAATGACGAGACGAA	59.894	20	TTGAATTGCTCTCCCTCCAG	60.331	20
CCCATAAAATCGGATGGCTA	59.751	20	ATTACGTCCAAATTGCTCGG	59.96	20
CAGCATACGCGAAGGGTATT	60.117	20	CCGAGTGCTTGTATGCAGTG	60.472	20
CTCAATAAAATGCTTCCAATCG	58.762	22	GCCACTCTTGTGCTTCCTTC	59.997	20
ATCCAAGGAGCACACCTGAG	60.261	20	CCACCTTCCTTTGCTTTCTG	59.846	20
TCCCCATCTCTCTCTCATGG	60.152	20	TCCTTTCTTCTTACGGCACC	59.312	20
CCAATTTGAATGGTTATCACCTG	60.457	23	TCGCGAACTCATAAATTGAAC	60.619	22
ATTTGGCCCTATAAAATGCG	58.96	20	TGACCGTCCGTTTTGAAGAT	60.495	20
ACCTCGCAGTCATTCCAGAC	60.269	20	CCAAAAGTGTTATTTTTGTTTC	59.766	25
AGGAGGGGGTATAATTTGAATAG	59.971	24	TGTTAATCAGTTTATGCATCTT	59.917	25
TTGAAATTGGATATTTTCAGGAGA	59.868	25	TGTCCTCCATTAAGCAAGCC	60.214	20
GCAACGCAATCAAAACTCAA	59.856	20	TGTGATGAGAGAGAGGGGCT	59.945	20
CCGGGGGATTATAATATGGG	60.069	20	CGAAGGTACGGTATGCGATT	59.982	20
CTGCTCCGATGAACCTCTGT	60.408	20	CCGGCGATAAGAGAGAGAAG	59.17	20
GACCTCTACGAGGCATACCAA	59.208	21	TGGCAACTGCAAGTTCAAAG	60.027	20

ATAGGGATTTCGGATTTCGG	60.109	20	TTTTGGGAGAAGTATTGGGATT	58.864	22
TCCACGGAGAGCGTCATAC	59.803	19	CCAATTTGAATGGTTATCACCT	60.457	23
CGAAACTGAGCTCCATAGCC	59.978	20	GTTATGCGTTTTGACGGGAT	59.829	20
GAAGCCCTTTCTTCCCAATC	60.017	20	TAAGGGTCATGAAACGGACG	60.883	20
TGAAACAACACGACCGGATA	59.964	20	ATTCACCTCTGACGACTGGG	60.112	20
CGGATGAATTTCACTTCACG	59.123	20	GTTTGCAAAACTCCCAAACC	59.452	20
TGTGTGTCGATGCCTGAAAT	60.12	20	TTCCGAAAATATGCTCCACA	59.112	20
ATCCGGTCACCTCTCTCCTT	60.073	20	AGAGGAGCCCCATTCATTCT	60.037	20
CCGTCAGTTTCAAGACATTCC	59.583	21	TCGATGTCGATGATGTCGAT	60.039	20
AATCCCCCAAACCAATTTCT	59.51	20	GAGGTTTGTGCCATTCGTCT	60.119	20
AGGGCTGAGTACACGAATGC	60.285	20	AGGGTCCCACCCTTTTGTTA	60.581	20
CGATGCAGAGAAGGGAAGAG	60.088	20	TATGAACCCACCAGCATTCA	59.924	20
CGGTTCAACTTCCCATGTTT	59.83	20	TTCTAAGCTCGAGGGCACAT	59.978	20
TTGACATTGAATCCCCTCATT	59.234	21	GCTAGAGGGTTTTGTTAATATG	57.693	26
CTTGCTTGCTGAGGTAAGGC	60.154	20	TTAAGGCCAACTTCCCTCCT	60.068	20
GGTAGCACCATCAGCAGACA	59.862	20	AAAGGGCTTCAGGAATTTGG	60.423	20
TAATGGCGCCGCTAATGTAA	61.44	20	GGCGGCGTGACTTATTCTAA	60.23	20
GTTCACCCCTACACGCAACT	60.035	20	GGGGGAAAATTATAGTTAGGG	57.532	22
CCACATAAGCGTCATCTCAAA	58.785	21	CGATAGATTCGATGAACCCC	59.344	20
AGGGCTGCAGGAATTCAATA	59.668	20	GCAATTGAAGGTTTGACCGT	59.978	20
TTTGCCATCATAAACTCTATTCG	58.344	23	GGCCTATTGAGCCAAGACTG	59.836	20
CAGGGTTGGAACTAGAACCG	59.587	20	GTGCATTTTTGGGAGCAAAT	59.945	20
TCGGAAGGTTTATCCTCAGTG	59.181	21	TTCAGAAACATGTCAACGTGA	58.825	22
ATCATTGCCGAACACCTTTC	59.939	20	TCTCCGAGTTCTTGCTCTCC	59.679	20
CCACTTTCCACAATCCTCGT	59.966	20	TCCTGGCTTCAAAACCAATG	61.001	20
TCTCCTCTCCTCTCTCTCTACTCTC	58.237	25	AATTGACCTTTGACGTTGGC	59.978	20
GGGTGGGTCTCCCTTACATT	60.052	20	CACACAGATGACTAGTGTTGG	60.133	24
ACCCTCCGGTACACGAAAAT	60.61	20	CGCTGGTTTTGGAGATCAAT	60.074	20
GTGGAACCAGAGTGGCCTAA	60.111	20	TCCGGTCCGATTACAATTTC	59.762	20
TCGCAACTTCACCTTTACCC	60.11	20	GGCTTTTGCATGGTGACTTT	60.118	20
TGTGGAACCAAACGATCAAT	58.824	20	CTTCCAGAGGGATACCGTCA	60.065	20
TTGGAATAGGTCCTTGGCTG	60.066	20	AAATTATCGCTTCGTGTCCG	60.096	20
TTTAGTGTTTTGACATGATTACTC	57.557	25	TGCGACCTTAAATTTGGTGA	59.157	20
GGGTTACCAAATTAGTTCGTCG	59.773	22	TTCACTTTTACAACTTCCACAT	58.721	24
CTTTTCGCTGCATGTGTTGT	59.911	20	GAACTAAATGCCCGAATGGA	59.901	20
ATAAGCCACCCAAACAATGC	59.829	20	TGCATGTCTCATTTCGTTTGT	59.188	21
GGATCATCTTCCCTCTCCCT	59.449	20	AAGCCATGGTTCAATCATCA	58.926	20
CAAGGCAAGGACCAGATCAT	60.073	20	TTCACAAACCCATGTCCCTT	60.21	20
AAGGAGGTGTTATGAAGGGATT	58.028	22	GGAAGGAAACATTCTTTTGGG	59.801	21
TCCCAAACTGATGGAAGGTT	59.381	20	CTGCAGGGGATCATGACTTT	60.073	20
ATGCAAAAGTTATGGTAACAAGA	57.459	25	AGATTGGGTACCCGACACTG	59.844	20
TTACCAAAACGCCCCAATAG	59.826	20	AGATTCAAGGGCCGAGATTT	60.039	20
TTGGTGAATGATTGACGATGA	59.916	21	TCCATAGCCGATAAAATGGC	59.892	20
AATCAATGGTCCACATCGGT	60.057	20	AAAATCAAAGGCCCACAATG	59.801	20
TCTCTCTTGGTTGGTGAAGGA	59.829	21	CGACAAATGCAAGGCTACTG	59.488	20
CGTGGTTGGTGTGAGATTTG	60.001	20	TACATACAGTCAACGGCGGA	60.134	20
TTACGATTCACCAATTCGCA	60.073	20	CATGTGAGTGGCACGTGATT	60.604	20
GCAAGAGATGAGCGATAGCC	60.088	20	TATCATTTTGCCCAACCTCC	59.762	20
GTAGTCGGCAGAACCCAGAA	60.255	20	CTGGATGGCAAGCTTTTAGC	59.982	20
ATCACTGCATTTCGTCCTCC	60.081	20	AGCGAATATTGCTTCACCGA	60.742	20
TGCCTTTATTTTAGCCTCCCT	59.26	21	AGCCTTGATTGGAACATGGA	60.461	20
GCCAAAAACTTTGATCCCAA	59.916	20	TGTAACCCAAACCAAGCACA	60.004	20
CCACCTCATTTTCAACACCC	60.21	20	AGAGGAGAGGCGAAGGAAAG	60.088	20
CTACGAGCCACGGTTACAGG	60.7	20	CCAGACCAACCAACACTGAC	58.992	20
AAACCGGGCCTACAAGATTT	59.835	20	GCCCTCAAGAAATGCCAATA	60.038	20
CACAAACAGCCCAAGGAAAT	59.971	20	TGAATGCAGGACAAGAATGC	59.805	20
GGAACAGAGCTTCAACGGAG	59.989	20	CTTTGCCCCTTTACTTGCTG	59.876	20
ACAATTGGGATGAGCAGGAG	60.073	20	ATGCCCACATTTCAGAGTCC	59.934	20

TGGTGGCCGAAAATTAGAGA	60.576	20	TCAACCATTTGTTTTTGCCA	59.946	20
ACCAGAACGACGACACCTTC	60.159	20	TTAACCTCCCGTGGACGTAG	59.986	20
CCCAGGCATAGAAAGAAAAGA	58.454	21	TGGTGGAGCGTCTGTTTTAAT	59.623	21
CGTCGGTGTATGACCTGTTG	60.025	20	ACCAAGAGGCGTTGGTAGAA	59.734	20
AACTTGCACCCAAATTCCAC	59.836	20	CGAAGGATTTGCAACTGGTAA	60.117	21
CACAGAACGCTCTTTTGCAC	59.64	20	GACCGCAGGTTAATCCAGAA	60.074	20
ACTATCACCCCACCCACAAC	59.555	20	TGTCTCCATTCTATTGGCCC	59.894	20
CTAAACCCAGGTGGCAGTGT	60.028	20	ACGCATGACTTTACCAACCC	59.859	20
TTTGAAGGAGTGGGATCTGG	60.042	20	ATTAGCGAACATGGAGGTGG	59.955	20
ACGGATCGGAATTTCTCAAA	59.505	20	TCCGAGACAAGTTTCGTGAAC	60.284	21
TTAATGGACGTCGTGAATGC	59.548	20	TCAAGTGGCATTTTTGTCCA	60.088	20
CTAGAGGATTCGGCATTGGA	60.17	20	TTATTGTGTGGGGCAGAGGT	60.375	20
GTTGGAAAAAGCCAATCGAG	59.685	20	TTTCCCTGAGCACGTTAGGT	59.734	20
GTTCCAGGAGCCAGATAGGA	59.239	20	GATTCTGTATCCGCCATTGAA	59.915	21
TTTGGAGAGATGGGGTTCTG	60.042	20	GGCCCCTAGGGTGGGATA	61.981	18
TCCATCCACCTCTGCTTTTC	60.195	20	TTCGTTGATGATGGAATGCT	59.079	20
ATTTGTCCAATGGTGCTTCG	60.894	20	ACCGCCGATGTGATTTTAAC	59.829	20
GGAACCTGAGAATGGGGAAT	60.133	20	TGCATTTCATTCACACACCA	59.516	20
CATGTGGATCATACAACAGGGT	59.598	22	CATTTTTCCTCATGGAATGGA	59.748	21
TCTACCAAGATCCTGCCTGC	60.362	20	TACAAGGCCCACCTCAAGAC	60.111	20
CGACTATTGTTTGTCATCGCA	59.744	21	CGGAATACAATTCGACAGAAA	60.01	23
TGCCTTGAGTAAGGGCATTC	60.214	20	GAGGGGTGTTTCCAGACAAA	59.943	20
TCACCACCTGAAGAGAGGCT	59.986	20	GTTGTTGAGGTGGTCTCCGT	60.009	20
CCGCTCCTCCTTTTCTTTTT	59.829	20	TCCCGGCTGAATGTTACAAA	61.389	20
AAGGAGGTGTTATGAAGGGATT	58.028	22	AGGTAGGCACAGGGGTTTTC	60.361	20
GCAGCACATTGTGGTCTTCA	60.885	20	AAAATCTCTGCCCAATGCAG	60.214	20
TTTGGGGGTGCATATTTCTC	59.762	20	TTGCCACCCCTCACTACAAT	60.375	20
AGTATGTGGATCTGGGCTGC	60.104	20	AATGCCCTCAGATGCTATGG	60.059	20
CTGCACCATCGCTATCTTCA	59.972	20	TCACCGAAATAAGGGTTTGG	59.795	20
TGCAGTTGAGATAAGGGAGGA	59.822	21	ACGGGTCGTGTCAGAAATTG	60.954	20
TGAACATGCTCATATTTTAATACA	58.521	26	TTGCACAATTCTCAATCGGA	60.197	20
CATCTCCAATGCCAGGTACA	59.522	20	AGGGTCCCACCACCTAACAT	60.489	20
TCGCATTCTTATTCCGATGA	59.212	20	CTCACTCCAGTTTTTCACCCA	60.133	21
TTGGGGTTATTTAGAGGGGC	60.143	20	GGAAGCAAAAAATGGCAGAAG	59.823	20
AGGCCCACCAATTACAACAC	59.717	20	TGACTAAGTTGTGTGAGCAGGA	59.966	23
CTTCTCTATGGCCCACATGC	60.624	20	CGTAAAAATGGTTATTATTGGA	58.395	25
CCCAAGAATGGGTTATTATTTGA	59.14	23	GCATCCTTTGCACCTTTGAT	60.081	20
AATAGCCACTGTCGCCTACG	60.292	20	GCCCCCAATTTCTCTCTTTC	60.017	20
CATGATCTGATGAGGCAGGA	59.743	20	ATCGCATTGATCCCAACTCT	59.513	20
AATGTTGATAGGCCGAAACG	59.96	20	CCATCTACGCAAACCCAGTT	59.993	20
GCCAAAAATGACGTTTTGCT	60.117	20	AAATTTCCAGATTCCCGTCG	61.173	20
GCTAGAAGCAGCCGTGACAT	60.569	20	TTGCGCGTGCTTTAAATAAT	58.524	20
CCGGAATTTTACGTGGTTTG	60.215	20	CCACGACGGTTAAAGGAGAA	60.103	20
CCCTTAGTATGCTGTCCGAAA	59.234	21	GGGGGTTATCACCTGATCG	60.142	19
TTCATGAGCCTTCTTCAGCA	59.673	20	ATTTCTGCAATTGGGGTTCT	58.504	20
TGAATTTGGTCTCCTTTGGC	60.051	20	TGTACCGTGACAAGACCTTTGA	60.583	22
TCGTGTCACCAGAATCAAGC	59.837	20	CCACAACCCTTTCATCACCT	59.82	20
CTCACATGAACGGACCATTG	59.96	20	CTCGCAAGCTTCGATTTCTT	59.73	20
TTGTCCATGCAACCTACGAT	59.002	20	CAATTACACTGCATGGGCTG	60.134	20
GCAGACAACTGACAATGCAAA	59.903	21	ACGTGATTCCTGCGTCTTTC	60.263	20
GGTGGAAAGAAGCTAACCCC	59.94	20	AACATGGCCAACCCAAATAA	60.053	20
CTCCTCCTCATCCTCGACAC	59.792	20	TGGCAGAAGTCGTTGAACTG	60.025	20
AAGCCAAGTTAGCTCCCAGA	59.077	20	CTCAGCATCGGAGCCATAAT	60.199	20
TTGTTAGAGGTTTTGACGGGA	59.595	21	GATGGATCTTCGTATTTGTTACT	59.819	26
AATGAATGGCCCATATTGGTT	60.274	21	GTTTTCATTTGATCACGCCC	60.318	20
CGAACATGACACAAATTGCC	59.972	20	ATGAGTTCGAGGCTCAATGG	60.218	20
CCTCCACGAATGGTTTTGAT	59.79	20	CACAAGCAGTGAGATTGGGA	59.831	20
ACACGGTCATGAATAAAATCGTT	59.664	23	CGTCCAGTTCACTTCATTGG	59.135	20

ACTGACCAAGCATCCTCGAC	60.269	20	ACCCTGAATTCTCCCCAACT	59.795	20
CATGAAAGCGGTGGAGATTT	60.074	20	AGTTCGTCAAACCTCCCAAA	59.569	20
AGACAAACAAAGCCAGGTGC	60.299	20	GAGAAAGTGTTTGTGGGGGA	59.943	20
TCCAATTTCTTCGCGTAGGT	59.708	20	AATCTTTGAACAGCCGATGG	60.074	20
CTACATGCTGAGATCGAGCG	59.722	20	CAACTTTTGCGGACAAAACA	59.746	20
AAATAAAGGCTGCATGGCAC	60.103	20	ACCTCTTCGAGTTCGTCCAA	59.844	20
ATTTGTTGCAGGGCAATACC	59.829	20	AGAGTGCGCGTTTTCATCTT	60.022	20
GCCGGATTCCCTTTTAAGAT	59.402	20	TCACGACATTATTTCCCTCAAA	59.451	22
ATTCCGTCCCAAAGGAAAAA	60.644	20	GTAGCCATGGAAGAATGCGT	60.103	20
ATGCCCTTTTCTCGAACATC	59.129	20	TCAGATCTTAATCGTGGCCG	61.129	20
TCGTGGCTGGTTAAGCTTCT	60.015	20	CCCGAATCCGTTACAACAAC	60.227	20
ACACATCTCGAGGGATCGAC	60.08	20	TGAAGTTAGGAAATAAGGAGG	58.743	25
ATGAAGTTAGGAAATAAGAAGGT	57.239	26	ATCGTGGGCGTAAATCATGT	60.221	20
CCTTGAAGATCAAGACATCTACT	59.685	25	ATCTTCCAATTGGCGTTGAG	60.074	20
AGGGCAATTGATCTTGCCTA	59.668	20	TCAATTGTCTTCGAGACGGA	59.369	20
TGGAAAAACACAACAACCCA	59.834	20	TGCAACTCCTCTGACCTCCT	59.986	20
ATGAGACCGGAAATGGATGT	59.218	20	CCACCACCAGAAGCAAACTT	60.149	20
TGGTGGAGGCTCGGTTATTA	60.46	20	GCATTACAGAAAGTTCCGCC	59.713	20
AGCTTCACCAAGCTTTTCCA	59.993	20	TGAACAAGGGTAAGATGAACC	60.221	22
AACCTCCTGCTGCTTATCCA	59.836	20	GCGGCTTCATCTTTACTTGC	59.988	20
AAAACTCCAAATCCCCCAAC	60.032	20	TTCACTGCTGACCGTGTTCT	59.467	20
AAAATGACCAACCATTCGGT	59.15	20	GTAAAGGGGGCACGAAAGTT	60.352	20
TCAGTGATAGAAATTGAGGGGAA	59.952	23	CAATGTTCAGCGAAGTGGAA	59.84	20
TTACGGGTTGGGCTGTAGAC	59.993	20	GGCTGGATTTCGTCCCTATT	60.286	20
AGAGGGTTATCATGGGATCAA	58.32	21	AAACGGTTGAAAAGCCCATA	59.451	20
ATGCCGACACCACACATATC	59.25	20	ACGTGGGGAGAGAGGAAGTT	60.111	20
GGTGCACCCTCACTTTTGTT	60.012	20	GTCACGGTGGTTCTTCATTG	58.984	20
TAGGGTTCGAATCCCCACTC	61.211	20	CAATCATCCACGTCCTTGTG	59.96	20
CATTGTAGCCTGCATTTCCA	59.688	20	CCACAGCTGAAAACGTAGCA	60.05	20
TGGGAGAATTGGGCTAAGTG	60.066	20	CTTGATGCACGAATTTGGAA	59.664	20
TTGGTATTGGATTGGAGATGC	59.776	21	AGAGACCAGACCGTTAGGGG	60.502	20
AGAACTTCTCCATCAGGGCA	59.803	20	CCACTTATGTCGAAGATTTTTG	59.933	24
TGATCTCAAAAGATCAACGGTTT	59.994	23	CTCTAAGGGATGATTGCACCA	60.081	21
AAAGCACGCCAAAATTGTAGA	59.772	21	ATGGCGCTATCTGGTTGTTC	60.103	20
CGATGGTTGGAAACAAATGG	61.118	20	CCCAAAAATAATTTGGGCCT	60.016	20
ATTCATGAACCACAAAGGGG	59.647	20	TGGTGGTGGAGTTGTCTGAA	60.129	20
TCACACCAAAGATGCTGCTC	59.992	20	GTTTGGGAAGGTTCGGATTT	60.166	20
AAGTATTGGGGCAGCAAGTG	60.132	20	CAACACACAAAGCCACCATC	60.008	20
GTGTTGTACGGCGCTAGGTT	60.197	20	AGTGGTTATTACCGGATCGC	58.93	20
CCACATAATGTTGCGCATGT	60.41	20	ACTTGGAATCGTGAGAAGCG	60.397	20
TCCCTGCTCAAACACATCAG	59.831	20	AGGAAAAACGTGGCAGTCAG	60.291	20
TTGTGGCTTCATGCAAATTC	59.67	20	TGCAGGGTATGCATGTTTGT	59.995	20
CACGTTAAATCCCTTGCACA	59.585	20	AGCATGGTTGCATACTGTGG	59.596	20
TGTGGTATCAGAGCCACGAC	59.707	20	CAAACAATGGGACCACAAAA	59.268	20
TCTGCAACAACAGAAGGATCA	59.43	21	AGTAAGAACCGCGAGCTGAA	60.154	20
AGAGAAAAACGGTGGGTGTG	60.005	20	GTTTTAAACCAAGGCCTCCC	59.814	20
AATGCAAAGGATTTGATCCG	59.901	20	AGGCAATGGACATGGAAGAA	60.461	20
CTGTTCCCTCCCTTCAACAA	60.081	20	GACAAGCACTCATGTGATGGA	59.698	21
GGACGCACCAGATTGTTTCT	60.119	20	GCATCTCTAATTGGACCCCA	59.894	20
TGTAAGGTGCTCCACCATGA	60.112	20	AGAAATGCAAGATTGCGACA	59.425	20
CCTCTTCATTTGCTTCTGGG	59.807	20	GTGCCGTGTACTTCCTCACC	60.577	20
CAAAATCGGCATTTCCATTC	60.268	20	CAGTCATTGGATTGCATTGTG	59.98	21
AAATGGCACTTCAATAATGGCT	59.87	22	ATGAAAATACGCGGGGAAAT	60.517	20
TTTTCTCAACCGAGCTCACC	60.375	20	CCTCTCGTGTTTCTTCACCC	59.697	20
TTCATGCAGTTGGGAGATGA	60.201	20	CCCCCACCACACCTCTACTA	59.837	20
GATGTGATTAATTCCCACCATT	57.666	22	CCGAATCTTTTCGTGAATCAA	60.06	21
AAGCGTCGTGGGCTTGTAT	60.672	19	GATTTTGGGGAGGACAAGGT	60.169	20
TTGAGCAATAAATCCAGGGAG	59.168	21	CCAAGTAAAGCTCGAACCCA	60.241	20

GAAAGAGTGCTGCGGCTAGT	59.786	20	TTTCATGATCCAGATGGACG	59.451	20
CGCCACTCCAAACTTCAAAT	60.11	20	GGAGCTACTCAGCCCATGAT	59.268	20
GGGCTGGATACAATCCATCTT	60.167	21	TGCGAAAAATTTGGTTCTTGT	59.617	21
CTGCTGTGCGTCGATTTCT	60.152	19	GTGGCACGATCATTGTTGTC	59.975	20
CTGCTGTGCGTCGATTTCT	60.152	19	GTGGCACGATCATTGTTGTC	59.975	20
CAGCAAATCACCTCATCCCT	60.073	20	CTCTTGCATCACCTTCACCA	59.831	20
GCTTTAGTAGGGTGCAAGCC	59	20	CGTGCTCATGTCAGCAAGTC	60.627	20
GCAGGTTAGCAGGATAAGGG	58.812	20	ATCAATGGTCCACATCGGTT	60.057	20
TGCAGGAGAACTAATCTTCAAAA	59.453	24	TGCGTTTTGACAATATATAGGT	60.083	26
TCTGGTTTCCAAACAAAGCC	60.088	20	AACATGGATGGAGCTTCTGG	60.073	20
TAACGCGAATATGCTGATGC	59.832	20	ATCGGTTATCACCGGATCG	60.697	19
AATGCCCCACTAATCCCTTC	60.152	20	AGCTATCAGGAACCTATGTTT	58.728	23
GGGAAACTCACTACTCTCATTTC	60.514	24	TCAAACAAGGCATAAAACTTT	57.096	22
CTTCCAGGAAACTCCACTGC	59.844	20	GAGAGGCTTCATCTTCTGCC	59.119	20
TTGTTCGACGTCACAGCTAAT	58.446	21	GCAAAGAAGGGACGACTGAG	59.989	20
CCGAATCCCGATAACTAAACA	58.953	21	CACGTGTCAGCACACAATTTC	60.214	21
TGCTGCCTTAATCCACACTG	59.864	20	TACAGCCCAGATTCCCAAGA	60.594	20
GAGGCTTCAATCCGTCACTC	59.81	20	TGATAGCGTTTTGCTGTATGC	58.998	21
ATGCACACCCCGAGATACAT	60.226	20	GCAGTGACTGAGGTTGGTGA	59.872	20
TGGCGGAGGAGTCTTCTAAC	59.43	20	ATCGCTTCTTCTTTCGCAGA	60.235	20
GGGTTATCACCTGATTTTCTCC	58.826	22	CCCCTGGTTGTTATCCTTGA	59.784	20
TAGGCCTTACATGCCGATCT	59.691	20	GTGTGACATTGGCCAGACAT	59.399	20
TGAAGGACAATGGAAGGCAT	60.461	20	TCGATAGGACGTGTATGACGA	59.163	21
GATGGCCGATATTTGCTCAC	60.444	20	GGAGAAATTTGATTTGTTGGG	60.164	22
GCACCTCTATGGTTGGGAGA	60.073	20	AACCCTTGGATCTGAAGCAT	58.595	20
CACTGCGAGTTCAAGGATCA	59.984	20	ATACTCTTCGATCCCGCGTA	59.691	20
TTTTGTCGCCAATTGTTTGT	59.062	20	TGCTTTTTGTCGCGAATATG	59.842	20
TGTGAGTGAGTGAGCGTGTG	59.624	20	CGCCGCCATTATCTCTACTC	59.829	20
CAGCCACGATGATATGACAA	58.069	20	CCCCACTTTTAAATTGCGAA	59.937	20
CGCTCTCTCTCTTTCCCTCA	59.82	20	GATTGCGTAGTCGTGTGTGG	60.183	20
ATTTCGGTGTGAATTCGGTT	59.292	20	TTAAACTACACATGTAATCCAT	58.07	27
TTCTACCACCACCCATCTCG	60.913	20	GGTTTGGCGGTTGATAAATG	60.188	20
ACGCGCGCTTTTAGAGTTTA	60.17	20	CGCGTTAACAGTGGAAAACAT	60.046	21
TTCATTTTTAAATCCTATATCAAC	57.503	26	TTGGGATGGAGGGAGTACAG	59.92	20
TCCCAACCAGGCTGAATAAG	60.066	20	ACACAGAATTCGCCCAAAAC	59.978	20
GGTGCTCAAAAATCCGAAAA	60.053	20	ACACCATCCACTCACCCAAT	60.096	20
CAGATTTGTTATGCGTTTTGACA	60.048	23	CTTTCTCATTCAACACCCCA	58.541	20
TCGCATGGGAATATAATGGA	58.792	20	GCTTAAGAATCGTGGCTTCG	59.982	20
CAAAGAAAAAATAAGGCCACCA	59.107	21	AGCAAAAAATAAAGGGGCTGC	60.566	20
TTCGAATGTCATTTCACCCC	60.702	20	AAAAAGTGGCAAATTGGGAA	59.429	20
GGAGCAACCGAGTGATTGAT	60.081	20	ACGGCACATCAAACACCATA	59.847	20
CAACAAAAATGGCACTCTTTCA	60.145	22	CATGGAACATCTGATCACGC	60.08	20
AACTCAGGAGCAATTGGGTG	60.111	20	GCAACAATGGAGCAGATCAA	59.805	20
CATCTCCCAATTTTGATGCC	60.274	20	CAAGCCTCCACAACACTCAA	59.873	20
GGCTGTCTCTCACTCCTGGT	59.43	20	TTGTATTTTGTCTGGCAGCG	59.872	20
TTCACACATGCACCTCACCT	60.162	20	AAAGGGAAAAGGACCGACAT	59.805	20
GCACTCAACCACAACCAAGA	59.726	20	ACCTCCCTCTTCTTTCCCAA	60.045	20
CGCCTAAAGCAATCAACTCC	59.845	20	GATCCCGACGACCTCTCATA	60.034	20
GGCCTTTCCATTTTCCTCTC	60.017	20	ACCCAACGTCGGTTACAAAC	59.757	20
GGGTGTTTTGACAATATCGC	57.943	20	CGGAGGCGATAGACAAAAGT	59.336	20
CCCTTTGGTATGAGAAGCCA	60.066	20	ATGGAGTGCACCTCCTCAAT	59.535	20
GAACTAGCAACCCCCTACCC	59.827	20	GGGGTGAATTTAAAGGGGAA	59.992	20
TATGCAGACGAAAAAGCGTG	60.014	20	TTGACTAGGAGCACGCGAAT	60.934	20
GCAAGGATTGTAGCAAAGGG	59.708	20	CACTGTCTGGGGCTTTGTTT	60.149	20
TAGCAATCAAGTCCCTTCGG	60.206	20	ACACACTCTTTCTCAGTGGAC	59.42	22
CATTGCTTTCCGACTGTTCA	59.84	20	CTTCACCAAGTTTCTTCCCG	59.705	20
TCCTTCCTTGCTCCTTTTCC	60.683	20	CACTTGGCATCACATGGTCT	59.551	20
TCGATGAATGATGAGAAGCA	57.844	20	CTTGTGGACAGTGCATGAGC	60.473	20

AACCGAAAAAGAAACCTTTCAA	59.181	22	TGACAATATTTAGTGTTTTGAC	57.78	26
GGTTTGCGTTAGATATGCCC	59.438	20	TGAAACATGATACCGCCAAA	59.93	20
ACTTTGATTTCTTGGTGGCG	60.11	20	GTCCCATTCTACTGCCCAAA	59.933	20
TACCGTGGTTTCTACCCCAA	60.22	20	CGTAAATCCGGCTTGAATTG	60.448	20
TCATTTGTAGCTGCACTCGC	60.165	20	TGCAGACATGAAGAGGGTGA	60.402	20
AAACTGAGTGATGCCAGCCT	59.874	20	TTACATGGCCAACGGGTATT	60.074	20
GGAAGGCGACATGTTTCAAT	59.939	20	TTCTCATCCTTTGCCTTGGT	59.67	20
AGAACCCATGGACATGGAAA	60.173	20	AAAGGGAAAATTGGCAGGAT	59.777	20
TTCGTGGAGCAAAAACATCA	60.234	20	TTCCCACCATGATTTCAACA	59.75	20
CTTGTGAGCCATGTTGTTGG	60.152	20	TTGTTTATGCCGTTGATACAAA	59.437	23
ACTGTGATGCCACTGCTGTC	59.905	20	CCTAAAATTGGGTCCGATCA	59.756	20
TCAAACCTTGTGACTCTGCAA	59.475	21	TTCATTGGGGGTAAAACCTTC	60.041	21
CATCTAATGTCCATTTTTGCCA	59.832	22	TGGTTTGAACCATGATTTATTT	58.773	23
TTTTCTCAACCGAGCTCACC	60.375	20	TTGGTTCGAGCCATTGTGTA	60.111	20
CCATCCTGCACCATCATACA	60.353	20	AAGTCCACAGTTACCCGCAG	60.171	20
AAATTGCACCTCGTCGACTC	60.263	20	TCATCATCCTCCTTTCACCC	59.862	20
GCAATTATGGGGGACAGCTA	59.923	20	AACTCCAAATTTTGATGCATGT	58.493	22
TTTGGATCCATAACATGAAAAA	57.065	22	CAACCAAAAACTCTCGACCC	59.569	20
CCTGCCAACTTTCTTCATCC	59.67	20	CTATCCCCGAATGTGCCTAA	59.916	20
CTCACCTTCAGGGGACAAAA	60.081	20	TGAAGTTTACACAACAAATCTA	59.348	26
ATGGGTTATTACCGGATCGC	60.903	20	CCTCTCAGTCCCAGACTTGC	59.986	20
TGTTGCGATTTTCATTTTCCT	59.578	21	ATAGCTCAAGGGTTTTCGCA	59.845	20
TTCGTCAGTGGATCTTGCTG	59.984	20	CGAGGGGTGCTAATAATTCAA	59.088	21
CATTTCCTTGCACATCCCTT	59.933	20	TGCAATTGTTCGTTCCTTCA	60.234	20
AGAACCACAACCCTTCTCCC	60.349	20	TGCCTACACAAATCCACCAA	59.964	20
CAGAAATTGCCTTGGTTGTTC	59.601	21	GGCAGTTATGACCGTTGGAT	59.82	20
ATATGATCGCTCTCGCCTGT	59.826	20	TCACGCCTTCTCTCTCCAAT	59.95	20
CGCCAAAAACACAAACAAGA	59.746	20	TCTGCTTCGTTTCCTCCATT	59.813	20
GAAACCCCCAATTGTCTCAA	59.767	20	ATCAACCCTCAACCCTCTCC	60.314	20
TGTTTTCAATCTTGGCCGTA	59.157	20	ATTGTGGCCCTCAGATTTCA	60.461	20
TGCGACATCATGAAATCTGG	60.631	20	GGTCCAAACCAAAATCGAGA	59.91	20
GATTTATCGATCAACCATTTCTTT	57.707	24	TGCTTCCCTCACAACAACAA	60.278	20
TCACCAATTTGAATGGTTATCA	57.873	22	GCGTTTTTGGCCTGATATTT	59.081	20
ATGGGCTCGAAGTTTCTTGA	59.813	20	ATCCAAAGAAACAGCAACCG	60.11	20
TCAGAGGCGAGAACCAACTT	59.989	20	CTGGGAGCATGTCAGTGTTG	60.309	20
TGGTTTCACCAAAAACCGAT	60.206	20	CTTACAATGTTGCCCCCAAG	60.357	20
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CCAGAAACCCCAAACAAAAA	59.811	20	CAGAGAAAAGTCGTCGGGAA	60.366	20
TCGGATCACCTAGGTTTTGG	59.926	20	GAGTTCCCGCGTCATAAAAA	60.074	20
TTCATTCACTCAGCACCGTC	59.837	20	GGGGAGAGTCAGGTAGGAGG	60.066	20
CCATACTTCTCACGTTGGCA	59.716	20	TGATGAATGACGACACATGC	59.037	20
CAGCTGCACCACAGAAGAAA	60.175	20	GGCGAGATTGTGGAAGAAGA	60.34	20
CACATGAATGGATGTGATTTGTT	59.606	23	TCAAACGCGTCTCAAATCCT	60.776	20
CCATTTGCAATGGACAAAAA	59.396	20	AAGCCCATATCAGGGGTGTT	60.578	20
CAGAGAGAAAGTTCAACAGGGA	58.574	22	CAATAAACGCCCACATGAAA	59.42	20
TCATGTCTCTTGGCCTTGTG	59.831	20	AAAATTCCAAACTCCGACCA	59.406	20
TGGGCAAAACCATCCTTTAC	59.801	20	CGAGTGCCGTACTTGAGAGA	59.187	20
TGGCAGATGTTCTCCTCAAA	59.369	20	GCGCTATTTTTAACCCCAAA	59.11	20
ATCGAATGCACACACTTCCA	60.12	20	TTGGTGATGAAATGCAGAGC	59.805	20
GTGCTGTGTTGAAACCCCTT	60.012	20	TTGTCTCTTGCATCACTCCC	58.802	20
CCCCAAATTGATGGTTTCAT	59.481	20	CACACATGTGGCTTTGCTTT	59.764	20
CCTTCCCTTGACGACTTACG	59.728	20	TCTTCACATTTCCTCCCCAG	60.042	20
TTCCACTTCTTGTTGTGATTGC	60.154	22	TCGCCTCCAATACCAAGTCT	59.694	20
GCATGCGGGGACATAATCTA	60.827	20	AGGGGCTCGAGAAAGAGAAG	60.088	20
TGCAATTGCTTATGAGGGTG	59.688	20	CGGTATCACGGACGATTTTT	59.823	20
TGGCCGAAAATTAGAGATGG	60.031	20	TCGTGTTCTTCGTCGTGTTC	59.88	20
AGCCTTCTCTCAAATAAGGGTG	58.914	22	CAAATCATGTTGAAAGGAACC	59.839	22

TCTCCACGTTTCCATCTTCC	60.05	20	TTGAGTGGTTCGGGGATTAG	59.926	20
GTCCGAGGATAACCCTTCCT	59.397	20	TCGATAAATAGCCACATGCC	58.603	20
TTTGAGATGCAGAAAGACATTGA	59.875	23	GGGACACCTCAGTGGTAGGA	59.962	20
AACGAAATCGAGACACCGAC	60.119	20	TGTGAGGGACACAATTCTTGA	59.124	21
TTTCTCAACTGAGATCCCCC	59.065	20	GGGGTGATTGGTAATAGCTCC	59.68	21
TTTAGTGTTTTGACATGATTACTC	57.557	25	TCATGAGCGTTCGTCATTGT	60.272	20
AAACTGGACTGGGTATCAACAA	58.486	22	ACCGACTCGAAACTGCAACT	59.914	20
TTTTGGCAATTCCCTTCATC	59.878	20	CGCTTTATGAATTCAGCCGT	60.23	20
AAAAAGCGTTGTCTTTGAGCA	60.046	21	AATTCCTATGGGTTTTGGGG	59.882	20
CGTGCCAAGACTCAAAACAC	59.339	20	TGGGAGAAATCGATAATGGG	59.717	20
CTGAGCCCTTCTTATTCATGTT	57.52	22	CAAAGGCCCACAATGGTTAT	59.685	20
ACACGTACAAAAAGCCGGTC	60.037	20	GCGCAATTGCATCTATTGAA	59.809	20
CCGGTTTGGGAGAAAAATCT	60.291	20	CAGAATTGGGTGTAGCAGCA	59.864	20
ACACACCCCAAAAGAAGACG	60.005	20	CTGTACCACGCTTTTTCCGT	60.168	20
TTTGCATTCAAACTTCACCG	59.706	20	AATTAGCTTCTTCGTCGCGT	59.138	20
GCACATCAACACTCGCAAAT	59.728	20	AAGTTCGCGAGATCCAGAAG	59.574	20
TCAAGAAAAAATGGGGAGACG	60.044	20	TGTTAATCTGTTCCGGCCTC	60.074	20
TCAGCTGAAGGAGGAGGAAG	59.673	20	GGGGACAATTCAACATTTGC	60.177	20
ACCCTCTTCACCTCCCACTT	59.968	20	CAAAAGGTTTATCCCAGTCTCT	58.333	23
TCATGCAATCACTATTAAGACTC	60.036	25	GAATTTTTGGAAATGGTGTTCA	58.831	22
CAGGACCCATCTATCGCTGT	60.096	20	TAAGACACCAGGCAGTTCCC	60.111	20
GCCTTGGAGCAATTGGAGTA	60.214	20	AGCTTGAAACACACACACGC	59.953	20
TGCACACTCGCAATTTCTTT	59.469	20	ATGAAGAAAATCTGGCGCTG	60.352	20
GGTCTTGCCGGATTCATCTA	60.036	20	TGAAGTCGTCGTAGGAAAGC	58.104	20
TCTGCATTAACCCCGCTTAG	60.223	20	CAAAGCTCAAGCTGATGCAA	60.28	20
CCCACTCATCTTCAACCTCAA	60.096	21	GGGGATTTCTGTCGCTTTTT	60.431	20
CCTTTTCTTAGGCGTTCTTGC	60.369	21	CGGTTGTATGCTGCACAACT	59.788	20
CTGCACCATTCTCTTTGGGT	60.111	20	CATTTCCACAGGGACACACA	60.416	20
GCGTGAGTCGGTGAGTGTAT	58.755	20	TAGGCCTACATCGAAGCCAT	59.691	20
GCTGAGGGGAGACTACATGG	59.679	20	GTGACCCTTTGTACCGTTCC	59.308	20
CGTTGGCAAGGTATCGATTT	59.96	20	AAGGAACGAACAAGTTTTCCA	59.543	22
GGATGGAATGGATGTTTGGA	60.526	20	GAATGTTGTCGTAGCCTGTCA	58.79	21
TCCATTTAATATGTCGATGACCAC	59.976	24	GACGCTAACGCCATTACGAT	60.124	20
CCTAACCTTGGGCTTTGATG	59.564	20	GTGGCATGGGGAAGCTACTA	60.096	20
ATTCGACTCTTCATCAGCCG	60.362	20	GAGCACGCAGAGAAGCAATA	59.326	20
ACTAAGGCTGATGGGGTTCA	59.55	20	GACAATCCGGCCAAATTAAA	59.773	20
AATCATCCCAAGCTCTGCAC	60.226	20	CTGGGACCTGATGGTCTGTT	59.962	20
TTGAGATTCCGTGAGGACTGT	59.712	21	GTATCAGCAGCCACCCAAAT	59.962	20
AAAACTTGACCCGATCATTGT	58.424	21	GCAAAGTGGAGATCATGGGT	59.934	20
CAGCAAAATCCTTCACCTCAG	59.861	21	TCTTTAACCGCCACCAAAAC	59.975	20
GCACCAAAAAGGAAAAATAATC	60.071	23	GAGAGCAGTTTCGGACATAAA	57.518	22
TTACCTCTGTTGGTGCAACTT	57.406	21	GCCAAAACTACCCCTTTCAGA	60.469	21
TTTCTTTGTTACCATGGGGG	59.657	20	TTCAGCAAACCAGCTCTCCT	60.134	20
TGGGACAAAACGGGAAATAG	59.795	20	TGCGAAGTTTGTTCTTGTGC	60.035	20
CCCGTATACACACCACGGAT	60.517	20	GCCTTTTGGGGTCTAAGGAG	60.068	20
CGGCATGTTCCTCAACTACA	59.716	20	TGGCTTTGCAATCTCATTTTT	59.712	21
TAGACGAAGGTCGAAATGGG	60.066	20	TGTGAAAGTGGAAAACACCCT	59.482	21
AAAGCATTAACAGCACGCCT	59.911	20	TGTCTCATTGTGCTCAAGCC	59.992	20
GTAGCTTCAAACTCCCGCTG	60.015	20	TCTTATCGTAGCTCGGTCGG	60.365	20
TGAGTAAAAGCACGATTTTGGA	59.758	22	AGGGGGTTATCATGGGATCA	61.3	20
TTTCGTAATTTCGTCCAGCC	60.074	20	GAGAAAGTGAAGAATCGATTG	59.717	23
TGCAAGCACACTCAGACACA	60.235	20	TCACGCAAACAAATTCCAAG	59.706	20
GAGGCAAAGCAAGGCATAAG	59.982	20	TTCAAGTGTTCCCATCACCA	59.935	20
TAAACCCAGGTGGCAATCTC	59.933	20	CCCAACTTTCTCCCCTCTTC	60.045	20
AACCAGACCGGACCGTTAAT	60.61	20	TGAAGCACAATGAAAACGGA	60.234	20
ACTTACCGTCATTTCCGTCG	59.993	20	ACCCCACAACTTTTCTCTGC	59.187	20
CACTAAATTGGTGATGGATGAA	57.487	22	TCTCAACAGCGTGTTTGGTT	59.339	20
GGCCTAGGTTTCGAGGTAGG	60.089	20	CTTTAGGCGTTCAAAAGGCA	60.368	20

TTTTCCCATGAAGCCAAAAC	59.916	20	TGAAATGAAATCATGCCCCT	60.274	20
GCGCTCAAACTTAAGCATCC	59.988	20	CATCCCCTTTATTCACCCCT	60.011	20
CAATGGTGAAATTGCGACTG	60.111	20	TGCACAACAAATAGGCAAAA	57.846	20
TGCACTCTGTGATGGGAAAA	60.24	20	TGGCAAAGCCCTTTCTACTT	58.973	20
GTGCAGCAAAATTGCTTTGA	59.999	20	CAACTCATTGTCAACCGCAC	60.16	20
GCCTTCCATTCCAAAAATCA	59.878	20	TTGCAAGGCTCTGAAATCAA	59.542	20
GAGTGAGGGAAAGTGAAGCG	59.989	20	AGGCTGATTGTGAACTCCAGA	59.859	21
TGAAGTTAGGAAATAAGGAGGTG	58.743	25	TCATGTTACACGTGGACGCT	60.183	20
TTCGTATTTGTCTAGCGCCC	60.23	20	CTCTTCCCAGCAAGAAAGGA	59.545	20
TCGGTTGGATTTCCTTTCTG	60.044	20	AATTGTTCATTTGCAACGGC	60.876	20
CAATCTGACGGCCGATATTT	59.923	20	TTAAATATTCATGGGCACGC	58.513	20
TGGTGCAACCATTGGAGATA	59.924	20	TCAGGCCTATCGAACCAAAG	60.206	20
AGTCAGCGGAACCGTATCAC	60.142	20	GTGACCCGCCTCATCTTCTA	60.218	20
TGAAGTTAGGAAATAAGGAGGTG	57.525	24	CAGGTTTATCAACAAGGTTTTG	59.795	23
ATTTCCTTTTCTTGGGTGGG	60.159	20	GCAAGCTAGAACCCACCATT	59.198	20
TTTGATGGCTTGAGTTTCCC	60.051	20	CCTCCTCCTTTTCCTTCCAG	60.175	20
TTCACCCTCACACACACGAT	60.005	20	TGCGTAGAACAGAGAGCGAA	59.888	20
CCGTAGTTCCGAATGGTTGT	59.853	20	CGAATTCTAGGCGATTCCTG	59.801	20
CTTTGCCTTGTGAGAGGGAG	59.982	20	GGGAAGAACGACGACGATAA	60.074	20
TCCCTCTCTCCCCATTTTCT	60.008	20	GGTTTGGTTGGAGAAAGCAA	60.088	20
AACTCAAGATTCTGCATCGGA	59.828	21	AAGCAACAATACCCCCACAA	60.227	20
CTGTGTGATGTGGAGTTGGG	59.997	20	AACCCTGTGTATCCCAGCAA	60.375	20
CAGGAATTCGCTTTCTCCAA	60.323	20	CTTTCTTGGACCAGATTGCC	59.67	20
TCACCCGGACCTCTTCTTAG	59.28	20	GTCAATCATGTTGGGTGCAG	59.967	20
ACTGTCAACCCCTCCCTTCT	59.968	20	CAAGCCTTGGACTTTGGGTA	60.103	20
CGAAATTGAGCTTTTTGGGA	60.181	20	AGGACGTTGATTTGTTGGGA	60.353	20
CAATACCACCCCAACACACA	60.128	20	AACCATGTGCTTACACCACG	59.49	20
TATATGGGCCGTTAGATCGC	59.913	20	CGGAGACTAGGGTTTGGGAT	60.319	20
AAGCATTTCATTGGGCAGAG	60.214	20	ACCCCAAAATCCATTTTTCC	59.867	20
ATTAGCGTGCCTATTGCACA	59.353	20	CTGCATGCACATAGAGTATTGC	58.346	22
AACGCCGTCTGGATTTTATG	59.96	20	CCAATATTCTTCGGAGCGAG	59.801	20
AAAAATATAAACCCTGTCGTATCT	58.581	26	GTGGGGTATGGTCAACGACT	59.703	20
ATCACGAGTTTTTCCCTTAAAA	57.036	22	TTGAAGATCGATTGGCCATAA	60.409	21
CACCGGTGAATGGAAAAATC	60.17	20	TTCTTTCTGCATCCACCACA	60.24	20
ATCACATTAAATTTGGCGCA	59.032	20	TAGGCCCATAAATGCTTCCA	60.415	20
GATTAGCAAATTTCGGGACG	59.547	20	GGAGTGAGGATTTGAGGTGG	59.505	20
ACAACAATCAGCACACGGAT	59.014	20	TTGACGAAGCAACCTCCTTT	59.853	20
TCATGATTTGGCTTTAGGGC	60.038	20	GGGCATGCACCTAGTCACTT	60.142	20
AACAGAGCATTCCGTCCTTG	60.255	20	TCCCTACGAGGAAGTCAGGA	59.797	20
ATTTCCCAAATACCAAGGGG	59.882	20	TTGGTTTTGTTTGGGATTGA	58.841	20
ACCCTCGACGAAGTTTCCTT	60.11	20	ATTTGTTGGAGGTTTGGTCG	59.83	20
ACAAGAGTTGAAAATCCTCCCA	59.976	22	TTTTTATTGTTTGCTCCGGG	59.937	20
TAGGGTCCCACCACCTAACA	60.224	20	TGTAGCCATTGGGGAAGGTA	60.323	20
CGCAACACAAACAGACATCC	60.16	20	CAACTCAAATGCATGGGAAA	59.518	20
ATCGGTTATTACCGGATCGC	61.031	20	GATGTGTGCTGGATGTCGTT	59.557	20
CGAGGATCGAACCCACTTTA	60.066	20	TCATTCATTCAGACTCAGGGG	60.058	21
TTCTCAGATGTTTGGTCGGA	59.215	20	TGTTCACCTTTTGGCCATTT	60.344	20
TGGGTTTCATCAAGATTGGA	58.897	20	ACTTTCTGGTCAACACTCACGA	59.809	22
AGTGGTAGGCCGAGTTCAAA	59.734	20	GGGATAAAATAAGGGGTTTCC	60.883	22
AGTTGGGTTGGAGCATTGAG	60.111	20	TTTGGGCTGCAAATGATAAA	59.146	20
TCAAGAAAGAATGTGGAGCAA	58.488	21	CCGTCTCCTCCCTCTACCTC	60.208	20
GCACATAGCGTCTTCGTCAA	60.019	20	AAGAGCAACACATGCCAACA	60.31	20
TTTCTTCCTTTCTTGCTTGTTTC	59.088	23	GTGTGTCTGGTGGGGAAGAC	60.421	20
TTTGGGGGAAGAAAAATGGT	60.514	20	GGGGCCAATCCAAATTTAT	58.563	19
TTTCCACCATGATATCGACAC	58.285	21	GAGCGCAAAGCACAAAAATC	60.896	20
GGCAACGGAATACCATTTGT	59.691	20	CGTGTTCATCTTCACCCCTT	59.966	20
TTTCCAATTTCACGAGGGAT	59.363	20	ACTATGCTCACCCACTTGGC	60.142	20
GCAGGTTAGCACGATAAGGG	59.73	20	CGCCCCACATTGTTTCTTAT	59.823	20

CGTGTCCATTGAGTACCTCGT	60.043	21	GGAGGAATGCAAGTTGTGGT	59.973	20
ACTGCCGATAAAAATGGCAC	59.967	20	AAAAATGAGCGGACCAAAAT	58.557	20
TGAAGTTAGGAAATAAGGAGGTG	58.743	25	GGGGTGAAAGCGGTTATTTT	60.184	20
ATATGTTCACCGGCCAAAAC	59.691	20	CGTGGTTTATCGGGAGTGAT	59.813	20
GTGGTTTAGGTGAACCCCTG	59.304	20	CTCCTTCCCAGACGAACATC	59.655	20
TGGTTCAAAACCATGATTCC	58.243	20	TCGTCCAACTTTAAGTGATTTT	60.037	24
GAAAATTGGCGGTACAGTTGA	59.989	21	TGGTTTGGAATATACCGAAGTT	60.115	23
TCTTTCCTTGTTTCGGCATT	59.685	20	GCGTAAGGGTGTTCGTGAGT	60.179	20
AAGCAAGCAAAACGAGTCAAA	60.046	21	ATGCCATGACACGAACAATG	60.399	20
AACGTAGGAACTTACACAAAGTT	59.917	25	GGCCGAATTATGCTTTTGAA	60.04	20
GGCATTGTTGTACATTGGCT	58.504	20	TGTGTCATCTTACACTTTCCAC	58.201	23
TTCAAATTTGTTATTGATACCGAT	59.229	25	CAATCTGCGAAACTGGGTCT	60.255	20
TCCTTCCACATCTCTCCGTC	60.199	20	TTCTTGGCCAGAAACCCTTA	59.679	20
AGTTCCTGCCCCTTCTTGTT	60.11	20	GAGAGTGCCTCACTTTTGTGG	59.899	21
ATGATGAGGTCGAGATCGCT	59.792	20	TTTCCTCATGTCCCGAGTTC	60.05	20
CTGTCTCCTCCACCTCTTCG	59.978	20	TTTCTTGGCGTGGTGTTGTA	60.149	20
ATCTCTGGCTACGCCACTGT	59.898	20	TTCATCGCCTCTCCTCTTGT	59.95	20
GCAGCCACAGTTGTTATGGA	59.722	20	CATTTGCAATGGAAAAAGGG	60.294	20
TCACGCGGAAATAAATCCAT	60.289	20	AGCGGTTATTACCGGATCG	59.93	19
AATGAAGACATCGGAGAGGG	59.09	20	AAGAGGTTGGGGGTGCTACT	59.994	20
GTTGCTTTGCAGACCCTCTC	59.997	20	CAAAGTCAATAGCCCAACCA	58.623	20
AACCGGAGATCCAATCTCGT	60.853	20	CGTTTGAGCTTTGTTTTCTTGA	59.553	22
CATCCCTATCAACTCTTTCGATG	59.973	23	GTCCCTTTTTACCCACCGAT	60.053	20
CCCCTCAAATGCACTTCATAA	59.946	21	GCATCCTCGTGTGTGGATTA	59.527	20
TTGAACACACAGTTCATGCCT	59.202	21	GCAAGACTCGATCAGGAAGG	59.95	20
GAAATTCTAGGTCCGCCTCC	60.039	20	TCCACTGTTCAAGTGGACGA	60.285	20
TCGAAGCAAAGTCCTCATCC	60.34	20	GTGGGGCCACACTTTTCTAT	58.912	20
TGCGCCATAGATAAACCTGA	59.281	20	CCAATTTGAATGGTTATCACCT	60.457	23
TATGGAGCAACACAACCACG	60.574	20	TCTCGTTTGGAGGAATTTGG	60.044	20
AATGGGTTTTACACATTGGCA	60.103	21	CCTCGTTTGCAGCAGTTACA	60.05	20
TGTGACTTCAAAAACAGCCG	59.881	20	ATTGCGGTAACAATTCGAGG	59.96	20
GATCATTTCCAAAAACAATGATG	58.349	23	TTGTTTTTCCGATTTCACCA	58.987	20
CGACCTTATAACATTTATTTTTCAT	57.518	27	CATATTTGATGGGACCTTACG	58.831	22
AAATCATGAGCGTCCGTCTT	59.7	20	GATTTTGCCCCCATATGCTA	59.757	20
AGACACCCTTTCCATCGTGA	60.51	20	ATCCCAAATTCCCAACCTCT	59.629	20
TCCATTCCGAAAATCAAAGG	59.872	20	CCGCCTGATTTGTTTCTCAT	60.074	20
GTTCAGTGTCGGCCTCGTAT	60.142	20	CCCCCTACATTTCTTCATGC	59.387	20
GTGTCAGGCATGTTTGTTGG	60.008	20	TCTTGTGGTAAGCAGCTCCA	59.591	20
TCGAAAGGGTCAATTGAATG	58.546	20	TATATCGGGGGCTGAGCATA	60.403	20
GAATCGTGTCCTTCTGGCAT	60.081	20	CAAACTCCACCATAACCGCT	59.993	20
TTCAAATTTGTTATTGATACCGAT	59.229	25	CAATCTGCGAAACTGGGTCT	60.255	20
GCCACCAATTCGAAAAACAT	59.807	20	AAGGGGACTTGCACAAACAG	60.149	20
AGATGTCTTTTGATCAGTTGGTGA	60.04	24	CGATATTGTGCCGGTTTGAT	60.721	20
AACCGAGAGCATAACCTGACA	59.749	21	CGGGTGAGAATAATTTAAAGC	59.887	23
CTGCATTATCGCATCAGGAA	59.792	20	CATCAGGTTCACTGGCAAAA	59.691	20
TTTAGTGTTTTGACATGATTACTC	57.557	25	AATAGGTCAAGATCGCCACG	60.096	20
AAAATAAAGCTGGGCTGCTG	59.496	20	TTCAATGCAGATGGGATTCA	60.009	20
AACTTCATTATTTGGGGGTGC	60.068	21	TGACATGGAATCAATGGTGG	60.177	20
CCTCCTCAACAGAGGATATAGGA	58.747	23	TTCATAATTTTGTTGCTTTTGCT	58.083	23
CCCAAATCGGCAAATAGGTA	59.789	20	AAATCCCAGCCACACATTTC	59.797	20
ATCCGGAACCTCGAAAGATT	59.903	20	TCAAATGGTAACCAATCACTA	59.328	24
TAGCCCTAACTCTTGCCCCT	60.221	20	CAGAGGCATGGTCTCAGTCA	59.98	20
CGAGCCTCAGCCAAAATCTA	60.481	20	TTGGAATTTGGAGGTGGAAG	59.903	20
TCCACATCACATGACCTTCTG	59.535	21	GCTTCCTCCCAATAATGCAA	60.038	20
TTGCGATTGTTGAAGTGGAG	59.84	20	GCCCACTCTTTCTAACCGTC	58.792	20
GTAGGGGGCAGACATTAGCA	60.096	20	CAGAAAAACCATGGGAGAGG	59.521	20
GAATTGAGACCCATGCACCT	59.934	20	AAAGCAAGCCTGGACTACCA	59.875	20
GAAATTGCTAGTTCGGGCCT	60.582	20	GCCAATTCCGATTCAAACTG	60.448	20

TTACGCTAGTCCGTGGGTTT	59.632	20	GGTTTTCAGATACACGTGCCA	60.939	21
TGAAGTTAGGAAATAAGGAGGTG	57.525	24	ATGAGGAGGAGGAGTTGGGT	59.929	20
TGCATGCATTTTAGCTTTGG	59.842	20	TCAAAGGCCTAGAAGTGTTTTG	58.562	22
TGGACATTTGGGTTTTCTCA	58.947	20	AGGAAATGCAGTGTTTTTCAA	57.411	21
AAAATGCCCTTGTATGCTGC	60.103	20	CAGTTTTCATTTGATCAAGCCT	60.122	23
ATAAAAATGGCACCTGGCTG	59.96	20	GCGGTGAGTGATTGAAGGTT	60.119	20
TGATTCACCTCCCATGATCC	60.692	20	AAGTAGCACGACCAGATGGG	60.134	20
GTCTCAATGGGGACATTTGG	60.173	20	TTCAATTGTATTAGCCGATTTTT	57.072	23
TTCCCGAAATCCGAATAAAA	59.367	20	GAGAACCAAGGGTCAAGAAAA	59.61	22
ACACAACTCGGAACAACGAA	59.187	20	CAAAAATCCAACACCTCTCAGA	59.513	23
AAGAGACAAACAAGCATGGG	57.797	20	TCACAATCGTCCATTTTTCG	59.518	20
GCTTTAGAGATGGGAGCACG	59.978	20	TGTGAACCAGAGTCGGTGAG	59.864	20
CATTCATATGAGGATGGCCC	60.118	20	AACCGTGGCTAATCTGATGG	59.955	20
GCCCCCTCTTTCAGTCTTTC	60.19	20	TGACTCAAGTCTTCAACCAACA	58.397	22
TCTTCACCACCTGAAGAGGG	60.229	20	GAAACGGAGGGTTGGTGTTA	59.83	20
TTTGCTTGATCCAACGGTCT	60.636	20	CGGTGGAATATGTATGGTTGT	59.996	22
CCAATTTGAATGGTTATCACCTG	60.457	23	TGAGCTCTTCCGTGTCCTCT	60.135	20
CAGAGGAGCCTCAAGATTGC	60.096	20	CTTGCACCACCACTTCCTCT	60.298	20
TCATGCCAAAATTTTCATTCA	58.994	21	GAGATTTCCTCCTTCCACAGG	60.059	21
CGAAACCCTCTCTAATTTGATTGA	60.785	24	TGCACACGCTACCTTAGTTGA	59.545	21
GGGTTATTATTTGATCACCTCCC	59.813	23	AAATGAGTTGGCTGTCCCAC	59.973	20
AAACGTGGAGCGAGCATAAT	59.736	20	TTTAAGGGTTATCACCTGATTTT	57.757	24
TGCGAGTCATGCTCGATTAG	60.119	20	TTAAACTTTCCATCGTCGCC	60.074	20
TAGACGGTTGGAGAGATGGC	60.218	20	AGTCCGGGGATAGTAATGGG	60.032	20
AACACCAAAATATCGTCCCG	59.685	20	TCGTGGAACGAAACATCGTA	60.111	20
TGAAGAAGATTCTCATCCCACA	59.67	22	TGAAATTAGGAAATAAGGAGG	57.424	24
CATTGTATTGGGCTGCTCCT	60.096	20	TGCCACGTAATCACAGCCTA	60.28	20
TCTTTCCCACTCGATTTTGC	60.192	20	TCTGAGATTTTCATTTTGTCGG	59.202	22
AAGTTGATGATCCCCGCATA	60.296	20	TCAAATGCTCAAGGATCAATT	59.162	22
GATTCAGAATTTCTCCAGATGC	57.874	22	GGCTGTGTGATCATGTTTGG	59.967	20
TGTGAGGGACACAATTCTTGA	59.124	21	AGTACCTGCCGACAAATGGA	60.517	20
AAAAATTCCAATGGTGGCCT	60.542	20	AGGCCACTGAGAGTGGTGAC	60.315	20
ATGCAAGTTTTGCTTCCCAA	60.617	20	TCAATGTTGATCAATGTGGGAT	60.059	22
GAGCAGGGAGATAAGAGAGAGA	59.318	24	TCATGCTTGAATCAAAACAACA	59.206	22
GCATTCTTGGAACCACTTGC	60.646	20	AGGTTGTCCTGATGGTGGAG	59.962	20
GGAGTTTCCGGTGTTGAAGA	60.088	20	CACTCTCACGAGCTCACACG	60.829	20
TCCACAATTTCGATCTCTCCT	58.729	21	TTTTGCCATTTTCGAAATCC	59.886	20
GGTAAACATGCACAGGTATAGAC	59.854	24	AGGAAATAAGGAGGTATTATGA	60.302	26
CGAGGCAGAAAAATCAAAGC	59.96	20	ATTGCTTCCAATCGAACACG	61.032	20
ATCAACCATTGATTCCCGAG	59.75	20	CACGAGCCGCCTAAAATAAA	60.218	20
TCAATCCTTGTCACCAACCA	59.935	20	TGCTGCAGAGTGTTCTTTGG	60.175	20
GGACACGCGGATCAGTATCT	60.104	20	TGCGAATGATAATCAACATGAA	60.329	23
AGGTCCCAGAAGCAAATATGA	58.659	21	TCTTTTACTTGCAATTTCTGTTT	59.4	25
AATGGGAGAGCCAAACAATG	59.933	20	AAATATTTCACGCCGCTGTC	60.103	20
CCCAGAAGCAGATCCATGTT	60.073	20	CCACGTACACCGACAAACAC	59.922	20
TCCTTGACCGCGTAAAGATT	59.708	20	TGATCAGCAGCTATGGAACC	58.826	20
TCATGCATTCACCATACGAA	58.492	20	GAATGATGGAAGCAATGCAA	59.628	20
CACCGTGTACTCTGCCTTGA	59.897	20	TTGGCAAAACCCTATTCAGG	59.931	20
CCACTTTTGCATTGCCTTTT	60.11	20	GTTGGTTACGGGAATTGCAT	59.691	20
ATTTGGTCCCGTACAAGCAG	59.993	20	GGCAAGGCTAAATGGTCAGA	60.214	20
CGTTTCTTCCCTCATTTCCA	60.044	20	GGCCAAAACATTGCTCCTATT	60.326	21
GACTTGCTTGCAAGAACATACA	58.108	22	GGACAAATATGGTGATGGCA	59.205	20
TCTGGAGTCCACTTCAAGCA	59.545	20	TTGGCTCGTACCAAGAAAGG	60.241	20
TCTCAGCCACAAAATTCGAT	58.298	20	ATATCACATGCATGACCGGA	59.763	20
GGGTTATCATGGGATCCATTC	60.225	21	GGTTGACTCATGGAAAAAGCA	60.103	21
AAGAAGCAATGGTCGCAAGT	59.882	20	AAAAGGTGATGGGTGTTGGA	60.21	20
AACTGGTTTGGTGGTTTGGA	60.246	20	CGTTTGGCGGATAGTTTTGT	59.996	20
TGGAGGAAGCATTGGACTTT	59.67	20	CGAAGGTGGGTTCTTGTGAT	59.966	20

CCTTTTTGCTTTATTAGAAACCTG	57.797	24	CCAAATAGGGCACAATCACA	59.395	20
TTTTCGGTTTGTCTCATCCC	59.91	20	GAAGGGAGGGAATCTATTGTG	59.42	22
TGGCGTGACACCATGTAAAA	60.967	20	TTGGATGAGATGATGGCAAA	60.009	20
TTTTTGGTGGCGGTAGGTAG	59.99	20	AGGTGCTGCCCAAGAACTTA	59.875	20
GTTTCCCTTTCGATGCATGT	59.939	20	GGCTGCATTTTTATCCCAAA	59.907	20
CATTGATGGACCTGCTCTCA	59.787	20	AGAAGCGTAGCATTGAGGGA	59.978	20
TCTACTATACCCTTGCAAATTATC	58.82	27	AAACCCCGACTTCTCCTTTG	60.467	20
TTTGCATCGAGACCAGTTTG	59.84	20	GAGGCGATTGCTTAGGTGAA	60.352	20
TGGTCCTTGACTAGTTCAATTTCA	60.035	24	GTTTTCGTTGTCCCCACAAT	59.694	20
TATACACCCCGCATCCATTT	60.038	20	AGACCCAAGCCTACCGAGTC	60.649	20
TCCAATTTGCCCTTTTATGC	59.907	20	CTCCTGTCCATGAAATTGGG	60.309	20
ATGCTAAGTTAGGCCTGCCA	59.867	20	CGTCCAGTGCCTGTGAATTT	61.096	20
CCAAATGAAATGAAAACCGTG	60.209	21	GGGTCGACAAGCTTGAGAAA	60.375	20
AAAATGGCGGTCAACTCAAG	60.11	20	AGGGAGGGAGAGTTTTGCAT	60.074	20
ACATGACTCGAGCCTGTCCT	59.866	20	TTTGGCACCCCTTTGTAATC	59.801	20
CCTACGAAGAAATACTGCGCTT	59.939	22	CTTCAAGATTATGGTGGGGG	59.24	20
TCTTTGTGGGGAAGAACAGC	60.232	20	TTCAACATGAAGTTCGACGC	59.847	20
TCACCTCCATCTCTGCTCCT	59.945	20	TCACCCGAATCTTTCGTTTC	60.051	20
GCATGCATGAGCAAGAGACA	61.154	20	CGATCGATCATCGGAAAAAT	59.862	20
TCGTGATTCCTCCCAAAATC	59.871	20	ATGAGGCCCATCAACACAAT	60.203	20
CAACCATTATTATTCCAATCGAAC	58.736	24	ATCATGGCTGATCAAGCTCC	60.189	20
GATCATGCATTCGCAAAGAA	59.775	20	TCCCAAAGTTTCACACGTCA	60.128	20
TTTTCCCCCAGATGTCTCAC	59.903	20	TGGGATTGATCCTACCCAAA	60.126	20
TGGTCGAACACTCAGCAGTC	60.03	20	TTTTCATGAATTGCCTTCCC	59.878	20
TTTTATGCGGCATTCATGTG	60.474	20	TTTAATTAGGTCCACGCGCT	59.742	20
CTGCATTTTCTGCTGGTTCA	59.988	20	AACGGTCTTAATGCAATGGG	59.823	20
ACGAAAACAAAAGGTACGGA	57.278	20	TGTCCGTGATGATCGGTTTA	59.924	20
TGATTCGGTTAATCCAAGGG	59.756	20	ATGTTGCAGCTTTTCATCCC	60.081	20
GAGGGGGTGAATCATTGGTA	59.605	20	TCATCCCAAGTCCAGAGCAT	60.622	20
TCGGTTTGAGAACCAATGAC	58.543	20	TTTTTCAGCTCACTTTGTGATG	58.081	22
AATCTTTCTTGGGGCCATCT	59.903	20	CCAGCAATAGCCCTCTGTGT	60.277	20
TGGCACACTCTCATTGCTTC	59.992	20	TGGTGATTGCTCATTCTGGA	60.201	20
GAACACCGAGAGCAAACCTC	59.851	20	GACCGTGTGCAATGAAACAG	60.16	20
ATGCGTGTGGTCGATGAGTA	60.144	20	GTGGCATGCAAACGACATTA	60.532	20
TTTCCCTATGAAAACCGTGC	59.938	20	GCTGCAGATCTAAGGCCG	59.654	18
GGAATAAACGGCCAATTCAA	59.773	20	TTAAAAGTGCGGGGCATTAC	59.964	20
ACAAAGCCACCGTCAGAGTC	60.307	20	CATGATGAGAGTTGGGCAAA	59.648	20
CGTGTACTCCGCACTTCAGA	60.049	20	ATCGGAGTTGATTTGATGCC	59.9	20
AATGCAATTGTGCATGCCT	60.096	19	TGGCGATTAATTTCCCTTCA	60.395	20
TCCGGTTTCAAATCCAAAAA	60.273	20	TGTCCAACTCAAAGAGGAAAA	57.441	21
TCATTATCATCCGCCTTCAA	59.065	20	ACAAAAAGCACAAACCCACC	59.875	20
ATGGACCAATGCACCAAAAT	60.059	20	GAGGTGTTACGCTCTCCAGC	60.02	20
ACAATTTGCTGTGGCTGATG	59.722	20	TGCGGAGTTCAAGACTGATG	59.984	20
TACGAAGCTGGAGGAAGTGG	60.388	20	CGGAGATTCTCTCTCTCCCC	60.292	20
CATGTTTGCCTGTTTTGTGG	60.004	20	TTGTGCATCAAAATAAACCCA	58.922	21
TGCATCGATGATCTTGAAGG	59.756	20	CCCCCTATTGCTCAGACAAG	59.688	20
TTGAGCGACGTATCTCCTTGT	59.89	21	TTGGGATTTCACGAAAGATTG	59.924	21
AGGAAAATGTGATAGCAGCG	57.999	20	TGCCGTTTTGTTCATGTTTT	59.062	20
CCGCGAAACAATGAAGGTAT	59.96	20	GGCTAATTGTTGGCCTTTGA	60.074	20
ATCCGGATCTGATTCGATTG	59.854	20	TCCGGATACGGATTATATCCA	60.36	22
TCCACAGAGATTTCCCACATC	59.918	21	TGCCTTAGATTCCACTTGGG	60.066	20
GGTGACGATGGTGATTGATG	59.769	20	ATGCACGTAGGCATGTTCAA	60.142	20
TCCAGAACATAAACACCGCA	60.111	20	CGAGCGTAGTCGTCGCTATT	60.564	20
CTGGTACGTGCGACGTATTG	60.195	20	TGAGCTCCTTAAGGGAATGC	59.41	20
TTGGTGAGTGCAAGAGAAAGAA	60.03	22	GCATGTAGCCGTCCACAAAT	60.925	20
CACTCAAGTGGGGGATTGTT	59.82	20	TCCAGCGACTCATGTTGTTC	59.837	20
TGATGATGATGGATTTAGCGA	59.079	21	GAGGGAGGGTCGTTTATCGT	60.328	20
AGAAGACTCAATCATGGGCG	60.218	20	CCCAAGAATGGGTTATTATTTG	59.14	23

TGAACTCTGCATCATCTCCG	59.942	20	CGAAATGCATGATTGAGGTG	60.073	20
GCTGGTCGGTTAATTCCTCA	60.074	20	CCCCGAAACTTTAGCGTAGA	59.357	20
TCCGAAAATCAAAGACCCAC	59.91	20	ACATGGATTGTGCTTTCGAC	58.572	20
GGAAGACTCATTGCCCAAAA	60.051	20	GGAGGGATTGAACGTAGGTCT	59.452	21
GCATCTCTCCCATCTTCTGC	59.917	20	CTTTTCTGGAAGGACCACCA	60.081	20
AGTGTTTTGATCGAGTCGCC	60.263	20	GCTTTGCGTGGTGGAATTAT	59.967	20
TTATGATATTTCCATAAGTCACAC	57.297	26	GCGAAAGAAAATGGTTTGAA	57.873	20
GTCATGGTGTTGGCACTGTC	60.013	20	TGTGCATGAAGTGAAAGGGA	60.24	20
CCACAAATCATCCATGCAAC	59.781	20	TTGAAGTAGGGCATTGAGGC	60.214	20
GGCAAGCGTCTTTGTTTGTT	60.292	20	GATAGTGGAGTTGTGAGCATCT	58.878	23
CCTTGATTTCCAGGATCCAA	59.864	20	TGACGACCGATAATTGCTCC	61.003	20
TCACATCTCATTGCCTCTGG	59.787	20	TACTGCAGTGGAGTTGCCTG	60.049	20
TAGGTAACCGGTTCGACCTC	59.052	20	CCAAAAACTGATAAATGATGCT	60.355	24
GTACGAAAATGCCCCTCGTA	59.96	20	TTTTTGGCCTTTGATCTTCG	60.181	20
ATGGAAGGTGGGCCTAAAGT	59.827	20	TTCGTGAATAGTGCTGCCTC	59.028	20
ACATTGAACGCTCCAAAACC	59.978	20	TTCTACCCATTCTTCGCCAC	60.074	20
GCCTCCCCATATTGCTTTTT	60.28	20	CGGGAGAAAATGAAAACCCT	60.291	20
TTTGGGCCTTTTTATTCCG	59.887	19	CGGTCTCGGTTTGGAATCTA	60.066	20
ATACTAGTGCCTTGCCCGAG	59.359	20	TCGAAAATGAACGATCGAGA	59.35	20
TTCTAAAGGGGAAACGACAAA	58.727	21	GCCCACCTGGTTTAAAGGAT	60.187	20
TTCTCTCCACTGTGGCAATG	59.831	20	GAGGGAGGGAAGATATTCGG	59.859	20
AACGCCTTTCACCCCTAAAT	59.835	20	TCCACCAAAAACCTGTCCAT	60.21	20
GCTACCCATTTCCCAGCATA	59.923	20	AAAATCCGAGCCAGTTGTTG	60.11	20
GGCAGAGTCACATTCCCATT	59.934	20	CGCTGCAACAAATACACACC	60.18	20
ACGAAACCACGAAATCAAGC	60.118	20	TCCAACCTTGTTTTTCCGAC	59.948	20
CCTCAGTTTCTCCCTCACCA	60.229	20	ATCACCGATTTGCAAACACA	59.972	20
TGCAGCCCACTAAATCACAC	59.722	20	ATAGGATTTCACTGCCTGCG	60.235	20
GGGAGATGGGTTGAAACAGA	59.903	20	TCACCAGTGCTTTGAGGATG	59.831	20
ATCGAACCATTCCTGCTTTG	60.074	20	TCACCTGATTTTCTCCCTCC	59.065	20
CACTTACTTAAAGTCAACTCCCCT	59.66	25	TTGCACGCAGCATATTATGAA	60.247	21
TCGAATGATTCAAAGATTCACAA	59.578	23	TAGGCCTAAATGGTCGCATC	60.06	20
AAAAGAGAAGCCCTCCAAGC	59.962	20	CCAAATCCAAACCACCATTC	60.029	20
CGGCAAAGAGTTATTCGGAG	59.839	20	ATTCTGCTCGATTCCCAAGA	59.773	20
AGTTGGTGCAAGCTGGAGAC	60.453	20	TTTGGAAAAACAGAGCACCC	60.088	20
TGATTTGGGACACTCACAACA	59.992	21	TTAATGGCCAAAAACAAGGG	59.805	20
TGAATTGAATAATCCCAAATCAAA	59.583	24	TGACATTTGTCTAACGATGGTG	59.415	23
TCACCGAAAAGATATGAAAATCAA	59.851	24	AATGTGATGCTCAGCAGTGTTT	59.809	22
TGCCAATACAAAACCAACCA	59.826	20	TGGTTTGGGGTAGGAAATTG	59.657	20
TGCGTTTTGACGATATATAGTGTT	60.194	26	AAAACGCGCTATTTTAAACCC	59.549	21
GAGAGTCGGAGATGACCTGC	59.952	20	TCACTGCATTAAACCTACTCCC	58.264	22
GCAATCGGTGACCTTTTCTT	59.174	20	TATGTGGTCTGGCAGTCGTG	60.745	20
TATCAGTTGGCAGGGGAGAG	60.21	20	TTATCAGACAATCCCGGAGG	59.887	20
TGTGATAGGATACGGCCCAT	60.177	20	TGACACGGTGATTTACGTGG	60.427	20
TGATGCTGCATTTTGTGTGA	59.833	20	TGAATCCTCCCCCATTGTTA	60.126	20
CTTCAATCCCACCACCAAGT	59.82	20	CTAATGCCCCAACACAGCTT	60.132	20
TGGATGTCATACCGGACTCA	59.918	20	TGTGCGCTAAAGGTTTTCCT	59.883	20
GAGCAGGATTCTGTGGAACC	59.661	20	CCTTCTTTGGGTCAGTGCAT	60.111	20
GGGCAGCTCACAAATCTCTC	59.957	20	TTGTCTTCATCAAACGCCAG	59.84	20
ACAATCGATTTCCCAACCAC	59.653	20	AGGGAGGTGGCTCCTGTTAT	59.957	20
AAAAGTGGCATTTTGCCCTA	59.586	20	ATGATTGCGAAACAGGAAAAA	59.578	21
GGAAATAAGGGGGTGTTATGA	57.796	21	GAGCGCATTCGAAGAGTAGC	60.265	20
GGACCAACTATGGCACAACC	60.24	20	TTCGGCCTTTGTATTGCTTC	60.209	20
CACTTTTCATCTCCAACCCA	58.541	20	TGAGAAGAACACATAAATTCG	59.772	23
TCGGCTCTTTTTCTTTCTCG	59.702	20	GTATGTGCGGTGAGGAGGAG	60.678	20
TTATGCAGCAAAAATCCGAG	58.912	20	CCTCCAGCTGTTAAAACCCA	60.103	20
AGGAGAACCACGCATTTACG	60.132	20	TTCGGAGTCTTCAGACAAATCA	59.853	22
CCATTCCTGAGACCAAAAGG	59.521	20	TCATGTGCTTCAGTCCTTGC	59.992	20
GGAATGATTTCCCTGAGCAA	60.014	20	AATGGAATACCGGTGCAAAA	60.188	20

TGTCCATTGGCAGTTAGCAG	59.864	20	CTCTCTCCCCCTCCAAAAAC	60.045	20
CCAATAGTTCTTCGGTCCCA	59.926	20	CCAAAATGCTTTCGTTCCAT	59.938	20
GCACTCGTTTCTTTCTTCGC	60.14	20	TCCGGTGACTGAAAATAGCC	60.074	20
TGAAATTCAATGATCGGACAA	58.954	21	ACTCCCTGTGCTTGTTCTGG	60.298	20
CTCTGCCTTAGGTGGCTTTG	60.008	20	ACACCTGGGTGAGACCAAAC	59.859	20
CGTGTTTGGATTTGGGTAAAA	59.723	21	TCCGATGGGGTATTCCACTA	60.148	20
TTACCCTGGCCAGTCAGTTC	60.111	20	GGCTAGGCTTGTAGCAAAAGG	60.389	21
CGAAAACCGGTTAAAAACCA	59.841	20	CGCATTTTTGGCCTGATATT	59.928	20
AGATCTTCCGATCGGTTCGT	60.99	20	TCCCCACCAAATTTAACCAA	60.024	20
GAAAGGGTGCGCAATATTCT	59.186	20	TCCTTAATTCATTAAATACATA	57.288	26
TCTTATTCTCCCTCTCGCCC	60.673	20	GACTCATACCACCCCAAAACT	59.259	22
GCTACGAGAACCGAAAATGG	59.708	20	CCCTCTCTCCCCTCACTCAT	60.605	20
TTCAGATGGTGTCAAAACCC	58.387	20	GTGTGATTGGCAGTGACAGG	60.162	20
TTGTAATAAATCTTTAAAATGGGA	58.149	27	GCACGGCAGTGGAAGAATA	59.814	19
CTCAGAATCCACTCCTGCAA	58.957	20	TCAGTACAATGGAGTGATGGC	59.621	22
GGGTGTGGTACTTGGGACAG	60.275	20	AGTCAGCCGAGGAAATTCAA	59.813	20
TTTTAGCCACTTTCTTGCCC	59.338	20	CGAAAAGCTGAGAAGATGGC	60.096	20
TGGGTTATCACCGAATCGC	61.806	19	CGGCTGTCAACAGAAGTTCA	60.025	20
CCGACCTTACATAGCGGAAA	60.089	20	TGGCATGTGGGGGTATAGTT	60.074	20
GAGAAATGGCCCATGACTGT	59.934	20	TTTTGAGACACCCCAAGTCC	59.943	20
GCCTCCTTTCATGCAATGTT	60.081	20	TGATTCGGGTTAATCGGTTC	59.762	20
GAGAAACCCGACATGCAAAT	59.939	20	TGGGACACTGTTTTCTTTGGA	60.514	21
CTCTCCTTCTGCGCACTTTT	59.757	20	TCCCCTGCTTCTAAAACCCT	60.068	20
GTAGGAACCGTGCAGCACTA	58.952	20	TTTCCCAACAAATTCAGCAA	59.133	20
AACCGCGTCTCTTAGTTTTATGA	59.362	23	TGAGAATGGTGGAAGAAGCC	60.195	20
TTGCACGAATGGTTTGACAT	59.972	20	TGGCTTGGTCTTGATCTGTG	59.831	20
TCATTTTGATTACTTTTACTATTCG	57.299	27	GGGAATAATGTATGAATGATC	59.487	24
AGTCGATTTTCTGCAACCGT	59.74	20	ACTGCCACCAGCCTTGTACT	59.792	20
AGTTGCAGCGAAAACATGG	59.856	19	TGTTTGTGATCCCAATTGAA	57.35	20
TTTTCTCAACCGAGCTCACC	60.375	20	TTGGTTCGAGCCATTGTGTA	60.111	20
AATGCAATCCTTTCACTGCC	60.081	20	TATCCAGTGTTGCTTTGCCA	60.257	20
GGGAGCGACGATAATTGGTA	59.923	20	AAGTCGAAATTTGGCAACAA	58.267	20
TTGGCAACTATCCCTAACGG	59.953	20	TGAGCACATGCCAAAATGTTA	60.126	21
TCAAAACGGTCAAACGATGA	60.088	20	CCATGGCTGATAAAAATGGC	60.289	20
ATGATAGGGCATGGCATTTT	59.258	20	CTAATGGGAAAAGCATTGGG	59.406	20
AAGCAGGAAGTCATGCCACT	59.874	20	AACATGATAATGCTGATAAAA	59.715	26
AGCAATTTGTGAAAGTGGGG	59.971	20	TCTTTGGCTCAATGGAGGTC	60.195	20
TGATTCGAGTTTTGATGGGA	59.049	20	ACTTGGAATCTGGACTCGGA	59.655	20
CAAGAAGAGGACTGGTCCGA	60.377	20	CAACCGGCAGCATTTTTACT	60.131	20
CCTCTTTTCGACCTTAATAAGCC	59.67	23	ACGGGTGGGAATGTATTAGG	58.646	20
TGAAGGTAGGAAATAAGGAGGT	58.703	23	TTAAGCCTACCACGCTGTCA	59.488	20
GCTTCCATGTTTAGGCTTCG	59.845	20	TTTGGTTGAAGGTGCATGTC	59.547	20
AAATCGAATCGTGAACACCC	59.797	20	TTACAGTCCCCACTGCCTTT	59.592	20
GACCCTAGCTCTTGCCCTCT	59.979	20	TGAGGCCACTGACTTGAATG	59.831	20
ACAACCGGCCTAATCCTTTT	59.835	20	CAAATAATGTGGCAATCCCC	60.016	20
TGCGTTTTGATGATATATAGGTGT	58.933	25	TTCATCTTGTAGCGTTTGAATG	59.772	23
ATGTTGCATGAGTGAGCTGC	60.024	20	CAACAAATGCATCATCTGCC	60.08	20
CGAAAAATGACTGGCCCATA	60.827	20	TCCTGATGGACAACTGACCC	60.934	20
TATGGGTTATCACCGGATCG	60.544	20	ATTTACCCATAGCGCACTCG	60.117	20
AGTGACGGCCTAATGACAAA	58.228	20	GGAATATGATCGGTCGCAAA	60.807	20
GTTACTCGTGGAGGTGCCAT	59.997	20	GGGTTCATCACCGATATGCT	59.78	20
TGCAAGAATGGTGAGAGTGG	59.831	20	TATCAACCCAAAACCCCAAC	59.523	20
CCCACGCCATATTCTCTCTC	59.653	20	TGTAGGGGAATCTCGTGGTC	59.927	20
CCGTTTCCATTTACCACTCA	58.475	20	AATTTTGGAGATGGACCGTG	59.79	20
CGGCAGAAGGAGAGAAGAAG	59.304	20	GGTAGTTGGCGTTGACTGGT	60.035	20
GCGTTAACTGGTATAGCGGC	59.769	20	GCTGACTAACCCATTCTTGTTT	60.048	23
CCTAATCGCAAAACAGCACA	59.872	20	ATCTGAACAAATGGGCTTGG	59.933	20
GAACCAAAACCGGATGCTAA	59.938	20	ATACGACAGCGTGTTGGACA	60.183	20

TCGAGGAGTTTACACGGAAGA	59.861	21	ACTACCCAAACGTCCCAAAA	59.331	20
CTCCCACCTTCCAACTCAAA	60.081	20	AATGGTGGGGGTAACAACAA	59.948	20
TGCGATCTATTTTGGCTTTTC	59.336	21	TCTTTCTTGGAACATCTCGTCA	59.853	22
TTGGAAACCTTTTACCCCAG	58.922	20	CCTGGTTCATTTCAGGGAGA	60.042	20
ATGCACGTAGGCATGTTCAA	60.142	20	AACACACAAACGAATGGCAA	60.011	20
CGAGGTTGCCCAAACTCTTA	60.241	20	AAGGAAACCTTAAAGGGCCA	59.939	20
TTGGTGGTCTGGTGACTGAA	60.129	20	GTGGTGGTGTGCGTTCATTA	60.436	20
AGGTGCACTAAGCCAGCACT	60.081	20	TTGAACATGCATCCAAAGGA	60.049	20
AGCTACATATTTTGATGCATACGG	59.481	24	ACCTGGAAACGCATATGGAG	59.955	20
ACGAACAGCTTCATCATCCC	60.081	20	CCTTTTCTGCATTTGGTGCT	60.249	20
CCTAACCCTTGACTGCAAGC	59.875	20	GATGCGCCACCTTTATTGAT	59.929	20
CAACTCCCAAATCCTCCAAA	59.903	20	GAGGCATTCCATGAGGAAGA	60.158	20
TCCCCCATCAAAATACTTGC	59.762	20	GCTTGAAGCGAAAAAGGAGA	59.708	20
ATGAATCCACACAAGTGGGC	60.79	20	TCACCTGCACACACATTCAC	59.101	20
CAAAATTGGAACGACTTGCAT	59.989	21	GGGGCTGTTGTGAAAGAAAC	59.574	20
GTTAGCATGGGAAGGGGAGT	60.328	20	TCAGTCAACCAACCAACTGC	59.726	20
CAAACAACAATTCAGCAAATACCT	59.494	24	ATTGCACCTCGTAAACACCC	59.859	20
CTCCTTCTGTTGATCCCCAA	60.042	20	ACGGTGTGTCATCATTGGAA	59.812	20
AGGACCTGCTGGATTGTCAG	60.261	20	TTTACACCACAAAGTTGCCG	59.627	20
CATCTGATTACCGCATTCTCG	60.611	21	AAGGTCCTTCTCATTGGGCT	60.074	20
AGAGGGTTATCATGGGATCAAG	59.307	22	CCCATATTGGCAAGCATTTC	60.289	20
TATATGGGTTATCGCCGGAT	59.127	20	AACTCAACAACCCGTGAAGC	60.156	20
CTGACTCGTGCCCTTATGGT	60.134	20	CAATTGTCTGACCCCCATCT	59.779	20
TTCGAAATCTAACGATCCGC	60.175	20	AGAAGCCAGGCAGCATAAGA	60.118	20
GGATCGAGTCCATGCCATTA	60.833	20	TGCTTGACAAGTGACATTGAA	57.882	21
TACGTGTATGATGGAGGCCA	59.948	20	CTTGCAAATTACCAAGGGATT	58.126	21
GAACCACCACTGCATCACAC	60.013	20	ACTGAAGCTCGAACCCCTCT	60.393	20
GTAGGCGCAGGACCAATTTA	60.096	20	GTGGCAGGAAGCATTCACTT	60.263	20
ACCAAACCAAACCAAGCAAC	59.875	20	AGGGGATTGGGATTTCTTGT	59.629	20
GGGGACCATCTCAAATGTTTT	60.046	21	CCAATCTCTTTCATCACTCTCG	58.934	22
GCAAAGTGCCACCAACACT	59.742	19	TGCTGGTTGCATACTTGCAC	60.876	20
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GCTGCAACGAAGAGTGACAA	60.183	20	TGTGCACTCGATGATGTTTG	59.248	20
GGGGTGCTATAAATGCCCTT	60.171	20	CCAAACAACTCCCTACCGAA	59.964	20
TCTCCTCCCTTCGTCTCTCA	60.064	20	AGCTCTTCATCGGTTGGATG	60.218	20
TGCTTCCGAAGATCTCGATT	59.917	20	CTGATGCATGTGGTAGGAGC	59.271	20
GGTTGCTCTTGCTCTTCGAG	60.277	20	CCATACAAAAGCGCCAAACT	60.131	20
TTCATGGATTCAAAAGGGGA	60.244	20	TGTAGCTCCTCCTAATTTCCTCT	59.445	24
GCGAATTTTGGTGTTGGAAT	59.807	20	CCCAACATCATCCCTCACTC	60.326	20
TTCAGTTGGCCGAATGATTT	60.448	20	AGTTCGAGGTGGGCTTTTCT	60.247	20
CAGCACAACGTTCCATTGAT	59.572	20	AATTTTGGCAACCGATCTTG	59.938	20
CGATCTAACGGCCCAGATT	60.044	19	CTGCCGGAATCACATCAGTA	59.673	20
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TTGCACTAGATCACTCCCCTT	58.803	21	TTGGGTTTTGATGATTGCTTT	59.442	21
GGCGTCGGTTGATAGATTGT	59.962	20	GTGGAAGCAAACTCAACCGT	60.156	20
AACTCCAGACACCACCTTCG	60.151	20	TGTGGCCTTTTGTCACTTCA	60.278	20
TGCAGTCTTACAGCCCAACA	60.449	20	CATTTGGGAGGACAAAGGAA	59.903	20
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GAAGACGATTAGCGTGCCAT	60.243	20	GGACGTCCAAAAACGGAAAT	61.08	20
CAAGTAATGCGGAGCTAGGG	59.861	20	GGGACTACCGTGATGGAAGA	59.927	20
ACCACTTCTTTCGCTACGGA	59.875	20	CAAGTGAAATTGGATGGTGC	58.976	20
AGTGTTGAGCAAAAGGGCAG	60.431	20	TGAGAACTTTGTGGGCATCA	60.24	20
CTCTTTGCCTTCTTCCATGC	59.955	20	GGTGCGGGATCAATAGGTTA	59.784	20
CTACTCGGCCTTGGAACTTG	59.869	20	AGGTGGGAGTGGAAACACAC	59.859	20
ACGTTTGAATGCATTGGGTT	60.235	20	AGTTGCTGTTCTGACCCGAC	60.307	20
ATATCCCCTTGAGCCTCCAC	60.293	20	CGGCATGATGCAGTAAGAGA	59.972	20

CATCCCTTAATCCCCATCCT	59.974	20	ATCCTGCCTTGTTCCTCCTT	60.074	20
AAAGTGATTGTGAAACCGGAA	59.462	21	TCGCTGACTTGTGGATTGAT	59.245	20
TGTTTTTCCACAACTCAACCC	59.861	21	GAAGGAGAGGAAGGGCTTTG	60.319	20
GACGGTATTTAGGTGTCCTCG	58.591	21	TGCCTCAACTTTGTGTGCTT	59.49	20
CTTTCCCCATGCATCATCTT	59.894	20	TTATGAGATTGGGGGTGGAA	60.126	20
TCTTCGGGTGTTCTCGTTTT	59.711	20	CATCACCGGCCTACAAAAAT	59.823	20
TTGAGGCGGTTAGGAGTTGT	59.734	20	TCACAGGCAAATGACCAAGA	60.24	20
ACCGGAATGAAAATCGGATA	59.23	20	TCCACATGGATGAAGTGCC	60.489	19
TCTTTGTTTTCAACGCCTCC	60.227	20	AGATTGAATGCAACAGCACG	59.871	20
CCACATGCTTAGAGATGGGC	60.624	20	ACACCATGGTTTCCAATGCT	60.24	20
CAAGTAATGCGGAGCTAGGG	59.861	20	CCGTGATGGAACAACCTTCT	59.966	20
AATCCCAGTTGAGGAAAGCA	59.67	20	AATTCACAAGCTCACAAAACG	57.947	21
TTGCGAGAACCAACTCTGTG	60.025	20	CTAGCAAGGCTTCCATCTGC	60.118	20
ATGACACGCATAAAGGGACC	59.82	20	AAAGGTGAAAGAGACATCAAC	60.026	23
ATGATTGCCCCCAGTTATCA	60.155	20	CCGCAACTTGACAATGACAC	60.16	20
GACGGGGTCGGATTATACCT	60.039	20	CATTATCTCAAACGAGCGGC	60.742	20
TTTGCCGTACACATCAGAGG	59.716	20	TGAATTGGCCTAAGCGAAAG	60.335	20
ATTCTCCATCCGACCATTCA	60.281	20	CGAACAAGAGTCTTCCGAGG	59.982	20
TCTTTGGTGACCTGTTGGAA	59.109	20	AAAGGCTCCTCTCTTCAGGG	59.95	20
CCATATTCCTCCGTTCCACA	60.713	20	TTGGGAGAGGGATAGTGCTG	60.21	20
TGCATTTTTAATTTATTTTCCTGA	57.15	24	TGCAATGCATCAGAGACTCC	59.95	20
AATTATGTGGCCGAGGACAG	59.955	20	CACCTCCTAGGCGCTATTGA	60.365	20
CAGTGAAAATGGACCCCTCT	58.989	20	CACATAAGCGAAAACGCAAA	59.88	20
GAGGTTTTGACCATATTTACTGTTT	60.393	27	TTAGTTTCATGAATGGAAGTGA	57.035	25
TCATAATGGTCTCCATCGCA	60.033	20	TTGGATCCTGATTCTCGACC	60.011	20
GGATTCATGAGATCGACGGT	59.893	20	TTGCTACACCTGCATTGACG	60.865	20
GCATATGCATTAAAATAACTTGA	58.448	27	TGTTGACGAACGAGACAAGG	59.873	20
GGCGGTCAGGTGTTAATTTG	60.365	20	TTTCGACAAATCATTGCAACA	60.103	21
TTTTATGCATCGTGCCAAAG	59.702	20	GGGTGATCATGGGAGAAATG	60.135	20
TTGAATCAGCTGTTCGCATC	59.955	20	AAGGCAGCATGCTTGAAACT	60.022	20
CAGCCAAAAATCTTGGGAAA	60.046	20	TGCATGATGTTTGCACGTTA	59.716	20
GGTTATCACCGGATCGCTAC	59.415	20	TGCACTCTTATGGCCTTTGA	59.42	20
AGTGGCACCAGTCGTAGGTT	59.646	20	TGGACCATTTGTGCACTTGT	60.008	20
AAAATCAAAGGCCCACAATG	59.801	20	TTTGACGAAATTGCCCCTAC	59.938	20
GCACCAATATTAGGCCATCG	60.31	20	GTGATTCAGGGTTCCGGTC	60.319	19
ATTGAGCCAAGGAGGAGACA	59.803	20	TTGGGGATGAGATGGGAATA	60.088	20
ATCTCGAAAATGGATGACCC	58.789	20	AATGGCCCAGATTTGTTTTG	59.801	20
CAAGTGCAATCTTGCTTTGC	59.614	20	CGAGAAAAGACAAAGAAGGGA	59.865	22
GCGAAATTCGTTGGTTTGAC	60.49	20	TATTTCGGGTTGTCCCTCTG	59.926	20
ATTACCGTCGTCATCTTGGG	59.813	20	CGTAGTTTAATTTTGCCGGG	59.489	20
TTTTTGGATGGAAAACCACT	57.037	20	TTGCGAGCAACTTGTCAAAG	60.172	20
TTATCATTGGAGTAAGCCCCT	57.708	21	TTGGAGTCCATGAGCATCAG	59.787	20
AACACATGGATTCATTGCCA	59.781	20	GGGGTAAAATCGAGGGGTAA	60.013	20
TCGCAAATTAGTGGCTTGCT	60.905	20	TTGGGGAATGTTGAGAAGGA	60.43	20
ATTTGGGTCTCTTCGACACG	60.111	20	CCTGCAGCTTTGAGTTCCTC	60.134	20
AAGCCAGCACATGCATACAC	59.753	20	TGGGGGAGAATAATGTTGGA	60.126	20
CATCGTCCATTGCTCGACTA	59.823	20	GAGTTGCATGATGGCATGAG	60.233	20
ATTGAAGACCGCCTCGATAA	59.668	20	TTAGGGATTAAAAGCGGCAG	59.341	20
GGAAGTTCATATTCACTTGAAGA	60.732	27	CTTGTGAAATGAATGCACCG	60.111	20
GGTAGCTGTCGTCGATGTGA	59.862	20	TATCGTTTTGCCGCCTTATC	60.061	20
CCGGGGTATGCTATAAACGA	59.81	20	CGCATTTGTGATTTTTGCAC	60.118	20
TCGTGAAACACTTCAACCCA	60.128	20	CTGACGAAGGAAGGTTCTGG	59.837	20
CCACCCATTATTTTGTTAGGAA	57.934	22	CACAGTTCACCCCCATTTTT	59.688	20
ATTTTGGCATCCTCTTTCCC	60.265	20	TTGAGGTGTGGCTGGTATTG	59.566	20
GAATATGCATTGAGCTGCCA	59.799	20	TTTCGGGGGCAATGTACTTA	60.315	20
TTTCTCTTGGCAATGATCCA	59.2	20	AGCCAGCAATAATCTCAGTGG	59.35	21
AAATAGTTCGGGTTTTCGGC	60.312	20	GGCTCGGCCTACTTAAGCTC	60.491	20
CTTCTTGACGGCAACGTTTT	60.284	20	TGCATGGCAAAGCTTCAATA	60.356	20

ATGGAGGTTGGGTGGTAGTG	59.697	20	AGCCGATAAAAATGGCACAC	59.967	20
CTCCACTTCACCGGCTTTTA	60.241	20	GGGTTTTGGAGATGAGGGTT	60.169	20
AATACCCTTGTATGCTGCGG	59.982	20	GGCCAGACGATAGTTACCGA	60.096	20
TGGAATGGTTCAATCCCATTA	60.002	21	CAGAATGGTGGCAACAAAGA	59.691	20
TTAAATACCGACAACCCCCA	60.046	20	TCGGAGACGAGAGAGGAGAG	59.81	20
CAACTGCACCACAAAGAACC	59.187	20	TTTAAAAACTTGGTTGGCGG	59.972	20
GTTTCCCACCCTTCACTCAA	59.943	20	CCTCACTTCACCCTCACCAT	59.962	20
TCTACCCCTCAGAATCCTCG	59.234	20	CGTCATAGATAACGGGGTCG	60.344	20
GTTTGGGTAAAATTGCTGGG	59.315	20	AATTTGATTGATGGTTTCGGA	59.264	21
GAAAGTTGCAGCCCAGTGAG	60.975	20	CGGTTCATGTACCAGCAGAA	59.716	20
AGTAATTGGCACCATACCCG	59.708	20	TTTTTGGATGCAGTGTGACC	59.547	20
CTGTCCGTCACGTTGAACC	60.146	19	GACTCCCTTGTGGAGAAACG	59.697	20
TTCAAATTGCGGATGGATTT	60.268	20	TTTGTATTCAAACTCAACACAG	59.53	26
GAAAATCAAAGGCCCACAAA	59.916	20	TACACAAAACCAACAGCCGA	60.149	20
TGCACTTGTTTTCCCAATATCA	60.356	22	TCTTGTGTATGCCTTGCTGG	59.864	20
CAATTTAAGTCGGCGAAGGA	60.202	20	TTTTTGACTTTTTATGGGGGT	57.539	21
AGGAAAAACCATCACAAAAATTG	59.298	23	AATAAGGGGGTGCATGTGAG	59.813	20
CAATTCGACGACCAAATCCT	59.933	20	ACCGATGTCCAGAGGAACAA	60.51	20
GCACAGAGCAACCAATCTGA	59.992	20	CTTTGTGTCGCAAGGTGAGA	60.025	20
AAATGCCGAACTTCCAAGAA	59.685	20	TTTTCTTCACCCAAATTTAATC	59.404	23
TCAGATCGCTATCGTGTTCG	59.972	20	ACGAAGAAGGTGTTGGTGGA	60.545	20
ATGCAGCCTCCAGCTTCTAC	59.603	20	TTGACAATATTTAGTGTTTTGA	58.99	27
AGAATAAATATGAACGAAAGCAC	59.536	26	ACGCGTTAACTAACCGGGAT	60.741	20
GACCCTGAACTCCCAAAACA	59.943	20	GCAGGAAGAGAGGAGAGGGT	59.952	20
GTATCCCAGGCCGAATTTTT	60.15	20	ATGTTTCGAGTTTGGTTGGC	59.978	20
CTTTCTGTTTGAGAGGAAAAACA	57.731	23	TTGGATTCCGGGTTCAATAC	59.622	20
CTGTTGCTGGGAGAGGACAT	60.261	20	CTTTTCTGGATGCAATGGCT	60.214	20
GGCATTGTCAGACGACGTAA	59.722	20	CGGTATAGCCCGAACAAAGA	60.089	20
ATATATTGTGCAGGCAGGGC	59.951	20	AAATGTCTTCATCCCCACCC	60.95	20
TGCAGTGCACTTGGACTTGT	60.51	20	AAACCCCCTCTTAAGTCCTGA	59.088	21
ACCTGGCAAGATTCATCGAC	60.081	20	CCACAAACACAAACGCAAAG	60.187	20
ATGATGGGAAGGGTGGGTAT	60.272	20	GTGGACGCTCCAGATTGTTT	60.119	20
ATTTTCATCGGAAATGCTGC	60.045	20	GAAGACGATACCGCTGGAAG	59.836	20
CGCAGCATCCTATTCACGTA	59.856	20	TGCTCACTCATCCTCCAGTG	59.98	20
TCCATGAAGGAGGAACAAGG	60.042	20	TTATCCAGTTTGGATTTTGTTCT	58.266	25
AATGACTCAATCTGCAAGCG	59.028	20	GTGTACCCTGAGGGACGGTA	59.844	20
ATTTGGTCAAATCGTGGTCC	59.653	20	AGTGGCATGATAATAGCGGC	60.088	20
ACCAGAACCAACAAGCAAGC	60.299	20	CCGTGGCTCTTTGATCCTTA	60.206	20
TTCATTACCCCCACCCACTA	60.044	20	GGAAAGGTACGAGGTGGTCA	59.966	20
GACGAAAGCAATGATGACGA	59.805	20	TCAGCTTCAACATCACCAGC	59.992	20
TCCGCCTTAATCCATCAAAC	59.901	20	GTCCAATAACGCCAGCAAGT	60.14	20
GATAGTCCATGCCCCATGAT	59.592	20	CAACGGTATTGTCATGTTATTG	59.311	23
TGATTCCTTTATGGCGTCTGA	60.591	21	CCAATTTGAATGGTTATCACCT	60.457	23
CTCTCGCCAACGTACCTCTC	60.012	20	CAGCTCATCGTGGATGCTAA	59.972	20
AAGCAGGACAGTAACAGCCG	60.453	20	ATCCCGACATGGTGGATAAA	60.014	20
TTCATAACATTTCTATCGGTATTT	59.71	26	ACAGGGGTTCGAATCAGCTA	59.694	20
GCACCTGAGGAGGTGTTATGA	60.126	21	TGCATCCAACGCTACAAATC	59.694	20
GGTAAAGACCACGACCCAGA	59.966	20	TTTTAACTAACTCCGGCCCA	59.581	20
CACGTTGTCCTGGAACATTG	60.001	20	TTGCCTGGTTATCCTCGAAC	60.074	20
ATGGACGAAGTGTGTGGTTG	59.441	20	TCCACAGTCATGATCGCATT	60.08	20
CCATGAGTCACGAGCTTACG	59.465	20	ACCAATGGTGGTATGGTGTG	58.984	20
TCCGGTCTATTCTCACCTCAA	59.679	21	CTCTTGGAGCGACTCCTCAC	60.135	20
TGCTACTTTGTCCCGGATCT	59.694	20	GCGTAGTGGTCAGTGGGACT	60.182	20
ATTCGAATCGCCATTTTCAG	60.038	20	GATCGAACGGGTTCACCTT	59.918	19
AACCCACAATACCACCCTGA	60.088	20	GGCACACATTATGGTTTGGA	59.251	20
GTTGCTTCGAAGGTGGATGT	60.119	20	CCACATCGGTGAAGGTAACA	59.415	20
GACGAAGAAAAGGATGTCCG	59.67	20	GGGATTCACACCTCACCATT	59.636	20
GAAAGCAGTGACGAAGGGTC	59.851	20	CCGTGCTTCCATCTTGTCAT	61.067	20

TCATCCTTAATTGGCTGCAA	59.257	20	GGACGCTAGAGAAAAGCGTG	60.154	20
TTGGTTGGTCACGAAAGATG	59.541	20	TTCCCTTTACTTCTTCCCCC	59.393	20
AAACCTGGAAAAGACAGCCA	59.711	20	AGAAAAGAGTTTCAGCGCCA	60.132	20
AGCTAGTGTGCTGGCTGCTT	60.364	20	AGCAGCTCGATGGAGGTAGA	60.119	20
GCATCATATATGCGGTTGGA	59.362	20	GGGATAGTATCGGATCGCAA	59.885	20
TCGTGTTAAAGCACGGTATCA	59.24	21	TACGGCGACTGAGACATACG	59.888	20
AATGGACGTCATGACCGAAT	60.203	20	TTGTGCCACATTTTTCCTGA	60.088	20
TACCAATGGACCACAAGCAA	59.964	20	CAACCCCACCTGTGCTAACT	60.028	20
CCCTTCAATCCCAAGGTTTT	60.159	20	TAGACGAGGCATTCTTTGGG	60.206	20
GCTGTTTTCCATTTGATCTGC	59.705	21	TCCGTCAACCAAACGTATTCT	59.485	21
GGAGAAAATAGCAGCGCAAG	60.117	20	CCTGCACCAAATTTTCCATT	59.801	20
CAAGGTGGCTTCACACACAA	60.757	20	CCAAGCCAACCAAAGCTTAC	59.747	20
ATTCAATGGCAATCTCCTGG	59.894	20	TGCTCATGAAATATCGTTGGTG	60.886	22
ATTGATGCCTGAAGAATGGG	59.894	20	TGGATTTACCTCTTGGTGTGC	59.985	21
TTGAATGGCAAGGATTGGTT	60.309	20	TTTTAAATGGACGTAAATGGAT	59.218	24
AAGGCAATATGCTGACGGAC	60.103	20	TTTAAAGTGTTGAGCGCGAA	59.625	20
TATCGCTATGAGTCCCCACC	59.917	20	CGTTAGTCGTTCCTGGGCTA	60.262	20
CCCCGACAATCATCACTCTT	59.927	20	TTCGGACCAGACTACGGTTC	60.111	20
CAACCCCTCTCCTTCTGTCA	60.229	20	TGGAAACAAGTGGATAGTTAG	57.815	23
ATGCTAATCCAAACGATCCC	58.86	20	CGCAATTATATTAACTTTGCGT	60.375	24
TGTATTTTTCCCGTGAAGCAC	59.989	21	CCACGTGGAATTATGGGAGTA	59.693	21
ATGCATTTTCCAAGGCAGAC	60.081	20	AGAGACTGTTGAAGCTCGGC	59.751	20
TCCAGGTCCAAATGAAAAGG	59.903	20	TGCCTCAATATCTGCTTCACTG	60.407	22
CGCACTCTGCAACACTGAAA	61.201	20	CTCCAAATTGAGGCGAAAAA	60.181	20
TTTCTCTCCGCACAATTCCT	59.813	20	TGCTGAAGAATCTGACACCG	59.984	20
CCCAATAGTTCAGCACCATCA	60.899	21	ATTCTACGCCGTTCTTCGTG	60.27	20
TGTTGTCAATCGAATTAAACCGT	60.619	23	GTTCCTGCTTTGTGGTGGAT	59.973	20
CATCTGATTCTGACGAGGCA	59.942	20	GTCCCAACTGAAGTTCCCAA	59.943	20
GGGGAGAGCAGGAAAATCAT	60.41	20	TCCACAATGGAAAAATGCAA	59.907	20
AAAGCTTCCGGTATCAGCCT	60.228	20	GTGGAGAAGGAAGGGACACA	60.088	20
CGTGATAAGCACCCTCCAAT	59.955	20	ATATAGTACCGACCGCCTGC	59.094	20
CATTGGAGGGAGAAAGGGAG	60.948	20	ACCCGAGACAAAAACCACAG	60.005	20
AGCATGGAGCCAAAAGAAAA	59.823	20	GTGAGGGAATGCTCTCCAAG	59.803	20
ATTGAATCTCCCACTTCCGA	59.483	20	TTCCTCCAGAGGCTCAGTGT	59.986	20
GGACTGCTCTCCTCATCTGG	59.945	20	ATACCTTTCTTTTTCCCGCC	59.442	20
CCGGCTATCTCACTCCAGAC	59.827	20	GACCAGAACCTAATCTTGGGA	59.101	22
AGATCCCGTATTCTCACCCC	60.154	20	AAAAATCAAAGGCCCACAAT	58.418	20
CAGTCACAAAAGGGGGAAAA	59.942	20	TCCTACAGCCCGTGGATAAC	59.955	20
CCTCCGGTTCAAAATCAAGA	60.044	20	ATGGCGACCATCAGAAACTT	59.556	20
ATTTCAGTCCCATCAGCCAG	60.073	20	TGAAACAAAAGGGAACGACA	59.145	20
AATGCGCTTTCTGCAAATCT	59.988	20	GAACATCATCGAGGTCGGTT	59.934	20
CAATTTGATAATTTGAAGCTCTAT	58.753	26	GAGACCAATTTTGCTATGTAAT	58.304	26
CGTAACGTCAGCTTCTTCCC	59.875	20	GAAATAAGGATGTGTTATGAA	58.049	24
CACATGTCACGAGCCAAATC	60.12	20	AAAGAAAGCTTCAAGCAGCG	59.904	20
TATGGTGGTATGGTGTGGGG	61.296	20	TCCAAGCCTGGAGACCTAAG	59.425	20
ATGAGGGGAATGCACCACTA	60.34	20	TGAGAATGGTGGGTGTGAAA	59.935	20
GCCTTTGACATCCAGGACAT	59.934	20	TACCAATCCATGTGCGAAAA	59.93	20
CCAAAATTGATGTTGCCCTT	59.801	20	CAGATTCTGGCACTGAGCAA	60.136	20
GCCGTTCTTCCCTTCTCTCT	59.957	20	CGGAATCATCAAACCCAACT	59.79	20
TTTACGCACATACCCCCATT	60.074	20	GAATCTTGGGTCCAAACCCT	60.169	20
AAAGGAAACAGGAGCAACCA	59.711	20	ACCAGGTCTCCTGGGTTAAA	58.498	20
CCCCGTCTTCCACAAAATAA	59.795	20	CGTCCATGCTCTGTTCTTCA	59.984	20
CCGAGTATGACGACGTTCAA	59.716	20	TTCAGCCTCCATTTACCTCA	58.298	20
AAGGAGGTGTTATGAAGGGATT	58.028	22	TCGAGATGCTCTGATGCAAT	59.507	20
ACATCATGTAGGAAAATGTTTAC	58.165	26	AGCTAGACACGTGGAGACGC	60.621	20
CCATTGACACGCATGCTTAC	60.142	20	AGGGGAACGAAAATCTCTCC	59.513	20
TCAAACTCATTGTTGTTTCACAAA	59.575	24	TGGGTGATCAGGAAAAATCAC	59.782	21
TCACCTAACCCCTCTCTTGG	59.133	20	ATGCGAGTGTTGCATCTGAA	60.423	20

CTCTTCGGTGATCAAGCGTT	60.397	20	TCCACGAAGAACCTGGTTTG	61.064	20
AGAGGATTTGGAGAAGCCGT	60.212	20	CCGCAAGTCAATAATGGAGG	60.46	20
GGAGGATCCGTGATGTTCTG	60.475	20	ATCGAAATCTAAACCCGCAC	59.046	20
TTGTAATGTGTACCGTCCGC	59.469	20	TGAAGTTAGGAAATAAGGAGG	58.743	25
GTGGGGGATGATGTGGATTA	60.404	20	ACACAAGTATGACCAGGGGC	59.851	20
AGGCCTAATTGCCGTCCTAT	59.951	20	AAGAAAGTATCAGGCGCATCT	58.111	21
CCGAGCTTCACATCCTCTTC	59.95	20	CCGAAGGCAACACCACTACT	60.171	20
AGAAACACAAAAATTAGCATACA	59.908	26	TGTTGAACGTGTACGTTGGG	60.463	20
CAACAAAAATCCTAGTCCATCCA	60.223	23	GCACGTGTGAATATTGGGC	59.947	19
AAAGGACCTTCCCACATTCC	60.169	20	CAAGCTTATTCCTGCCCAGA	60.344	20
GGGCCTACACTATCTCTGCG	59.859	20	CATGGTGTGGGCCATATATTC	59.915	21
AGATGTTGCCACCTCAGCTT	59.874	20	TTTAGTGGCTGGAACCGAAG	60.241	20
TCATGACTCACGAGATGGGA	60.205	20	GGCTCAAAAAGTTTCATATTTC	60.022	25
CCCAAGCATTAAAGCCCATA	59.922	20	CTGCAGTTTAAGCGACACCA	60.05	20
GGGGTGTTGAATTTTGGAGA	59.767	20	TTGGGTTAATCCGTGTAATCG	59.707	21
CCCGTTATGATTCGTTAAATCG	60.543	22	GTGAAGAAGCCGGAAGTGAA	60.375	20
AGCCCCAAATGATCCAGACT	60.853	20	TTGGAGAGTTGGGTACAAGC	57.797	20
TTGAGGGATGATGCATACGA	60.033	20	TGCATGCCGCATACTATTACT	58.368	21
GTGCGCAACATGTAAGAGGA	59.871	20	CCGATTTTTGGTATATTGGGC	60.385	21
GGGCTAAAATGGTGTTGGAA	59.801	20	ATGATGTATGTGCGATGGGA	59.763	20
TTTCCTGGAGGATCTGCATT	59.629	20	CCCCCAATTTGTTTTACTCG	59.311	20
CTCGACTTCATCCGTTTGGT	60.111	20	CCTAATAAAATGGCCATGCG	60.295	20
TTCAAGCTAACCAGCCAACC	60.249	20	CTTCTGGTTCCAGCAGCATT	60.397	20
CTGGTGCCATGATTTTCATC	58.926	20	CGGAGACAAAGGGTCATTTC	59.526	20
CCGTGGAAGACAAGGGATAA	59.926	20	CGCTGACAAACATCATCACC	60.12	20
AAACGCAAACACATACGCAA	60.177	20	CTCGATCAAGACCCTATCGC	59.797	20
ACGATGTCGTGTAGGGAAGG	59.989	20	AAGCTAGGGCAATACGTCCA	59.73	20
CGAACATTGTCACCGTCAAC	60.008	20	GAAACGAATCTGTCGGTGGT	59.973	20
TTGGCTCTGGTTTGTTACCC	59.971	20	CACGACAAGAAAGCCATGTG	60.301	20
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AAGAGCAAAACCCAAAGCAA	59.861	20	CACTCGAACCAGTCAAACGA	59.873	20
GAAATTGTGTTGCAGGCTCA	59.847	20	GACCACAACCAACCACATGA	60.27	20
CGCAATGCAATAAATGCAAC	60.103	20	CTCACGCGAGGTCTTTCTTC	60.134	20
AGCAAAAGAAACAAACGGGA	59.724	20	AAATAGATCTTTTGTAAAGCCC	58.02	23
GCAAAATTGGTCTCTATGTGTAGA	58.813	25	TGTCTCCATTCTATTGGCCC	59.894	20
AAAGGAGGTGGATCGGTTCT	59.935	20	GGATGAGGAAGAAAGGGAGG	60.008	20
AAATCAATCTCAGCCGCTTG	60.352	20	CGGTTGACAGCCGATTTTAT	59.96	20
CCGGTTATCCAATCCATTTC	59.091	20	GAGAGGGAGGGAGAGAGGAG	59.489	20
GGCCAGATTTCGTCCCTAGT	60.464	20	GCATCGTCTCAACCCTTGAT	60.081	20
CGTGGGTGTAGTGATGGATG	59.831	20	TCCCTCCAAATCGTTGCTAT	59.528	20
TGGCATCGTGAGGAGTGTT	60.263	19	TGATAGGGCACACAACCCTT	60.375	20
AGCCATGGAGTGGATTCAAG	60.073	20	TGAGATATTTAAATCCTTCCGTT	57.452	24
ACCCCCACTTCCTCTGTTTC	60.349	20	GTCCTTTCGACATTCTCCGA	60.195	20
TGCATGAGAAATGAGCGGTA	60.366	20	GAAAATCGACTCCCATTCCC	60.641	20
ATGAGTTATCACCGGATCGC	59.923	20	TCAAGTAAAATTTCCCGTTCG	59.107	21
CGAGAATTAGCTGCCACTCC	59.978	20	CGTGCCTTCTTCTAACTGGC	60.015	20
CCGGCTCCGATCTATACAAA	60.053	20	TTCCCTCAGCTCATCCATTC	60.158	20
AAAACCTCCAATCCCTCCAC	60.169	20	CTCATGTTGCTTGGATGCAC	60.272	20
GCATTGGCGTTTGAAGAAAT	60.081	20	TCATGTTCATCCAAGTTGCC	59.502	20
ATCCGCCAAACCTTCTTCTT	60.074	20	AGAATTTGCATTGGGTTTCG	59.938	20
GAACCACCGAGTACCAAGTGA	60.02	21	CGATTTGAAAAGCTTGCTCC	59.96	20
AACGGTGGGAGAAATGAATG	59.79	20	GTCTCCATGCTTGAGCCAAT	60.226	20
GGTTATCACCGGATCGCTAC	59.415	20	ATAATTAAGTCATAGAGCAGG	59.136	24
CAACTCAGCAAGTCCTGCAA	60.175	20	CCTCTCTGACCTCACGTCTTG	60.034	21
TTCATGTGGGTCAGCTATGC	59.679	20	AGGTGGAACAAGTAACGCAA	58.283	20
AACGCTCCAGTTCATAGCGT	59.904	20	TGAACCGGGTCTCTCGTAAC	60.111	20
ATCGTTGAAGATATTCCGCA	58.187	20	CAGCCCTCAGATTTTAGCGA	60.481	20
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AATTACATTGGGCCATCCTG	59.645	20	ATGTTTCATTTTGCCTGGCT	59.574	20
CAGCAAACATTGCGAAAAGA	59.992	20	GGTTTCTTCCCCAACGCTAC	60.856	20
TCCAAATGCAACTGGTGAAA	60.088	20	AGGCACATCGTGTGAATCAA	60.12	20
CGTCGCAAGCACATAACAAT	59.759	20	CGGACGTTAAACGAAGGAAA	60.103	20
TTCTCGGGATTTAACGTCCA	60.439	20	TGTTGTAGTATGGCAAGATCC	58.174	22
TAAGCTTAAAAGGCCGGTCA	59.847	20	CCCAAGGCGAGCTCTAAGTT	60.884	20
CCCAGATAATTTTATATGTGGTGA	58.345	25	CAGTGTAAAACCTTATTGGGG	59.641	22
GTGATTGGTGGTTTTGTGGA	59.241	20	TCAATGCTCTTTTCAACCCTT	58.823	21
GGCTTCTTCTCTACCCAATCG	60.214	21	CGTGCGATCCAATTAAAACA	59.562	20
TCTCCAAAAACAGTCCCTCTC	58.363	21	ACTTCCCAGTCGTGGATGAG	60.112	20
GAACTTCACCGCTTGGACAT	60.119	20	CACTCCTGAAGAATTTCGGC	59.813	20
AGGCGTCAAAGAGGAAGACA	59.989	20	ACACCCCTAATCCGAACACA	60.232	20
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GGTTACTTCGAACCCTGCAA	60.11	20	AGTTCAATAGAGGCAGCGGA	59.978	20
CATGCAGGTTTTGTCCAATG	59.964	20	CGAAGATGAAAAAGGGCATC	59.645	20
GCCGCAATATACATGGCTTT	59.956	20	TCTAACGGCCGAGATTTGTT	59.708	20
GGTTCTTTTTGCATTAGCCTTT	58.863	22	CGATTTCTACACCATTGTTCCA	59.861	22
CTAGCAAATTTCGGGATGAAA	59.199	21	GTTCGGGTGTGCAAAAATTC	60.352	20
GGAGTTTTGACCTAATTAAGACC	58.571	24	GATGAGCATCAGAGGAAGGC	59.917	20
TCTCATGTGACTGAGGGCAA	60.402	20	CTCTTCCCTGCAGATGATGG	60.758	20
TTTATGCCCCCTCAATTTCTT	59.795	21	ATGACTTCCAGTGCCAGGAC	60.12	20
TGTTGCCTTGCAAATTATTTCT	58.808	22	GCTCCAAAATGATTACGTGG	58.093	20
CTTCTCCTTGCTTTCCGTTG	59.986	20	CCCGACAATTTCACCCATAC	60.051	20
TTTCGTGTTTCTTTTGATTTTTCA	60.019	24	AGGTAGAATGGTTGCGTTGC	60.14	20
ACTCAATGGACACATGCCAA	59.967	20	TGCTCCTGGAGTACATGACAA	59.621	22
CGCAACCTCTAGAAACCCAC	59.734	20	TGATTTGACACGAATATGACA	58.956	23
CGTCTTAGATCCCTCCCACA	60.065	20	TGCATCACCTTGCTTCTCAG	60.136	20
GGCCTGGGCCTACATAAGTT	60.34	20	ATCTCAACCCTTGATTGCGT	59.556	20
CACCAACATCACACTCGACC	60.005	20	AATGCTTCGGACTTGCTCAT	59.843	20
GCTTTTGGAGCTGTAGTCGG	60.015	20	AAATCCTCAATGCAAAAGCAA	59.712	21
TGGTTATTAGGGGATGGTGA	57.736	20	GGCTAGCATGGACAACCCTA	60.096	20
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ATTCCAAAAATCAAAGGCCC	60.13	20	AATTGTTGTGATGTGAAGAATT	58.947	26
GGAATTCAATTGTTTATTTGTTGC	58.881	24	CAAAGGCCCACAATGGTTAT	59.685	20
TTGTGTCGTGTTCGTGTCAA	59.751	20	CACAACCAAACCAACCATCA	60.255	20
CCTCACTGGAGGAAGGATCA	60.191	20	CGGATTTGGGTTTCTTCAAA	59.91	20
GGCAACCCACTTGTGAAACT	60.012	20	TGAAACGGAGGTTTGGTGTT	60.388	20
TGATATTCTCACCATCCTACTCAT	60.153	26	AAAACCGATGCAATTATGCC	59.801	20
TTTCCCTACTGGGACCCTAA	58.502	20	CCGTTTGCAACAATTGAGAA	59.706	20
CCAAAATTGGCGGATAACTG	60.315	20	CGAAAAGGTCAAAATCTTGGA	60.102	22
GAGCGCACTCGAAAAGTAGC	60.3	20	ATCGTTTATCCGATTGCTGG	59.923	20
AATCCAACGGTAAAACAGCG	59.996	20	GCACCGGATTGTTTGCTAGT	60.14	20
ATTTGAATCCCAGGCCTCTT	59.903	20	ACAGGGGAGAGAGACAAGCA	59.986	20
CCGTGTGCGTGTTGAATATC	59.995	20	CGCTGGTTTTGGAGATCAAT	60.074	20
ATCATAGCCATCCATTCCGA	60.26	20	TATAAACGCTCGTCTGCTGC	59.234	20
TGAGGGGGAGCTGAAATAGA	59.767	20	CAAGGGTAAGGGAGGTGACA	59.959	20
CAGCTGGTATCTGCGGTTCT	60.419	20	ACCGATCTCACCCCTTTTCT	59.935	20
CGTCAATCACCAAACGTCAC	60.008	20	TGAAAAGGCTTCAATTTGGG	60.046	20
CAGAAAGAGCCCATAGCCAC	59.836	20	ATCACGGATTTGGAGGACAA	60.317	20
TCAGCATGTTGCCATTAGGA	60.22	20	TCATTGGGCAGTTTTGTTGA	60.088	20
AAGGAGGTGTTATGAAGGGATT	58.028	22	GCTTTGGGTTCAAATGGTTG	60.344	20
ATCTCTTCTTCTGCCCCACC	60.596	20	CACTTCAACACTCCCCACAA	59.565	20
TGTTCCTCACGCACTCTCAC	60.03	20	ATCGGTTATTACCGGATCGC	61.031	20
GGGGTTCTTCTCCTTTCCAT	59.373	20	CCAATTTGAATGGTTATCACCT	60.457	23
GAGGTGGCTTCTTTAGGGCT	59.848	20	TCGTGTCGAGTTAGCGTGTC	60.056	20
CAGCATGTTCCATGTTCAAGA	59.707	21	GTGGAGGGGGAGTATGGATT	60.015	20
CAAAGTTAACCACCCCCAAA	59.696	20	TATGGTGGAACAAACTCGGC	60.894	20
TTGGCCTCACGATAGCTCTAC	59.49	21	GGTGCAGTCAAAGGAGGAAG	59.844	20

TGTTTGACGATGAAATCCGA	60.049	20	TGAGAGCGAGAAAGGGTTGT	59.989	20
GACGGCTAGATTCGATCCTG	59.797	20	GAAATGTTCACACACGTCGG	60.008	20
ACACCTTTTTCTTCCCCAGG	60.332	20	ATTGGCAATTAACCGTCAGC	59.967	20
ACACAACGAATTCCTACGGG	59.853	20	GAATTTTGCCACCGATGTTT	59.807	20
TTCAAACCTTTGCCACTTCC	60.088	20	TTCTCCTTGGGCAACTCACT	59.844	20
AATAAATTACGGGATGCCCC	59.88	20	TCCGGCAAAAACCAAATTAC	59.81	20
ACCAACTCGTCAGACAGCAA	59.467	20	GTGGAGGGTTTTTGTCTCCA	59.943	20
AGAAGCAGTTGGGATGATGG	60.073	20	TGAAGGGAATGGAAAGTTGG	59.903	20
ATGCCCATCTCATTTCAAGG	59.894	20	GCTGCTCTTTTCTGGGTTTG	59.993	20
AAGGGATGGTATCATTTGATCG	60.041	22	GCTTCAACGGTATCCAGTAACA	59.947	23
TCTTATTGGGTTGTCCGAGG	59.926	20	GATGCCAACGTCATATTTGCT	59.981	21
AAAGAGAGAGTGCATGCGTGT	60.073	21	TGGCACGAAATTAGTTGTTTG	58.736	21
TGTGAGTGTGTGTCTCGTGTG	59.352	21	TCCCCCTCTCTCTCCTTCTC	59.883	20
TTTGAAGGAAAACTCGTCCC	59.146	20	TGCAGCTCTTGCTCTTGTTC	59.47	20
GTGCCTGCTCCACTTTCTTC	59.997	20	GCACACTCGAAAGGCAATCT	60.406	20
TGTGCAAGTTTCGTAGGCAG	60.05	20	GGCCGTTTTAAAATCGAGTG	59.586	20
TGCAAGTTCCGAGTTCAAGTT	59.906	21	AATGCATGCACCTGATTACAA	59.055	21
TCTCAGCTCGATAAGTGGCA	59.697	20	GAGCTGTTATGCGTTTTGATG	58.452	21
CATATCCTTTGAACCGGCAC	60.331	20	AGGTTTAACTTTTCAAATGGAA	59.667	27
GATCGATCTGGGCTCTCTTG	59.91	20	GGGCCTTGAAGTTCTCTGTG	59.844	20
GGTGGAGAGTGAGGAAGCAG	59.986	20	ATCACCTCATCACCGCCTAC	59.957	20
TTGGAAGAGGAAAGTGGGTG	60.081	20	AATGAAACACCCCCAAACAA	60.066	20
CCACGATGATTTCGATACACA	59.41	21	GATCCGGAAGGTCCAAAACT	60.306	20
CTATGCAGCCTCCAGCTTCT	59.74	20	TCCAACACAAAACTCTAAATTT	59.821	25
AGGTCCATAAGTGTTTTGAGTTAT	59.42	26	CGTCGAGAGATGCAACGTAA	60.011	20
TGGTCTTGGTCACGATTCTCT	59.712	21	CCTCACGTGATATTTTTAGCAC	59.197	23
CGGAGAGATTTGTGGGGTTA	59.926	20	ACGTTGCAAGAAAAGGTTGC	60.292	20
CCAAGCATGTGCAATTGTGT	60.584	20	TGCAATGTACAGCAGAAGTGG	59.92	21
CTGGACGCATTAGTGGGTTT	59.993	20	GTCGACTTCTCCCCCTCTTC	60.194	20
TATAAGGATCAACCGCCTGC	60.06	20	TCACCAATTTGAATGGTTATCA	57.873	22
GGGGCTTCAGATGAAATCAA	60.014	20	TCCCCTTCTCTTTCCCGTAT	59.897	20
TGGCTAGAGCATCAGACCAA	59.547	20	TAAAGGTCGAAAATGGCGAG	60.202	20
TGGTGCAGATGTCCTGGTTA	60.112	20	TTCCCCTTTTAAGGTTGATGG	60.163	21
TTACATCTCTACGCAGGGGC	60.235	20	ATTAGGAAAAGGGGCAGACG	60.443	20
GTGATCGCTGGTTCTTTCGT	60.263	20	GCAGCAGCACCCTTTCTAAC	60.022	20
AGGTTGCGTCAGATTGGAAG	60.255	20	TCATGCAACCATGAAAACAAA	59.961	21
ATAACGATGATCCCGAGGC	59.869	19	TGCCGGAAAACACCAAAATA	61.214	20
AATGATGTTAATCCAGCGGC	59.929	20	GTGTCAGAATCTGGGCTTCC	59.661	20
CATCTTCACCCATCTCAGCA	59.787	20	CCGGTTCTCCTATCCGATTT	60.278	20
CATGCGTAAAGGCACAGTTG	60.316	20	CATCGCGTCCACAAATACAC	59.995	20
GTAGGTTCGCCACTGCTCTC	60.02	20	TGAAAGGAGCTCTTCATGACC	59.42	21
CAAGTATTCTCTCCCCAGCC	58.741	20	CGACTGCATCAGCAAACTGT	60.056	20
TCATATCATTGTTTCCGCGA	60.035	20	GATCTTGTGGAATGAAGGGG	59.336	20
CCACCTCAAAAACAAATGGTG	60.248	21	GCTGCTTTCTCGCTCATTTC	60.243	20
ACAAATCACGCGAGGAAATC	60.081	20	TCGCCCATTTTCTCAACTTC	60.192	20
AAAATGTGTTTGGGGTGGAA	60.066	20	ATCGGTTATCACCGGATCG	60.697	19
CGACTTGTACTGCGACGAAA	60.05	20	GGGATTCAGGAAACAGGACA	59.903	20
GGTGGTGTTTGCCTGTCTCT	60.159	20	TCTCGCTAAGCAGCCTTTTC	59.867	20
CCCAACTGGAAAAGTCCAAA	59.942	20	TGCCACGACCAAAACCTATT	60.365	20
CGCAGATCCCAGATTTGTTC	60.603	20	ATTGCATCCTCCACGTTACC	59.82	20
TGTTGCTTGAAGGTGATCAAT	58.215	21	GAACCATCCGACCTTGAAGA	60.05	20
ATATCAGGCCAAAAACGTGC	59.967	20	TGCTGATCTTATAACGCGAA	57.172	20
CAATGAGGTGTCTGCCCTCT	60.261	20	TGGCACTTAGCATTGAATGAA	59.315	21
CCCGAACTCCGAGTACAAAA	60.103	20	ACGGATTTAAGGGTTATTACCT	57.667	23
TGCTGATCTATTTACATGCTTTTCA	60.158	25	GTGGCTTCTGTCTGGAGGAA	60.386	20
AAAAGGAGGAGCGAGAAAGC	60.096	20	TTTTCACCCGACAAATCACA	59.941	20
GAAGATTGAAGCTCGGATGG	59.773	20	AACCTCATTGATTTGCAGGC	60.081	20
TAGCTGATCTCACGTGGTGG	59.855	20	CTGCATCTTGTGTCCTGGAA	59.831	20

TTTGAGCAAATTGATATTTTAATG	58.728	25	TGAGATTTGGGCAAGCTTTT	59.823	20
AATTGTTGTCCATACATTTTGGAA	59.793	25	TGAAATCCAAATAGGTTAGAA	59.664	25
ACCCAACTGGGTAAACCCTT	59.593	20	TTCGTTTGGCACGTTTTGTA	60.147	20
TGGGGATGGATTGATGAAGA	61.221	20	CGCTGGTTTTGGAGATCAAT	60.074	20
AAAATCCTTTCCACAACCCC	60.032	20	AGGGAAGGCAAGGAAACAAC	60.476	20
AGATGTGGGTGGTTTGCTTC	59.973	20	AATTCTTGCACGCCATTTTC	60.081	20
AGGGGTCCAAAAGCAGAAGT	60.11	20	ACCCTAGCTCGGAGAAGGAA	60.34	20
ATGAGTTATCACCGGATCGC	59.923	20	TGATTCATTTTCTGCACGGA	60.197	20
TTTTCTGCACAGATTTGATGG	58.759	21	AATCGTGCTATTTTTGCCTGA	59.734	21
AACCGGGCAAGAAGAAAACT	60.11	20	CTCCTTGGCTGACTAGGTGC	60.012	20
CGTTCTTCATGAGCCTGTAGC	60.03	21	AAAAATATGGCATCCCGGTT	60.389	20
GCTTCGATGTTGATGCTTGA	59.955	20	GACGAACCCCTGAATCATGT	59.786	20
TCGATCTGCAACTATAAGCCG	60.37	21	TGTAGCAGCGAAATGCAGTC	60.165	20
ACCCAAAAATGGGTTATTATTTGA	59.753	24	TCTTCCGGATTTTAGGAGGC	60.522	20
CAAGGCAGTGTCCACTTGAA	59.873	20	AGTGAACCCAGTGGGAGATG	59.962	20
ATTGATGCCCTGGTTACAGC	59.962	20	CGTCTCGTTTTTCTTCCTCG	59.986	20
TGCCAGAACTTACCGACCTAA	59.755	21	GGCTGCGTTTTCAGTTTTTC	59.867	20
TCCAAATTTTGATCAATTTCCAA	60.501	23	TTCGGTTAATCCAATGGTCA	58.818	20
CCCTCTGTGTGTGATTTCCG	61.513	20	GACAAAGTTGTAATTTGCGGC	59.644	21
GTGTGTTTGTTTGACGGTGG	59.897	20	GCAAGAAACACAAGCCCATT	60.118	20
ATCTTGCATCGGCAAGAGAC	60.37	20	TTTTTATCGCACAAATATTTTG	58.231	25
AAATCGATATTGAATTAAAGGCT	57.153	24	TTGGAATGAATAAATGGAATG	58.357	23
TTCACAAAGGGCTTTTCAGAC	59.345	21	ATATTTCAACCCCGCAACAG	59.823	20
TTGGGTGGAATAGACTTGGG	59.784	20	AATGCCGACTTTGTGGATGT	60.384	20
CAACATCATCATCAACATACCCA	60.496	23	TTTGATAAAAATTTGGCGGC	59.913	20
AGCACTGCAACGCAACATAC	59.942	20	CCAGCTTCCCACATCATTTT	59.933	20
GCCTGCGAAAATCACAAGAT	60.221	20	GAGCGCAGATATGAAGGAGG	59.939	20
TAAGGGCGGTATCACCTGAA	60.46	20	TGCATGCCTATGCTACACAA	58.885	20
GGGTAGGATTTTGGAAGCGT	60.32	20	CCATCTGTTCACACTCACGG	60.154	20
TCAAAACCGGTGATTAACTGC	59.989	21	CTTCTCAGCAATCATCGCAA	60.096	20
GGGGTTCTGATCATTGAGGA	59.862	20	TCCAAGTTTTGAAGATGACCT	58.293	22
TGTTTTCGTTCTGAGAGGGG	60.224	20	AAACAAAATCAACCCACCCA	60.066	20
GGTTCCCAGTTGGCATGTAA	60.755	20	AGTGCGCTCTGGGTAAACTC	59.501	20
GCCAGAATTCGAGTAGGCAG	59.978	20	TATGGTGGTATGGTGAGGGG	60.452	20
AGTCCATTTCCACCCCTTCT	59.795	20	ACGTGGATGTTATGCACGAA	59.995	20
GTTTCACAGGAGGCGGTTTA	60.11	20	TGCAATCCTTCCAATCCAGT	60.461	20
CAGATTCAAAGACGGCGTTC	60.776	20	TGTTGTGCATGACTGGATGA	59.658	20
TGAAACCTGGCATTCACAAG	59.691	20	AACCAGAGACGCAGCATTTT	59.882	20
CCAGCCGTATTCTTTTCCAA	60.067	20	GAAGGAATGTCCACCGAGAA	60.05	20
CGCGCACACAGTAGAGAGAC	59.801	20	CCAACGGTCCCGTATTATTG	60.067	20
CGCGAGATTCGATGGTAGAG	60.894	20	GGATCAACGGTCAGCATTTT	59.939	20
GATCACTTCGTTCCCCCTG	60.459	19	TGGTACCTCCTCCTAATTTCCT	59.854	23
TGCAGGCCGAGAAGTTTTAC	60.386	20	GCCGGTAATTTCGTGTAGGA	59.96	20
CCCACACACAATGCAAGAAT	59.42	20	GAATCCTCACCTCCCCAAAT	60.133	20
ACCCCTTTTACCCTTTCCCT	60.048	20	GCTTCTGCTTACTGCCCTTG	60.154	20
GTCAGCACGCAATTTCTCAG	59.596	20	GAGACGCTGATGGGATTGTT	60.081	20
TTTCAGACATTTCGATCCCA	59.049	20	TCCCGATTAAAGTTTCCATGA	59.397	21
AAGTTCCACTTGTTCACGGC	60.156	20	CGAGTGGAGTGAGAGGAGAC	60.592	21
CAAGCCCAAATCAAGGAAAA	60.046	20	AGGATCCCCTAGCTTCTTCG	59.805	20
TCTCCTCTTTCTCCCTCTCCT	58.627	21	GTAGAGAGAAGTGGGCGGTG	59.867	20
TAACAATGCAGTGGCTGACC	59.722	20	TGATGATGGAGCATTTGGTG	60.481	20
CCCGAAAAATTACTCCCACA	59.795	20	CTCAAGCTTTGATCTTCGCC	60.096	20
TCAATTCCCAAACCATATCCA	60.002	21	CGCCTGTATAAATGCCTCG	59.291	19
TCAGCTTGTTAGTGTTCAGTTTGA	59.13	24	TACAACAGGCCAAAATGGCT	60.502	20
TTAACCTTCTTGCCCTGCAT	59.708	20	CCAGATCAAAGATCCAACGC	60.603	20
AGTTAATCCGACGGCTGAGA	59.836	20	TCCATGTCTTTTTCCCTTCA	58.117	20
GGTGGTGAATCATCAGCTTT	57.577	20	TGAAGTTAGGAAATAAGGAGG	58.743	25
TCAAAACATTTATTTATGCACACA	59.969	27	AAGAGCGAGCAAGAACTCCT	58.43	20

CCAATGATGGGTAACGGAAT	59.505	20	AGCCCTCGTGAACATAGGAA	59.694	20
GTTTATGTTGCGAAATCGGC	60.465	20	GTTTGGTTCGGTTTTACGGA	59.839	20
AGGGATTTTGGATGGAGAGC	60.41	20	GGTTAATCGGTTCGGACTCA	59.933	20
ACATGCAATGAAAATGCCAA	59.937	20	CTCAAACAGAGTGGGGAGGA	60.229	20
ATTCTATGGTGCCCCCTCTC	60.293	20	TGTGAAGCACTGGTTTTGGA	60.278	20
CACGAAAATTTTGCATATCGG	60.321	21	ACGGCTCCCATTGTTTCTC	60.065	19
GAATGATGCATGCTCTCACC	59.201	20	CCATCATCACAAGATGCCAC	59.925	20
GCCATGGTTTCGATTTTGTT	59.807	20	TAAAGGGGGACCATTTTTCC	59.992	20
AGGATCTTCTCATTCCATCGAG	59.674	22	TGGTGAGGATTTAACGGGAA	60.301	20
GCAGCACCATACCAGAAACA	59.722	20	TCGTGTGATGCCTTGGAATA	60.073	20
GTTCCTTGGAGCACCGACTA	60.255	20	ACTTGCTTAGTTCATGGCCG	60.27	20
TGAATGAGGGTTTTTGTGGG	60.724	20	AAGTGTTGTCGTTTCTTTGGA	57.376	21
CTTTCCCTGCGTTGCATAAT	60.096	20	CTGCCTTGCCTTTTAAGCAC	60.018	20
CCCTGACCACCATCAATTTT	59.647	20	CGCAACTGTTATTCGGGACT	60.132	20
TGAGTGGATATATTGGGAAGGG	60.034	22	TTAAGGGGGTTATTAGTGGATC	58.807	23
GACCACCCCTGAAACTTGAA	59.943	20	CCCACCCATGCCATTATTAG	60.031	20
TGGAAGTTTTTGAATTGGGG	59.772	20	TTGTTGAAACGAATCCGACA	60.088	20
AAGCGATGCTCCAACTTGAT	59.843	20	TTTTGCACCCTATTGGCTCT	59.708	20
GCAGATGGTGGCTTCAAATC	60.613	20	TCGAGGATCAATCTCGGAGT	59.761	20
GAACTGGGGTCAGCATTGAT	59.934	20	TAAGTTTCTATTCGCCCCCG	61.27	20
TCTCTCCCTTCTTCTGCTTCA	59.294	21	TTGATGCTGAGGCATTTGTC	59.805	20
AAGAAAGAAAAGTGTTGGGGG	59.486	21	AAATATTGAGGTGGGGGTCC	59.881	20
CAAGATGGCATCATCCATTG	59.883	20	TGATAACAGGGAATGGGGAG	59.744	20
AGCATTTGGCCTTGTCTGTC	60.263	20	TATTGCCCCTATCTATGCGG	59.907	20
TTGTTCTTGTCCGTCGGATT	60.495	20	TTAGCATAAATTTAGCCACCG	57.12	21
CCAATTTGAATGGTTATCACCTG	60.457	23	TGGACTAGGGGCTGAAGAAA	59.807	20
TTTGTGGGAATTCTATCGGG	59.756	20	CACCTCCCTGGGGATTTTAT	60.011	20
GTGGCAGCCATATATCCGTT	59.813	20	TCGCCCATGACTACACCATA	59.948	20
GCAGTTTCCTCACCTCCAAA	60.232	20	TAATGTAATTGGCCCCGAAA	60.144	20
CGCTCTTGATGCAAGTTGTC	59.596	20	TGGTTGTAATTGCACCAAATTT	60.045	24
ATGGAATTGGGATTGATGGA	59.952	20	AGCGTGAGCTCATTTTCGAT	59.985	20
GCACAACCACTCCACAAAGA	59.726	20	TTTCGTGTGTGTTCCTCTCG	59.873	20
TTTTGATAATGGTTTTGTACACATT	58.037	26	ATGAGTTATCACCGGATCGC	59.923	20
GATCTAAGGGCCGAGATTTG	58.74	20	CAACGACCTTCATTCGATCA	59.648	20
CTGTCGGTGCATTTGATGAT	59.527	20	TTCAATTGGCAACAAACCAA	59.946	20
TCCACCATTGATTTATGCGA	59.891	20	TGGTGAAAACCCCCAATAGA	60.162	20
TGCTTTATGCCTTGCCTCTT	59.982	20	GATCGTACGTATCGCCGTCT	60.125	20
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GGCAGTCGTTTTGAGACGTT	60.299	20	CATCCTGCCAAACCAAGAAT	59.933	20
GATCGCGGGAATCAACTTTA	60.038	20	GTGCACTTGAAATTGCATCG	60.265	20
TCACCTGCATCTGGGTAACA	60.112	20	TCAGAAACAATCTTTGTCTGTT	58.992	25
TTCCTGAGTTGGTGAAAACG	58.746	20	CACCAAGTGGGAAATAGTGC	58.076	20
GGTTTGGGGAAGAAAAGGAG	59.912	20	ACCCTCTCTCCACTCACCCT	60.112	20
TTGCTATTGAGAGGAAGCGA	58.747	20	TGGCATATTTGTGTTGGCTTT	60.37	21
CTTTGGCAAATCAGGCGTAT	60.096	20	AGGTAGAAGAATAGGTGCATG	58.501	24
GTGCTGCTGCTGCTGTAAAC	59.818	20	GGACCGTGATGGACTGACTC	60.537	20
AATGTTATCGATGGCGTATGG	59.696	21	CGTATCATACAAGTATGCTGTC	59.985	25
CCAGACAAAATCCCCTCTCA	60.042	20	AATCAATGAGAAACCCACGC	59.939	20
ACATGATCTTGGATGGGCAC	60.758	20	GTTGAATTTTCACCCCGGTA	59.662	20
TTTCTGCATGATTTGGATGA	57.609	20	AAGGAGGTGTTATGAAGGGAT	58.028	22
AAAATGAGCAGAGGCCGTTA	59.845	20	TTGCAACACAAAGCACGAAT	60.302	20
TTGAGCTGGTTGATTCATTTTG	60.11	22	TTAGTCCATTCTTTCGGCGT	59.708	20
GTGGGCGCAAGTAAAGAGAG	60.015	20	GGCTTATGCATTGACCGTCT	60.103	20
TTGAACTTGTTTCAAATCCATGA	59.483	23	GCATCTTTAATGGTGGCCTG	60.469	20
TTTGCTCTCTCACACATGCC	59.992	20	AGATCGGCACAAAAATCGTC	60.081	20
ACAGTGCGTGTGTGTGTCAA	59.818	20	TTTGGGGACAACACTGACAA	59.976	20
ATCACCCCCTCTCCAAGAAT	59.755	20	AATCCCATCCCTCCATTGAT	60.354	20
TTTCGAACTTCCATCCTGCT	59.813	20	ATGTAATGCCTCGCCCTATG	59.945	20

ACCGCCGTCTGTAATAATGC	59.988	20	CCCAATACCTCCCCTCTCTC	59.89	20
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TGCTGTGGAATACCTGGGTT	60.375	20	AACAGTTCGGTTCACGATTTG	60.023	21
GGAGAGGAGGAGGAGAATGC	60.3	20	CACCTCCATCTCCGATCATAA	59.902	21
GCTGAGATATACGCGGTGGT	60.125	20	GTGAGGAATCCACTCTCCCA	60.048	20
TGATTCTATTCTGTGCTTCGGA	59.845	22	TTTCAGGCTTCAAAAATCCA	58.334	20
CCGATGGAAAATGGAAATTG	60.124	20	TTGTATCAACGGTCCGGATT	60.192	20
TATGCTGCCAAGTGCTCAAA	60.545	20	TTGATCGCGACATTTGATTT	59.115	20
TGGGCCAAACCCTATATCAA	60.146	20	TGAGGCATCTCTCTCTCACATT	59.043	22
GGATTGTGGACTGCCTGATT	59.934	20	TGAGGCAGTGTTGTTCTTCG	60.025	20
CCAGTGTTGAAGCAGTCCAA	59.873	20	CTGCCAAGGAACCACAAAAT	59.971	20
GGGTTGATCGTAATGGGATG	60.014	20	CGGATTTAAGGGTTATTACCTG	58.81	24
TCCTCCTTCCGTTTGTTGAG	60.224	20	TTGGCCCTACTAACTTGAGCA	59.89	21
GGGATTGTGCCCAAAGATAG	59.387	20	TGAAGCGTCAAATCACAAGC	59.995	20
AATTGTTCAACCTCTCCGCT	58.792	20	TCGTTTTGCTTCTCACCCTT	59.853	20
CATGTGGTTGAATTTCGTTCA	59.43	21	AAACCACCCGAGTAACAACG	59.891	20
ACGCAAAAGCAAGACACAAA	59.512	20	TCGTGTCTAGTGCAGCATGA	59.141	20
GAATCAACATTTCATCGCCA	59.48	20	TCTCATCCAACGAGCTGAAA	59.522	20
CATTGTGATAGGGTTCCGCT	59.955	20	TCCTGTAAGCTCCACCCAAG	60.246	20
CACATATAATCAGGGGCGGA	60.681	20	ATTATATGCACTGGCGGACC	59.813	20
CCTGCAAGAGAGAGGTCGAG	60.275	20	GGATTCCGAGTTTTCGATCC	60.777	20
TGGGTGGGAGATAAGAGGTG	59.92	20	GGCATTATCGATCTTGGCAG	60.574	20
AAAAACCAGCACCAATCCAG	59.971	20	CGGAAGCAAAATTCACGAAG	60.742	20
TTTTCTCGACACATAGAGTCCAA	58.893	23	TCAATTTCTCTCTCCTGCACC	59.42	21
TCATCCAAGTTCATGCAAGG	59.648	20	AAAGCAGCCGCAAGAAGATA	60.117	20
GCTCCACTTCTTCTTGCTGC	60.285	20	AGCAATCGTGATAGGCAACC	60.103	20
ATAATGGCGGGTACGTTGAC	59.713	20	ATTTAACAACGGACGAACGC	60.003	20
TCAACTGCTGCAAATGATCC	59.805	20	CTTGCTATGGTTGATCGGGT	59.955	20
GCGTCTCACCTAACCTCACC	59.727	20	GCAAGGGTTTGATTGCATTT	59.945	20
TTCCCCAGAGCTTGAGAGAG	59.673	20	ATCGAATCGGAAAGTTCCCT	59.903	20
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CCAGATCATGGGTCACTCAA	59.473	20	AAAAGAACTTTCTCCTCTGGCA	59.521	22
AAATCCGATGGTTGTAGTGGA	59.302	21	TCAAACCCGACAAACCATTT	60.206	20
GTCGGCGTTTTCAGCACT	59.992	18	TCAGGCAAATCCTTGGGATA	60.405	20
GATAAGCCAGGGTATGGCAG	59.551	20	GGAGGCATTCGATCTTTGTG	60.603	20
ATATGGGATTTTGCATGGGA	59.979	20	ATTGCAGATGGATGTAGGGC	59.923	20
ACAATCCATGCGTCCCTAAA	60.331	20	TCATTTTTCGGTTGTCACGA	60.088	20
ATGGCATGACTCTTGAGCCT	59.834	20	GCTGTGCTAATTTGCGGAAT	60.238	20
TTCTGATATGGAAATGCCCC	59.722	20	CAAAATGGACCCATCCTCAG	60.309	20
GACGTGGTTTGCAGGCTATT	60.14	20	TTTGGAAAGGAAAGCTCGAA	59.931	20
GGTTTCCCTCCCAAAAACAT	60.032	20	AGAAGTGAATCAAGTGATGGC	59.771	23
TGTCCCGGATATAAGCTTGG	59.916	20	TGGAATGTCAAGTCAACACAA	57.556	21
TTCAGACTCCAAAAACAAAGCA	59.898	22	TTCGTCGGAGCAGGAATAGT	59.836	20
TACCCTTGCATGCACATCAT	59.955	20	GTCATTGTATGGTGCGTTCG	59.995	20
AGAAAGTTGCAGGCTGGCT	60.149	19	AGTCCCATGTTGCTGCTTTT	59.74	20
CCAGCTGACAATCCCCATAC	60.34	20	AGGCACTGGCTTGGATTATG	60.096	20
ATCCAAACTCCAACCTCCAT	58.297	20	TGATTGAGGCTTGGAACAAA	59.247	20
GCATGATCAAAGAGGCCATT	60.043	20	GCACAAACAGACCATCTCCA	59.682	20
TCCTTGGCATACATTCTCTCTC	58.411	22	GCTGCTGGAAATGATGATGA	59.763	20
TACTTTAGCCGCCAAGGAGA	59.975	20	CATGGATTTTCTGGGTCTGC	60.461	20
TCCCACCACCTCTACCCATA	60.187	20	TTGACCAACGCTAATCACCA	60.111	20
ATGTGATTGGGGAAGAATGG	59.605	20	TCGAACCACGTAAATCCTTTG	59.982	21
CACAGCTGTCAATCAACAAGAAG	59.966	23	CTCTCTAGCACCGACCCAAC	59.867	20
CTGTCTCAGTCACCGTCGAA	60.022	20	AACCCTCCATCGTTAGCCTT	59.962	20
TTACACTGCAGTACGTCGCC	59.935	20	CTGTGAAATCCGAAAAATGGA	59.924	21
GACTTCTGGTGGACGACGAT	60.12	20	CTCTTCCCAAAGCCAGAGTG	59.982	20
CCCTGTCCATGGAAGTGAGT	59.962	20	AAGGTCTCCTCTCCCACCAT	59.929	20
CTGCAAGAAGGTTGCTCCTC	60.134	20	CACAACAAAAAGCAACCCAA	59.603	20

CCACCCTCCATTGCTCATAA	60.853	20	ACATCTGTTCTGTTGCGTGG	59.751	20
GTTGCTCAGATTGAGGAGGG	59.803	20	CCATAACGCACCCAAGAACT	59.993	20
ACCTGGGTCAGTTTCTCCCT	59.968	20	TCTCGAGAAAACGGGATTTG	60.184	20
ACGCGTGTGACATGTTCCTA	60.183	20	AATGGTGTGATCTTGGACCTT	58.364	21
CGCGAGACATGAACGAATAA	59.833	20	TTCAACGTAACTGGCAGCAG	60.05	20
TTGGCCTTGTCCTCGTATAAA	59.595	21	GAGCCTGACTGGTGTGGTTT	60.159	20
TCGATTGTATTTAAGCACGCA	59.365	21	TCAGCAGATGTTCGCATAGC	60.127	20
TTGTCACTGCACTACGAGATGA	59.515	22	CTTTTAGCCAGCCCAGTTTG	59.876	20
TTGTTTATGCATCCAAGCCA	60.073	20	TGTGGAGCTGAAAACCACAC	59.726	20
CCCATAAACCACACTAAAGATGG	59.654	23	GTGAATGTGCATGGAGGATG	59.925	20
CAAGGCAAGACTTGTGGTCA	59.873	20	TTGTTCCTACGCACTCACATTA	58.372	22
CTCCCGTGAGGTAAACATCC	59.405	20	TGCAAGTGTGCAACAGATCA	60.029	20
CCGACATTCAGCAGATGAGA	59.942	20	GCAAGTAACCTAGTGGCCAAG	59.717	22
AACCTTCGGACAGCTCTTGA	59.989	20	CACCTTCGAGATTGCTAGGC	59.978	20
ATCAGTGATCACACCTGCCC	60.968	20	CCGTTTACGTTTATCCATACCC	59.52	22
AAACATGGAATGAGTTAAGGGAA	58.919	23	GTTCGGGGATAGAGCCAGTT	60.464	20
GGTGTGCCTTGTCCAATTTT	59.836	20	TATGGCGAGGAAGAAGAGGA	59.91	20
AAGAGGGCCAGGAACAAAAT	59.94	20	TTCCTGCCTACCATTTCAGC	60.214	20
GTCAAATCGTGAACACCCCT	59.827	20	CATTAAAGCTAAGGCCCCAA	59.208	20
TCAAACCATTATACCTACCGCA	59.385	22	TCCGTAGTTGGTTTAGGTTCTTT	58.328	23
TGCTTATCTTTTCGGGCTGT	59.845	20	ACCATCAGATTCATTGTGCG	59.527	20
CTACGTAGCTCGGTTCTCCG	60.03	20	CATCACCTTCCAATTCACCC	60.173	20
AGAGTGGTCCTGCCCTTTTT	60.11	20	AACAGAAGTGATGGGCTTTCA	59.726	21
GAGTGGAGGATTCGGTGAAA	60.05	20	TTTGTTCCTCCTCCCTCCTT	60.045	20
CTGGAGCAGATCCCAGTCTC	59.945	20	GGCATCTCCTCTTGTCTTGG	59.803	20
CTGAGGCCAATTCCTCAGTG	60.791	20	GTCCGCTATAAAGCCCAGC	59.821	19
ACCACTACCACCAGCACCTC	60.033	20	CATTGCAAAATCTCGCTTCA	59.953	20
ACAAACGAAAGGGACCACAA	60.388	20	TTTCGGTTTCTGCAATTTTTG	60.095	21
TCAGCAGCCATTGAGACATC	59.95	20	CTCAGACAGCTTCAAATCCCT	58.537	21
AACAAAACAAAACAGGGGCA	60.378	20	CATCACCGTCATCGTCTCAC	60.121	20
CGAACCACGTTAAATCTCTGTG	59.671	22	AAGATGTTGGGTTCTGACCG	59.966	20
AGCTCAATGCACTTCCCAAT	59.7	20	TCACCAGATCATACCTCCCC	59.737	20
TAATCGTGTTGCATTGCCTC	59.694	20	CATAAATCGCCGCCTCTTAC	59.704	20
AGGAGTCGGAGTGAAAAGCA	59.989	20	GTTGGACCGGTTGGAATAGA	59.79	20
TTTTGGCGATATGCAATCAA	60.037	20	AAGCAGCCATAACTTGCCTC	59.481	20
TTCACTTTTGGCATGTCAGC	59.847	20	GGAATTCTATCCGAGCACCC	60.797	20
TGCTGAGACAGTGGAAGGTG	60.022	20	TGTCTGTCTGTCTAGGCCCC	60.261	20
GCGTGGTTGTGAGCGTATAA	59.759	20	CTCACCGCCAACTCTCTCTC	60.135	20
CTGCTTTGTGTTGCGTGTTT	59.951	20	TCGTTGGTCAACTTCAGTGC	59.88	20
TTGCCAAGACATTTAACGCA	60.251	20	AATTGAGACACAAAAGCGGG	60.11	20
TTTACAAGATCAATGGTCCCAA	59.315	22	TATGCCCTAAGGGGGAGGTA	60.644	20
TAACATCAACGGCTGCAAAA	60.251	20	CGACTTTTCACTATTCTCCGC	58.986	21
TCGACGTCTACAAAACGCAC	59.911	20	AGGGGTCCTCCGTCATAAAC	60.19	20
AGGAGGACGAGTGTGGTGAC	60.161	20	TTCCAACGACAATAATTCCATT	59.616	23
CATTTTTAATTGCAAAATTAATCC	58.536	25	GGAAATAAGGAGGTGTTATGA	59.323	24
CATGCACGTATGCATGTTCA	60.145	20	GAAAAGCTTGGGAATGGTGA	60.051	20
AAGGGTTATCACCTGATTTTCTC	57.73	23	TTGCCACTTTATCCCTCCAC	59.933	20
TAGCAAAAACGAAGCCACCT	59.883	20	CACTGCGATTGCAGATTCAT	59.83	20
CCCAAAATCAACGTCCAGAT	59.79	20	TTCGTGCCTAGTTGGAAACA	59.317	20
ACGATCATCAAAGAATCGGC	60.043	20	TTCCCCTGCAATCAAAGAAG	60.184	20
CGATTGTTTGGTTAATGGGG	60.046	20	TTGCTGAAAAGCAAGCCTCT	60.27	20
CACAAACCACTGAATCGCAC	60.16	20	CCCTCCTATGCACTCCAAAA	60.066	20
TCTGCGTTACTTGCTTTCCA	59.609	20	GAGTGCGCTATGCCTAACAA	59.09	20
TGAATATTGATTGGTCCATGC	58.296	21	TACTCGCCATTTTCCCCTAA	59.542	20
ATTACCCGCCAAAAAGGAAG	60.305	20	TCTCCCATTTCCAACCTGAG	60.042	20
ATGTGCACAGCGAGGTATTG	59.746	20	GGTTCATTCACATGCGTGAC	59.975	20
ACCAAAATGCACCAACACAA	59.864	20	TGTGGCATGTTCTTCGAATC	59.654	20
TTTCCCCTATGAAGCCCAG	60.014	19	TCAGATGAAGCCAAAGAGGG	60.331	20

ATCACTTCCGATCGAACCAC	59.934	20	GTAGAGTAGCGGCTGCAGGT	59.668	20
AACTACGGCCACATGAGCTT	59.763	20	CGCTCCCATTTTTGGTAGAA	60.067	20
ATTTGTTCACCCTGGACGAT	59.263	20	ACCAAACACCCCCTTAGTGTT	59.646	21
GATTCTCACGCCATTCTCAA	58.799	20	GGGATGTTTGGAGAGACGAA	60.05	20
AAGCTGGCTTGTTCCTGTTC	59.478	20	ATCAGCAGCAACCAAGTTGA	59.445	20
TGGACAAGAAGCCATTGAAA	59.247	20	CACGACGAACTTTTCACTTCA	58.96	21
GTTTCCTGTCCAATTCCCAG	59.381	20	CCCACAGATCTTGGACTGGT	59.962	20
TTTCATTATTTATTGCAAGTTTTCG	58.765	25	GGCTGGATCCAATGGTCTTA	59.894	20
ATCATCAATATTCCCGACGC	59.751	20	GCTGACAACATGGTCGCTTA	59.871	20
TGTTGAACGTCTCCAACTCCT	59.754	21	AAGTTTGGGGGAGGAGAAAA	59.912	20
GAGAAAAGGGGAGTTGAGGG	60.045	20	TTCTTCCAGAAGTGGGCATC	60.195	20
GAGCAGAAACTTGCGGAGTC	60.142	20	AACCCTCCTGAACCAAATCC	60.169	20
TGGTGATTCTTTGGACTCCC	59.903	20	AATTGTACATCAAAGGGGCG	59.823	20
GTTAACCTTGCAAGCTGCCT	59.522	20	TCAACGGTTGCAATTTGATT	59.016	20
CTTGCTCCTAATCGTCGGTC	59.836	20	AACTCCATCTCTCTCCCGCT	60.358	20
GCCATGAACTATATTGATTTTCCA	59.28	24	GGTGGAAGGAAGAGGAAAGA	59.677	21
GCCTCAAAATATCTGCTCCAA	59.31	21	TGCCTGATGAATTTCTCCTG	58.797	20
GGTTTGGCAAAAGCCTCAAT	61.339	20	CAATGGTGAATATTATAAAGG	59.607	26
TCCTTTCTCAAATGAAGAGAAAC	59.411	24	AGTGCACTTGTGCCCCTAAA	60.689	20
TGCAGAGATTTGTGGCAGAC	59.992	20	AGAATTTCCCCGCGTTATTT	59.808	20
TTTTCAGTGGTGTTTGTTGTTT	57.248	22	TGTAAAAGGATTCCACGTATTT	58.128	23
TATAAAAATGCAGCCAGGGG	59.922	20	ACCAGCCTGACCTCAAATCA	60.656	20
CAAACATCATGCAGAGGACG	60.263	20	AGAGCTCAGGATCTTGCGAA	60.24	20
AAAAACGCGGAAATCACATC	59.945	20	CATGGTGAGAAGCGTTGATCT	60.27	21
GTCGTCGTTTCCACCTCTGT	60.159	20	GCTCGCCTCCTCTTTCTTCT	60.233	20
GCGGCTCTGCAACTTTTAGT	59.66	20	AAAACGCGCTTTCATACCAT	59.614	20
TCAGGTTAGCCTTGTCCGTT	59.734	20	AACTCATCCAACTAAGCCGC	59.34	20
TTTGTTGGCCATTCTCCTTC	60.051	20	ATGAACCTGCTTTTTGTGGC	60.118	20
GCCCAAGATACTCCATCCAA	59.894	20	GGAGAATCCGGTGGATAAAAA	60.137	21
AGGCATTGGTTTGTTGGAAG	59.971	20	TGTTCACCCACCTTTATCCTTT	59.741	22
AAGGAGGTGTTATGAAGGGATT	58.028	22	GATTTATTGTGCATGCCGTG	59.96	20
ACTGACCGCCCAATCATAAG	59.955	20	TTAAGCAAGGGGATGACTCG	60.206	20
GGTTGATGTCATCGTCATGG	59.769	20	CCGGAGTGTGTTGATTTCCT	59.966	20
CGGCACAGATTACAGCACAC	60.333	20	GGCGGCTTACATTGTTTCTC	59.713	20
ATGAATGCAAAATGGGCACT	60.339	20	AACGTCAAACGGTCTATGCC	60	20
TGAAAGGTAGGGTTTTCGCA	60.608	20	ATGAAGGCCAACGTTCACTC	60.119	20
TGCAAGTAAAATCGTCGTGC	59.879	20	CGGAACTTCGTTCATTGTCA	59.691	20
TGAAGTTGACGAAGAAGATGACA	59.906	23	AGAAATCAGGAGCTGCCAAA	59.955	20
TGGTTGAACTGTTGTCCTGTCT	59.664	22	CACGGTAAGTCCCGACATTT	59.853	20
TTGAATCTCCGGCTGAAACT	59.813	20	AAGCTGCTCCTTTCAAGCAA	60.27	20
TTGGCCACAAATTAAAAGGG	59.805	20	TGGTCGTTGCTGGTTTAATG	59.585	20
TGAAACTCTCAACAGATTCCCAT	59.99	23	TGCGTTCTGAGTTTGTTTCG	60.027	20
CACTTAAGGGGGTTATTAGTGGA	58.515	23	TGAAAATTGTTTTATTCCACAT	58.048	24
TGGGAACACTCTTCAGGACA	59.23	20	CTCGCCCTAACTAGCGACAC	60.037	20
TTCCGGATTTTTCATTGGAG	59.872	20	TCAGTTATGCTCTTCTCCCCA	59.822	21
CAGATTTGTTATGTGTTTTGACAA	57.29	25	TTTATTTGGCCGAACTGACC	59.938	20
ATGGTGGCTGAAATGCTTGT	60.526	20	GACTGATTCAATCTCCTCCCA	59.079	21
TTCTGCCCTTAAGGCTGTTG	60.378	20	GTGGCGGCTAGGTTTACAGA	60.27	20
CTTCTAAAGCTCCACCACACG	59.921	21	GATCATGGGCTTGCAATCTT	60.043	20
GGAACAGGCAGTTCGACATT	60.119	20	AAGGAGAAGCAACAGCGGTA	60.015	20
CCAGGATGGTGATACATTTGG	60.059	21	CGATTCCGGCGTAGAAAATA	60.054	20
GGAGAAATCAAGAGGAGGGG	60.008	20	TAATTTCGGCCAAAACCTTC	59.055	20
TAAATAATGACCGCCATCCC	59.621	20	ATGAGCTCTTCGTCATTGGG	60.218	20
ATTTGAGGGGGAAAGGAGAG	59.508	20	GGAACACGACTCTTTCGAGG	59.844	20
GGCATAGGTTTGGGTTTCAA	59.801	20	GCACGAATAACTGCAAAAGG	58.439	20
AGTGAGCATGTTGTTGTGCC	59.758	20	CCAGACTGGGAAGTCAGCAT	60.261	20
TTCCCTCCTGTTGATGCTTT	59.67	20	GCCATTAGCCTTGGAGATGA	60.177	20
TGTTCGAGGCGTTTTCTAGG	60.378	20	TCAAAGGGATCAAAATTCCC	58.808	20

GCAACGAAGGGAGGACTTTA	59.312	20	TGAACGGTTAAAATAATTGCT	59.91	24
TTTGATGGGATGGTATGTTTATGT	59.399	24	CCCCTTGAGTATGTCCCATC	59.213	20
TTAACCAACATCCCATCTCCA	60.177	21	GGGAGGTTGCATTTCGTATG	60.331	20
AAAAATCAAAGGCCCACAAT	58.418	20	CCAGCCAAGACCAACTCTTC	59.844	20
GCCATCAAAAGAGGAAACGA	60.192	20	CCATGTAGGCGTAAAAATAGG	59.119	23
CGAATGAAACAAGTTGGGAAA	59.961	21	TACAGGCCCTGCAAGAATTT	59.708	20
TGATTTCAGTTGGTAGCAGGAA	59.747	22	CGGGTTTTTCTTCAGCAGAC	59.853	20
TTGCAGCATTCTCACCATGT	60.272	20	CACCCGGCCTCTTTATTTTT	60.305	20
CTCTTCTTCCCAGTTTCCCC	60.045	20	GGAGTCGCGGAATCAAATTA	60.038	20
GGGTTATCATTTGAACGCGA	60.837	20	CCGGAGCTTGAAAGATGAAG	59.948	20
CCCAAGCAAAAGACGACACT	60.291	20	ACATGAGTCGATGATTGGCA	60.08	20
AAGCTTCTGACATCCACGCT	60.02	20	CCACGTTTTGGGGTCCAC	62.219	18
TAGGTGAAGGTGGATTTGGC	59.933	20	TCAAACAACGTGAATGAGCA	58.835	20
TCTTTTGCAGCCCTCCTTTA	59.953	20	GTTCCCCCAACTGAGAATCA	59.903	20
GAAAAATGTATGGGGTCGGA	59.622	20	CGTGTTTCCTATGCTTCTGGA	60.256	21
AGGGACTTAACAAGCCATCG	59.195	20	ATTTCCTCCCCTCTCTCTCG	59.772	20
TTTCTCATACAAAAAGACATTTCT	58.494	26	TTCTGTCTTCCGCGAATTTT	59.823	20
GATGCTCACAAGCAACCAAA	59.847	20	CCCATTTCAAGCTTGCTCTC	59.955	20
ACCTTAGCAACGAAGGAGCA	60.015	20	CATCCGGTTTTAGTTTCGGA	59.931	20
GCAAGTCTGGTACTTGGGGA	60.111	20	CATGTTACACGTGGACGCTC	60.183	20
TGACTGTCATTTTACCTCTTTATGA	57.131	25	TCAACTGCCTGCATTGTTTC	59.847	20
CATAGCTTGCTCACCAACCC	60.657	20	ACCCTTTGTCGGTGGATTTA	59.288	20
TCGGTTCTGACCACTAAACG	58.773	20	CACCAAATTTCATCATTTTTAG	58.144	25
TTTGGATCTGTTTGTCGAGTTG	60.147	22	GTCCACGGGGGAAGAATAAT	60.017	20
AAGACCTATCACACCGCCAC	59.997	20	TTTTGGTCTGGTCTGAGCCT	59.844	20
ACCCTTTGTGGGAAGAGGAC	60.349	20	GCAAGTTCAACCTTCTTGGG	59.711	20
AAGGAGGTGTTATGAAGGGATT	58.028	22	TAATGCGTGCAACACACAAG	59.354	20
ACATGGGCAATAAGTCAGGC	59.962	20	GGCTATCAATGGTTGTTGGG	60.192	20
GAAAATCTGCAGTGGGGTGT	59.973	20	ATGCACGTAGGCATGTTCAA	60.142	20
CCAATCCGATCTCTCTGGAA	60.15	20	AGTCCGATTTCAACCAGGTG	59.966	20
GGGCATAAGCTGTCAGGTCT	59.313	20	CTGCATCCCCCAAAAAGAG	60.578	19
CCCAGCATCCGTTAGTTACAA	60.004	21	TTGGTTATGCAAGTGGAACG	59.585	20
CAAGTCCGGTTCCAGTTTGA	61.064	20	TTCATGAGCTCGCTTTTATTGA	59.985	22
GGCAAGGTAGTAGAGCCACG	59.898	20	CCTATGGTAGTATGGTGTGGG	60.365	22
TCCCTTCTCAAACAACCCAC	59.943	20	GAAGGGGCGGAATTATCTTC	59.873	20
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TAGCGCTGCAGAATTCAAGA	59.856	20	CTCCCAAGCCAAACACTCTC	59.844	20
GTAAATCACGAGACCGCCAG	60.657	20	TTGAATCTGGCCTTCGATCT	59.773	20
AGAAATCCAGCAACCAATCG	60.074	20	ATTGCAGTTCAGCCTCTGCT	60.164	20
TGAGGAATGAGAGCGTAGGG	60.353	20	ATCTTGACAGCTTGTCGGCT	60.02	20
TCGTGCAAAATAGCACCAAG	59.872	20	TTGCCTTGCACTTCATCAGA	60.539	20
GATGTTAATCCAGCGCCCTA	60.06	20	TGATTCCTATGCCTCGTGGT	60.483	20
TGTAGAGCATGCGTTGTCTG	58.6	20	GGTCTCCGGTCCCTAAAATG	60.683	20
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ACCCACTGCAATTACCTGGA	60.375	20	TCATGGTTTCTCTGTTGCGA	60.39	20
CAGAGCGCACTCGAAGAGTA	59.49	20	TGGCGTTGAAAATCTCCATT	60.448	20
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TTCAAAAATGCCACTGCTTG	59.849	20	TGATTCTGACGAGGCAGATG	59.942	20
GGATTTGCATCTACCATTGGA	59.776	21	GCCTGCTACACAGGGTTTTC	59.74	20
CGGTTATCACCGGATCGC	62.397	18	CCTTTAGCTGGCAGGCATAC	59.867	20
TCTTGCTGCTGACACCAATC	59.992	20	TCCCTCCCTCTTTAAAATCACA	59.939	22
TCAACAACGGTAAGTTGCTCTT	58.951	22	TCAAGCCCGCGTTATTAGAT	59.704	20
CCCAGCACTTTCCTGTCATT	60.111	20	CCGACGTACAGATGATGCAG	60.287	20
TCAAGAATCCCTTTAGCCGA	59.778	20	TTTTGTCCTTTTCATGGATGC	59.93	21

CCCCATTACCATCTTTCTCG	59.382	20	GATCCTGCAACAAACCACAA	59.547	20
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CTTCCCCTTCGCTCCTACTC	60.34	20	TCAAAATGGTCATGAAACACG	59.43	21
TCAAAAACCGAAAACCGAAC	59.953	20	ACCGAACCGAACTGATTTTG	59.971	20
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GCTTGCGATAGGCTTTCTTG	60.117	20	CAGACCTCCAAAAGCAGGAG	59.982	20
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TAAGAGTTGTCCGGAGTCGG	60.246	20	CCCACATCTCCCCTCTCTCT	60.605	20
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GTCAATCATCCAACACACCAA	59.256	21	ACCCGAGACAAAACACGAAC	60.012	20
CGCGAGGGTTGTGATAAACT	60.132	20	AATCACTCTGTGTGAGGCCC	60.12	20
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TGATGTGAGATGGGCTTGAG	59.787	20	TGGAGATCGTGTGAGAGGTG	59.82	20
CCTACCTAAGGAGGGAGGGA	59.526	20	TGCAGCAATGCTAGAACCTG	60.157	20
CCCTACGCACTCGTTTTTCT	59.378	20	CTGAGGAGATTTTGGCAGGT	59.284	20
CCTGCTGTTGATTTGATGGA	59.648	20	GTTGCAATAAATCCGTGGGT	59.691	20
AAATGGAATGTGGCGAAGAC	59.939	20	TGTCATGGGAATTCACGAAA	59.9	20
GAAAAATTCGTAAGTGGCCG	59.586	20	AACCAAGCATGCTCATGTCA	60.272	20
GGGACAGAAAGGAAAGCACA	60.232	20	CTGAGGTGACCTGGACCATT	59.962	20
CCAACAATTTCGGTTTGACC	60.206	20	TGCATGAAAACTCCCTCACA	60.24	20
ACCAAACCCATTCTTGTCCA	60.21	20	GAAACAGACCCACAACCCAT	59.679	20
TTGATGGATTTTTCAAGCCC	59.878	20	GAAAATCGCCCAAAGATTCA	60.016	20
GGCAGGTCAAAGGCTGTTTA	60.249	20	CCAATTCCATCAAATCCAGG	60.126	20
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AGGGAGCTGCAACAAGAAAC	59.478	20	ATGCGGTCGGATTAGAATTG	59.923	20
GTTATGATGGGAATGGTGGG	59.871	20	AAGCTAGCACGTAAATGGGG	59.248	20
AATGTGACCTCAATTGCAAAA	58.134	21	ACGAGACCATCGTTCCCATA	60.34	20
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TCCCCTATTTGGACAAGGTG	59.784	20	TGAGAATGTGCTCAGACCGT	59.42	20
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TCGTGCATTACTCGGTTACTTG	60.186	22	GTCGGTCAACATTGCTTTCA	59.697	20
GGAACCAATCTGGTGCATTC	60.326	20	CAAACTGGTGCTCATGCTTT	58.926	20
CACCACCGGACATACTCCTT	59.844	20	CGTGGAGACAACGTGAAGAA	59.873	20
CGCACACACCATCTGTGAAT	60.604	20	GGTCGTAGTCTTCCTCGTCG	59.867	20
TTCCTCTTGAATTTGGTGGG	59.903	20	AGGGAATGGAATGAGCATGA	60.426	20
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TGGAAATGGAATCCGAAGAC	59.871	20	ACTCGAAGAGTAGCGGTTGC	59.644	20
CTTCAAGGATTTGAGCCGAG	59.948	20	TTGGGTACTTCCGACAGCTT	59.734	20
GCTTCTTCTTGCTGTGAGTGG	60.186	21	CTTGGCCACTTATGAATCGG	60.46	20
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ATATTGTCACATGGTCCGCA	59.805	20	CATGCAACAAACCAACCAAA	60.393	20
TGTGCCTTGATTCATTGAAAA	59.147	21	AGTTGAGATATTGGAGAAGAT	58.004	27
TCAAGATTTTGTGTGGCTGC	59.847	20	CCATATACAACAAGATGCCAA	58.927	23
CACCCCTGAAACTCCATCAT	59.779	20	ATTGCTTCCTGAGTTGACCG	60.255	20
GACGACGATGAAAATCGTGA	59.654	20	TCCCCATTACCTTAGTTAGCAG	59.194	23
ATATAAGGCAAAAACGCGCA	60.591	20	TGACGACCGATATGTGCTTC	59.679	20
TGTCGGTGGACTGATTTGTG	60.57	20	GGCGAGGAAATCAGAGAGTG	59.95	20

CGTGAGAAGCGTTGATATGG	59.297	20	TTCCTTTCATTACACGTGCC	58.625	20
CCTCTCACATGTCTCCACGA	59.82	20	TGATGCAATGATCTCATTCTTTT	58.709	23
TGCGTCCATTTCACTCAATC	59.654	20	TGCACAAGCATGTTTTTCATT	59.22	21
CATGGAATTAGGGCTCAGTCT	58.28	21	TGTAAACAGGCTAGGTCGGA	58.379	20
CACCAAATGTATGTGCATGAGA	59.469	22	AATTGAAATGGCGGAAAATG	59.773	20
TGGGGATGGGGGTAAGTAAT	60.258	20	TCTGTTTTTGTTTTGGTTGCC	60.004	21
TCAACCGCCAGATTTTCTGT	60.636	20	GCTAAAGCCATCTCCAATGC	59.813	20
TCAGCTGCCAAACCAAGATA	59.42	20	CCTGGCAGCTTTTGATCTGT	60.397	20
AAAGGTCCCTCACCAGTCAA	59.549	20	TTTCCCCAGTTTGTGTGCTT	60.529	20
CTTTTCTCTGCTTATGCGCC	60.117	20	TAGCAAAGCCCAACCTCATC	60.214	20
GGTGCTGCAACTGAACTGAA	60.032	20	TCTCATCTCTTCTCCTCGCC	59.636	20
CTGTCACGTCTCTTCCACCA	59.864	20	GAGGGAATGATCAAAACCGA	59.871	20
TGGCTATAGGACATCGAGGG	60.051	20	CTGTGTTTGAGGTTGAGCCA	59.873	20
TTTGCATGGAATAAGAATTTTGAA	59.858	24	TTGGATCAATTGGAAGCACA	60.049	20
AATTCAAATTGTCGAAGGCG	60.074	20	TTGGGGATTAGTTCGCAAAG	60.067	20
TGAAGACGAGATTTCAGGGC	60.34	20	ATGCAGTTCCCTTCTCCTGT	58.744	20
AGTGGCCTCTGGCTGTTCT	60.001	19	AAAGAAATTGGACAGTGGCG	60.11	20
CTCCACTGATGTGTGGATGC	60.121	20	AATCTTCAACCCCCACCTCT	59.795	20
CATGAATTTTTGGGAAGCTGA	60.06	21	TTTTCTGCAATCCAAAAGGG	60.046	20
CATGCAAACTGCTGGAACAT	59.722	20	GGGAAAAAGGGCTTGTTGTT	60.332	20
TCTGTTCAGAGAATGCTGGGT	59.859	21	TTTGAACACTCAATGCGCTC	59.995	20
CATGACCCAATCAATGCAAC	59.781	20	GCAGTCAACAACCACGAAGA	59.88	20
TGAAAAAGAAAAACGCGTCA	59.462	20	TTCTGTCCAAGCATGAATCG	59.799	20
TGTACGTGCGTACGTGTGTG	60.293	20	CGGTCGGAAGAAGATTACGA	60.206	20
TCCTGTTTGATGAAATGCCA	60.049	20	CTGAAGATGACATCCCCGTT	59.927	20
GTCTGAGCGAGAGTGTGTGC	59.771	20	CCGACCTCTCCTCCTTTCTC	60.328	20
CAAATGAGATTGGTTCGAGCTT	60.612	22	AGTGGGAATCCGGACACTAA	59.405	20
ACAAAGGTTGGAATGGCTTG	59.971	20	GCTTTCTTTTCTTCCCCCAC	60.053	20
AAGCTCGGGCCTGAACTATT	60.228	20	CACCAGACCGGCTCATTTA	59.658	19
ACTCAGAAATCCATCCCACG	59.927	20	CCCACCTCGAATATCCCCTA	61.023	20
AGAAACCCATGTGCAACTCC	59.973	20	GCAACACGCTCCATCTTCTT	60.406	20
CGCCTTTGCATCTCCTGTAT	60.235	20	CACGTGACTTATTTGGTGGAAA	59.898	22
CATTAAAATGTGTATGCACCTGA	57.669	23	TCAATTCGAAACTTGAGGTACT	60.162	24
TGGGAATTTCTTGATGGAGG	59.864	20	CCCCTGGTTGTTGAAGAAAA	59.942	20
AAGGGGGAAAAGAAAAGGGT	60.156	20	TTCGCCCAATCTTCTCATTC	60.155	20
TATATGGCGGTGGAGATGTG	59.375	20	TGTTTAATTTTTGTTAAGCATGC	59.958	25
ATAACCATTGTGGGCCTTTG	59.685	20	CCGGGGTATGCTATAAACGA	59.81	20
TAAAAATGGGAGATGAGGCG	60.031	20	AGACAAGGAAAAAGAGCGCA	60.132	20
GCGGCCAGTTCAATACAAAT	59.967	20	TGCGTGAAGATAGTGATGTGTT	58.31	22
AGAGAGAAAAAGCTTCGGGG	59.955	20	GTTTAGGTGCTTGGTTGGGA	59.971	20
GATGATCCGAGGATGAATGG	60.244	20	GCTTGATCGTCTCCTGCTTC	60.104	20
TACCTTAGTGCCACCGATCC	59.955	20	GGTGGAGCAGTAGAGGTGGA	60.261	20
AGACCGGACCGTTAGGTAAT	57.55	20	CCTAAAATGCCCTCAGATGC	59.668	20
CTCAGTGTTAGTGCGCAAGC	59.812	20	GTGGAGTGGTGGAGCAAGTT	60.159	20
TCCAAGATGAATAAATGAAAGGG	59.344	23	TGAGACTTTGGTACGGGAGC	60.255	20
GCAAGAGAAGCCCTCACAAC	59.997	20	AGGCAGAGAGGTGACTGGTG	60.458	20
CGTTTCCAGTGTTTGCTCTG	59.485	20	GGAATTCCATCCATCTCGAA	59.831	20
ACGGATTTAACCCCCAAATC	59.888	20	GGCATCCATACTTGCCACTT	59.962	20
TAGGGGCCACTTTCTGTCAC	60.111	20	GCATGCATACAAAACCAAACG	61.284	21
ACTGAGAACTGCTGCGTGTG	60.251	20	TCCTGCAATCTCTGAACCAA	59.369	20
TCCCCTCATCTTTTGACTGC	60.195	20	GCATCATAGGACCCCAAAAA	59.762	20
TTTGATTCCCCACCTTCAAA	60.28	20	GCTGCTTGATCCTGAATCCT	59.39	20
TGTTCGTGTTCTCGAACGAT	59.293	20	TACCATGCGGAAGGAATGAT	60.296	20
GTCCAATAGCTTTCGGCAAA	60.209	20	TGTTCAGCACACAGAAACTTCA	59.534	22
AAAGCAGCAAACTTCCGATG	60.386	20	TTTTTCTTTGGGTCATGTGATG	59.839	22
TTCGCTTGTGGTGAAGAAGA	59.566	20	ATTTGATCCCCCAATTCAAA	59.067	20
GGTTTGGAGCAATGACGAGT	60.119	20	ACTCCTCTTTCGATCTGCCA	59.95	20
ACTTGTCGCTTGCCAAGAAT	59.882	20	GAGTGCAGAGTGCAAAACCA	60.032	20

AAACTCGGTTTGGGCTTTTT	59.98	20	ATGTCCTTGCAATTCTTGCC	60.081	20
CGCTTGTCCTGAGTTGTGAA	60.025	20	CAATGCCTTCTTTTGGCTGT	60.249	20
AGTTGCCGATTGGTAAGCAC	60.14	20	TCCAACAACTGGTCAGCATC	59.682	20
TATGAGAAGGGCATTTTCGG	60.031	20	TCTGGATGCATGAAAATTGA	57.609	20
TCACAGTTTGAAGTTTTATGTCAT	59.466	27	ACCAAATGGCTTAGGTGACG	59.993	20
ATGTCAGTCTGCCAAAGGCT	59.874	20	CTCCGTGTTACCATTTTGCC	60.365	20
TCACGAACCCACATTTTTACA	58.928	21	TAGAGTCCTCCGATTCCGTG	60.21	20
TCGTAAAACATGAACTTCTTTGGA	60.037	24	TGATGTTTGTATATGTTTCGTTC	57.233	24
AAAGCTGCGAAGAAAGTGGA	60.132	20	AATGAGGTCAATGGTCAGCC	59.934	20
GAGGCTATCGAGGCTTTTCC	60.307	20	TGGCGTGCTAACTGCTAAGA	59.776	20
TCCACCTTGAAGCTCTCGAT	59.95	20	CCCCATGAACACACACACAT	60.138	20
GATCCCCTTTTTGCTTCGTT	60.431	20	AAAACTCCGGCATGGTACAC	59.859	20
TCCACAGACAGATTTCCCAA	59.059	20	ACCGAACCACGTACATCCTC	59.851	20
TTACGCGTCAACTGGGAAAT	60.502	20	CCGTTCCATCAAGCATTTTT	59.938	20
CATCATCTTCGCTCCTCTCC	59.91	20	ATTCGATGGATTTCGACGAG	60.036	20
AAGAAACCCCCATTGAAACC	60.032	20	CAAAGCAAGTGTTGCTCCAA	60.027	20
CCACAATGTAAGGAGCACAAAC	59.54	22	ACTAGTGGCAGCCATGTCCA	61.688	20
TTCGCCTTGCATTGACATAA	60.215	20	CGCCGATATATGCGTCTTTT	60.082	20
TCAAGAAGGGAGAAGGGGTT	60.045	20	CAACTGTGATGTTCTTGTTTTG	59.707	23
TTTTCGACCGTCATGAGATG	59.648	20	TGCCATCGTTCACTTTACCA	60.111	20
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TTTGAGAAATGGAGCAGCCT	59.955	20	GTAGTGGTCGACGGGCTTTA	60.132	20
ATGGCGTTGTTATCGTTTGA	59.041	20	TCCAGTGTAGTTTACCCGGC	59.993	20
CCAAATTTCCAATACAAGGCA	59.818	21	GATTCCATGTCCAGACCCAT	59.593	20
ATATTTTCTTCCGCCGGAGT	59.93	20	ACGAACTCCTTCGATTCCCT	60.074	20
GCGGGGTTGTTAAAGAAGAG	58.834	20	TTGGTTGACGTGGTTTGCTA	60.149	20
AAATTCAACCTTGGATGCTACA	58.629	22	TCCGTTCCGGTCTTCTACAT	59.55	20
CCGGTTTGCACCAATTCTAT	59.823	20	GCCAAGTCATATCAAATCCGA	59.915	21
TGGGTCAATTCCAATTCAAAA	60.153	21	CTTGCAAATATAAACGTAATGA	58.479	25
ATCTTGTTGCCATGCTGTGA	60.272	20	AGCTCCCAAGTCTGAGTGGA	59.986	20
TCAAACCTTTAAATTGGCCG	59.937	20	ATTTGGGTGAGAAATCGCTG	60.074	20
TTCATTGCCTTTGCGAAGAT	60.721	20	CCCATTGAATTATGGGGTTG	59.872	20
TTCCAATTATCCATGTTTGCAT	59.193	22	GAAATAATATGGGGCGTCCA	59.621	20
TGGCAAGAAATAACAGCATACC	59.146	22	ATGTCTGCCCAGCAGAGAAC	60.418	20
CCCCCACAGACATATTGACTC	59.274	21	TGCACAATCATCACACATAAC	60.306	23
TGCAAACATGGGACTAATATGAA	59.376	23	ACGGGAGATTTTGCTTGTTG	60.11	20
ACCGCTTCAAACAAAAGCAG	60.42	20	ATATTTGTTCCTCCGGCTCC	60.286	20
GGAGAGTGGAGGTTGTTGGA	60.088	20	AGGTGAGCCAGATGTAGCGT	59.898	20
CGTGCATTTCCAACTCACAC	60.16	20	AGAGCGACAGCGAAAATGAT	59.985	20
CCCAAACCTTAATGCCCTTT	60.177	20	TGTGTTGAAACCCTCATCCA	59.935	20
CGAGCATCCCATTTTCTCTC	59.773	20	TGGTTGCCAGCTTACTGCTA	59.632	20
TCCACCCTTTAATGTCACCA	58.821	20	TTGTCATGATTTGCGGGTTA	59.93	20
AATTGCCCATGTTGGTTAGC	59.829	20	GGGAAGAGAGTGAGAGTTTTG	59.507	22
AGCCAAGAAATGGAGGGAAT	59.903	20	ACAACAATGTTCGCATTGGA	59.972	20
GGCCTCCAACGTTTTCAATA	59.938	20	TTGATTCGGGTTCGATTCTC	60.014	20
CGTCGTTGGTGCTATACCCT	60.015	20	GGTGATATGCATTTGACATTCG	60.217	22
GGAACGCAGAGGATCAATTC	59.635	20	TGCTTTGACAATATTTAGTGTTT	59.901	27
ATCTGGGCTACCGATTTGTG	59.955	20	CGTCACACATCCATGTTCGT	60.45	20
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TGGCACCAAGAATCCCTAAC	59.933	20	GGCAGACAAGCCATCATTTT	60.081	20
CCAACGAGAAGTCGAGAAGG	59.982	20	TGATTGTGGACCAACAGCAT	59.967	20
CTCCATCCCTGCTCTCTCAC	59.945	20	TGAAGGTGTGTGGGGTGTTA	59.848	20
GGTGTTATCTTGATGGGTGGA	59.662	21	TGGACAAGGGAGAAAAAGGA	59.641	20
ATTAACGCACACACGTGACA	58.628	20	CATGGCGTAGTGTTGGAGAA	59.716	20
GGCCTACCAAACACGTTACAA	59.912	21	TCAATTAGGTGTCCCACCGT	60.232	20
TTAAAATGAATGAAGGGCGG	59.901	20	TTGAGTTCGGTCATCACCAT	58.933	20
GCTCTTGATTTGCTCCATCC	59.78	20	TTCCTTCACTCTCCACCTCG	60.377	20
TCTGGGCTGCTAAGAAAGGA	60.088	20	GGGTTCAAACTCCACTCAACA	59.997	21

TTTGCTGATGCCATTGAAAG	59.809	20	TGTGTGTCATTTGTTTTGTTAG	59.464	24
CCGAATTCCGACCTAACAAA	59.931	20	TGAAGCTGTGAACATCGCTC	60.144	20
GAGGGAAAGAGGGAAGGAGA	59.749	20	CGTTGTAATGCCCCGTAAAT	59.72	20
AATCAATCGGCAAATTCAGG	59.901	20	GTTCAAGCCCAAAAATCACC	59.41	20
TCGGAAAAAGATTCCCATTG	59.872	20	CAAAGGTAAAGGGTCCTCCC	59.799	20
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CATGGCAGTATTGGCATCAC	59.955	20	TCAATCTGCAAAAGAACAGGG	60.234	21
CATAATGACCCGCTAAAGGC	59.569	20	TTATCCTGTGCTTTTGCACG	59.872	20
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TAATAGCGGCCGATCTGAAG	60.323	20	GGCTTATTTGGCATGCTCTC	59.813	20
GACGTCCTACTCGCCCACT	60.277	19	TGCGTTTTGATGATATATAGGT	60.054	26
GCAGGTTTCCATATGTCGCT	60.103	20	CCATCTTGGACCACACCATA	59.215	20
GCCAACATGATGACCTGAAA	59.502	20	TATTCTCGCAAACAGTGCCA	60.401	20
TCCACCCACTGTCCCTAGTC	59.962	20	AGCTGCTTGCGTTTCTTGAT	60.162	20
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GAGAATGGAACTTGCCTCCA	60.195	20	GATGCTGAAGGAGCCAAAAG	59.955	20
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CGAAGATTTATGCGGGGTTA	59.922	20	TCTCTGCAACAGCCAGAAGA	59.855	20
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GCCATGGATGCGATAAAAGT	59.929	20	GCAGCCTCAAATCCAACCTA	60.214	20
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GGCTCAATTATTTAGGCCCAT	59.33	21	CCGTTGGAAAAAGGATGAAA	59.91	20
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ACTGTGCCGTAAGTGTGCTG	59.97	20	CCAGAATTTCGAACCTCCAA	60.044	20
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CGCTACAAACAAGGCAATCA	59.872	20	CCTCAGCAAAATGCAGTTGA	59.988	20
ACACAAGGATTGTTTTCCCG	59.83	20	TAGTACCTGCATGGGGTTGG	60.766	20

CCTATTGCTTAAGACGACATGCT	59.826	23	ATGCACATTGTGTCCCAAAA	59.823	20
CTCCATTGGTGGAACGAGAT	59.927	20	ATTTGGACCCCACCCTACTC	60.052	20
TAACCAATCGAATTCCCAGC	59.901	20	TGACAAGATTCAATAAAGCCA	59.639	23
TGCAATTTATATGCTTTTGCAC	57.955	22	CCAATCCTGAACTTCCTCCA	60.042	20
CATAACAAGTGGCGAAAGGG	60.493	20	ATGCAGTCAAAAGCAAGCCT	60.022	20
CCCGCAAAATTGCATTATCT	59.928	20	TTTTTGGTGTTTGATTGCGA	60.088	20
GGAGTCGGCCATGTAGCTTA	60.235	20	TCTGTGTTCAATACCGCAGC	59.871	20
TGCACAATCGATTTACGTGG	60.523	20	AATAAGCCCGTTGGAAAGGT	59.835	20
TGTCAGGAAATTGTTTCGCA	60.234	20	AAATGCATCTCAATTTTTGGAT	58.916	23
TTGTTCATCAAGGCCTCACA	60.24	20	TATCACCAAGAGATGCCCAC	58.516	20
AAACAGCAGAGAAGCCCAAA	59.993	20	ACGAGAAATGGAGTGGTTGC	60.119	20
GAATTCGGGGTGTTTTGAGA	59.91	20	CCCAAGAGTCCAGAACCAGA	60.229	20
TGCGTTGTTTTACCATTGGA	59.969	20	CTGTACAAAAGCTATGCTTTCA	59.901	25
CTCGTCCAGGACAAATCCAT	59.927	20	GAGGTACCCTAGGCGAGAGG	60.225	20
CATTGCCGCAAGATCAAGTA	59.833	20	TGGTATGCTGCTTCTCCCTC	60.362	20
ATTCTAGCACCGTGAAACCG	60.132	20	GTCGATGGGGCAGAAAAGTA	60.074	20
TCCCAACCCCATTTACAAAA	60.024	20	TTTCGAGTATCGCTCCGACT	59.978	20
GTGGGTTTACCTAGAGCGCA	60.27	20	CGATTTGATGAGAAGTGGCA	59.799	20
GGAATGAAGTATGTGGAGGAAGA	59.473	23	TCTCTCAGCATTAGCCCCAG	60.495	20
CGCCCTTTTAGTTAAAACCTTG	59.246	22	AAATAAGGAGGTGTTATGAAG	59.323	24
GCTGGAATCCTGATGATGCT	60.189	20	AACTTTGCAGCTTCTGAGCC	59.763	20
ATATAGCCGTTGGGCTTGTG	59.982	20	TTTGAAGGAAGATTGCGAGG	60.323	20
TTCCTCCAGCGAGTCGTAGT	60.012	20	ACCAATGCGGATGCTCTAAC	60.103	20
TGTGAGTTGCCACTCTCCAC	59.872	20	GAAGCCCAAAGATGAACCAA	60.051	20
AGCCATGAATTTCACCAGCA	61.588	20	CCTTCGTCACCAACGAAGTT	60.149	20
TGATTCTTGATGGAAAGGCA	59.2	20	ATTGAACTCAAAGCCCTTGC	59.316	20
GGCCAGAAACTGCCATAAAA	60.074	20	AGGTGGCAGGAAGTTGTACC	59.065	20
CCTCACAGGCAAATATGCAA	59.688	20	TTTTGGAATCCGAGATGAGG	60.006	20
CGCCAGCTCAATTTTATTCC	59.682	20	GGTGAAGCATGCAAAGATGA	59.805	20
CTTGAGCAATGTGGAGCTTG	59.591	20	CCTAAAGTGACCCCATTCCA	59.784	20
TTAGGCTTCCCATCCCACTA	59.523	20	GGATGGAGAGATTGCAGCAT	60.189	20
TTTCGCTCTGATATCCCCAT	59.486	20	CATCTATGCTCGCACATTCG	60.388	20
TATTCCCGGTATGTAGCCCA	60.167	20	CTCGCAATACTTCTGCCTCC	59.978	20
TCTCTCTGCTTCACACACGC	60.343	20	TTATCAAGCTTGTCAGCCCC	60.214	20
CCACAAAGCTCTTGGAAATAGG	60.122	22	AGTTGTGATGCAATTTGAGCC	60.133	21
TAGTATTGGAGGTTGGGGGC	61.061	20	GGAGAAGGTGATGGGGCTAT	60.293	20
GATTCTGCACAGCAATGTGG	60.272	20	CCCTGTAACAGTTGGTGCCT	60.028	20
CGTTCCTACTTTGTGGTGGA	58.621	20	CCCTTGATTTAAGAGATCCAAT	59.004	23
CAGTATCGGGAGTGAGAGGG	59.673	20	TTCAGAAATGCAATAAATTCCG	59.11	22
GATTTGGGGTTTCGGAGATT	60.131	20	CCGGCTTGGCAGTAATAAAA	60.089	20
CCCTACCCATTTACCCGTTT	59.939	20	TGTTCGCACAGGTGAATCAT	60.12	20
TTCGAAATGAATGGTCGTGA	60.049	20	GGCCGTTTGTTTTATTGGAA	59.81	20
TCAAATCCTAGCCACACACG	59.716	20	TCAAATAGGTGGGTGGTGGT	60.088	20
TGCCAATTTAAGTTCGAATGAG	59.253	22	TTCTCGCAGAGCATGTGTAT	57.013	20
AACCGGTTTGACCGATTTTC	61.08	20	TGGTGCAAATTGTGTTGAGAA	60.142	21
TGCACCGGATAATACAGCAG	59.712	20	GATGCCCTAGGGACGTATCC	60.682	20
AAGATCAGCTTTTCCCACCC	60.443	20	ACCAGAATAGCCCAGTGGTG	59.989	20
AGTTTATATCAATAGTTTTGTGTCC	57.108	26	TGTTTGTGTTTTGACGTTTGC	59.665	21
GCAGGTGTAGGACTGGAGGA	60.261	20	GACCGCAGGATAATCCAGAA	60.036	20
TTCAAGGAGTTTGAGAGGGG	59.255	20	TTGTTAGTTTTGGATGGTACGA	59.817	24
TTCATTGCTGCTGCAGTTTT	59.614	20	TTTTTGCAGGGAAAAAGCAT	59.699	20
TTCACCACCAGCCTTGATAA	59.123	20	TGTGATCAAAGAAGAAAAATGA	59.549	25
GGCAATGGCTATTTTGGCTA	60.061	20	TAGTAAACCGGACGTGGCAT	60.386	20
AATTGTACAGGTTGAGGCGG	59.993	20	TATTGGAAAGGGATCTGCCA	60.405	20
GTTCGTACCGAACAACACCC	60.277	20	TGGTGTCCATCCCTCTCAAT	60.326	20
CAAAGCTCAGCCGACCTAGT	59.639	20	AGCACGTATCGACATTGCTTA	58.478	21
TGCAAGAAAAACAAGCCCTC	60.365	20	GTGCTGCGTCTCATGTTGAT	59.87	20
TTGTCGCTGGACACGATAAG	59.864	20	GGTAATGTCGCAGGCGTACT	60.162	20

TCGACTGAAAATTTTGGCTAATC	59.637	23	CCGGAGTGATGCAGTAGTTG	59.314	20
ATTTCCCTTATGCCACTCCC	60.152	20	GCTCAATTTTAGTTGTGAAATC	60.065	26
CACGAGCTGTTAATCACCACA	59.773	21	TGCTCTCAAGAACACGCACT	59.776	20
TGGTTAACTCAATCTCAGCCG	60.256	21	CGCCTCTAAGAAAACATAACT	59.482	23
TTAATCAGATGAGGGCAGGG	60.029	20	ACAATCGTATGGTCTCCCCA	60.195	20
TGGACCACACCTATCATAACCA	60.11	22	ATCCTGTATCGATTATCATTTT	58.075	25
GAACTCTGTGGGCGTCAGAT	60.269	20	TCTCAGACAAAACCTTCGCC	60.375	20
TTGGATTGGACATTGGGTAGA	60.177	21	GCTGATGTGCAAACAAAGAAA	58.956	21
ACACTCCTGTATGTAGTGACACG	60.034	25	TGGCTAGAGAGATTCCACGA	58.543	20
TTTGGTTTTTGGTTTGCTCC	59.953	20	ATCAAGACCGGCCATTCTAC	59.009	20
TCACCAATTTGAATGGTTATCA	57.873	22	CCCAGTGAATGATAAGGGGA	59.744	20
CGCACGAGTTAGCATAGCTG	59.799	20	CGATATGTTACGTAGGATGAC	59.374	24
TGAGAGTTTCTGCGTTGGTG	60.025	20	AATGTGTTCCATTGCGGTTT	60.235	20
GTTGGCTTTTTGTTGCCACT	60.154	20	CCTGAAATCTCAATAGCCCG	59.662	20
CATCTTGATGTCCCCATTGA	59.296	20	ACGAAAATCAAAAAGCCCAC	59.067	20
GCTTCAGTTCTGTGGCATCA	59.992	20	CAAAGCACAACAGGGTCCTT	60.149	20
CCGCAAACACCTATTAACCG	60.368	20	TTTTCTACGTCAGCACACGC	60.058	20
TGGATTTAGCCGATTCCAAG	60.031	20	TGATTGGGTGCAACTGAGAG	59.831	20
TCTGTGCTAACTCCGTGTCG	60.049	20	ACCCGTTCCACAACCTACTG	59.884	20
CTTTGCACTCTCCAGCAATG	59.591	20	TCAACAGCCAGCATTGTTTC	59.847	20
GGTGAAGAAAGTGGGCTTCA	60.232	20	CTGCACACACAAACCCTCAC	60.203	20
AAGCAGTGGAACGAGGAAGA	59.989	20	GAATGTCGTTTCAAAATAAAA	60.107	24
CGCATTTCATCTGCTTTTCA	59.953	20	CATTGCTGACATGATTGCCT	59.679	20
TTTTATTGGGGGTGCAACAT	60.053	20	CCGAAAAGGCGATAAAATGA	60.033	20
AAGCCTGGGCATTACATTTG	59.96	20	TGGGTATGGGCTTAAAATGC	59.795	20
CACCGAATATTCCCAACTCAA	59.809	21	AATTGTGAACAGGTGGCAAGT	59.511	21
CCTTCCCTTAAGCCCATCTC	60.032	20	TATCACCCTAGCTCCCCTGA	59.647	20
TAGCTCTGAGGCTGGTGCTT	60.299	20	ACAAAGTGATACATGCGCGA	60.288	20
CCACTTCTCCCATTTGCATT	59.933	20	ATTGCCTCAGGCGTAGTCAT	59.723	20
CCGTAGCTGTTATTGATGGAAG	58.787	22	TCTTTTCGGCAACCAATTTC	60.053	20
CACCAGAATTTAGGCGGAGA	60.206	20	ATGGATTTTCCCATGAGGTG	59.605	20
CCGAATATCCCCCAACTAAAA	60.023	21	AATCCCAAATCCCATCACTG	59.605	20
GTCTGCGTCGTCAAGAAGGT	60.453	20	TACCCATCTCTTTGCTGTCG	58.874	20
CATCTGAGCATTTGCAAGGA	59.948	20	AAGGTCCGTAGTCCATCACG	59.989	20
TTTGGCAACAGACAATTTGC	59.712	20	TTCTTCGCGAGCTTCTTGAT	60.235	20
CACAAGCTCGGAAGGGTAAA	60.241	20	TAGGCTCCTGGTTTTTGTGC	60.249	20
GCTGCAAAACTGGAGGAGAG	60.134	20	AGCGACGCATGACCTTATTC	60.243	20
ATCGATTAGGTCGCACAAGG	60.096	20	CTAGAAGGTTGATGGCACGG	60.647	20
GCGCTGTAACCAACAACAGA	59.911	20	CGGCTTATAGTCCCCAATGA	59.916	20
AACAATGGCTTTAAAGGGGG	60.177	20	ATGGGTTATCACCAGATCGC	59.78	20
TCTGCAACTCGACATCAACG	61.023	20	CGATTTACACACGCGCAC	59.859	18
TACCATTTTCGTCCGTCACA	59.964	20	CGCGGAGTTTAAGGAATGTT	59.225	20
TGGTTGATTAGATTACCGCTACA	58.71	23	CCCGATTGACATCCCTAATG	60.148	20
TGTCTCACGAGGATTTTCGAT	59.685	21	AAGATTGTGCCGATGGTGAT	60.348	20
AAAAGGGCCTATATCCAATATGA	59.2	24	AGGCTGAGACTGAAACCACG	60.444	20
CAACTGCTCACCAGACATTGA	59.889	21	GTGACAAAAGGGCCTGAAAA	60.088	20
GGGGTTATCATGGGATCAAG	59.055	20	TGAGTAGAACAATCGTGCGG	59.864	20
AACGCAGATCTGATGGCAC	59.81	19	AGAATTGGGAAGGGTTCCAC	60.169	20
AGCCGTGTACTCTGCCTGAC	60.476	20	ATGGAAAATCCCCAAATTCC	59.83	20
AACAATGCAGTAGCTGGTTGG	60.183	21	TCAAATGACAAAAACGCCAT	59.016	20
GGTGATTTTTGATTATAGGAATAT	59.773	27	AAAAATCCGTCACTAAATGGG	58.802	22
GGAACAAAGACACCATTGATAAA	59.311	24	TAGTACGCGGGCCAATTAGT	59.63	20
TTTTGATAACGTCAAATCCAACA	59.394	23	CAACGTGAGTTTGCCAAGAA	59.881	20
TAAATGCCAATATGGGGGAA	59.976	20	TGTGTTAACCTTTGGCTCCC	59.971	20
TTTCATTGCAATATTCTTCGACA	59.616	23	TATGTGGATGAAACCAGGGG	60.572	20
TTTGTGCCTAAAATGCCCTC	60.074	20	GTTGGCATTCAAATCAACCA	59.375	20
CACTCCCAACTCACAATCCA	59.52	20	AATTGTCTTGCTTTCCAGCC	59.316	20
TATTTGCTGTTGTGGGGTTG	59.439	20	TGGGATGGACTTGGAATCAT	60.135	20

ACAAATGAACACTCCGGCAT	60.384	20	TTTAAGGGTTATCACCTGATTT	58.625	25
AGGCAGAAAAGAGGAGGGAC	59.817	20	TCAATCTCACGCACTCAACC	59.837	20
TTGGAATGAATTTAAGGCGG	59.901	20	TCCCATATTGCCACCCTTTA	60.146	20
CTCGTTAGCAAGCAATGCAC	59.638	20	AGGCTGGCTCTGATCTTCAA	60.096	20
GAAAGAAGAGGGCTCCACAA	59.405	20	TTTGAAGCATGTGTTAATTGCC	60.006	22
GCTGAAGAGGTCCAGCAATC	59.957	20	AATGCACAAACAATCCACGA	59.972	20
TTCATGTGAGGATATGGCGA	60.033	20	CTACAATGGGCAAGGCATTT	59.96	20
CAATGTCAGAGTGGTGGTGG	59.997	20	TCCAGACACTGGGTTGTTGA	60.129	20
TCTTCTCGCATACCAAAGGT	57.422	20	ACAAAACTCAGGCCACTTACG	59.295	21
ATTTGCGTGGGGAATAATGA	60.153	20	AAATCCAGAAGCAATGCCTG	60.214	20
CCCAAGAAGCCCTTCTCTCT	59.95	20	TGAAGCTGCATTCACTCTGC	60.296	20
AAATGGATGCTGATAAATGGA	57.059	21	TTTTTCGGGCTCCAAACTT	59.671	19
CGAGAGAGCTTTTCCTTGACA	59.743	21	ATTGCCTCCTTTCATGAGCA	60.744	20
CAAACCCTTAAACTGAGCGG	59.741	20	GGAAATTTTCGGGTGAACCT	60.166	20
TTTCCCCTCCCTCATTTACC	60.124	20	TTTGCATCGCATTCATCATT	60.043	20
TCCGTCGTTGTAGGAAATACG	60.004	21	TTAACATCAAGGAAAGCCCG	60.067	20
TTCCTCTGTGGTGAAGGGAC	60.088	20	ACTTGCAGGTTCTTGGCAAT	59.74	20
TGCAACGTGAGTAGTGACTCG	60.104	21	AGGTTGGGAGTTGGCTAGTG	59.208	20
AAGGTACAAGTGGGTTCCCC	60.088	20	AGCTTGTGGAATTGTTTGGC	60.118	20
TACCCAGACCCAAAGCAAAT	59.429	20	CCGCTTCCTACAGTACTCCG	59.891	20
CAACAAAAGCGTGTTCATGG	60.149	20	GGGGTTTCTGAGAGGGTTTC	59.912	20
GACCGACGAGATAGCGAGAG	60.119	20	AATGCCATGTGACAAACCAA	59.823	20
CACCACAAAGCAATTGGAAA	59.561	20	TCGGGAAAATTTGTGGTTGT	60.206	20
TGGGTGCCATTTCTATCACA	59.924	20	CTGAAATGGGGTTTGAATGC	60.309	20
TTAATGAGGGGCCACAAAGA	60.439	20	TTGGCAGAGGTGTGAGAGTG	60.022	20
TGATCTGGAAGTAAGGAATCCTA	59.657	25	CTTTCAGGCGAGGAAGAGAC	59.162	20
TCATTTTCCTAGGTGAGGCG	60.206	20	TCTCCACAAGTTCCCGTTTC	60.088	20
TGGGGCTCTTGAGTTCTGTT	59.844	20	TGGGAATATTGGCATTTTTGA	60.137	21
GGGAAAAACCGATGAGATGA	59.871	20	AGCAGCAGCAAACCAAGAGT	60.201	20
TTCCCCAGCTCAAGACCTAA	59.807	20	TTTCTGGTGAAACCGACCTC	60.088	20
AAGTTGCATGCCATTTACCA	59.041	20	GGACGGATGGATTTGTAAGC	59.391	20
CTATTATGCCCTGCCTGAGC	59.829	20	TCAGCCTTGTTTGATGCTTCT	60.008	21
GGCTTGCTGACTTGGCATA	59.964	19	GGTTCCCGCGTCATAAAAT	59.776	19
CCAAAATTGCGTGCAAAGTA	59.742	20	TTATGAAAACCGCAGCAGTG	59.872	20
GGATTTTGGATTGGTCGAGA	59.871	20	ATTATCATTTCCACCGCCAC	59.651	20
CAATGTTGGTGACGTCTTGC	60.16	20	AGTTGTGGGGCTGGAGATAA	59.55	20
TCACAGCTGGCATAACCAAG	59.864	20	GCCTCTGATGCAAGTCCTTC	59.957	20
TCACGGATTCACCAACTGAA	60.088	20	ACGATCCCATATTTGCCAAG	59.784	20
TTGCAAACTTAATTGGTGCG	59.742	20	CCTCTGATGCCGGAACTTAT	59.15	20
CCTATATACGGGCATGGCATA	59.688	21	GGTCTTCGGGTCTGGGTATT	60.19	20
TATGAGTCGCACACAATGCC	60.697	20	ATGTCGGCATTCAAGGTTTT	59.434	20
ACTGGGTTGGTAGTTGCCAG	60.028	20	TCAAAGCTTGAAGGCCTAGC	59.73	20
AGAATTTCAAGGTAATGGGGA	57.54	21	TCCACAAAAGATCATGCCAA	60.049	20
GCACGTCTCTCGGACATACA	59.862	20	GGTGCAAAATTATGTGGGCT	59.829	20
TCAAACTTACCACCCGAACA	59.021	20	TTACGTAAAAATGGGTTATTAT	57.411	26
TTTGCACTTAAGAGGAGTTTTGA	58.249	23	ATATGGGACGTCCAAAAACG	59.685	20
TCCACCGACAAACAACAAAA	59.981	20	CCAGATCTAATGGCCTCGTC	59.653	20
TGTTTAGGCCCAAATGGAAG	59.931	20	TAGGCGGATTGGTTTTTGAC	59.938	20
GAAGCTAATGCATTCTGTCGC	60.003	21	ACCTTCCATAGGTTGGGAGC	60.328	20
GTTAAAGCCAAAAGTCGGGC	60.958	20	GAGAAAGAGTGGGGGAGGTT	59.534	20
ACAGCAGCAAGCAATAACGA	59.638	20	TTGTGAGAAGCCAAAGCTGA	59.716	20
CTCTTCCCAGGAGACGAATG	59.797	20	ATCATTACTGGCCATGGGTG	60.603	20
TTGCACTTCCTGGAGAACCT	59.844	20	TGTATTCAACCAGCTGGCAA	60.257	20
GGATCCATTTTGTCGCAGTT	59.939	20	TGGCATAGTCCTGAGTGGTG	59.701	20
CACACATGGAAAAGATCTCCAA	59.971	22	TTCTTCTATCCCAATTTGCTTGT	59.175	23
ATCGCTCCCAATTATGGACA	60.296	20	TCCCATTTCTTTTGTTCCCA	60.28	20
ACAGCTTTAGTGGGGCAAGA	59.875	20	AGAAATCCCCCTCCTCATGT	59.755	20
AACACATTTCTTCAACATTCATCA	58.541	24	TTTTCTTTTTGCAGGATATTCG	58.439	22

TCAACGGTTCACATCGGTTA	59.964	20	CATAGGTCACCGAATTCCATC	59.259	21
TGGAGAACTCATTCTTACTGCG	59.517	22	CTTGCACTGCGTAATGGAGA	60.011	20
ACGAACACACACGCACTCTC	59.948	20	AGGGAGGAATAGAGCCGAAA	60.166	20
GGCCAGATTTCGTCCCTATT	60.286	20	CAATCTGACGGCCGATATTT	59.923	20
TGTTTGCACGTGAATAAGCC	59.735	20	AACGGTATGCTCGGATTTTG	59.96	20
GGCTTAGCTGTTCGTGGTTC	59.882	20	TTTTCGTTCTTTCTCAATTTCG	58.542	22
CGCCGACCAATCATGTAGA	60.637	19	ACCAAATATTAGGGTTATCACA	58.348	24
GGTGGAAAAACTGATGTGGC	60.362	20	TTTGAGTTTGCATCTAAGAAGG	59.828	24
ACCCAAAGAAGAAAGCACCA	59.711	20	AGAGGGTGAGAGGGGACCTA	60.066	20
TCTTTGACGTTAATTTTCGGAGA	60.115	23	CGTAGATCCCTGTCGGGTAG	59.569	20
CCTGAAAGAATTTGGGGGAT	60.124	20	AGGTTGTGGATTTGTGAATAAA	58.883	24
ATCTCTGCCCCCATCTCTCT	60.179	20	GACCGGCCGTAATAATGGTA	59.682	20
CCCACTTTTATGGCCGACTA	59.953	20	GATGTTTTTCCAATGTGGGG	60.029	20
CATGTCGTGTCGTGTCAGAA	59.265	20	TCGTCTCACGAGCAAAGCTA	59.888	20
TTTCCTGCCTTGTCAGACCT	59.844	20	CCCTTTTTCATGGTGGTTGT	59.688	20
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CGGCATCGATAATGGACACT	60.884	20	GTAACCTGCCACCCCTGATA	59.813	20
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TCCGCAATTAACTTGGAAGG	60.067	20	TGGGACCCGTCTTCTTATTG	59.926	20
AGGGCTATGGGTGGTAGGAC	60.212	20	TCGTAGTAGGAGCACGAAAAC	59.941	22
CAATAAAGCCCGTCACGTTT	59.996	20	GGATGCCAGAATCCATGACT	59.893	20
GGCAGCCGATTGTAGTGAAT	60.103	20	CCCCCTAACATATCCACGTTT	59.952	21
AGCCGTGAGATTTACTTTTAACTT	57.02	24	TCGGAGTTCACAAGTTCGAC	58.854	20
GCGTTTTGACAATATATAAGTGTT	59.394	27	AACGAAAACCACACGGGTTA	60.262	20
CCAAACCAAAACTCATCAACC	59.322	21	GGGCCCATCCTATCACACTA	59.773	20
TCTCCCAACACACCTTTTCC	59.943	20	ATGGGGGTGGGAGTTTAAGA	60.549	20
GGAAAAAGGAAAGGTGAGGG	59.912	20	GGGAAAACTTCCCACCAAAT	60.032	20
CAACTCCCCCGTAGTTTTCA	59.964	20	GATCCACTTGCCTTGATGCT	60.226	20
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TCGAGCTGAACGAAAGAGGT	60.134	20	TTACCAATCCGGGTGATGTT	60.051	20
CCCCACCTTAGCGTTAAACA	59.99	20	CCCTGCTCCACTTTCTCAAT	59.284	20
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GGCAAAAACACCAACGAAAT	59.845	20	TGATTGACTCATATGCCCGA	60.033	20
ACTCAACTCTGATCGGTGGG	60.112	20	CATCCAAGAACCACAAAGCA	59.691	20
GGAGATGGAGGGTTCAAGGT	60.314	20	TCCGGTAGGGTGCATAAAAC	59.823	20
ACAAAAATGCCCTTGAATGC	59.945	20	TGGATTGAAATAAGGGGTCG	59.756	20
TGATATGGTGTTGGGAGGTG	59.215	20	GAAATCAGCACGAATCACACA	59.713	21
AAACCAGAGAAATCCCCCAC	60.169	20	AAGAGGAAGAGGCAGAAGGG	59.95	20
GCTCAATGCGTAGGCTTCTC	60.125	20	AGTCAACCATGGCGTCTTCT	59.727	20
AAACCGCACTTTAGCTCGAA	60.018	20	GACCGCCTAGATTTGTTGGA	60.074	20
CCCTTGTATGCTGCGTTTTT	60.131	20	GCTGAGCGGATTTAATCGTG	60.742	20
AGTTTCGATTCGATTGACGG	60.074	20	TGCAAAACGAGCAAGTGAAG	60.172	20
CGTGAGGGCCTAAGAATGAC	59.694	20	CGAGACATGGGAGCTCTAGG	59.966	20
TTCCAACAATCTCAGCATCA	57.743	20	ATGGGGAGCAGGAAGGATAC	60.293	20
AAGTATTGATCGACGTGGGA	58.019	20	ATCTGCGAGGATCTACGGAC	59.268	20
GCACACAAGTTTGGGAGGAT	59.973	20	GCCGTTGTGTCGTTTTCTTT	60.154	20
CTGCCTCCCTTGTTCTTACG	59.869	20	TCTCATCAGCAAGGCCAGAT	60.914	20
CCCTAATCATCTCCCCTCCT	59.35	20	GGTCAAATCGAGAACAACCC	59.386	20
CCTAGAGCACACTCGAAGGG	60.005	20	TTGTGGATGGTGCATTTTGT	59.823	20
CCTCCTTCCATAGCAGCAAA	60.344	20	CATCGGTCCAGAGAATCTGAG	59.812	21
TGATCAAAATCCACACCTCG	59.496	20	TTCAGGTTTCCACCTTTCTTG	59.201	21
CAGAGTTTGTTTCGCAACCC	60.668	20	CCATGGCCAAGAGTCTTATCA	60.081	21
GCACTGGTGGAAACTGGATT	59.973	20	TGCTTCCAATGGTTGCATAG	59.688	20
TCCACCTCTCTGCTCCACTT	59.986	20	TTGGGTGATAGGCCCAGTAG	59.948	20
GAACCCAAACCTCAAGCTCA	60.232	20	TAGCCGACCCCAATTTAGTG	59.953	20
GGAAGCGAGGTAGGCTTTCT	59.983	20	AGGTAATTTCGGTCGCACAC	60	20
AGCCAGATTCTCTTGGTGGA	59.803	20	CCACCACCATCTTACAAGCA	59.566	20
CCTTTCTCCATGGGCATCT	60.019	19	ATCCTCAATAGCACCAGCGA	60.765	20

TTGAGATTGGTCGACTGCTG	59.984	20	TGCACCTTGAAGTTGTGGTT	59.187	20
TGATTGGACAAAACGACCAA	59.941	20	GTTGAAGGGGCTGACAACAT	59.973	20
GTTTCTCTCACCTCCTCCCA	59.228	20	AACATGATGAAGGTCCGAGG	59.927	20
AGGGCCCAACAATTTCTTCT	59.94	20	TGTGCTTTGAGCAACTCCAG	60.175	20
GCATATGCATGGTTCTCACG	60.104	20	GCAGTCCCAAAACAAGCAAT	60.118	20
TGGTCCACCATTCTTTTACTGA	59.471	22	TCAATTCCCCCACCAACTTA	60.162	20
TGAAATTAGATTAAAGAAAAGAT	57.681	27	ATAACGGGATTGAAGGAGGG	60.145	20
TGGGGTGAATCAGTTCAACA	59.935	20	GCCTACATCCACTGGTCAAG	58.158	20
GGAAATAAGGAGGTGCTATGACA	59.515	23	TATCATTGTTTCGCGAGCAG	59.976	20
TGCAGCTCAAAAAGACAGTCC	60.565	21	GGAGGCTGCTGACAAGATTC	59.957	20
CACTTTTTGTGAAACCCCTCA	59.994	21	GCCAAGTGCTTCGTTTTGTT	60.292	20
AGGGGATTCCTGCAATTTTC	60.265	20	TTGGGACCCCTTTCACATTA	60.162	20
AGTGGCTGGACTAAACCACG	60.171	20	GATCAGAGAAAACAAGCCGC	59.962	20
TCCCCATTAATCCCATCAGA	60.088	20	GACCCCAGTTTTCCTTCCAT	60.169	20
TGCTACTACTGGCTTCCGGT	59.898	20	TGGAGTGTTGGATCTGTTGC	59.682	20
TCCGTGTGCGTATTCTTGAC	59.722	20	GCCCAAAGTTAGATGTGACCA	59.985	21
TTTACATACAAGGAGACAGAATAT	57.852	26	ACGAAAGCGGAGTTGAAAGA	59.993	20
ACTTGTCAATGCCGGTAAGC	60.14	20	TCATTGCCATCGGAACATTA	59.891	20
TCACAACGGGGTCAAATGTA	59.816	20	CCCTCCTCTCTCTCTCCCTC	59.489	20
ATCAGGCTCGAGTCCATGTC	60.231	20	ATGACCGATGGTCGTGATTT	60.203	20
CGGCATGAGATGAGATGAGA	59.9	20	ACTAGCAAATTTCGGGACGA	59.708	20
AACAGAGCAAGACGAGGCAT	60.02	20	CTCCTGCCAGTCTTCAATCC	59.803	20
GCCAAGGAAAGCATGGTAAA	60.074	20	GCAGAGGTGTATTCTGTTGCC	59.755	21
AGCCAATCACTAACCAACACG	60.045	21	AACTAATCCATGCTGCTGGC	60.243	20
TCCGCCCTCGTGTTTTATTA	60.448	20	TTGCAAGACATCCAACATCA	58.62	20
CAGCATCCTTCATTTCGGTT	60.074	20	TGACAATCACTTGCCACCAT	59.967	20
CATTGCCATTGCAGAAGCTA	59.976	20	CCCTGTGCAATCACTCAAAA	59.691	20
GTGTCAGAGGCGGTTGTCTT	60.307	20	CCCTCATTTGTACGGACTTGA	59.978	21
CATGATGCATTTTCCCAGTTC	60.324	21	TAGGGACATCTGGGTGTGTG	59.388	20
CCAACCAGCTTAGCGAAAAA	60.368	20	TGGAGGACCTCACGTGTGTA	60.154	20
CCAAACCCAATATCACAGCC	60.192	20	TCCTTGAACTTCTTCGGTGG	60.224	20
AAAAAGTCCCCAGCCAATCT	59.94	20	CACGCCAATTCAATCATCAC	59.931	20
CCCACTAACCTTGTCTCCCC	60.736	20	TGGTAAAAAGCGCTCGTACA	59.509	20
GGTGTGCTCGGATCTTGATT	60.081	20	CTTGGATGGGCATTAACCAC	60.192	20
AAGATTCTCTCTTGTAGGTTGTCC	59.72	25	TCTCATTCTGGTTTGAGGGG	60.042	20
CATCACGGCAAAGCAAGTAA	59.872	20	TCACTCTTCCGACTTCCGAT	59.803	20
CGCAATGATAGACCACAACG	60.134	20	CTCCTCTCCAGCCATCTCCT	60.891	20
CCACCACTTTCTCTCTCCCA	60.229	20	TGCTGCTTCTGGTTGATGAC	59.992	20
AGCCAGGAAACGCTGAAATA	59.845	20	ACAAAGCTCGAGTGGCATGT	60.865	20
CCAAATTTTAACAACTGATGCAA	59.076	23	CAAAACTATCGACCTTTTCGG	58.751	21
TTTCTTGCCCATATTCCACC	59.762	20	TGAAGTTTCCCCGAATTTTG	59.91	20
AGAAGCTTGTTGTCCGCTGT	60.058	20	CAGAGTGCCTCTCTTGGGAA	60.523	20
AATTGTTCCTGCTCGTGGTC	60.119	20	GTTTGGGTCGAATTTGAGGA	59.91	20
CACTGGATCTGCCGATGTTA	59.673	20	CTTCATCTTGAGAGAGCGCC	60.24	20
CCATATGATGCTGATGCGAT	59.485	20	TATGACCGGCCAAAGTAAGG	59.953	20
AGTCACGTCTATTCATCATTGACA	58.654	24	GGCGATATCCGACTCACTGT	60.104	20
GGACTGATGATCCGGTGACT	59.928	20	ACCATCTCTCGCTCTGCAAT	59.981	20
TTTAAGATGTGCATGCATTTGA	59.217	22	ACGGCAGGATTAAGTCCCTA	58.671	20
GAAATTGTTGTTGTGTTTGCG	59.122	21	CGGTTTCAATCATGACTGTCC	60.368	21
AAATTTTGCACCGCCATATC	59.801	20	AATGGTGTTTCCACTTTTTGC	58.986	21
ACGCGAAGTAGCATGGTTTT	59.775	20	TGCCGGATACAGATATGCAA	60.058	20
ATAGGCTATGCACGGTCCAG	60.118	20	GTGAAGAGGAGCAAATGGGA	60.195	20
ATGCCACCACTTCCCTGATA	60.34	20	CGCTTCCTCGTTTTCATCTC	59.955	20
CCAGATGTGAGGAGCAAACA	59.831	20	TCGAGTTTTGGTTCGGAAAA	60.587	20
TTCTAACGGCCCAGATTTTG	60.067	20	TGATTTGACATTTTTGGAGAGA	59.984	24
CAAAAATCTAACGGGCCAAA	59.937	20	ATTGATGCGAGGCATGTGTA	60.104	20
CCACGCTTCATTATCAACCA	59.542	20	CGTAGTGGGTGAGGAATACCA	59.861	21
TGCTCTCAATTAAATACACCCG	59.143	22	TTTTCAGTTTCGAATCAGTTAG	58.445	24

GCCAGCAGTAAAGAGGGTGT	59.357	20	AAACCCCTCCAAACCCTAGA	59.799	20
CAAAACGAAATAAATGCGGC	60.444	20	TCTAGGCATCGAGATGCAGTT	59.992	21
TGCCATTATGGTGCATTGTT	59.816	20	ACTATCATGGGCTGGAGGTG	59.95	20
GCGCTTTTTCTTATCATGGC	59.822	20	GAGGGATCGAGAAAGGGAAC	60.015	20
CAAGATGATGAGGGCCAAAT	59.894	20	GCTGACTCCAGGGTATTCCA	60.073	20
GGAGACCAATTCTTGGCTGA	60.195	20	GTTCTCTAGCTGTGCCCCTG	60.012	20
CAATAAATTGGGGTCGGCTA	59.789	20	TGCGTTTTGATGATATATAAGT	59.361	27
TGGTTATTACTGGAACGCGA	59.182	20	TTTCTAATGGGCGCTGAAAT	59.682	20
CCGGCCTATCGTCTTCCTAC	60.968	20	TCACGCAAGATGCAACAAAT	60.265	20
TGCTAATGGCAACTCGATCA	60.366	20	GCACCAATTATAGGATTTTGG	59.588	22
GATACAGCTTGGCTTCTGGG	59.836	20	TCCCTCTGCATATTTGTCCC	59.894	20
GCAAAAGTGCCTACTTCACCA	60.298	21	TGAATAAGTTTGCGAACCGC	61.131	20
AAACCAACTATCTCGGTGCG	60.132	20	GCTGGAGCTACGATTAACCA	57.999	20
TGACCTGGTGTCCCATCTCT	60.527	20	ATTCCTCAAGCATCATTCCG	60.036	20
GCAATCTATCCCATACAAGGC	58.547	21	CGAATGATGGAACGGAGATT	59.894	20
TCCATCTTCTCTCAGGTGGG	60.191	20	TCTGTTCCACTTTCTCCATGC	60.248	21
CAACCAATTCAACTTTCATTATGC	59.788	24	ATTCGTGTTTGCAGTAGGGG	59.993	20
CCGGATCATTGACATTTGTT	58.271	20	GGGTTTAATTTCTCGCATGG	59.411	20
TCCTGCCCATGACATAATCA	59.883	20	GCTGTGCGTCGATTTCTTTA	59.066	20
ACAGTGGCTAAAATGCACCG	61.08	20	TGTGGATGGACGGATTTTCT	60.317	20
AACACCTAGGGGCTTTGTTG	59.097	20	TTGGGATTAAGGCTTTGGTG	59.931	20
CCTGCATCACAAAAGCAAAA	59.849	20	GAGATGAGCTTCTTGCTGGC	60.249	20
TTTCTTGACTGTGGATTTCCAAT	59.864	23	ACCTCTTCTCCTGCACCAAA	59.844	20
TGTTGGTTTGTGAGGTCAGC	59.726	20	TTGGGAGTTGCTTCAGATCC	60.195	20
CGTCTGATTCGTCGTAGTCG	59.465	20	ATCGGTATAGGGCTTGGGTT	59.688	20
ATCGGATTCTGGGGGATAAC	59.981	20	TTCCTTGTGCTTTGGCTTTT	59.861	20
GCATGCAAAGTTGCAAACAA	60.827	20	GCTGACATTGACGGCTTACA	59.871	20
TTTATCTCTCGGCCAACACC	60.074	20	AAGTCCGAGAAAGCCTCTTG	58.67	20
TGATGAAGGCACAGAGCATC	59.95	20	ATTTACGGGTTTGTGCTTGC	60.003	20
TTGGGGGAGGGTTTAGGTAG	60.172	20	CATCAGCGTCACCTCAAAAG	59.44	20
CATATGGTGTCAGGTTTGGG	58.695	20	CCTAAATGGGTGAGCCAATC	59.387	20
CATCAGTTGTAGCTGGGGGT	59.989	20	GTGAGTGCATGCAAGTGGAC	60.328	20
ACATGCCCTAAAAACCGATG	59.823	20	TGTTTGCAATTATTTCGTGGT	58.084	21
AGACCAAACCTCAAGCATGG	60.111	20	TGGCCTGCTATTATTGACCA	59.136	20
GGCCACTCAGTTACAAAGGTG	59.648	21	TCGAACTCAACGACCAAAAA	59.293	20
TTCCAACAGCTCAAACAGCA	60.574	20	GGCTGGTTTGCTTGAACATT	60.118	20
GGTGGAACTGATTGGGAGAA	59.903	20	TTGCATCAGAGCAAAACGAC	59.995	20
AAGTGCCTTGTGTGTCACGA	60.357	20	CACGACCCAACACACACATT	60.333	20
GTCCCTTCTTACATATGGCCC	59.68	21	TGCATGATTGCTCCATGTCT	60.233	20
ACGACCCCAATTTTTGTCTG	59.83	20	AAGCTATTGGCGGAGTATGC	59.347	20
ACCATTATGTGTGCGAGTGG	59.445	20	CCTCGCGTAAACCCTTGTTA	60.124	20
AAAACCACGTCGTTCTTGCT	59.78	20	GAGGTTCATCTCAACCACGG	60.51	20
CCAATGTATCATCCCTCGCT	59.917	20	CGATTGGGCCTATCCTATCA	59.878	20
ACTGCTCCTCTCATGGTCAA	58.379	20	CCATGACCCTGAACAATGAT	58.201	20
AATCCAATTCGAATCCCCTC	60.096	20	GGTGTGTGTGGAAACTGACG	60.047	20
TGATTCCATGAACACCCTTTT	59.278	21	ACAAGGCATCACTTCACACG	59.751	20
CAGGGGATCTCAAGCCTGTA	60.21	20	CCATGGCGATGAATGTAGTG	59.948	20
CCCATGCTTGGGTTCTCTAA	60.066	20	TTAACCCACCAAAAAGGTGC	59.839	20
AGGATTCACGAGTGACCCAG	60.112	20	AGCTCCTCAACTAAAGCCCC	59.848	20
TTCCACCATGATTTCGACAC	59.348	20	CCGAATCTTTTCGTGGATCA	60.972	20
GCGAGCAGACCAGAAGTCA	60.287	19	CTTGAGGCTACCATGGGAAA	60.066	20
AAGGTGGAAGGGAAGAATCC	59.373	20	TGGAGATTACCGGGTTTTGT	59.288	20
TCGTGAGAAATTAATGGAACAAA	59.885	24	GAAATCAAGCCATTTCCGAG	59.645	20
GCTTGGAAAAAGGGAGGAAT	59.532	20	GCCATTACGGGTGAGGAATA	59.784	20
CATGCACATCCCTCTTTCAG	59.241	20	AAGGCGAGATCAATGTTTGG	60.074	20
GCCAGTTCTTTTTCATGGGA	60.051	20	AGCTGTCCGGAGACTTTGAG	59.598	20
GATCAAACACGCATCACCAC	59.975	20	AGGGGAGGATATGAACTCGG	60.285	20
ACAACACGGAACCACTAGGC	60.035	20	TCCTCTCTCTCTCTCCATCACA	59.127	22

CATGAACTCCATGAAGCATGA	59.664	21	AGACGTACCTGGGTCATTGG	59.844	20
ACCTGATCACTTGTCCGAGG	60.112	20	CACTGCACATGCTGCCTTAT	59.895	20
AGTGAACCATGGGTCCGTTA	60.232	20	GGAGGGGAGAGTTTGAATCC	59.874	20
GTTCAGCAACAGCTTGACCA	60.032	20	CCTCCCTCACCTCCACACTA	60.104	20
TCCGATAGGCAAAACGACTC	60.214	20	CCCTGTCGAGTCTCAGCTCT	59.732	20
CAAAAACCGAAAAACCGAAA	59.951	20	CGAATTTGCAAAACCGAAAT	59.943	20
GAGAGCAACACATGCCAACA	60.885	20	TTCGTTTAAATCGATTGGGG	59.767	20
TCATTTGTTAGAGGTTTTGACCA	58.663	23	GGGCGCGACAGTTATAGAAG	59.867	20
ACATCGGCTCAAACTCCAAA	60.636	20	TGGATGTGAATAGGGTGGAA	58.77	20
ACATGCCATTGCTACTGCTG	59.895	20	TCCTGTGAGCAGAAGGGAGT	59.986	20
TTTGATGATATATAGGTGTTTTGA	58.476	27	GCGTAAATTTTGAAAGAAGCA	57.304	21
TTTGTTATTGGGGTATGGGAA	59.042	21	CAAGCGTGATTAGCCATCAA	59.833	20
GTCACCTGTCACCAGAGCAA	59.872	20	GTCAGAGGAGCAGAATTGGG	59.803	20
GAAAGCCCCCTTTTCTCAAC	60.053	20	CCGAATGCAACGGTTTTAGT	59.996	20
GCGTTCACGAAGAGGGTAAG	59.875	20	TTCATGTTTGCTTAGCCGTG	59.872	20
CGGACAAACACGACAACATC	60.008	20	TTGCAAAGTCATGGCTAAAGA	59.89	22
TAGGGATTCTGCTGAGGGTC	59.239	20	GGATGGTTCTGTGCAGGAAT	59.934	20
CGTACTGCTCCATCTTCAACC	59.749	21	CGAACACAGGGCAATAGTGA	59.716	20
CAAGAGTAGAGAAAATCCTCCCA	60.121	24	TGTCCATTGATTGCTTGATCC	60.859	21
GGAGTGGAGTGTGAGTGGGT	60.006	20	ATTTGAATTTGGGAGGAGGG	60.124	20
CAACTGACCAACAACAGCCA	60.757	20	AAAAGCTCCTGCACTTCTCG	59.757	20
TTTCTCTCTCCTCTCGCTGC	59.973	20	TCGTCGGATGAAAAAGAACC	60.051	20
ATCTCGGCCTAGCTGGATTT	60.194	20	TTGAGGACAAAAACCCGAAG	60.081	20
TAGACCCAGGCTTCGAGGTA	59.83	20	CTCGAGTTCGGCCTATTTAGTT	58.973	22
ATTCCATCACCCAACTCTCG	59.927	20	CATCGGGGTTTGAAGGTTTA	59.795	20
TAAGGGCGTGGGATACTGAG	60.088	20	CGTTTTGACGATATATAGTGTT	58.68	26
TCATCAACGAAGAAACGCTG	59.988	20	TTTGAATGCCAACAGGTGAA	60.088	20
GATGCCCTCCACATCAGATT	59.893	20	AACCGTCGCCGACTTAAATA	59.609	20
GTAGTTTACCTGGCTGGCGT	59.266	20	TTTTATGTCACTGGGGAAACG	59.847	21
TGTGAAGGCCTACGAACTGA	59.44	20	TTGGAGTTAAAAGCACCATTG	59.625	22
ATCTTGACCGCTGATTTTGG	60.074	20	TGATGACGCCATGTTTCAAT	59.931	20
TTTTCTCTTGACCACGACCA	59.262	20	TCAAATTTTCTTTCCGGTTCA	59.551	21
GGCACCTCAAATGCAAATCT	60.081	20	TGCTATAGGGGAAACAACCG	59.953	20
TGCTCCATTGCAAGAACATC	59.805	20	CGGACCGTTAGGATTAGCAT	59.067	20
CAAATTTCCATCCCTCTCCA	59.864	20	TTTGAGTTTGCATCTAAGAAGG	59.828	24
AGCAATGAGCAACATTCAGC	59.031	20	GAGGAGTTGGGAGAGCAGG	59.929	19
TTTTAATTCACGCACAATTACATTT	58.984	25	AATTTGCTGTCGACGGAATC	60.081	20
TGTTGAATGTTGTGCCTCGT	60.16	20	ATGAGTTTGGTGTGTTGGCA	60.008	20
TACAAGCACAACAACACGCA	59.944	20	TCGCAGATAGGATTTTTGCC	60.175	20
TCAAACACTGCGCTTCAGTC	60.183	20	TGTGTAGTCCTGTTCCTGCG	59.897	20
GGTTGCACCTCTGTTTTCGT	60.156	20	TTCCTCGACAGATTATCCGC	60.177	20
TCCAACTACGTGGGTGGTTT	60.269	20	CAGAAGTAAACAGACGGCCC	59.734	20
GACCCCACTTGCCAAAATTA	59.801	20	TTGGTCATCGCAATTCGTAG	59.688	20
CACAGGGAGAAGACGAACTCT	58.533	21	TTGCTGCCCAAAAAGAAAAA	60.701	20
TGTGTTGGTCTGAGAGGCTG	60.022	20	CCCAGAGATGCGGAAAATAA	60.031	20
AGGTTTTTCAAGGAGTGCCC	60.476	20	ATTTTCCGCCCTAGTGGAAT	59.799	20
AATGTTTCTGGAATCACCTGG	58.898	21	TATATAAGAAACGGCGGCCA	60.424	20
TAAAGAATGCCCACTCCCAG	60.066	20	ATGGAGACAGATGGAGTCCG	60.072	20
GCAGAAGGCACCGAACTTAC	59.882	20	CGTCAAGCAATGCCAGATAA	59.833	20
TCCCCTACTTGCGTCCTCTA	59.83	20	ATGATGCAACATCCCTTGTG	59.374	20
AATGAAAAGGCCATTCGAGA	59.645	20	CAGAGGGTTTCCAAAATGTCA	59.956	21
GAGCATAGGGAAATGGGGTT	60.152	20	GAAAAATGGCAGAGTGCTCC	59.82	20
CAATGGCTTCACCAACCTTT	59.971	20	CCTGGGTTCTTGGTTTTGAA	59.942	20
CGGCTTGGATTATTTCCTATTTC	60.169	23	AAATCCAAGGAGGCGAGATT	60.039	20
TTAGTTAGTACCGATTTCAGGGTT	57.499	24	TCAAAAATATGTTGTCGGCG	59.562	20
CCGAAAATACAGGCGCATA	59.671	19	CCACAAAATCTGGGGTCTGT	59.82	20
AAAGGTTTCCTTAACTCTGCGA	59.433	22	TGCTGTTTGCATTTTAAGATGA	60.186	24
CAAAAACAACTTCAATATGGATCT	58.211	25	AGACCGAAAGAAGTCCACCC	60.489	20

TTCCCCGATCAACAATCAAT	60.133	20	CACAAACTCACACAATGGGC	60.008	20
CCAATTTTCTCTTCGGGCTA	59.292	20	GTTCAGGACGGAGGAGTTGA	60.238	20
ATTGTACGAAAAACCCCGTG	59.724	20	AAAGGTTTTGATTTTCCGGC	60.292	20
AGACAAACATAGGATGCCGC	60.103	20	ATGGGCTTTAGTCCCCTGTT	59.827	20
CCCGATACTTCACCCTTTCA	59.926	20	TGGCTTCTGTTTCTCCATCA	59.369	20
GTCTGATAGGATTGGCTCGG	59.653	20	GGACTGGAAGGAAGGGAAAG	60.045	20
GAAGGTTCTGCAACGGAAAG	59.853	20	CACCGTTCTCTGCAACAAAA	59.881	20
AGCACGTGTTGAGGCTTCTT	60.058	20	TGGGTGGTGTGATAGCATTG	60.39	20
GGATGGAGTTCGGTCTGAAA	60.05	20	CTTGCAGGACATCAATCGAA	59.799	20
GTGTTCTCGGTTGATGCAGA	59.837	20	ACATTCATCCGAGCAACTCA	59.245	20
CCATGCACGTAAGCATGTTC	60.142	20	GTAGGAGGCAAAGTAGGGGC	60.096	20
TATTAGGCCACCCCCTAACC	60.034	20	CCCCAAAACACCCCTAGAAT	60.046	20
GCTTGCTCTTGCAACCTCTT	59.763	20	CTCATGCTTATTTTGCAAGGG	59.728	21
CCCAACAAACCCTTTCTCAA	59.942	20	CACATGCCTGGAGCATACAC	60.144	20
CATGGCATGCAAAGAAGAGA	59.948	20	ACCAGCTAGTCTTTTGCCCA	59.875	20
GAATGGGAAGTTCGGAATGA	59.871	20	AGATTTTGCACCAACAACCC	59.836	20
CTTCCATTCCATTCCACACC	60.173	20	CACCCAATTTGGTCGTTTTT	59.702	20
CCCAAAAATGGTTTCACACAC	60.118	21	AACGCTGGAAGAATGTGACC	60.119	20
TCCGACCTAATGAAAGCGAG	60.344	20	AAACCGTGCATGAACTTTCC	59.978	20
GTGAGGTGGGCAGAGTCAGT	60.315	20	AGTATTGGTTGCGGGTTCAC	59.859	20
TCCAACCAACATCAAATGGA	59.75	20	AAACAGCAGCAGTATGCCAG	59.101	20
CAAATGGGAATCCATGAAGG	60.126	20	TATCCGCAGGCCAAGATAGT	59.691	20
CCGACAATAAGAAGAGAGGCA	59.462	21	CAGCATGAATCAAACAACCA	58.099	20
GCCACTGAACCAAGTGACCT	60.159	20	ATTATCTCGATCGGCCTCCT	60.024	20
ACAATGATATTCGCGAAGGC	60.067	20	AAACGACAGAAGAAAGGGCA	59.853	20
GTGGCCTCTAATCAGTTCGC	59.843	20	GCATCGGACATTGGAGCTAT	60.066	20
CCAAAAAGAGGATCCCAGAA	59.097	20	AGTTTTTGCGCAGGAATGTT	59.752	20
TGATATGACCACAATGGCGT	59.805	20	TAGCCGATAAAAATGGCACC	59.928	20
AAATTCAAAAGCTGGGATGG	59.019	20	CCATTCCATTCTCACCCTCA	60.86	20
GAGATTTAGTGCGCGAAAGG	59.982	20	CTCCCATTTGTGCTTCAACA	59.691	20
GGAAAAGGCATATTGTGGGTT	60.068	21	TGCGTTTGTTCTAACTTTATCA	59.734	24
ATAGCTGCGAGGTAACGTGG	60.292	20	CAGGGGGACTTTAATGGGAT	60.011	20
GCACCACCCTACCCTTCTTT	60.361	20	AAGTTCCAAGTGATCGGTGG	59.966	20
AAGGTGTAGTTCGGGGTGTG	59.884	20	GCGAGCAAACTCGGTTAAAG	60.018	20
GTTTCCTCGAAAATCCACCA	59.91	20	AAAACATGTGGAGGGCAGTC	59.973	20
TTTTCAAACCCTGAACACCC	59.807	20	TGTAATGCCTCCTTTCAGCA	59.42	20
TTTCTCGCATTGGTCAATCA	60.197	20	TGCTTTTCTTCTCGCTCTCC	59.836	20
AGGTGCTGTGTGATGATGGA	60.121	20	GACAACAGAAAAACCACGCA	59.74	20
TGCTCGCTTTCATTTCACAC	59.995	20	TCGGGGCGAATAGAGACTAA	59.801	20
CCTCTTTTGTTTTCCATGCC	59.546	20	GGGATTAATTCCCAGCATGA	59.722	20
AGACGGAGGAGAAGAGGAGG	59.945	20	GCCACGCTCTTTCATTTCAT	60.221	20
AGAGCTCTTCAGTGGCGAAA	60.277	20	ATTGCATTCTTGGTGTGTGC	59.577	20
GTCGGGCTAACGTGCTACA	59.879	19	TTTTAACGATGGATCATGTAAG	59.748	24
CTCGTGTAGAATCGCCTTCC	59.836	20	ATTTCACTTTGCCAGCAACC	60.118	20
TTTTGGGTTGGAGATGGTTT	59.264	20	CAGTCGGATTCGTTTTGGAC	60.495	20
CAAACGAAAAATTATCAACTGTA	59.853	26	AATTGCATCTTCGGTTTCGT	59.574	20
ACCAAGTTGAGGGCATTGAA	60.495	20	CAGGTTTAGTTGTTAGGTGTTT	58.77	25
CTGACCGGATCTCTCACTCC	59.792	20	GCACAATCAAACCTTGCCTT	60.118	20
GACAAAACCATCAGCCACCT	59.973	20	GAAAAGAGAGGGAGATGGGG	60.008	20
GGGGACTTTTTAACCAACCA	58.785	20	TCAACTCTTGTGGATAACTATT	59.968	26
TGTGAGTGTGTGTGCAATGA	58.12	20	GTTGGTTTGCGTTTGATCCT	59.978	20
AGGGAATATCAGGGGAATGG	59.974	20	TTGCACAGCTCTAACAAACAC	59.578	22
ATCGAACTGGAGGAGGCTTT	60.212	20	TTCTCAGTGCTGATGTTGGC	59.992	20
GGAAATCCAAGGCTACACGA	60.074	20	TGAAGCGCCTGTTTCTCTCT	60.277	20
ACAGGATAACGGATGCCTTG	59.955	20	ACCTTTGCCAGATTGTTGAAA	59.601	21
GGGGTGGTCCTCATTCTAAA	58.836	20	AAGAACCACGCGTAATCGAG	60.27	20
TCGCGTGTCATTCTAGACCA	60.413	20	TGCGTTTTGATGATATATAGGT	58.933	25
GGCCTTCAAGCAAAATCAAA	60.188	20	TTGCATGTCTGCCATCTTTC	59.805	20

GTCATCGAGCCTAATCGAGC	59.946	20	TGGTGTGGTTTTGGAAGTGA	59.976	20
GCGATTTTAACAAAAACGGG	59.472	20	TCAACTCCCACGTCCACATA	59.96	20
CATTTTCCCAAACCCACAAC	60.066	20	CGGAGAGGAGCTGGTATTTG	59.83	20
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CATTCAAAAGCTTGCTTCCC	59.823	20	ATGATAACAGTGAGGCCGGA	60.483	20
CTGTCCCCACGGTCTAATGT	59.844	20	TTATGATGCCTAGTGGTTGGC	59.974	21
CGCATTTGTCTCTCACCTCA	59.984	20	ATCCAGTTTGCCTGGTTTTG	59.971	20
AGACTGCACCTGCGGTAACT	59.937	20	TTGGATTGAAGCTCAGCAGT	58.597	20
CCTGGTGTCCACTGTGTTTG	60.039	20	TCAAAGCAAACGACTTGTTCC	60.277	21
TTGTTTTGGTGGGTTTGGAT	60.066	20	CAGATAATGGTGGGCCAAAT	59.645	20
ACCTGAGGGAGTTGATGTGG	59.962	20	TTCAAATGCCAGTTTTCACG	59.706	20
TCAAGGTCTGACGAAGTCGC	61.546	20	CATTTTTGGAGGAGATTCTTCG	60.068	22
CAGCCCTTGGCTCTTTTAGA	59.587	20	TTATGATGGGAATGGGAGGT	59.055	20
CCTACAAAAAGCAAGGGCAA	60.236	20	CGTTTATCGATTAGCACCCG	60.468	20
CATCGATTGAACCAAACACCT	59.845	21	TTTGCGTGTGAACATCAACC	60.562	20
CCAAGCAAACTACAAACCCA	58.673	20	TAAGTTCGATGCCCGAAGTC	60.214	20
TCCAACGTCAAAGTTGCTAGG	60.29	21	GCATAGGAATGCCAATTCAA	58.577	20
TGTCTATGCCGGTTTTTGAA	59.157	20	TAATAGCCACGAAAGGGGTG	59.953	20
AATTTCGGTTACATGGCAGC	59.967	20	CCACTTCCCAACCATCTACC	59.259	20
TTGTTAGAGGTCTTGACGGGA	59.72	21	GCCCTCACCCTTTATGGTTT	60.187	20
TTGGGGAGGAGAAAAGAGAA	58.833	20	GATTCTTTGAATCATATTCCAC	58.865	25
CTTATCCAACTCAATTTATATGAT	57.452	26	TCTCTCTTCCTCACCAAGCA	58.669	20
ATGCGATGTGTGGTCGAATA	59.955	20	AGGGGTAAAGGTGGAAATGG	60.046	20
GGGTTATCACCTGATTACTACCCT	58.775	24	TCCTTGTCATTGTGGATGGA	59.893	20
GTCGTGCGATGTATGATGTG	58.517	20	CCTCGGTCTATCTCATTTTTATC	58.715	24
GGGAGGAAGATGCAACTCAG	59.803	20	TGATTGGGATGCCATGTTTA	59.745	20
AAAGGCCACGTGTTAATTGC	60.003	20	CAAGGAATCCGAAAAATGGA	59.872	20
GCTATGGCTCGTATTCCTTCC	60.075	21	TGTGCACCCCATTAAAGGTT	60.227	20
GGAAACGATCGTAATACGCC	59.438	20	CCGTACATGTTGATTGCCAC	59.847	20
TTGAGACGATGTGCGATAGG	59.823	20	TACATTCCATTGTTTCGGCA	59.93	20
ACTAGGTTGTTGTGGCGGAG	60.171	20	TCCTGCTCTTGCAAATGAGA	59.673	20
TCATATATGTTCCTGGCGGC	60.827	20	CAATGCTCCTTACGATGCAA	59.833	20
GATCGATCGGGAGTCAGAAA	60.158	20	ACGGATTCACCAGAACAAGC	60.119	20
TAGATTTGGATCGGTTGGGA	60.266	20	AGTCAACATTTGGCCCACAC	60.823	20
GTGGCTTGCTTGCTTCTTTC	60.14	20	GGGAAGACTGTGTGAAGGGA	60.088	20
ATCACCCCAACATCACCCTA	60.05	20	GGTGTGCTCGGATTTTTGAT	59.939	20
TTGATTTTTAATGGGGCAAAA	59.313	21	TGCGAAATTTAAGCCAAGTG	58.958	20
GCTCAATTCTTGGACCTTGC	59.82	20	TTGGACTAAACCACCCATCC	59.647	20
ATGGAGAAACACCAAGCGTC	60.119	20	ACTCCTTGATGGTGGAGGTG	59.962	20
GCTCATGATTTGGCCAGTTT	60.081	20	GATTGTCGTCAACCTCCCAT	59.786	20
AATTTGTGTTGGCTTCAGGG	59.971	20	AGCATACAGTTCTCCCGAGG	59.308	20
GCGATCATTCTCGTGAAGAAA	60.346	21	TCGGCGCTGTTTACTCTTCT	60.154	20
GCTTGTACCCGTAGCGTGTT	60.197	20	ATAAAGAACCCAACTGGCCC	60.187	20
GTAGAGGGCGAGAACGACAG	60.012	20	TCTCCACCACCATTCTCACA	60.088	20
ATAATTGCCTAGCTGGCGTG	60.251	20	TTGTTTTGTGCGTTATGTGGA	60.022	21
TTCCCACCATGACTTCAACA	59.935	20	TTCGGAAGCGTACATCAAGA	59.42	20
CCGGTGCACCATTTGATAAT	60.585	20	CACGGTTCTTCAGCAACTCA	60.025	20
TCGAGCAATCTGTAAGGTGAAG	59.517	22	AAGGTGGAAAAGGGTTGCTT	59.976	20
TCTGCGGGATTTAGAGGATG	60.17	20	TCTTCCTCCACCATTTTTGC	60.051	20
TGAATTGCTCCACATACCCA	59.924	20	ACGGAAATTTCACTATGCCG	59.96	20
CTGTTTGTTGCCCCTTCAAC	60.529	20	AAGCAAAATGGATAGCGTGG	60.096	20
GTGTGGTCTGCAAAGTGTGG	60.203	20	CGAACTCCAATGGGGTAGAA	59.926	20
AATCGCTGAACTGTTTTCCG	60.249	20	GGTTCAGGTTGCGAATTGAT	59.939	20
CACACACCTACTTTAATGACGCA	60.102	23	GCGGTATGACTTCATGGGAT	59.78	20
GGCCAACATGATTAGCATCC	60.304	20	TCAGGAATGCTCCATATTCTCA	59.668	22
TCTTGTCAGCGCGTTTAATG	60.014	20	TGTTGGATTTGGGATCCTCT	59.336	20
TTTGGTGGTTTTGCAGATGA	60.088	20	ATTTGCACATCAAACTCCCC	59.797	20
GGGACACCACGTAAGCATTC	60.384	20	GCCTTTCTCGCTCTCCCTAT	59.947	20

GAGGAAAAATGAGCACCGTC	59.676	20	GGTGGGGGTTATCTCCTGAT	60.015	20
GCTAAACTCCAGCGCAAAAC	60.025	20	AACGGATGAGAAAGCGATTG	60.214	20
CTCGCTCGGAAAAGCAATAC	59.982	20	ATTGGGGGTAAATAGACGGG	59.903	20
GGTCACGATTGTTGGGTTTT	59.694	20	CGTGTATATGCTCGAGATGGG	60.496	21
TTTGGGATTCCTCTCGAAAA	59.617	20	TGTGTGATGGAGCTTCTTCTTC	59.478	22
ACCTCGGACGCCTAAAGAAT	60.096	20	TGCCACTCTGCAGGTACAAG	60.049	20
TGACGAGTGCTGTGAATCCT	59.42	20	CCCTTAGCTACCCAAAAGCC	60.089	20
TTGAACTCCGTAGCAACCAA	59.317	20	CACACGCACACACAAAATCA	60.204	20
GCCATGTCTTCCTCTTCGAG	59.95	20	CAACTTTCCGCTTCTCCAAC	59.853	20
CTCACCTGCATCGTCTTTCA	59.984	20	GGGGCCAAGAAAAGAGTAGC	60.208	20
CTGCTCTCCAGAAGCAAACC	60.134	20	AAATGCACAGAATGTGAGCG	59.871	20
CCCATGGAAACTCGGAATAA	59.756	20	ATAAGAAGGGCTGCCGAAAT	60.061	20
CGCAGGATTGTACGGTTGTA	59.609	20	CTGGCAATTCCAGTTGTCCT	60.111	20
TGAAGTTAGGAAATAAGGAGGTG	58.743	25	ATTATCCCAACCCAACCACA	59.91	20
TGCGACAGTTTGTGTGATGA	59.868	20	CTTGCTTATCCCTCGTCCAA	60.206	20
GGATTCGAGTTTTTGAAACCA	59.054	21	ATAAAATGACAGCCCAACGC	59.967	20
TTGGTTGAAAGATGAGGGAGA	59.656	21	ACAGGTTGAGGCCCCTTAGT	59.994	20
TCGATTAACTTGACAAGGTTTGAA	60.037	24	TAACACGCATCCGATGAAAG	59.688	20
GGAGACAGGCGTGTTTTGTT	60.156	20	GCATGGCCCTGTCAATTAGT	59.962	20
TATGAGAGACGAGCTCACGC	59.297	20	GAATTGGGCAATGGAGAAGA	60.014	20
TTGGTTATCATTTTGTCACAGTTTT	58.935	25	CATGGACCCCACATGTCATA	60.048	20
AGGCCCACCATACCACAATA	60.074	20	CGATTTCGAGTTCCTGGGTA	60.066	20
CCCTCGTCACTTGTCTGTCA	59.864	20	GACATTCGTCGTTGAGGTGA	59.682	20
AAGAGCAACAGCGGAAGAAG	59.757	20	TCGAAAAAGGAAAAATAAAAT	59.468	25
AACGCCTTTCCAAACTTTCA	59.724	20	TTTCGAAGATCAATGGACGA	59.2	20
ATTTGTTCAAAATCCGCGAC	59.945	20	GTGACGAGAGGATCACGGTT	60.12	20
AAACTTTGGAATCGACATTGCT	60.007	22	AAAGGAGACTAGTGGCTGCG	59.639	20
GTCGAGCAACAGCAGGTGTA	60.056	20	TTGGCCTAATTTTGTGTGGTT	59.37	21
GGTTTACCCATAGCGCACTC	59.597	20	GATCATACTGAGCTGAATAGTT	59.641	26
TTCTCCTCACAATGCTTCCA	59.369	20	AGGATGGAGTGCTTCAGGTG	60.261	20
ATTAGCTCCTTGCTGCGTGT	60.044	20	AAAAACATGAAGTCGGGCAC	59.978	20
TCCCAAGAATGAAGCCACTC	60.195	20	AACGACGGTGGGTTGTTAAG	59.891	20
AAGCTCAGTAGCGTTCTCGC	59.927	20	TTGTACTTCGCACTTTTCCG	58.964	20
ATATTGGTGGTCACATGGGG	60.317	20	CCACCCACTGCATTCTCTCT	60.261	20
AATGATTCCTCCCCTTCCAT	59.588	20	CGAGGTTTGTACCGTTCAATTT	60.269	22
CCGGTACATTCGGTAGATGG	60.206	20	GGATGGTAGCTCTATGCCGT	59.178	20
TTGAGCATTGATACAGTGGAGA	58.379	22	TCCCTTCTTCTGATGTTACCG	59.181	21
TCTCGATTCAACTCATCGGA	59.322	20	TCACATCTTATAGCGTGCGG	59.856	20
TCATTTCGGAAGGAGCAACT	59.813	20	CCGTTTCAATCGACACAACA	60.552	20
TGTTAATGAAATTTACGCACACA	58.225	23	TGGTGGATTGGAGATGGTTT	60.173	20
TGACAACGGCTTGTATCTGC	59.871	20	ACCGTTGAGACAGTTGGGAG	60.151	20
GGGCTGTACTTCAGAGGCTG	60.012	20	TCGGAATTGATTTGATGCCT	60.414	20
TCACACGCTCAGTGAGGTTC	60.03	20	TGCGTCTGCTAATCTCCCTT	59.978	20
GTTCCCACAAAAACAGGGTG	60.246	20	AATGTTCTTCAAGGTTGGCG	60.11	20
AGCGATTTTAACCTCCCGTT	59.966	20	AGGGGATTCGAAGCTTTTGT	60.074	20
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ATTTGGAAAAGGCCCGTTAG	60.305	20	TTGGCCAGGAACTTAGAAGC	59.452	20
GGGGAAAGATTGCAAATTCA	59.878	20	GTGTTGAGATGCCTCAATCAA	60.118	22
CATCTTCACCGGCTTCTCTC	59.95	20	AGGAGAAGATGCCTTGCTTG	59.574	20
ACATTTCAGCCACCATCTCC	59.934	20	GAGTTTCTGCGAAAAGTGGG	59.853	20
CAGGAAGTTTCACCGGAAGA	60.224	20	TTGCCATTTTCAATGATCCA	59.867	20
GTGGCTTGTGTTTCCTTGGT	60.012	20	TTGGGTGTTTTCAAGAAGCC	60.088	20
GAATTTTTGAGATCGACGCC	59.651	20	TTGTTTTGTAAATGGTGCTTGA	59.562	23
TTGATTCTCGCCATGTACAAA	59.172	21	GGCTCAAGTTGATTGTAGCG	58.529	20
TGAGTAAGCCGGTGCATTTA	59.325	20	GCAGAAATTTGAACCGGGAT	61.184	20
GGCGTGCATGTTTTATCTGA	59.694	20	GAGAGGGAACCATTTGACGA	60.05	20
GTGTATGCTGCCCATGTGTC	59.999	20	TGATCTGTTTCTGGCTTCCA	59.369	20
TTGATTTTGGCAATTCAACG	59.538	20	GCTCTGCTTTGATCAGCTCC	60.249	20

CGCTTCGCCATTGTAATTTT	60.095	20	ATAAAATAATCCGGGTCGGG	59.874	20
ATGCCAACCCACGCTAATAA	60.343	20	TTGAATGTTTCTGCTGACGG	59.84	20
ATGAGAGCGAGCAAGGGTTA	59.978	20	AATGGTAATCCGATTGGCTG	59.784	20
TGATTAAAAACTGAACCGGACA	59.492	22	CGAACCGAATTCCATGTTTT	59.801	20
AGAAATTGGTGGGAATGCAG	59.933	20	AAATAAAGCGGCAACCACTC	59.229	20
CACCGCCTCGTATCTTCATT	60.096	20	AATGCAGCCGACTCTTTCTC	59.579	20
ACCTCGTTTTGATGCCAGTC	60.119	20	TTGCAAGTATTCTCTTCGCA	57.257	20
GGCCTGATCTTACCTAGGGG	59.919	20	AAAATCAAAGGCCCACAATG	59.801	20
CGTGATTCATGCCATATTTGA	59.391	21	AGGGTTTATTTGCTGGCTAGG	59.638	21
GGTTAATCCAACGGCTGAGA	60.074	20	TCCACCTCTCCACCAAATTC	59.903	20
GCTCCTCCTATCCACATCCA	60.034	20	CTGCAAAGCAAACAACAGGA	60.027	20
TGGATGCGTTGATTGAAAGT	59.127	20	TGGCCTTGCACAAACTAAAA	59.344	20
TTTCACCCAAATCACGAACA	59.941	20	TCGATTCAGTTTCCCCACTC	60.05	20
AAGGGGAGTGATTGTGTTCG	59.966	20	TATTTAATGCCGCACCTTCC	59.928	20
TCGGTTGGTGAAGTTGTTGA	60.128	20	CATTTCAAAATCCTGGCTCC	59.505	20
ACACGGATCGGAAATCCATA	60.155	20	CCAGAATGTTGTTCGTCTGC	59.293	20
TCCAACGGAAATCCTTATACTCA	59.851	23	TGAATATATTATCAAATCCAAT	57.918	26
AACCCACTTCCACAGAATGC	59.973	20	GTCGTTATTGCGTTACGGGT	59.889	20
TGCACATGCAAAGCTAAAGG	60.014	20	CTGGATCATGGATGGTAAATCA	59.645	22
CGATCACTGTAAGAACCGCA	59.864	20	CGCCTCTACCAGACATGGTT	60.134	20
AGACCCAAAATCGCACAATC	59.939	20	TGAAATGGGCTGTGAATGAA	60.049	20
GCTGGGATATTTTGCCATGT	59.791	20	TCCATACGCACTGCTCTTTG	60.011	20
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TTGTGGGCTTATTTCCATCC	59.762	20	TCACACACACTCACACGCAT	59.772	20
ATTGTGTTGGTGCTTGATGG	59.42	20	TGTCAACAAAAGCTTAAAACT	60.192	24
TGCCATTTGATGGAGAATCA	60.009	20	GATCATGCTTTTCCTGACCG	60.603	20
AAGCGAATCCAGGTAAGGCT	60.228	20	GAATTTTAGTGTTCGGGCCA	59.938	20
GGCAGCAAGTTAAACAAGGC	59.889	20	TACTGGAGTGGTCTGTCCCC	59.962	20
TCTCTTTCCCCCTCCTTTTG	60.54	20	AAAAAGAGTGGCTTTTGCGA	59.996	20
CTCCCCACTTTCCTTCAACA	60.081	20	TGCCGGTCTGAAAACATACA	60.111	20
GCCATTGCACTTATGCTCCT	60.243	20	GGGCCATTTGCTCTATTTGT	59.046	20
ATGGACTTGCTGAAACACCC	59.973	20	AGCTGCTAGGTTTGCGAATG	60.543	20
ACGTTTTCCACCTTCAAGACA	59.624	21	GGCATATTTGGGGAGAGGTT	60.152	20
AACTCAATGGGGACATCAGG	59.779	20	CCACACTCTCCTCCAAAAGG	59.691	20
TGCAACTGCATGGGATAGTC	59.679	20	TCTAGCCCAAAACTGCCAAT	59.708	20
GGAGGAACTCCATCTCCCTC	60.012	20	TGTCCGAGGTTTCGTCTTCT	59.844	20
GAGACAAAAAGCATTTGCCC	59.691	20	TCCCAATGTGGTCCAATTTA	58.669	20
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GGTGAAAGGCCATGTGAACT	59.973	20	CAAATGTCCCGGTTGAGTCT	59.966	20
TACACCAAATCTTGGCTCCC	59.933	20	GATCATGCAAGAAAACGTGG	59.127	20
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AGACTGTTCAAGGGCAGCAC	60.453	20	TCACAAACCCTTGCTTTTCC	60.088	20
GCACTTTGTCTTGACGCTGA	60.183	20	TGAGGATGAAGTAGCGTTGG	58.874	20
CCTCCGGTGGATACGTTAAA	59.817	20	GGACATATTTTGTGGGACGG	60.051	20
CCAAGCACATCAGCTGAAAA	59.988	20	CCTTGGAGATGGGGAATCTT	60.264	20
TCCTGCTTTTCATCGCTCTT	60.096	20	GTCGCCTCTCTTTCAACGAC	59.997	20
CAGAAGGCTTGGAGATTTGG	59.807	20	CGTATTCAATAGACACATTGCC	59.903	23
CACTAAGTGGTGCTTTCGAGG	59.921	21	CCAATTTTCCCCAACTCAAA	59.772	20
CACGTGGGACTACTGACCCT	60.026	20	GAAGCAAGAAACCGCTTGAG	60.132	20
TCTCATCCCCTGTTTTCACC	59.903	20	GGTCGATTACTCCACCCTCA	59.927	20
TGTCAGCAGACATAGCAGGG	60.008	20	CCAATCTGTCAGCATTTGGA	59.648	20
CCAGTCGAACCGACAAGATT	60.111	20	CGACATAAAATTAAGTCAAAT	59.071	25
CGCTTTTACTCGAACCCAAA	60.236	20	TTTGTTCCACCACTCCATCA	59.935	20
GGCTGTTGTAAAACCCTTGC	59.615	20	AGATGAGTGAGGCTGGAAGC	59.56	20
AAAGCAATCAGTCAAAGGGG	59.17	20	TATTCGGAAACTGGAATGGC	59.901	20
GAGAGCAAGCAACAATCCAA	59.002	20	TCCACCAAATTCAAGCAATG	59.518	20
TGAGTGAGTTGGCGAGAATC	58.96	20	TTTACATCATGTGGTCGCGT	59.995	20

CTATATAGGTCCCCCGTCCC	59.51	20	ATTTTAGGGCAAACCATGCC	61.039	20
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AAGTCCTCCGCCTCTAGCTC	60.117	20	ATCTCGCACGCGATAAAAAT	59.71	20
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TGAGAGGAAAATGGTTTGGG	59.903	20	CAAAGAGTATCGGCTGTGGG	60.647	20
CCTCGATGGTAGACATGCAA	59.673	20	TAGCAGCCACACCTGACATT	59.318	20
GTATGACAAGCAGCAGTGCC	59.476	20	GCAGAAAGATTTTGCAAGGC	59.967	20
CGGATTTAAGGGTTATTACCTGAT	58.81	24	AATAAGTGCTCCGACTCCGT	58.817	20
TTTGGCTTGAACAGCACTTG	60.027	20	TGCAAGTGATGACCCAAAAG	59.691	20
TTTTTGGAGCCGAGAAGAGA	60.066	20	TGTACTGAATGCATCAAAACC	59.867	22
GCGGATTATAATGGGTCGAT	58.741	20	TCCCCATTCCCTCTCTCTCT	60.149	20
GAATGTGGGCGATCTTGACT	60.081	20	CTCTCCACACGCACTAGCAA	60.199	20
TATAAACCCGGAAACGACCA	60.181	20	GTGGGAGAAATGGGGAGAAT	60.133	20
CACTTTCCATCCAAAATGCAC	60.359	21	TGCAATAGGTAGAGAAAAGTT	60.507	26
GCACAAATTTTCAATTCACGTT	59.036	22	TGTTATTATTGGAACAGCACCC	59.786	23
GATGATGGTGTTGCATGCTT	59.533	20	TGTTGACTCCCACATGTTTCA	59.992	21
ACCATTTAATTTCCAAAGGGTT	57.897	22	AGTGGTACACGTCGGGAAAA	60.41	20
ATGCTTACGTGTTTCAGGGC	60.14	20	ACCATCGATCTCTGCTTGCT	59.981	20
ACCTTGCATATGATGGTTAGCA	59.501	22	AAGTCAATTCCGTATGACAAA	57.752	23
GCGCAAGAGCTTTTTCTGAG	60.407	20	AAGCAAAAAGTTCTCCGGCT	60.373	20
CACATTCTTTAAGCCATGGGA	59.946	21	AAAACTGCTGCCTTTTGCAT	59.889	20
AGATCCACGTTAGAACCCCC	60.19	20	CATCTGCACCCATTTCCTTT	59.933	20
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TGCAAATGGTACTAGGGACG	58.649	20	TTTTTGAGTAGGGGGAAGGC	60.423	20
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GTAAAGCCCATTTGAACCCA	59.801	20	TCATTTGCGCTTGTCATTTC	59.816	20
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CCTCAATTTCTGCAGCCTTC	59.955	20	CTCTTTTCCATGGGGTAGCA	60.066	20
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TTGATGGCATCGATGAGGTA	60.033	20	ATGGTCTATGAAATGCCCCA	60.155	20
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TCCGAATTCCGAAAAGAAAA	59.633	20	GGGCAGAGAACGTGCTTTAT	59.34	20
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TCGTCCTCTCCCTTTCCTTT	60.183	20	GCCGACTCACCAACTTTCTC	59.851	20
TGACACTCACGATTTACCGC	59.722	20	TCTGACTCGCTTTGATGTCG	60.136	20
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TGGCAGAGTGGACTTCTCAA	59.545	20	CACTCTCTGTTGCCCAATCT	57.87	20
CAGCCTGGTCCAAATAGCAC	60.657	20	TGTGAAAACGTTGGTTGTGAA	60.035	21
TAGGTTTGGATACCCGTTCG	59.817	20	CTATGGACGCAATCCTTTCC	59.528	20
GGAAGAAATTAAAAACCCCCA	59.195	21	ACCCAGCGAAGTCACAAGAG	60.444	20
CTGGGATGGGAATGAATGAG	60.272	20	CGGGAGAGCAAGTTTTGAAC	59.853	20
TCCTCAAAGCAATAACGCTAA	57.757	21	TGATGTTGATAAAACTGATAA	57.4	25
TGATGTTTCATAATTTGGGCA	58.876	21	TCATCCAATGGTTTGGTTTG	59.222	20
TCAGGCTTACAGCCATCCTC	60.362	20	TGCTTCCAATCAATTTTCCC	59.878	20
TCATCCATTCCCAGTTCTCC	59.862	20	GGTTGGAGGAGACGATGAAA	60.05	20
TCGCAGTAGGTAAAAGGCGT	59.904	20	AGTGCCGATTGAAGTGCTGT	60.865	20
CACAAAAGGATGGGAATTGG	60.162	20	TGAAGTTACGAAATAAGGAGG	57.535	23
ACATTTTCAACGGCACGATT	60.374	20	TGGTTTTTGCACGATAGCAG	59.872	20
TCGCACAGATCGCTTCATAG	60.119	20	GCTACAGCAGCCATTGATGA	59.979	20
CTGCACCCTGCAAAAGTACA	59.904	20	GTCGACAATCAAGTTGCAGG	59.293	20
CCATTGATAGCATGCGTGAC	60.104	20	GATAAATTAATCGCTGGCTGG	58.73	21

CAGGTGGGATTGTTTGCTTT	59.971	20	ATTTTGGAGGGAAAGTGGCA	61.728	20
TTGCTAATCTTCGATGTATCAACC	59.545	24	TAAATGAACCGCAAATTCCC	59.773	20
GCCTTGCATTGTTGAAACTG	59.322	20	TACAAAACCATAACACGCGG	59.486	20
TGACAGATGCACTGATCCAAA	60.256	21	TTTCCTTGCAAGTTCCGTTT	59.724	20
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TGATACCCTGCTTTAATGAAAAA	57.906	23	CTTGCAGCATGGTCAAAGC	60.555	19
CGCAGCCTGAGTTGATTTAG	58.675	20	TCACCACAACCAAACACAAAA	59.889	21
TGTGATGGAACGAGGATTTG	59.496	20	GCTCTCATTGTAATCTCCACCA	59.198	22
TGAAGATACGAATCCTGGGC	60.036	20	GCGGTTATCACCGGATCG	62.397	18
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TCATGTCCTCCAACATCCAA	59.893	20	TTTGGTACTTCATCATTTAAAA	59.446	27
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GGTTTGGGCCTCGTGTAATA	59.823	20	TAGGGCCCTTAGTTCGTGTG	60.125	20
TGAGAGAGAGAAAGATAATCCTA	58.331	27	GGGAATTACTTTGGTTTTGGG	59.575	21
CCGAAATCGGAGTTAGCATT	59.182	20	TGGACTCTGGAAGCTGGAGT	59.986	20
GCATAGGGAGATTTGCGGTA	60.06	20	TGCCATAGATATGCACCGAG	59.67	20
AATTCGGTGTATTTAGCCCC	57.948	20	GAGCTTTGGTGGAAACATCC	59.532	20
TCGGTCAATCCACAACTTCA	60.088	20	CATGAACAGGTCCGCGAATA	61.965	20
TTTGGCCGGACTAGTTATGG	59.953	20	AGCTTCCGCAACAAGTTCTC	59.621	20
TATTCTCTTTGCCACGCCTC	60.352	20	CGGTGTGGATTTTGTGTGAG	60.001	20
GATTGGAAAAGGGTGGGTTT	60.032	20	GAACTGGTTTTTCGATCCCA	59.91	20
CCCACAATCAACTTGCACAT	59.42	20	TCATCGGGTAAGCAACATGA	60.073	20
AGAGATCACTGATTATCTTTTCAA	57.297	27	ATGTCATTGACCAGACCCG	59.329	19
GGCTATTGTGGCATGGAGAT	59.923	20	CTTGTTGCCACGTATCCTCA	59.716	20
GATAAAGGTCGGCGTCAAAG	59.708	20	AATGTAGTTGCAGCACGCAC	59.942	20
TCGAATTGACATCTTCGTGC	59.805	20	GGGACAAACAAAGGAAGTGG	59.425	20
TGTGCCAAACCACTCTTGAC	59.726	20	GGCAACAGTGGGATAATGCT	59.962	20
TTCTCATGCCCCTTCAAATC	60.014	20	GCAACAACGTTAACAGCAGC	59.541	20
ACAAAGACATGGTGGTGGGT	60.135	20	CCTCCAGAACCACAGCAAAT	60.111	20
GTCTCGATTGAATTTTCGCC	59.651	20	ACTCAACCAAGGAAGTGTTGG	59.097	21
CAATGAGACCATGTTGGTGC	59.967	20	GCAAAATTGGTCTAGAGAATT	57.367	25
AACATTGGCTGGATTTCAGG	59.933	20	ACGCATGTGCTTCTCAATCA	60.423	20
TGTGTCCGGTGGTCATCTTA	59.96	20	GACTCCCTTCCTCAACCCTC	60.05	20
CCTTCCACCGCTACTCTCAC	59.867	20	GAATGCTTTTGCTGGGGAG	60.729	19
TCCCCAGTCAATTTCACACA	59.935	20	TTTCGTCAAATAATCCAAGCA	59.603	22
CAGCGTTTTTGAGTCCATCA	59.84	20	GTGGCGTCTGGCTGATAAAT	60.103	20
ACGGTGGTGGAAAAGATGAC	59.827	20	TCGATTTGGTCTATTTCGGC	60.038	20
TGCATTGAAATTGACAGGGA	60.049	20	GGCATGTGCTGGCTATCTTT	60.243	20
TTCCTAGAAATGCTCTCTTTCTGA	58.845	24	ATAAGGAGGGTCCCTTGCAT	59.789	20
TGCTAACATACGCATGAGGC	59.862	20	CCACCAAAAATGATTGCAGA	59.518	20
TTGACAGCTGTACCTGCTTGA	59.649	21	CAGGAACAAATGCCATTGAG	59.123	20
CGACTTGCGCTAGAATCGTT	60.543	20	CCAGAGAAGGGCTGAAAGAA	59.545	20
CCTCCCCCATGATTTTCTTT	60.124	20	ATCGGTTATTACCGGATCGC	61.031	20
TGGAAAGTCCTGGACCTATGTT	59.864	22	TCCATTGATTGCCACTTTCA	60.049	20
ATTCCTTGTCCACTGCTTGC	60.263	20	ATGGTGGATGAGTAGGCGAG	60.096	20
TTTCCATCAGCATCTTGCAC	59.805	20	GGTCACCCTAATGGCAGAAA	59.933	20
CCCATATTCATTAACGCTTGC	59.468	21	CGGAAATTTTCAACCAATTCA	59.797	21
GCCCCTGGTTTTGGTCTATT	60.187	20	GTTTCGTATCGGACGCCTAA	60.096	20
CATCTGCTGCTTTGTTTGGA	59.988	20	ACCCCATTTTGCTGTTCATC	59.797	20
TTTTAATCGCTTCCGCATTT	59.696	20	ATTGGATTTGGTGTCGAAGC	59.939	20
CCACCTGAGGGAGTTGATGT	59.962	20	TCAAAATGCCAGTCTTCACG	59.84	20
TGACAGCAAGCCAGATTGTC	59.992	20	GTCCCATTTCCACTTCCATC	59.192	20
GAATCAAGCTTAGGCCCACA	60.214	20	GAATTAGGGTGGGCGAAAAT	60.15	20
CCTGCAGATGACTGGCTACA	60.008	20	CACTGAATGAGGGGAAGCAT	60.073	20
TCATTTCAAGCAAAATCGCA	60.334	20	GTTAGTGTTTTGACATGATTAC	58.688	27
GCATTCTTAAAATCCTCGGG	58.647	20	CCGGATATTGGGAGAAATTG	59.227	20

GCTCAGGCTTACATGGGTGT	60.142	20	CTTTCTCGGCAATACAAGCA	59.062	20
AGCTACACCTGAGAGTGCCC	59.48	20	TGAAGTTAGGAAATAAGGAGG	57.525	24
CTTATGGTGGTATGGTGTAGAGG	57.59	23	CAAGTTCGAGTCCGAAGACC	59.844	20
GCGGGTCAAGTTGAGGAATA	60.074	20	AAGTTGAGGAAGCCGAACAA	59.853	20
TTTCCCAGAATTTGCCTTCA	60.555	20	GTGTTTCTGCGGTGGAGAAT	60.119	20
AGGTTAGTGGTGCACGGTTC	60.035	20	ACGTCCAGGGTTAGAGTCCC	60.371	20
TGGTGGTGAATAGGGGACAT	60.05	20	CCCTGTCCCAACAGTCATTT	59.82	20
TGGTATGAGTTGGCTTTTTGG	59.982	21	TTAGCACAGTGGTTTGCTTTG	59.024	21
CTTTGGTTTTGGCAGGTCTC	59.711	20	CCGAAGAAATGGATCCTCAA	60.006	20
ATGCGAAACGAGAATAACCG	60.096	20	AACAGTATGAGCAGCCAGCA	59.621	20
TCTCTCAGAACCACGACACG	60.022	20	AAAGGTGTGAGAGGGTGGTG	60.002	20
ACCACAACCCATCACATTCC	60.497	20	GGAAGGGAGCAAAGGTGTTT	60.476	20
TAACGATGGACTAGGGGCTG	60.088	20	ACCCTAATTGTTTCGGGCTT	59.835	20
AAGACAAAACTCGCAATGGG	60.11	20	TCTAATCCTCTCCCCTGTCG	59.234	20
TCTTGTTCCAAGTCCCTTCG	60.224	20	GGGGTTGAGTCCTTCCATTT	60.169	20
TTGCTTTGGTCATACAAACATT	57.253	22	CCACATCAAGAATCGGTGAA	59.496	20
TTGGGTATTGTTAGCTCGGG	59.953	20	ATTGTGCGTGCATTTTTACG	59.631	20
TGGAACCTATTTCCTCCACG	59.926	20	GCATGAAGTCGGGTATTGCT	60.103	20
AGAGTTAGGCGGAGGGTCAT	60.096	20	ACACGGGCTTTTGAATTTTG	59.975	20
GCTTTGTGCCTGCATTATGA	59.839	20	ACTAAGTTGGTTGGGACGGA	59.449	20
GGGACGTGGTTAGCAGATGT	59.997	20	TCCCACATCATCCCTTCATT	60.135	20
ACAGCTGGCCTTGGATGATA	60.624	20	AAAGCAGCAAAAACCCACAG	60.284	20
CACCTGCAAGAGAGGGAAAA	60.366	20	GCACTGAAGTGGTGAGTGGA	59.872	20
AATAGGTCGGGTTTTCAGCC	60.32	20	TCAAATTTAACAGGCCGACAT	59.465	21
AGTCAGTGCTCACCGGATCT	59.866	20	TGGCTCGAGGACTCATCTCT	60.096	20
TCCATTTATCGGAGTTACGG	57.579	20	CATTGTCCGGGACTTTGTCT	59.966	20
GGTTTATTGGTGCTGGTGCT	60	20	GATTGTGCAGCAAATTCCAA	59.67	20
GAATTTAGTTTGGGCTGCCA	60.074	20	AAAGCTAACCTCCCCACCTC	59.576	20
GAATAAGCCTCCACACCCCT	60.328	20	AATCTCTATCGGCATGTGGC	60.066	20
TTGAACCAAACACCCCCTAA	60.198	20	GGAAGACAAATATGGGACGG	59.244	20
GCCATGTGGAGGTTGATTTT	59.797	20	TTCCATGCATTTTTCATTATGTG	59.725	23
TTGGTGAAGATTCGATTCCC	59.871	20	TCATTGGATAACAACCGCAA	59.93	20
TTTACTCCGCCACGGTTAAG	60.124	20	GGACGGCCTTTCTTCTTTCT	59.827	20
ACAGGTGAAATGTCCAAGCC	59.973	20	CACTGCGAAGCTTGAATCTG	59.74	20
GAAAATGTCGTGAATGCCAA	59.523	20	TCTCCAGAGCCTGCCTCTAC	59.703	20
TGTGTTGATGCAAGTTTGGAC	59.606	21	TTCTACTGCCTGGAAATGCC	60.214	20
ACGATTTACGCCGAGTTAGG	59.248	20	CCCTTGGTGCTGTTATGACC	60.375	20
AAGCCTCCCAAGTCTCCAAT	60.074	20	CAGTGATCGCAGGGGTTATT	59.955	20
CCCCGAAAAAGTAATGGTGA	59.795	20	ATTTGGGTAGAGGATGTGCG	59.955	20
TACCCCTGCCATTAAACCAA	60.181	20	GGTCAAAACATTGACCATATTT	59.949	26
TTGGGGTGGAGAGAAGTGAG	60.229	20	GAGGTGTGGAAGGCGAATTA	60.074	20
GTGTTGGACTTGGGTCATCC	60.223	20	ACATGCCTCTTCCACAACCT	59.579	20
TCAGTCTGCACAGCTGACAA	59.293	20	TCTGGAAGAGCCGTTGTTTT	59.853	20
ACGATGGCTTTGCTGTTCTT	59.882	20	GAATTCATGGGCGTTTCTTG	60.448	20
AGGGCGTGCCTAATGGTATT	60.711	20	TAGCTGTTTGTGCGATGACC	59.871	20
ATGGGCCTGCCTATTAGTGA	59.551	20	TAGAAGGAGCTGATGGCGTT	59.978	20
TTTCTGGGGAGTTCATGTCC	59.903	20	TGACGCCATTTCATCATACC	59.355	20
GGGGTTATCATGGGATCAAG	59.055	20	AAATCATTCCCGTCATGGAA	60.133	20
GGCCAGGAGATGAGTCAGAA	60.349	20	CCCGCATTTTGTTATGCTTC	60.456	20
CCAAGATCAATGGTTCCTAAGTG	59.879	23	CATCGATTAATGGAGGCACA	59.499	20
GAATGGCTTCGAGCTTACCA	60.352	20	CTTTATGACAGGCGCACAAA	59.872	20
GATGAGCCGAGGAGCAATAC	59.803	20	TCCGCACCTTGGTTTAAAAG	60.103	20
TCCAATTCCGATACCTGACC	59.75	20	GCGACCTCACAATCATAGCA	59.83	20
GGCTGCAAACATTTGAGGAT	60.081	20	GCAGACATAAAAAGGGCTGG	59.708	20
TTTATGAAAAATGGCCCCAA	60.123	20	TCTCGCAGAAGGTGGATCAT	60.769	20
GTTCCGATACGTCTGAAGGC	59.7	20	TTAGGACAGATTTGCCCCTG	60.066	20
GGTAGGAACTGCATGACCAAA	59.985	21	AAAGCCTCCAAAGCATGAAA	59.823	20
CAGGATAATCCAGAATCAACACA	58.962	23	ATCTTTCACTCAGCATGCCA	59.399	20

AATGTGCATGGTTGAAGCAA	60.119	20	GGCCATCGCTAGGAAGTTTA	59.32	20
TTTCAACATTCAGCCGATCA	60.197	20	AAACAAGAGCCGAAAAGGGT	60.11	20
TTTCTTCCACGCCTTTCAAT	59.685	20	CGTTGTCAATGGGATTTTCC	60.17	20
CAGGACAAAGCAGATAGGGG	59.688	20	ACCATATTTAAGGGTTATCACC	57.552	24
GGAAGGAACAAGTGTGGGAA	59.943	20	GAGGCTGGAGCAAGAGAAGA	59.827	20
TGAGCACCTCCATTTCTTCC	60.195	20	TTGGCTTCCATTTCTGTTCC	60.051	20
TTTGAGTTGTGATGTTTGCATTT	59.549	23	CAAAAGGTTGGGGAGTTCAA	59.942	20
GCTAGAGCCAAGGACATGAAA	59.467	21	CAAAAGTAGTGGGGGCAATG	60.357	20
TATGAGATCTCGCCATGACA	57.71	20	GGGAACACCCTTGCTTGAG	60.64	19
CAAACAAAAGTCACGGCAAA	59.746	20	TTATCCCTTCGCTTTCTCCA	59.778	20
GCTAAATATGAGTTTCCTCTTCCA	58.073	24	TTGCACATACACGCAGCATA	59.892	20
TCAATCAAATCAAGGGGAGC	60.014	20	CACGCAACTGAAAAACCAAA	59.746	20
GCCATCTATCTTGTTCGTGACA	60.14	22	AGTGTAGTTCCGGGGGAGTT	59.856	20
TAATGCCCACATGAGGAATG	59.35	20	GTTTTTGGGCAGTGATTGCT	60.118	20
TATCCGAGTTTTGCCAGGTC	60.074	20	GACGATGCTCTGCACTCAAA	60.144	20
TCCGCAGAAACATATGACCA	60.073	20	TTTACAATGCAATCGCCTCA	60.215	20
TTCCAGTCTTCTGCCAATCA	59.369	20	AGAGAGAAAAGAATCCCCGC	59.789	20
TGCTTTCGTTCAGGACTGTG	60.025	20	CTGGTTCCAGCTCCAATCTC	59.803	20
GCAGCATAAGGCATAGGGAC	59.696	20	CCACGATAAATGCTTCGGTT	59.96	20
GCAAAATCGGCTAAACTATGG	58.775	21	CAGGTTTATCAACACCATTTAT	58.008	24
TACTGGTCAGAATCACGGCA	60.263	20	TCAAGGGCGTTTTTATATTTGA	58.675	22
GTTTGATGACGTGGTTCGTG	60.008	20	ATCGTTTTACCTTTTGGCGA	59.586	20
GTACGCGTTATTTGCCAACC	60.384	20	AAGTACATTGAACGCCCTGC	60.14	20
TGGAAGTTCTTGAGGTGCAA	59.415	20	TCCGGCTCTTTAGTAACCTCAG	59.907	22
CGGTTTCCTGTTTTCCTCTG	59.705	20	CACTTCAAACGTCGTCCAAA	59.734	20
CTGTCTCCAGTGTCTTGCCA	60.022	20	CGAAAATGCTCGGTTGAAAT	60.074	20
GGCGTCCTCATTTATGATCG	60.435	20	GAAAGCTCCAACCACTCTGC	59.997	20
CCATACGTTGGTAATGCAACC	60.124	21	GGAATGTGGAGTTTGGTGGT	59.679	20
TCTGCAAGTACCCCCAAATC	59.933	20	TGGGTGCTGGATACTGACTG	59.701	20
CCACTGCATCACAACCATTC	59.967	20	GGGCTCTTCATCACTACCACA	60.126	21
AAGGTCGTACTAGCCAGCCA	59.898	20	GCTGCAGCAATGAATCTGAA	60.104	20
TTGCCTTCATATGTGGGGTT	60.192	20	TTTTTCCGATTTGTGTTGGTT	59.348	21
TGATGGCCCATGATTAAAGA	58.917	20	GCCCTCCATCAATACAGCAT	59.923	20
AGCTATTCCCCAAACCAACC	60.187	20	TCGAACCAAATGCAAATGAA	60.051	20
AATATGTGCTCTCATTTGATTACA	57.519	26	CCTCGCTCTAATTTGGCTTG	59.975	20
AAATTCGTTCGACTGTTGGA	58.201	20	GCACCCTGCTTAAACCAGAC	59.74	20
TGATGATTTTTGGCCTTTGTC	59.93	21	CAGTAGCCGATGAATGCAGA	59.972	20
TGGCGAAGAACTTCAATGACT	59.867	21	GAGAGGCATTATCCAGGTCA	57.676	20
TTACAATTACGAACGCGTGG	59.625	20	CCAAAATCCCTTCTTTGTCTTC	59.992	23
CATTCAGTTCATCATTTTCATGG	59.329	23	TTTTCAATTCCTCGATAGCAAG	60.207	23
TTGACCGTCCAACAATTCAA	59.941	20	TTCGGTATGTTGACGATGGA	59.924	20
AGCACAAGAGGACGTATGGG	60.134	20	TGTAAACAGTTCTTGGGTGGC	60.023	21
CCACGACCAATTCTTACAGC	58.228	20	GGCATCCACAACGATTAGAAA	59.952	21
ATTCTCTCCAGCCCCTTCAT	60.037	20	TCGTAGCCAAGAAAGCGAAT	59.982	20
CCGGTTTATGGATGAGGAGA	59.887	20	GGTGGTAGTGGTGCAGACAA	59.597	20
ACGAACACCACGACAACAAA	60.049	20	AAGAATGCAGGGCCTTAGGT	60.096	20
TCATCATGTGATGCAGACCA	59.61	20	CACATCATCGCATCGATTTC	60.041	20
TGCCTGTATGAAAAAGCATCA	59.315	21	TCTTTACCGCATACACACTCTA	60.121	25
TGAATGGAACACACACACCA	59.376	20	GACTGCTCTTCAGGCTCTGG	60.284	20
TTCGGTAGGCCTGAATTGAC	60.074	20	TTAGACCTCACACACCGACC	58.566	20
TTTGGGTGAAGGGATTCTTG	59.903	20	GCTGCTACCTTTCAGTTGGTG	59.928	21
AGGCATTCGAAAAGCTCATT	58.93	20	TTTCGGCATTCGTAAGGTCT	59.708	20
TCCTCTGGTTTCTGTTTGCC	60.232	20	GCTTTTGCTTAGAGGCGGAT	60.84	20
CATTGGCTGAGGTGGCTAAT	60.096	20	TGGACGCCCTAGATTGTTTC	60.074	20
AGGGAATGATGGAATGGTGA	60.135	20	GTGGTTGGAGTGGGAGACAT	59.817	20
TTTGCAAAACAAAGCACGAT	59.349	20	CAAAACCACAAAACTGTGACG	59.13	21
AAGAATCGCCGTGAAGAGAA	59.955	20	CCGCATCCACTAAACCCTAA	59.953	20
AAAACAAGTCATCCATGTCCC	58.755	21	GGGCTTCTTTTCTGGCTTTT	59.835	20

TCTTGCCTCCAAATTCAACC	60.051	20	AAGTCCACCACCCTTGTGAC	59.859	20
CTTACCTGCGTGTTTTACAACTG	58.932	23	TGCTATTCATCTCATTGCCA	57.8	20
GCCACAGTGGAAGAACCAAT	59.973	20	GCACCCCTTGTTTACTTGGA	59.971	20
GGCCATTGGGCTTATCCTA	59.87	19	TGACAGTGGAGGGAGAGAGA	58.446	20
TCGTCAGTAAACCCGAATGA	59.123	20	CCCTATGTCAAAAGTGTGGGA	59.838	21
GCCTCGCATGCTATTGCTA	60.096	19	GCATTGGCTTTGCTTACTCC	59.851	20
GCTTGAGTGTGGCACATTTAGT	59.313	22	AGGCCCAGACTTCGACATAG	59.308	20
TCCTACCAGCCAAAACATCC	59.933	20	GGGATGGTGCTACCTTTTGA	59.933	20
TGTCCTGAGAGGCAGGAAAT	59.803	20	CAGGATCACATGTCCCAACA	60.378	20
TGGAATCGTTTGTCCACTTT	58.048	20	TCGACTGCCTTCAAGTAAAGC	59.646	21
CTTTGCTGTTCGTGGTTCAA	59.881	20	TTGATCGCTTATGCATTCCTT	59.696	21
CCATAGAAAACGGCCAGAAA	60.067	20	ATGTTCCTGTGGATGGTGGT	60.096	20
ATTTTTAGCCATGGTCCCAC	58.765	20	GCTGTGTTTTGTGGCATGTT	59.621	20
CTTCGTCTTCTCCAACTCGC	60.134	20	TTCTGCAACACCAGCTTCTC	59.165	20
TTCACTGAATTTGCCTGAAAAA	59.736	22	GCTCGGTTTCATTGCCATAC	60.478	20
GACCACTAATCCAACCCCCT	60.052	20	GAATGCTCTCCTTGCACACA	59.992	20
GTTCGTTGCGTCTGTCTTGA	60.032	20	TTGGGGGACCATTTTGTTTA	60.024	20
TCGCAAAAGTGATCTTCGTG	59.988	20	TCTTCCACATTTGAGGGGAG	60.042	20
ATGCGTGGGCGATATTATGT	60.203	20	GAAAGTGCAACGGAACTGGT	60.156	20
TCAACACCCATCAAGATGCT	59.09	20	TTTCCCTGTTTTCAGGATGC	60.051	20
TTCCACAATTGGATGCTTCA	60.049	20	TTTTATCAATTCGGGGCTTG	59.901	20
GACCCAAACGGAGCATCTAA	60.074	20	AGGTGGGAGGTCAATTTGTG	59.82	20
TCCAGAAGCAGTGAAGCACA	60.745	20	CCCTGAACAGGTATGGATAAG	59.72	22
TTTTCCACAGAAATGTTGGC	58.599	20	TTTTATGCACAAGTGGCAGC	59.879	20
TCGTCTTCATGCTCACTTCG	60.136	20	GGATCAAACCCAATCCACAG	60.173	20
AATGATGAGCCATGCAACAG	59.679	20	GTGGACGTCCCAGATTGTTT	59.827	20
TGTCACGGTCAGCACTTGTT	60.357	20	GCCCAAACTACCGAATCAAA	59.938	20
TCGGGGGAATAATAAGGGAA	60.45	20	ACGCGTATGCATTGGTCATA	59.983	20
TGGGTTTAGGGATTAGCTGC	59.182	20	GCCTGAAAATCCATTTAGCG	59.682	20
GATCCAATAAACAGCCCCAA	59.762	20	TATTAACACAAATCCGGGGC	59.66	20
GTGACGAGTTTGCGTGAGAA	60.032	20	TGAGTGGCAGGGCAGATTAT	60.624	20
ACCCAAACACCCATTCAAAC	59.55	20	AAGTAAAGGAAGGCCGAAGG	59.72	20
TCCTTGAATCAGCCACACAA	60.24	20	CAGCACTGCACTTCTGAGAGTT	59.856	22
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GAACCTCCTCGTTAGCTCCC	60.212	20	GTTTGGGAGTATGGTTGGAAA	58.798	21
TTATGCCCTCCATTCTCTGC	60.177	20	TTTGTGGGAAAAGTTGGGAG	59.942	20
TTCTTTTATGGGCCATGAGG	59.894	20	TTCGGATTCGATGCCTTATT	59.507	20
CATTTTGCACCCCTCAATTT	59.801	20	CCGAAAATCCCAAAGATGAA	59.872	20
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TGCTTCATGAACCGACAAAA	60.234	20	AAAAGGGAATGAAGCAGCAA	59.823	20
GGAACTGAGCTTTGAGGGTG	59.844	20	CCTCTGCAAAATCCAGGAAA	60.184	20
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AACAAGGTTCCGTTCTGCAC	60.156	20	CACCTCGAGATGGTAGGCAT	60.096	20
ATGCACACCAACTGCCATAA	59.995	20	TCAGCTCTTCTGCACGTCTC	59.446	20
TGTCAAGTAACCATTCAGGGC	59.985	21	CAGGGCAGATATATTGGGGA	59.739	20
ACCACCTGCCCAACTATCTG	59.989	20	GGAGGTGGATGGAGTGTCAG	60.527	20
CAACAAGGTACTCGAAGAACACA	59.337	23	GTTGTGCCTAAATTCCGAGG	59.569	20
AGCCTGGTTCCAAATTTTCC	60.299	20	TTTTCCCCACCAACAATCAT	60.029	20
CCTCATTGCTGTCGCTATCA	59.972	20	ATGTGCAGCTTTATGGGAGC	60.243	20
ACAATCGGAGTGCCATTTTC	59.939	20	CATCTGAACTTTGCCAGTGC	59.445	20
ACAGGAACAAGCCCATCAAC	59.973	20	TGTGGCTGTACTCCGTTATGA	59.209	21
CAGCCCTGAGTGGTTTTTCT	59.328	20	GATGCACTTAGTGGTGCCAG	59.318	20
GAGAGGGGTGTTTGGTGCTA	60.111	20	TGATTTTGGGAGTAATGGGG	59.617	20
TTTAGACAGTTGCACCCAGC	58.926	20	CAAGAACCGGGGATGACTAA	59.926	20
GAAGTGCTTAAAACCCTGCG	59.883	20	TGCATGTGTATAATAACAACC	59.808	23
CGGGAGAAATCTCGTTGGT	60.058	19	TATTGACCCACTTGTCTCCG	58.569	20
GAGGAGTAGAAGTCGGCGTG	60.012	20	GGTTTTGGGTTTAATGGGCT	60.055	20
ATGACGCCATGGGTGTATCT	60.226	20	CCAATTCCACCCCTCTTTTT	60.159	20

GCAGTGGAAGAACGAATATGG	59.583	21	GGGTCCTGTTGATCTTTTGCT	60.49	21
TGAAGTTAGGAAATAAGGAGGTG	58.743	25	CCTGTTTGGTACATGTCGGA	59.415	20
GTGGAAGCCCATCTCCATAA	59.894	20	ATAGCGTCCACTCCACCAAC	59.997	20
GCCATGATGCCTGTGAAGTA	59.679	20	GGAAAATCTATTGCAGGTGCT	58.341	21
GGAATTTAGACGATTGATCCG	58.521	21	TTTTCCTTCTCTTTGCAGCC	59.569	20
TTCCACCAGATACGGAGACC	59.927	20	TCCGTCATCAGAAACCACAA	60.088	20
ACGGATTTATTGGTTATTACCTGA	58.008	24	TGTCGTCTGACATTGCCTACA	60.317	21
ACGACACATACGAATTGCCA	59.995	20	ATTCTCAACACCCACAAGCC	59.973	20
GTGGTCCATTGCTCAATCCT	59.934	20	CCACCATTGCTAATCGTCCT	59.955	20
TGAAATTTGGCTTGCATTTG	59.679	20	TGCAGTTTTAGGCATATCGAA	58.458	21
TTTGAAATGGCAAACATCAA	57.606	20	ATGCATGCAGCAAGTTGTTC	59.878	20
ATGCAAAAATTGGTCCAACG	60.732	20	AAAGGTTTTCAATGCAAGGG	59.064	20
AAGAAGGGGGATTGTTGCTT	59.94	20	AGAACAAACGACTTCCACCAA	59.624	21
AGGTCTTTCGAACCCCCTTA	59.934	20	CTCTTTGATTCCAACCCCAA	59.903	20
TGGGAGCTTTATGATTTGGC	60.038	20	GGCTGGTAACCCATCAAAGA	59.933	20
ATGAAATGCATCAAATGCGA	60.043	20	TGTGTGTGGCCACTAAAATGA	60.019	21
CCCTTTTTCTCAAGGGAGGA	60.54	20	ACACATCGTCCCTTAATCGC	59.962	20
GATCAGCTTGGCGAATTCAT	60.185	20	CCTACAATGCCACACCTCCT	59.989	20
CATGTTCATGGCTATCATTTGC	60.351	22	TTGTGGTGTGGAAGATCTGG	59.52	20
CAGGAGAATTTGGATTCGGA	60.006	20	TCCCTTTTGTCCCTTTCGTA	59.541	20
GTGACCGGTGGTTGTCTTCT	60.009	20	CCTGGCAATTCCCCTTTAAT	60.143	20
CTAAACTCCGCCAACTGCTC	60.015	20	TACCTTGAGGTTGAGGGTGG	59.959	20
CTGACATGGAAAGCACCCTT	60.111	20	TTTGGAAAAAGGAATCGTGG	59.91	20
AAGAATACCACCGCCAACCT	60.743	20	TCTTGCAAAAAGCGCTACAA	59.764	20
TTGAGGGTATCACCAATCTGC	59.947	21	ATTGCGCTCAAAGATATGGC	60.203	20
TTATGGAAACCACCCGAAGA	60.301	20	CCAAAATTACATGGTTCGGTG	60.096	21
CTGTTGCTTGGTGCAAGAGA	60.175	20	TCTGGTAACCGAATTGCCTC	60.074	20
GATTACGTCGATCCAACGGT	59.82	20	TCAGGTTTATCAACATCATTTAT	60.138	27
TTTCAATTCCTCCTGGCTTG	60.184	20	GCCCATTTGCAGAATCCTAA	60.038	20
CTTTTCCATTTCCGATCCAA	59.872	20	GAAGGAAAAGGGCCATCTGT	60.443	20
TGCACGTAGGCATGTTCAAT	60.142	20	TGAAGTTAGGAAATAAGGAGG	58.743	25
AGATGTGCATTCAGAGGGTGT	59.594	21	TGAAGTGCTGACAAGGCATC	59.992	20
CATCGTTAATGTTGATTTTTATTCG	58.943	25	CCACTTTTTGTTTTGGAGCA	58.794	20
AGCCCTCCACGATAACATTG	59.955	20	AAATGGGTCAATTTTGGCAG	59.801	20
ATGACATGGCCATAACGAGG	60.744	20	ATTGGTCCAGCAGGTTTGTC	59.973	20
CAGCCATTTCGGACTAAGGA	60.206	20	TGCATCTCCTCCACCTATCC	60.034	20
GGTGGTGGTGTTGAATAGGG	60.088	20	AGCACAGCATGTGGAGTGAA	60.473	20
TCACGTATGGATAAGGCTAAAGA	57.995	23	TTGTTGCGCAATGAAGACTC	59.995	20
GTTCGATGTCGGGTTCGTAT	59.82	20	CATCATTCCCCTCCTCTTGA	60.003	20
CTGTGTGCCTCCTCCTTTGT	60.298	20	ACATCCGTCCATTTCCAAGA	60.317	20
AGCCAATTGCCAACCAATAA	60.323	20	TTGGGATCTTGCATGAACAA	60.049	20
TCGATTCTTGTCATCCATGC	59.61	20	TTTCAATCACACCATCCCAA	59.75	20
CGGTCAGTTACACTCCGTGA	59.745	20	GGTCAAATTGGGGATGAATG	59.991	20
TTTCTGATGGGGTTGAGGAG	60.042	20	CAACCCTTGATGTGGAGCTT	60.111	20
TCTGAATGCCTGTTGGTTCC	61.046	20	CCGCAAAAATCCTTCACAAT	59.938	20
TCAGAAACCACTCCCTCACC	60.088	20	CCCTCTGGAGCTCTTCTTCA	59.673	20
TTGAGAGCAACCTACCTGGG	60.246	20	TGCCTTTCCATGAACAAAAA	59.133	20
CACATTTCCATTTCCATTGGT	59.537	21	CAATATTGGGCAGAGGGAGA	60.029	20
CACGCTTGCTAGACAACGAC	59.664	20	ATCCCGGACTGAGTGAATGA	60.475	20
AAGAGAGGTCAAAGCTGCCA	60.134	20	GAAGAACGAGGTGGGAGAAA	59.259	20
CATCTCCGGAAAATGGACTG	60.452	20	GGCGTGACACTTTTTCGATT	60.118	20
GGCGGTAGGTAGTTGTCGTC	59.621	20	ATTATCATTTCCACCGCCAC	59.651	20
TACACCCAATTAACCCACCC	59.406	20	TATAAATTTTGGCGCCGTTG	60.797	20
TTTGCTGAGCATGTCATGTG	59.409	20	CCCAAACATTTATTCCCCATT	59.774	21
TGAGCAAAGAAGCCTCGAAT	60.096	20	CGAACAAAGCACACATGAGG	60.301	20
CAGAGAAGCAGACATGAGCG	59.88	20	TGGCACAACAAAAGTAGAGAG	59.562	22
AGCTTCATCTCTGCGTCCAT	59.981	20	GTTCAAATTCTCCCTTCCCC	59.744	20
CATCCAGGTCACCCTTTTGT	59.82	20	GGATGTTGATCGAATGGAGG	60.281	20

AGGCCTCGATAAATCCGTCT	60.06	20	TCCGGAGAGAAAAAGACACG	60.366	20
CTCAGCAATTGCCAAAGACA	59.988	20	GCGCTATGTACACGGTGTTG	60.203	20
TCCCATTCAGGCTTGAGGTA	60.594	20	TTTGCTTTGGGGTTGTGTTT	60.378	20
TTTAATCGGGATCCGGGC	62.966	18	CGCAAAGAGAGAAATCGAGG	60.088	20
AGAGGGCTCCATGGAAATG	60.019	19	TCATACTCTGGCTGCTCGAA	59.697	20
ACCTCTGCCCACTGGATATG	59.95	20	TTTGTGCATGCTTCAGTCTTG	60.042	21
TGGTTGGTTGCTGTCACTGT	60.203	20	AGAAGCCCATATGGCATGAG	60.059	20
CCAACTGCTTCTGGGGTAGA	60.246	20	TAGTGCATCCTGCCTGTTTG	59.864	20
TCCGACCGGTTTTTAAATCA	60.294	20	AGTGAATCTTGGTGGCTTCAA	59.726	21
TCAACTAGTGCTGCGAATGC	60.165	20	AGTGAAGGGAAATTCCAGGG	60.298	20
CCCCAGTCCCTGCATAGATA	59.91	20	AATCACAGAATAAACGCCCG	59.96	20
AAGCAGCCTCACACAAGTCA	59.622	20	CACCTAGCAGCAGTGTGGAA	60.049	20
CCAACGCATCCATATCATCA	60.307	20	GCAGTTGTCGGAATGGAGAT	60.081	20
GAATCTGTTGCGTCGTCTGA	59.992	20	CAGTTGGCTTGTAACTGGCA	59.904	20
CAATTCGAAGCCCAAATCAT	59.901	20	ACATATGGTGGTATGGTGCG	59.152	20
CACCACATTTAGTGGTTATCATTT	59.605	25	GCTTGATAGTGGGCATGTTG	59.152	20
ATCGAACGTAGGATTGGCAG	60.096	20	GCTGCATCCCGATATGGTAG	60.457	20
AGCACGGTCCCTTGTACATT	59.478	20	CTGGGGTTTGAGAGAAGCTG	59.982	20
AATGAAACGGAATCCAGTCG	59.933	20	AACTAACGTCCTCCCGTTCC	60.361	20
CTTCGCTTTTGGCTATCTCG	60.11	20	TTCGACTTTTCAAGTTATTTTTC	59.74	26
TGCACTTGCAAATTTAAGCTG	59.155	21	GTTCGCTTCACCGGATACAT	59.962	20
CAGAGAGAAAATCGGTGGGA	60.187	20	GGATGTTTACTATGGGGTGTTT	59.531	23
ACGACTCCATGTTCCGACA	60.105	19	AGCAACCTCAAACCACAAGG	60.149	20
TTGGAGACCCTTCTTTGCTG	60.366	20	TGCTGGATTCATAACACGGA	60.073	20
CCAGACTTTTGGTCTCAATATATC	59.335	25	GGTCAGGCTACCCAACAGAG	59.721	20
CAATTTGCGCTCTTGTTCTG	59.609	20	TGCCATCAAATGCAAGTTTC	59.67	20
GAAGTACCAACCGGTTCCCT	60.225	20	TATTGTTGCTGCTGATCCCC	61.003	20
CAATGTGAAGGGAACTGCAA	59.691	20	CCCATCAGACCAGTTGACAC	58.94	20
TTTTGGCATCAGCAACAGAA	60.379	20	GGAAACCCTGAAGAAACGAA	59.146	20
AAATTCCCTCCACCGTCTCT	59.935	20	ATTCAATCTCTGGGCTGTGG	60.073	20
GGATCTTCGAGGAGTGGTGA	60.199	20	ACCTCCACCGTCAATACCAG	59.844	20
CTATGCAATGCCACCACAAC	59.995	20	TTCTCTCACATCCATCGCAG	59.942	20
CTTCCGCTTTCAATCTTTCG	59.953	20	CGATACCAGCAGAACCCATT	59.955	20
CTTCGAGTTTGAGAGGTCGC	60.134	20	TCCCATTTCCTCCAAATTCA	60.244	20
TGTGTTCAGACCGAGTCAGC	60.03	20	GTCAGTGGCAACACTAGGCA	59.905	20
TATGATGCTGGACAAGTCGG	59.673	20	ATTGAGCTCATGTCAGCTGGT	59.889	21
TTAAGCCTGTAATGGGGCAC	59.96	20	AGCCTGCTCAACCTCAATTC	59.434	20
TCTTTGATTTGGCTGCTTTGT	59.875	21	TCAAACTGGTGTGTGTGGCT	60.203	20
TCTGGGATTGGGCTTTATCA	60.405	20	TGCATGTGGTGATTGGTAGAC	59.435	21
TGTTGGTGTGATGGTTTTGG	60.255	20	TCTGCTTTTTAGAGAGAGGGA	58.924	23
TCTGACAAGCAACAAATGGC	59.847	20	CTTCTCATCCTGCGAACTCC	59.95	20
GGAGAAAGCAAAGAGCGAAA	59.708	20	AGCAAAGCAAACAAGAACGC	60.564	20
TTGCAGCAAATGGATCTGTC	59.805	20	AAATTTGTCCCCCAGACTCC	60.169	20
TCTTCTGCCGTTGATGTCTG	59.984	20	CTACAAGGCCAGATGCCAAT	60.096	20
CGTCTTGGTCTCCATCAGGT	60.112	20	TCTAACACGCAGCATCAAGG	60.011	20
GCGAAAACTAGATGCCGAAC	59.851	20	TTGCCTTTATTTCTTGGCAGA	59.84	21
CGATGTTTCTCGTCTCACCA	59.831	20	CATTAATGCAGAGCAGCCAA	59.976	20
TGCTTTGCCTAGGCCTATTAAG	59.904	22	ACGAGGCATATCATGTTCGG	60.884	20
ATCTTGCCGCTGTTAAGGAA	59.845	20	TTTGCTACCTCGCATTGTTG	59.872	20
TCCAGTTTCCGGTCAATGAT	60.317	20	CCCATCACCAAACAAAACCT	59.688	20
ACAATCTTGGTGGTTACGCC	59.859	20	GGCGCCAAATGATAGAGTGT	60.103	20
TGAGCCTTGCTGACACTGTT	59.622	20	GAAGTGCAGCATGAATTTGC	59.43	20
CAAACCCCGAGTCTGATGTT	59.966	20	CTCGAAAGCACCAGTAAGGC	60.015	20
GACCCCTCAGCAGTGACAGT	60.315	20	CCTCTGCAGATTCAAATCCC	59.629	20
ATTGCTGAATGTTGATGGCA	60.08	20	CCCAGCTGCCTTCTTTTCTA	59.587	20
CCGATAAGAATGGATGTGGG	60.148	20	GGCATACGGCTCACTCTACG	60.817	20
AGGGCAAGCATATCGTGTTC	60.103	20	CCCATTCCAACCATAGCAGT	59.813	20
CGTTAGAGGTTTTGACGGGA	60.103	20	TGGCATTACGCATTACCACA	60.926	20

TGGTGAATATAGAAGGGCGG	59.916	20	AATGCAAGAAACCTTGGCAC	60.118	20
GGGTGAGTCGAGAAATACGC	59.7	20	TTTGTTCGTGTTCCAAAGGA	59.145	20
CACACGCTGGAACTGCTTTA	60.05	20	TGTTTGGTTTGTGAATTGGGT	60.118	21
AACTCCTCACAATTTCCCCC	60.169	20	TGAGCTGTGTTTAGGGCTGA	59.591	20
ATCGTCTCAATAGTTGCCCC	59.009	20	TGATGGTGAGGATGCTGCTA	60.376	20
ATAAAGTAGTAGGCCCGCCC	59.485	20	TTTGTGTCCCAATAACACCAAA	60.124	22
ACAAGAAACGGTGAGAACCC	59.04	20	ATCCATAGCCAAGCACAACA	59.152	20
CTGATGCAGATGCAGACAGT	57.466	20	GAGCAGTTGGAGTTGCTTTTG	60.045	21
GTTCGTGCTCTTGAACGTGA	60.032	20	TCTGTGGGACCAACTTCCTT	59.549	20
AAATGAAGTTGGGCAGTTCG	60.11	20	ACTCCATCCACTCAACACCC	59.817	20
CAAGTTTGAAGGGTTTTGCTTT	59.682	22	ATGTTTCTGGCCCCAAATTA	59.273	20
CGACGTTTAACAGCCGTAGC	60.821	20	CGTTTCTTGGTAGTTTGCCC	59.609	20
TCAGGATGTTGCAGTCAAGG	59.831	20	GCATATTTAAAGAAGGCCAAG	59.301	22
GTGCAATGTGAGTGGACGTT	59.603	20	GTCTTCGGGAAAGAAGGGTT	59.553	20
GGTTCGAGTTTCGATGAGGA	60.195	20	GAGGTTTTGACGGGATTTAGG	59.822	21
AAGCACGTACCACACAGCAC	59.826	20	AGCATTAAAAAGGCCATCCA	59.547	20
CCAAGAAATCAAGGATCGGA	60.006	20	CACTTCCACCATTGATGCAG	60.112	20
ATGCCAAGGAACCTGTTGTT	59.454	20	TGTGCAAAATGCTACAGGTGA	60.309	21
AACGTGCTATTGTGTCGTCG	59.788	20	ACGGGAAGAAAGAGGGCTTA	60.2	20
TGACTTTTGGGGTTTTCGAG	60.081	20	TCCCTTTCACTCACACACCA	60.129	20
TTGTGGTTGAGTACGCCAAT	59.05	20	CCAACAGTTGAATATGCCTAC	59.536	22
GAATGGAAGGGTCGTCAAGA	60.05	20	CGGGAGATGGTTGTTTGAGA	61.034	20
TGTTCTTCAAATGGGATGTCA	58.961	21	AGCAGAAGCCCATCTCCTTT	60.349	20
CCCAAATCAATCAACTTTCCA	59.787	21	GAACTTTGGTCGATCGTCGT	60.119	20
TGAGCTGGACGGACATTGTA	60.263	20	GCACACCAATCCGAAAATCT	59.939	20
CAAGGCGTTGGAAAAATGAT	59.938	20	TCAAGAACAATAATCGGTGCA	60.131	22
TTTTGCTTCCACTGCTTGAA	59.585	20	CGCTTTGGTGCATCATCTAT	58.749	20
CCCTCTTCGTGTTCCAACTG	60.68	20	TTGGAGAAAATTTTGTGGGC	59.916	20
GGAGACTTATGGAGGGGGAA	60.264	20	ATTCTCCGAATCCAGCACAC	60.081	20
GAGCGTTAGCTCTTTCGCC	60.25	19	GGAATCGGAACCCTTTTAGC	59.909	20
AACCTGTATTGGGACATCGC	59.82	20	GGAACATTGCACCCAGAGAT	59.934	20
GTTTATCTTCGGCTTGCTGC	59.988	20	TCACTCATGGCTTCACGTTC	59.837	20
TTATTCATGGTCCCCTTCCA	60.126	20	GGAAAATGGGTGATGAGTGG	60.173	20
TGAATTTGCATCTAAGGAGGAG	58.467	22	AGCACCTAATTGTACCCCTGT	57.62	21
AAGCAGCAATCTCTGCCATT	59.985	20	ACCCAAGCTGGTGGTTATGA	60.375	20
GTGTGGATGTCCATCACTGC	59.97	20	AGACTCGTGTTCCAACATTCA	58.201	21
AAATCTGCATGCACCTGTTC	58.726	20	GACCATTCACTGGCATTTCA	59.502	20
AAACTTTTGTGGGCAAATGG	59.839	20	TTCCAAAAGCTGCTCGAAAT	59.96	20
CTCACCACAGAAGAGGGAGAA	59.435	21	GGCTAGCTGAAGGATTTCCA	59.41	20
ACTCGAACGGGATCTTGATG	60.073	20	GTTGCCTCTCTATCCGCAAA	60.352	20
CAAGCAAACACCACAACACC	60.049	20	CGTTGGCCCGATATTTAGAG	59.564	20
ATATATTGTGAGCCCTGGCG	59.945	20	GAGGAACAGAGACGGAGGTG	59.835	20
TTTCTCAACCATGCATCCAA	60.049	20	GCTGCTGCTGTCTAAATCCA	59.178	20
TTCTTCAATTTGCCTGTGGA	59.247	20	TGAAGATGGCACCTTGAGTG	59.831	20
TCGCCTCTCAAGATTGTGAAT	59.828	21	CGTGCATCACATAGAATGGAA	59.557	21
AACACGCACTCTTTCACACG	59.946	20	CGGGTGATTATAAATTGGCG	60.165	20
TAATTGGGAACGGTGGTGTT	60.088	20	CGCACTGACACCATCAAACT	59.751	20
GAATAAACGGCGGTAATGGA	59.795	20	CGCCTTCTCAGCTATGATCC	59.939	20
CGTCATCGTATTGGCTTCCT	60.096	20	TACCAAACCACAAAGCAGCA	60.293	20
TTTTGGACCTCCCTTCCTCT	60.045	20	GGGTGAAACCCAAACGTAGA	59.83	20
TCTCCTCCGTGGACGTAGAT	59.679	20	GCGTAAATATTGGCATGCTTT	59.148	21
GCTCTGATGCCAAACTGTTG	59.445	20	TGACCATGTATCGGTCTTTCAG	59.993	22
AGTGGCAAATGAGGAGATGG	60.073	20	GAATTCGTGTTTGGTGGCTT	59.978	20
TTCACAATGAATGACCAGCC	59.502	20	TGCGTTTCTGCGTTTTTATG	59.88	20
TGAGTTGTTCATTTCAGATGTTGT	59.961	25	TCACGGAAAACTGCACAATG	60.699	20
CAGTTTTTGAGTTATGATGCTTTC	59.727	25	CGGTTCGAAATTGGATTCAT	59.762	20
TCTCTCTCTAACACACAAACAGA	58.829	26	ATCTTGGCAATCCAAAGCTG	60.214	20
GACTCGATTGGGACATCAGG	60.475	20	TAATCTTCGTCTTCGGCGTT	59.845	20

CATTTTGCTTTGCAGGAACA	59.849	20	AAAGCCTTTCAACAGCCAAA	59.861	20
TACCGATCGGGCTACAAATC	59.923	20	CTTCGTGGAGCTGCAAACTT	60.571	20
AGTGAGAGAGAAAGTGCCGC	59.751	20	ATGAATTCCGCTGGAAACAG	60.074	20
CTAAATCCGCTTCGAACGTC	59.845	20	GATGATTTATCACCGAATCGC	59.387	21
CCGAATCCTTTCATAGAGCG	59.801	20	TTCCACCATGATTTCGACAC	59.348	20
CCGATCCCAATCTCTCCATA	59.848	20	CAGCATTACCATTTCCCGAT	59.784	20
GTCCGTTGGTTTACCCAGAG	59.449	20	TCCTCGATGTTTGAAAACCAG	60.096	21
AGGAGTGGTTGAGAGGTGGA	59.682	20	GTGCATGTGTGTGTGTGGAA	60.053	20
TGACCACAAATGTTTCCTCG	59.541	20	GCAACATGCTGATGGTGGTA	60.549	20
GCATCGAAGGGATGACATTT	59.9	20	ACGATCATCACATGAACCGA	59.925	20
GGTTCCAAGCCGTTTAGACA	60.11	20	CGAAACGATTAGTTGAATGTG	59.652	22
AGGGGTTATCATGGGATCAA	59.055	20	CGGAACACAATTCGACAGAA	59.691	20
AACTTGCGTAGCATCATCCA	59.301	20	TAAGCCAAGCACACATGAGG	59.864	20
TCGATGCATACTTGTTGGGA	60.073	20	GGTGCAAGAGATTCATGGCT	60.226	20
GAGGAATTGCCAACCCATAA	59.762	20	CCAGTCAAAGTCACCAGGAA	58.695	20
TCGTCACGTGCGATTTTAAC	59.735	20	CAAAATTCCCCCAACTCAAA	59.772	20
CCCAGTTCGTCGAGAAAGTC	59.844	20	AACTTGCAGAGTCGGGTGAT	59.727	20
CAGACCATCTGGGAACTAATCAA	60.359	23	CTGAATTTGTGGTGGCAGTG	60.152	20
TGGAGCGCAGGCTATAAGAT	59.967	20	GGTTCTCACTCTCTCTCAGCC	58.201	21
TCTGCATTTGGTGGTACTGG	59.566	20	GACGATAATTCGTCCGTTGG	60.331	20
GAAGCAACGGAAAGAAATGC	59.829	20	CCACCCACTCTCCCCTTAAC	60.736	20
GCAATAAAAAGACCTTGCATTTG	60.019	23	GATTGGCCACTGGTGCTTAT	59.962	20
GGAATGGGATCTCTTCCACA	59.862	20	GAGGCAAACACCCAATTGAT	59.797	20
CCAGGAAGACTCATTCGATCC	60.974	21	GTCAAAACAAATGCTGTGGG	59.024	20
ACTCACACCCACATCCATCA	59.801	20	TGTGACCAATATCACAGATTCC	58.502	22
ATTGAAAGCCTCCCGTTTTT	59.945	20	CTGCATAGCTGATATGTCCCA	58.761	21
CGGCTTTCTCAACACCTTTG	60.796	20	TCGGAAGGCAAGATCACTAGA	59.963	21
AGCAGACTGGTTCCAAAAGC	59.478	20	TGACAATTTCCAGCAGCAGT	59.445	20
GGGGCTGCTTTCTCTTCTCT	60.096	20	ACTGATTCACCTTCTTGCGG	60.255	20
TACTGCAAATTCCGCCTCTT	59.845	20	TTGGCTGTAGGAAACCTTGC	60.249	20
TGGGTCTCAGATTCTTGGTCA	60.64	21	AATTGGAATGAATGGAGCGT	59.391	20
GGGTATGCATCGCTCAGATT	60.066	20	TATATCTCCACGGACCACCC	59.629	20
GGTACTGGTGGAACTGCCAT	59.851	20	TCCCTCTCCACAAAATCCTG	60.042	20
AATGTTTCCTGCCACTCAAA	58.201	20	CTTGGTACAATGGCTGGAGG	60.508	20
GAACCATACAAGCAGTGGCA	59.722	20	CTTCGCTTTTCGCGATTTTA	60.456	20
GGGAAACAAACTATCCCATTTG	59.588	22	TGTCCAAAATTGTTGTCGCT	59.174	20
AACTCTCTCCGCCATGATTG	60.218	20	ACTCGGCCTAGTTCGTTGAA	59.875	20
TTCAGTACTTGGCCCACTTG	58.773	20	ATTACCTCTCCTGCCCCAGT	59.957	20
CCATTTTCTTATCTCGCCCA	60.031	20	GGCGTTTAATTCGTAATCCG	59.455	20
TGCTGACAGGATTAATTGATGG	59.96	22	GCTTCAGTTGGCAGGTATCC	59.7	20
TAAGCAAGCAAACAAAGCCC	60.376	20	CAAGCATGAAAACAACCGTG	60.149	20
GGCCACATGCTCAATTACCT	59.962	20	GCGCCTGCAGTTATTTGTTT	60.272	20
TGAAGTTAGGAAATAAGGAGGTG	58.743	25	CGGTACGGTATGGTGTCGTA	59.342	20
GATCCTTCCTCTCGTTATGGC	60.053	21	CCACCTCTGTGATCCATTCA	59.473	20
TCGCGTAAACAACACGATCT	59.347	20	ATTTCACCCACAAAATCATCA	57.778	21
TTATCGGCTGTACTCTCTCGC	59.629	21	AGGCGGCATTCTCTAATTCA	59.807	20
TCCTACAACTCCGGTTCCTG	60.103	20	GGTGTTCTGGGTGGAAAATG	60.21	20
TCGGGACAACAATATCAGGTC	59.805	21	TGTTGTTGGTGGAACTTGGA	59.976	20
ATCCCTCGCGCTCACTACTA	60	20	TAATGCAACAGCCAACAAGG	59.729	20
TATGGGATTGGGTCTTTTGC	59.762	20	GAGTCGGAAGGCATATGTGA	58.672	20
ATTAAAGCACCTTTCGCGTG	60.264	20	TGGGGAATGACTCACCACTAA	60.36	21
TTGTCTACCTTCTCGGGGTG	60.103	20	GATTCGAGTTTTGCTTCCCA	60.192	20
CTGGTCCATTCAAACCTGCT	60.111	20	GCCTCCATGCTCCTATTCTG	59.797	20
CCGCATCTTCTAACGAGAGG	59.971	20	TGACAATATTTAGTGTTTTGAC	57.78	26
TCGCCGTCTCTCACAAATAA	59.42	20	TGGGAATAGCGATTTTCCTTT	59.922	21
CTCTCCCTCCCTCAATCCTC	60.149	20	CACGCACACACAAATTCACA	60.204	20
TATCATCCACCAAATTGCGA	59.891	20	ATCTGAAAAACACTCGCGCT	60.022	20
TTTTCGAGTTATGAAGTTAGCACC	58.926	24	ATGCGAATGGAGGTTGACTC	60.081	20

CCGGCGTTCTGTTATCTTTC	59.708	20	CCGGAAAAGAAAACCCACTT	60.324	20
TGAGGTATGTTAGCCAAGTTCA	57.454	22	TTGTTAGCGAATTTTTGGTGG	59.986	21
AACCAACATGCACAACCAAA	59.864	20	TTGGCTCCATTTTTCAAACC	59.916	20
GGGTTCCTGCGTCATAAAAA	59.938	20	CCCGATTCGAGTAGCTGAAA	60.344	20
AGGAGAGAGAGTGTTGGGTAGAC	59.945	24	AGCGCCACCTCAAAAGTAAA	59.883	20
ATATCAGAAAGCCACACGGC	60.103	20	TGATCAGGCTGCACTTTACG	60.011	20
CGCCGGTGCCTATCATATT	60.832	19	ATTGGTGCGTGCATGTATGT	59.878	20
GAACACCTCTCCAGAGCCAG	59.986	20	AAAGCTCAGTTCGATCCCCT	60.212	20
CAGCAAATACTCTGCACCGA	60.011	20	CATTGGAATGTAGGGAACCG	60.184	20
TATTCCGAGTTTCATTCGGG	59.894	20	CCAAATTTTCTCCACGCTTT	59.202	20
GGAAATTGAAGCTGTTGCCT	59.316	20	GCCCATACAATTTCACAAGGA	59.815	21
CGGGGTACACATTTGGAACT	59.711	20	CCTTCTTCCACTGCTTTTGC	59.993	20
GTAGGGGTGCAAATGAATCG	60.331	20	ACCTCAAACCCTTCTGCGTA	59.734	20
TTTCATCGTCTGCAACAAGC	59.995	20	GGGGAAAGAAAAGCAAAAGG	60.048	20
TCAGTCGAAACATCATGGGA	60.048	20	ACCCCTACCCCTACCCTACC	60.309	20
GCGTTGAGAGGCTCACTTCT	59.751	20	GCTTCAAACTGGCTCTCGAT	59.579	20
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TTTATCCCCCTTGCATTCAG	59.894	20	AATCGCCATGATTCTCCAAC	59.9	20
GGAGAAAGTTGATTTGTTGGG	58.54	21	TGAATTTGCCTTTGTACATTTTG	59.076	23
AGTGTGCTCCAACACAGTGC	59.948	20	TGCAGAGGAATTGGTTGTCA	60.24	20
GGCCAACCCATTTGACTTTA	59.801	20	GTCGGATTGGATCGGAGATA	59.854	20
GGGTGGTATGGTGGAAGAAA	59.647	20	TGGGGTGATATAAGATGATGC	57.38	21
CATTCACCACATGAGATGCC	59.925	20	ACGAGAGGTGGGAAAAGTGA	59.697	20
CCCTTTGAGAATAATGACATTGG	59.724	23	TTGGTTCATGTAGCCGACC	59.512	19
TGAACCGTCACCGTCAATTA	59.964	20	CAATATGGGAACTTCGCGTT	59.96	20
GCGACATCCACATAACATGC	59.963	20	TCCCCTTCTCCGTATCATCA	60.417	20
TTTGGGAGTGGGTGGAATAG	59.784	20	AAGTCCCTCTCGGGTCGTAT	59.957	20
AGCCTTCAAAAACCATGCAA	60.617	20	GGAAGCTGCTCTTGAGTTGG	60.134	20
GTTGATTCCAGCAGCTTCGT	60.406	20	ATCAAATTTTGGATCCGTGC	59.768	20
CCCAAGACCCCAATTTGAT	59.59	19	GGTTGCACACTCCAACACAT	59.446	20
TCGTTGCCAGGGTAAATGAT	60.331	20	GAAGCCACAAATGCAACATC	59.131	20
CCGTTACCCTCGACTTTGAA	60.103	20	TGGACTGATCAGCAGAGGAA	59.499	20
AGTTGCAGCAGCATTCCTCT	60.164	20	CTCCCAAAACCTCACCTCCT	60.48	20
TCTGATCAAAACTGCTTCGG	58.999	20	GGCATTGTCTTGGTTGTTCA	59.547	20
CGATCGGTGGATCTTGAACT	60.073	20	GCCAATCCTAGCGATGAGAA	60.318	20
GGATCGAGTAAGCGGAAATC	58.742	20	CAGGACGGTTCCTCTCTTGA	60.377	20
TGCATCAATCTCATTTCCCA	60.009	20	CCAAAGAGTTGTTGGAAGCC	59.711	20
ATCACTCTCGCTCGTCGTCT	60.167	20	GGCTTGACACCGCTACTACC	59.763	20
GCCATTACATGCAGGGTTCT	59.962	20	AAGCATCTCCGAGGGAAAGT	60.212	20
AAAATGGATTCATGTTTGGGAG	60.055	22	TCCAAGACCCCAATTTGATT	59.22	20
TGATCCCATGTTTTCTGCAT	58.926	20	TCCAACCCATCTCCCATTTA	60.126	20
TCCCTATAACCGATACACCGT	58.341	21	TGGTTGGATATTTCCCCCTT	60.37	20
CTTTTTGTATGGGTCGCGTT	59.996	20	CAACGAAGAAACAGGGTTGG	60.52	20
GCTTTGGAAGTTATGGTCGC	59.713	20	TGCCATTGCAGCTAGTCTTG	60.157	20
ATCGGGTGGAGATTGTTACC	58.717	20	CTTTCACCACCGCGTACC	60.112	18
CACCGGCAGCAGATTAAGAT	60.235	20	AATATGTCAACTTTCCGGCG	59.96	20
ATAAAGTGGCGGAGCTAGGG	60.593	20	AACATAAACAGTGGCGGAGC	60.14	20
TGCTGCATGAAAAATGAAGG	59.809	20	TTTGTCGGAATTAGGGATGC	59.901	20
CCACAGCATTGACATTAGGG	58.999	20	ACCGTGGAGATTAGGAGGGT	59.817	20
CTGAAATCCCATTCGCATCT	60.036	20	AAAACTTCTCGCCCCATTCT	60.074	20
TGTAGCCGACCCCAATTTAT	59.297	20	CAATGCCGTTTGTGATCATT	59.4	20
CATTTCCAATTTCCCTATCAAAA	59.243	23	TTCACTAAACTCGTGGAAATGA	58.798	23
ACAAGTTCGAAACCTGGACC	59.04	20	TTGGCAGCAACTACTACCATAC	57.048	22
CCCAAGACCCCAATTTGATT	60.91	20	CTGTGGTTGATTTGTGGGTG	59.848	20
AGTATGACGGCCATGGGTAA	60.214	20	ATGTAGCCGACCCCAATTTA	59.297	20
CTCAATATCTTACAATATCACAAT	59.306	27	GGTGCAGTCTCTTTCAAGGC	59.997	20
TGTTCGGACTGAACTGGTGA	60.285	20	TTGGTCTCGGGTTATGTTTTCT	59.871	22
CGAGGCTGAATTTATGGCAC	60.606	20	ATTTTGTAGCCGACCCCAAT	60.562	20

CGAAATGATGACCCTCCACT	59.927	20	CGATGCCCTTGAGAATCAAT	60.036	20
GCTGCTAATGTCGAGCTAACG	60.187	21	TCCCACCAAGTATTAATATGCT	59.768	24
GATTTTGCGGCGTTTGTATT	59.971	20	TTCAATCACGCTCCTCTCCT	59.95	20
GAAGCTTCTCACGATTCTTGG	59.066	21	CCAGCCTAAATTCCATCACC	59.387	20
CCAATATTTTTGGTCTCACGG	59.325	21	TTATCAGAGTCGAGCAAGCG	59.322	20
TGTTCGGTGAATGTTTTGGA	59.941	20	CCAATTTATTGGGATTAAGGCT	58.465	22
AGCAATGCGAGGATGAAGAT	59.803	20	GCAGCAGAAATCGTGGAGAT	60.37	20
TCGCCTCGCTATTTGATTTC	60.31	20	CGGTTGTATGAAACCGTTAGA	57.706	21
TTTTATTAGAATGCCGGGGA	59.389	20	GCAGTTTGCTGTGCTTGTTC	59.646	20
TGAAAAAGATGGTAAAAACCTTC	59.776	24	CGAACTCGTAGCCCATCAAT	60.096	20
CAGCCAAACATTGAGCAGTT	58.926	20	TCTGCAGCCATCTGTTCTTG	60.136	20
TTTTCCCACCCAGATATCCA	60.126	20	TGATGGGGAAATGGTTGAAT	59.991	20
CAGAGCGCACTCGAATAACA	60.157	20	GAGTTTATTGCACCCAATTAGG	59.687	25
TTCGAACCTTCTGCAAAATATAA	58.036	23	AGAATTTGGGAAGAAATTTCA	58.672	24
AAGAACATTTATGGCAAACAACA	58.601	23	TGAGATGTCCACAGCTTCCA	60.402	20
CTACCACTGCCGGAAAACAT	59.993	20	AACCATAAGCCTGCCTTTCA	59.708	20
TGCCCGCTAACCACTTATTT	59.609	20	TTTAGACGGGCTCTTCTTGG	59.448	20
TTTCTAGCCCACAACTTGGC	60.249	20	TCGACAACATCTCCGATCAC	59.637	20
AAATAATCAGGCTTCGTGCG	60.23	20	TTTGATGGCTTCTGCCCTAT	59.668	20
TCCTGAAACGAGTGATGCTC	58.96	20	CCTTTGATGCCGATGTTCTT	60.074	20
GTGTAAGGTTGGAAGCGAGC	59.882	20	CGTAAAGAGGGGTAGGGGAG	59.949	20
CCACCTACAGGTGCACAAGA	59.745	20	TTCTGTTGGTCATTTTCCCC	59.767	20
GTTACTTGGGAGATGGGGGT	60.052	20	CACCAATCCCACAACAACAA	60.255	20
ACCTTCTTGCAACCAACGTA	58.283	20	TGAAATACCATCCAGTCTGTCC	59.878	23
ATCGAACCGTGAACACCCTA	60.375	20	GACTTGCCTTGTGACTAGCG	58.677	20
TGAAAGCTCCTGCTTCACCT	60.134	20	ACACCAGCCGAGAACATCAT	60.542	20
ACAAAAATCCAACAAACCCG	59.702	20	TATGCAGGCACATACCGAAC	59.572	20
TGTGATTTCATTCGCATGTTC	59.538	21	CCACACGATGTTACCGTTCA	60.427	20
CTATTCATCTGGCCGACCC	60.432	19	TCTCACGCAAAGAACCGTATT	59.761	21
TTGTACTGTGTTGGCTTCATGTT	59.593	23	AAAGCTGATCCGTTCCAAAA	59.685	20
GGTTTTAATTGTGGGCTCTCAG	60.001	22	GCAATCAACAAAGCAACGAA	59.856	20
TTTTTCACGGTTGGAAAGGA	60.452	20	ACATCTAAAGAAGCTAAAGGG	57.122	23
TCACCAATCAACACTTGAACA	57.556	21	AGGCCTGCACTCAAAAGAAA	59.993	20
CCAAGGTGATGTCAAGTGTGA	59.581	21	CAGCGGACCGGCTATATACT	59.229	20
CCAATTTATTGGGATTAAGGCT	58.465	22	TTCGATTGCTTAGATTGGTGG	60.081	21
CAGCAAAACAACTTCATGTACGA	60.214	23	AGGATACATTGCATTTGGGAA	59.287	21
TGTCAGGCACTCCAAAATCA	60.24	20	GGGAGTCGGGCCCTATAGTA	60.299	20
GATGTGGAGGTTGACGGAAC	60.372	20	TGAGTTGCAACCAAAACCAC	59.591	20
ATGTAGCCGACCCCAATTTA	59.297	20	TCAAAATGGAAACGTGGACA	59.941	20
TACAAATCAAGCACGCAAGC	60.021	20	GCACCTTACCCTCAAAACCA	59.971	20
GTGAATTGGGTTTGACAATCG	60.22	21	TCATTCCTCTTGAATTTGGTGA	59.546	22
GGATCAGCAGTGGCTTTTTC	59.82	20	GATCGGGTTTTTCGGGTATT	60.02	20
GAAATAGCTTGGCCCTCGAT	60.551	20	GTGGATGAGAGGGTTTACCG	59.405	20
ACCTGCTCACCGATCAAGTC	60.269	20	GGAAGTGCATACGAGTGGGT	59.997	20
CCACAAGTTATCACACCCCC	60.088	20	TGTGATGTGATTGGGAGAAA	57.41	20
TTTTACGTTGTACGAATCCTATCTT	58.735	26	TACATCCATTTCACACCGGA	59.774	20
ACATCGCATACGTGTATGTTTAAT	57.646	24	CCGACGAATTCCTTTCAGTT	59.17	20
TGTCAACGACGAGATGGAAA	60.24	20	CTGTGATAACACCCTGCCCT	59.989	20
GGGACCTTTCAGTCACCAGA	60.088	20	CTGCACATGCTTTAGTCCCA	59.864	20
ATGCTGGAAATTCGATTGGA	60.414	20	CAGGAACATCGTTGTTTGGA	59.541	20
CATCGTCATCGTCATCCTTG	60.072	20	CTGATGGTGATGGTGTTTCG	59.96	20
AAAGGGTTGTCCTTCACTCG	59.183	20	GCACCCCCACCTTACTTTCT	60.361	20
GTGATGCCATAACATCGTCG	59.955	20	CCCAAGACCCCAATTTGAT	59.59	19
TTTAAAAATCGGACCGGAGA	59.52	20	CATTGGCTTGTGAGTTTCGAC	60.684	21
TCGTGCAATAAAACTCGTGC	59.879	20	CATGGCATTGATGATGAACC	59.738	20
CCAGCAAGGAGTAATTGGGA	60.066	20	CGGAGGTAGTTGGCATTTGT	59.993	20
TGAAGGACCCGTCATACAAC	58.415	20	GACGTGGTTTGCAGGCTATT	60.14	20
CCATTTTTATCGGCTCTGGA	60.031	20	TGCTTAATTCTTAATGTAATAT	59.009	26

TACGGCCGGGTAAATTACAT	59.212	20	CAACCACAACAGCAGCCTAA	59.904	20
TTACCTTGTCGAAACGGAGG	60.103	20	TCCTCCAAATTTCTCTCCCA	59.6	20
GATTGTTGAAGGCCGACAGT	60.119	20	GTGAGGTGCATGTGGATCAG	60.121	20
CATGTAGCCGATCCCAATTT	59.784	20	TTTTTCACACCAGAAACCAAA	59.151	22
TGGCAACTCAAAAATGCTCA	60.379	20	TGTGCCCGTATATTTATGGCT	59.358	21
ACTCCCCCAATTTTCTCACC	60.169	20	AGGGGAAAAGAGAGAGGTGG	59.671	20
CCACCAGCAGAACAAGAACA	59.873	20	TCAGAACCCGTCTCTGCTTT	59.989	20
GCGACGGGTACATTCCTCTA	60.096	20	TCATCGAACAAGTCCTCCAA	59.215	20
GCCCAGTTTTGGTCGTACTG	60.55	20	GTTGGGCAGCCAAATATTGA	60.837	20
ACCGTCCACGTCAGTATTCC	59.851	20	GTAGCGTTGCTATCCCGTCT	59.364	20
ATTTCCTTGCTTCCTCGCTT	60.34	20	GATGATCGCTGATGTTTGGA	59.61	20
TGAAAGAGCCTCCATCCCTA	59.767	20	CCCAAGACCCCAATTTGATT	60.91	20
TAGTGTAGGACCCCTCACGC	60.134	20	CCGACTAAAACGACATGCAA	59.729	20
TTACCAGGTGGCAACATTCA	59.964	20	GGGGTTGAAGATGCCCTTAT	60.152	20
ACCCTACATAGCGGGGAAAG	60.332	20	AGGGCCTGAAATCTGTCAAC	59.141	20
GAGGGGGAAAAGAGAGGATG	60.008	20	ATCGAACCTCTCCACCTCAA	59.655	20
ATGGGCGTCCACTTGTAGAG	60.134	20	GCGATTCGCCTTCAAATCTA	60.31	20
TCGACCCAAATAGAAGACCG	60.066	20	GTTTCCGGAGCAGTTGTCAT	60.119	20
CAAGACCCCAAATGATTGGT	59.647	20	TGGAGGATAAAATTTGTAACA	59.782	24
GTGGTCCACTCTAATGCCGT	59.997	20	ATGTAGCCGACCCCAATTTA	59.297	20
ATCAAGCGAAGAAGCAGAGC	59.866	20	GATGCTACTCCCACAAACCC	59.41	20
AGGAATAAAGGCTGGTGGCT	60.096	20	AAGTAGATTCCGGGCCATTT	59.799	20
CATCTTCTTCTGGATGCGGT	60.218	20	AAGGAAACCACATCTAACCTG	59.817	24
CCAAGTTATTCACGGATCCTTTC	61.027	23	TGCCCTATTTTTCCTCCTCA	59.64	20
CATCGATTTTGGGCCTACTG	60.46	20	TCGATCCCACGTATTGTGAA	59.924	20
GGTAGACGCCAGCCAGTTAG	59.898	20	CGATGCTCCTGTGTCAAAAA	59.84	20
CAAACACGCCAATCATCAGT	59.572	20	AAGGTTGCGTACACCTGACC	60.035	20
CGCAACCATTTCATTGTGAC	59.972	20	TCCTCATCCCCATCAACATT	60.135	20
TGGGCCTATCCTATCAGTCG	60.051	20	ATGTTGAGCCCAACCCAAC	60.774	19
AGGGTTTGAATTTTGTGGCA	60.344	20	TATCGGTTCCAAATCACACG	59.395	20
TTTGTGTCGATCAACTTGTGTG	59.658	22	GTATTGGCTTTACAACTGGGC	58.642	21
GGCATATTCGTCTTACGGGA	59.923	20	AGGTTCGGGGAAGTCTGATT	59.935	20
CGAAATGGAGATCCAAATCCT	60.272	21	TTCGAAATTTGGTGTTAGCC	57.754	20
GCAGCCAATCTCCTCTCATC	59.917	20	TCTGAACAATTTGCAGCTCG	60.134	20
CCGGATATCCAGTTTCATCC	59.2	20	GGCTACTGGTGCAACCCTAA	60.132	20
CAGCGAATCAATACGTGCAT	59.718	20	CCCAAGACCCCAATTTGAT	59.59	19
CGCCGAAGTCATTAGGTCTC	59.836	20	AAGGGATCCTCTCCTTCTGC	59.778	20
AACGAGCAAGAGGATGAGGA	59.95	20	CGTCGGGTAGACCAATGACT	59.989	20
ATTAGTTGGTGGAATTGCGG	59.823	20	TGTAGCCTACCATTCCGTAGA	58.787	22
TAAGGTTGGCTGTAATGCCC	59.96	20	TGGACAAAATCATCCTGCTG	59.648	20
CCCAAAACCCCAATTTGATT	60.754	20	CGGCATAAAAATTGGTCAAGA	59.95	21
TTTTTCCACCACTTATTCTTTTGA	59.107	24	TGATTGCTAATTCAATTTTTAT	58.242	26
TCGAATGTTGCTGCTCAAGT	59.596	20	TGCAGACACTTCAAAGTTCCA	59.475	21
AAGAAGAGGGAAAAGCCCAA	60.18	20	CCGGATCGGTCTTAACTCTG	59.688	20
CCCAAGACCCCAATTTGATT	60.91	20	GTGCAAAGGACATCGGTAGG	60.517	20
TTTCATGGGTACACATTTGAGC	59.867	22	TGCAGTATTGAATTACTTTCCG	57.911	23
GGGAAGGGGACAACATTTCT	60.169	20	ATGTGGCCTGATCTACAGCC	60.104	20
CGGATCCACTTTTCTGCTTT	59.312	20	TGGATGATCAAGGCTCTCAA	59.322	20
TGATCACACACGAGTCCATTT	58.999	21	CGCGGCTAAATTTGAAAGAG	59.979	20
CGTTGGTGAAGAACAACTTTGA	60.182	22	TGATCAGAATCAAGCAAGCG	60.096	20
CAAAGGGAATCAAATCTGGG	59.359	20	TGGCAACTGTACAAACAATTC	59.132	22
GATGGCCTCCCACCTTCTAT	60.293	20	ACATGTCAATTAAAAAGAAGG	57.538	25
TTTGGTTCATTTAGCCGACC	59.938	20	TTCGTCCCTTACCCTTTGTTT	59.858	21
TTCTCTCTTGCCCAGCATCT	60.096	20	CTTGCAAGGGAAGACGAAAG	59.986	20
AGGAGGATGACGACGATGAT	59.491	20	CTGCTAGACCCAGTGGTGGT	60.174	20
ACATTCTGGTCCGTAGGTGG	59.844	20	GGCGATTGTCAACTTGGTTT	59.978	20
CCACCATCGTCGTCTCATC	60.063	19	TTGGGTTTAGGGTTGTCAGC	59.971	20
CCACTCCACGTTTACGCTCT	60.312	20	TGAATATCACAGAATTTGGGA	60.19	23

TCTACTTAGAGCAGGGCCGA	60.11	20	TTCTCCAGGCTGATGTTTCC	60.195	20
AACCTTGGCTGGCTCCTAAT	60.096	20	ATGCATGGTGTAGGATCACG	59.399	20
TTCGAAGCTTGGAGAACGAT	59.955	20	GCCAAGGGTAAGAGAAACCC	59.94	20
CAAAACCTTGGTGAACAGGC	60.529	20	CCCAAGACCCCAATTTGAT	59.59	19
ATGTAGCCGACCCCAATTTA	59.297	20	AAAATATAGCCAGCCCAGCC	60.428	20
GCATTCTTCCTTCCTTCGTG	59.813	20	CAGCCAACACGATCAAACAT	59.572	20
CGTCAAGCTCTATGCTTCCC	59.978	20	CTTCAGCAATTCTTCCTGCC	59.955	20
TCAAACCTAAGACCGGGATG	59.926	20	TGATGGAGAATTTGGAGGCT	59.629	20
GGCTCGAATTACAAAAACCAA	59.111	21	ACTTCCTGGCCAGACCTTTT	60.11	20
TGCACTGCTTATCAGATTCAA	57.113	21	ATTGTGCAATGGGAATGGAT	60.021	20
GTTGAAATGCTTGCATGGG	60.065	19	TGCAAAGCGAAGAGAGACAA	59.864	20
CTGCCTCAGACTCTTCCACC	59.986	20	ATGGATTCCTTGTTCGATGC	59.9	20
TGCTCCTCCACCTCTGTTCT	59.986	20	CTACCCGGACTTGGATGTGT	59.844	20
GGTTGTGTGCCATCATCAAG	59.967	20	TGTAGCCGACCCCAATTTAT	59.297	20
AACTTGTGACTCCAGCTCCG	60.444	20	GAGAGAAGCCAGGGATGACA	60.349	20
TTCTCATCTCCAGTCTCCATGA	59.803	22	TTGCATGGTCGGTAAACTCA	60.111	20
AGAGGTTGGAGCAATGAGCA	60.945	20	TGTAGCCGACCCCAATTTAT	59.297	20
ATTCTGGTCGCTCCACAGTC	60.269	20	ATTCTTCGGTTGGAGGTGTG	59.966	20
CACCCCTATTCTTTTTGCCC	60.664	20	CTCGGGAAATTGAAAAGCAA	60.181	20
AGAAGATTTTTGCCACCCAA	59.546	20	TCAATCACCAATCAACAAAAC	59.708	22
CCATGACCCTCGACTTTGAA	61.034	20	CGAATGAGAAAAACTGGGGA	60.044	20
TTGCTGTCTCTGGCTCTTTCT	59.367	21	CGACGGATTGATGCTAATTG	59.136	20
CTTGCCCACTCCACCACTT	61.117	19	ATAATAACCCCGCAAGGGTC	60.041	20
AATGCAGGTTGGAAAAGGTG	59.971	20	ATAGTTCCGGTGACCCAGTG	59.844	20
GCTTTCGTTGCACATCTTGT	58.929	20	ATGTAGCCGACCCCAATTTA	59.297	20
CACATGTTGTCAAATAGATTCACT	60.218	27	TGTAGCCGACCCCAATTTAT	59.297	20
CAATCGGTCATGAGTTCGAG	59.241	20	GGTGTTTTCTAGAGGCACGG	59.734	20
ACAGAATGAATGCCCCAACT	59.41	20	CAAGTAAATGCTCGGCACTG	59.488	20
TGTAGCCGACCCCAATTTAT	59.297	20	GTGGGCTTTTAGTGCCTTGA	60.249	20
TCGGATTCTATTAGTGATTCAAGA	57.142	24	GACAGTAGCAAAGCCACACG	59.515	20
TCAAAATCATCACTCTCCACTCA	59.726	23	GCAAAATTGTTTGTTGTTCTGT	60.793	24
GGCTCATTACACAAAAACGTAGG	59.946	23	ATCATTCAGGAGGGCGGTAT	60.682	20
CCTTGCAGAAAAAGGCTTAGG	60.362	21	AACGCAAATGCAAGGAAGTC	60.257	20
TGGCAAGATTTGTTTTGACAG	58.808	21	AACCGCTTCTCAACTCCCTT	60.247	20
ATTCAAGGCCAACAATCCAG	59.933	20	GCAATGCATGAACCACACTC	60.128	20
TCACACATGGAGAACGAAGC	59.837	20	ACACCAAAGAACTTGCCCAC	60.012	20
TTGTGATGGAGTAGAGGGGC	60.073	20	AATTGAAGGGCAGTTGATGG	59.933	20
TCAGGCCTGTTTACACCCTT	59.592	20	CTAAACCCTTTCCCCGAATG	60.655	20
ATGTAGCCGACCCCAATTT	59.259	19	GAAATTCCCGATAAGTTGGAA	58.049	21
TCCGATGTTCGATTTTCCAT	60.274	20	GGGATTGTTATCGTGATGGC	60.163	20
CGTACATCCCCAAAGTCCTG	60.366	20	CAGAAGAACCATGCCAAAGA	59.861	21
CTTCAGCAGCAACTGATCCA	60.136	20	GCATTGGTGACATTGATTGC	59.939	20
AGAATGTACCTTGGGTCGCA	60.517	20	TGAAATATCATGTCCAGGTTTC	57.62	23
CCCAAGACCCCAATTTGATT	60.91	20	AATTTCTCCAAGCTGATGCAA	59.837	21
AGACCCCAATTTGATTGGAA	59.22	20	ATGGAAAAATTTGCAGAGCG	60.209	20
ATTTGCTCGCAACGATGTTA	59.329	20	TTATCGGTTTAGCCAGCACA	59.325	20
ATCTAACGGCTGGCATTTGT	59.597	20	AATATGATGGTGCGGTGGTC	60.613	20
CCATATGCAAACATGCGAAG	60.096	20	CCCAAGACCCCAATTTGATT	60.91	20
TCATCTGTTTGGCCTGTCAC	59.682	20	TTAAACCTACCCCTTCGCCT	59.96	20
TGCATGAAACTTTGTAAAACCATT	59.822	24	ATCCGCCCTTGATACAGGT	59.376	19
TGATACCACGTCAAGCAACC	59.572	20	TCAAGCAAAAATTGAACCCC	59.916	20
AGGATAAAAGAGGCAGGGGA	60.032	20	GAGGCGTGACTTTGGCTAGT	59.501	20
TGTAGCACGAGTGATGAGGC	60.016	20	GGTGTTGAACAACCAGACATA	60.182	24
CGATCATCCCTCATCTGACA	59.585	20	CAGCAGCCATCTGTTCTTGA	60.136	20
TAAAAGCGCACTTTGACGC	60.148	19	GGACACCCGTGTTGAAGTTT	59.867	20
CGGAGGTGATCTCAAATGGT	59.927	20	CTCGACCCGTGATACCAGAC	60.533	20
CAAACCATGAATAAGCAATCCA	59.832	22	TTGTCACAAGTTTGGGAGGG	60.923	20
TTTGCTTACGGAAACAGCAA	59.486	20	TGCAGCGAATGTTGTTTTTA	57.997	20

TTTCCCCCTCCTCTCATCTT	60.008	20	TTCACTGTCGTCAAAGCTGG	60.025	20
ATGGAAGCTGCATTGGAGAG	60.362	20	TCGATCAAAATAACACCATTG	59.838	22
TGAGTAATTCCCCCATGGAA	60.126	20	GATTTTCGAGTTGCAGAGGC	59.962	20
CCCAATTTTCCGCATTTTT	59.759	19	TCAGAAGGGGTTATGTCCTCA	59.827	22
ATGTCCTTGAAGATGCTGGC	60.226	20	AGACCAAGCTTCGTTGCATT	59.882	20
GGAGAAAAGCATACGGGTGA	60.074	20	GGCAGCCTAATATTGAGCAGT	59.784	22
TGGTTCAAGCACATTTCCTG	59.691	20	GGACCTAATTTTCCCCAAGG	59.639	20
TGTCAAGTAGATCATGGGCG	59.673	20	ACCAATGGTGGTATGGTGTG	58.984	20
TCTCCACATGCTGTCTCACC	59.827	20	GAGATGGGAGGTGGTCTTGA	60.048	20
TGGAGATTCCGGAGTTCTTG	60.187	20	CGGTGCTCCTTGTATCCATT	59.955	20
CGTTGTGTGAGTGTGGTTGA	59.15	20	GCACAATGCCAAGTAGCAGA	60.019	20
TGGGCAGCCAAATATTGAGT	60.469	20	CAGCAGCCATCTGTTCTTGA	60.136	20
TCGACTTTGTTTGGTTCGGT	60.529	20	TCCTAGCTAGCTTTCCAATTCA	58.299	22
CGAGGATCCTTCACAACCAT	59.927	20	CGATCCCATCAAATCTGAGC	60.57	20
TTTGTCTTTCCCTTTGATGCT	58.823	21	TTCACTCATGCATCTTCCACA	60.256	21
ATGTAGCCGACCCCAATTTA	59.297	20	CCTACTTGCATTGTGCTCCA	59.864	20
CTTTCGGAGTCACAGAAGGC	59.989	20	AAAAGTCGCAATCAGCAACA	59.469	20
GGAAAAGTTGTGCATGGGTT	59.836	20	TCTTTTACAAGGTGGGTGGC	59.971	20
CCGACCTCACATAGTGGGAA	60.913	20	GACTGGGCTTTTTGGTTCAA	60.088	20
CAAAATCGATCTGCAACCCT	60.074	20	ATGTAGCCGACCCCAATTTA	59.297	20
TGCATTCGTATAAAGAAAATCGC	60.449	23	CCCAAGACCCCAATTTGATT	60.91	20
AGTCGATCTCGTCGGGTATG	60.096	20	GATGGACGTCGACGATTTCT	60.081	20
GCTTGTGATGTAGAGAAATGAAG	59.329	24	TAACCAGCAGTCCCCAAAAT	59.429	20
CGAGGGTATAAGGGACGACA	59.948	20	CGACGAGAAAGTCGTGTCAA	60.025	20
ATTCGAAGGTGTTGATCCCA	60.317	20	TGCACCAACTTCCTCTCCTT	59.844	20
CACAAAATGTTGCTGCTCAAA	59.903	21	GGAAGCCAATTTGTTTGCAT	59.945	20
CAAACACCATCGCAAACAAG	60.149	20	CTTCCCTCTCAAAACCATCG	59.665	20
GGTGAGTTTGAAGCATTGCATA	60.138	22	ACCTTTAGAACTTGCTCCACCA	60.165	22
GGCCCAAAGATCTCAAACAA	60.051	20	AGAGAAACAGAAGTTGCAGC	58.796	22
ACAAATGAAGGCGAACAAGG	60.11	20	TCAAATTATCTGCTTCCCGC	60.175	20
TCCTATCTATTCCGCGTGCT	59.829	20	GAATTGGCGACGTAGGGTTA	59.96	20
AATCAATCAACTTACCACCACC	57.839	22	TGATGCAGACTCGAGGTACG	60.008	20
GGAAATCCAATTAATACAGTCAG	60.572	25	CCCAAGACCCCAATTTGATT	60.91	20
GGAGCATCCTTGGTTGAATC	59.488	20	TCTCCCCAATTCACCCTACA	60.309	20
ACCCTTGAGCTTGCATCTGT	59.874	20	GCTCAAGTGGCTTCTATGGG	59.836	20
TCGGTGACGAGGTGGAGT	60.252	18	GTAAGCACCTCCTTCCACCA	60.111	20
TGGAACCATTGCAGTCAAGA	60.24	20	GAACGGAAAAGCTTCGTTTG	59.861	20
ATGTAGCCGACCCCAATTTA	59.297	20	CCCTTGACTTTCAACCCAAA	59.942	20
TGTGTACGTAGTTGAGCATGTTG	58.837	23	CCTTAGGTAATGGTCGTCCTTG	59.886	22
ATTGCTTCCGCAATATCCAC	59.929	20	CCCAAGACCCCAATTTGATT	60.91	20
ATGTTGAGCCCAACCCAAC	60.774	19	TTCTTTTATGTGGGTTGCAAAA	59.511	22
TGTAGCCGACCCCAATTTAT	59.297	20	CTTCCTTGCATTCGTCATCA	59.799	20
TTCGATGGTTGATCTTGATTG	58.56	21	TTGATGGAGGCCTTATTTGC	60.038	20
ATTAGCAAATTTCGGGACGA	59.547	20	GGGATTTGGTGGTGAAAATG	60.029	20
TGATGGATCGAATATTCTCACG	59.923	22	CAACCCCTACTCTTTTCTTCCT	57.968	22
ACACGATAGCCATAGCCGAC	60.125	20	AAAAGCACGAGAAAAGGGTG	59.355	20
CACTCTCATGCTCCTCCTCC	59.945	20	TGAAGGACCTCCTGATTCGT	59.655	20
GAAGTGGTGGCAGTCCATTC	60.52	20	GACAATGGATGAAATTCCCG	60.133	20
AGCAGCCCCTCTTTTGAAAT	60.208	20	TTTCCAGGTCCTCTGTCGTT	59.697	20
TCTGATTTAAACATGGTGGCT	57.23	21	TTTCATTCCTTTTTCCTCCTTT	58.307	22
TCTTGTGAGACTGTTGTTCTGGA	59.938	23	TCGCCACCTAAATGGAAAAG	60.067	20
CCCAAGACCCCAATTTGATT	60.91	20	TGGTGCAGATTTAAATGTTATA	60.495	26
CCCAAGACCCCAATTTGATT	60.91	20	GATGCCTGATGAACATCCAA	59.456	20
CCCAAGACCCCAATTTGAT	59.59	19	GCCCAAATACCACTTGAAGC	59.574	20
GATGGATGAAAACCCACACC	60.034	20	GTTTACCTGGCTGACGTGGT	60.035	20
CCCAAGACCCCAATTTGATT	60.91	20	TTCAAGCGGAAGTTCATTCA	59.395	20
TGTAGCCGACCCCAATTTAT	59.297	20	CGATGCGCAAATAAAAGACA	59.842	20
ATGATCGGATTTTGTTGGAGA	59.377	21	CCCAAGACCCCAATTTGAT	59.59	19

TTAAACTGGCACCCATCAAA	59.013	20	CTTTGCTTTTGCATCTGGGT	60.249	20
TTCCCTCGTTTGTTCCACTT	59.569	20	GCCTGAGATGGTAGACACCG	60.678	20
TGCATAGAGGAAATTGCATAGC	59.371	22	TCCCTAATGCTGCCTTTGTT	59.708	20
CCTATAATTGAAGCCGCCAA	60.054	20	GGGCTAGGGTTATCAGGGTC	59.789	20
GGAGGAGATCGAGAGTGACG	59.945	20	GACGACTACAGTGATGGCGA	59.862	20
TTGCAAAAGTGATGTGACCG	60.699	20	AGGGCGAGTCTCAAGAAACA	59.989	20
TGGGCAGCCAAATATAGAGC	60.196	20	CAATGACGAATAGCAGCCAA	59.833	20
CCCAAGACCCCAATTTGAT	59.59	19	CCTCGATCGCTTGGATCTTA	60.309	20
TCAACTTTCCAACTGATGGC	58.697	20	TTTGTGTCATAGAAGGCCCC	59.933	20
AGCTGTGTCTCCAAACTCCC	59.305	20	CCGTGGTCGCTAGCAAATTA	61.139	20
TGTTGATTTGGCTGTCAAGG	59.691	20	CCGAGGTGAGATTCAAAGGA	60.187	20
CAACGGTTTACAAGTGTTGTTG	58.187	22	TGACAATGTACGCACGGAAT	59.995	20
AGCTTAAAGGTGGAGGATAGTGG	60.031	23	ATCTATGGCTTCCGCTTGTG	60.235	20
CGTTTTTGTCAATGCGTCTG	60.293	20	ATAAATGCATGCAACGTCCA	59.96	20
CCCAAGACCCCAATTTGATT	60.91	20	CGGCACTAACCAAGTTCTCG	60.817	20
CTCATCCCTCGCACATTTCT	60.218	20	CCGAAGTGCTAGACCCAAAG	59.869	20
TTCACTTGCTCCTCTCCTATCA	59.077	22	TTTCACGTGGTTTGGTCTGA	60.128	20
CATATCATAAAGATAAAGACAGC	57.413	27	TTGGAGTGATTAATATGCAATT	59.389	26
AGCTGCATCGAGCTTTGC	60.409	18	GCATACCTATCCGAGGGACC	60.682	20
CCCAAGACCCCAATTTGAT	59.59	19	GCTTTCTTCAGCATGTTGTCC	59.874	21
AACCCAGCAACCATCAAAAA	60.344	20	CCCAAGACCCCAATTTGATT	60.91	20
CAATTAAGTTCTACGAATTCATTT	58.761	27	CCCAAGACCCCAATTTGAT	59.59	19
TGAACCACGACTTGAATGGA	60.088	20	CCCTGAATTTGATCCTGGTG	60.309	20
CAGGGTAGGAGCAAGGAGTG	59.861	20	CTGCTTTCTTGTCCTCGTCC	59.989	20
TGCAACACAATCATTATGGC	57.987	20	TTCGACAATGTGTCTACATCCA	59.05	22
TTGATGAGCCATAACCCTCC	59.894	20	CAATGACGAATAGCAGCCAA	59.833	20
GTCCCAAAAAGGCAGAAACA	60.088	20	TCTGCACATCTGAATTTACAAA	57.528	23
GAAATTTGGAAGTGCCTGGA	60.051	20	AATTCCGAACCTCGAGTCCT	60.074	20
TGATTTTGGATTTTAGGCGG	59.901	20	ACAATGATCGGTTTCAAGGG	59.79	20
AATGAATAAGTTTGCATTTAAGAG	57.268	25	TCCTCTTCGGTTGGTTTTGA	60.605	20
GCTCGTGTCCAAATCAAACA	59.697	20	CTCTCCGTCCACGATGAACT	60.261	20
GCAATGAACACTTAGCAGCG	59.638	20	GTTCCAAGGGAAAAGGGAAG	59.912	20
TCAGGTTTGACTTTCATTCTCGT	60.158	23	TGGAGGACTAGATTTGGGGA	59.478	20
CCGAAATTAACGTGGAGGAC	59.429	20	AACTTTGTTGAATGAGCCCC	59.031	20
TCACAAACCGCTGTTGTTTC	59.74	20	GATCCTTGGCCCTTTTCTGT	60.443	20
GCCCGAGGTTGAAGATGATA	60.036	20	GGAAAGTGATCCTTGGGATG	59.336	20
TGTGTTGTTTGATGTCTTTGTGA	59.133	23	GGGCTACGACAACGGTTAAA	59.996	20
TTTCTTTTTCCTCAACAATTTCG	59.647	23	AGGGAGCAGCTGACTAGTGG	59.622	20
TTTTGGGAGTTCTCCTCCCT	60.045	20	AATGATGACCTCATCTCCGC	60.042	20
CCTTTCCCTTGCGTATCTTG	59.702	20	CCCAAGACCCCAATTTGATT	60.91	20
TGAATATGCGGGAAGAAAGC	60.175	20	CCCAAGACCCCAATTTGAT	59.59	19
CATGGCTGAGAGGAAAAGGA	60.331	20	GCTGCATCAATGGAGCTTCT	60.514	20
TGCTGAGATGGAACTTGACG	59.984	20	GCCTTCTTCAGCTCCTTGAA	59.694	20
CAATGAGAAGGCAAACACGA	59.84	20	TGGGAATAATCCAGGAACCA	60.126	20
CCAGCCCAATAGAGGTGAAA	60.066	20	GGTTTACCCAGAACGCACTC	59.598	20
TATGATCGTACACGATGGCG	60.51	20	CCAATGAGACACACTCCCAA	59.52	20
TTTTGTGTGTGTTTGCAACG	59.221	20	TTCTGTGCATTGCCATTGAT	60.08	20
TTGGCGAGATCATTTCCTTC	60.155	20	TAACTGACCTGCAGCGGAAT	60.796	20
CGATTGTGGTGACGAAGATG	60.112	20	GCAAGCTTTCCCACTCACAT	60.263	20
ATCGTTGTGAATTTGGGGAA	60.17	20	AAAATGGTTCGTAACTGCCC	58.952	20
GCTTCCAGATCTGCCAAAGT	59.434	20	GGGTTTAGACGTCATGCACA	59.572	20
TGGCATAACAAGCTAGGACAT	57.408	21	CCCAAGACCCCAATTTGATT	60.91	20
ATGTAGCCGACCCCAATTTA	59.297	20	TCGAAGAAGCGAAAATCACC	60.331	20
CGGTGGTTTAATGGAGTTGC	60.365	20	AGCTTCGTAATATGGGCGAG	59.343	20
GGGCAAAAGCCAATGAAATA	59.907	20	TTGGGAGTCAACTGATTGCTT	59.726	21
AACGAACGAAGCTGAGCAAT	60.022	20	TCGAGACGGGACTGTGAATA	59.241	20
CCCAAGACCCCAATTTGATT	60.91	20	GAATCCCATATGCGAGGATG	60.26	20
TGTAGCCGACCCCAATTTAT	59.297	20	CCGATCGAGCTGAGAAAAAG	60.088	20

TGACTTTCGGATTTTCGACC	60.051	20	GATTTTCTTGGATCTCATGCC	58.586	21
TAAATTTACTCGCTGGTCTATCTAT	57.426	26	TCCGCACTTGAAATTCCATC	60.983	20
CCTGAGGTTCAGGGTCCAT	59.905	19	CCCAAGACCCCAATTTGATT	60.91	20
GATGAGATTCCCGAGGTTGA	60.011	20	TCAGCAGCCATCTGTTCTTG	60.136	20
AGAAATGCAAAGACCAAGAACA	58.882	22	CCCAAGACCCCAATTTGATT	60.91	20
TGTCAACCATAATATATGCATCGA	60.127	25	AAATTGGGTGGTCCATCAAC	59.508	20
CCCAAGACCCCAATTTGATT	60.91	20	AAGAATGCAGCGCAAAGTCT	60.162	20
CCCAAGACCCCAATTTGATT	60.91	20	TTTTGCCGGTCGATAACTCT	59.708	20
GCGAACACAGTTTTTCAGCC	60.817	20	GCACACGCTGAAGGATCATA	59.83	20
GCTCTTGAAATTTTCTTATTGTTCC	58.842	25	TGTCTTGTGCTGAAGATGGTTC	60.299	22
TTGTGTCAGACTTGTTCGGC	59.88	20	TGGCTCAAAAGTAAATGGGG	59.931	20
CCCCCAAACTTATTGACAAATG	60.443	22	AGATGGTGCAGTTCTTTGGG	60.111	20
GTCAGCGAATTGTTGCAGAA	59.995	20	ATTGACGTCGTTGAAGAGCC	60.263	20
TTGCATTTTTCATAGCCCAA	59.146	20	TGTGTGTAGAGGGACAACGC	59.751	20
CCTCAACCAGAGTCTCCTCC	58.819	20	AATCCGTTATTTCTCCCGGT	59.666	20
TATTCCACCACGCTCCTTAT	57.184	20	GAGCTGATGGAAACACTTCG	58.443	20
CCCAAGACCCCAATTTGATT	60.91	20	GGATGTACCAGCATTGCCTT	59.962	20
GTGAATAGCTGCTGGTGGGT	60.142	20	AAAATCGCACGACGAATACC	59.967	20
GAGAGCAAAGAGTTGGCACC	59.997	20	CTCCTTCAATTGCCCTTCAC	59.67	20
GATGGATGGATCAGAACCGA	60.839	20	CGTTCCGACCCTTCAATAATC	60.678	21
AACAATTCGTGTCATGGTCG	59.42	20	GATTCGAATAGGAACGCGAG	59.807	20
CTTGCGGTCTTGAACATGAA	59.84	20	ATGTCATGATCTTCCCAGCC	59.893	20
TGGCAGATTCCCTTGATTTT	59.505	20	AGGCTGGTCTAAAGCGCATA	60.003	20
TGATAGCAGAATGATTGAAGCAA	59.867	23	TCTGATGTGAAATGTGTGGATA	57.465	23
TGGGACGATAAGGGATAGTG	57.488	20	ATGTAGCCGACCCCAATTTA	59.297	20
TGAGATTTTTGGTGTCAGTGGT	59.496	22	GCATTTTTCACTTAGCCGAGA	59.488	21
AGAACCCGGTTTGATCTGTG	59.966	20	GGGTGAGGGAGAAAAAGGAA	60.414	20
GTTAGTTGTTGGCCCGGTTA	59.861	20	GAGGATCGACTGCTCTGGTA	57.97	20
TGGAATTCAACATCAATGGTTC	59.668	22	TCACCAAATAATATAGTTATCA	57.39	27
CGAGATGTGAAGATTGAGGC	58.388	20	GGGATTTCATCCAAAAACCTG	60.528	21
CATACCTCGGCCTTTGATGT	59.955	20	GAGCAACTTCTTGGCTCGTT	59.621	20
TACGCAAAGGCACTTCTCAA	59.609	20	AAGTAGATCCATGTGGCCGT	59.434	20
GAAGTACCTGCCTACTCGTCTGA	59.957	23	CATCTTCATCTGCCAGTGCT	58.987	20
GAGGGAGGCACTAAGAAATGG	60.082	21	TGTATGTCGAGTCGAGTGTGA	57.825	21
GTCTCTTGGTCTGAGCCTGC	60.143	20	GTTCGATCGTTTGTCCTCGT	60.119	20
ACGCAATTCATCACAACTGC	59.728	20	CGGCTTAGGGCAGATAACAG	59.861	20
CCCAGAAGCAGAAGAGGTTG	59.982	20	AACACCGGATTCACTTTTGC	59.978	20
GGGTCCACCTCTTTTTCCTC	59.912	20	GAGAGGAGCGACACCAGTTC	59.993	20
TGTAGCCGACCCCAATTTAT	59.297	20	GCTGCACATATTATGCTTTGC	58.485	21
CAGCCGAGAACATCATCAAA	59.799	20	AGGGGATCGTAAAGCCTGAT	59.925	20
AGGTGGATTAGTTGTCGTTTTGA	59.92	23	ATGATCTGAAGAAGCGTGGC	60.37	20
TGTATATTCCTGAAGACGATGGC	60.346	23	AATCCCACCCTTCACCATTT	60.422	20
GGCATGCATAATGTGACACC	59.812	20	AGCATTGGCAAAGACGACTC	60.406	20
TGATGATTGAGTAAAAACGACAA	58.721	24	TCACAAAAATATTTCCCGGC	59.773	20
TGACACATGCACATTTCACG	60.164	20	GAACAAAACATTTCGGGGTG	60.206	20
CCGTATCAAGCCACCAAGTA	58.649	20	CATTTAAGGTGCAGCCTGGT	60.132	20
TCGAGGAAGGAGAGGTGTTG	60.377	20	TTCGTCTTTCCCGTTCTCAG	60.366	20
CCCAAGACCCCAATTTGAT	59.59	19	AATAAAATGTCGTGAGCCCG	59.96	20
TCTTTGCGATGAGCTCCTTT	60.096	20	TCCGTTGGAACAATAGGGTC	59.79	20
TTATCCCATCCCCCTTAACC	59.846	20	GGACGATGAGGAGGAAGATG	59.612	20
ATAAACTGTTACTCCTGGGTGC	57.318	22	TTAATGGGAAATTGCGTTGG	60.671	20
CTGCCACCGATTTGAACATT	60.894	20	CGGGCCAGTTAAGCTTGTTA	60.257	20
GACGCTTGGTTGGATAGCTT	59.34	20	TCTGCCTGAATTTGGAAAGG	60.184	20
CCGCCTCCGTAAATAAACAA	59.958	20	CACAACAGAGCATTAGGCCA	59.864	20
ATTCGCTACCGTGTGGAGTC	60.142	20	GATCGAGCTAGCCCAGTTTG	59.978	20
CGGACAGAAGGATGGCTTTA	60.206	20	GGCCTCAAGGTATGAAGCAG	59.836	20
TGTTTTATTGTGTCTTTGTCATTGT	57.745	25	GCCAAGTTGACACACACAGG	60.203	20
CATAAACCACTTCGAACGGC	60.502	20	CCAGAGTTCGTTTTGGAAGG	59.705	20

TGTAGCCGACCCCAATTTAT	59.297	20	ATGTGTCATTGTTTCGTGGAA	58.888	21
CAGCTCTTCAAACTGGGCAC	60.975	20	CAAAAGGTTTTTGACTCTTACC	60.077	25
GATGCCACAACTTAGAATCGC	59.728	21	TGGGCTTTTAAGGAAGACGA	59.817	20
TGATGTTAAGAAACATTAAAAAG	57.883	25	TTGATTGCGTTGCTTAATGG	59.702	20
AGCCAAAAGATACTAAACTTCCA	58.898	25	GCAGCCAAATACACTCAAAAC	60.173	22
AATAAAGCGTGCCTCACCAC	60.14	20	GACTCCGCATAGTGGAAAA	60.074	20
GATGATGATGCCACTCTTGG	59.04	20	CGACGCTGAATGAGCTAGAA	59.322	20
AAACGGAATCGAAGGTGATG	59.933	20	AATCGAGAATGTGGACGGAG	60.073	20
GGAGAAGGATGAGCGAAATG	59.773	20	GAGCGTGCGGAGCTAGTATC	60.147	20
GTGTGAAGGCCATGATTCCT	59.934	20	GGTAGGCTGGTAAGGGCTTC	60.096	20
TTCAGCCCAGCCCAATAATA	60.415	20	GTGGTATGCTGTGGAGGACC	60.395	20
TCCTCCTGTCCTTGCAATCT	59.803	20	CCCAAGACCCCAATTTGATT	60.91	20
TGGGCCGATCCTATCACTAC	59.917	20	TTGCTTCCGTGTTTTATCCA	59.157	20
ATTCCCGAGACTGAGATGGA	59.612	20	CTGCAGCCATCTGTTCTTGA	60.136	20
TTTCTGGTGGAGTTCATTGAGA	59.711	22	TGGTGCTGGAGGTGACAATA	60.112	20
TTCTCTCTGTGCTGATCGAAA	58.736	21	CAAAACAACCGAATTGCACA	60.535	20
GACAAGGCGTGAAGGTGAGT	60.307	20	CAAAAACGAAAGCAAGCTCA	59.226	20
CCCAAGACCCCAATTTGATT	60.91	20	AGCACAACCCAAATGGTAGG	59.853	20
CTATAGGCACGCCGAACAAT	60.117	20	GAAAACGTGCAGCTCAACAA	60.035	20
TGTAGCCGACCCCAATTTAT	59.297	20	CTACCACAACACATGAGGCG	60.175	20
CCCTTTAAGATAAAAATGAATATT	60.57	27	ACCGTGTGCCCCTAAAAATA	59.338	20
GCCCGAGGTTGAAGATGATA	60.036	20	GGAAAGTGATCCTTGGGATG	59.336	20
ACAATCCCAATTGTATCCGC	59.651	20	CCCAAGACCCCAATTTGATT	60.91	20
TGCAATAATTTTGGCCAACTC	59.957	21	AATGCTATTTGGAGCCATCG	60.06	20
ATTAGCAAATTTCGGGACGA	59.547	20	AATGGGGTGTGAGGAAATGA	60.173	20
ATTTGGGAGTGTTCGGACTG	59.966	20	ATTCGAAAGTTTGCCAAAAA	57.431	20
ACTCGACTCAACCTATTTAGCAA	57.311	23	GGCCGATATTTTGGCCTTTA	61.096	20
AGTGGAGCTAGTGAGGGTGG	59.325	20	TAAAGTTTGGTGACGACCGC	61.06	20
TGACCTCGTGTAACTGGCAA	60.301	20	CTATGCCCAAAAACGCTAGG	59.736	20
TTCCATGGGTACAGAGGAGC	60.073	20	CATCATCAGGGGGAGTAGGA	59.879	20
AGGAAGATGAAAAGACAAGCG	58.591	21	AATGGAGTAGATTTTCCCATG	57.552	22
TGCATCAGGCAAAAACTTATCA	60.619	22	TTAATTATGGGACGGAGGGA	59.227	20
AGCAGCTACAACGGTAAGGC	59.545	20	GAGCATGTAACTCATGTGTCC	60.438	23
TGTCCACCAAGACCAAATGA	59.935	20	GGATTCGCAAGATCGACAAT	60.043	20
GTGGTTATGGAGGAGACGGA	59.927	20	AGTAAAGGGTTTGCGCTTGA	59.883	20
GGCTCCGTTTGGTGTAATTG	60.365	20	ACGAATTAGCGTTTGATGGC	60.103	20
GAGAGAAGCCAGGGATGACA	60.349	20	CTCCTGCACCAGAACTCTCC	59.986	20
ATTCACACCTGCTCCAGTCC	60.12	20	AACAAGGGTTTCCATTGACG	59.83	20
TGGGATCTATTTGATGAGGGA	59.329	21	TCCAAATGTAACTCGACCCAC	59.845	21
TTAAGCCTTGGTCCATGTCC	59.933	20	GAGCAACTTCTTGGCTCGTT	59.621	20
CGCATCTTTTGGGATGATTT	59.901	20	GAGGCTCCTTCAAACACTGC	59.997	20
AGCTGCAGACCAACATGTCA	60.473	20	CCCATCACCCACCACATAAT	60.317	20
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CCTCCGGAACTCTCCTAACC	60.067	20	ATACAGTGCCACCACCACCT	60.307	20
AAATTAAATAACCTCGCCGGA	59.824	21	TCCAGATTCGTCCCAAAAAC	59.91	20
GGCTCGCCAAGGTAGATAAA	59.32	20	GAAACTTGATGCTGGTCGCT	60.406	20
ATGAAGCCAAACCCTCAATG	59.933	20	TTGCTGACTCTTCAGCCATC	59.116	20
GAACTCAGCGTCTCTACGCC	60.164	20	AGCTAAAGTCGGGCCAAGAT	60.228	20
TGTGGAGAAAGGAATGGGAA	60.43	20	TGAAACTCCACTGCCCAAAT	60.495	20
CCATGTAAGAAAAGTGGAAGGG	59.865	22	TCGAGGGGAGTGTTGAAGTC	60.238	20
CAAAATTAAAAATGCCCCCA	59.648	20	AAATGGTAGAAATCGCCGC	60.052	19
TCATTGGCTATGGAGGTGGT	60.34	20	TGGATTATGTAGCTGACCCCA	60.337	21
GAACGAGGTTGGCGTATTGT	60	20	TAGAAGGAAACCGAGAGCGA	60.088	20
CATGAGGCTGCTGAACTCAC	59.577	20	GAGCCTTGGAGGAAGGAGAT	59.778	20
ATGTAGCCGACCCCAATTTA	59.297	20	ACGGGATTGAGTTCACGTTC	59.973	20
CGGGGTTCGAGTTCATATTG	60.323	20	TATGCCCAAGACCTACCGAG	60.088	20
TGCTGCCACACTCTCTCTGT	59.764	20	TCGAAAGCTTGTCAGCAAGA	59.864	20
CATCAACATCATCCCCATCA	60.137	20	GGTGAATCAGCAGGGGTTTA	59.933	20

TGGTTGAGCTAAAATCTTTGAGA	59.453	24	TTCAAAAGTTATTTTCGAGGAC	59.667	23
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TGCTAAACGATGAGCTTGGA	59.566	20	AGGTCATGCGTTCAAGGTTT	59.598	20
CGTCGTCGCTACATGAAGAA	60.011	20	TGATGCCACAGTTGGATCTC	59.637	20
GCCGTAGAGTAGATCGGTGG	59.717	20	CATTGCCACTCAAGAATCCA	59.648	20
CCCAAGACCCCAATTTGATT	60.91	20	ATGAAGTGGCATCGCAGATT	60.634	20
ATGCGAAACCGATCTTTCTG	60.214	20	ATGATCCATATAGCCGACGC	59.914	20
CGTGGAGCCTATTTGGATGT	59.955	20	CTTCAGCAGCCTTTGTCTCC	60.134	20
CAAAAACCCCGAATTCATTG	60.16	20	AGAGGGGGTTTGAGGTTTGT	59.834	20
TATGCCCGTGAAAAAGAAGG	60.067	20	ATCGGAAGCTTCAAGTCCAA	59.813	20
AAATGGAGTCGAAGCAGCAT	59.843	20	GTAGGAACCGGATACAGCCA	59.955	20
GGCGTCTCAAACGTATCTCC	59.7	20	GCCGGATGATCTACAAGCTC	59.803	20
CAGCAAATGCAACAACACCT	59.764	20	CCTGAGGACTGATGGTGGTT	59.962	20
GTGTGGCTGTTCATTCTTGG	59.139	20	CTTTAAGGACAGGACAGCCG	59.869	20
ATGTAGCCGACCCCAATTTA	59.297	20	GGTGAAAAACCCGAGTTCAA	59.948	20
GGAGCAAAGCTGTTGAGGTC	59.997	20	AAAATGCCCCTCTTCTCCAC	60.443	20
TTCAATCATATAGAATCTGCTCTT	59.283	27	AACCCTAAATCTTCATCACAC	58.124	22
ATATGAGAAGAGCAAACCCACA	60.014	23	TCATGTAGTCGACCCCAATTT	59.302	21
TGCATCATTTAGCAATCTGCAT	60.617	22	AAAAAGATTTTACGTGTTTCAC	59.169	24
TCAACCAACTGGCACAGAAG	59.873	20	CTCATTATGATGCTCCGCCT	60.199	20
GTGCGCTCTGATGACTGAAA	60.144	20	CCTCTTGCATATTGTGGCCT	60.096	20
GAGGTTTTGGGGGTTGAAAT	60.032	20	TGCATTGGCTGAAGAAAGTG	59.988	20
TGAAACTCCCCACAATCTCC	59.903	20	CTCTTTGAGGGACATTCGGA	60.187	20
ACACACGCATACACACACGA	59.649	20	CACAGCGCTATAGGTTGCTC	58.703	20
TGTGAAACCTCCTTCATGGT	57.971	20	CCCAAGACCCCAATTTGATT	60.91	20
TTGCCTCTAATTTTGGCTCC	59.297	20	AATCAATACGGACTTTGCCCT	59.849	21
TCTGGTCAACATCAATCTGAGC	60.263	22	CATGTCCCCAGAGATGAAAGA	60.058	21
ATCGTTGGCCAGTCGGTTA	61.452	19	TGACAGGAGGAAATAATGAGA	59.502	24
TCTAAATTGCAAAAGCGCAA	59.602	20	TGTAGCCGACCCCAATTTAT	59.297	20
TATTCCGGATCAAGAGGGTG	59.887	20	TGACTACAACGACGATTCGG	59.716	20
TCCAGCCTTTACCTCTTTTTGT	59.304	22	TGATACTTCGCATCTCACGG	59.823	20
CCCAAGACCCCAATTTGATT	60.91	20	AGGCTACATACATCCGCCAC	59.985	20
CCCAAGAATGACTGGGGTAA	59.784	20	TTTGATTGGGAATAATTGGGT	58.163	21
CTCTATCACAACCCAAGGCG	60.647	20	CACCTCCAATCCAGTATCGC	60.483	20
TGTAGCCGACCCCAATTTAT	59.297	20	GCTGCGTTTGTATGGAACTG	59.347	20
GGTTCGTCTTCAACCACGAT	59.973	20	TTCCCGGTACGACGAAATTA	60.315	20
GCAGGGCATGAACAAACAAT	60.905	20	CCTTTGTTGCACTAAGTTCCAA	60.746	24
GGCATTTTAACTTTGATCATTAAC	59.267	25	TCGATTGTCCACAATTGCAT	59.931	20
TGTAGCCGACCCCAATTTAT	59.297	20	GGCTAAAATCGGTCAAAACG	59.586	20
CTTCCTCTCCTTCACCCTCA	59.375	20	TGATGAGGATTCTGTGGTGC	59.637	20
GCATGAAACTTGGAATGGAAA	59.93	21	TGCTTAGAAAATAGGAAATGT	59.212	24
CGTGTACGAAGGTCACGATG	60.175	20	CCAGCCTTCCAAATTACCCT	60.312	20
ATAAAATGGGAGCGGAGAGG	60.411	20	GATGTCCGCCGTTTCATAAT	59.791	20
GGCATGAAACGGAATAGCAT	59.929	20	CCCGGATTGACACTCCTAGA	60.065	20
AGAGGACCAGCACCAGAAAA	59.844	20	CCAGCTCTTTCTGAACCCTG	59.982	20
TGTGAAATTCTCTGGGAGCA	59.369	20	GTTCCTGAAACGAGTGATGC	58.287	20
TCTTGTTGTCGCGTTTAATGA	59.359	21	TTGGGACAAAAGAAGCTGAAT	58.823	21
TGCATGAAATCAAACTCCCA	60.049	20	CGATGAATTGGGGGAGATAA	59.717	20
AAAAACCAACTGAATTGCAAAA	58.698	22	CCCAAGACCCCAATTTGAT	59.59	19
CCGATTCGTGGAAACCTGTA	60.883	20	GGTTATGGTTTTTGCACCCA	60.597	20
TTTGGAAGAAAAATTCATCGG	59.042	21	AATGGAACTAACCCAAGTTGA	57.663	22
GAAGGGGGAGACCGAAATTA	60.258	20	TGTAATGCATGGGGGAGAGT	60.34	20
AGATCATCAAAGCCCCTCAA	59.629	20	GGTCCATGAACCCTGGACTT	61.152	20
GTGTTTGTTGTGTGTCTCCCA	59.477	21	CCGTCTCACTCCAATTGACA	59.676	20
TCAAAACTCGGTCTTGCACA	60.427	20	ATGCAGATATGGAGCAATTTTT	57.795	22
AGTCCGTGTTCCGATGAGT	58.067	19	CATTCTATGCCATGCAGACG	60.243	20
ATTAGCCCCATCAAGGGTTC	60.152	20	CCCAAGACCCCAATTTGATT	60.91	20
TGAGCAACCTGAAAATTGAACA	60.648	22	CCCGTGGACGTAGATCAGTT	59.989	20

CAGGTCAACTGAAATCTGAAAGA	59.799	24	GCAGACCAAAGAGAAAGAGTA	59.595	23
TCCCCTTTCTTGACCATCAG	60.042	20	AGGTGTTTTCCCACGTCATC	59.827	20
ACGAGAACCCTCACATCACC	59.969	20	AGAGTGGGGGAGAAGACGAT	60.073	20
TTGGTGCAAAATGTGTTGAT	57.442	20	CTCTAACCCAGCAGCAGACC	60.012	20
CTACAGTCCGTGTTCCGATG	59.161	20	TGCTCATTATTTGATTGGCG	59.662	20
TCCCACATAGGAAAAACAAAA	57.157	21	ACGATGCACAAGACATGAGG	59.707	20
AGAACCCCCTTGATCATTCC	60.133	20	GGCAAAATTCGTTGGAGAAA	60.053	20
CAACGCGTTCTGCATTACAA	60.838	20	GTCGACAGGCATAAGCTTCC	59.843	20
GGTTCATATAACCGACCCCA	59.505	20	TTGGTGCGATAACAATGGTG	60.379	20
TCCCACTAATTTCACCTGGA	57.992	20	CCCAAGACCCCAATTTGATT	60.91	20
GTCATACCCACTGCTCCCAC	60.395	20	GGTCACAACGGAAACAACCT	59.867	20
TGTGCATATTGTTGGGGAAG	59.395	20	CACCCAAGTTTCTTCCAAGG	59.563	20
AGACGAGTGGCTGCTACCTG	60.611	20	AAACCCCTCGTGTTGTTTCA	60.388	20
TTGATGAGCCATAACCCTCC	59.894	20	CAGCAGCCATCTGTTCTTGA	60.136	20
TTGGATTCCCACAATTCCAT	59.991	20	TTTGTTACATGCGGAACCAG	59.585	20
TCGAACTCATCAAAGACCCA	59.215	20	CTTAATGGGTGAGAGACCCG	59.545	20
AGCTTCGAACCCTGACCTTT	60.247	20	CTTCCCGCAAAACGTTGTAT	59.996	20
TTGGGCAACTTGAAGATTAAAAG	59.667	23	ATTTCCACCGTTCAGACAGG	59.966	20
CCCCCAAACTTATTGACAAATG	60.443	22	TTGCAGTCTGAGCAAGGAGA	59.855	20
AGAGGGAGAGTTCGGGAGAG	59.945	20	AATCAGAATGGTTGGTTGGC	59.797	20
TGCAGCAGCCAAGACTTAGA	59.888	20	AGGGCCTGTGCTCATAGAGA	59.973	20
CTCCAATCCATAGCAACCAAA	59.946	21	TGAGGCAAGCATCAGAAAGA	59.673	20
ATGTAACCATGGGCCAAAAA	60.053	20	GCTAGTTGCACCCCTGTCTC	59.874	20
GAATTGGTAGGGTTTTCTGTCG	59.871	22	TGGAGAAGGAGGATCCATGT	59.46	20
GTCCAAATGTGATTGCCCTT	59.797	20	GGAAACCCCATCCAGAAGAT	60.133	20
CGGCATTATCAGTACGACCA	59.566	20	AAAGCTCGAACTTGTGGCAT	59.882	20
CGTACGGAAATCTGATAGGAAAA	59.528	23	CCTTAGCCCAAGTTGTACCC	58.577	20
CCAAATTTGTAAATGCAAACAA	57.71	22	GGTGAATTGTGTCGCTCCAT	60.935	20
ACCAATGGGTGAAAGAATATGG	59.945	22	AAGTTTGCCCTATCAAACAGGA	60.001	22
ATGTAGCCGACCCCAATTTA	59.297	20	TGGTGGGAATCTTTTCATCG	60.832	20
TACTCCCTCCGTCTCACTCC	59.254	20	ATTGGGGAATTCACGGAGAT	60.526	20
CCTCTGAAAGCTCGGTTCAC	59.989	20	CCTTCGTTTATTGGGGATCA	59.756	20
CAAAGCTCTTGGATTCAGGC	59.955	20	TGGAAAACCATCATCAACCA	59.75	20
TCAGTTCCGTCTAGGCTTCAA	60.001	21	TCTTCTAGCAGATGACCCTTTT	59.9	23
CAGCGTTTGAGTCCAGGTTT	60.291	20	CCTCCGATTTCTTACCATGC	59.528	20
GGTCATGTGTTCGAGTTTCAA	58.61	21	TTGCTAGCCTCATCATTCCA	59.375	20
ATGCAAGGTGCATGTGTCTC	59.714	20	GCAAACAGAAAATGAGGGGA	60.051	20
CCTTTTATACGGGTCGGGTT	60.068	20	ACCAGCGCTAACACGAAATC	60.278	20
CGGAGATTCGCAAGTTCAGT	60.397	20	TCCCACCAATTTGTCCTAAAC	58.798	21
CGTTGGCTCGACGTTATCTT	60.27	20	GAGCAGAAAATCGTGAAGGG	59.813	20
TGGACCGAGTCATCTCTGTG	59.82	20	CCACTATGACCATGCCCTCT	59.95	20
GCAACGGAAACAACCTCTTT	59.218	20	ACACAATCAAGGCATCAGCA	60.272	20
TCTGGCCTGATCTACAGCCT	59.973	20	GCTAGCACCTCTTCTATTGCTG	60.183	23
CTCTGCTCAGCCCCTTCA	60.221	18	AGAAGAGGATGTTGGCGATG	60.218	20
GCTGTAGCTGACCCCAATTT	59.198	20	TGTCCATCATTCCAGGCATA	59.883	20
GATGCGTTTGAAGGGAAAAA	60.053	20	GCCCCTACAAGGAGTTCACA	60.111	20
CCGAAGAGCATAGTTCAGCC	59.978	20	CTGCCCTTTCAAATGTTGCT	60.249	20
ATAAGGATTCCGGGTTTTCG	60.143	20	TCTCCAACGGCATCTCAAG	59.926	19
GGTTATTTATTAAAGTTGGAGGTG	58.455	25	AAGTGCACAAGCACTCGCTA	59.812	20
AATTCGAAAATTGCGTCTCC	59.162	20	GCAAGGCTGGAACTGAAAAG	59.993	20
ATCACCTATGCATGTTGCCG	61.862	20	AACGTGCAACGAGAACTTCA	59.49	20
CCATGTCACAAGTCACTCGC	60.319	20	GTAGTGGTATGGTGTGGGGG	59.966	20
TTCAGTCACAAGAGCACCCA	60.44	20	CAAAATTCCATGACAACCGA	59.371	20
TTTGATTGGGAATAATTGGGT	58.163	21	GCGTCCAAATAACCGACACT	60	20
ACGGGTTAAAAATCCCAACC	59.924	20	CTGATAGCTCCGACAACCGT	60.277	20
TCGCATCTGGGATAATGAAA	59.065	20	CCACCGCTAATTTGGAGAAA	60.067	20
TTTGATTGGGAATATATTGGGT	57.28	22	GGTATGGGGTGATGTCGATT	59.488	20
CCACACCCCTTTTGACTGAT	59.82	20	TTGATCCACCCTATTTTGCAT	59.287	21

TGCTAGGCATGTATTTATTATTGGA	59.043	25	TGAATTCTTGCACGTTCTCG	59.988	20
CCTCGTGCAAGCATTACAAA	59.872	20	TGTAGCCGACCCCAATTTAT	59.297	20
TTCAAGGTTCTCGCTCTAATCC	59.856	22	TGTTTTCATTTGAATAAATACGT	58.972	26
GCATTATGTAAGCTCAAATAGGCT	58.177	24	TGATTCGTGAACATTAGGCTCT	58.861	22
CTCAAGATGCGAAGCAAACA	60.134	20	CGGATCAAACCCTAACCCTT	60.18	20
CTGATCACCCTGTTTTGCCT	60.111	20	TCACTGCATGTTCGGAAAAG	59.84	20
TTCGCTTTGATTATTAAATCTTCTT	59.313	26	GCGATATAATCTCTGACGATTG	60.102	23
GAAAGAAGCTCCCGAAGGAC	60.328	20	CTCGAGAAGTAATCGTCGGC	59.978	20
CAAGACCCCATTTTGATTGG	60.162	20	CACTGGAATGTCAAGGCAGA	59.831	20
CACCGGTTGGACCGTCTT	61.968	18	GGGGGCTATCTTGTGAGCTA	59.292	20
TCATGATGGTCCTGATGGAG	59.425	20	AGCGTTCTTTCCCGAGTCTT	60.382	20
TGTGTTGGTTGCAGGTTCAT	60.008	20	TGTAGCCGACCCCAATTTAT	59.297	20
CAGTTGACACTTGGGGGACT	60.002	20	TCCCATGTTCCATTCCTCTC	59.862	20
CCATGCTAATTTCAGGGGAA	59.894	20	GTTGAAAGTCCGGTGACGAT	59.973	20
AGAGGATGAAATTCCCGAGG	60.401	20	AGCCAATCTCCTCTCAGCAG	59.703	20
TGTGGAACCAACACGATTTT	58.874	20	TTCTACGCGGCCATCTCTAT	59.829	20
AAGGGGCTTCTTGTTGGAAT	59.94	20	CCGGCAGTTACATATTCGCT	60.117	20
GGATCTTACGGAGTTGAGCG	59.836	20	ATAATCAAGGGTGCAGTCGC	60.103	20
AAAGTTGGTGCCCAGAACAA	60.529	20	AGGTTGCGTACATCTGACCC	59.997	20
TGCCGTCGACTTTATCAACA	60.257	20	GCCCCGCTCAGATAAACATA	60.06	20
GTTTGGAGGTCAGGTGTTCG	60.545	20	TGGCAATTGTACAAACAATTCA	59.288	23
CCTTGTGCAAATTAATCCCG	60.315	20	CATCTCTTGCATCACTATGGGA	60.096	22
TAGGGAAAAGTCATCACGGC	60.074	20	ATCGACAGCACTTCCAGCTT	60.02	20
CTTGAATATCGGCGAAGTGC	60.742	20	GTTGGGCAGCCAAATATTGA	60.837	20
ATGTAGCCGACCCCAATTTA	59.297	20	GATGCCATATGCGATGATGA	60.427	20
ACATCCATCATCATCAGCCA	59.882	20	ATGTAGCCGACCCCAATTTA	59.297	20
ACTTCGCCACCAGTTTGTTC	60.156	20	ATTGACATCGAAATCCTGGG	59.75	20
ATTATTGAATGGGCCCAAAA	59.124	20	TCTCGTTTCAGCACCAAATCT	59.867	21
TGGCTATCCTCAGCTGCTCT	60.263	20	TTCAGCTCCTCACCAAATCC	60.195	20
TATATGTGGCCTTCTTCCCG	59.916	20	ACCATGTCCGGCAACATAAT	60.081	20
CCTCCACTGGACACACCTCT	60.153	20	CAAGTTGAATCAGAACGGCA	59.84	20
TCACTTATCCCTCCGAATGC	60.036	20	GGTTCAAGTGTTTGGGAGGA	59.943	20
TAGCTCTGTTGCAGCCGATA	59.735	20	CCACTAGAGATGACCTACAAG	58.848	24
AAAGCCAATTTTGGTGGGTT	60.573	20	TGGTCTCTGTCCATTGTGCT	59.261	20
TCCAATCACTTACCAAATGCAC	59.867	22	TCCATTTCTAGACTGCGAGG	58.048	20
TATTCAATTACCTTGCCGGA	58.109	20	GCTTGCACTTTTCGACCAAT	60.257	20
CTTTCCCCAGCATCAACATT	59.933	20	AGCAAGCGGAAATCACCAG	61.332	19
CGTGTGAACCAGCAGATGAG	60.463	20	CTTAGGAGTCGGAGTGGGTG	59.715	20
TCAGAAGGGGTTATGTCCTCA	59.536	21	TCAAGCAATAGGTCTTTAATAT	58.367	25
CAAGTTCTTTCAAATTGGTGGAC	59.9	23	TCCACCAAACAATTTATGGAAA	59.208	22
CACATGGCTCAGACGACACT	59.897	20	ACGAACCAGGCCGACTAATA	59.592	20
AACACTCACAGGCGGAGTTT	59.769	20	ACTTTGAAGCTCGGAAACGA	59.993	20
GGTACAACATCATGCCACCA	60.249	20	ATAATGAGTAGGCCGCATCG	60.081	20
AACCTCTGCCGTGAAATCTG	60.255	20	CAGCAAAGTCACGAGCATGT	60.056	20
TGACCCTAGTGGTAACACGG	58.496	20	TCCCTGTAGAGGCAATGGAG	60.21	20
CAGCCATGAATGAGAGTGGG	61.63	20	TGCCAAGATTTTTGCTCCTT	59.823	20
GCTCTCGCTGCTTCTGTTCT	60.043	20	TCGTTGATTGTACGAGTCGC	59.871	20
ATAAAACCTGCCGGAATCG	59.908	19	GGTAACGTTTTCCGACCAAA	59.839	20
AAAATTGGAGACGGCATTTG	59.938	20	GCGAAAGGTTTTGGAAATCA	60.053	20
TCCCTAATTCCCCATTCCTT	59.6	20	ACACATAGGGACGGTGGTGT	60.159	20
GGGGGCCAAACAAATATACA	59.525	20	TTTCCCATGACTTGCTGTTTT	59.601	21
GTACTTGTTCGTGTTGCCCC	60.419	20	GATGACAATGATCCCCAAATG	60.006	21
CTGAAAGGTCCCAGGTTCAA	60.081	20	ATTGCACCATGCATTCCATA	59.775	20
GGCATTATGTCATGGTTCCC	60.021	20	AGGTTGCGTACATCTGACCC	59.997	20
TGAAAAAGGGGTAGATCGGT	58.503	20	TGTACTCAATGAAATAGGGTGT	57.629	24
TATGGTAGCTGGCTCGACCT	59.859	20	TTTTTAGCCGACCCCAATTT	60.645	20
TCGCCAACTTCCTCTGATTT	59.813	20	TGTCACACGTATTTTTGCAGC	59.79	21
ATGCCCGAATTTTCCCTAAC	60.15	20	TCGAGGCAGAGAGGAGAGAG	59.962	20

GTGGGCACCCAACAAAATTA	60.597	20	ATGTAGCCGACCCCAATTTA	59.297	20
ACGTCGGGTAGACCAATGAC	59.851	20	TACAGTCCGTGTTCCGATGA	60.112	20
AGAAATACATGCAGGGCTGAG	59.35	21	TGTAGCCGACCCCAATTTAT	59.297	20
ACCAAGGGTGCGAGAATATG	59.955	20	AAGAGCAGTCAGTGGTTGGG	60.298	20
TCCTCTTGGGTTGTTTCACC	59.943	20	GGATTCAGACGTAAGGAGCG	59.836	20
AGAAAAAGAAGAGGGAGCGG	59.955	20	AGTCTCTGGATCGAATCCCC	60.421	20
CGATTTATTGCTTGCCAATG	59.169	20	GCAACGGAAACAACCTCTTT	59.218	20
CATCATCATGTCCACCGAAA	60.33	20	ACCCTGGGGGCTATCTAGTG	60.34	20
CGAGGAGGAGGAAGAGGAGT	59.945	20	GCTCCCACCACAACCAAT	59.318	18
GCTTTGCAACACACATTTGG	60.157	20	TCCATTCCTTGGGAAGACTG	60.042	20
ATAAATCGAACCTCCCCACC	60.017	20	GGCTGTGGCAGAAAAGAGAG	60.134	20
AATGCAACCTGAAAACCTCG	60.11	20	AGCCGACTTCACATAGTGGG	60.134	20
GTCAGAAAAGCCCACCTCAA	60.232	20	CTCGAAACCACTCAACCCAT	59.966	20
TACCCTCCCCTGTTTTACCC	60.046	20	CGACGGAGTTGGAGAAGAAG	59.982	20
GCTACATCCAATGCTGGTGA	59.679	20	TTCTTGCCCGACTTCTGAAT	59.813	20
ACCGATATTTTGGCCTTCGT	60.692	20	TCGATCTTAGTCGGTCCAGC	60.362	20
CCATTGAGACTCGAACCCAT	59.927	20	GTTGGTGGGATTTGAACCTG	60.21	20
GATTTTGCCCAAGAATACCG	59.411	20	GCGTGCTGAATCTTAACCGT	60.278	20
CTTCACCGATCCAAGGAAAA	60.044	20	AGAATTCCGGTAAGCCCAAT	59.799	20
CACACATTCAACTGGATGGC	59.967	20	TTCATGTAGCCAACCCCAAT	60.192	20
GGTTTGAATCCCACCAACAC	60.073	20	CCCAAGACCCCAATTTGATT	60.91	20
TATTGTGGCACTCTCCCCTC	60.073	20	AACAACAGCAGCAACAGTGG	59.946	20
TGGAAGATGGAAGAGGATGG	60.003	20	GAGCAAAGCAGCTCATCTCC	60.249	20
CACCTCAGCCACCCTAGAAG	59.861	20	TGAATCGACAGGCTTGAGTG	59.984	20
AACAGATCGTGTTCGTGTCG	59.751	20	TTTATTGGGGGAGAATTCTTGA	59.782	22
ATGAGTCGGTTTGTTGAGGC	60.119	20	TGGGAGTGAGTGAGTGTGTG	58.154	20
GAAAGACCACGGCGATTTTA	60.074	20	GCGACATGGAGGAGGGAC	61.66	18
TTACCGGTTGACAAATTCCC	59.662	20	AATGCTGTTAGGTGCATTGAA	58.307	21
TCCTCGACGCTGAATGATCT	60.914	20	GATGATGATGCCACTCTTGG	59.04	20
ACATGCAAATCCATTACCCA	58.697	20	CACAAGCACACTTGGGAGAA	59.873	20
ACGTGGAGGACAGTGGTCTT	59.604	20	CTTTGCTTGAAAATGCCGTT	60.244	20
CTCTTCCTTCCCAATTTCCC	59.875	20	ACGGTAGGGGGCAAAAATAC	60.075	20
CAGAAGATTCATATTGATTTTGAG	59.034	26	TGGCTTGATTTAGCCCATTT	59.547	20
AAGGCGGTGTATTATGTCGG	59.845	20	TCGTATTCTTAGGTTGCATAAC	59.924	24
TGATCTCTCCCGTGAAAACAT	59.541	21	GTTTGATGTATGCGTCGCTG	60.288	20
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TTTCCAACAATAACCCCGTG	60.587	20	GTCGCAACGGAAACAATCTC	60.646	20
GCTCGCTGGATCCCTAGAAG	61.383	20	TAACCCAATCGCAGATTTCC	59.901	20
TTGAAAACCGATTTCCCTT	57.113	19	TTTTGCATACCTTCCGATCA	59.112	20
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TGAGGTTCCAATTATATCCTTATG	59.654	25	TTCCCAGCACTCATCTGTTTT	59.726	21
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TTTTTGAATGGCCGTTTACC	59.81	20	ATGTAGCCGACCCCAATTTA	59.297	20
TTGTCAAGATTGGCTTCGTG	59.84	20	TTGAATGCACAGAGAGATGGA	59.384	21
CGGCTTTTGTTACATGCTTTC	59.772	21	TGCCATGCTATCCTAGTATTCG	59.257	22
AAACATGCCCAACATTCAGC	60.905	20	CAACGGTAAGGTTGCGTACA	59.65	20
CTTCCAAAATAGGGGGTTCC	59.639	20	GTCTATGTGCGTTTTTGGCA	59.735	20
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TCAGGTCGATATAATTTTGGGTTT	59.978	24	AGGCATGATCAATCAGCTTGT	59.714	21
CCCTTGGCCATTACTTGTGT	59.853	20	CAGCAATCGCAACTTCAGTC	59.596	20
TCTCCCTACTCTTTCGTTGCTC	60.019	22	TAGGCAAAAAGGAAGCATGG	60.202	20
GAACCCCATTTGTGGAAGAA	59.767	20	ATGACGCGGGTGTTCTTATC	59.962	20
TTTAAATGTATCCGCCGTGA	59.029	20	TTTAAGTTTATTCATTTATGTTG	57.211	27
TTGAAGATCCGGAAATTTGT	57.125	20	GGCATCATCAATAGCTTGGG	60.435	20
GGATCGTAAAGCCTGGTGAA	60.074	20	GGCTGGGAACCAATAATCCT	60.152	20
GAGAATGTTCCCGCTACTGG	59.694	20	TTCCCAAATCATCTTCACCC	59.727	20
ACAGTGGAGGAGCTCGCAG	61.753	19	TCTTCGCCTTTGTCTGGAGT	59.989	20

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CGGACCAGACTCCAACTTTT	59.183	20	CAAATTGGCCCCTGATCTTA	59.894	20
GCACGTCCAGAGGAGACCTA	60.408	20	CCAAATCCCCTTTTGACATTT	60.041	21
AAAATGCGGCATCTGAAAAC	60.081	20	TCGTCAGGATAAGGGTGGTC	59.927	20
CTTCATAGTACGCCACCCGT	60.015	20	TGAATCATGAAATTGATAAGAT	60.205	27
TTCCTCAATTTTGGGACCAG	59.903	20	TGGTACAAGAGGCCGAAAAG	60.241	20
TGATGTACGCACTTGGTGGT	60.032	20	ATCATACTGCACCCCTACGC	59.985	20
GGGGCGTGACAATATCAAAG	60.331	20	CGATGCCAAAATGTAGCAAA	59.702	20
CACGTCAACAGGCGAGATTA	59.864	20	GATCCTCATCCTCCTCCTCC	59.973	20
GGATTCACGGATTGAGCCTA	60.036	20	TTGGATAAAGTTATCAAGCTCT	58.188	25
AGGCCAACTGACATCTGGAA	60.656	20	GAAGTGGAGGTACAGCCTGG	59.721	20
TCACTATCCTCATCGGAGGC	60.181	20	CATGGACTTTACACATGCCG	59.988	20
TGTGACGGCAACCAGAAATA	60.111	20	TGTGGCAAGGTTTTAGGAGG	60.103	20
TTTCATGTGTGCTTATTGTTTTCA	59.575	24	AGGTTTACCACACAATTCAATC	59.687	24
TGCAATGGCTTTTCATTGTT	59.161	20	CCCAACCTCAACATTCTTGG	60.345	20
TCTCCAACAAAATTTCGGGA	60.418	20	GGTGACCAAGTGGCATTCTT	59.973	20
TGTCACCACGCTCCCTAAGT	60.711	20	TGACATTTTTATGCTAGTTTGAC	60.189	25
TCGTGAAAATCCGATTAGGG	59.894	20	TTTCGAAAGGCACAAGATCA	59.395	20
CCCCCTCTCTCAGCTAGGTT	59.834	20	CCCCGCTACAAAAGATTGAA	60.067	20
AGTTCTTGTTCGCGATTTGC	60.395	20	AAAACCCTCAACATCCATGA	57.835	20
CCCTGCTCAGTAGATTCCTTTG	60.254	22	TGTTTTATCTGTGCCGTTGAA	59.216	21
AAGCTGCAGGGACAATTCAT	59.7	20	ATACGTCGCACAATGACCAA	59.995	20
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ACCCGCTATCAATGTTCCAC	59.82	20	CTACCCTGGGTTTGTTCCTG	59.444	20
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GACGTATGCCAAGCATTTCA	59.694	20	AGTTCAAGGATACCCCCTGG	60.183	20
ATTGTGGAGTTGCCCATCA	59.909	19	GCCACAAACCTGAACCAACT	60.012	20
GTGCATGCAGCTGAAGATGT	60.024	20	CATCATCGGGAGGAGTAGGA	60.027	20
GGAGGTATACTTTGCTGCAGGT	59.68	22	GTTAATAGGGCAAAATGCCA	57.662	20
TCAGCAAAGAGTAGTTTCCCA	57.622	21	CAATTTCAAGAACCCCCAAA	59.772	20
GTTCGGAGTTGGGTAGTTGC	59.598	20	GGAAACCACATCTAACCTGTTC	58.572	23
ACCGACAAAAGCTAGGATCG	59.336	20	AAGCTGGAGCTAAGGGCTTC	60.117	20
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CACCTCCTTCCATGCAAACT	60.111	20	CGCATCCAAATACTTGTTCG	59.182	20
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TGGTGGAGGTTCTCCCTCTA	59.649	20	ATGAACTGGTGGAGGTGGAG	59.962	20
GAAGCTGAGCAACGAGAAGG	60.277	20	TGCAGTGATCGGTTCTTCAC	59.837	20
AAGGTAGGTCTGCCCCTGTT	59.994	20	AAATGGCCCGTAGTTTAGGG	60.197	20
TCGTCTCTCCCTATTCCCTCT	59.29	21	GGATTCTTGAGCCAAAAACG	59.685	20
ACACCAATCACACCGTTGAA	59.855	20	GTTTCAGGGCAGACTTGCTC	59.997	20
CTCCCAAAACCTCACCTCCT	60.48	20	AAAGGGGCTTCCAATCATCT	59.903	20
CGAAACATGTCAGGCAAAGA	59.84	20	ATGTAGCCGACCCCAATTTA	59.297	20
CCGTGCACAATTAGGACTGA	59.716	20	AAGTTGTCATTTCGGCCTCA	60.636	20
AATCCCTTGGGAAATGAACC	59.996	20	TTCTCGGCATTCTCATCCTC	60.303	20
GGGTCTAAAGATGTTGCCTCA	59.184	21	TCTTGGTTAATGGCGATGGT	60.331	20
CACAAACCAAAGGTGCATGT	59.465	20	TCCTGAAACGAGTGATGCTC	58.96	20
TACTTTAGCTGGCAGGCACC	60.407	20	TGTTGAAATTGGACCAGCAA	60.088	20
ATTTTGAACGGTAACAGCCG	59.996	20	CCATTCGGGACATCTTGTTT	59.79	20
TGAAACTCCCAACCCATGTT	60.21	20	GGGGCTGCTGATAGTGTGAT	60.104	20
CAATGTTACGTTCAGGCCAA	59.585	20	AGGCTTAACCAATTTTGGGA	58.556	20
AAGCATTGGCTTCAGCTGTT	60.022	20	TCCATAGTGTGCGGTGACAT	59.992	20
CTGGTGCTAGTACATCCGGC	60.678	20	CAAAATAGCCCGAGGTTGAA	60.067	20
GATGGGCCTCTTCATTTTCA	60.014	20	GCATGTGAGGGTGGTTGAGT	60.999	20
CCTACTCCCCCGTAAATTCC	59.661	20	TTCGTGATTAATTCCGACCG	60.827	20
TGGGCAGCCAAATATAGAGC	60.196	20	CTGCAGCCATCTGTTCTTGA	60.136	20
AAATGCCAAGAAAAACCGAA	59.564	20	TAAGACCAGTTTTGCCCTGG	60.103	20

GCCAAAACCGTGTAGTTTGG	60.399	20	TCAACGACGAGCTGCTTAGA	59.888	20
ACTCCGTGTTCACCTTCTGC	60.307	20	GTGTGGGTTCTTTTATTAATTC	59.323	26
TGGAGTAATTGCATTACATTCGA	60.374	24	TCATGTGATTCAGGGTTTAGG	59.429	22
TGAACATTAAAGAATATCTACTC	57.829	27	CTTTTGTACGGGTCGGGTT	59.838	19
GAATATTATGGCACCATGGGTA	58.585	22	TTGCTTACGGAAACAGCAAG	59.108	20
TAGCCGACCCCATTTTATTG	59.789	20	ACGCAATTTACAACCATTATCT	59.375	24
CAAAACCATGGCATTTTTGA	59.396	20	ATATAATGGCGTAGCGCAGC	60.241	20
TGTACAAGAATCGTCACCGC	59.722	20	CGACTGGTCCGAATCTGAGT	60.261	20
CGTATCATTTGGTGAGCTTGA	58.785	21	GCGACATTTAAGAGTTGGGG	59.569	20
AATCCTCAAGGACTGATGCAA	59.685	21	GCCTAACAATTACGAGGACAA	59.569	23
AATTGGGGTGTTGGAACTTG	59.688	20	TTTCTTGGAAATTCTCCTCCC	59.519	21
TCTATAAGCTTCGGGAGGCA	59.938	20	GGCAAGGTTCGAGAAAATGA	60.192	20
GCAATCATGCATCACCACAT	60.371	20	TGCTCTCTCTCTCTCTCTCCG	59.164	21
GGCGTGTGTTTGCCTTAGTT	60.176	20	ATGTAGCCGACCCCAATTTA	59.297	20
TTCTTGGTCTCCAAAGTCCG	60.224	20	GCACTCCAAGACACCTGGTT	60.159	20
TTGAAGATCCGGAAATTTGT	57.125	20	CACCAAAGCCTTAATCCCAA	59.931	20
TTATCGTTAGCATACCGGGG	59.81	20	TGAACACAATCAGTATCGTAA	60.514	27
AGATTGAGCCCGAAAATTGA	59.645	20	TTGCCAACCTCATTTGTTTT	58.12	20
TGGTCAATGAACCAAAGCAA	60.088	20	ATGTAGCCGACCCCAATTTA	59.297	20
GTAAGTAAGGCGGTGGCAGA	60.27	20	GCAATCATGCATCACCACAT	60.371	20
CTTTCGATGCTCCTCTCGAC	60.096	20	GATCCGAACGCAAAACAATC	60.457	20
ACTCCTGATGAACCCCACAT	59.232	20	GCCGCGTACTCTTGTCTCAT	60.428	20
AAGAGGCGTTTGGGAGAGTT	60.247	20	TCATGTAGTCGACCCCAATTT	59.302	21
CTTTGCCCTCTCTCCATCTG	59.943	20	AAGCACTTGAATCCCACGAC	60.119	20
TTTGGTTCATGTAGCCGACC	60.894	20	ACCCAATGGCCGTTTATGTA	60.074	20
TGCAGAAGCATTATTCATCG	57.477	20	TGTGTTGATGGAGCAAGAGG	59.831	20
CAGCCGAGAACATCATCAAA	59.799	20	CAAGGGGACAGTAAAGCCTG	59.728	20
CGCCCAGTTCTGGTCATACT	60.134	20	ACTCCCACCAGCACGATTAT	59.434	20
CTAGATTGCGGGTTTTCCAA	60.067	20	GCTGGAGCAAACTCTTCTGG	60.134	20
AGGGCTTAAACTCGATTGGC	60.582	20	CATTGATCGTATTTGGGATCTT	59.693	23
AATTTCGAGCTTTCCCCAAC	60.431	20	TGCAATGGCTTTTCATTGTT	59.161	20
AGAAGATCCGGACGAGGATT	60.037	20	CGTGGCTGCCATCAGTATAG	59.322	20
TTGACGACGAAGCGATAAAA	59.443	20	GATCTCCTTCACCACCTCCA	60.048	20
TCAGAAGGGGTTATGTCCTCA	59.536	21	CCATTGCCATCAACTTTGAATA	59.832	22
GATCCCCTGCAAGTGTGACT	60.12	20	AAGAAGCTGGAGCTAAGGGC	60.117	20
AGCATCTAAGGAACATGGATACT	58.74	24	TCCCACATTCACGTTCTACG	59.566	20
CCGGAAGAAAGAGTGGGTTT	60.467	20	ATCATGTGCAACTGTGTATGCT	58.187	22
CAATATAAGAACATTTATGGCAA	58.564	26	AGATCATCAAAGCCCCTCAA	59.629	20
TGTGATTCGTTGTGTTTTGCT	59.234	21	TTCCACTTGCTCGACTCTGA	59.701	20
TCCCAAACTTGAATCCTTCG	60.044	20	AACAGCAGTGGCAACAACAG	59.946	20
CAAGCTCCAAGATTCTCCCA	60.331	20	AAGTCTGCTTGATGTGGCCT	59.874	20
TAACTGTGATCACGAAATGCG	59.744	21	TTTGATTTCGCAATATGGTTTG	59.84	22
GATGCAGCAACTTCCTCTCC	59.957	20	CTCCTGCTTCACCTCGATTC	59.95	20
GGTTCTCCCTACTCCCCCTC	61.195	20	CATGCAACACCAAACAATCA	58.966	20
GTGCCCACACTGCTCAACTA	59.905	20	GGAGGTCGAGATTCATCCCT	60.421	20
CATCATCAACGTTCTTGGGTT	59.845	21	CCTGAAACGAGTGATGCTCC	60.801	20
TGTAGCCGACCCCAATTTAT	59.297	20	GTGCGGTACGGAAAGGAATA	59.96	20
AATCCGTACCAAATCCCTCC	60.017	20	TTGGAGTTCTTGATTTGGGC	60.051	20
CGGTTAGAGTGACCGTTGGT	60.028	20	TTTTGAGGATTCTGGATGCC	60.014	20
ATGAAATTCAAAAGGGGGCT	59.777	20	CCGGACAAGGATCTTAGCCT	60.59	20
TCAAATGCGAATGGTGTTTC	59.523	20	TTCTCTCTCACACACACGCA	59.126	20
CCGAAGTGCTAGACCCAAAG	59.869	20	GTCCCATCAAAATCGGAAGA	59.871	20
CCCCAAACTTATTGACAAACG	59.366	21	ATGAGGAAGATGAGCCGAAA	59.773	20
GGCAGTACTTGAACCTTCGC	59.882	20	AGCATCATGAGGAGGAGCAT	59.792	20
TGGCGACTCTCTGTCTCTGA	59.846	20	GCGGTTCTTCTCCATCACAT	60.081	20
AAATTTATTTTGAGCCGGGG	60.142	20	GAGCTCTGCACTTCGTCCTC	60.292	20
ACGTTTTCTTGCCCACAAAC	60.015	20	TGTAGCCGACCCCAATTTAT	59.297	20
AGGGGAACACTCGAAAATCC	60.306	20	GAGGCGGGAAGGGTTGAC	62.969	18

TGGACCATCAATCTCAATTATCA	59.287	23	TTTTTCTTATTTTATCCCGATTT	57.886	25
CCCAGAACACCAGTTCACAC	58.992	20	CATATCTCTCTTTCTCCTTCTCT	59.63	27
TGACCTCGAGTCATCAACCA	60.246	20	GACCCCACATAGTGGGAAAA	59.647	20
CTTTGTGGAGCGATGTTTGA	59.84	20	GTGGGGAAAATGAGATGGAT	58.641	20
ACGAACTAGCAAACCGGCTA	59.904	20	GATTCTGTGGTACGTGCCCT	59.997	20
GGAGAAAAGCATACGGGTGA	60.074	20	GTTGGGCAGCCAAATATTGA	60.837	20
TCCCCTTTCTCTCTCTCTTCG	60.074	21	TCTTGGAGGAGGAGGATTCA	59.731	20
CCCACAAAGGACCAAGAATG	60.345	20	TTTCGAAATTGGGGGTTTTT	60.5	20
AGCCGCGCCTAAATAGTTTT	60.239	20	GCCCCTCGTATATAACTAAAG	60.536	27
TTGATGAGCCATAACCCTCC	59.894	20	TCTGCGTCTCCAAGTTCTCA	59.701	20
TAATTCGCTGAAGCAGCAAC	59.21	20	GTGGAGAAGTTAACCAAGGG	59.85	21
GCTCAACCTTCCGATGCTAA	60.352	20	AAACTTCAGCACTATCATTGTT	58.398	25
ACTTTTCTGCTTTGGCTGGA	59.993	20	CCCCCAGTGAACGAAAATTA	59.795	20
CTGGGCAGCCAAACATAGAG	60.786	20	CTGCAGCCATCTGTTCTTGA	60.136	20
ATGAAAGCATTTAACCGCCA	60.456	20	TGCCGATAAGACCTCTATGTG	59.73	22
GCACAGGTAGTGTTGCATGG	60.183	20	AAGATGAAGTGTCGTTGCGA	59.445	20
GATCAGATGCAAATGGAGCA	59.763	20	TTGGGATTAAGGCTTTGGTG	59.931	20
AAGCCCAACCACCAATTTC	59.782	19	CCAGATCGCTCGTTCTGATT	60.362	20
AAAGACAGAAAATCAGAGAGGC	59.535	23	GACATTAGGGCAAAAGCCAA	60.074	20
TTTTAATTCCCCATATTACCAACA	58.654	24	TTGTCACGAACGGTTTTGAT	59.024	20
AATGGGACAACTCATCCTCG	59.927	20	CCTTGTTGTTTCCATTCCGT	59.83	20
GATAGCCGTTGGTGGTTGAT	59.82	20	TGACAGCTAGAGAGCCCCAT	59.973	20
TATTTTCTCACTCCCCACCG	59.926	20	AGAGAAGGAAGGTGACGGGT	60.111	20
TCGGATCCACTTTTCTGCTT	59.813	20	AGTAGAGGTCGTGGACGAGG	59.325	20
GAACCCCTTCAGGATTCTCC	59.874	20	GGCCTTCAACTCTCTGCTTG	60.134	20
TAGCCAGTGGCCACCTTATT	59.592	20	TTCATGTAACCGACCCCAAT	60.051	20
AAATGCGGCTTCCATTTAGA	59.682	20	CTTTGACGTCATGGATGCTG	60.263	20
ATTACCTTCACTCGCCGGA	60.609	19	ATTCCCTTCAGTTTTGTGCG	60.11	20
CCAGATCTGCCAACGTTTTT	60.11	20	GATGAGGAGGATGAGCGAAA	60.303	20
TCTTTTCTTTTCCTTTTATGCTCG	60.234	24	AGGAAATGATCACAGGCCAT	59.366	20
TATAAGGCAATTTGCGAGGC	60.192	20	CCCTTTAATTGGTTGGTTGG	59.175	20
CGCCTAGGGCTTCAACTTCT	60.884	20	AAATCTCCTAGCCGGAGACC	59.674	20
GTTTTGGGTCCTCCACAAGA	59.943	20	GAAACAACCGAGCAGAAACC	59.717	20
CTTCGGAAGCGATCTCAAAT	59.41	20	GGAGATGGAGGATGTGAAGC	59.617	20
GACGAGGATGAGGTTGAGGA	60.199	20	TCCCCATCTAAGAATGGTCG	59.887	20
CCCCTCATGGATATCGTTTG	60.148	20	CCCAAGACCCCAATTTGATT	60.91	20
CTGCGACAATTGCTCAAAAC	59.469	20	CTCGTTACTCCCACATGCAC	59.165	20
TGACCCACATAGTGGGAAAG	58.414	20	TGACAATTTATCATTTCCTGTA	58.939	26
GATGCAGATGAGGACGTGAA	59.794	20	TCCCTATCTCCGGGAAGAAC	60.401	20
TTCTTCGCTACGGCTACGAG	60.669	20	CTATGGTGGATTGGTGTGGA	59.215	20
AAAGGTTGAGAACCATGATGA	57.096	21	TTCAAAACCAAACATGCTTCC	59.967	21
ATGCCGTGATTGAAACACAA	59.972	20	GAAGAAGGGGGAATTCATGG	60.632	20
GGAGAAGAGGATTTCCAGGC	60.154	20	CCGGTACATGACTTCGAGGA	61.055	20
CTCCTTCTTGCTCTTCGTCG	60.269	20	CCAAGATTTCCGAAACCAAA	59.91	20
GAATCAAGTATCTGATCTGAGCC	59.752	24	AGCTGATGATCCTGAGAAAAC	59.899	23
TGCTGCTGCTTTCTTCATTG	60.28	20	GCACTTCATTTTCAATTTATGC	59.916	24
GAGAAAACAAAAGATAGATGGA	60.139	25	GATTTTGTGTGGCGGGTTAC	60.235	20
TTGCAGAATCCAACTGCAAG	59.988	20	GAGAGCATGAAATGCCCAAT	60.043	20
CGAGATTTCAGAATGCCTCC	59.773	20	ATCTTCTCGCGATCAGTGCT	60.127	20
AGGGAACCACGAAGCACTTA	59.734	20	ATAGTGGCAGCTCCATGTCC	60.104	20
TGCGATTAAGGCTTTGGTGT	60.637	20	TGAAACTCGTATGGTCACAGG	58.635	21
GGTGGAGGCGAAAGTGTAGA	60.255	20	ACGGTATTCAGGCTCGGAC	60.088	19
GCCAGTCGTATCTAACCCGA	60.096	20	CACCGTTTGAAGAGTTATGTG	59.677	22
GAAATTGCATTGTCGTGTCG	60.119	20	ACCATGAACTTCAAATGGTGA	57.908	21
AAACCAGAGCCCTCTCACAA	59.844	20	TTTTTGCCACATTCCCTCTC	60.051	20
ATTTTCAAACCGATCGACCA	60.309	20	GTTTGGTCCGGTTAATGCAC	60.235	20
GTTCATGTAGACGACCCCAA	58.415	20	TACGCTGCGCTGCACTAATA	60.706	20
TTCGATCTCGTTGTGTTTCG	59.84	20	CTGAAATAGGGGGAATGCAC	59.387	20

TCACATCGCTAGAACCACCA	60.263	20	GCGAAAAATATTTCCAGCAA	57.92	20
TGGCTCCACAATTCATAGCA	60.22	20	CGAAACAAGATCCGTCCAAT	59.933	20
TTGTTTGAAATGGGTATTCCG	59.685	21	TCATGATGCATACGAATGATA	59.373	24
CGACGCTGAATGAGCTAGAA	59.322	20	ACTCTTGGCGGTTTCGGT	60.656	18
GCCATGCCTTCAGTTTTGAT	60.081	20	TTTGCCTTTTCAACCATTTTG	59.965	21
TTGCACGAACAAAATTCGAC	59.712	20	TTTCAGATATTTAATTTGGCGG	59.832	23
CATCGAATCAAATCCATCAGG	60.281	21	TAGCAGGCCAAAGAGGAAGA	60.088	20
AAGCATCAACTGCGGCTAAC	60.416	20	GGAAATGGACCCACAACATC	60.034	20
GATGATGATGCCACTCTTGG	59.04	20	TGCTGCATGTTCTGAAAACC	59.847	20
AGGATTGGGGCGTGATAAAT	60.531	20	TGGTTTGATGTAACATTCCGA	58.881	21
TTTCGCGCCTTATTTGTTTT	59.732	20	AATAGAGATTGCACTCGGGC	59.297	20
AAGCCGATTCTGAAGTTCCA	59.813	20	CAAATATTTTGGGCTCCCCT	60.143	20
GCCGCCAGTTAGTTGTCTTC	59.882	20	TTTTCCCTAACTCTCATCCTTTT	57.568	23
CCGTGCTATGATGAGCCATA	59.67	20	CAGCAGCCATCTGTTCTTGA	60.136	20
ACACCCCGTATTTTCGAATG	59.685	20	AGCATCATCATCATCAAGCAT	60.073	22
CATTGGCATTGCATGATAGC	60.066	20	TTCTCAAGAATTTGGCACCC	60.051	20
CGAGGCTTAATGGATCGTGT	60.096	20	AGGTTGCGTACATCTGACCC	59.997	20
TAGATGTGGGCTTTTTCCGT	59.569	20	CGTGCAAGCATCTAAATGGA	59.833	20
GCGACGACTCTCCGTCTATG	60.966	20	CCCATCACATGCATCAAGAG	60.072	20
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AAATTCAATTACCTGCCGGA	59.411	20	GTTCATGCAAGATTGAGCGA	59.955	20
ATGACGTCGGCGGTGATT	62.522	18	ATTTCGAGTTTCGGGCTTTT	60.075	20
TCGGCTAGTTTCATTGGAGG	60.206	20	TCCAACCCTATCTATGGCTCC	60.293	21
CATCCTTTCAATGGCAATCC	60.274	20	GTAGGCGATTAGTGGAAGCG	59.867	20
TTGGCTCTATTCATGGAGGTG	60.081	21	TTTTTCTTGAAAGTACGTACAC	58.23	27
GAGAAAACAAAAGATAGATGAA	59.404	26	ATGGGTTGGATTTGGTGTGT	59.95	20
AACATGTTTTCAATCTTGACCGT	59.797	23	GGAGAAGGAGAAGCAGCAAA	59.694	20
TTGCACAGACATTATCGCATC	59.709	21	AGGCAGCTTCTTCGTCAAAA	60.132	20
AAACCTCCACCAGAAATTAAAGA	59.02	24	TTCATTTGGGGTTTTTGTGC	60.712	20
TGCGTTAACGTACACAACTTCA	59.341	22	GCCTTTTGTGGAGGATGACA	61.046	20
GTCCCAAGTAAGGTCGGTTG	59.449	20	TGTAAGCTCTGGAACGGAGG	60.388	20
TCGAGGACGAATCCTTTCC	60.142	19	CTCGGGATCAATGACATTCC	60.281	20
CAAATTTTCCCCCACTCAAA	59.772	20	GTACCCCACACGAAGACACC	60.284	20
GGCAAATAATTGATCGCCTT	59.038	20	ATTCGCAAAGGGCTAGGAGT	60.228	20
AGCATTTCAGGATATTAAAAACC	59.378	25	GCCGAACCCACTGTGATATT	59.82	20
ATCGTTCATGGCATATTCAGG	59.799	21	CACTGATCGTACACGATGGC	60.144	20
ACGCTATGTACCTTGGGTCG	60.015	20	ACTTTTCGGGTATTTTCGGG	60.177	20
GATGATGCTGGGAACCAATC	60.289	20	AGGGGATCGTAAAGCCTGAT	59.925	20
ATCATAACGAGGAGGAGGGG	60.285	20	ATATGTGGGGATAGGGGTGG	60.652	20
CGGGGAATTATATAAGTATGTCTT	59.636	27	CAATTCCTTACTGAATTTGGGG	59.711	22
ACGAGGGTGATGTTGGAGAG	60.112	20	GGTCACCCTAGATGGGTTCC	60.575	20
TCAATGCTTTGCCTATGTTCA	59.315	21	GTGGGACGGACCAAAATG	59.737	18
TGTACCGGTATCATCCCCAC	60.461	20	TGGGGGCTATCTTGTGAGTT	59.55	20
GTGCTCCAGTTTGTCGTGAA	59.88	20	GGAATTGGAGTGGTCTGTGG	60.363	20
CCAATTGGTTGACAAGACCC	60.21	20	TTTATGTAGATATGGAGCGATT	57.561	25
ACGATCATCCATCCATCCAT	59.978	20	CTTCATCGACTCTCGCATCA	60.096	20
TCAACGAATACCTGCTACCAA	58.307	21	CAACAGCTCGCAAGATGAGA	60.287	20
GAGAGGAGGGTGACGGTGTA	60.112	20	TTATTTTTGCGGTAAAGGCG	60.089	20
CCACCATCGTCGTCTCATC	60.063	19	AAACACGAACTTGCCGATTT	59.615	20
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CTGACGTGGGTTCCATTTTT	59.83	20	TTTTGTAACTTGAGCAATTTAT	59.966	26
GATGATGATGCCACTCTTGG	59.04	20	CCTCAGTAATCGCCTGATGG	60.615	20
GTGGGGCAGCCAAATATAGA	59.923	20	CCGGAAATCATGGGTGTAAA	60.555	20
GCGTCCGACTCCTCAACTAT	59.313	20	TGATGAAATCAGTTGTTTGATA	59.457	26
TTTGTTGGGAAGGTCGTAGC	60.11	20	TAGCAGGCCAAAGAGGAAGA	60.088	20
CGTAGGCCTAGTTGGCTCTG	60.03	20	GCGTGCACAAAATGGTAAACT	60.053	21
CATCGGTTAGTTCTCCCACC	59.405	20	CGATCCCACCCCTTAATTTC	60.502	20

ATGGTTGCCTTTGTTTGGAG	59.971	20	AACATCAAATGAGGCTTGGG	59.933	20
TGGCTCTAACGATGCCTTTT	59.845	20	TCGTTCATTCACGTAGAAGTTC	59.799	23
AGTCAACACTCCACCAAGCC	60.159	20	TTCAGCGGATTGAGTGTCA	58.88	19
GGGAAATCCAAGTCCCAACT	60.169	20	GAGCTGGATTACCAGTGCGT	60.285	20
TCGTTACCCGAGTTGAGGTC	60.111	20	AGTTGCTTTTGTTTGGAGCG	60.42	20
CCCCCAATACCCAAATTAGA	58.621	20	ATCTCTTTCGCCGCACAC	59.95	18
AGTGTGGGTTTCGGTGTTTT	59.353	20	CGAAAGAAACACACGTGAGA	60.318	22
CACAAGTTATTGGCGAGGGT	59.993	20	CATCAACTCAACAAAGCCGA	59.84	20
TCTCGAACCAAATTTCAGCC	60.192	20	AGCCTCCCTCTTTAGCCATC	59.811	20
AAGGAGGAAAAGAACCTGCC	59.691	20	TCACGTTTGTTTGAATCCCA	59.941	20
TATCCAGCATGAGGGGAACT	59.508	20	GCAACGGAAACAACCTCTTT	59.218	20
GGTTTTTGGTGGGAGGAAGT	60.204	20	CCATAGCTTGTGAGGGCATT	60.096	20
CTCTATAGCCGCCTGCATTT	59.479	20	AGATTTCATTATCCACATTGGG	57.808	22
TGTATTCCGGTTCAACCCTC	59.79	20	TTGTGTGCATGTATTGACAGG	60.035	22
TTGGAGTTGCATAAATTGTGG	58.544	21	CGAACCTTCTGCAAAATAATG	59.253	22
ACAATGAATAAACGGGGCTG	59.823	20	TATGGGCATAGGATTTTGGG	59.616	20
TGTGAACACAGCCTCACCTT	59.31	20	GGCAAGAATCCTCACCAAGA	60.195	20
GCTAGGAAGGCTCTTGGGAT	59.811	20	GCCTGCACAACAAATTTCAA	59.712	20
GCAGCAACTTCCTCTCCTTC	59.166	20	AGGGGGAGAGTTCTCTTGGA	60.186	20
CCTGCCCTATCTGCATCAGT	60.24	20	CCTGAAACGAGTGATGCTCC	60.801	20
ATGACTGCAGGAGATTCGCT	59.981	20	ATGTAGCCGACCCCAATTTA	59.297	20
CGAAAAATGGGATGCTGAGT	60.074	20	TGGGTTTAGACCGATGTCGT	60.375	20
GAACTAACTGCTGCAAGGAAAAA	59.946	23	TTGGAAGTTGGAATGGCATC	60.843	20
AGCAGTGAACTGGGACAAGC	60.453	20	GCATCACAGTTGAATGTGGG	59.967	20
CTTCTCAGCCTCAGCCTCTG	60.422	20	CCTTAGGAAAGGCACGACAC	59.734	20
TTGCTTTGGCTCACAGTACG	60.05	20	TTCGTAAACGAGTGTTGGAAA	59.663	22
ATTTGCAGGAATTGGTGAGC	60.081	20	TCCCATAAAGCGAAATGGAG	60.031	20
CACGTGGAGAGCAATGACAC	60.319	20	GACAACACTGGAGCTGTGGA	59.872	20
TGTCTCCGAGTTTGTTTCCC	60.088	20	GGAGTGCATGCTCCAGACTC	60.989	20
GGGAGTGGGTTATCGGTTTT	60.053	20	CAGACGTAGGAACGGAGAGC	60.012	20
GGAACTTGATTATGTATCTGATGA	58.072	26	GTTTACTCGCTCTTGCTCGG	60.154	20
AAAGCCCACCTTATTGTTCG	59.087	20	TTGTCATATGAATCATGAAATT	57.088	24
AGCCTTTTGTGGAGGATGAC	59.141	20	TATCATCCTCGGAGGCAATC	59.998	20
CACGACGAGGAGCATTATGA	59.823	20	GGCAGTACTTGAACCTTCGC	59.882	20
CCCTTCCCTCTATTTCCGAC	59.897	20	ACAGGAAACGTAAAGGCCG	60.118	19
GAACTCGCAGGTTCTTTGGA	60.375	20	TCTTCTTCCTTGAGAACGGC	59.55	20
GCTCGTTGCAAGCATATGAA	59.983	20	AGCTTCCCCTCTTTGGTTGT	60.11	20
AGTTGGGAGTTGGGAGTCCT	59.968	20	AATGTTAGCGACCCAGCATC	60.103	20
GATCCATGTGTCCACGTGTC	59.808	20	ATGTAGCCGACCCCAATTTA	59.297	20
CCTCACTCTCTCCCTCCCTC	60.336	20	CTCACCGGAGAAAACCTCAC	59.697	20
CTTCAGCTTGGTTCTGGAGG	59.982	20	CCATAATGTCCGGCTGAATC	60.296	20
TCCATCATTCCCTTTCTTGG	59.864	20	GGAGGAAACAGTGGTGGAAA	59.943	20
TTGCCAAGCTATCCAAAGGT	59.708	20	CCCGAACACTAGTGGGGTTA	59.846	20
GCTGGATCACTATTTGGTGG	58.019	20	CACTCGTTTAATGTTACACTTT	59.213	27
ACCCGAACCGGAATACAAAT	60.431	20	TTGTTTATCGTTTCCGTGTTTT	58.589	22
ACGGCACCCACAATAAATTC	59.691	20	GATTCGCTCGATTCTGAAGG	59.917	20
CCGGACAAGGATCTTAGCCT	60.59	20	TGGGATGAAATTCAAAAGGG	59.733	20
TTCCTTACTGAATTTGGGGTTG	60.21	22	TGGAATCCGAGAAAATCAGG	60.006	20
ATTCGAAGGTGTTGATCCCA	60.317	20	AAAAGTTTCCACACTTGCCG	60.147	20
AGGTTTTGGAGTTTCCGTCA	59.569	20	TTCAAATATTCGACTCCGGC	60.038	20
TTCTCCTCCCTTGTGATTGG	60.042	20	AGAGTCTTCCGACAAACCGA	59.844	20
GCTAATAATTCGGTGGCAGC	59.71	20	GGTGGTCATTTTGGGGATATA	59.787	22
TCATCCTCGGAAGCAATCTC	60.303	20	CGACACATGAGCTATTGGGA	59.673	20
AGTACCATTTCGGCCATTTG	59.823	20	TTGGATCCACACCTTCAAAA	58.947	20
TCGTCGACCACCATCTTAAC	58.57	20	CACCACCCCAACCAAATAAA	60.452	20
TGACGGTGAAGAGGGTTGAC	61.113	20	CCCACTAAGCTAGCTCCCCT	59.864	20
TTTTCGTTTCTGGTTTCGCT	59.861	20	AACGGGATTTCGAGTTGAGA	59.67	20
GAGACCTCGAGTCGGAGATG	59.945	20	CGACCTGCTCCTTTTCAATC	59.813	20

CTCGGGGGTCAACACTACAT	59.844	20	ACATACACGACGGCAGCATA	60.165	20
ACGAGGGCGAACTGTAGATG	60.277	20	TTTTGATGAAGGCGGGAATA	60.395	20
TGTAGCCGACCCCAATTTAT	59.297	20	GGATTCGAAAAGACATCCCA	59.871	20
TTTTCCCTCCAAAGCCAGTA	59.679	20	CTAGGAAACAGCCCTCAACG	59.869	20
TGTTGCAATTCGTGTTAAATCTT	58.733	23	ACATGCCGAGTTTTTCTCATTT	60.007	22
CGCCCAGTTCTGGTCATACT	60.134	20	GGCAGCCAAACATAGAGCAG	60.934	20
TCACCAACATGCCCGTATAG	59.42	20	AACAGGGATTTTGAAGGTGC	59.031	20
TCCTCTCGATCCTCGTTACA	58.387	20	CCGACTAGGACTAAGGGTCCA	60.493	21
GGCTTGCATTTGAAAGTACAGA	59.406	22	TTACATCACATGCCCCACAC	60.249	20
CGATATGAACGAATGCGATG	60.058	20	ATGGGGGTCAAGGACAAAAT	60.422	20
CATTGCCACCATCCGAAC	60.915	18	GTCGTCATCCCCCTAGTTCA	59.927	20
CTTTGCTCGATCTATTCGGC	59.945	20	TTCAACTCACACCAAGTGGG	59.565	20
AGCTTCTTTCAATCGCCTCA	60.096	20	CTCATCTCGAGCCTTTGGTC	59.95	20
TCAAAATTATACCTGCCGGA	58.109	20	CGTCAGTTCCACCGAAATCT	60.111	20
ATAATTCCCGGCGTCATCAT	61.42	20	GGTGGTTTTATGCACGCTCT	60.14	20
TGGGATAGGATTTGGTGTCC	59.605	20	GGAAAAAGTGACTGGGCTTG	59.711	20
TTTTCCCATTGCACCAAAAT	60.167	20	TTTGGTGGTTAGGGAGCTTG	60.103	20
AGGGGATCTTGGGAAGTGAT	59.755	20	ATTGTCAAACCAGCGAGAGC	60.406	20
CCCGTGGAGACGAGGTATTA	59.948	20	TTAGGTTCGAGACCCATTGC	60.074	20
CGTGGTGCACTTGCATACTT	59.788	20	TCATTTTCACGTGACCCTATTG	59.861	22
GGAGTGGAATCGGTAGCAGA	60.218	20	CGTCGGAGGGTTCAATAGAG	59.688	20
TGAGTGGGTCTCTGCTGTTG	60.022	20	GCTGCTGTCCATGAAGTTGA	59.992	20
CGAGACTCATCCACTTGCAG	59.571	20	TGTAGCCGACCCCAATTTAT	59.297	20
GTCAGACCAGCTCTCCTTCG	60.135	20	GTTAATGTAGCCGACCCCAA	59.823	20
GAACAAAATAAAAATTTGGGAGG	59.637	24	CACTACCCAAACCCACCAAC	60.126	20
AAGGGGCACTGGTAAGGTCT	59.994	20	CGAGCCCATTGTCTATCCAC	60.483	20
TGCTTCCGTGTTTTATCCATT	59.465	21	GTGTTCCGATAATCGCCAGT	59.962	20
GTCCATTTCTAGACTGCGGG	59.694	20	AACAACATTAACAATCATGCC	59.288	23
GCGGAATTCCTCAAAGAAGA	59.387	20	CTCCTCGCCTCCTACATCTG	59.966	20
TTGGGGGTGACGTAGTCG	60.523	18	CCCACTAAGCTAGCTCCCCT	59.864	20
ATGTGTGTGGCCATTTTCAA	59.823	20	TTTATGTTAACGCACAATATTC	59.715	25
TGCGTCAGAAGATCCATTACA	59.287	21	GGTGTGTTTCAAGGCAAATTC	59.467	21
TGCAGCAACTTCCTCTCCTT	60.134	20	TCCTTCCCTTTCCTGGAACT	60.045	20
TGTCACACCCACGCATATTT	59.847	20	TCTGATCTCCGGTCGACAAT	60.622	20
GGGAGAGTTCTCTGGGGAAG	60.186	20	AGCACAACAACCACTAATCCG	60.045	21
CAGTTCAGCAGCGGAATTTT	60.386	20	CTTGGCTACCCCTATCGTGA	60.088	20
ACCACTCTCCCTTGGCCTAT	59.957	20	TTGAACCCGATTTCTTGTCA	59.097	20
GCGGAATAGCATTCACGTTT	60.103	20	TGGTGGCAAAGCAACTACAG	59.904	20
TCCAAAAACCATGCAATGAA	59.907	20	TAAATTGCCGTGTGAAACCA	59.969	20
ATGGCGACATCAAACACAAC	59.425	20	CAAATGCATGTTTGTCGTCC	59.972	20
GTCGCCAATTATTGATGCCT	59.929	20	CATTGTCCAAAAGCTCAGCA	59.988	20
CATCACAGGCCATTAGTTGG	58.999	20	GCAGAAGCACGATGCTCTTA	59.326	20
TGGTTCCCTTCTTGTCCTTG	60.081	20	TATGCAAATCAGTGCCGAAA	60.215	20
GATGATGATGCCACTCTTGG	59.04	20	CCTCAGTGCAGAAATGTCCA	59.831	20
TCCATTTTTCTTCGTGCATTT	59.578	21	TGCAAATCCAATCATCTCCC	60.812	20
GATCGTTCTGCAGGAGCTTG	61.087	20	AGGGCTAAGAGGAAAGACCG	59.842	20
CACGATCATCCCACATCTGA	60.496	20	CCATAATTACCGGCGTCATC	60.175	20
TTCCCGAGACTGAGATGGAC	60.199	20	TTCCCATAATTACCGGCATC	59.621	20
TTCAAACTTTGTTCCGCAAA	59.321	20	CGTCAGAATATTTATTCCATGT	58.462	25
GGTAAGGTTGCGTACATCCG	60.386	20	GCGTAAACTAACTGGTGGGC	59.637	20
CGTGTGAAAATGAAATCGCA	60.644	20	TGTAGCCGACCCCAATTTAT	59.297	20
TCGAGTGATCGTGCCAATAA	60.22	20	ATCGGGATGCTGCTAAAAAC	59.186	20
ACGATCGAATGATCCCTGAG	60.034	20	ATCCCGGAAGAAGAACGAGT	60.074	20
TATAGGTGCTGGGGCTAACG	60.11	20	ATGTAGCCGACCCCAATTTA	59.297	20
AGTTCCACGAACCAACCAAA	60.388	20	GCTCCGCCAGTGACTGTATT	60.285	20
TCCTCGCTCCTAACTTGCAT	59.978	20	TCCCCAACTTCTTCCTCCTT	60.045	20
ATTGTATGCGGGAAAAGTGG	59.823	20	TCTATTTCCAAGGCCAATGC	60.038	20
TGTTTAAAGTCCATTCGGGC	59.938	20	TTCCTAAATCATGATGGTGAAT	57.949	25

CGGAAGTAGGCAAAAATGGA	60.067	20	GGTTCGAAAACCGTTGTTGT	59.875	20
AGGTGCACGTGACTCCAAC	59.728	19	GGATTGGATTTCCTCACCAA	59.727	20
CCCCTCCCCCTCTCATATT	60.096	19	TGGGGGAATGTAATATCATTG	60.261	23
ATACCTCGGCCTTTGATGTG	59.955	20	CTTGGCTCATTGCAAGCATA	59.976	20
CATTGAAGAGCTCGCTGGAT	60.504	20	CTTGTGTCCGACCTTGTTCA	59.72	20
TGAGGTCGCTCACAGATGAC	59.988	20	TTCCTCCTTCCTTGAGATCG	59.356	20
AATTTGGGAAGGCCTTTGTT	59.814	20	GTTCGAGTCTCAATGGGGAA	60.05	20
TAGTACTGCAGGCGAAGCG	60.309	19	CGGCATTCAGCAAGAAAAA	59.938	19
CCTTTAGAACTTGCTCCACCA	59.364	21	GAAGCGTGGGAGAAGCTAAA	59.592	20
TCCTTGGGGATAGTATGCTTG	59.054	21	GTAGATTTCGGGCCATTTCC	60.642	20
AGGCCTGAAACTGATCGAAA	59.813	20	ACCAATGGTGGTATGGTGTG	58.984	20
CCCCTTAGGGTTCCTCATGT	60.183	20	GCCATTGCCACGATGAATA	60.447	19
CCTTCCACTCCTTGCTTGTC	59.844	20	TCTTCGGGATTCTCCATGAC	60.011	20
GAGGATATAGGGCATGGCAA	59.885	20	GCGGGCAAATTTCTTTTTCT	60.547	20
AGAGGTATTGGGGGATTTGA	58.307	20	GTCTTCTTGACGCCGCTC	59.663	18
AATCTCTCAATCTTGCGTCG	58.048	20	TCTAATGTTTCCTCCACCGC	60.074	20
CTAACTGAGCTGGCGGACTC	60.156	20	GCAACAAGACTAAGGCGGAG	60.015	20
GTCGTCGAGAGAAGCTCACC	60.143	20	ATAAGCAAATTTCGGGACGA	59.547	20
TTAGACGTCACGCACAGCAT	60.481	20	GTACAGCTAAAGCGGGGGA	60.22	19
CTGTGTCTCCAAGCTCCCAT	60.261	20	TTGATGAGCCATAACCCTCC	59.894	20
CATATGCTCCATACAGCCGA	59.67	20	TAAAGTGCAATTTTCCCCGA	60.427	20
GGCGGCTCCTCCTATGTAA	60.185	19	GAGAAGCCTTTGTTCTGGGA	59.405	20
GGTCCGATTGAGGAGATGAA	60.011	20	CAATGGGGACAGACGAAAGT	59.966	20
GGGATGAATGAAAGAGGGGT	60.133	20	TCGATTCCACATATCTCCACA	58.938	21
TCAATCTCCCACTCTTGCCT	59.803	20	TGTGAAACTTGACGGAATGG	59.541	20
GACCGATTTGTGGAAACCTG	60.353	20	TGGGTACAGGTTGTGGGTTT	60.126	20
CCCGCTTCGATATCATTTGT	59.923	20	TGAATAATCCTGCATGGCTG	59.646	20
ATGTTGAGCCCAACCCAAG	60.908	19	TGGGTTGCAAAATTAATCCG	60.671	20
CCTCTGTCAAACCGAACCAA	61.064	20	CGTCAGTTCCACCGAAATCT	60.111	20
GCTGTTGTATTCCTCCTCCG	59.694	20	CTCCTCGCTCTCTCCTCTCA	59.962	20
CCAAATATTACAATAGCTCACAA	58.68	26	TTTGTCCTATGCTCTTCCCG	60.206	20
TGAGAAAGTTTGCTTCGGGT	59.853	20	CCCAAGACCCCAATTTGATT	60.91	20
TTTTAATACCCCATTTTACCAACA	58.695	24	TTTTAAATGATGTCATGGGAGC	58.946	22
CCGAAGTGCTAGACCCAAAG	59.869	20	AAAACACTAGCAATGACACTT	58.511	23
GAGTCACTCACGCTCTTGCTC	60.345	21	TCAACCGTCTTGAGATGCAG	59.984	20
TTCAGCATGCAATACCAAACA	60.126	21	ACCCACTAACACCCCTCACA	60.275	20
AGCTCCCTTCCTCATCATCA	59.761	20	ATCGGAGTCTGGTGGCTATG	60.096	20
TCCATACTTGGCATCGGTTT	60.331	20	GGTGCGAGGGAGATTATGAG	59.653	20
ATGTAGCCGACCCCAATTTA	59.297	20	CACCCACTCGTAGAATCCGT	59.989	20
TTGTTTTCTTAAGTTGTGATTTGTC	59.865	26	ACCAGGTTTGAAGTTGTCGG	60.005	20
TTTGTCATATGCGAACAGCAC	59.75	21	CCACCAGGTTGTACAGCAAA	59.609	20
TGAGCTGCACTTGTTTTGTCTT	60.096	22	CAACTTGATCCCTATCACGC	58.173	20
GATCGAAAGGTGATTGGTGG	60.317	20	CAGGGCGTGACAGTAACTCA	59.897	20
GATGGGACCCACACAATTTC	60.034	20	AGGAGTTCACTGTGGGATCG	60.112	20
ACTCTCCTTTTCCTCCACAAA	57.896	21	CCTTCTCGGTTGAGTCTGCT	59.598	20
ATCAGGCACATCACCATCAA	59.925	20	CAAGACACGGGGAGGAATAG	59.545	20
TTTTTATTCCGTGACCCTCG	59.931	20	AGCAAATGGTGGAAATGAGG	59.933	20
TGAAAGTAATGCCCATGGAAC	59.815	21	ACAGAAGACCCGAGCCTACA	59.867	20
ATGCAGCAAAAGTCTGAGCA	59.746	20	AAAAGCAGGAGATGACAGCC	59.434	20
GTTAATACCGCTGATGGCAA	58.653	20	TCATAACATCGATGAGTGTGG	59.874	23
CACGTGCATTAATTATTGTTTTCA	59.015	24	ATGGGGCTTTTTAGGGCTAC	59.463	20
TAGCAGGCCAAAGAGGAAGA	60.088	20	AGGCCAACTGAAATTTGAAAG	60.109	22
AGCTGGATGTGTAGCAAAGC	58.132	20	CAAATCGGCATTATTTAATGGA	60.052	23
TTTCCTCTCTGAGCCTTCCA	60.065	20	TATTGGTCTGGAGGTGGAGC	60.073	20
ATGCCTTATATGCCGGACAC	59.813	20	TTGGGAACAAAGAGTGCAAA	59.293	20
AGCATTCTCTAAATGGTTTCCA	57.888	22	CCGTCTAGGGCTTCAACTTC	58.934	20
GATCTCGATCGTGACCCAAT	59.893	20	TCAAAAACTCCCAATTTATAAC	58.928	25
GGGAGTTTCGTTTGAGCAAG	59.853	20	GCACATCACCATCAAAACCA	60.376	20

TAAATTGGGGTCGGCTACAT	59.297	20	TTTTTGTCAATGTGGGATTGAT	59.182	22
GGAGTCCGTGGTGAACAAGT	60.009	20	GACGATGGTTGCCTTTGTTT	59.978	20
CACCATTCTCTAAATGGTTTCCA	60.223	23	TTCATCAGTCCCGTCTAGGG	60.065	20
GTAGCTCCCTTCCCAACAGA	59.284	20	ACGAGAAAGAGAGAGATGGG	59.825	21
TTTTCAATGTCCACACCCCT	60.21	20	ACTCATGGTCCAAGAATGGC	59.934	20
ATGTCCTCAATCGATCCCAG	59.886	20	TTACAAGGGAAAGGTTGCGT	59.609	20
CTCACGGTTGGAAGAAGAGC	59.989	20	AAGAGCGCCAGTATGGGTAA	59.73	20
TCAAACTGGACCATCCAACC	60.758	20	GTTCATGTAGCCGACCCAAT	59.82	20
ACCCGGATTACTCCGATGAT	60.546	20	CCTCATCAATGCTCAGCCTC	60.914	20
GAGTCTCCGAGATAAGGCCC	60.176	20	GAGAACCAGATTGTAGCGGC	59.843	20
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GTGGCTTCTATGGGCAATGT	59.962	20	ATCTTTCAAAACCATGCGGA	60.448	20
GGGCTGCAAATAGATGGAGA	60.177	20	CAACAGGCTACCTCCTCCAC	59.721	20
ATGTAGCCGACCCCAATTTA	59.297	20	ACCTTGCGCCCTTTAAAACT	60.129	20
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CGGATGAATTTTTGTTCGCT	60.074	20	AGAAACCGGTGTTCCATTTG	59.83	20
GAGCACGTTATTGGCTGGA	59.814	19	CAATCAACCATCACATCCCA	60.177	20
CCTTGGAGTTGTCCAGCATT	60.111	20	TCCGATCCTGGACCTTAGAA	59.623	20
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ATCCAAGGGGATCGTAAAGC	60.286	20	GCTGGGAACCAATCATCCTA	59.894	20
AGAGTCTTCCGACAAACCGA	59.844	20	ACTCACCTCTCCCTCGACCT	60.258	20
ATTGGGATTAAGGCTTTGGT	57.552	20	AAGGTTTCGGAAAGTGGGTT	59.842	20
CCCACTCGAAATTAACCACG	60.357	20	GGTGAATTTGGTCCTTCAAA	57.488	20
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AAACCTTAACGCCCTCACCT	59.998	20	TCTCGACTTCCTTTTCCGC	60.467	19
ACTCCGACATGGAGAACACC	59.969	20	CCTTCCAATTCTCTGGGTCA	60.042	20
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CGACCCGGTCCATATACAAA	60.576	20	ACCAATGGTGGTATGGTGTG	58.984	20
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CCGAAGTGCTAGACCCAAAG	59.869	20	ACACTGGTAATGACGCTTCG	58.802	20
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CTTTGCTTTGACTTTCGGGT	59.355	20	AGGCTCGAACCATGCATATC	60.066	20
TCAGCAGGCATAAATTTCCC	60.038	20	GAGGTGGAGCTGAAATTTGG	59.67	20
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ATCGAAGATCTCCGCACACT	59.834	20	CTCCTCGCCTCCTACATCTG	59.966	20
TGTCACCCAACTTATAAAAGAAG	58.381	25	AATGGTAGAAATCGCCGCC	62.223	19
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CAGGGAATTGAAGATTGATGG	59.373	21	CACAAGTTATCACACCCCCA	59.262	20
GCCACATGCTTTGTGTGAGT	59.758	20	GGGCTGAGATGGATTTGAGA	60.158	20
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TAAAATTGCCCTATTGCGCT	59.717	20	CACCAACATCGAGTTCTTCG	59.288	20
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CATGAAACATTTCAAAATATCATC	58.726	25	ACATCTGACACCCCAAGACC	59.817	20
GGGAAACCACCCGTATTTTT	59.924	20	ATAATAGTGCCCCGAAAGGG	60.164	20
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ACCCTCCTTTCACATGTTCG	59.966	20	TTGCTCCTTAAAGCTCCTGC	59.73	20
TCAACAATTTACGGGCTTCC	59.938	20	CTTCAGCTCCAGGGTTTTCA	60.366	20
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CTCTTTCGCAGCCTCCTCTA	59.853	20	GACACGGCCTTTGAGTCAGT	60.307	20
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CCCAAGACCCCAATTTGATT	60.91	20	GCAGGATCCAAACAATCCAT	59.756	20
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CAGCCTCAGGACTCCTCATC	59.945	20	TGACCTGGTGAACGATAGCA	60.263	20
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TCAAAAACCATGCCACTGAA	60.088	20	TCTGGAGCTGGATGATGATG	59.743	20
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CTTCGGCAGATCACTTAGCC	59.978	20	ACCCCAATTTGTTGGGATTA	58.995	20
GCTTTGAGGGTCAAACCAAG	59.711	20	TTCTGGGAGGTATCTGCTGG	60.21	20
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GGAGGTGGGGTTAATAGAAGG	58.834	21	CGCAATGTACCTTGGCTATG	59.206	20
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TCACCGGAAACAAATACATCAA	60.223	22	TGGAGCTAAAAAGATTTTCAC	60.238	23
TTCTTCTGTACAATTAATGTCCAA	59.121	27	GCTCCCTGATACCACGTCAT	59.957	20
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CCACCATCGTCGTCTCATC	60.063	19	CCTAGGTTCAAATCCCACCA	59.784	20
TGTGATGAGATCGTGAACCTG	59.692	21	CCTCTCAATCCCAGACTTGC	59.803	20
TCCATTTAATCCCCCTTCTTC	59.257	21	TTGGAACGGGATTCGATCT	60.41	19
CTTGGCATTCTCTTTCTCGG	59.948	20	TCAAATAGCCCCTTCGGTAA	59.542	20

AGTTATGTAGCCGACCCCAA	59.452	20	CGAAATCTCACGACGCATTA	59.833	20
CGCGGAAAGAGAGAGTTTTG	60.125	20	AACCGTGTACACCCCTACCA	60.149	20
ACCCAGTGAAAATTGACCCA	60.21	20	CCCAAGACCCCAATTTGATT	60.91	20
CACCCAAGGCAGAGAAAAAG	59.846	20	TGCTCGAGATCCCAATATCC	59.998	20
GCTGCAGAGGTGGTGTGTAA	59.905	20	TCATCACCACAAAAATCCCA	59.75	20
TTCAGGTTGAAGTCTTGGGC	60.232	20	GGTATGTCGGTCAGCGATTC	60.492	20
TCGTTTGAGTTCGAGCAAGA	59.716	20	AATTCAATTACCTGCCGGA	58.024	19
TTGTATGGCACGAGTTCTTGA	59.332	21	TTCACTTTGGAGGGAAGGAA	59.641	20
ACTCGTCCTCCGTGGATATG	59.95	20	GTGGCAGAGATGGAGGATGT	60.08	20
GCGCAGTTGCCAAACTTATT	60.272	20	TTGCCAAGCTATCCAAAGGT	59.708	20
TATCCGAACCGACCCAAATA	60.146	20	AAGCAGAAGAGTGCATTAATC	59.471	23
GGATGGAGAGGAGGAAGGTC	60.012	20	TGGAAGGGCAATTTAGTCCA	60.439	20
TCAGAGACGGAAGAAGCACA	59.701	20	CAAAGACTACCTACAGATCCC	60.241	23
TGCCGACTCTTTCTTCCTTC	59.55	20	GGTCAGAGTGACCGTTGGTT	60.009	20
GCCTGGATATCTTGCTCCAA	60.177	20	CAGCTACCCATCTGCCAAGT	60.277	20
ATGTAGCCGACCCCAATTTA	59.297	20	ATGCAACAGAAAATGCCACA	60.119	20
TGATATTTTCAATGATGGATCG	57.46	22	GCAAAGCATACTTACAGAAAC	58.516	23
CAAATGCAAATCTACCTGGGA	59.946	21	CCGCTGAGATAATGCTCGTT	60.374	20
TCGACGCGGAAGTAAATCTT	59.845	20	CGATGGGGTCTTCTGATGAT	59.886	20
TTGCCCATGCATACACATTT	59.816	20	ACGCGCCGTCTAAATAATGA	60.608	20
TTTTCGGTTACCATGTCGTT	57.999	20	CATGATGCAAAAATTTAATTAG	58.335	24
AAGGATGAGGAAGGCAAGGT	60.074	20	GCTTTGAACTCGAGCTGTCC	60.142	20
CAGCTGTGGAATCCCATTTT	59.933	20	CAAGATTCCTCTCACCCCAA	60.042	20
GAGAAAGAATCAACTGCGGC	59.962	20	TTGAATTGTGTCTGCTTCGG	59.84	20
TCTTTTCTTTTCTTTCCCCCA	60.034	21	GCTACAACGAGCCCACTCTC	60.02	20
CGTGGAGGGATTCTTGGTTA	59.926	20	GCCAACACCTCCTTGATGAT	59.934	20
TCGATCTCTTGCAGAAGGGT	59.95	20	ATGGTGACAATCGTGCTGTC	59.557	20
CGAGAAGATCTTGAGGTCGC	60.096	20	GGAACCTCCTCTGTTCCCTC	60.05	20
TTTGGTTCATGTAGCCGACC	60.894	20	TGAGAGGACACCCAAGTGGT	60.563	20
ACGGAGAAATTCGACTCAGG	59.284	20	TGAGAATTAGCAATTGAAGTT	58.584	25
CCCACCATCACCGTTATTTC	60.051	20	TTGCTGGCAGTGAAGCTCTA	59.888	20
CGGAGAAATGGTTTCTGCAT	60.074	20	CCCCAAATAGCTTAGGAGGC	60.055	20
ATGAGGATGATGACGAAGCC	60.042	20	AGCCAGTCTCAGTCCTCTGC	59.738	20
TTTGCACCAAAATGGACAGA	60.088	20	TGCTTGTGGACCAAAGATTG	59.691	20
AATCATGTACACCCGGTTCG	60.636	20	GCCCCATCCCTAAGAACATC	60.662	20
GAAAGTGGGGGTTGATTGAA	59.767	20	CGCTTCGTAGCCCTGAATAC	59.867	20
AAATCGGGGTCGAAAAATCT	59.777	20	GACAACGATGGATACCCCAC	60.057	20
AGGAGCAGGGGGATTTGTAG	60.455	20	AGGCCACGTAAATACGAACG	60.018	20
TTGCACAAGCTCTTGCACTC	60.333	20	TCCTCCCAAGATCACCATTC	59.862	20
TTGTTGGCTATGCTCCAGTG	59.864	20	GGAGGTGGGCTCTCATGTAA	60.073	20
GATTTTACACCTGCAAGGGC	59.574	20	CCTGTGTTCGGGCTAAATGT	59.993	20
TATGACACAATGTCCCGTGG	60.24	20	ATATCGCCGTAACTGGGTTG	59.845	20
ACCAGGAACCAAACACCAAA	60.246	20	GACCACCTGCATTCACAGAA	59.682	20
TTAGCACGCTTGGATGTGAT	59.301	20	ATTTGGAACCTTGTGCGTGT	60.419	20
TCAAACCTTTCTCCAATTGCTT	60.109	22	TTCCCTCAACCTAGACCTCG	59.28	20
ATAGATCCGGAATGATCGGA	59.3	20	TCGTAGTGCATGTCTGATTCTG	58.952	22
TGCCTACATACCGACGTGAC	59.596	20	ATGCCACATAACGCATTCAA	59.96	20
AATTCCCACCACCACAAAAA	60.066	20	ACCAGCATTTTCAGAGCCAC	60.263	20
CTGATCTACTCCGTCCCCAA	60.065	20	GCAACCACGTACCATGACAG	60.032	20
TGCAAGAGAAAACACATCCG	59.84	20	CCCAAGACCCCAATTTGAT	59.59	19
ATGGTGGAAACCAAGGCAT	60.188	19	ATGGAAACATCAACACACGC	59.425	20
GCTGTAAATGAAACTGCTGTATG	60.212	24	CTGAGTGCGTTTGTACTCAACC	59.842	22
CAGAGCGCACTCGAAGAGTA	59.49	20	CTCTGGATAAACCCACGGAC	59.405	20
TTGTCATATGAATCATGAAATTTT	58.012	25	AAAACGCATTTTGGAGTTTGT	58.664	21
GTTCGCTGAGGCAACAACTT	60.44	20	CCATGAATGAGCACACAACC	59.967	20
CTGACTGCGCGACTTTGATA	60.157	20	AGGCGGGACTGTGAATAATG	59.955	20
GGCACCGGGTATTACATCAA	60.585	20	CAATGAAGACTGAATCTCGGA	59.312	22
ATGCAGCTCATGTCTGATGC	59.982	20	CCCGGAAGAAAGACACAAGA	60.224	20

AGCAAAAGGTCGTCCTGCTA	60.015	20	CCAAGACCTACTGAGCCAGC	60.012	20
TTTAGGCCAAGTTGTACCCA	58.147	20	GGATATCCGGTTTTGCTCAC	59.391	20
GATTCAGGGGAAATTCACGA	59.871	20	ACTCCCCTCCATTCTCCATC	60.278	20
TGGAGGCGGATTATAGATGTG	59.93	21	CGTGTTAAGTTGTTAACCAATA	59.456	25
GCGAAGCTATAGAGATCGGG	59.046	20	TGCACCAAAGGAGGTTCTCT	59.844	20
TCCAAAGTTGGACTTATGTAAAA	57.079	24	CAAGTGGAATTCATGATGCG	60.073	20
TGAGCAACTGCCAAAACGTA	60.436	20	GCACAATCACCAAGATCGAA	59.654	20
TCGGAGAGAGAGAATGGCTG	60.634	20	GATTTTGTAAACTGCCCGGA	59.938	20
CATTGCGTCATACGATGTATTAAA	58.997	24	GAGCATATCTTGGGGGCATA	59.885	20
CTAGCCCAGCATATTCCCAC	59.551	20	AATACTTGCCGTCGCCTATG	60.117	20
CAAGCCATTACCATCACCCT	59.813	20	GACGTGGTTTGCAGGCTATT	60.14	20
TTTGAGCACCGAGTGGTTTT	60.668	20	AGGTTGCGTACATCTGACCC	59.997	20
TTCTTCTCCCTCTGCTACGC	59.717	20	CTCGGAATCATTTCCCGTTA	59.894	20
AGCGAATCGAGATAGCCAAA	59.945	20	TTTGTGGATATTTGTTTATTGTC	58.939	26
AGCCACTGACAGCCACAGTA	59.493	20	TGCGATGATTGCAAGGTTAT	59.14	20
CTCTCGCTCCCTCTTTCTGA	59.82	20	TAGGCATGGATTGCATTTGA	60.035	20
GCAAAATTAAAAATGCCCCA	59.783	20	CCAACATTGGATTCGAAAGG	60.301	20
CCCTAAGTTTGCATCTCCCA	60.066	20	TGCTCGGTTTGGCTAGATTT	59.845	20
AGACGTAAATGGGCGTGAAT	59.457	20	TGGGAGTAGTCCAATTTTCTCG	60.474	22
TCCTATTACTTCCTCGACTTTAAT	60.245	26	AGCCGAAATTTTTAGGTATCG	57.509	21
TCATTGGAGGTCCACACAAA	59.935	20	CCGTGTGATAGGAACCATCC	60.195	20
GGCGGCTTCATTGCTTATAG	59.838	20	ACTACGATGTTCGCCACCTT	59.621	20
TATATCTGCTAGAGGGCGGC	59.438	20	GGACGCTTAGGTGGATGTGT	59.997	20
CTTCCGCTTGCTTGTTCTTC	60.132	20	CCAATATGGTTTAAAATTCTTC	59.976	24
AGCGTAATAGCGTGCAAACC	60.293	20	ATCTCACATACATATAATTGAG	57.101	27
AAAATTTTGTAGGTAATAGCAATC	59.665	27	TGGAAGTAGCAGATTGCGAA	59.566	20
GCTCAACTTCACCAAAAATCG	59.738	21	TTGATGAGGAAAACAAGTGGG	59.956	21
GGCTACAAAGGGACATCCAA	59.933	20	CAGGATACTGGCAAACAGCA	59.864	20
CCCACATTTTCCACCTTAGC	59.429	20	CATACGGAAGCCTTTGTGCT	60.27	20
TGCTCTTCACGTGAGTCTGG	60.178	20	GACGATCACCGGTTCTTGAT	59.934	20
GGCGGGTACACCACACTACT	59.914	20	CCTGAGGATGAAGTGGAGGA	60.191	20
AAGATTACGACGGCGATACG	60.117	20	ACCTTCGCACCACTTCACTT	59.769	20
CTCCCATCATCCTTTTTCCA	59.864	20	CTCAGCGTCTTGAAAATCCC	59.813	20
ATCCCGTTGAAATATGCGAC	59.791	20	ACCTTCAAGGGCATCATCAG	60.073	20
ACTCTAAGGGATGAATGCACG	59.208	21	TGATCCACGCAACTCAAAAA	60.234	20
CATGCGCTCAGCATAAAGAA	60.118	20	GGTGTGGCATATTTATCGGG	60.038	20
GGATCAGCAGTGGCTTTCTC	59.957	20	GTCCAACTGGAGGATCAGGA	60.048	20
TTGGGATTAAGGCTTTGGTG	59.931	20	GCCCAATACGTCCATTTGAA	60.701	20
AAACTGCCAAGTGCCAACAT	60.559	20	TCGAATCCTGTCAACACTGC	59.837	20
GAACCGTCTCAGTTGTTCGC	60.844	20	TCAGTTCCATGCTTGTCTGC	59.992	20
CAAGACCTTTTTGTTCGCTT	57.158	20	AGCGGATTTACAATTCGTGC	60.103	20
GGTTCGAGCTACCGAAACAA	60.249	20	GGAAAATCGGCTGAAGTCTG	59.813	20
TTTGCTGGATACCGCAAGTA	59.325	20	ATGTAGCCGACCCCAATTTA	59.297	20
GAGAGGGAGAGAGAGGGGAA	59.883	20	CTAGCCGATGACCTCCAAAG	59.83	20
TAATACCCCGAGTCTCCCCT	59.783	20	AGGGAATAGCCCACCAAACT	59.827	20
TTACGCGGGAACCTACAGAC	60.132	20	CAGCTCCATGATACTCCTCTAC	58.585	24
ATGGAGGAGGAGGAAAAGGA	60.008	20	TGGTGATGATGGTGCTTGTT	59.967	20
TCGTTCAATTCACACACGTTC	59.606	21	AAAATTTTCACCCGCAAAGA	59.564	20
GGGGGTTTGAGGGTTAGAGA	60.298	20	TACCGACAATTTTTGCTCCG	60.989	20
GGTGGCTGAAGATAGGAATGA	59.14	21	CTGCAGTGGTGACGGAGTAA	59.897	20
AGCAGAGTTTGTTCGTCGGT	59.914	20	CCAAGGAATCAGCAAACACA	59.691	20
TGCGGAAGTAGCTTTGATGA	59.566	20	GCTTGGGAGACGAATCAATC	59.635	20
GAGCCATTGATGGCATTTTT	59.907	20	GTGACAAGTGTTTGAGGGAGG	59.607	21
CAGAAAGCGCTTCGAGAACT	59.898	20	AGAGCTTCTTGATTCCATGTCA	58.936	22
GGTTTCGGAGGTATTGAGCA	60.074	20	GGTCGTACTGGTGCCTGAAG	60.711	20
TGTTTGGATTTCATGAATTAGTAT	58.5	27	TTGTGGGAAATTGGGAAAAG	59.772	20
GGGGAGGAGGATTGGATAAG	59.722	20	TGGTGGTAATGCCAAGAGAG	58.722	20
ACTGACCACCATCTTCTCCG	60.112	20	TCGAACTTGTTCAGGCACAC	59.88	20

TCGCTCCTCCAAGAACAACT	59.989	20	GACACAGAGGCTGACGATGA	59.988	20
TGCTGTTTATCACGACGAGC	60.019	20	CCGCCTCTATTTCCGTAACC	60.811	20
AACTAGCGAAAAACGGACGA	59.883	20	CCGATCGATCAATCTGAAGG	60.56	20
AAGGTCAATATGCGGTGGAG	59.955	20	AGGAAATAAATGGATTTTCGT	58.914	23
CTCGAAAAACCAACACCCAT	59.83	20	TGTTCCTTTACCAGAGGCGT	59.734	20
CCAACCAAATTGGACTTGTG	58.871	20	AACACCGTTGGTCGAATTGT	60.277	20
AATTTTGAGCAAGGCCAATG	60.074	20	TAATTGCCACAGGGAAAAGG	59.931	20
CCCAAGACCCCAATTTGATT	60.91	20	TGGTACAAAAGTTTGCCCAT	57.999	20
CGCCTCTTGATTAACCTCCA	60.206	20	AGATGTACGCAACCGTACCC	59.882	20
TTTGGTCCCTTTCGAATCC	59.856	19	GGCACTGTCACCGGATTATT	59.82	20
GGGTTAGTTATGGAACGATGC	58.456	21	ATGTAGCCGACCCCAATTTA	59.297	20
CATGTCACAACATGGAATCTCA	59.42	22	GAAATGGATCCGAATGAGAAA	58.963	21
CAGGATGGTTTGAAATGAGGT	58.898	21	TTTGATTGGGAATAATTGGG	57.289	20
TAATTTATCGATGGCGGACG	60.792	20	GGGGCATTTTGGGGATATAA	60.694	20
TTGATTGCTTTAAATCCGGC	60.04	20	TCGTGTGGTTCGAATATGAAAT	59.343	22
TTTAAAGTTGCCATTTCAGCC	59.244	21	TCCATTCCCGAACAAGAAAC	59.91	20
GCCAAAATCTGTATACCCCG	59.297	20	ACCTTATGGGGTACTGGGCT	59.713	20
AACCTTTTTGAGCTCCGCTT	60.373	20	ATGTAGCCGACCCCAATTTA	59.297	20
ACATGCATGACTTGGTGCTC	59.714	20	GGAAGTGGGTTCTGTCCAAA	59.943	20
TGTAGCCCACCCCAATTTAT	59.158	20	GCCAACTAAGCGATCCATGT	60.103	20
CGCTGAACGAGCTAGAACTTG	60.332	21	GATGAACCCCACATCCAATG	60.995	20
GAGGAAGATACGATTTGAAACCT	59.531	24	ACCCTGGCCATCTTCTTTCT	60.074	20
AATGGGTGAGAGACCACGAC	59.969	20	TCACAAGGAGGGTCGAAATC	60.05	20
TGTTCTTTGTCGTGGTTTCG	59.734	20	ATAGTGGTATGGTGTGGGGG	59.405	20
ACAGGAATTGAAATGACGGG	59.79	20	GGCCTGCATGATTTTTATGG	60.289	20
TGCACAAAAATGTTTTAAAATTGC	60.26	24	GAACAACCATTCACCATCCA	59.193	20
CAATAAGGATGGGTTTCCGA	59.756	20	TAGGGGTTGGCTCTCTGATG	60.21	20
TGGATTTGGAATCGGTTTTC	59.739	20	CTCCACTTTTCGAATGTCCC	59.526	20
CAGCCATGAATGAGAGTGGG	61.63	20	ACAAGAAAATCCATCGCCTG	60.074	20
TGTAGCCGACCCCAATTTAT	59.297	20	CAAAGCCATATGCGGTAGGT	59.982	20
TCATTTATTTCCTTTTTATATGTGC	59.326	27	AAGAATACCAACAACTAAATA	59.137	27
TTCAAGTGTGCTTCCACCAA	60.278	20	TTGCACCGTGTGCAGTTATT	60.18	20
TGCTAGCATTCGTGTTTCCA	60.401	20	TTCCCACTAACCAGCTCACC	60.111	20
CCCAAGACCCCAATTTGATT	60.91	20	TCTTTAGTTAGCCCTTTGAGCC	59.933	23
CGACCGATCCATTTTAGGAA	59.894	20	TCCTTTTGACACAAGAAAACC	60.365	22
CGAACCTAGGAAAAGTTGCG	59.876	20	AGTGCTCATTGCATCCTTCC	60.226	20
TGAACTCCTCCCAAGTCAGG	60.229	20	AAACGAGAACTATGAAGCACC	58.906	22
TTGATAAGCCAGCCACTTGA	59.42	20	CGTTTCTGGCAATCTCCTTC	59.813	20
GGGTAATGGCTTCAACTCCA	59.933	20	CCAGCCTTGTGAGACAGTCA	60.022	20
GCCGACCTGCACAAAGTTAT	60.14	20	GGGTCAGATGTACGCAACCT	59.997	20
CTGCATGGGCTATTTCCACT	60.096	20	AATCCACATTATTTCTCACTCA	58.455	24
CGACACATGAGCTATTGGGA	59.673	20	TCATCCTCGGAAGCAATCTC	60.303	20
AAAGCAGTTAATAACGAAAAACC	58.442	24	TTTTAGATAAGCATACACCATC	59.08	26
AAAGTCTCCTGCTCGCTCTG	59.891	20	CCGTGCCAGTACCTCCTCTA	60.269	20
ATGTTCCACCTCCCAAGGTT	60.607	20	AAACCCACGGACTAGCGTAA	59.632	20
GACGGGTGTGGGCTAAAAAT	61.099	20	CCGATAATTGCAACGACTCA	59.688	20
ACGTGTGCATGTGAAATTTTTAT	58.493	23	CAGGCACCAACCAAGAGATT	60.111	20
TCCAAATCGCTCAAACATTG	59.664	20	TCACAGTTTTCCCCCTTTTG	59.942	20
ACCTAGACTCCGACGAAAAGC	59.899	21	GCTTACACACGTTCTTGAGGG	59.788	21
CACTCTCCTCAATGGCGTC	59.356	19	GTGACTTCGAGCGCAGTTTT	60.581	20
TGAGACTCAGATGAAATGTAGCC	58.475	23	ATTTTACGTCACACAACTCGAA	57.364	22
TTTATGCATTGCCGTGAAAA	60.074	20	TTCAATGGTTAAATTGGTATTT	59.073	26
ATCAGGATCGAGTAAGCGGA	59.797	20	TTTCCCCAACCTCAACATTC	59.767	20
ACTTGTGAGACAAAGAGAACAAA	57.292	24	TAGCCACCACACTCAAGTCG	59.897	20
CACGTCCCTCATCACTACCC	60.386	20	ACTCGCTCGATCGTTGTTCT	60.02	20
TCACATTTACAACCTACATCGG	57.573	22	CCGAGACCCCAATTTGATT	59.735	19
TGGCATTTATTTTCGATTTGA	58.162	21	GAATGCAGCATCATCACACA	59.202	20
TTATATGCCACTCTTCCCGC	60.06	20	TTTGGAATGCAGGTGGAAAT	60.309	20

GTACTACCACCGGCGAAGAA	60.132	20	TCATTGAAGTGACCCAACCA	59.935	20
CAACGGCCTTTCTTTAGCAG	60.011	20	AACTGCAACCCGTAAATGGA	60.365	20
CTTGGGTGCCAGAGAAAAAG	59.846	20	CATCCCAACCACGTTAGCTT	59.993	20
GCGATTCGGGCAGATACTAC	59.696	20	AACTGATGCTGCTGCTGCTA	59.918	20
GCATTGGAAAATATTACTGGGG	59.588	22	GATCGATTGAAAGGGACTCG	59.629	20
TACTTGGGACGGGATGGTTA	60.184	20	ATGTAGCCGACCCCAATTTA	59.297	20
AGAAGGCGAAGAATGCACAC	60.406	20	ACCTTCATCATCCTCATCCC	58.741	20
TGTCGTCGTGGACAAGAAAA	60.278	20	AGGTCATTGCAAGGAATGCT	59.7	20
TCTTCTATACATAGTGCTTCCGGT	58.446	24	TCAGACTTCGTGGTTCGTCA	60.44	20
GTTCGGTTCCGGTTTCAAAT	61.08	20	AAGAGTGAGGCGATAGGCAA	59.978	20
CTTCCACAGGCATTGGGTAT	59.813	20	TCCTGTGTCAGGGCTAGCTT	60.012	20
ACAAATCACCAATCAACAAAACC	60.014	23	AAGGCAGCGACTGGAAATC	60.355	19
CCCAAGACCCCAATTTGATT	60.91	20	TTTGGTGAAGTGTTATGCGG	59.585	20
CAATGGATGGTGAAAGGCTC	60.461	20	TGCAGAGATGGACGTGTTGT	60.319	20
GTTATGAAGGAGAGCGTGGC	59.843	20	ATAATCCGGTCCCTTCCAAA	60.502	20
AACCCTCAGCAATATGCCAA	60.469	20	GCAAGCCTTAGTCAAGCCAG	60.154	20
CGACAGAGTTGCAAAGAAGTTG	60.088	22	GCCAACCCGCCTTATCTAAA	61.281	20
AATCCCACTCTTTTTGCTGC	59.316	20	TTTCAGTTTGGAACTTGCGA	59.439	20
TCACGAGTTGGCTCTTTGTG	60.025	20	GCAACCCATTCGTATCCTTT	58.906	20
GCGTCTTTGAGGTTCTCCAC	59.851	20	TCACTTCATAAAGTCCGCCC	60.074	20
GAAGGCAGAGACCGTGAAAG	59.989	20	TCCGTCGTCTTTCTTTGCTT	59.993	20
CCGACTAGGACTAAGGGTCCA	60.493	21	TCTCGATCCTCGTTACACTGG	60.262	21
AAAACAAAGGCCATGCTGAC	60.118	20	TGTTGCTCATGACAAATTCAAT	59.996	23
CAGCAACCACCAAATACTCTTG	59.671	22	TCAGAAATTGGGAGCCCTAC	59.126	20
AAGATCAGGGAAAAGGGAGC	59.651	20	AGGGTCACACGAAAGTTTACA	58.675	22
AATCTGCAGCTTGGTTTTGG	60.249	20	CACTGTGGTGGCATATCAGG	59.984	20
CCTGTCAAGACCCAATACGAA	59.978	21	CGTTCAAATCACCAACATCG	59.964	20
TCCAAAATTAGTACAAGCATCAAA	59.168	25	GTTGGAAGCCTTGACATTGA	58.697	20
TCGCCTTCTTTTGCAGCTAT	60.117	20	AGGGGAGAAATGAAAAAGGG	59.393	20
TAAACTGTAAGCAGCACGCC	59.136	20	AAGGTTTTAACAGTCCTCCGA	57.854	21
ATGATCTCGACCTCCCTCCT	60.035	20	GAACGAGCTCTAACTCCCCC	60.212	20
CGTAAGGCTCTCCTCATGGA	60.353	20	CCAAGAGCAAGACGACAACA	60.025	20
TGAAATGAGTTGGAATGAGGAA	59.546	22	CCAAATGAGCTCGGTTGATA	58.721	20
CACTGAGGCAGAGATGGAGA	59.074	20	GCAAAGACTCACGAGCAAGA	59.318	20
CCATTCTCACGATTGTTGATG	58.987	21	AAAAATTTATTGGTCGGCCC	60.022	20
TGTGACGTCTAGCTCGATCC	58.987	20	TTCACACATCCAATCCAAGAA	58.961	21
TTTCCACAAAGCGTCGTACA	60.293	20	TCACATTAGAGCACATGGAGG	58.736	21
GGGTTGGGTTTTCTCCATTT	60.032	20	TGATCATGCTTTTCGTCTCG	59.948	20
TCCACTGATTCCAGATGGTG	59.473	20	GCTAAAGTGCCTCGTGCTTC	60.162	20
TAATGAAATTGGGTGGGAGC	59.762	20	CGCCACAAGATTAAACCCAT	59.823	20
CCGACTCCACATAGTGGAAAA	59.978	21	TTCGAAAGGGAGATTTGAGC	59.387	20
TTGCTTGCGGTATTGTTTTG	59.742	20	TGCACTGCATTTCCTTCGTA	60.401	20
AAACCTCACCACAAACGGAG	60.005	20	ATCGAATTTCTTCGACCCCT	59.903	20
TGTTGTTGAAAAAGGCGACA	60.271	20	TCAGGTTGGGATGAAAGGAG	60.042	20
TAGGGCTTTTGTGTGGTTCC	59.971	20	GATATGGGGCACAAGAAACG	60.331	20
GTCTCAATGGGGACATCTGG	60.326	20	ATAGGCCAATTCGTCTCGTG	60.096	20
TGAGCAAGAAGGGTGTTGAA	59.415	20	ATTCTCTCTTCTTCGCCACG	59.574	20
CACCCAAATTTTCTTAAGCCC	59.83	21	GGTCCCAAAATCGACGTAAA	59.801	20
TGTAGCCGACCCCAATTTTA	60.315	20	ATCAAATCCACCGTCCAAAA	60.17	20
ATCCATCCATGCATTTTGGT	60.021	20	TCAAAATCGAGAAAGCGAAAA	59.95	21
ACCCATGGATCCAACTTCAA	60.173	20	GTGAAAATGAATTGGGGTGG	60.029	20
GGTTCATGTAGCCTACCCCA	59.813	20	ATTCAGCCCTTAACTGCCAA	59.708	20
GAATGTCAAGATGAGAGATGGAA	59.598	24	CATCTAAGGCTCCCAAGCAT	59.292	20
CCGAACAACACTCAACTCCA	59.72	20	TTTGCACATGAACAATCACAA	58.588	21
GGGTTGAGGCCACTATATCC	58.334	20	GCCATTGAAATTACCTGCAAA	59.957	21
TTACTCCTCGAAAACAGCCG	60.378	20	AGAAACTGCTGAGACGGAGG	59.598	20
ACGAAGCAATACACTTTTGAAGA	59.391	24	TTCTCGCCCTCTAAGGTTTTC	59.843	21
CGCCTTTCTGTAGCCAAGAG	60.147	20	GATTCTTTCGTGGAGTCCGA	60.195	20

AGCTCTTTCAATAAACAGAATCCA	58.528	24	TCCAACCCAAGGTGAGTAGC	60.111	20
GCACAATTAAAAATGCACCG	59.077	20	TGAGGGGGAAAAGAGAGGAT	60.008	20
CAAATCAATCGTTCCCCTTG	60.301	20	AAACCAAAAACCCAAGACCC	60.068	20
TTCAAATTCCACAAACACGG	59.415	20	TTTTCCATTGGCATAGTTGAAAT	59.741	23
ATACCGCAGATCCCTTTCCT	59.925	20	GATGAGCTTTGGCTTCTTGG	59.955	20
TTCGGACATGAGCAATTGAG	59.799	20	AACTCAACCCAACGCAAATC	59.978	20
CACGTAGGCGGCTTTACTGT	60.326	20	TGGGGGATTGTTGGAATTTA	59.988	20
GGATTCGAACCTGGGACTTT	60.306	20	CAGAGCGCACTCGAAGAGTA	59.49	20
CCCAAGACCCCAATTTGATT	60.91	20	TCAACATACCCAATTATTCCCA	60.292	23
GATTTTATCCGGACGGGTTT	60.02	20	TCCTCCATAACTTTTTCCTCACA	59.987	23
ATCCACGATCTTTGCCTTTG	60.074	20	AAGAACTCGCAGGTTCCTTG	59.473	20
GTTACTAAGGGTTGCGGGCT	60.503	20	GGTGAGAAGTACGCATGCAA	59.871	20
TCATTTTGGGACGGAGGTAG	59.926	20	GGCAAGAGAATTGAAGAGCG	60.096	20
AACAATCCCGGGAGAAAAAC	60.166	20	TCTTCCCCAAAAGTCACCTG	60.081	20
TGATATCCCACCCGATCACT	60.158	20	TAACATTTTTCGTTGCCGGA	61.344	20
GCACAAATTGAAAGCACACAA	59.767	21	TGTAGCCGACCCCAATTTAT	59.297	20
TTGGTATGATGGAATGGGGT	59.871	20	CTATTTGCTCGAATTTGGGG	59.542	20
CCCAAGACCCCAATTTGAT	59.59	19	CCGTGTGCATTTGTGTCAAT	60.436	20
CAGCTGCTGTCATCATCGTT	60.016	20	TGAGGTTTCCATCACAACCA	59.935	20
AGTTCCCCATTGCTGTTTTG	59.971	20	GCCCATGTTTTGAGAAATTG	58.066	20
TGAGCCTACATCTGTGCTGG	60.008	20	GAGAAGGGTTTGTGTCCGAA	60.088	20
GCCGGTTAATATGCATTTGG	60.172	20	TCTGTCTCCACTTCCTTGGC	60.386	20
CGGAGAGCTCGGTAAATGAG	59.971	20	CCCTCAACCACCACCATATC	60.05	20
AAGGAGCAGCTGTCTTTTGTG	59.671	21	GGGAAAGAGATGACAACCCA	59.903	20
GCGGGAAAGGTGTAATCAGA	60.074	20	CAGCCTCCCAGCAAGTTATC	59.836	20
GATTGGTTCAGCTATTCCGC	59.674	20	TAAAAATGAAACCGGCCAAA	60.287	20
GGCTGGATTCTTGAGGTGAG	59.803	20	AGGTTGCGTACATCTGACCC	59.997	20
AAGAAGTAAGCCCGACCTCC	59.713	20	CTCCGGATTTGGAGACTCTG	59.797	20
CGCAACTATCTGCACCATTC	59.301	20	GGCTTGTATGGTTTGGGAAA	59.801	20
ATGTTGAGCCCAACCCAAC	60.774	19	TCAACATTCAAAATTGGTATGA	59.665	25
AATCATTCGATTTGGCAAGC	60.045	20	CAAGTTTTTATTAGCATTTTAAA	57.364	26
GGGAGGTTTCGTCACACAGT	60.009	20	CTGGCCTGATCTACAGCCTC	59.973	20
GCAACGGAAACAACCTCTTT	59.218	20	TGCAGACCACTTTTGGTGAA	60.278	20
GGTAGCAGGTGAGGGTGAAA	60.111	20	GCCTCGATCCTAACGTGTGT	60.142	20
GTGGGTTGCACCAATTAGGA	60.755	20	ATCTTCGAATCAGCCACCAC	60.081	20
GCAGATAATCACGATTTAGTTGG	57.86	23	CATCTTCAAGCAAACAACACCT	59.286	22
AAGGGATCAATGAGCCACC	59.878	19	ATGGGAAGGGGTGGAGATAC	60.015	20
GATGTCCCCATTGAGACTCG	60.475	20	CGGTTGTCATAAGACCACTTCA	60.03	22
GGTGGTATTGATCATCCGCT	59.78	20	ATGGGATAAATTCGCTCACG	59.923	20
GAAGCCAGGGAAAGAATGAA	59.244	20	GCAGTGACACCGATAGACGA	59.862	20
TCGGCATTTGAGTTTATCCC	59.901	20	AGGACTGCCGACCTCTTTCT	60.393	20
TTATTTTTGATGGCGTCGGT	60.323	20	AAAAACATTAAATCAAACTGTA	57.811	26
ATTTTCGTCGCCCCTCTTAT	59.93	20	AAGGGAGCTACAACCTTTCATC	59.685	23
GTTGCGTACATCTGACCCC	58.948	19	CTACAAGCATGACTTGCCCA	59.864	20
GCGGGACCTAGAATGTTGAA	60.074	20	AGTCATTAAGTGTGGTCTCGGA	58.721	22
CTGCCCTTAGCCGTTAGATG	59.861	20	AGACAAAGGCTCTGCCCATA	59.836	20
CCTTCTCACTGACCTGCACA	60.022	20	CCCAAGACCCCAATTTGAT	59.59	19
TAATTTACGGCTCGGTTTCG	60.089	20	CAGCAGCCATTTGTTCTTGA	59.988	20
AAATGGCCGAAGAGATTCCT	60.039	20	AAGCACGAGTGCTGTGATGT	59.498	20
TGTTTCTGGTTTCAAATTGGC	59.967	21	TGCTGTTTTGTTATAACCCCG	59.876	21
ACGTGCCCTGTTCTCTCACT	59.907	20	CTAATGGAGGCGACGAAGAC	59.836	20
CACGTCCCAAGTCCTCATCT	60.112	20	GAATGAATTCGAAGTTTGGGA	59.009	21
TTCCTTGTGAAGCACAATCCT	59.726	21	ATGTAGCCGACCCCAATTTA	59.297	20
CCCATACATTTGTGGGGATA	58.011	20	TTGAACAATGGTACCTCCTCC	58.898	21
ATCGTGACCAACCCAAACAT	60.096	20	TTATAACGTGGGAACCAGCAG	60.004	21
GACGATGTTTTGTTGCGATG	60.119	20	AGAATCAAGCAATGGATGCC	60.043	20
GTCTACCCCGCCAGATCC	60.439	18	CGGCGATGGCTAGAGTGTA	59.98	19
AACTCACCCACCTTCTCCCT	59.968	20	GAAATGCGAGAGGGATTTGA	60.155	20

AAAATGAACGAGCATCCAGC	60.221	20	CTGAAGGCGGAGGTTTCATA	60.206	20
TTAGGTTTTGCCCAGGATTG	59.931	20	TCGAAGCACTCCACTGAAGA	59.701	20
CCAAAATCTCGGCTTCAATC	59.645	20	CAAGACGGGTTGTGGGATAC	60.232	20
GTTCGAAGGGTTGAGGATGA	60.05	20	CTTTGTTTGGAGCGCGTG	61.555	18
GGGTTATATCCCCGTCTACCC	60.623	21	AGGTCTTTAATATCCCCATTTG	57.99	23
TGACTTATGCGTGCATGTGG	61.713	20	GGACCGATTTGAGCATTTTG	60.448	20
GATGGACTCCGACGATGACT	60.08	20	CCTTGGGATATTGTTTGGCA	60.692	20
TCACTCCGGATCAAATAGGC	60.036	20	AATGGGATTATGTTTGGATTTC	59.454	23
AATTCCATGACATTGCCTACG	59.837	21	TGGCTTCTTTTGCACCTCTT	59.993	20
GATAAGCGGCTGAAGGTGAA	60.352	20	AGTCATTCCCTCGTCTCCAA	59.655	20
TGCAGCAACTTCCTCTCCTT	60.134	20	AATTTGTACCCAGCATTCCG	59.823	20
ATCCTGTGGTGGCATGTTTT	60.24	20	GAGAGCAATACCGATGGCAG	60.765	20
TGAGCGCACTCGAAAAGTAA	59.752	20	GTGTGGGAAGAATGCGAAGT	60.119	20
AACTTTAGTCGTCGTCATCATCA	58.781	23	CGGCTCAAAGGACAGATAGG	59.83	20
GATACCACCTCGATCGCCTA	60.059	20	TGAATCAGCTCCGTAGGCTT	59.978	20
GGCGGAGTTCGATAACAAAA	60.074	20	TCCACAACCTCTCATCTCCC	60.048	20
CCTACCAAGACTTGACCACCA	60.013	21	TCCTCACTGAGTCTTGATATTG	57.06	24
CAGCAGGAGTGGTGCAGATA	60.008	20	CATTTGACGGTCCATGTTTG	59.816	20
CTCTAACATGCCATGGAGCA	59.823	20	GCGATATCACGTTTAACGGC	60.485	20
GAGAGTCGGGTAACTGAGCC	58.894	20	ACCTTCCAATCAGCCTGCTA	59.836	20
CACTCCATCGGATCCAAGAT	59.886	20	ACACAATAACCATTCGTTCTCA	58.552	23
TGTTTAGGCTGCAGGAATCA	59.42	20	GAGAGAGGGAGAGAGATCGG	60.043	21
CAACATTTCCGTGGTGTGTC	59.855	20	TGTGCAATGCAACAAGATGA	59.833	20
TCAATTGATTTTCGTAATCCTGG	60.187	23	TGGAATTGAGCAGCCTTTTT	59.823	20
TAGGACGATAATTCCCACGC	59.923	20	ACGTCTTGACCAGTCCCACT	59.604	20
GCATTAGTCCTGGTGGCATT	59.962	20	GCTGCAGAAAGTGTTGGTGA	60.032	20
GATGCAGTTGGAAAGCACCT	60.263	20	TGAGACTCGAACCTGTGAGC	59.129	20
GTGGGGCCTTACACCAACTA	59.853	20	TAAGGTGGGTTTTTGCCTTC	59.064	20
CTCAATTTTTCCGGCGAAT	60.024	19	TACCTGCCGGAATGTTGCT	61.591	19
GGACTGTGATGGGCTAGGAA	60.073	20	CGCTAGAATCTCATCCAGTTGT	59.797	23
TGCGGATTAGGGTAGCTTTG	60.223	20	TGATGTACGCACTTGGTGGT	60.032	20
AGAAACCAGCGACACATTGC	61.248	20	CCACAAAATAATAAGGCGGC	59.455	20
CCACAAATGGGGTTGACTTC	60.21	20	TCCACAAATCATGCGAAAAA	60.051	20
ACCAAACGATGCAGATTTCC	59.939	20	CAGCTCCGAGCAAGTTATCC	59.978	20
CAAATTTGATTGGCTCTGTGA	58.759	21	TGCCATTATGCTCCAATGAA	60.035	20
GCCCTTACAAGACCATCCAC	59.41	20	ACCGATCTCACAAGCCAGAG	60.408	20
ATGCCGGATCGAATAATCAG	59.885	20	TTTTCCCATCATTCACGACA	59.9	20
AATATCTTCCTCCCCTCCCA	59.722	20	CTGAGCCATCGAGGTATGGT	60.096	20
TGTATGCCCTGCAAAACAAA	60.111	20	TACCAAACAGCCCACTCCAC	60.954	20
AAAAGAGGGGATGAGGCAAT	59.903	20	AAACAGAATTGTGCTTGGGC	60.118	20
CCAATTTATTGGGATTAAGGCA	60.037	22	CCTCCCTCCAATTTCCACTT	60.298	20
CCTCATTTTGAACCCGAATG	60.301	20	GCTTGATGGTGGATGTTTGTT	59.851	21
CCCCAAACATCCAAGAAAGA	59.903	20	ACCGTACTCCGAATGAATGC	59.962	20
ATGAGATCCTTGCGCAACTC	60.37	20	CGGGACCGTGAATAATGACT	59.813	20
CGTTTCCAACACCGACCTAT	59.853	20	GGCGGATGGTATTGAAGGTA	59.784	20
CATTGGAGATGCCCTTAGGA	60.029	20	GAATTCCACTGGACCTGCAT	59.934	20
ATTGATTCCGAAACCTGCTG	60.074	20	ATTGTTTGTGAGCTTCCGCT	59.882	20
CCGACCACTCTCGTTTGAGT	60.298	20	AATTGTGCTATTATCTGCGCC	59.251	21
GCTAGGTTTGTCTTCTGGCG	60.015	20	ATGTAGCCGACCCCAATTTA	59.297	20
TTCTCCTGAATGTCCCCACT	59.505	20	TGCATGCATCTTTTTCTCTTTT	59.013	22
TCATCCAAACCTCAACCAGAC	59.958	21	CGGTAAAGGGTTCGATTTCA	59.931	20
TTCATGCCTGTATTTCAATCG	58.639	21	CGACCACAAGGTTAAGAGCC	59.734	20
ACCTCAACAAGTGGGCCTTA	59.592	20	GACAGGCCTGAGTTCGGTAG	59.867	20
TTCCAGTAAACAGGCCCTTG	60.103	20	AGGCTGCAGCTGATCAAAGT	60.164	20
GAATATATCTTGCCGTTGCCA	59.942	21	AGAATGCATTGAGTCAAACAT	59.24	25
TCACGTTTCACGCTTCCTAA	59.464	20	TTTCTTTTGGCCAATGTTGA	59.133	20
CGGACCAGCCTAGAATTTGA	60.206	20	ACAAGAATGTTGACCAAGAGC	59.78	22
GAATGGCGAAGAAGTGGAAA	60.192	20	GCTCTTACACCCATCCGAAA	60.074	20

CGAACCATAGTTGTTGGACG	59.047	20	TGTGACTGGGCACGATTTTA	60.111	20
GCATAATCGAACTGGAGCTG	58.477	20	GGGTGTCCTCGACATTTTTC	59.386	20
GCAAACAATGATGGCACAGT	59.577	20	ACGAAGTGGCTGAGGAAATG	60.255	20
GCCACCAAAAATCACACAAA	59.42	20	ACGGCTGCAACTTTCCATAC	60.14	20
CCACTCCAAATCTCCCTTCA	60.042	20	AATTACCTTCACTCACCAGAAA	57.008	23
GCTGCACACATCATTTGGAC	60.128	20	TGGAACATCGTGAATTTCCTT	59.42	21
TGTGGAACTCATCATCTAATCCA	59.443	23	ATCGAGGAGTTATGGGAGCA	59.653	20
GCACAAATTGTTCCCATTCA	59.375	20	GACGATGCTATGCAGATGGA	59.788	20
TCGTACAAAGGAACTTGGGC	60.11	20	ACTTGATATGGATCCGAGGC	58.962	20
TCCCCCTACCCCAAACATA	59.992	19	ATGGGGGATGAGTTTGTGAG	59.779	20
GGGTTTTACCGCCGTTATTT	60.076	20	CGGAAAGTGACCTCTGAAGC	59.989	20
TGATTTCGCACGAGTGTTGT	60.31	20	CGGTTCTTACCATTACCCGA	59.817	20
CCATTTCCGGTGGAAGAGTA	59.926	20	CGCTAGTCAAAGATGATGCG	59.59	20
GCTTGACGACGCACTTGATA	60.019	20	GGGCTTGAAAATGTAAGCGA	60.209	20
AGCAAGGCTTGGATCAATGT	59.7	20	GAACCCGACCACAAAGGAAT	61.115	20
AGGCTTTGCATAGCTGTCGT	60.044	20	CAAGCCCCAAAGTCAAAAAG	59.719	20
TTCGATTCAAGGTCTCACGA	59.369	20	TGTAGCCGACCCCAATTTAT	59.297	20
AAATGGGTGTGACTTGGCA	59.951	19	TTGATTATCATGTCGCTCGC	59.799	20
GCGGTGGATTTAGGATTTCA	59.901	20	TGATTGTACACGATGGCGAC	60.549	20
GTTGCGTACATCTAACCCCC	59.316	20	GCGGATAAGCTCGAACAGTC	59.985	20
AAATACAAATTCAAGGATTATACA	57.021	26	CCCACATTTACTTGATGCATTCT	60.25	23
AGGCCGCAATCTTTTAATCA	59.682	20	TGTCAGGATATTGACAAGGTG	60	22
TTAATTAAACCCAAACCAAACTCT	58.59	25	TGAATATCGGTTTCATCGCA	60.035	20
TGGGATTAAGGCTTTGGTGT	59.429	20	ACCCAACACCAAATTATGCC	59.551	20
GTTGCAAAACGACTGGGAAT	59.978	20	TGGATCGGAATACTGTGTGG	59.369	20
CCATCGATGTCAAACCACAG	59.96	20	ATTTAATCCCGTGCAACGC	60.852	19
CCTCTTTCTTGGGTGATGGA	60.042	20	CTTCAGGGCCAAATGTGAGT	60.111	20
GCGATTGTCGGTGAGGTAAT	59.962	20	TCAATTTTCACAAAATAACGCA	59.542	23
GCTATCCTCAGCCTTGCATC	59.946	20	CTGGTAAGGCTGTTGGGGTA	59.986	20
AAGGGAGAGAGAGGGGAGTG	59.801	20	CTCCTGTGGCCAAACAATCT	60.111	20
ATCGCAATCTCTCGGACACT	59.834	20	GTTCGGTTGTGAAATTGGCT	59.978	20
ATTGGGCCTGAGTTTTGATG	59.933	20	CGAGCCATAAGCTCGGATAG	59.96	20
CGCGGTTATTTATGTCCGTT	59.853	20	TCGTCCTTTTCAGTCAGCCT	59.989	20
GTCTAGCATCCTTTGGCAGC	59.985	20	CGAAAACTGAAGATCGGGAA	60.184	20
ATGTAGCCGACCCCAATTTA	59.297	20	GACACTTGGTGTGCAAATCG	60.16	20
GGGTTTGTTCTAGTTCATCCCA	60.221	22	GATGACGGATTGAAGGCTGT	60.081	20
CCGAGGCTGAGATGGACTAC	59.827	20	ATCTGCAAAGTGCTGCTGTG	60.207	20
ATTGAATGGGAGTCGCTGTC	60.081	20	CTAGGGTTGACCCACCTCAC	59.425	20
TGATGGGTGAGTTTTATATGATGC	60.102	24	TATTTTGGTTCGATCACGCC	60.837	20
GCTGCAGATCACAGAGCAAA	60.296	20	GTGCTCAAGGTTTGAACTCG	58.497	20
ATCCTTCCCACCTCGAATTT	59.766	20	TAGTCTCTGCCAAGTGGGCT	60.012	20
TGTAGCCGACCCCAATGTAT	60.214	20	TTTCCAAGACCGGAAACAAG	60.081	20
CCCCCATTACTCACATCAGAA	59.799	21	AAGGCTTTCGCCTTTTTCAT	60.204	20
TGAAACCTTCTGCCCTCAAT	59.67	20	AATGGCGAAGGCAGTATTTG	60.096	20
AGCATGAGTACATACATTTCTAG	57.669	26	AGGTTCTCAATTATGTTATTAG	57.915	27
TGGTGTAATTTTGGAAGGGAG	58.936	21	TGGGCGTAAAATAGAGGTGC	60.096	20
AAATCCCCAAAAGAACATGG	58.738	20	GCAAGCCCTTTCAAACATTC	59.691	20
AGCCTTTTGTGAATGATGGC	60.081	20	AGATCGCTCCTCCAAGAACA	59.95	20
ACTGCTTTCTCACAACGCCT	60.058	20	ATCAACCCTTCGGATGAAGA	59.483	20
AGGATTCGATGTCTGCCAAC	60.081	20	CCTGCAGATCATTCACATGTTT	60	22
CTTGGGATATTGCTTGGCAT	59.923	20	TTCGATGTATTGTTGGATAATGT	58.808	24
CAAGGTGGGTAGCAAGAAGC	59.875	20	ATGCAATCACAGACTGCCCT	60.688	20
GGGTCGTCGATTTGGACTC	60.468	19	CTCGGCGATACTTGTCTTCC	59.836	20
ATCCAAGGGCTCGATTCTCT	60.176	20	CTATCGCCCTCTGCTTTCAA	60.481	20
CGATCGTTGAAAACCCACTT	59.971	20	TCACCATCACCATCACCATC	60.189	20
TTGTCCAAGTGGGAGATTGTT	59.439	21	ACACTAACCTGAAGCCATGAGA	58.865	22
GGGATTTTCGTTTGGATGAA	59.739	20	TCAAATTTTTCAGCTTCGCC	60.323	20
TTTCAAATACCTTGACCAACGA	59.492	22	ACCCAAATGGATTGGGTTCT	60.422	20

ATTATTTGATGGGGGCACAA	60.016	20	CCGATTTGCCGTTCTATCAT	59.923	20
CGATCATTTCGGATAACGCT	60.06	20	CCCCTTTCGGTGTAGACAAA	59.964	20
TGGTATGTGTTGTATGCGTTCAT	60.187	23	CCCGAGGGAGTCACAATTTA	59.926	20
TGTAAACCGCCTCAAACCAT	60.365	20	CGCACGTTTGTATTTTTATTTTT	57.532	23
TGGAGGCGGATTATAGATGTG	59.93	21	ATTACGCATCAGCACAATCG	59.718	20
TCGACACAGTTCATCGGAAG	59.831	20	GTTACATCCCACCGGATTTG	60.051	20
TGCCTCATGTAATGGTGGAG	59.522	20	GATGGCAAGCAAACTGATGA	59.805	20
TTTGCTTCAGCATTTCCTCA	59.542	20	CTTCAATCAATCCCCCTGAA	59.864	20
GTCGGGGTAATCCGACCTAT	60.039	20	ATGGACACGTCCAGATGAGA	59.05	20
TTGACCGTACTGGTGATGTACC	59.78	22	TTGAGCAAACTAAATTACAAC	59.322	25
TGCAAAATTTGTGGGATGAA	59.907	20	CCATGGCTTTTCAACCAGAT	59.933	20
TCATCGAATCAAATCCATCAAG	59.901	22	TAGCAGGCCAAAGAGGAAGA	60.088	20
CCATTTTCCCATCAACATCC	59.991	20	TGTGATTCACTTGCTTTGCC	59.847	20
TTACTATGCGGACTGGGACC	59.955	20	TTTGTTCCATGCCTCTCTCC	60.195	20
AAGGGAGCTACAACCTTTCATC	58.783	22	TTATCTCCCCATTTTCGTCG	59.894	20
GGAGACAGCGGCTAGTAACG	60.037	20	GTATGGTGTGCAGAAAAGCG	59.347	20
GAATGTTGGAGCTACGAGGC	59.843	20	AAGTAGGGTCAAACACGTGAA	58.304	22
TCTCACACTGCAGAGGATGC	60.146	20	GCCCATCTGACGATAGAAGA	57.834	20
GTTTGTCGATCATTACGCCC	60.339	20	ACTCCTTTCGTTGCCAAATG	60.11	20
TTCATGTTTCGCGATTCAAC	59.67	20	TAGATCATCAAATGCGCCAC	59.652	20
GGAGCTGGTTTTTGAGATGC	59.82	20	TTTGGTTCATGTAGTCGACCC	59.845	21
GAATGGCATGTGGATCTGTG	59.925	20	AGAGTAACCACCTTCAGCCG	59.353	20
ATTTGTTCAAAATCCGCGAC	59.945	20	GCGACGATTGAATGGTATCAA	60.852	21
TACAGCTTGGTTTCGGAGGT	59.734	20	TTGCATTTAGGAGAATCCCG	60.031	20
GCATAGGATATTTATTACACCACG	59.916	25	TCATGGTTCGTCAATAACGG	59.395	20
GCCCTCAAATCTGACCAAAA	60.051	20	GAGTCTGAGGTGGAGGTGGA	60.243	20
TCACCACCACCATCATCATC	60.189	20	TTATCCAACCCAGCCAACAT	60.192	20
ACAATTTGATTGTGCGATGG	59.4	20	TCTGTCTAATGTTTCCGCCG	61.157	20
TTCACGCTATGATCCGTCTG	59.823	20	GGTAGCTACTTCAGTGGCGG	59.898	20
AATTGGCCCTCATTTCCATT	60.511	20	AATAGCATCGGCTGGTGAAT	59.556	20
TGCTCATCAAAAAGTTCCCA	59.247	20	CGTCCAGCTGATGGTAATGA	59.673	20
GCTGCCATGGAAACTCTGAT	60.226	20	TCCCAAAGAGCAAACAGCTT	59.993	20
TGTACGGTGTAATGCTTGTGC	59.67	21	CTCGGCCTCCGTCATTATTA	60.053	20
GTGAATCCTGGTATCCCGTG	60.195	20	AGGCTGTGCTCATCCGTAGT	59.898	20
CACGAGATGGGGACTCTTGT	60.112	20	ATGTAGCCGACCCCAATTTA	59.297	20
ACAAGTATCCACCACTCGCC	59.997	20	ACCCATTTTCAAGATGTGCC	59.797	20
CCTCCTCTATTGCTGATTTAAGGA	60.108	24	CCACTGTTGTTGCTGCTGTT	59.946	20
GGCGTTTCTTTGTTGAGAGC	60	20	CCCCTTTCTCCAGCTTTTTC	60.18	20
AATTGTGCTCCATTTCCCAG	59.933	20	CCCCGTACACAGTGATTTTTC	59.345	21
TCATCGAATCAAATCCATCG	59.43	20	AGCAGGCCAAAGAGGAAGAG	61.027	20
CTGGTCCACTTCCAGCTTTC	59.844	20	GGGACAAGACTCAAACGAACA	60.141	21
ATTCTACGGTGATTCGTCGC	60.103	20	TCTCCATCACATTGCTCTGC	59.95	20
AGGCTTGCTCAACCAAATCA	60.776	20	AGCCCTGCCACGTTCTATTA	59.73	20
TGACGGTGTCGTGGAAGTAG	59.745	20	GGCAGCAGCCTCTTAATCAC	59.985	20
CCCAAGACCCCAATTTGATT	60.91	20	ACCCAGCATATTCCACAAGG	59.813	20
TTCTCAGTGCTATTTTGTTCCG	59.402	22	TTTGGGAAATATGGATCGAA	57.882	20
AGAGGAGAAGAAAGCCGAGG	60.088	20	CCTGCGAACTTTCCTAGCAC	60.015	20
AGGAGTTTTCCTCTTTCCGC	59.827	20	ACGATGAAGACGTCGGAGAA	60.801	20
GTGCATGCAAGACAACAAGG	60.31	20	CCGCACTTGACTACTCAGCA	60.199	20
TCCATCTGTCATCTCATCCA	57.404	20	TTCGGGATCTTGATGGTTCT	59.483	20
GCTTACGTGAAAGTGGGGAA	60.11	20	CCAAGAAAGTGGAGAAGCGA	60.508	20
TTCTAAGGCGTGCGTATTCC	60.23	20	AGAACTGTGGAACTGCAGGG	60.298	20
AGCTTTGGTTCATGTAGCCG	60.27	20	CAGCGGAATCACTGTCACAT	59.707	20
GGGTGAAAATTCGCAAACAC	60.352	20	TACCTTGTCGGTAAATCGCC	59.96	20
ACCCTAATCAACATCTGCCG	59.955	20	AGGGCTAATAATGCCCAAGG	60.292	20
GCGTCATCGTGACGTCTG	59.981	18	CTTCAGCTTGGTTTTGGAGG	59.846	20
TCGTGTCACCAGGTCAAAAC	59.571	20	CATACACGGTCACGTCTCGT	59.622	20
CGACCCACATAGTGGGAAAA	60.745	20	GCAGGGAACCATAAAAGTGC	59.574	20

TCTTCCATCCAATAATTCCTGT	57.552	22	GGCCAAAGTGGTGAATCAAG	60.495	20
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CGATTTCCTTCCACCAAGAA	60.044	20	AACACAAATATGCCATGCAA	57.506	20
CTTCGCTGCCATTTCTTCTC	60.096	20	CGATAGCAAACCTTTCCGAG	59.839	20
TTTCAAAAGATGAGCTACTAGCA	59.573	26	GTTGAGGAAGCTGTTGGAGC	59.997	20
CCTTTAACCAAAAGTGCCCA	59.968	20	GGTCAATCCCAATGACCATC	59.995	20
CATCTCTGCGTATGCATTCTT	58.012	21	TCCCATGCAAACTGAATCCT	60.461	20
GCCACAATAACTTGTGAAACCA	59.904	22	CAGTGGCTCTTTCGCTTACC	60.015	20
ACCACGTTGGGATCTTGGTA	60.232	20	GAACCGATGAGCAAAGTATTC	59.229	22
CCTTTTTCTGTTTCTTGCGG	59.855	20	TTCGTCCCACTCGAGAGTTT	59.844	20
TGGGAAAAGAAAATGGGAAA	59.36	20	GGGAAGTTAGAGGAGGTGGG	59.928	20
GTATGGTGAAGCGTCCCAAG	60.517	20	TCCAATTAGGACAATCAAACC	60.055	22
AACTGAGGACGGAGGGAGTT	60.111	20	TTCTTGGCTCGTTCCTTCAC	60.375	20
TGTTCACACACCCCACCTTA	59.848	20	TGTGTGGGTGGTTCATGTTT	59.701	20
CATTTCAACACAAGGCAAGC	59.322	20	GTCGTCGCAGAGCTAGTGAA	59.344	20
CGTGGATATAACTCGGCCAT	59.807	20	AACAGCAATTGGAACTCACTG	60.054	23
CCCCATATGAATCCTTTCCA	59.576	20	TGCTGGGAACTGTACTGGAC	58.725	20
TGTAGCCGACCCCAATTTAT	59.297	20	AACAAACATATGCTTTCCCAA	59.891	23
GCAGCTGTTCATGCTGTTGT	60.064	20	TAGCCAAGACCCCAATTTGA	60.439	20
TGGAAGTGGAGGAGGATTTG	60.042	20	AACACGCGAGTTTAAGGGAG	59.378	20
GGGGTCCTTGTCGTATAGCA	59.955	20	ATCAGGTTGGACCAAAGGTG	59.82	20
TGCCTTCTGAATGATGGACA	60.201	20	AGGTTCGGGGAAGTCTGATT	59.935	20
GTTGTTGTTGGTGTTGCTGC	60.207	20	TGCTAGCACCTCCTCTATTGC	59.629	21
TGATGTAGATATGGAGCGATTTTT	59.073	24	AGGCCCCCTTGTCAAATACT	59.827	20
ATCAAGGGCCAGTCTGCTTA	59.836	20	AACACAATAACGGTACCCGC	59.752	20
ACAGTGGAGACGGAATCGAC	60.12	20	TTGGTAATCTGATCCGAGGC	60.036	20
TCTACCCACCAATGACAGCA	60.112	20	GGATCAGCAGTGGCTTTCTC	59.957	20
CGAGCAGCTTCTAAAGGACG	60.284	20	AAGCAAACCAATGCAACACA	60.157	20
ATTGGCCTGAAAACACGAAG	60.11	20	CTCTTCCACCTGTCTCACCG	60.85	20
GAAGTCATGCACGATGAAGC	59.404	20	AGGTTGCGTACATCTGACCC	59.997	20
TGTGGTTGTTGGTGTTGACC	60.309	20	TGATGCTTTTGCGTTTTCTG	59.992	20
TTGGAGGGGTTTAGGTTCAA	59.401	20	TTGTTAACCCATTCCCACAA	58.719	20
TCGGGCTTTGATTTCAAGAT	59.645	20	AAAAAGAGTTGACAGGGGCA	59.711	20
TGCAATTTCAGGCACATCAT	60.08	20	GAAGTCGAGGAATTTGCTGC	59.962	20
TCTGGTTCGGATTGACATGA	60.048	20	CAATCCTTCATTCTCCCTCG	59.623	20
TTCAGAATCATTTACTTCCAAGTT	57.589	25	TCTTGATATCTTGGGCAATTGT	58.642	23
AAGAGGATTCTGTGGTGCGT	59.727	20	CCTCTCATTCACCCTCATCC	59.46	20
GAGAGGAAGAAAGGCTGTCG	59.162	20	CTCTCTCTTCTCCCTCGGCT	60.23	20
ACGATGTTGCCACAATTTCC	60.765	20	CCTTTCTGGACATGGATCGT	59.927	20
GGTGTAGATCTGGCGGGTAG	59.574	20	CGTTCGATGAATGGGAGCTA	61.129	20
CGGTCTAAAACCGAGCTGAA	60.378	20	AACCCACATACTCGAGGCAC	59.997	20
CAAAAAGGAACGCAAAAACAA	60.129	21	AATACGTAAGGCCGAGAGCA	59.867	20
GATTGGCCCAAACATCAGAC	60.326	20	CTTGAAACCGGGGTAGGATT	60.18	20
TTGTCAACTTGGTTTTGCCA	60.127	20	CGTGTTCGTTCCTAGCTTCC	59.875	20
TGAAAGGCTGCAGCAAGATA	59.712	20	GATCGGAGATGGTGACGATG	61.474	20
GGGGCGTGACATTAACACTA	58.502	20	TACACTTTGAGTGGCGATGG	59.716	20
GCCGGAAGAAAAGACACAAG	59.853	20	CCTCTCTTCTCCACCTTCCC	60.186	20
ATCCGCAGTCAAAACGTACC	60	20	ATCAATGACATTCCGGTGCT	60.348	20
CCCCAACCTTTTACTCCTCC	59.799	20	AGATGCTGGTGGTACTTGGC	60.142	20
CCCAAGACCCCAATTTGATT	60.91	20	ATATGGCCCGTCTGGATTTT	60.531	20
CGCAAGATGTTTCAGGGATT	60.074	20	CTACTACATCCCCATGCGCT	60.118	20
AATGTTTCTACGCATTGGGG	59.823	20	TTAGGCAGGACACAAACGAA	59.317	20
GGCAAAATCTCAATTGTAGTGC	58.768	22	TGACGTGCACATTTGTTATGG	60.43	21
ACATGTGGTGGCAGGTTACA	59.88	20	TATCAGATGCCGGTTGATGA	60.033	20
TCTAGCCTGCTCAGCCTCTC	59.997	20	TCATGATGGTCCTGATGGAG	59.425	20
ACTGGGCTTCTCCGACCTAT	60.096	20	ACCAATGGTGGTATGGTGTG	58.984	20
GCTCTCCGACCCATATACCA	59.917	20	TTTCTTTTTCCCCGTCCTCT	60.046	20
TGTAGCCCGTGACTGTACCA	60.175	20	GAGAGTGGAGGAGTTGCAGG	59.986	20

ACCCTCACTAGTTTCGGTTAGA	57.065	22	TGGACAAAATTTCAAAGTGGT	59.876	22
ACAACCAAGCAGGTCCAAAA	60.529	20	TTGAAGTCATGTGTCCTCCATT	59.454	22
CGATACCCATAACGGGTGAG	60.206	20	TTTGATTGGGAATAATTGGGT	58.163	21
TGGTTTTGGGAGGAGAGAGA	59.773	20	ACATTCGGGGGAGAAGGTAT	59.651	20
CGATGGGATCCAGAAACTGT	59.927	20	GAAGACGACGATGTTGGGTT	59.973	20
GAAAATGCTGGAAATGAGGA	57.735	20	GCCACCTACAAGAATGCCTC	59.7	20
ACGGCTAAAATCAGGAGCTG	59.476	20	TTACAAGCAACATCCATCGAA	59.172	21
TAAATCCTTCGAGGTCACCG	60.066	20	TTTGATTGGGAATAATTGGGT	58.163	21
GAATCAGTGCTTGCCGATCT	60.37	20	CTGGGTTGGGATCCTCAGTA	59.92	20
GTGGAAGCATCAAAGCAGGT	60.263	20	TCAACTGCAACCGAGCTCTA	59.74	20
CGTTATCGTGACGTCGGC	61.269	18	TCTGAACAATTTGCAGCTCG	60.134	20
CTTTTTGTTTTGGAGTGGGG	59.443	20	TCTGCTTCAAGCTACTCGGA	58.9	20
TAGCAACTGCACCAGGATGA	60.413	20	TGGGCACTAAATCGGGTAAG	59.953	20
CCGGATCCACTACAAGTTCC	59.405	20	ACAATTGTGGTCGTGGGAAT	60.096	20
TGCATCTGAATACACGAGGTTC	60.14	22	CGAAGGTGTAGATCTGGCG	59.405	19
CAATGCCAACACAACCAAAC	59.864	20	CTCGTGCATTTTCCTTGACA	59.84	20
AATTGCAGCCAAAAGCATCT	59.851	20	GATCTTCATTGCGGGGATTA	59.862	20
TTCGACCCCAACTCAATAGC	60.074	20	GGTTTTGAGGTGGAAGCACT	59.187	20
TAGCCGACCCCAACTTATTG	59.953	20	TGACTTTCATTTGTTAGCCCA	58.28	21
TGAAACCCCATGATTTCCAT	59.991	20	AATCACAGCCCCGATAATGA	60.296	20
TTGCTGCACATTTTCCATTG	60.644	20	TCTGCACAAAACCTTTTCCC	60.088	20
TTGGACAGATTAGCACGGAA	59.272	20	CCACCATTCTTGTTGTTTGACA	60.817	22
AATTGGCATTTTGTAGGCTCA	59.6	21	TGTCTCTCAACACGGCATCT	59.42	20
AGCTTTGGTTCATACAGCCG	60.27	20	AGCATTCCGAGTTTTGGATG	60.074	20
ATAAATTCACCCGGAACTCG	58.903	20	CCACTGCGCCATAGGAACTA	61.176	20
AAAGCAAACCGCTAACCCAT	60.849	20	TAGTTATTCCGCAACGGAGG	60.089	20
ATTCTTGCCTGTGTCATCCC	59.934	20	CTCAAAACCGAATGGAGGAA	60.044	20
TGTAGCCGACCCCAATTTAT	59.297	20	ATGGACATGATTTGGAGGGA	60.135	20
GACCCCAATTTGATTGGAAA	59.599	20	TTTTTGTTGTTGACTGGAGGC	60.139	21
GAATCGATCCGACGACTCAT	60.042	20	ATTCTGCTGCTGTGACGATG	60.016	20
CAGGGTTAGCAGCAGCAGAT	60.559	20	GCGACTAGTGCTGTAGAAGGC	59.304	21
TGTATTGTCTTGATTGCAGGAAA	59.639	23	ATGGTGTCAACACATTGGGA	59.656	20
TGTAAAACCCTGACTAACAAACA	59.189	25	AGGCCGAACCACCTATTTCT	59.962	20
CAGAGCGCACTCGAAGAGTA	59.49	20	ATCACGTGAAGCCACACAAA	60.16	20
ACAGAGGCACAGATTAGCAGC	59.659	21	TTGTGCCGATTCCCTTTTAC	59.938	20
TACTGCTGATTCAAGTGGCG	60.011	20	ATGCTGATGGATGTGGATGA	59.882	20
GCTAACCATTTACTTGCACATTTT	60.288	25	GGACGATTGCGTCACTGTTA	59.722	20
AAAGCATTCACGTAACGGGT	59.499	20	ATTTCATGTAGCCGATCCCA	60.296	20
AACACTATCCCACAAATCACCA	59.218	22	CAACCAGTCTAAGCGGCATT	60.27	20
TTCTTCGATGTATTGTTTGGATAA	57.787	24	CCCTGCATGTCAAATTGCTA	59.688	20
CGGATTGCATCCAAGAAAAA	60.941	20	TCAATGTCGCATATATTACTTT	59.79	25
TCCGTCATTTTCCCACTCTC	60.05	20	AATAGCTCGATTGAGCCGAA	59.945	20
TGCATTCAACATCATTACAAAGTC	59.059	24	CATGCGCTTCTTATATTTTGC	57.667	21
GGACTTTGGTGTGAGAAAATTG	58.602	22	TCCTTCCTCATGTCTTTGGC	60.195	20
TCTGAATTTCACCAATCGGG	60.832	20	TGAAGGATGCATCTTGCTGA	60.504	20
GAGATTCCCGCATCCTATCA	59.998	20	TTTATCGATTGTTGCCCTCA	59.112	20
CGCCCGACTGAATTATCATC	60.435	20	TGTTGTGGATTCAACTGGGA	59.935	20
AGGTTGAAGATTCGTGCGAT	59.7	20	GAAGGTGGTCGTGTCGAAGT	60.159	20
AGATTTTGGATTCGTGGCTG	60.074	20	ACCGACGACCAAATGGATAA	60.192	20
CCTCAAGACCCCAATTTGATT	60.173	21	ATCATGTTCTGCCTGTGCTG	59.862	20
CCCAAATGATTTCAAAATGGA	59.624	21	CAATTCATGATGGTCATTTCAG	59.815	23
GAAGGTGGGAGATGGAGTTG	59.505	20	TAGTCGTGGCACACAGGAAC	59.751	20
TGAGTGGTGAGGAAATTTAGGAA	59.987	23	AGGGACGCTATCGATTTGTG	60.096	20
CCCAGGCTCAAATTCCTACA	60.066	20	ACACAAAACATGCATCAGCC	59.577	20
TTGTTGATGGTTGAGAGGTGTC	60.012	22	CAAACCACGCCAGACAGATA	59.716	20
AGAATCACAATGCTCCTGGC	60.226	20	TTTCAGGGCTGCTGAATGAT	60.744	20
AAAATGATGATTCCGGGTCC	60.891	20	GCCCAAACAAACTAGCAAGC	59.889	20
TCAATATGAATTGATCGCCG	59.478	20	TGGAGGTTTTAGGTAATTGGA	58.952	23

ATTGCTCGATCCACCTCTTG	60.218	20	GCGAATTTCCATGTCATCAA	59.48	20
AAATCAAATTGTGTCGAGGCT	58.709	21	AGCCATCTCAAGAGTCGTGG	60.408	20
CTGGGTCTAAAATTCGGCAG	59.702	20	GATAGCCACCGTGATGCTCT	60.249	20
GGACTCCCATCGTCTCCATA	59.886	20	TGGCTTCCATTTTAGCAACC	60.074	20
GGAGCTGAGCAATGAGAAGG	60.096	20	CATCATGTTTAACTGGATTGTG	59.397	23
TGAAGTTTCGAAGACTGGAAGA	59.097	22	ACCACCAAAGCCTTAATCCC	60.187	20
TTTCACCGTTGTCATAGCCA	60.111	20	GGAAGTGGGGGTCGGTATAA	60.929	20
CGTCATTCCGATCATCTCCT	60.034	20	GGTATGCTTGGAGGGTTGAA	59.933	20
TGTAGCCGACCCCAATTTAT	59.297	20	ACCTTTGAATGGATTGCTGG	59.933	20
TGAAAACGATTTAAACGTGGG	59.855	21	GTGCTCTGCTCTGCTGTTTG	59.929	20
CAAATCATGGAAACAGCACG	60.111	20	TCCATGGCAAGTGACTCAAG	59.831	20
GGGGAAGGAGAGAGAGAGGA	59.883	20	ATCAAGCAAGCATCTCAGCA	59.704	20
TGCATACCAAGTTATTGGCG	59.585	20	AAACTGGAGCACAAACCGAA	60.668	20
AGGGGGACCAAAATGAAAAC	60.032	20	TTTTGCAATCGGAGCTCTTT	59.96	20
ATTTTCTCATGGGTGTGGGA	60.173	20	GGTCGTTGGTAATTGGACGA	60.755	20
CTGCCATCTGGTACAACTGC	59.318	20	GAAAAATGCCAAGAACCTCG	59.685	20
TATGGATGCACCGGTTAGGT	60.214	20	TGGCTTGCAGAATCAAGAAA	59.542	20
GCAAAAATACCTGGCGACAT	59.967	20	GTGGTCATTTTAGGGGATGC	59.249	20
ATGTAGCCGACCCCAATTTA	59.297	20	CTACCCACCCAGGTCATCC	60.183	19
TGATCACAAACTTAGCGGACA	59.332	21	TTTTGTGAGCCATCTGCAAC	59.847	20
GCCTCGATTGATCCACTGAT	60.042	20	TGGTTCGTGATTGACGTCTC	59.682	20
AGACCGAACCACCCAATACA	60.232	20	TCGTTGGAGTCTGAAAACCA	59.262	20
AGTTCTAGTAGCCCGGAGCC	59.87	20	ACCCAATACCCAAACCCATT	60.166	20
TGCGAATCATTCAATTCTGC	59.775	20	TGCAATGGCTTTTCATTGTT	59.161	20
GCAGACCTAACATAGTGGGAAAA	59.552	23	ACCAATTTGAACGGTTTGGA	60.206	20
CTCCTCCACCCGTCTACAAG	59.715	20	GGCGGTGGTGATTTGTACTT	59.859	20
CGAACCCATTAAGCCTCAAA	60.067	20	CTCCAAGAATCCCTTCCAAA	59.097	20
GGCTGGCTCTTTCAATCAGA	60.483	20	CGAAGACGTCAATTTGGTCA	59.691	20
GCTGCAGAAATGAGAGGAGG	60.096	20	TTTTTAAGGTGGGGAGAATGT	57.596	21
TTGGCCTAGACTTCACATTTTTC	59.659	23	TGTAGGCATAACTATGATTGG	58.532	23
AATGCTTGCAAGGGTGTAAGA	59.761	21	AATCCAACTTATTGCATGTTGA	58.556	23
GTACCGATATCATCCCCACC	58.937	20	GGGAAACAATTCTTTTGGCA	59.916	20
AGGTCAGATCGAAGGTCTCG	59.405	20	TGTTGGTGGGATTTGAACCT	60.21	20
GCATCTGGATCCTCCACAAT	59.893	20	TTTGCGTCCTTCTGCTATGA	59.566	20
TTGGTCGGATATTGCATTGA	59.891	20	CCTCCCTTCACCTTCAAACA	60.081	20
AGGGAAGTGTGGGGAAGAAG	60.48	20	AATCCGCGTGTGCAATAAAT	60.351	20
TGGCAACTCATACTACCCGA	59.148	20	CATATCACGCGGATACCACA	60.366	20
GTGATCTTGAAGGAGCTGGC	59.957	20	ACCTCAGGTTGCTCCGAAC	60.253	19
GGTGGAGGTTATGGGAGGAT	60.015	20	TTACATATTTCTTGCGGCCA	59.169	20
GCGTGCACTTCAAGCAATAG	59.638	20	CAGGGCCCTAGAAATTAGCA	59.315	20
TGAAGTCTTGACAACGCATTT	58.419	21	CGGGCTGATGTAGAGGAGAG	59.966	20
AGTCTCCCTCGCCAGAAAAT	60.212	20	TCGTTTACAGCATACGCGAG	60.037	20
CAAACATTATGCACCAAGCG	60.133	20	AAGCTTTATCAAGGGCTGGG	60.573	20
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TGAGAGAACCTCCCCCTTTT	60.045	20	ATGAGCTACTGGAGCGAGGA	60.119	20
CTCATGCCGGAGTTAGGAAG	59.83	20	ACCATGGAGACGTTCGACTT	59.579	20
AAGCCCGTGAAAAAGAAGGT	60.11	20	TCAACGCTCACCTTCACATC	59.837	20
ATGTAGCCGACCCCAATTTA	59.297	20	GCGTGGTTCCATCTCAAAAT	59.939	20
GCCTTCTCGAATTTGTCTGC	59.962	20	TGGCCAACTCTCCCTTCTC	60.333	19
ATGTAGCCGACCCCAATTTA	59.297	20	CCAATGGCTACTTCTCTGCG	60.924	20
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TCACGGGTTTGGGAATTAAA	60.16	20	TTTGGTTGGTGATTTGGGTT	60.066	20
CCTTTGTTTAGGGTAGCCCC	59.829	20	CAGCATTCTATCTGGGCCAT	60.059	20
TACTTGCCCTAGCGACTGCT	60.176	20	TCAGGCAGAAAATGGGATTC	60.014	20
AACGTTTTATCTTCGGTGCG	60.131	20	AGCCGTCCACAACACTTACC	60.035	20
TTCATCTGTAACGGGTGGGT	60.232	20	TACTTCTGACCCCGCAAGAC	60.255	20
ATCAGGTTGCCCTCCTTTTT	59.94	20	ATTTAGGCCAGCCCAGACTT	60.096	20
GTGGTATGGTGTGGAGGACC	60.096	20	TTACCGGTCGGTTACCAGAG	59.986	20

TCTTCGTGTTTGTCCATTCG	59.691	20	CGTGGGAGGTGAAGAGATTC	59.655	20
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TCTCGGATTCCATGCCTAAT	59.486	20	TTTTTCTTGCACCAAATAGGTT	57.875	22
CACAATTTGAGGTGTATGGCA	59.454	21	GATGGGAGCACCTCAACAAC	60.52	20
GCATTTGACAATCATGCACA	59.078	20	AAAAGTCGCCGTTACTGGTG	60.168	20
ATCATCCCCAAAGCAAAAAT	58.368	20	GTTGCCACAGCGGTTCTAAT	60.14	20
TCGTAAAGAATGGGCTGGAT	59.528	20	TGCAAGGTCTTCTCCAACCT	59.844	20
TTTGCAACGTGGTCTTCATC	59.697	20	AATTTACGGGACCCTCAAGC	60.32	20
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GGGATCCATTTCAGCACAAG	60.461	20	AGTCCTCCAATGAAGTCCCA	59.505	20
TTTGGATTGCAACCTCCTTT	59.546	20	GGGGAAATGTGCCAGTTAGA	59.933	20
TCCTACCAATGCCTTCTTGG	60.066	20	AATTTGGATTGAAAATGAGAG	57.344	24
CGTCCCCCTGAGATGAAATA	59.887	20	ATTTTGAATTCGGCTTGTCG	60.074	20
AAATCCAGAACGCAGGTTTG	60.11	20	CAGGGTTTCAACATTTCAGC	58.201	20
TGGAGTAAAAGATGGTGGGG	59.784	20	AAGAAAAGAGAAGGCTCCGC	60.096	20
TTTGTGCTCACACTTCTCTCG	59.224	21	TGTTATTTTGTCGGGTTGGG	60.587	20
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GCCAAACTTGTGCTGCAATA	59.879	20	GCCCCTGTTTGCAATGTAAT	59.829	20
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AATCCCCCTTTCCTAGGGTT	60.014	20	AGAGAGGGCTTAGAGACGGG	59.972	20
CTCCATCGCCCACATTATCT	59.917	20	GCCAGCGTGATACTGATCCT	60.249	20
TCTGCTACCCACCAATGACA	60.112	20	GGATCAGCAGTGGCTTTCTC	59.957	20
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TTCTGTCAATTTATGTGTTAACTTC	58.056	27	CTTATTTTGCATGTGATATTGG	58.153	24
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CTTTGTCCTTTCCTGGCTCA	60.366	20	GAACCCGATGAGGAAGATGA	60.011	20
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CATCCACCTTCACACCATCA	60.378	20	TGGTGTCTATGCTGGGATCA	60.072	20
ATAATTTACCGGCAATGGTG	57.401	20	GGAGGGGTATTTTGGGGATA	59.846	20
GAAAACTGAGCCAACCCAAA	60.088	20	TTCCCGAAATAGCCAGATTG	60.031	20
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TGCCTTCTTTAACAGCCCAT	59.708	20	TGGAATGGAAATGTTTGGGT	60.029	20
CATGACAACTTCATCAGGCG	60.263	20	TTTTTAGGAGTCCCGAACCA	59.541	20
TCCCACGAGGAATTTGAGTC	60.05	20	AAAAGTGCACCTGAGCCATT	59.74	20
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ACAACTCGTCTTCCGTGGAT	59.579	20	TGTGATTGTTGTGGCAAACC	60.413	20
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GGCTCTGCAAGAATTTGAGC	60.103	20	CCGGTACATGACTTCGAGGA	61.055	20
AGTTTGGGTATCCGCTCCTC	60.464	20	AGGAACCATTTCGTTAAAATTA	60.032	26
AAGCCGAATTCGTTACAACA	58.294	20	GGTCCAATAAATGTGGGCCT	60.94	20
TCCGGTAATTCAACAAAACGA	60.342	21	TTCGGAAACACCTAGAACGG	60.103	20
CGTCACAGTTAGTGCCAACG	60.361	20	TGGTCTGGGAGAACTCCACT	59.682	20

AAACGCATACCACATAAGCCA	60.391	21	TCACATTTAACCTATGAGTCTG	59.565	24
AGAAATCCAGCAGCAAATCG	60.352	20	CTTTTGGTGATTGGGATGGT	59.647	20
CCGAGAGATGTCTCCCAGAA	60.34	20	TTTGATTGGGAATAATTGGGT	58.163	21
CGGGAATTCAAAGCATCACT	60.074	20	TGTTTTGCGCAGTTATGGAG	59.872	20
ACCTTGCTCGTGTACCCATC	59.997	20	CGGCCTAATTGTAACCTTGG	59.469	20
TTGGGAGCAAATTTCAAGAG	57.945	20	TCACCCAAGTCCAATCTATTCA	59.429	22
AAAATTGGTGCGGATGTCTC	59.939	20	CAACGGGGAAAAACAAATTC	59.292	20
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CCGGCTTAAAGGTGAAATGA	60.067	20	CAAGGTGACTGCATCATTGG	60.112	20
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ACCCTCGAGCTCTTTTGGAT	60.212	20	AGCGTGCATTTTCAGAGGTT	59.882	20
GACGACTCAGCTTGACCACA	60.03	20	TGAGGCTACATCGGTGATGA	60.225	20
AAGGAAGTGGCATGCTTTTG	60.249	20	GGTCTCTGGATCAGGTTGAGA	59.243	21
TTTTGCTATTGTGGTGTTTCAA	58.264	22	ATCACAATGCCATCACCTCA	59.925	20
GTGTGAACTTCCTCCAACAACA	60.051	22	CCCAAGACCCCAATTTGATT	60.91	20
CCACCAGTACCAAAACCACC	60.126	20	CGTTAGAGGGAGTCAGGCAC	59.867	20
GAATTTGGCCAAGTCGATTC	59.51	20	TGGAGAAGTGGATAAACCCG	59.926	20
AAGCTTGCAAGTAGGAGGCA	60.154	20	GAGGTGATCGGTTCATTGGT	59.786	20
TGTTGAGGCATGGCTATGAA	60.22	20	CGTGTCTATTGAAACGATGAA	60.056	24
ACAGTTCAGCTCCACAACCC	60.159	20	GTGCCTCTCTCCCTTGTGTC	59.841	20
CATGTGCATCAAACGGAAAC	59.972	20	AAGAGATTCACAGGATGCGG	60.218	20
TGCTTACCTCCGGAATTTTG	60.067	20	CGAGGGTGATGAAGGAGCTA	60.353	20
TGAGATTCACTTGCCCCTTC	60.195	20	TCTAAAGTGCAGGATGGCAA	59.42	20
ACTTCCCAGACCTTGTTCCA	59.549	20	TGTAGCCGACCCCAATTTAT	59.297	20
CTTCTTGACCAATAATAAAGAAAA	57.082	27	GATCACCTCGAACCTTCTGC	59.81	20
CCAAACCAACCTCGCTCTTA	60.241	20	GTAGCTTGTTTGTGGGCGAT	60.14	20
AAGAGATAGGGGAAGGAGCG	59.805	20	CCACATCCCCCAAATCATAA	60.384	20
CAAACATGGGAGGGTTTTGT	59.688	20	CCGGACGTCTATACCAGGAA	59.948	20
CCAGACATCGAAGAAGCTGTT	59.487	21	TGAATGATCTCAGCTCCGGT	60.769	20
AGCCACCTGATGAACACCAT	60.395	20	ATCTGCATTGCAAACTGTCG	59.871	20
GCTTGTCCTCCACTTGAAGC	59.997	20	TTGGTCTCTTAATGGCCACC	59.933	20
GGGAGGTTTCGTCACACAGT	60.009	20	GCCAAGTTGTCTGGAAGGTC	59.703	20
ATGTAGCCGACCCCAATTTA	59.297	20	TCGAGGTAAGTCGATCAGGC	60.362	20
TGTACAACCAGTTGGGTTCG	59.46	20	AAACGTGAGGTTTTGACGAGA	59.766	21
CCTAAGCAATTGATAGTGCCAA	59.275	22	AGAAAGCCCACCTGATCACT	58.744	20
TTTTCCACCAAGGTTGCATT	60.344	20	TTCATCTGTATTCGACTTCTCC	58.847	23
GATTTTGGGTTTGGAGACGA	59.91	20	AAAAAGTGCCTCCCTCGATT	60.074	20
TCGGTTTATACAATAACCAATTTA	57.809	27	CGTTCCAGTGGTTCAAGTCT	57.771	20
TGACATTCCTTTCCATTGGC	60.843	20	CAAAGCGAAACACGCATCT	60.003	19
GTCACGGGTTCGAATTTCA	59.486	19	GCGATCTTGTCACTTACGCA	60.019	20
GCGAGTTTCTTGAGGTCGTC	59.997	20	TACCCACCACCAACATCAAA	59.667	20
ACTCTGGGACGCTTTACCCT	60.132	20	GGGAGGGTGTTGAGATTCAG	59.505	20
TCGTGCAAGTTTTCAAGATCA	59.454	21	GGGAGATGAGAGGGGGAATA	60.228	20
ATTACACGGGTAAGGTTGCG	59.883	20	GCATCATGCTTTCCATACTCAA	60.103	22
AGGTGCTAGCAGCATGGAAT	59.866	20	ATGCCAACCAACAAGCATAA	59.041	20
ACGATCCTTCTGTCCCTTGA	59.655	20	ACTGCCCAACACCGACTTAC	60.035	20
AAATCCCCTTCCCATCATTC	59.959	20	GGCGGATTTAGGAGTGTGAC	59.556	20
ACCGTTGTGGTTCGGATTAC	59.717	20	ATGTAGCCGACCCCAATTTA	59.297	20
TCAATTCAAAATCAAACCATGC	59.816	22	CATGGGGGTCTGCTATCATT	59.773	20
TTGAATGTTCACGGCAGAAG	59.84	20	TTCTTGATACATGGGCGTCA	60.073	20
TTCACATAGCCGACCTCACA	60.263	20	ATTGCTTACTGCCGGATTTG	60.096	20
GGTTAATGCATTTTGCCTGC	60.465	20	ACCGGGATCCTTTTCAACTT	59.805	20
ACTTGGCACGATCCAATTTT	59.434	20	AGGTGTGGCTCCTTGAAATG	60.111	20
TCCCATGGCTGTTGTTCTTA	59.123	20	ATTGATGACGATGACGTGGA	59.925	20
TCTCCTGTACTTCGTTTAGACATC	59.377	25	GAAACTTCAAATGAATCTTCAA	57.492	24
TGCACCGGTTAGGAGGATAG	60.088	20	TCCTAGAATTCCAATACGTGGT	58.941	23
ATGTTCATGTTGGGTGCTGA	59.967	20	ATCCAAGCAAGAGATTATCAC	59.997	24
GGGATCCAAACCTCGACATA	59.75	20	TAGAAGCCTCTGAACGCCAT	59.978	20

GACGTCGCAGAGGAGAACAT	60.418	20	AGCCTTGCTCACGCATCT	59.688	18
AGCTTATGTTGCATGGAGGG	60.096	20	ATTGTTGATTTTTGCCAGGG	59.801	20
TGCCATGATTGTTGAAGGAA	60.049	20	AAGCCCGAACCTGACTTTTT	60.11	20
TCCTATGCATCCATTTGCAG	59.646	20	GCTGTCTTGATTTACCTTCACG	58.906	22
GATCAGCTCCAAAAGCTTGC	60.103	20	TCAGCTGCGTTTCATTCATC	59.955	20
GGGCTGTTTTTGAATCGAGA	60.192	20	GGTCACACCCTACAACAATAA	59.818	23
TGACATTGTGACCTTCAGGC	59.682	20	TTGTAGTCCTTCCTCACAAAGA	60.198	24
CCATGAAACTAGCCAAGCAC	58.379	20	GGCACGTAGGCTACAGCTTC	60.044	20
GTCCACTCAGGCCCTACTTG	59.721	20	CAAAAGGTGGAAAGTCACCAA	59.994	21
AAATCTTTTGGGGCGTTCTC	60.431	20	CATCCTCTGCGTCAGAATCA	59.942	20
TGGAATTCAATCCAAGGACC	59.727	20	TCAAAGTCGATCTCGTCGTG	59.984	20
TCAAACTGGAAACCGAAACC	59.948	20	CCCAAGACCCCAATTTGAT	59.59	19
GGACGGTAACGAGCACCTAC	59.621	20	GCTTCAGAACAAGGAAGCCA	60.517	20
GCATTTGTTGTTGTGGCATC	59.979	20	TCAGTTGACTGCCCTCACAG	60.022	20
ACAAAACACAACAACCCCGT	60.171	20	TTTGGACAAAGAGGGGTCAG	60.081	20
ATGCGGATGTTGTGGGTAAT	60.081	20	CTCGGAAATCTGGTCATTGAA	60.059	21
TGTCAAGCTCTTGCATAGCAGT	60.219	22	TGGTTTGGGTTTTGATCACC	60.594	20
AATAAAAGGCGGATTGACCC	60.15	20	TGATTTAAATAAAAATATGTTG	58.957	27
GGATACCTGGGTCCAGACAA	59.779	20	AGCATCAAGCCTGCTCAACT	60.164	20
TATCCACTTCACTGGGGGTC	59.779	20	TCCTCTCCCCACTGAACAAC	60.088	20
CCAACCTCAGAATCATCTTTCA	59.17	22	TTCTCAAATGGCGAGCTGTA	59.566	20
TTGATCTCAGTCAGCCATGC	59.95	20	GAGCAAAAAGGAGCGTATCG	59.982	20
AATCAAAACATTTAGTTGGCACA	58.601	23	CACAAAATGAACGTGGTTCG	60.004	20
AGACTTCATCATCCCCATCG	59.886	20	TCGAATCAAGATTTCTCACGC	60.346	21
ATATAGGCCCAAATCTGGCA	59.392	20	CACACACATCCTTCTCTCCG	59.257	20
ACTCGGATGGGATCTTGATG	59.886	20	GCAAGACTGGTTCCAAAAGC	59.859	20
AAGCATATGCCTTGCTTGCT	60.01	20	CGAACTAGCTCACGAGTCGAA	60.715	21
AACCCTCCCCTCTCCAAATA	59.761	20	GGATTGATGCTCCATTGCTT	60.043	20
CAATGGACAACCAAGCCTTT	59.971	20	ACTTCAGTTGGGCAATTGGT	59.454	20
TTGGTCCAGTGCCCAGTATT	60.375	20	CAGTGGGCAAACCAGATTTT	59.971	20
CCGTGTTCGATGACTACGTG	60.175	20	ACACCTCCGTCAACACCTTC	60.009	20
TCTCGCAGAGGAGGTCAAAT	59.95	20	CCATACGATATCACCGACCC	60.036	20
AAGAAAGACGAAGCATGGGA	59.813	20	CTTTCTTGCATGATCCCACA	59.648	20
TAATGCGGGTAAAAACCCAA	60.178	20	CCAATGATTGTGGAATGAATG	60.564	22
TAGACACATGCCAACTCCCA	60.112	20	GCTTGAACATCCGAAAGAGG	59.813	20
ACGACGACGGAAAGATTGAG	60.255	20	AATCTGAGCTGGAGTTGGGA	59.803	20
AGGGACAACGGGTTCTGATA	59.405	20	TCCGCACAAAGAAAATGATG	59.664	20
CCAGCAGACACGAAACAGAA	60.025	20	TGGTGGTTATGGAGGAGGAG	59.92	20
CACCAACAGCTTGGTCTCAA	59.873	20	ATGCCCTCGATGATGATGTT	60.312	20
TGGTTTGGGAATAATTGGGT	58.995	20	TGAAGGCCCTCTCATTTCTC	59.361	20
TAGGAGGCTGCAGAAAGAGG	59.711	20	TTGACTTTACCCTCGGACCA	60.486	20
GGGTGGTTTATGGCCTTTTT	60.055	20	CCACAATGTCATCACAGATGC	59.983	21
CATTTGGGGGTATTACAATTTTT	58.2	23	CGCAACAAAATTCGAACTGA	59.849	20
GCGTTTCTTAAACTGCCTGC	60.025	20	AGGCTAGTAGTAGTGGGAGGA	59.049	24
GACAGCTGCACGACATGATT	59.87	20	GTCGGTTAGCGTTGCTTGTT	60.313	20
TTGGTTAATGTAGCCGACCC	59.823	20	AAACCTTGAAGGAACCCAGG	60.332	20
ATGTTGGAGTCGGGAAGATG	59.927	20	GCTTGAAAAATCTCGAAGCG	60.096	20
TGTCCCCTTCGTTCTTGTTC	60.088	20	AGCAATTTCTTGGCTCGTTG	60.386	20
TGGAGGGGATTTGTGTTTGT	60.21	20	GTCTCCACCACCTCCACCTA	59.962	20
GAGTTGAATGGCGTATTGGG	60.331	20	TTTCCAATCCAATTCCTTGAA	59.374	21
TGGTGTGCATAACGAGATTAGT	57.332	22	AAATGTCACGTGGATGCTGA	60.12	20
AAATCTCACAGTCTTGCGCC	60.406	20	AACTTCTGCTTATCGCCTGC	59.62	20
GGTTTGGATTGACAAGTCGG	60.353	20	TCATGAAAATGAAAAACGCAA	59.179	21
GTTGTTCTTGGGATTGGTGG	60.21	20	GCCGGTCCCATAACAAGTAA	59.823	20
GTGCAGATGTGTCTGTCGCT	60.063	20	TTGCACCCAGAGCTTCTTCT	60.134	20
AGGCCACCGAAACTCTTACA	59.734	20	CCCAAGGCTGATGATCTTTT	59.126	20
AAAGAGGTTGTTTCCGTTGC	59.218	20	TGCTGGATCTGATCTGTGGT	59.212	20
TTCGTAATGATGCCACAGGA	60.073	20	TCGTTCTTAAAAGTTATGGCAC	59.569	23

CGTTGACTGCTGGAGAATGA	59.984	20	TGCCGGATTTGGATAGATTC	59.862	20
CACAAAAGCTGACCCAAGGT	60.149	20	CCCAAGACCCCAATTTGATT	60.91	20
ACCTGCACCACCACCAAG	60.59	18	GGTGGTGGATTAGGACATGG	60.05	20
AATGATTGGGTGTCCATTGAA	60.044	21	ATGTAGCCGACCCCAATTTA	59.297	20
ACAGCAATTCAAGTCCCACC	59.973	20	ACACATTTACAACCCGGCAT	60.118	20
AAAGGTCCCCTTTCCAAGTC	59.415	20	ATTTTGGTGCGAGTCTACCG	60.132	20
TAGGGATGAAGAACCCGTTG	59.926	20	CTCAAGATGCGAAGCAAACA	60.134	20
CCCATCTCTTGTTTTCTTCATCA	60.469	23	TACACCCCGTTTGCTTCTTC	60.11	20
TCCCGGATCACTTGGTACTC	59.927	20	TAGCATGGAGTTGTGCATGG	60.687	20
GGCTTGCGGGTCTTACTTAG	58.997	20	GGGGATTCCTACAAGAAGCA	59.126	20
ATACTTCCGTATTGCCGCAC	59.988	20	TGGATTGGATACCAAAAGGG	59.617	20
TTGCAATGTGGCATTCATTC	60.476	20	GCATTACAATGAACCACCGA	59.4	20
TTTGCTGAATTTTCTTCGCA	59.562	20	TCAAACACCAGAATTGCCCT	60.495	20
GGAAAATTGCTTTGAAGGTGC	60.953	21	CGAGGAATAGCTTGAGTGGG	59.83	20
TAGTGGGGGTCAGAACATGC	60.924	20	GTTATTGCACAAGCGAGCAC	59.498	20
ACCACAACTGGTCGGTATGG	60.69	20	GCATGTCAATTGTCGAGCTT	58.879	20
GCAGCAGCAACATACAAACC	59.351	20	CACCCGATTCTTCTTCTCCA	60.187	20
ATTAAGCTTCTTCCTCCGCC	59.82	20	TCCGATGATCAGTTGTTGGA	60.048	20
TTTGTTGTGGAGTTTCAGGTGT	59.538	22	TGTAGCCGACCCCAATTTAT	59.297	20
ATTGCCTCCACAAGAATTGG	59.933	20	GAGTCCGCATAGGTTCGATG	60.624	20
AGCATTGGCTTTGCAAGACT	60.022	20	AACCTTATCCCCAAATTCGC	60.15	20
CCCAAGACCCCAATTTGATT	60.91	20	GCGAGTCGCGACCATATAAA	61.124	20
GTTGTGCGTGCTTTTCTTCA	60.035	20	ATCAATTCCCCAATCCCTTC	59.959	20
ATGTAGCCGACCCCAATTTA	59.297	20	GAGTGGGCGTTATGGTGACT	59.997	20
GTTCGAACTCCACTGTTCCA	58.697	20	CCGGGAAAATTACATAAACAA	60.01	24
CATGTCACACTTCGCTCACC	60.319	20	ATGTAGCCGACCCCAATTTA	59.297	20
AATTATGGCGTTGGGTGAAC	59.691	20	TTCCCGTGATATTCCACTGA	58.923	20
TTCATGTAGCCAACCCCAAT	60.192	20	GAGTCGATCACAAACAGCCA	59.837	20
GCTACCTCTCCCTCTCTCCC	59.396	20	TGGTGGGATTGGATTTGATT	59.991	20
CCATAGTTTAAGCAAGGGCA	57.927	20	TTGGTTCATATAGCCGACCC	59.784	20
AGGTTGCGTACATCTGACCC	59.997	20	ACATCAACCCAAAAAGACCG	59.83	20
GGGGTTGCAGAAGGTAATGA	59.933	20	CAGCCATTCCCCTAAAGTCA	60.066	20
CCCCACAATGTCTCGTCTTT	59.966	20	ATCTTTGAACCGTGTGCCTT	59.598	20
TGGACCATTATCGGACGTTT	60.192	20	TTTGATGATGTTGCCTGGAG	59.648	20
CGCCTTCTTTGCACCTACTC	60.015	20	CTTGCCGGAAAATCAAGAAC	59.685	20
GGATTTGGCCCTGTGTGTAT	59.676	20	CGGAGAAGAACATCCTCAGC	59.95	20
AGGAAAGGACATGGCATTGA	60.461	20	TTCGTGTGTGTTTCCTCTCG	59.873	20
GTTTCCAACGAAGTTCCCAA	59.948	20	ACCGAGCTTGGATTTTTCAA	59.685	20
CAAGACCCCAATTTGACTGG	60.345	20	TTTTGCTCATCTTGTCTGGG	58.847	20
TAGATGGCTGGGAAAATTCG	60.031	20	ACCACCTTGTTGTGGATTCAA	60.262	21
GTTTTAACCTCTGCATCCCG	59.569	20	TTGCCATCATCTTCAATGGT	58.926	20
GTTTTAACCTCTGCATCCCG	59.569	20	TTGCCATCATCTTCAATGGT	58.926	20
CGACCGAATAATCCTGTGGA	60.853	20	CTCAAAGAAAATTGCGGGTC	59.685	20
CAGTGCTGTCCAAACCTCAA	59.873	20	TGCATATTGAATACAATGTCGA	58.464	24
AGAAGGAAATGGGAATGGCT	59.903	20	TCTTGTCCAAATGCCTCTGA	59.369	20
AAAATGGTGGCTTTCTTCCC	60.299	20	AGCCCTCAATTTTATACTCGAA	58.417	23
GACAACATGGGGTTTTGGAC	60.073	20	TGTGGTGGATCTTGTTGAGC	59.682	20
AACACGAGGTGGAGGATGAC	59.969	20	ATCGTTATTGCCGGATCCAT	61.42	20
TTTCCTCCAACATTGCTTCC	60.051	20	AGAAGTGGCTAAGCCCATGA	59.836	20
CCAAGTCACCCAAGAATTGC	60.495	20	TCTGTGCACCATCAAACTCA	58.784	20
TTTGTTGTGGGTTACCCGAT	60.088	20	TTTCAAGAGAGGGCCAAGTC	59.405	20
TGTAGCCGACCCCAATTTAT	59.297	20	GCAAGGGTGGTGCTCTTATT	59.198	20
GATTGTTGAAGGCCGACAGT	60.119	20	GAGCATGTGGGTCAGCAGT	59.844	19
CAGCGATTCCAATGTCTGAA	59.799	20	TTCCTCATTCTCCGCAGTTC	60.34	20
ATGTCAAGGGCTCAAGGCTA	59.836	20	CCCAAGACCCCAATTTGATT	60.91	20
TGTGTGACTGCATGGAAGGT	60.162	20	CATCATCATCCTGTTGTCGG	59.918	20
CATAGCCGATCATTCCCAGT	59.917	20	TATCGATGCACAAGATTCGC	59.799	20
GTTTACCTGGCTGACGTGGT	60.035	20	TTTTCTATGACGCGGAAACC	60.074	20

TATCCGTTCGGCTGTACCTT	59.592	20	TGCTTGCCTCGTTTAATTTGT	59.772	21
GTCAATGGGAACAACCGTCT	59.827	20	TAAGGCCTTTTCCCCTAAGC	59.695	20
ATTGCAAGCAAAATCATCCC	59.907	20	GGTCATTAGCAACCGAGAGG	59.694	20
CCCCATCTCAACCAAATGAG	60.309	20	CAAGCACAAATCTCGATTACC	60.131	22
CCAATCATACATGCAAAGTGC	59.055	21	GTTCAAATTCCATGTGTCGC	58.979	20
ACCATGACCGACATGCAGTA	59.992	20	CAAAAGGCAAGCCTCTCAAT	59.452	20
GCTGCTCCTCATTGTCATCA	59.95	20	CATTCCTATGCCAGTCCTGC	60.624	20
CCGTAAATGCCTGTCAACCT	59.993	20	ATGTAGCCGACCCCAATTTA	59.297	20
AATCATGTACACCCGCTTCG	60.914	20	TCTCCCAAAACATCACCTCC	59.903	20
CAGCACCACCAGCGAGAA	62.247	18	GCGCTATTTATTGAGCACCC	59.71	20
GCGGATAATACAATGGAGCA	58.603	20	CAAAGAAATCATTCACATTCGC	59.451	22
TGGCAGTCCATTCATCTGTC	59.637	20	TCTGAACAATTTGCAGCTCG	60.134	20
TGGAAAACTTTATCATTTCCCTTG	60.534	24	AATGGCCAATGACCAATACC	59.51	20
TGGCCTTTTAATAGGATGCG	60.054	20	GCGGGTGACCTAATTCCATA	59.784	20
TTGGGAATTTCTTTCCATGC	59.878	20	AGATGATTCTGTTGATGCCAA	59.574	22
TTTGACCAAACGGAACAACA	59.981	20	TGTAGCCGACCCCAATTTAT	59.297	20
GTCCAAAAGCTTATCGGCTG	59.845	20	AAATGGTTTCCATTCCTTCC	57.821	20
TGAAATCCCTCAAATCTTACCA	58.556	22	ATTTTCCCAGCCCTTCACTT	59.94	20
GAATCTTAGGACGCGACGAG	59.978	20	GCGGCACTGATAACTTCTCC	59.843	20
CGAGTGAGGCTGGAAAGAAC	59.989	20	TGCACGTAGATGTCAGAGGG	59.855	20
CCCATCATAGGGAAAGGGAT	59.974	20	CCCTTGCCAAATAGGTTTCA	59.931	20
CCGACCCCACTTAGTGAAAA	59.964	20	TCCTAAATCCCAATTACGGG	58.759	20
ATTCAGAACTGGCCATGGAG	60.073	20	GGGACCTTTCAGTCACCAGA	60.088	20
TGGTTTATGTAGCCAACACAATTT	59.72	24	GTCGGCATACTAATGATAATGT	58.115	24
GGTTCCCCATTCTCCTCTTC	59.874	20	GTGGTGCCATCTTCTTCACA	59.682	20
ATTAGCGCACCCACAAATCT	59.597	20	GGTTGCACAAAGTAGCTTCAC	60.347	22
GGTGCAGGAGTAGGTGCTGT	60.329	20	ATGGGCTTTTCTCACCCTTT	59.94	20
TCGTCTTGATTTTGTTCTGCAT	59.752	22	CGTCGTAATCCGAAGTTCCA	61.021	20
TCGTCTCTACGACGAAACCC	60.255	20	TGTGAGAATCCACAATCGGA	60.048	20
TCACAGACTCACAGTGTTGGC	59.931	21	CTCGAGCATGTGGTGGTTC	60.263	19
TGGATGATGGAAGAAAATCG	58.493	20	TGTGGAGCTTGATACGACGA	60.413	20
ACTAAAAGGGAAAAGCCCCT	58.273	20	TGAATCCCTATTGTCGAGAGC	59.283	21
TAGTTTGCAACAGTGACGCC	59.911	20	TGAAACTGCGAGTTCAATCA	57.968	20
TAGTTTGCAACAGTGACGCC	59.911	20	TGAAACTGCGAGTTCAATCA	57.968	20
TCCCTTTAAAAACACAAACCTTTT	59.397	24	ACCAAAACACAAAAGCCTGC	60.154	20
AAGCACGTCAGATGAGGGTC	60.269	20	AAAACCGTAATTTCACCCCC	59.924	20
TTCATGGCTTGACAAACTCG	59.84	20	TGAAATCGATCCCGATTATTCT	59.772	22
ACAACCCGTAAAACTCCACG	59.891	20	CGATGCGAACAAAAGGTTTC	60.617	20
ATGTAGCCGACCCCAATTTA	59.297	20	TTAATGGCTTGTGAATACGGC	59.978	21
ATGTAGCCGACCCCAATTTA	59.297	20	ATATCATTCCCCGAGAGGCT	59.888	20
AATGGTACCCCAACTTCACG	59.711	20	TACTCGCTCCAAACTCCACC	60.255	20
CGAGATTTATGAGAGCCCCA	60.17	20	CCCAAGACCCCAATTTGATT	60.91	20
GTTGGTGGATTTTGGGAAGT	58.741	20	TTTCGGCCACCATTGTTATT	60.188	20
TCTCGTGTAACGAACAAGCAA	59.521	21	CTTGACCCCCAGACTCGATA	60.065	20
CGTTGCAGAAGTTTGCTTGA	60.172	20	AAGGTCCATCAATGCCCATA	60.155	20
CTTTTCGTCGTCCACGTTCT	60.291	20	AGTGCGTGAAGCAAGTACGA	59.664	20
AACACCACAAGCGACAAGAC	58.78	20	TCGTGGGTAAACACACCAAA	59.857	20
CCTCACTCTGATGCTCTCCC	59.945	20	AGGTGGTGTGGTTTCAGGAG	60.002	20
AACAGGTTTCAACAATCGGG	59.83	20	ATGGCGAAAAGTGCAAAATC	60.081	20
CAGCACGATTTTGACTGGAA	59.84	20	CAGCTAAAATCCCCAAACCA	59.931	20
AGCAAGCTGCTCTGGACAAT	60.164	20	CACAACAAGGACTTGCATGG	60.152	20
GGATGATGATGTTCAGATGGG	60.15	21	TTTTTGATTTCCAAAACACATTC	58.924	23
CATCCTTGCCAATTTCCATT	59.762	20	ACGTGAATTGTCCCACATTG	59.267	20
ACCCCTTGCGGGGTAATA	60.148	18	ATAGCTTGTTGGGAGTTCCG	59.195	20
CACGAACACCCCTGCATATC	61.329	20	ATTATTACCTCAACCGCCCC	60.041	20
GCTTATCTGGACAACCCCAG	59.55	20	TTTTTCAAGCCCCACAACTC	60.088	20
GGCAACCTCAATGTCCAAAA	60.874	20	CGGTATACGGCGAGGATTAG	59.586	20
TATGGAGAAAATCCCTCCCC	60.089	20	GCATTTGATACCGTAGCAGTTC	58.792	22

TTTGAAGGGCAAACTCTGCT	59.993	20	AACGAGGTGTGAAGGACCAT	59.43	20
CGTGTTGCAATTATTGGGTTC	60.237	21	AGTCGACCTTACGTAGCGGA	59.898	20
CAGGAGCAGGAGCTATCTGG	60.111	20	GCGAATTTCATCCGTTTTTG	60.436	20
TGCATTTTCACGTGCATTTT	60.118	20	CATCCTGCACCACAACAAAC	60.008	20
TCGAAGCTGGAGATGTGACTT	60.005	21	GGCTACTACATTTTGCCCCTC	59.979	21
CATGCAACCAAAACCACAAT	59.297	20	CCCAAGTCGGTTTCAACTTT	59.073	20
GCCGAGGGTGAAATAGATGA	60.036	20	CATCATTGGCTCCCATTTTC	60.274	20
TCCACGTTTCCTTAAAATATGG	58.067	22	TCAGTATGTGATCCGCCTTTT	59.583	21
GGCCGTTTGGAATAGGATTT	60.15	20	CACGGATTCGAATTGTCTTC	58.145	20
TAATCCATGGAAGGCTCCTG	60.029	20	AACGGAAACAACCTCTTTGC	59.218	20
TTGGTACTCACAAAACCCCC	59.688	20	AGCCATTACCAACGGTCTTG	59.993	20
GGAAATTGCTATGTTGGGGA	59.762	20	TTCCGGCAGACAATGATATG	59.499	20
CAATGATGGGGTTGCTTTTT	59.801	20	GGTTGTGTACATCTAACCCCAA	60.028	23
GGTTTCTTGCAGGAGAATGC	59.82	20	ACTACCCGAGCTTCTCCCAT	60.096	20
TGGAATGTCTTCCATTAAGTGC	59.091	22	GATACGACCTTGCTCGCTCT	59.603	20
GGACGGTTCACCAAAAATGA	60.734	20	ATTTGGAGGTGGGTCGATCT	60.714	20
TAATGGGGAAGTCCTAGGGG	60.138	20	TTGGCCTCCCTTTGTAGTTG	60.103	20
ATACTGGCGGACAATATGGG	59.668	20	GCAAACACCCCCAATGACTA	60.755	20
ACCACTGAATGCTACGAGGG	60.134	20	ATTCTCCCATGCCCATCAC	60.708	19
TGGGCAAGAACGCTAATTCT	59.845	20	GCAAGAGATTCTTTGTCGCC	59.962	20
TTGCAAGAAAATTGTCCCGT	60.481	20	CCTTCATAATTCTCGAAAGGTT	60.785	24
CACCACCGCCCTACAAGTAT	59.875	20	GGTGGTGGAGGTGATTCGTA	60.78	20
ACGATGGCGACTTATGATCC	59.923	20	TCAAACTCGTGTGAACCCAA	60.128	20
TAATTTCCCCCAATTTTCCC	59.833	20	GCCGCCAATAAGTTGTCTTC	59.713	20
CTCACTCGAACTCGTCTCCC	59.986	20	CCGATTCCTGAACCAGAAGA	60.187	20
GCCTAAGAAGCCCAAATTCC	60.041	20	GTTATCGAGGAGGTCGGTGA	60.073	20
TGAAGTCCGGATCAACTTACG	60.118	21	TTCTTCTTTAACCGACCACCA	59.595	21
CAGCCATGCTTCTTATGCAA	59.976	20	AGATTCCATGGGCATATTCG	59.745	20
AGCCGATAAACTCAGCGAAG	59.615	20	AGGTTGCGTACATCTGACCC	59.997	20
TTGCAAAATCAAGTATACGTTTGG	60.277	24	ATTGTTTTGGCGTTTTCTCG	60.11	20
AAACACTGTGGCTCCAGCTT	59.914	20	GTCTCAGGGAAGAGGCAGTG	59.986	20
CCAACTGATGTGGAGGAGGT	59.962	20	ACCCAATTGTTGTGGATGCT	60.24	20
CACTGGCGACCTAGCAAAAT	60.27	20	TCCGATGGAGCCTTAAAATG	60.031	20
ACATTAACCACAATGGAGGC	57.39	20	GTCCAAATTCGTGTAAGAAATC	58.175	23
GGAGCCCTGCATTTAGTTGA	60.214	20	GACGTGGATCGATGTGATTG	59.925	20
GGATGCCATTTCTTCTCCAA	60.014	20	TCATTCGAAACCGCTCTTCT	59.955	20
CTTCCGATTTTCTCGGATTC	58.715	20	TTTGGTCACTTTGCACCTAAAA	59.663	22
GCTTTCAAAACCAGCACACA	59.888	20	CCACCACCCACTCCAATACT	59.697	20
GTTTCTTGGACAAAGCAGCC	59.859	20	TGGATGGAGAAGGTCTGGAG	60.191	20
ATCGGATGAAAGTTGCGATT	59.533	20	ACCGACTGTACGACTCAGCC	60.329	20
TGCTTTTGAGCCCTCTGTTT	59.993	20	ATTGAAGAGCGATTCCGAGA	59.917	20
AGGCAGCGAAAAATCAGCTA	60.117	20	AATTTTCGCCATTTGCTTGT	59.592	20
AAGGCAATGAGGCAAGAAAA	59.823	20	TCATCGAGTCCGCACATTAG	59.823	20
CAATACATGGCATTGGTGGA	60.197	20	ATCGACATTGAGGTCAACCC	59.786	20
CCTCTGCAATCAATCAGCAA	59.948	20	TCGATTGCCTCTGCAACATA	60.366	20
CTTGTGGTTGTTGGTGTTGC	60.049	20	ATGCCATAACGGCTAGTCTCA	59.744	21
TTCGAAAAGCCTAAGCCTGA	60.089	20	TGCATTATATGGCCGTGACA	60.896	20
ATTTGCAGGGAGAGCAAGAA	59.955	20	AGATGCGACTTTTGTTTCCG	60.249	20
CCAATTTATTGGGATTAAGGCT	58.465	22	CCGACGTGGAATCTGAAAAT	59.933	20
TCGCCCATTTTGAATTAACAC	59.824	21	GCCAACAGATAATCGAAGCG	60.742	20
CGGAAGGCATGAAGAAGAAG	59.948	20	AGACCAAAAAGTCAATGCGG	60.11	20
TACCTCTTTTTCCACGCCAC	60.11	20	TATTTGCTTAGTCGTGGCCC	60.096	20
GGCCTTTTCTATCTCCTCGG	60.166	20	TTGCACTTTTTATGGGGGAG	59.931	20
GGCCGACGCATATACATTTT	59.822	20	TTAGCTACAGGTGGGGTTGG	59.986	20
GAGGTGAGGTTCCATCTCCA	60.048	20	AGCTGAAAGTGGAAGCGAAG	59.757	20
ACAAAAGATCGCAGCAGTCA	59.596	20	TTTTACGCAAATCCGAAGGA	60.56	20
AGTTTATGACCATCAGCCGC	60.103	20	CGTTGCAAAACGAGTGAGAG	59.634	20
GCCATGAACCTCATTTGGAT	59.756	20	CAAACTGCACCTCGTGAGAA	60.025	20

AAAAATGTTTCTGTAGTGGTTGTT	58.647	25	TTGGACACGTACACTTGCGT	60.222	20
GTAACTCCATGATGCCGACC	60.348	20	AGGATTTCACGGAGTGGATG	59.927	20
AACATGGACTGGAAGTTGCC	59.973	20	GAAGGGCCTTGTCTTCCTCT	59.817	20
TCGCCAAATTCTTCAACAGA	59.395	20	AATTCTTCCTTGGTGGGCTT	59.94	20
TTTTTATTCCGTGACCCTCG	59.931	20	GAAAATGCTGGAAATGAGGAA	59.148	21
CATTTCCCATATTCTCCCCC	60.337	20	CACATCTCCGTTGGTGTCAG	60.154	20
TGATGATGATCCGCCATAGA	59.993	20	GGATGTATCAGGTGGTGGGT	59.511	20
AGCTGCGCTAGCTGAACAAT	60.321	20	ACTGGAAGCGATCAATCCAC	60.081	20
TTGGTCCCAAATCCCTACAA	60.162	20	AAGGGATCAAAAGCCAACCT	59.94	20
CCAAGTTACGTGGCGTAGAAC	59.685	21	ACATTTCATTGCCATTTCCA	58.82	20
CTCGATTTGTCCCCTATCCA	59.887	20	GGTTTTGATAAATACGATTTGC	58.457	24
TCCCACTCCCATTCAACTTC	59.903	20	GTGTCGCAGATGAATCCCTT	60.081	20
AAGCAAAAGGGAAAACCCAC	60.332	20	CGGGGATCAAATGAAATCAA	60.64	20
TTCCACAGACCAAAACCCAT	60.21	20	CCTCACAATTCCATGCACAC	59.967	20
GGTCATTGCCTCGGATTAAA	59.901	20	TCTGATTGTACATGGTGGCG	60.539	20
GCTTTTCCAGTGAAAATCCG	59.685	20	ATGTAGCCGACCCCAATTTA	59.297	20
TGGGACTTGGAACTAGGGTG	59.959	20	AATGAGAGGGGAGAATGGGT	59.755	20
CAATGATTCATCCTCCGTTG	58.923	20	AAACCAAGACCCCAATTTGA	59.264	20
TGATGATAATGAGGTTGCTGGT	59.457	22	AGTTCATGTGGTTGTTGGCA	60.008	20
TTTTGAAAAAGTGTTGCCCC	59.953	20	GTCTCCCATTTTCCCGAAGT	60.306	20
GCTGAGCTGAAGGAGATCCA	60.645	20	GTGGCGGCTAAAACCCTAAT	60.332	20
TTAGAGGTGTCAAAACGGGC	60.11	20	TAATTCAATCTTTGTCGCCG	58.769	20
GTTAAATTCGCAAGGGGACA	59.938	20	CAGAGCGCACTCGAAGAGTA	59.49	20
GGACTGGAGCAGGTGTGAAT	60.12	20	CCCTACCTGCAACCTACCCT	60.374	20
CAATCAACAAAACAAGCCCC	60.344	20	TTGGGAGTGGGAGAGAGATG	60.191	20
AATCACCCTCGAATCAGTTTG	59.042	21	TGGCTTTGTCACGTTTCTTG	59.881	20
GCATAGGAATGAATGGAGAAGG	59.93	22	GCATGCACAACTAAAAAGCAA	59.019	21
AGTTTGGGTGAGAACGAGGA	59.697	20	AGGTTGCGTACATCTGACCC	59.997	20
TACTCCTCCGGATGATGAGC	60.181	20	ATATCACCACCTCCACCACC	59.511	20
AAAACGGAATCTACTTAGGGGA	58.224	22	GGATCTCAAGATCTGACGGC	59.768	20
TTGGTTGTTGAAGATGTGGC	59.547	20	CCCCGAACAATTTTTCCTTT	60.157	20
ACTAGAAGCATTTGGCGCTC	59.62	20	GATGTCCGCCTTATGAGGTT	59.009	20
ATGTACACCCACTTCGGCTC	59.997	20	TATGGGTTGGTGGTTTGGAT	59.91	20
CGTTGGATTGGATTCCTCAT	59.75	20	CCAAGATGACCCACCAATTT	59.647	20
TTGAAGATGATACGTTGAACCC	58.952	22	TTTTGTTTTGTCCCCATCAA	58.841	20
TGTAGTTAAGGCGGTGGTGA	59.195	20	AGTTCCAAATTGTGCCCTAA	57.217	20
GGCATAATGATGTTGATTTGGA	59.666	22	GGAGGGTGTTGAGTTTGAGG	59.549	20
AACAGGGGGAGAATGGAGAT	59.755	20	AAAAGCGTTGGAAAGCTGAA	59.996	20
TGGGGTCGACTACATGAACC	60.78	20	CCACCATGGAAAGTGCTTGT	60.954	20
ATCCTCAACTCCATCGCTTG	60.218	20	CTCTCCTTCAACCTCCTCCC	60.186	20
AAATTCCGTGACCAAATCCA	60.17	20	TGGATATCATTGTCGCTGCT	59.256	20
AAATTCCGTGACCAAATCCA	60.17	20	TGGATATCATTGTCGCTGCT	59.256	20
ATTAACTCGGGGTGCAGTTG	59.993	20	GTCCTTTTCTTCATCCTCATCC	59.037	22
GCAAACCCTAATCGGCAGT	60.088	19	AGTCGACGGTCAATTTCCAG	60.111	20
TCGAAAGGTCGGAAGAACAG	60.366	20	TCGCCGCTTCCAGATATTAC	60.196	20
TGTAGCCGACCCCAATTTAT	59.297	20	CACGACAACCCAACACAAAC	59.897	20
CACAAAATTTGCTTCAACTTCG	59.795	22	TGTTTCATCTGCTTGTTCGG	59.84	20
TTCCATGCACTCTTTTGTGC	59.847	20	ATTATTGCGCTCGAAAATGG	60.061	20
AGCTCGGGAGCAAGTACAAA	60.015	20	CGGTTGACCTCACCACGTAT	60.833	20
TCACCCTCAAACATTCCACA	59.935	20	AGCTCCGGTAGTGATGATGG	60.096	20
TCTGTTTTGTGCGAGTCTGG	60.025	20	AATTACCTTCTCTCGCCGGA	61.08	20
TGTTCAAATCTGTGAAGGCA	57.806	20	GGACGAAGCTACATTAGCCG	59.867	20
TTCCATGAAACATAAATCTTGCC	60.194	23	TTGAAAAGTTTGGATAATTCAC	59.885	24
AGGCCAGAAGTCCAGCCTAT	60.233	20	CGGGACTGTTTCCTGAGTTC	59.697	20
TGTGAAAATCTCGGTTAATCCAT	59.729	23	GAGTTGAGCGCGACAAAAAG	61.08	20
CAATCAAATTGGGGTCTTGG	60.162	20	ATTCGAAGCATAGATGCCCA	60.574	20
GGGTTCAATGCATTTACTTCTTG	59.891	23	TTTGGGAGGTTGGATGGATA	60.126	20
ATATAGCCGACCGCACAAAG	60.117	20	TGGAGTCTTCTGCATTTGGTT	59.726	21

TGAAATTGAAAACCTTAAAAATG	57.09	24	AGAAAAAGGGAGCATGAGCA	59.955	20
TTCCTTTTCAAGGTGCTTCA	58.475	20	CCCAAGACCCCAATTTGAT	59.59	19
GAGGACCTTCAAGGGTGTCA	60.088	20	GCATGGATTCCTTGTTCGAT	59.9	20
AGATTGCTGTGATGTGGGTG	59.551	20	CAGAAGTTCACCGTCGTTCA	59.873	20
CCTCCATTTCTCATGCGATT	60.036	20	TATACACCATCATGACCGCC	59.23	20
ATTTTCCTGATGCCGATCC	59.846	19	TCTGCAACTTCAGCAGCAAC	60.333	20
ATGATCATCCAACGGTTTCA	58.772	20	GATACAGAGTCGGACGATGAC	60.142	22
TTTGGACCGGGACTGTAATC	59.79	20	AGATTGCGTAAACCTGACCC	59.056	20
TGTGGATGGTCTGAATGGAA	59.893	20	CCCAAGACCCCAATTTGAT	59.59	19
GCATCAAAACATTTCAGCCA	59.67	20	TGGATAGTAGGATATGATAAG	57.698	26
CAGGGTAGGAAGCCCAAAGT	60.488	20	ACGTGGCCAAAACGATTCT	60.511	19
CCATCAGTTCCTTCTAGGGCT	59.721	21	GGAGACCCCTTCGAAAAATC	59.881	20
ATGTAGCCGACCCCAATTTA	59.297	20	TAAGGTTAGCAGTTTGGCCG	60.257	20
CTCGCACCAAATGGGTTAGT	59.993	20	TCCAATCACGAGAACACGAG	59.831	20
TGATGAAGAGACACCGAACG	59.831	20	GAATCCGCCACATTGCTTAC	60.478	20
TCTTCAACATTCCTGGGCTC	60.195	20	GTAGAACCTTCCAATCCGCA	60.074	20
CATCGGGTGCAATGATTAAG	58.991	20	AAACTGAAATAGGCGAAGCG	59.496	20
CCCAAGACCCCAATTTGATT	60.91	20	AGCCATGAAATTCCCATCAC	59.756	20
TAACGGGAGAAATGGTCCAA	60.301	20	GTGCACCGACAGTTTTTGTG	60.199	20
TGATGGTATGGTGTGGAGGA	59.762	20	AACACGTCACCGGGTTATTC	59.717	20
GGTGTGGAGGAGCAATTCAT	59.934	20	CCTCCAAAAAGTCACCCAGA	60.081	20
TTTGTTGGATCTCCCGATTC	59.871	20	ATACGCGAGACCGTGTAAGG	60.154	20
GGGTTTAGGGTTTCCCATGT	59.919	20	TAACAATGCACCCGAGATGA	60.073	20
GTTTCATACCCCCACCACAC	59.95	20	TCCTTTTTCGGACGTCTCAC	60.232	20
GAACACATTGCTGAGAGCACA	60.048	21	TGGAAGGTGGAACCTCATTT	59.381	20
GTTTCTGATGTTGTTGCCGA	59.697	20	AACGAGGTGATTTGGACCAG	59.966	20
ATCTCATGTCCTCGCCTCTG	60.372	20	TCATAACAGTCTTCGACTAGCT	57.073	24
ATGTAGCCGACCCCAATTTA	59.297	20	TGATGTATGCCTGTGGGAAG	59.522	20
TGTTTTTGAGAAGAAACAAGAAG	59.141	24	ACTGTATTCATGGCCCTGCT	59.579	20
ACCGTACTCCCCAAGAACAA	59.449	20	GGTGACCAAAGAGGTGGGTA	59.82	20
CACGCAATATCTAGGCTATGGA	59.257	22	AATTGTTATCTCAGGCTACGCT	57.267	22
ATGTTGATGCTGTTTGGAGC	58.726	20	AGTTTAAACCCTCCCAACCC	59.191	20
GTAAGGATCGAGTGGGCAAA	60.074	20	CGAGCAAACTAGTCCGTTTCTT	59.948	22
CCTCCATCAGTTCTGTCTAGGG	60.124	22	GGATCACCAAAGGGACACAC	60.223	20
GTCCGGGTATTGTCTGCTGT	59.997	20	TATTCCCTAACCTGCGTTGG	59.953	20
AATGAAATCGTGCGAAAATG	58.627	20	TTTTGAGCAGGAATGTTCTTCA	59.861	22
TGAGGTGTGTGATTCCATGC	60.544	20	CCTCAATAATCAAACCTCGGC	60.807	21
TCATTTTCATTTTCATTTTCTTTTG	58.685	25	TGAATTTGCGACATTATTCATT	59.854	23
GGCACACTATTTTGGAGGGA	59.933	20	CAAGTTCACATTGAAATCGAC	59.663	23
TCGAATATTCCGGTGGTTTC	59.762	20	TACAGTTGCCGAAAAATGCC	60.999	20
AATAACATTAAACCCTAAACCCT	57.104	26	TCCATCGCTGAAAGAAAACA	59.395	20
TTTGATTGGGAATAATTGGGT	58.163	21	TTTGTGTTAATTATGTTTCAGTT	58.306	27
ATCCTCCATTTCCCATTTCC	59.959	20	GAGATTGACTCCCACCAGGA	60.048	20
AACTGGGCTGGCTAGGTGTA	59.757	20	TCCCACAAAACCAAACACAA	59.834	20
GCGCAAGCTCACCTTTCTAT	59.62	20	TTTCATCAAAGCCTGAAGCA	59.542	20
AAATCAGCCCGACTTGAAAA	59.685	20	CTCGGGATCAATGACATTCC	60.281	20
ACCTCATTCCTCCCAATTCC	60.133	20	TCGGAGTTGGAGTTCTTGCT	59.989	20
CTGTTGCCGATCACTTCAAA	59.84	20	TGGGTTCATTATCAAGAATTGC	58.946	22
TCATATTTTTCGTCGGAGGG	59.894	20	GGGTTTTAGAGGGGAGTTGG	59.799	20
TAAAGAGATGCTTGGTCGCC	60.352	20	GTTAGCCAACTGTATGCCCC	59.457	20
ATAGTGGGGCCTCGTCTTTC	60.464	20	TTAGCATGTGACATTTCCCG	59.542	20
AAATTATCAAATTTCGGGACGA	59.693	22	ATAACCGATCCACCTCCCTT	59.651	20
CAATCAAATCCAATCCCACC	59.991	20	TCTCTGAATCCGGCCTAGAA	59.91	20
AGGATCTCGGGGAGCTAGAA	60.306	20	CTTCATATTGGGGCCCATC	60.103	19
CGGGCCAATAAAATCTCAAA	59.901	20	TGCCCTAATCACACATTTCC	58.423	20
CGATCAAGGAACACATGCAC	60.12	20	CAACAACATAAGGGAAGGGG	59.284	20
CAATGAACAGTTCGTCGGTG	60.152	20	ACAGTGAATGTGAGGGAGGC	60.12	20
AAGACGAAAGCTGTCGGAAA	59.993	20	GTGGGACCTTGCTACTGAGC	59.874	20

GAAGGGGTAGGAACTGGACC	59.795	20	GACAACGATGGATACCCCAC	60.057	20
ATGATGGACTTGCTTTTGGG	59.933	20	CTCCCAACAGGACCAATGTT	59.82	20
TTTGAATTGCTTTAATTTGTTGC	58.42	23	ATTAAAATGGTGCGAATGGG	59.66	20
TGAACGCCGTTAAGTTTGAA	59.344	20	CGAAATCGCGGTATCTTGTT	60.096	20
CAAAGGGGCTGAGTTGAGAG	59.982	20	AGGGGTGAAAACCGGATAAT	59.532	20
TCAAATTTTGGCACTGTTGC	59.712	20	CAGCCTTCGCCACTACTCTC	60.156	20
TCAGTTCGGTTTTCGGTTTT	59.587	20	ACAATTGCACGATGTTTGGA	59.972	20
TCCGTGCAGTAAAATGAAAAT	57.327	21	CAAATTATTTTCAACCCTCATA	60.324	25
ATCCACGTTCGATCCAAAAC	59.797	20	GCAGTTGTTGCGGATAGTGA	59.871	20
CGCCTCTGCTCTCTCTCTTC	59.579	20	ATCAGTGGAGAAAATTGGCG	60.074	20
TGGTGCAACTCCATCAAATC	59.502	20	TCCAAGGAACTTTTCTCCCA	59.641	20
AAACTCAGCGAAGTGGCAAT	59.882	20	TACCCTAGCCCTACCGGAAC	60.332	20
GGAGGAGGGGAAGAGAGTTG	60.186	20	CTCTCCCACTATTCCCACCA	59.92	20
CCACTTTTGGCGTTTGATTC	60.481	20	TTTGCCAAGAGACACGACAC	59.88	20
TTAATGGGATGATAAGCGGC	59.892	20	CACGTAAAGCACAACGCATC	60.324	20
GCTAAGTTGATTATGGTGGGC	58.595	21	TCGAATTGAATTAATTTTATGA	60.204	26
TCAGTTGCCCTTGGGATTAG	60.066	20	GCCCCACCAGAAAAAGGATA	61.173	20
CCCATCCGGAAATCTCTACA	59.887	20	GATTAAGGGGTTGAGGAGGG	59.761	20
GCATCTTCCCACAAGCAAAT	60.081	20	CGTTTTTGCAGACATGAAGC	59.469	20
TTTGCTGAATTTTCTTGGCA	59.42	20	CGACACAAACCCATTAAGCC	60.365	20
GCAGCCACAAATGACAGAGA	59.992	20	GACAGAAACACAGCGGGAAT	60.119	20
CATGAAAAATCCTCAATCCCT	57.98	21	TCGTTGATGATGCAAAGAATG	59.679	21
GGCCAAACGTTTAGTCTACTTGA	59.716	23	GCATGAACCAAAACTTGCTG	59.322	20
TGTTTCCATCTACACCTTGAGAAG	59.69	24	CCAAGTCCCCCTCATACAAA	59.784	20
ATTCCAGCCCAACACCATAG	59.813	20	GACATCTGGCCCATTTTCAC	60.326	20
CGGCATCCACATAACATGAA	60.343	20	GGTGAAAGACCCGAATTCAA	59.91	20
CAATTGAGATCCATGGGGAA	60.66	20	AGGTTGCGTACATCTGACCC	59.997	20
TGATTTTGCTTTTGCATCGT	59.305	20	GGGCTTCGTTTGATGACTGT	60.119	20
ATAAACATTGGGGGTGGGTT	60.166	20	ACACGGGTGGAAGTGAGAGT	59.604	20
TTCTTATCTCTGCGCCGATT	59.945	20	CATCCACAGTGAAGACCACG	60.154	20
GGAAAACGCATAATTCACCC	59.277	20	CCATCAGCTCCTCACTCTCC	59.945	20
AGGATGAGGAAGGCAAGGTT	60.074	20	ACACGACGGACGTAGAGCTT	59.937	20
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GGACTCGGCTTTTGAATCAG	59.813	20	CTTGGGAGTTGCTTCGTAGG	59.869	20
TACATCTGACCCCAAGACCC	59.779	20	TTGGGTCCTATCCAGTTTGG	59.784	20
TCGGTTGCGTTGTTATTTGA	60.111	20	GGAGAGGCGTGGCAATAGTA	60.235	20
AGCCATTCTTAAAAGCCTCATTT	59.675	23	TGCCATACAACACCACTTGC	60.584	20
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AACAGGTTCAAACCAGTGGC	60.012	20	TGCACCGGTTAGGAGGTTAG	60.125	20
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TGGAAAATCGTTGTTGACCA	59.941	20	CTCTACCACTGCACCACGAG	59.487	20
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GACACCAATGCATTAACCCC	60.059	20	TCCGGTCAAAAACAGAAACC	59.948	20
TTGAGGCAACATGCTTTTGA	60.379	20	CCTTCTTTAGAGGTTGGGGTG	59.977	21
CCCAAGATGACTAACCGCTC	59.694	20	CCGTCGGAATCAATTACCAG	60.323	20
CCTTAAAATCAGTCCCGCAA	60.067	20	GCGACCACTAAGCAACAACA	59.911	20
CGGCCCAATATTTAGGCAT	59.765	19	TCGATCCTTTATGGATTGGAT	58.33	21
ATGTAGCCGACCCCAATTTA	59.297	20	CAACTTGACATAGCATTCCCA	59.996	22
GAGCCGAGCTCAGTCTGTTT	59.751	20	CTCTCTGCTCACGCTCTTCC	60.431	20
ACCAAGAGACTGAAAGCTCCA	59.076	21	CCCAAGACCCCAATTTGATT	60.91	20
TTTGGGTTTTAAATTCGTTGAA	58.567	22	AACCAATTGACAATGAGAGGA	59.99	23
ATCAACCTACACCGTCCACC	59.703	20	TAACGGGAGAAGAGTGCAGC	60.538	20
GAAATCCAAAAGGCAACGAG	59.685	20	TGCCCTAGATCTCACACACG	59.855	20
AAGGCCGCATCCTTTGATA	60.559	19	TGGTGATATTATTGTGATTCCC	59.801	23
TAATCCTTGAACTCGGTGGC	60.074	20	GATCCATTTAGCAAACCCCA	59.762	20
CAAGTCGGCAAAAATTGGAC	60.481	20	TTTTCATTTTTACTTACGCGTCT	57.35	23
GAGTAATCGTCTCCGCTTGC	59.985	20	ATTCTCGTCGACACTTTGGC	60.263	20
CTTGCCAGGTTGCAATTATG	59.182	20	CACTCCCATATCATCCCTGG	60.15	20

GCATTTGAAACAATGCCAAA	59.543	20	CAGTCCTTGAAATGCCGACT	60.255	20
AAAGCCCAGAACTTGTAGCG	59.517	20	AGAGACGGTGACGTATTGCC	60.142	20
TCTGTGGTTGTTGGCATAGC	59.722	20	CTGGGTTTTATTTTTGCCGA	59.937	20
CCCTTCAGCCACTGACCTAA	60.246	20	TCTCCAAAATCGCAAACCTC	60.192	20
ACCATTGCACTCCGAATAGG	59.955	20	GGACAAGGGTTCGAGTCTCA	60.238	20
ACTCACCTCTCCCTCGACCT	60.258	20	TCCCTAGAAGCGCACGAGTA	61.06	20
CAGGAAAGAAGCCAGCAGAG	60.269	20	CAGCAGTCTGGATCTCCCTC	59.945	20
CCTGGGTAAATCTACGGGCT	60.332	20	TAAAAATGAACGAGTCGCCC	60.074	20
AGATGATGAATCCGCAGCAT	60.601	20	GACCACCTTTCTTTCCACCA	59.943	20
CGTGAGAAGATTGGGAGGAA	60.187	20	TCCTATTTTTCAGAGTTGAACC	59.203	24
GTCTGGCCTTCTTCGTGTTC	59.851	20	TTGGGTTTGGAGTGAAAACA	58.995	20
GAATTCCCAACCAAAGCAAA	59.916	20	TCCACCTTGAATTGACTGCC	61.046	20
AAAATACCCGCAAAGTCGGT	60.721	20	GCCTTTCTCATACCCTCGTG	59.694	20
TATTTGAGGGTGTGCTTCCC	59.933	20	AGGCACGGTTCATGTGTGTA	60.032	20
AGGAATCCCAATCAGAGAAAAC	58.578	22	TGCCAGAACACATAAATTTTG	59.524	23
CTTCAGCTTGGTTTTGGAGG	59.846	20	ATGACGGATAGCAGCCAATC	60.066	20
AAGCTCGTCGGATTTCTTCA	59.955	20	AACAAACCCATCACTCCGAC	59.827	20
GCAATGTATATTGGGTCGCA	59.405	20	CCCAGTACCGAACGAGTACAA	60.038	21
ATCTACAACAGGCGGCGG	62.174	18	CTTGGATGAAGAGGGAGGGT	60.447	20
TGTGTTTTGCCTTTCTCACG	59.881	20	CTCTTGGTTCTGGTGGTGGT	60.002	20
AGTTGGGACGGAGGGAGTAT	59.817	20	TTGACGCGCTTGAAGTAGTG	60.195	20
CTCAAACCCATCATGAAATCC	59.234	21	CCTTTGAACAAAGAGTGGGG	59.563	20
CGACTAATGCTCAAACGCTG	59.632	20	ATGTAGCCGACCCCAATTTA	59.297	20
TTCCCGATTTCAGTTGTTCC	59.91	20	GGAGGCATAAAAACCCCAAT	60.02	20
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CATCTGGGTGTGTGAGTTGTG	60.055	21	GAGGTGCAAGAATTTCCCAA	60.051	20
AGTGAGTTGTGGTGCGTGAG	59.94	20	CACAGGGCTTAGGAATGGAA	60.066	20
GAAATTTCCTCCCTCGAGATG	60.025	21	GCTTAGTGCTTGGTGCTGAA	59.224	20
GGGTCCAACTACGGATAATGC	60.576	21	CTGGGTCCTTGCTAAATTGC	59.708	20
TTTCAAGCAACCTCGCTTTC	60.502	20	TGTTTGGTTTTGAGGGCAAT	60.344	20
GACTACGATGAACTGGGGGA	59.927	20	TGCCACCACTCTTCTTACCC	60.111	20
CAGTGAGCTCTCCGAAAAGG	60.126	20	GGAGTCATCCACCTCAGGAA	60.048	20
AAACGGACAACCACTTTTCG	60.008	20	ATGTAGCCGACCCCAATTTA	59.297	20
TCGCCACTGAAAGAAAGAGG	60.508	20	TCACGCCTAATTAAACCATTG	57.731	21
TCCAACCCTAATTCGTGAGC	60.074	20	ATGAGCAGGGTGGAGAGAGA	59.945	20
CATTCAAAATAAAATGATGATGA	57.394	27	AGCTCAGGTTGTGCACGATA	59.47	20
CACTGCCTACTCCACCAACA	59.745	20	CATTATCTAATGATTAACAGTT	58.894	27
ATTGGCTGCAAATGTGTCAA	60.119	20	TCAATGATCCAATCCCCACT	60.135	20
GGCGTTTGTAGAGAAGCTGG	60.015	20	TCTGTGTTGTGGGTTGCAGT	60.203	20
TGACTCGCGTAAAAGAATATAAA	58.574	25	AGGGTCCCTCCTTATTGACA	58.446	20
CGAAATTAATTAAGGAAAAGATT	60.089	26	GATTTTGGTCCAGTGGCAGT	59.973	20
CACCCTTTTTGTGGAAGCAT	59.971	20	GGGTCGAGTAGAAGAACCCC	59.935	20
CGTGAGAATCTTCGACCTCC	59.803	20	GCGCAAAACAAAACACATTG	60.155	20
ACGACATGAAGCTTCTGCAA	59.596	20	ATGTAGCCGACCCCAATTTA	59.297	20
TCACAATAAACCTCCAGTTCCC	60.221	22	GAAAATCGGCAGCACTCATT	60.221	20
ATTTTGCTCACCCTGCTCAT	59.7	20	GTTTCGACATCGCATCTGG	60.217	19
AATGGGGACATCAAGTTGGA	60.173	20	TGGGGATTGAACCCAGATAA	60.126	20
TCTAATGTTTCCGCCTCCAG	60.206	20	GGTGGCTGTTATCGAAGGC	60.619	19
ATTTTTATGGATTGTGCCGC	59.801	20	TTTGCACAGCAATTCCACAT	60.119	20
TTTTTGTTTTTGACGGGTCC	59.817	20	AGGAGTTGGCTCACGATACG	60.277	20
CGCAGTTGATCTTCTGTCCA	59.984	20	GAAGGAACAGAAGAAGCGGA	59.55	20
ATGTAGCCGACCCCAATTTA	59.297	20	TGCAGCTCCTCAAAAAGGTC	60.517	20
CCGCATCACAATTCCAAAAT	60.701	20	TGGGGGTGCATTTAATGTTT	60.053	20
TAACGATGCCTTGCTTTCCT	59.845	20	CAGAGCGCACTCGAAGAGTA	59.49	20
CGCATCTTCCGAGCTATCAT	60.339	20	TAACGTGGGGTGTACGTTGT	58.825	20
TGGGCTAGTAATCTGGGTCC	59.006	20	TGTGTGAGTTTGGTTAGCCG	59.758	20
TCCTAGGAAATTGCTGTCCAA	59.693	21	GCAATAAATTTCTATGTTGCTC	59.562	24
ATGTTGATGCTGTTTGGAGC	58.726	20	AGTTTAAACCCTCCCAACCC	59.191	20

GCCACTTGTAACCTCCCAAA	59.971	20	TGGGACAGAGAAAGAATGCC	60.195	20
AATCTCGATGCCATCTCCTG	60.181	20	ATGTAGCCGACCCCAATTTA	59.297	20
TGCTAAAAACAAATGCCAAGG	60.116	21	CACGTGACAATGAAAAGGGT	58.469	20
TGATGGTGATAACACAATTGAAA	57.94	23	CTCCCCAATTCATGACCCTA	59.744	20
TATCCGAATAGGCGAGGAGA	59.762	20	CACCACCCCATCACAAATAA	59.097	20
AAAAATTGGTGCGGGTGC	61.826	18	AAGGCCCCCTTGTCAAATAC	60.187	20
GGAAAATTGGGTCATATAGCTCC	60.057	23	TTGCTCAAATATTTCAAAAAGC	58.963	23
TTGTTGCAGTAGCCATGCTC	60.019	20	AACACCTCCCGAAAGAGGAG	60.619	20
TGACGACGAACGAATTTGAG	59.84	20	AGCGATTCTCTTCGAGCAAG	59.859	20
TGTCAACGTAAAAGGAGGGC	60.11	20	GTCCAGATCCAGAGACCCAA	60.048	20
CCATTCATCGTCGAAGACCT	60.073	20	TGGCCAGCAATATGGAATTT	60.289	20
TGTTATTTGCACAATCATTTCC	57.572	22	AAAAAGCCACGACCTCTTCA	59.853	20
CGCCTAATGCTTTGCTTCTT	59.63	20	TCATCCCTTCCAACTTCTGC	60.195	20
GATCAGCAGTGGCGTTGTC	60.429	19	AGCCACGTCAAACTGGGATA	60.517	20
CATTCTTTCTCCGTCTTCCG	59.807	20	ATTACTCGCGAAACCGACTG	60.27	20
GCTTTTCAGTTGGCATTTTTG	59.75	21	TCGCATTCTACTCCATTTTCC	59.172	21
CACTTGCCTTGCACAACAAA	60.876	20	ATGGCAGCATTCATGTAGCA	60.251	20
TTGGCAGCTAGTGCTCATTTT	60.032	21	AGCCGATTTGTAAATTTGAGG	58.262	21
CCCAAGACCCCAATTTGATT	60.91	20	GTCGGACCATGATGGCTAAT	59.78	20
TGTATGGGGTCATCCATCCT	60.011	20	TAAGGCTTACGTATTGGCGG	60.109	20
AGGATAGAATGAGGGTTTTCCC	59.685	22	CCCAATGAAAATCTGTCGGT	59.79	20
CGTGCGTGTTGAATTCATGT	60.584	20	TTTGATTGGGAATAATTGGGT	58.163	21
CGTGCCAATAATGACACAAA	58.046	20	AAAACAGACCCACCAAGAACA	59.482	21
CGTTGTGCTCTTGAAACTGG	59.485	20	TTTGGTTCATGTAGCCGACC	60.894	20
GTTTCCTCACTACACCCCGA	59.966	20	TCCATTATTGCTTCCACCCT	59.387	20
GTGGATCAGCAGTGGCTTTT	60.263	20	GGGAGGTTTCGTCACACAGT	60.009	20
AATCAACTAAGCAGCGGTGG	60.27	20	GCAAAGGTTTTCCGATCAAA	60.053	20
CATCAAAAGCAGAGCAGCAC	59.746	20	ATCGGGAAAACGAGGAAGTT	59.94	20
ACGCATACGATCTTGATTATGG	58.992	22	GTAGAGGTGTCAAAACGGGC	59.598	20
TTGGGATTAAGGCTTTGGTG	59.931	20	ATCAAAACCGGAACCGTACA	60.227	20
TGGTGAAAAATCAAATACTTGGAA	59.763	24	TGACGTGCATGAAAGTTGCT	60.459	20
GGTGAAAAATCAAATACTTGGAA	59.788	25	GGCAAACCACCCTTTTCTTT	60.332	20
TGGAATAGCTTGATAAATGATTTG	60.207	26	TAATAAGCAGCAGGGCATGA	59.425	20
AAATCATCACAAGCCCCAAA	60.309	20	CGACGAAATCGATGACTGTG	60.263	20
TAGCCGACCCCAACTTATTG	59.953	20	GCTTAAGCGAGAAAAGCGG	60.237	19
GGGGGAGAAAAATAAAGAAAAA	57.789	22	TTGGAAATTTTTCAGAACACG	57.797	21
CGAGAACCAATAATGATGAGCC	60.821	22	GGCGTGTGGATGATTTCTTT	59.939	20
TTTGGTTTTGCTCCTCTGCT	59.993	20	ATCGAGTCCACTGTGCAAGA	59.42	20
TGTGACCTTCTTCCTTGTTTCTT	59.309	23	CTTGAAGGGACCCGTGAGTA	60.103	20
GAACGAACAGAGGCAGCATA	59.028	20	TGGCCTCTTCAGAAGGAGAA	60.065	20
CTCTCCTCCTTCTTCCCACC	60.186	20	AATCTCGCTCACGACTCGAT	59.981	20
AACCTTGGTTCATGTAGCCG	59.993	20	GGTCATCTCTCCCAAGTCAAA	59.979	22
ATTGACAGCAGGGAGGTGAT	59.535	20	TCTCTTTTCTCTCCCCCGTT	60.183	20
TTTGGTTCATGTAGCCGACC	60.894	20	TACCTACAACGTGAAGGCCC	59.993	20
TGGTAAAATTCCACTTCGGC	59.938	20	CCTTCTCAGCCTCAGCTTCT	58.917	20
AAATTACCGGGAGTTGAACTTT	58.141	22	GCTCAAATCGGAATTCAAACA	60.067	21
AATGGCAAAGGTAAATGAGCA	59.6	21	ACCGACTGGGCCTATCCTAT	59.811	20
AACCATTTAGAATTTTTCGGGA	58.902	22	ATGGGCCCAACACCAGATAA	62.413	20
CCCACCTTAGATACCGTTCG	59.448	20	AAAATCCTGTGTAGCAGGGC	59.198	20
CAGCACTCCCAATTTATTGCT	59.238	21	TTTCCAAGGTTTGGGTTTCA	60.314	20
AGGCGAGACAACGAAATTCT	58.936	20	TTTGATGCGCTCTAGTTGGA	59.566	20
CCCAAGACCCCAATTTGAT	59.59	19	CCCAAGACCCCAATTTGATT	60.91	20
TGGAGAGTTTGGACATTTTGA	58.187	21	AATCAACGAAATGAAACCGC	59.945	20
GTAGCAGCTCGGTGAGGTTC	60.02	20	AATCAGTGAGGCACCAATCC	59.934	20
ATGGTTGCCTTTGTTTGGAG	59.971	20	TCATTGCCCGAATAGAGTCC	60.036	20
TGTTGGTGGTGGTGTCTTGT	59.89	20	GGGAATATCCATTCGTTCCA	59.581	20
GAGAGCAGTCCTTTTCCCG	59.935	19	TTTCATTTGATATTTCCAGAGA	59.436	25
CGTTCCTTGCAACAACAAGA	59.881	20	ATTCAATGAAGGAACGCGAC	60.081	20

TTTCTTGCCTCGATTCCTTG	60.323	20	GCCTAAGAATGACTGAAACGG	58.847	21
TTGACCAGATAACATCGGCA	60.073	20	AAATTGGGCACCAGAATCAG	59.933	20
TGTGGGGACGATTATTCCAT	60.014	20	GTCTGGACAGACAACTGGCA	59.872	20
CAGGAAAACCCAGAAGTGAGA	59.314	21	TGTAGCCGACCCCAATTTAT	59.297	20
GAAGCAAAAACAAACCCACC	59.452	20	CCCAAGACCCCAATTTGAT	59.59	19
AAAACCTCATAAAACTGTCATGT	57.456	25	AAAAATACAGCTAATCGGTCC	57.848	22
CTCTTGCTGCTTTTTCCACC	59.993	20	GTGCAGCAATACCAAACCCT	60	20
AATTGGGGTGCAAAACAAAG	59.839	20	AATGGGATCTGTTGCTGCAT	60.492	20
GAACCCAAGAAGCAACATGTAA	60.048	23	ACGTGAGTTGGAGGAGTTGG	60.151	20
GTAGGGTTCATGTCCGGTTG	60.232	20	TGTTGGGCCTTTGACCTTAG	60.103	20
CGTTCCAAACTTCGAAGAAAA	59.366	21	GGGAGACGACATTCTTCAGC	59.81	20
TTGACAACATTGCCACATACC	59.312	21	GAGCTTTAGTGGGACATCCG	59.694	20
GTGCATGGAAACATCCACAG	59.967	20	TACAATGGCCTGAGCAAGTG	59.864	20
TCCAGCTATCCCGTTTTGTC	60.074	20	TCGGAAAGGAACTCTTCGAG	59.545	20
TGCAGTGGCGTTGAACTAAC	59.911	20	TTCACCCCGATTTCTTTTTG	59.91	20
CCACCTCACGCAAAAAGAGT	60.291	20	TAGCTTTGCCGGTGTCATAA	59.325	20
AAATAAGGCATGGGTTGTGC	59.829	20	GGAAATGGAAAGGCAACAAA	59.916	20
ATAAAGAGGGGCAGGGGTAA	59.793	20	TTTGGGATACGACCTTGCTC	60.074	20
CGAAGTCTCACGGTTGATTG	59.288	20	TCAGTTTTCGACTTTTTGGGA	59.71	21
ATTCCGGTGACGGTTGAATA	60.192	20	AGTTTTAGGCGGGAAAGCTG	60.731	20
AGAAAGGGGGAAAGCAAAGA	60.18	20	CACCGCAAATATACGAAGCA	59.725	20
ACTTCTCCTTCCACCGCTCT	60.393	20	CTCGAACACCATCTGATCCA	59.631	20
CTTGGAGAACTGACTTCGGG	59.837	20	ATGCTGCATGCACTATTTGG	59.718	20
ACAGTAAAATGCTGCCCAGG	60.132	20	CGGAAACTGACATCCACCTT	59.966	20
ACTCAGATCACTCAACCCGC	60.269	20	TTCGAGCAGGAAATGTGGAT	60.603	20
CGAAGCATCACATTTGAACG	60.257	20	GGGACAGGCTCTTGTGTTGT	60.159	20
CCACGTCGAGCTAGAACCTC	60.012	20	GATCGGCAGTGGCATTTT	59.61	18
CAATGAGGACATCCGAGGAG	60.612	20	CGTGCAAGGATGCAATAAAA	59.702	20
TCCTCTGTTGTGTTGGATGC	59.682	20	AGCTGTGCACACCACATTTC	59.758	20
ACAGACCCTCACACCATTCC	59.817	20	CTATCAGGCATTGCCCAACT	60.096	20
TGTGTGCGATTTAATCCTAACCT	59.912	23	TCTCTTGCAGCACTATGGGA	59.547	20
TCCATAAGCCATAGCTAAAAGAG	60.125	24	GTTAGTTGTTGGCCCGGTTA	59.861	20
GACACAACCACAACACCTGC	60.055	20	TTCATATTCCTGGCGAATCC	59.862	20
TCATCATTTTATCATGAATCCCA	59.137	23	TTGTTTTAATGCATCGGCTG	59.702	20
AACCTTCTCTCTGGTGCCAA	59.844	20	GCGACAACCATCTCTTCCAT	60.081	20
ATGTAGCCGACCCCAATTTA	59.297	20	TTGGGGACAAAGCAAAATTC	59.916	20
GGAGAAAAGCATACGGGTGA	60.074	20	GTTTCGGAGGTGTTGGACAG	60.545	20
TCCCATTCTTCACATCCACA	59.893	20	CAGAAAGGGGCAGATTCTTG	59.807	20
CTTCGCCGCATATGAAACTT	60.23	20	CACCAATTTCCCCGATCTATT	60.027	21
TTGAACTCGCTCCTTCCATC	60.34	20	TTCCCTCATTTGAACAAAACG	59.961	21
AGGAAAGCATGAGTGGAGGA	59.803	20	CAAAATGAAGCAGACTGCCA	59.988	20
AACCCTTTCACCGTCCTCTAA	59.984	21	ACATCAGATCTCCGTCAGCA	59.372	20
GCAAAATGTGTTGATTGTTATTCC	59.67	24	TGATCTTGAAACCGTGATGG	59.496	20
TTTTAACCACCATTTCCCGA	60.16	20	AAATGGACCCAACGTTGAAA	60.206	20
ATTTGCAAAATGCTGCTGTG	59.879	20	TCCCTAATGCAAGGATGGAC	59.894	20
TCAGAGGTGCACTCGAAGTT	58.594	20	GCGTGGGATCATAACTGTCA	59.527	20
GACCAGTTCACAAAAGTCCCA	59.997	21	ATGCAACCTCCTGCTTCCT	59.818	19
ATTACCCACCGGACACATTC	59.532	20	GATGAGACGAGAGAGGGGGT	60.615	20
ATATTTGGTTGGTTCAGCGG	59.823	20	CTGGTTTTGGCAAACTGTGA	59.734	20
AACTCGGCAAGATGAACTGC	60.406	20	TGCAAGAAAACTGTCCCGTA	59.317	20
CCGTGCCCAATAAATCCTTT	61.029	20	TGCAGGAACACCTGAATCAA	60.24	20
CACATGCCATAACCGTTCAG	59.988	20	CCGCAGAGGCGATCTCTA	60.201	18
TCAGAAAGGATCCTCCTCCA	59.731	20	TTCAGCTCATCAAATGGGGT	60.461	20
TGGGTGTCAGAGATTCGTCA	60.246	20	TGATGGAACCGGGAAGTTAG	59.926	20
CGTGTAGGATGGGAAATTGAA	59.809	21	CCAACCGAACTAGCAGAAAAC	58.893	21
CGATCTCACTTCGTGGGAA	59.771	19	CCATTGCTTAAGCTCCCTTG	59.839	20
ACATGAAGAGGACGAAGCGT	59.874	20	GTGTTGGGGATTTGATCCAG	60.173	20
ACCGCATGTCACTTCGAATA	59.152	20	CAACCATGTCAGCCGTTAAA	59.585	20

CCTATTTCCCAACCCAAACA	59.657	20	TCGCATTCAATTACCCAACC	60.701	20
GCATGGATCTTTGGGAGAAA	60.014	20	TCCAATTTATTGGGATTAAGGC	60.052	23
GCCGGTCTCAGTCTGCTATC	59.981	20	GTAATCCCCCTACTCCTCCG	59.783	20
GCAGCCTTGGTTCTTGTTTC	59.859	20	CGTTGCAGAAGTTTGCTTGA	60.172	20
AGAGTTATTCAGGCCAGCCC	60.599	20	GTGGTATGGTGTGGAGGACC	60.096	20
GTTGCTCAAATTCTTCCCCA	60.051	20	CATCAAGTGGTAGGCGGATT	59.955	20
GTTCTGATGCTCTACCAAAACG	58.906	22	TGATTGGTTAGAGAGTATGTG	59.971	27
CACTGATCGTACACGATGGC	60.144	20	ATGGGGGTTTGAAGTTGGAT	60.422	20
GATAGGCGTTCGAAGGTGAC	59.7	20	CGGGTTCATTCTGGTTCATC	60.317	20
ACGATGCTCGAGGTTCAGAG	60.555	20	TTGATTTTGCTTATTTTGACCTA	57.586	25
TTCCATGTTCTGGAGAAGCC	60.195	20	AAATTGCAGCAAACCCAAAC	59.982	20
CATTCCACCGGAAGGTCTTA	59.926	20	TCTTGCTTTTTGCCATGTGA	60.379	20
TGAAAACCCCCACTCAACTC	59.943	20	AGAGATGCGCTGGATAAGGA	59.939	20
CATCGAGACATATGCAAAAACA	58.701	22	AACGAAAGAGCAAATGGGAG	59.312	20
AATTTGAATTTGGAAAAGTATGG	59.244	25	TATGCATGGATGGTGTACCG	60.22	20
TCCGGTGCTGTCTTTTCTTT	59.853	20	ACGATCGCCTACGAGAAAAA	59.845	20
GCACTCGAAAAGTAGCGGTT	59.522	20	CAATTGCAAGGAATTTCCCA	60.807	20
ACGTCAACGCTCGTACCTTC	60.321	20	TGTTTAAAAGTTTCCTGCACAA	57.571	22
TGATGAACTGCTGCCAGAAC	59.992	20	GGCCATTTTCTGCTGTCATT	60.081	20
TGCATAATCAACGGTCAATCA	59.945	21	ATTCCCTTTGGGGACGAATA	60.502	20
CAAAAATGGCATTCAAGCTG	59.301	20	AGGCAAAACCCATGAAACAG	59.971	20
TCTTTTCAACATGTAGCGCA	58.075	20	CGCCGATCCCTACTTTTCTC	61.08	20
TGAGCCACGCACTCTGTAGT	59.648	20	GACCAAGAACCACTGCGTTT	60.156	20
TTCTTCTCCTCTGCCTCCCT	60.468	20	CCCCTGAAAACAAGAAACGA	60.081	20
GAAGTTGGTGGGTTGTTTGG	60.246	20	TTCAAATTAGCAACAAAAATG	58.007	24
CCCAACTTCCAACATCGAAT	59.79	20	TTTCATCGTCACAGCAGCAT	60.423	20
AAATTCCCCACCATTTCCTC	59.996	20	GTAGTTCTGGTCTCTGGCGG	59.867	20
CGCCTTGAGTTTGGGTAAAA	60.103	20	GATGCCAATGCCATAACTGA	59.504	20
CAGATTGAATGTGGAACGGA	59.496	20	TCCTCTTCTGCCATTTCAGC	60.483	20
TTCATGTAGCCGACCCAAAT	60.331	20	TGTGGCAGATGATCAAAGGA	60.201	20
TGTTCTGTTAAAACTTCACATCTC	58.054	25	TCAGGGAGTTCCATGACTCT	57.183	20
TCGATCCGGGACTTGAAATA	60.405	20	AGCGACGAAGAACGAAGGTA	60.015	20
TTCAAATGAATCTTCAACAGGA	57.338	22	AAAATTTTCATCAGTTATTTGC	58.388	25
TGAAGCCCAACAGATTGATTT	59.56	21	TCAAATTTTGGCTCGAAAGG	60.181	20
GAATTCTGAATGCATGGTTCTT	58.188	22	GGGATGCTCAAAGTCTGCAT	60.226	20
ATGGCGAGGGAGAGAGGTAG	60.746	20	TTCTCCCCGTAGAAGCCAC	60.203	19
TCAAAGTCCCTAACCATCCG	59.926	20	AAACACCTCCTCCCCATACC	60.052	20
CGACCTCACATAGTGGGACA	59.545	20	TGTTGCTTGGGAGCTTGATA	59.42	20
GTGCACATGTCAAGTTTGGG	60.008	20	CCATCTCCTCAAAGCACCTC	59.803	20
TTGACCCCAATCTCGACTTC	60.05	20	TATGCATGCTCATAATGCCA	58.679	20
CCGCTGATCTTTCTGCTCTT	59.717	20	TGAATCAGCGAGTGAGGATG	59.942	20
GATTGCCTTGTTTACCCGTG	60.365	20	CTACACAACACCCTTGCGAA	59.758	20
AATCTGGGGTTCAACAATGC	59.797	20	TGCTTGTTTCTGCTTTCAGG	59.195	20
CGGAGGAGTAGGGGGATTAC	59.783	20	TTACTGGCTCGTTCATGCAG	60.011	20
TGGGCGAAAATTCAACTAGG	60.067	20	GCAACGGAAACGTCTTTGTAA	60.159	21
CCCAAGACCCCAATTTGAT	59.59	19	TGAGACAGGTTCTCGTCGAA	59.545	20
GTGAGCGAGGTGAAGAGTCA	59.129	20	AGGTTCGCTACTGGTCATGG	60.134	20
CCAATTTATTGGGATTAAGGCT	58.465	22	TTGAAGTTGAGGGATGCATTA	58.227	21
GACACGCGGATCTGTGTCTAT	60.157	21	AGGTCAGAGGTGACGGTTTG	60.151	20
TGTGTGCAATTTGGTTCCAT	59.823	20	AAAAATTTAGGGCGTTACGAA	57.906	21
TGGTTGCCTTTAATGCTGTG	59.729	20	TTCAAACATTCTCCTTCCAAAA	58.716	22
TCGTAAGTTGGAAAGGGTGC	60.11	20	ACATGTCTTGCCTCAAACCC	59.973	20
TCCCAAAATGAAACTTGTAAATC	59.763	24	GAATCCTTGCACGAACGAAT	60.081	20
AAGGGCCTTAACACCAACAA	59.471	20	GACAAAAATTTGGCGATGCT	60.081	20
TGATTCATCGCATTTACGGA	60.035	20	ATCGATGATCACCCACATCA	59.724	20
GCGGAGGTGGATATTGTGAT	59.78	20	GGGTCGTTCAGCCAATCTAA	60.074	20
AAGCTAAGAGCTCCTTGGGG	59.976	20	ATGTAGCCGACCCCAATTTA	59.297	20
GATTGCCACGTGTAATGGGT	60.646	20	TTCTCTTTGGCTTTTGCAGG	60.493	20

GCAGCGAAAAATCGTAATCC	59.688	20	TTCCTGACGCTGAGGAAGTT	59.989	20
TTTGGTTCATGTAGCCGACC	60.894	20	CAATTGGAGGTTTGTGGTGTT	59.743	21
ATTCAGCTCTTGTTTCCCCA	59.67	20	CACGGCAAAAGCATCTATGA	59.833	20
GCACGAACCCATGACCTATT	59.82	20	GAATTCTTTGGCGAGATTGC	59.791	20
CTCGCCCTTCTCTGTTTCTG	60.126	20	CCCACTATTTCCCCTGAACA	59.784	20
CCCTGTTTCACATCATTCCC	60.173	20	CCCAAGACCCCAATTTGATT	60.91	20
CTTCCACACATAATGCCGGT	60.776	20	GGCTAACATGATATTGCACCA	59.859	22
ATGCATGCAAACCAGGATCT	60.492	20	TACGACCACTTGCTCCCTTT	59.734	20
CTACCGGAGGAAACCATGAA	59.926	20	TGTAGCCGACCCCAATTTAT	59.297	20
CTTCCACCCTTGTTTTCCAA	59.942	20	AGATATGCGTACTTATCCTTAC	57.953	24
ATGGTGGTAAGGTGTGGAGG	59.697	20	CGAAGACCTAAGCCACAAGG	59.869	20
AGATCCCTCCCTCGCTACAT	60.059	20	AGGTTTCGCCTTCAATCGTA	59.708	20
GGGTGGTGAAGAATGAATGC	60.326	20	GTTGTCAACCCAACGCTACA	59.615	20
CAAAACCTTCAATGGCCAAC	60.344	20	ATCCACCCTAGCATGTGGTC	59.81	20
CACCAATCCGTAGAGAAGGC	59.694	20	TTTTCCCATTTTGGTGCAAT	60.167	20
TTCTCTTGCAATGCTTCACG	60.134	20	CTCATGAAGCTTCTGTCGCC	61.087	20
GGAAGAAGGCAAGGGAGAGA	60.842	20	TCATCCAAGTTCGTGTGAAATC	59.978	22
GGTGCGGGATAAAAATGTTG	60.188	20	AATCCAAAATCTCGGCTTCA	59.645	20
ATATCAGCTCGCACAATCCC	60.066	20	TTTTTCATGGCCCTTTGTCT	59.546	20
ATGTAGCCGACCCCAATTTA	59.297	20	GAGCTCGTTGAAGCTGGAAG	60.277	20
TCCATTAACTCATCGTTAAAATTC	59.009	25	TCTGATCCTTTGCATTTAGCA	58.52	21
GGATGGGGATAGTGATAGGCT	59.279	21	GGTTGCCTGCACCAAGTAAT	60	20
CATATTCAGAGTCGTTTGAGCTT	57.727	23	TCTGTTATGTTTTCTCTAGTTTC	57.187	27
TCAGAAAAACAAGTGGGGGT	59.425	20	TGGTGATCTACATCTCTTCCCA	59.55	22
TGAACTTTTTGTTCCTGCGA	59.439	20	ACCACGACTATCAAGGCGAA	60.657	20
CGAACAAGAAACGGGGATAA	59.931	20	GGCTAAATTGACAGTCCTCGG	60.991	21
TGGTTGCTCAATTATGAAGGC	60.089	21	TCGGACAACAATTCATTGAGA	59.112	21
TCAATGGGGACATCTGAGTG	59.473	20	ACTTCCCACTCCACCACTTG	60.002	20
CCAAGTGTTAGTGGCCAACC	60.41	20	CCCAAGACCCCAATTTGAT	59.59	19
CTTTTGCTGCTCACTTGCAG	59.928	20	TGAAGGAAGAGAGAGAGGCG	59.82	20
ATGTAGCCGACCCCAATTTAT	59.585	21	CCGTCTGCGCCTTAAGTTAG	60.032	20
CCAATGTGATTGGCTAGTTGC	60.517	21	CACGGAAAACCTAAGTGGCT	59.238	20
ATGACCGAGGAGCAAATTGT	59.556	20	ATCACGCTTCATTTCATCCC	59.9	20
GTCGGATATGGGTTGTTTGG	60.051	20	TATCGATGGAGCAGCAATCA	60.329	20
GTAGAGGTGCCTGTGGTGGT	60.033	20	CTCGTCTTCCGTGGATAAGC	59.836	20
CGAGTAGCTGGGTCTGAAGC	60.156	20	AAAGGAAATCCCCTCACCTG	60.298	20
TGTCAGTCAGGGATTCTTTTGA	59.711	22	CTTGGGCAATATGTCGAAGC	60.606	20
TTGAGCATATTTTGTGTTGCTTG	60.177	23	CATCGACCGGCTTCATTTAT	59.923	20
TTTAGTGGGAATCACGGGAG	59.926	20	GTTATCTCCGACTTTGGGGC	60.826	20
TCCTTTCTTGGCTCCACATC	60.195	20	GAATTCAAGCCGGTTTCTGA	60.192	20
AGTCGCAGCAGAGGATTGTT	60.02	20	AAGTAAAAACAGGCGAGGCA	59.883	20
AACCCGAGTATCCTAACCCG	60.2	20	GAACCCAAATCACGGAGGTA	59.79	20
CCCAGTTTATTGGGATTAATGTTT	59.443	24	TTCTTTCCCTCACAGCACCT	59.844	20
CCTTGCATTAGGCAGAGCTT	59.615	20	CCCCAATACCCCAATTTGAT	60.614	20
CCCAAAAGGGAGGAGTGAAT	60.298	20	TAGTTGCTGGTGTGGTGGAG	59.745	20
GACAATGCTGATCTCCTCCC	59.617	20	AAACCAGCTCATTTGTTGGC	60.118	20
CCCCTTCATTAATGCACCAC	60.192	20	ACGCGGATTTGAAAATGAAA	60.436	20
ACGTTGCATGTCCATGATTC	59.379	20	TCGTATTCTTGGGTGAGCAA	59.272	20
CGAGCTCGATCATGCAACTA	60.119	20	GACACTGATCGCATGCCTTA	59.83	20
TGGTGAAAAGTAAGCATGCAA	59.359	21	CTAAAGGTGTCAAAACGGGC	59.609	20
ATGTCATTACTCCCACCGGA	60.195	20	AGGATTTTGAGGATGCGTTG	60.074	20
TTCGAATGCAACACTGGAGA	60.39	20	CTGATCGGCCAAAAACTAGC	59.845	20
TTGACGAGCTTCCCTCTTGT	59.989	20	CATGATAAATTAAACGTAAGT	59.371	27
AGATCGGACAACCCATCAAA	60.317	20	CACCAGCTTCGACACACAGT	59.94	20
TTTTGCTCACCCCTAACCAC	59.971	20	TGTTCGAAAACATTGGTCCAT	60.22	21
TCTCCACCCAAAAACCTCAC	59.943	20	GCGGTGGCTCTGTAGAAGAC	60.02	20
GGGGCGTTACATGGACAATA	60.585	20	CAATCAAACCCCAAGACACA	59.389	20
CCAAGGTTGAAAGGGATCTG	59.521	20	GCAGTATCAAGGGCTCTCGT	59.459	20

CCCAAACTCATGCAAAACCT	59.971	20	GAAATGGGGAGGAGGATAGC	59.866	20
TTACCTAGCAAGGGTTTGGG	59.084	20	CACTTTGCCCTTCGTTTCAT	60.11	20
AGAGAGACGGGGAAGAGGAG	59.945	20	TCTCCGAATCAGAGCCTTGT	59.95	20
GCCCATAAGCCCATCAAATA	59.757	20	CTGAAAAATCGGCGACATCT	60.214	20
AATGGAAAATAAGCAGGGGC	60.28	20	CAAAGCAAAAAGTTGGCGAT	60.244	20
CACACTTCTCCTGCAACCAC	59.31	20	AAGGGTGCCGACCAGTAATA	59.452	20
GGGAATCTTGTTTTAAGTATCCGA	59.762	24	TTGCTAACAAATATGCATTCCA	59.526	23
GCTCGTCTCGAGCTGTGTTT	60.743	20	TTCACGTTCAATCCCTCACA	60.088	20
TTTTTGATGACGCAGGAACC	61.012	20	GATTCGGGTTCAAACCCTCT	60.306	20
GAACCTCCTCTGTTCCCTCC	60.05	20	ACCCTTGTGAACAAACTCGG	60.005	20
AAAGGGTATGCAGCAGGATG	60.096	20	ATACGCACGAACATGAGCAA	60.288	20
GAGAATTCCCGCAGATCAAA	60.155	20	TCGGATTCCTTGGTTTTCAG	60.044	20
TTTGGTTTGTTGAACCCTCC	59.807	20	TTTTGGAAGGAGTGGTGGTC	59.943	20
CCACCCCCTTCTTTTTCATT	60.159	20	TGAAGCGAAAACTGAACGTCT	60.045	21
AGTGGCATCAAGACGAATCC	60.081	20	ATCCCCTCCAAATTCCAAAC	59.996	20
ATTGCATCTTGGCCCAACTA	60.469	20	TGCTTTCATCACTGGCAGAC	59.992	20
GGCATGCATAGGTGTAGGCT	60.125	20	AATGTCTCCCGAGTTTGCTG	60.255	20
GTGAGCTCTGTTGGTCTTTGG	59.899	21	TCAATTACCTCCCCAGAACG	59.926	20
TGTAATGATCTTGCATCGCC	59.652	20	GGTTCTGGGCTGTAACCAAA	59.971	20
TGGAAGAGTGCCCAAATACA	59.123	20	TTCATGAGCTCCGTGTTGAA	60.39	20
CTTCGGCTCTCCAACTTCAG	60.126	20	CCATACCCACATTTCCAAGG	60.044	20
CAGCTCCAATGCAGTAGCAA	60.157	20	AATTCATGAAGGGCTCGTTG	60.074	20
TTTCCAAATTTTCTCCTCCG	59.131	20	ATGTAGCCGACCCCAATTTA	59.297	20
AGATGGATGTTCGAGTTGGG	59.927	20	TCCACCACCACCCAATACTT	60.088	20
GGCGAATTCTAAAGTGATCAAA	58.386	22	AAAATCCTAATTGCTTTGCACC	59.525	22
AGGGCCAAATTTTATGGGAC	60.02	20	ATAATTTATCCCGCAAGGGG	60.002	20
TCAGTTTGCACACTTTCCCA	60.278	20	TTGCCAAGGGATATACCCAA	60.146	20
CATTTTTCTTAACGGATTCTCCA	59.507	23	AGGAACATGCCAACTTCTGG	60.111	20
ACATGGTGGTTAGGGAGCAC	59.851	20	TGTCTTTTGGTGTGTGGGAA	59.976	20
GCAGGAACCATCGAGAAGAG	59.95	20	AACCGACTTGAAACCTAGCG	59.378	20
GCGTGGGAATTGTTTCAAGT	59.978	20	CTAGAAGTCACCGGAAGCCA	60.388	20
CATCATCCGTAAGCTCCCAC	60.483	20	CCTGTTGGGAGGTTCTTCAC	59.549	20
GGGGTCCCTGTCTTATAGCG	60.836	20	ATGCAAGGCAGAAATCAACC	60.081	20
AGTCCCCATTGCCATAATGA	60.155	20	ATGCCTCTGTTCTTCATCCG	60.218	20
CCGTATAGTCCCGAGCAGAG	59.853	20	AAAATGAGGAGTGGGTGTCG	59.966	20
TGCCTTGCGAATTGTGATTA	60.215	20	ATGCCGAATTCAGTTTTTGG	59.938	20
CATCCCCCACTTTTCGTTTA	59.795	20	ATCAGCAAGAGATTGGTGGG	60.073	20
AGCCCATAAGCAACACGAAT	59.597	20	CACAATACCCCTGGTCAAGC	60.375	20
TGGGTGCGAACAACATTATTT	60.237	21	GGTTCTCTCATCCATTGGGA	59.862	20
GCAGGCGATAAGCAGAAGTT	59.62	20	TATGCTAACTCCCCTTCCCA	59.523	20
CCCAAGACCCCAATTTGAT	59.59	19	GTGAACTTGGGAGCTTCCTG	59.844	20
AGATCCAATCCAAATGCTGC	60.043	20	TTCTCCTCGTCATTGGAGAAA	59.799	21
GATTCCAACACTTGGGCTGT	59.973	20	GCAAGAACCCTCATCTGCAT	60.226	20
CACGTGTAGGATGGGAAATTG	60.234	21	CGCTTATTTTTGTAATGGAATTT	59.049	24
ATAGGTTGTTCAAAGCCGGG	61.217	20	CCGACCTCACATAGTGGGAA	60.913	20
CTTTGGGAGTGAATGGGAGA	60.042	20	ACAGGATGCCAGTTATGGGT	59.288	20
CGCCTAGACGCAGAAAAATC	59.982	20	TTGCTTCAACACAAATTTCACA	59.25	22
ATTTCTGGCTATGCCTGTGC	60.243	20	AGCCAAAATTTCCTCCAAGG	60.423	20
ATTTCCACTCATGGAACCCA	60.173	20	TCCGACATCAATGGCAGTAA	60.073	20
CCAATCACAGTCGAAGACGA	59.831	20	CCACTGGGACTAAGCGAGAG	60.005	20
GCGGCTACAACCAAATTCAT	59.967	20	CCCCGCACTTCTTAACAAAC	59.609	20
CATGCCTCGAGTATGTGGTG	60.136	20	TCGAAAGTAGGCGGGTTATG	60.089	20
CCCAAGACCCCAATTTGATT	60.91	20	TTTCCTTGGGTGTCTTCGTT	59.569	20
CCAATCAAATTGGGGTCTTG	60.162	20	CTCGCCCCTTAGAAGAGGTT	59.842	20
AGCAGGCTCAGACCAAGAAG	59.745	20	CATCGCTTCAACCCTTGTTT	60.11	20
TACTTCAACCCACGTGACCA	60.001	20	TGATAGCACGATCCACGAAG	59.823	20
TCGGCAGCAGTTACATCTTG	60.011	20	CCCAAGACCCCAATTTGATT	60.91	20
AGAGAATGTGGTGGTGGAGG	59.962	20	GCAACAAAGATGGCCAAGAT	60.081	20

AATTGTTGCATCTATTTTCTAAAT	57.596	26	CGTATTCCTCATTAAGCCCC	58.533	20
CAAGACCGTGACAGGCACTA	59.897	20	TGAACTTTTCCCTGGACCTG	60.081	20
AATTGTCCCTCCACACCACT	59.279	20	TTGAATCCCGAGATGGTAGC	60.036	20
AATCGCATTTTCTCGACGAC	60.221	20	AGTCCGGAAGTCTTTCCCAT	59.935	20
CAGCCAAGAGCCCATAGTTC	59.836	20	ACTAGGGAAGTTGGGAGGGA	59.928	20
TTTGGTTCCGATCAGAGCTT	59.813	20	TTATGTCATCTTCCGCTCCC	60.036	20
AAAATTTGTCCTTTCTACACGCA	60.05	23	ATTCTTGTGACGTTGGAGGC	60.119	20
AAAACCTGCCTCAACCCAG	60.096	19	CTGTAACCCAAAATCTCGGC	59.569	20
CCCAAGACCCCAATTTGATT	60.91	20	GCCAATTCAAATCTCCACCA	60.843	20
ATGTCCCTGCTTCGCATATC	60.066	20	TTTGGGATGATGGTTTGGTT	60.029	20
AAAACCCAATCAAACGCAAC	59.845	20	CCCAAGACCCCAATTTGATT	60.91	20
GGCAGAATTTGAATGGGAAA	59.878	20	ATTTCCTGCCATCCAATCAC	59.756	20
GAGCAACCTGATGGAGATCAA	60.211	21	CTCCAAATGTGATGTCACCG	59.96	20
GGAGGTTTGAAAGGTACCTGAA	59.499	22	CATGTAGCCGATCCCAATTT	59.784	20
CCGTCGGCTAAAACACTACC	59.632	20	AGTTTGAAGAAGCCGTGGAA	59.853	20
TCGATTTTGTTTAGGCTCGC	60.343	20	CATCCATCACCGTTAATCCC	60.014	20
AGGATCATGTTCGGCTCATC	60.042	20	CAAAGAGTTGTTTTACAGACC	59.626	25
TCAAAAACCAATTGATAGCACA	58.213	22	GCTTGAGTTTCAATGGGCAC	60.646	20
GAATTCTTTCCTCCATGCCA	60.014	20	AGGAGGAGAAGCCAAAGGAG	59.95	20
CCTCCCAAACTTGAGACCAA	60.081	20	CAACAGGAAGCCGTCAATTT	60.11	20
GAGGCGCAAAACACTTCAAC	60.817	20	ACCATTTTTCCACTCCTCCC	60.169	20
GCAGGCCAAAGAGGAAGAGT	60.903	20	CAGGCCAACTGAAATCTGAAA	60.234	21
GCTTTGGACTCGGAGTTTGA	60.375	20	CGCTGGTCGGTTAACTCTTC	59.875	20
GACATTATCCATTTTATTGGGCA	59.934	23	TGCAGCTAGTCCCTGCTTTT	60.154	20
GATCAAAATGGGCCTCAAGA	60.014	20	TTCTGTGCTCAGCTTCTCCA	59.855	20
CAAGAAAGCGAAATGCTTCA	59.182	20	GCATAGTTCGAAGGACAATAT	58.613	24
GGAAGCACTCGCAAGAAAAC	60	20	CACCCAGAGTCCATTCCACT	59.962	20
GTCACCCCCATACCCACATA	60.317	20	TGATGTCAAAAGCGTTCTCG	59.988	20
TGTAGCCGACCCCAATTTAT	59.297	20	CAATCGACCACCCGATATGT	60.603	20
GGAGTGGGTGTCGGTTTTTA	59.83	20	TTATTCTATGCCTTCAGCAAAT	58.474	23
CGTTCGATTTGCCGTTTTAT	59.964	20	CCGTCTTTGGAGCATGAAAT	60.074	20
TTTGGGTTTTAAATTCGTTGAA	58.567	22	AAAACCAATTGACAATGAGAG	59.864	23
AGAACCAGACCTGCTTGCAT	59.874	20	CATAGGCCAAGAAGGGAACA	60.066	20
CGACCCACATAGTGGGAAAG	60.366	20	CTTCCATCGTTTTCAGGGAG	59.665	20
TTTCGACGGTTTCAAAGAAAA	59.723	21	AGAGGGAGGAAACTTGACCC	59.534	20
CTTTTGATTGGGAATAATTGGG	59.562	22	TGTGGTCACACACTCCATGA	59.518	20
CTCTTTTGATGGTGGCCAAT	59.933	20	GCAGTTGGATGACTGGGTTT	59.973	20
ATGTCTATCGTTTGGGCTGG	59.955	20	TGGAAATTGTCGTGTAGTGG	57.023	20
AAGTAGACACGTGGGAAGCG	60.312	20	CAGAAATGGCAGCAGAAACA	59.988	20
GGCTGACTCATGGAGAGGAG	59.945	20	TGGTCATAGGAATTCGAGGC	60.036	20
GCACTGCCTCATCCAAACTT	60.263	20	GTTGCAACTTCCCACCTGAT	59.973	20
CCCCTATCCCCCACTGTTAG	60.56	20	GATTCATTCATTTGTCAACACG	57.999	22
CCCTCGGACACTTTGACATT	59.966	20	TGTGCAGTATGTTACCGCGT	60.203	20
TTCATGGTGGGGTGAGTTTT	60.21	20	TCTCTCTTCCGTGTTGGTCC	60.238	20
GATTCTGGTTCGGTGATGCT	60.081	20	TGGCAGAATGAAGTCGACAG	59.984	20
GCTCGTACATCGAGTGATGC	59.43	20	GTTGTTGCAGAAAAGGGGAA	60.088	20
GTGGAGCTGTGGTGGGTTAG	60.567	20	GTTCCTCGCGAAATTAGCAT	59.324	20
TGCACCATGTGTCAGAGGAT	60.121	20	AGACATGTTGCGTTTCCCTT	59.598	20
AATGAGAAAATGAGGCGCAC	60.221	20	GATCCTTAGTGGATCGAGCG	59.797	20
TGGCCAAAGACCAACCTATT	59.429	20	GTTCATGTAGCCGACCCAAT	59.82	20
CGGATTGTTTTTGGAAAGGA	59.91	20	CGACGGATAGAAATCTCCGA	60.17	20
AAGCTCTTGTTCTGCGAAGG	59.757	20	TGATATTCACTTGCCCCTTCTT	59.966	22
CCGTCTCCATTCTTCCACAA	61.034	20	AGATTTGCGGCTTCTCACAT	59.843	20
AAGGCCCTCTCAAAACCAAT	59.94	20	CCTCGAAATATCCTCCTCCC	59.859	20
GAAGATGTATCAGGGCGAGG	59.653	20	ACGTTCACAACAACACACATG	59.97	22
GCATGAGGAAAAGGGATGAA	60.014	20	TAGTGCAGCATGTGGTGTGA	59.894	20
CGGATGGTTGTTTCCATCAT	60.582	20	ACCTCGTGCAAAAATTCCAG	60.11	20
TCTTATTAGGGGCTTGTGCG	60.223	20	GGTTTCCAAATTGGGGTCTT	60.032	20

TTGGTTCTCCTTTGGAGACG	60.224	20	TTTTCTCATGAACCATCCCC	59.727	20
ACGCGCTTGAATCAATTAGG	60.23	20	GACTTGAGGACATACATAGTG	59.96	26
GGAGATAGAGAGGGGCCAAC	60.037	20	CTCAGTGGCTCGCTCATACA	60.16	20
GCTGATCATCTTGGGGGTTA	59.894	20	AACTGCTCCGTCTGCATCAT	60.833	20
ACGAGTTGTTTGGTTGAGGC	60.156	20	GCAGGGTTTTCGACAAAAGA	60.227	20
AACGTATTCCTTCCCCCACT	59.691	20	TGCTTAATTCCTCATCCGAA	58.308	20
TTCCCCACCATTTCATCATT	59.991	20	ATGACAGAGGCTCGTGAGGT	59.866	20
AACATGCCATCTCAAGGGTC	59.934	20	GTCCTTTTTCTCGAACGCAG	59.993	20
GAAATTGCTCCCCTCTATCAAA	59.572	22	GGATATCTATTTGCGCGCTT	59.331	20
TACGAGGTTAATGGATCCGC	59.923	20	GCTCTTCGACGACCTCAATC	59.957	20
CCCCAAGACCCCAATTTTAT	59.882	20	GTGAGAAACCCATTTTGGCT	59.031	20
TACTCCATTACAGACCCCGC	59.955	20	CCATTTCTCCTTGCATCGTT	60.074	20
GCACCCTCTCATGGATACTCA	60.088	21	GTTTTCCGGTTGACAAATCG	60.344	20
TTTGTGATGGGCAACTGGTA	59.964	20	ACACCACCAATTTCAGAGCC	59.973	20
AAGTCGTCGTCATCATCCTC	57.644	20	GGTTGGTAGTGGAGCTGGAA	60.111	20
GAGCATGCCTAGATGTTGCTT	59.495	21	GCAGGCTCAGACCAAGAAAG	60.134	20
AGTCTCAATGGGGACACCAG	59.962	20	TTCGAATGCTCACGTTGAAA	60.379	20
ATCCTCCTCAGATCCTTGGC	60.563	20	GATGCTGTTGAACCATCCCT	59.934	20
TGTAGGCCAAATGTGTTGGA	59.964	20	CAGCCATTCAACCAGCAGTA	59.864	20
CCAAATGCTCCTCTACCGAC	59.694	20	ATTCTCGTTTTCCACATGCC	59.939	20
GGCTCGCAAAAATAACCAAA	60.075	20	TCATCGAGTGCTGCAAAAAG	60.134	20
TAGTCGGAAAGTGGGGTGAG	60.103	20	TCACCATGTTGATGAAGCGT	60.12	20
CCTAAAGCCAGATCTCCGGT	60.59	20	TGGAGTTCACGTAGCAAAACA	59.376	21
CACTTACGAAATGTCAAGACGC	59.813	22	ATGTAGCCGACCCCAATTTA	59.297	20
TTAGGACTACCGGTCCGATT	58.528	20	CACCTCTTGCGGGGTATTATT	60.21	21
CCGAATGATGAGAAGTGGGT	59.927	20	GAATGCTTTGACCGCATACA	59.694	20
TGAGGGAACTTTGTGAACCC	59.943	20	TACATGTACGCCCCAAACAA	59.849	20
AGCTTAGGGCAACACGAGAA	60.015	20	CATCATTCCCATCACCATCA	60.137	20
CAATTCTTTTGTGCGTGAGC	59.469	20	CACGTATTTTGCTCCAACGA	59.729	20
ATCCATAAGCCGACCTCACA	60.483	20	TGACCAATGAGTCGACTTGC	59.837	20
ATGGACCCAATATGTCATAACCA	60.197	23	CCGTATTTCTATGCCACGGT	59.845	20
GAAGGGGGAGACCGAAATTA	60.258	20	GTTGGATGGTTGGGTGATTG	61.025	20
TGTTGAGCGACCACAATCTC	59.837	20	ATTCGTCGATGGATGACTCC	59.893	20
CATCATTTGATTGTGGTCCG	59.774	20	AATTGGCATTTGATGTATATTG	59.506	24
TCGAAATTGACACGATCCAA	60.049	20	CCCAGGAGAATTAGGGTTCG	60.807	20
TGGTTAAACTCCACCTTGGC	59.971	20	TCTTTCTCCAATGCGACCTC	60.34	20
GAACGAGCATCCATGTCAAA	59.654	20	CTCCTCGCTCTCTCCTCTCA	59.962	20
ACAGAGAGGCGGTGGTAAAA	59.734	20	CCATCCTTTAAGTACTTTGACT	58.83	26
CCATTTTGATGGAGACCGAG	60.452	20	CCCCAAATTCGACAAACAAT	59.662	20
TGTAGCCGACCCCAATTTAT	59.297	20	GGGGAAGAACTCATGAACGA	60.05	20
TCTCTCCCTAGAAAACGGCA	59.948	20	ACCACAAATTAATCGGGCAC	59.691	20
TTTCCCTCTCAAAAACATCACA	59.587	22	TGGAATAAGGCAAAAAGGAA	57.376	20
AGTCGTCTCCTATCCCATCG	59.116	20	GTGACGAGGAAGTAGCCCAG	59.867	20
CGGTCAAAACCAAATTACGC	60.356	20	AAGATGTCATTTTGTCGCCC	59.939	20
ACATGAATGTGTGGTTTCATCA	58.751	22	TGCGTGTTTGCATCCATTAT	59.96	20
TGCCGTCTACAGAAATGTGG	59.716	20	CCACTCACTCCAACAGAGCA	60.022	20
CGAGGAGAAATTCTGGATGC	59.773	20	GCTTGAAGCTCTATGCAAATC	59.636	22
ATTCGGCATCAACCAACTTC	59.939	20	GCGAGGCAATAGATGTGTGA	59.83	20
TCTGCATGAACGCTTCTCAC	60.144	20	CCTCTCCTCGAAAACCCTCT	59.811	20
CGCCAGCTACCATCTGAAAT	60.235	20	CATACCGGAGCAGATCCAAT	59.917	20
GCAACCATGATCTCATCGAA	59.61	20	ACGTTATACTCACGCCCTGC	60.162	20
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TTGTCCAGCCCAATCTGAAT	60.461	20	CAGCTGTCTCGCACAAGTTC	59.776	20
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CCATTACCGATGCCTTACTTG	59.483	21	TTGGCCAAGGACATAACCAT	60.192	20
GACAGCGGTTGGTTCAGC	60.412	18	GCAAAGGCTTGTGTTTCTCC	59.859	20

TCGTAGGTTTGGGTTTCCAC	59.83	20	TGTGGAGTGGACCTCATTCA	60.088	20
GGTGAGCGATCAAAATCCAT	59.9	20	CCCTTTTTGCACTTGCACTT	60.284	20
TTCTTTTCTGATGAGGCGGT	59.813	20	GGTTCAAGTGTTTGGGAGGA	59.943	20
AGAGGGGTGTTGAAGGTGTG	60.002	20	GCGATGAAGAACAAGACCCA	61.188	20
CCTCCGGCGATTACTACAAA	60.089	20	ATGGTATGTGGGATGGCACT	60.081	20
TGGCTTCAGAAGAAACACCA	59.415	20	TTCCTGAACTGATTGACCCC	59.903	20
GGTGGATCAAATGTTTTGGG	60.029	20	ATGAGCACCTTGACAATCCC	59.934	20
ATGTAGCCGACCCCAATTTA	59.297	20	AATTGAAGAAAGCCGCACAT	59.713	20
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CTGCAGATGAGGGTCCTAGC	59.973	20	ATCTCTTATCTCGGCAGCCC	60.702	20
GGTGTGCTGGAGATACCGAT	59.957	20	GCAGAGTCCCATAGCTCACC	59.834	20
ACTGCTCGCTATTTGGATGC	60.382	20	TCCAATCAAGGTCAATGCAG	59.648	20
GTAACAACGGTGGAAATGGG	60.088	20	TCCATCATTCCCTTTCTTGG	59.864	20
TAAAGTGAACAACCTCCGGG	59.964	20	ATGGGCATTCAGTGGGATTA	60.155	20
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AAAGAACAATGCCCCATCTG	59.933	20	CCAGTTGCTTTCTTTCCAGC	59.993	20
CGTTCTTGCCAACCCTCTAC	59.734	20	TGTTCCAATGGAGGAGACAA	59.059	20
TTGGCTCAAGTCTTTGCTGA	59.716	20	GGCCCATTTACATCATTTGG	60.016	20
TCCGTTGCTCCTACATCATTT	59.583	21	GGAGTGGACAACGTAGGGAA	59.966	20
GGCATAGCCACGATTTCAA	59.637	19	ACAAAAAGGAAATAGGCGGG	60.305	20
GCGAGTTTCTTGAGGTCGTC	59.997	20	ACTTTGTCACCACTCTCGGG	60.151	20
GTGCATGAAACATCTGCTGG	60.272	20	AAAAGGAAACAAAGCAGCCA	59.861	20
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CATTTTGTTACCCGAGCGAG	60.628	20	ATGCAAACAAACCCGTACAA	58.942	20
AGATGGGATGAATCTGGCTG	60.034	20	GAAAAATAAAAGACATACGAA	57.263	26
TCAAATACATAATTAGCACGGAG	59.504	25	GATCGAATCCGCTTTCATGT	60.043	20
TCTGGATGCCTTGAAAAACC	60.051	20	AACCCCATATAGCGGGAAAA	60.508	20
AAGAGGAAGGAGGTGACCGT	60.111	20	CTTCCAGCTGAAACTGTGAGA	58.229	21
TGGAGCATCCAACATGAGAG	59.787	20	TCAAAGCATCCCTTCTCTTACA	60.243	23
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CGACATGGTCATAAGGGTCC	60.195	20	ACAAGCAGGACCAAAACCAG	60.149	20
CCCAAGACCCCAATTTGATT	60.91	20	TGCAAGTACACTCCATTTTGTA	59.12	24
AATGAAATCGTGCGAAAATG	58.627	20	TTTTGAGCAGGAATGTTCTTCA	59.861	22
CGGAGACGGTAGAAGAGGTG	59.861	20	ATACAATGACGAAAACGCCC	59.829	20
ATGTAGCCGACCCCAATTTA	59.297	20	GTACCAACGCAAGGCAAAAT	60.003	20
AGAGCGTAGAATCGCGAGAG	59.882	20	CATCGAGTGATCCATTGTGG	59.918	20
AATCCCAAATTCATCCCTCC	59.959	20	CGACATCGGATTCCAACTCT	60.073	20
GGCCAAAATTGCCTCTATCA	60.038	20	CCCAAGACCCCAATTTGATT	60.91	20
GCTCAAACAGAAGTCCCTGG	59.844	20	GCCCTGTCATTTTTGAGCAT	60.081	20
AAATAGGCTGGCAAAGGAGG	60.573	20	CTAATCACCAACGCCCACTT	59.993	20
CCAAAGCTTGAAGAAATGTTTG	58.919	22	CACGATGCATATGTTCTGGG	59.948	20
GCAGACGAATTTAGTCGGGA	60.214	20	CTGGCAATGCCTATGTCAGA	59.823	20
AAGTGATGAAGGCTGCCACT	59.874	20	TCGTCAGAATTTTTGGACCC	59.91	20
AATCTCAAAAGACGCGAGGA	59.955	20	AACATGGACGACCACGTGTA	59.88	20
TCATTAGATTGGGAATAATTGGG	59.101	23	ACAGCTTTCTCGGATGGAAA	59.813	20
AGCTAATGCGGGAGAAGACA	59.978	20	GTTCCCCAGAACGTCACACT	60.009	20
CCTCCTCCTCCACATTTCAA	60.042	20	ACTGCTAGGAACGCAAGGAA	60.015	20
ACTGGCAGCAACTCATTTCC	60.263	20	TATTGCATGGTAATCCCGGT	60.038	20
TCCTTTTGCGTTTTATGTGC	58.819	20	CCCACATATTCTTCAAGCGA	58.721	20
GGACTCGGGTGAGTCTCAAG	59.835	20	ACTCCCACCAATAGTCAGCG	60.134	20
CGGGTCGAGTTGAGTCATTT	60.111	20	TTATGCCCAAACCTACCGAG	59.953	20
TTGGGATAAAATCTCCGAAAAA	59.791	22	TTTCTCCATTCGTTACTGCAT	57.379	21
TTTATCCCAAAATTGAGGCG	59.901	20	CTTTTCCTCAGGCCTCACAC	59.844	20
AAACCGTTCCCACCCTTTT	60.575	19	GTTGAACGGGAACGGAACTA	59.971	20
TGCAACCATCCAAATCCTTT	60.309	20	GAGGCGTATGAGATGGAGGA	60.181	20
TCGGAGAACGGAAAATTGAG	60.184	20	TTCGATGAAGGGAAGAAGGA	59.744	20
GTCCATGTCCTCGTCCTCAT	59.928	20	GAACATCGAAGCTTTTGGCT	59.457	20
AAGCTTGGAAATGCCTGTTG	60.249	20	CCCAAGACCCCAATTTGATT	60.91	20

GCTTCTCTGAAATCCTCCCC	60.154	20	AATCCCTCTTCTCCTCCACC	59.492	20
AGCAGGCTGAGAGAATGAGC	59.857	20	GCACAAGAAAGAAACCCTGA	57.923	20
TGCACAGAAGATCCTGCAAC	59.992	20	AGCAGGTTAGATGCCGACAC	60.285	20
TTTAAATCCAACTCACACATATAC	58.233	27	AAGAGTAGCTGCTGCGGGT	60.171	19
CGCTTTATGTATGCCTCGGT	60.117	20	GATTTCCCAAATCCCGTCTT	60.131	20
CCACTTCCCAAATTTCCCTT	60.159	20	AAAACGGAAATCGAACAACG	59.975	20
ATCCATGGGAATTGGACAAA	59.991	20	GAGAGGAAGCTAGCAAGGCA	59.859	20
GTAATCAGGGCCATTCCCTT	60.152	20	TGGGCCTCTTCCAACTTAAA	59.679	20
TTCCACTTCTTCTCCTTGGC	59.405	20	GCGGCGGAGATAGTCTACTG	60	20
TTGTATCCCCCAGTTTCGTC	59.79	20	TAAACACATGCCACTCCAGC	59.722	20
ATTTCAACTACGACGGCCAC	60	20	GTAGACTCCACCGCCTTGAG	59.867	20
CACTCGAAGAGTAGCGGCTG	61.263	20	TTGGTGCTTGCCTGCTAAAT	60.772	20
TGTTTTTACCTGCGTATCTGTCA	59.698	23	CATGTGTTTGGTGATATAAAAT	59.589	25
GTTGACGGTTGGAAGATGGT	59.827	20	CCTTGGTCGATCTCATCACA	59.631	20
GTTTACCTGACTGGCGTGGT	60.035	20	TCGAGTTGATCTTGCCTTTGT	59.867	21
AGACACCCTGGAACAACACC	59.859	20	GGAAGAAAAGTGCGATGACG	60.776	20
AGTGCTTCGGTCTGGATGAC	60.269	20	CCATACATGTGCTGGCAAAC	59.995	20
AGGTCGGCATCATCTTCTTG	60.218	20	GATGAGGGAGGCACTAGACG	59.827	20
ATCTCCACTTGTTGTCTCCAA	57.211	21	TGAGGGGTAGAGTTCCATGC	60.073	20
ATTCCTCGGGTTCTTGGAGT	59.935	20	AATGACTAATCTTGAACATGCC	58.779	23
TGATTTAGTAAAGTTGGAGGTGGA	59.098	24	GAGCCACGACTACAGGCAA	60	19
AAGGACCCTTTGTGGGATTT	59.668	20	TGCACTCATTAATTGTTTCGG	58.688	21
GGTTATGGTGCGTCGAGTCT	60.142	20	CCAGCTTAAGCCTGCATTTC	59.982	20
TCAAATGTTCGTCTTGCAGC	59.995	20	GTCGGGTGGTGTGTAGTTGA	59.441	20
AATTGAATTCAGAGCACCCG	60.074	20	ATGTAGCCGACCCCAATTTA	59.297	20
CCGACTACGACTATCCTCGC	59.859	20	TCGTAACGACAAATGGGACA	59.964	20
AATCGTCGAATTCGGTTTCA	60.448	20	GCGACAAAACTTGGTAACGG	60.534	20
AACATACCATCGTGGCCAAT	60.081	20	TGTAGCCGACCCCAATTTAT	59.297	20
ATGTAGCCGACCCCAATTTA	59.297	20	AAAATCATCCCAATTCCCAA	59.067	20
GGATTTCATTTCAGCGCTTC	59.791	20	ACCTCGACAAACTCCACACC	60.009	20
TGTAGCCGACCCCAATTTAT	59.297	20	TGTGGAAGGCGGAAAGATAC	60.074	20
TCAGAATATGCAAGGGGGAG	60.029	20	AAAAGTGTTCTGCTCCAGCG	60.571	20
ACGGATTCGAGTTTCAACGA	60.636	20	TGAAGAGTTGAGAAGGCGGT	59.989	20
CAGAGGGAGCATGTGACCTT	60.261	20	TCATTGGGAAAATGATTTGG	58.255	20
TAGTCATCGAGCAAGCCAAA	59.566	20	GGTCGATGAAGGAAGATGGA	60.011	20
TTGACCAATCACCAATCAACA	59.808	21	AGTCGAACCGGATCATATCG	59.917	20
AGTGCAAATGTTGACGGGTT	60.419	20	ACAATCCTTTTGAGCCTGGA	59.67	20
CACGAGCTACTCTCCGCTTT	59.78	20	CGAGGATGCTCTATCCGAAG	59.933	20
CCCAAGACCCCAATTTGATT	60.91	20	GGTGCTTTGCTGAGAAGAGG	60.134	20
CACGCCAACTTACAAACTATCG	59.706	22	GGGAAAGCAGGAGAGTAGGC	60.349	20
CAAGCCTTGGACTGAGAGGT	59.45	20	CTTCCCTCATTCCCTCCTTC	60.008	20
CCTTGAGCTCGTCAAAGTCC	59.989	20	TCTTCTGGTGCTTTCCTTCC	59.405	20
ATTGTTGAGAGCCGAAATGG	60.074	20	GTTGAGGAAGGAGAGCATGG	59.803	20
TTGGTTCATGTAGCCGACC	59.512	19	AGGGGCAGTTAAAAATCGGA	60.792	20
AAACCACCATTTCCGAAACA	60.206	20	ACAGGCAATCTGCTTAGCCA	60.934	20
TTGCCCAGTTCTTTTGTTGA	59.293	20	TGTAGCCGACCCCAATTTAT	59.297	20
TCTGTTTTATTTCCCCGTGC	59.938	20	GGAGAGGTCGTGATCCAGAA	60.199	20
GCTGAACAATGCCTCGAAA	59.94	19	TGCAACACCTCCATCATCTC	59.637	20
TGCATTTCATCGCTTTATGC	59.809	20	TTTAGGAGTCGTGGGTGGTT	59.449	20
GCCGTCTGATTGGAGGATTA	60.036	20	AACCAGCCCATCCCTTTATC	60.152	20
TTTTAAAACCGATCCCCACC	60.883	20	GTAAGCTGAACCCCAACCAA	59.971	20
ATGAGCATGATGTGTCTTGAAT	57.135	22	CAATTTAGCTGAAATCTCAACC	59.296	25
GCCGTCTGATTGGAGGATTA	60.036	20	TTTCAACGTCTCTGCCAATG	59.84	20
AAATATTTTAGAAAGAACAGATTT	57.114	27	TGTGGCATGAAAAGTTTTGG	59.561	20
GGAACAAACCCGACGTAAAA	59.839	20	CCCCTCACCTTTCTCTCCTC	60.186	20
ACCGACCTTCCAAATTGTTG	59.83	20	GCTTTTGAAGTCCTTCCACG	59.853	20
ATGGGTAGCCAGTTTCACCA	60.375	20	CCAACCTAACGCCACCTTA	58.635	19
CAGTTCCATGTCACAAACGC	60.16	20	TTTCCAAACCAAGCTATCGG	60.067	20

CCAATCAAACCCAACGAAAT	59.662	20	TCAACACATTCAGCAGGCTC	59.992	20
CATTTCCGACAACTCGATGA	59.648	20	CTCAATCGCAACTGCAAAAA	59.992	20
CATCATTCCCTGCAATCCTC	60.426	20	AACGTTCGCTCCAAACAATC	60.118	20
TACCCATTGTAAACCCCTGC	59.685	20	CGCAATTGAATAAGAGGGGA	60.031	20
CCAGAACCATGGACACACAG	59.997	20	AGCAATGGACCTCGCATAAA	60.606	20
ATTGACAATTCTCGGGTTGC	59.939	20	CTCTCTCCTAGGTCCGTCCC	60.208	20
ACTGCTAGACCCAGTGGTGG	60.174	20	TGCAATGCTCCGAGTATGAG	59.972	20
AGGGTTGTAAGGGGTATCCG	60.068	20	TTGGAGGAAAGCAAGGAAGA	59.926	20
GAGCAGCTCGACAATGATGA	60.104	20	GAACGGTGCTTATTACGGGA	59.96	20
GGCCACCAAGAATCTCAGAA	60.195	20	TGTTGTGGGGAAAAAGGAAG	59.942	20
GGGTTGTTAAGATTTAATGATTAT	57.624	26	TTTTTAATGCATAACGTTCATTT	58.651	25
ATGGTCGAGAGTGTTCCTGG	60.112	20	TTGGGATTAAGGCTTTGGTG	59.931	20
TCAAAGAAAGTGAGTAGAATCCA	58.56	25	TTTCCTAAGTCTTCCGCGTG	60.378	20
TTGGTTCATGTAGCCGACTC	58.724	20	CGTTTGATTCGCCGATAAAT	59.928	20
TGTGTTTCATGTTTGTTGTGATAA	58.06	24	TGGAGGTGGCTGTGATGATA	60.072	20
TTTCGAAGACTGGAAGATTTGA	58.949	22	GCCGGTTCTTTGTGAATCAT	59.939	20
TCAGTATTCATCGTGGCTGG	59.673	20	TTCGAATTCAAAAACTCCCAA	59.551	21
TGAATATTGGGGTGGGAAAA	59.988	20	CAGCGCTTCTTCTGCTTTCT	60.037	20
AATCACGGGACCAAAATGAA	60.17	20	AGCTCCATTGTACGTTTCCC	59.056	20
TCTCCAGAGCAAATCGACCT	59.95	20	GTTCAACAGGAGGTGAAGCC	59.703	20
GCACATGTTAGCCAGAACTTTG	59.813	22	GGCGCACATTAGACATCCTT	60.103	20
CGATTGTATTTGTGCTGCAAG	59.382	21	AGGCTTTACTCGGTTTGGGT	59.998	20
TCATTCTCTTCACCGGAAGC	60.34	20	ATGGTTCCTCCAATGTCTCG	59.927	20
GTGGAGGATTTGGTGGGAAT	60.95	20	CACTTCCGCCACCATAAGAT	59.955	20
TGTAGCCGACCCCAATTTAT	59.297	20	GAAAGAGAGAGAGAGAGTCA	59.828	25
TCCTCCATTTCCCCACAATA	60.126	20	CTGTCATGCAAGCAGCAACT	60.207	20
ATTTCCTGTTCTCTTCCCCG	60.434	20	ACCGGAACATAAGTGCCAAA	60.365	20
CCCAAGACCCCAATTTGATT	60.91	20	AGCATCCAAGCTCGACAACT	60.02	20
TCATGGATTCATGGTGCAGT	59.925	20	CAGAGCAAGAAAACATGCCA	59.988	20
CCCGTTCAGACCACCTTTTA	59.964	20	TGGGGGTGATCTGAGAGAAG	60.191	20
GAGTCTCCATCCCCACAGAA	60.048	20	GCGAACCAGATGCATTATCA	59.652	20
CCCAAGACCCCAATTTGATT	60.91	20	TTTTCTGTTTTTGTTCTCCTGCT	59.462	23
TGTTGGTAATTGGGATGAGGA	60.177	21	CGTCGATCACTTCAACCTTT	57.797	20
GTCGACGCATCAGAAGACAA	59.992	20	AAGTGGGGAAGTCTCGGATT	59.935	20
CAGTAAACCCCATGGTCTGG	60.224	20	GGTGGCATCATCAACAACAA	60.376	20
GGGGATCACCAAACTGAAGA	59.903	20	TCTTCCAAGATCACACAGCCT	59.859	21
CTTCTATGAAGCCCTCAGCG	60.11	20	ATCCTTCAACCCCAAATTCC	59.996	20
TGCAGAAGGTCTCCTCCAGT	59.986	20	AGTTTTCGACGTGGATCAGG	60.111	20
ATGGTTGCCTTTGTTTGGAG	59.971	20	CGAGAAGATCTTGAGGTCGC	60.096	20
CAACATTGCAAAATGGGACA	60.357	20	GCGTGGTGGGGATTTAAGTA	59.823	20
CCAATTTATTGGGATTAAGGCT	58.465	22	CAACCCCTGATAAGCAGAGC	59.836	20
TTACACGTGTGGGATATGGA	57.249	20	TTCCTTTCTTAAGCTTGTGAACT	57.936	24
GCAGCGCATCATCTTTTTCT	60.499	20	GTAGCCAATGAGTTGGGGAA	59.933	20
CACGTGAGGGAGGGTTTAGA	60.103	20	AGGTACGTTCCTGATCACCG	59.989	20
TGCACCGGTTAGAAGGGTAG	60.125	20	CACAAAAGGGCCTCTGAATC	59.67	20
GGCAATTGACCACCGTAAAC	60.235	20	ACGAATGCTTCGTCGTCTTC	60.406	20
GGGATTCAGTGATTAAAGCGTC	59.972	22	ATGAGCAGACTTGATGCGTG	60.016	20
CGTTTAGTGGTGCGAGGAAT	60.132	20	CCTCTTCCCCTTCAAACTCC	60.045	20
CACCAGTAGTTTCCGGTGGT	59.884	20	ATTCGTACACCCAATCAGCC	59.82	20
GGCGTAAGCAAATTTCAATCA	60.089	21	GCCACAGACCACAGTGCTTA	59.905	20
TGTTGCACTATTTGCTTGGG	59.729	20	CAAACCGCCAAATTCAGATT	59.938	20
GACTATGGCCCAAAACCGTA	59.823	20	AGCGTGATGAATGTCACGAA	60.272	20
AGGACATCGGTCTGAGAGGA	59.792	20	AATTAAACAAGCCCCTGCCT	59.966	20
GTGATCCATATAGCCGACCC	59.228	20	TTTTCCATGCACATGTAAGTTTT	59.822	24
GGTTCATGTAGCCGACCCTA	59.955	20	TTTGCGGGTAAATCGAAGAT	59.547	20
TCACAATCTCCCTACCCAGC	60.073	20	GGAGGAGAGGGGTAGAATGG	59.89	20
TGACAAATCAAAATAATTGCAAA	58.304	24	TGTAGCCGACCCCAATTTAT	59.297	20
ATTTGACTTTTCGTGCGAGC	60.395	20	GAGTCGGCGTTAAGTGAACC	59.74	20

TGCTTGATTAGCATTTTATGGG	59.132	22	CTGTCCAACCAATGCACCTA	59.566	20
TTGAGGAAGCCGTTGAAGAT	59.813	20	ACCTGATCGGTGCGATTAAC	59.962	20
CCTCCGAAAAATTGGGAAAT	60.123	20	CCATCCCATCATTCCATCTC	60.096	20
CTTTGCCTTTTCTGCCTCTG	60.125	20	TTCTGGAGGAGGTCGCTAAA	59.948	20
ATACGATCCATTTTGCCGAC	59.791	20	CTGCAGCATTTTTCACCCTT	60.249	20
AATCCTCAGTGCCATCAACC	59.934	20	TGCTCCTCATCCTCCTCATC	60.312	20
CAGGTAAGTCCGCCATTAGC	59.73	20	CATACCTCATCCCGCAGATT	59.917	20
TCGAGGCTCGGTCAGTATTT	59.836	20	CGTGGAAGGGTGACTTGAAT	59.966	20
TGGTCTCGCACAACACAGTC	60.951	20	GCTGACCTCACATATTGGGAA	59.947	21
AGCAAATAAATCGGCAGAGG	59.32	20	ACACCATTTTGGAGGGAGAA	59.381	20
GTCGAAGAACCTCGACAACC	59.703	20	GGTCGGGGAGAGTCAAGAGT	60.648	20
TGCTATTTTCATCTACCCACCA	59.474	22	TTCGTCTCCAAGGAAAAAGC	59.429	20
AAACGCCTAGCTCTCCACAA	60.015	20	TGTTTGTTGCTGCAGTTGGT	60.347	20
GAGAATTGGGTAACCAGCCA	59.933	20	TGTGTGTGTGTTGGTCGTGT	59.482	20
ATGCTTGGGTCAGTTGCTTT	59.74	20	CCCAAGACCCCAATTTGATT	60.91	20
GGCATGGTGCCATACCTAGA	60.884	20	TGCAAATACATCGAGCGTAGA	59.481	21
CAACAGCTTTCTGGTTCTCG	58.648	20	CCTTTGGAACAGGGTATGGA	59.784	20
TGAAGGAAAGGGATGGGTAG	58.978	20	TTTAGCTTCTTGCGGAGGTC	59.592	20
GACGAACTTTCGCTCGTCTC	60.142	20	CTCCGCCGGAAATTTTGTA	60.946	19
ATCTCGTGGGGGAAGACTTT	59.935	20	TTCACTGGGTTGCTAAAACTTA	59.613	24
GCATTTCCACGTTCAGAGGT	60.119	20	AGGGGCATAGCATAGCCATA	59.552	20
TTCAACACTATTCAACACGACTGA	59.715	24	ATTGGAAGGCAACTGCTCAA	60.776	20
GAATGGAATTGAAGCAAGGC	59.651	20	CCCAAGACCCCAATTTGATT	60.91	20
GGCAGTTGCCAATTCTTCAT	60.081	20	TGATCATAGGGTTCTTCGGC	60.036	20
CGGCAGTTAAGGCTCAAAAG	60.011	20	GGCAACACCAACAACAACAG	60.049	20
TGAAGGCCTTAAATCACCAA	58.214	20	TCTAGCTGTGAGATGTCTCTTG	58.903	23
ATCCATATACCGACCCCACA	59.894	20	TGCATCCACTTGGTGAGAAA	60.24	20
TTTAGGGGCTTTGTGCAATC	60.074	20	CCTTCCTTCGTCGATGTTGT	60.111	20
CCTTCCGTTGCAGTTTGATT	60.11	20	GCAAAGGAAATTCACGAGGA	60.192	20
CCTTCCATTTGAGGATTGACA	59.918	21	TGGTTCATGTAGCCGAAACC	60.894	20
CTGGGTAAACCCACGGACT	59.829	19	TGTCGTTTGCTCCTCTTTCC	60.375	20
GACAGAGGCCTTGCAAGATT	59.434	20	TGAGGTTTAACGAGTTCGCA	59.464	20
AGGTGCCGTTGATTATCTCG	60.096	20	TTCTATCGAAGACCGCATCC	60.177	20
TTCAGGTGTGATCAATGACAAT	57.922	22	CGGAAGTGATCACAAGGGTT	59.966	20
CTGAACGCATTTCCACTTCA	59.84	20	GTCCTGATTAGGGATGCCAG	59.508	20
TGTACACAGTGAGGTCATACTTAC	57.473	25	AGGGAAATTTGAGTGGATGC	58.984	20
GGTGACATCCACTACCTGCAT	59.866	21	CGTCGTCGTCGTCATCTTC	60.419	19
ATAATTCCCAGCCCCACTTC	60.152	20	TGTTTGAACGACTGCCTTTG	59.881	20
ATTCAAATGTGCTGCTGGCT	60.807	20	GCCGACCCATTACTAATCCA	59.784	20
AAATTAAGATGAGATTTGTCCTTC	59.826	27	CGGTATTCTCAAATGCACGA	59.688	20
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TTCTCCTCCTCTCGTCTCCA	60.064	20	TTAGGTGAAGCCAACATCCC	59.933	20
GCCATATCACGGTGGAAAAG	60.331	20	CGACTGGAGGAGGTCTTGAG	59.978	20
TGTAGCCGACCCCAATTTAT	59.297	20	GCATAGCAAAAAGAAGGCCA	60.343	20
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TTTACCCGATCTTGCTTTGC	60.209	20	ACTCCGATGACGATTGAAGC	60.226	20
CACCGGAACCAAAACCTAGA	59.964	20	CTCTCTCTTCGTTCATCCGC	60.096	20
GGTTCTCCAAATTCTTCCTCA	58.227	21	GAAAATTCAAAGATTTGGGGG	59.645	21
GGAATGGACGCAAGATCACT	60.081	20	TCCCTCCAAGATCCAGATTG	60.003	20
GTACATCTCCCAAGACCCCA	59.779	20	GTGCACATGCGGTCTGTATC	60.152	20
GGTTCATGTAGCCGACCCTA	59.955	20	TGTGGACCATGCATGCTAAT	59.955	20
AATGCTCAGGGGAGTCACTG	60.261	20	TGGCTGAGTTAGATGCCCTT	59.836	20
CTAGGGCGGACTACCATCAG	59.711	20	TTTGCAGCCGAACTACTGAA	59.609	20
ACCGTTTTGTTACCATTTTGC	58.912	21	ATGTAGCCGACCCCAATTTA	59.297	20
GGATACATGACACCCGTCCT	59.661	20	ATGACGACAAAGCTGAGGCT	60.02	20
AATCAAACCAACCCCAACAA	60.066	20	GATGCTAGCCGGAGATGTTC	59.803	20
CGCAGCGGAGAAAACATAGT	60.407	20	CAGTGGAAAGCAAAACCAAGA	60.269	21

CATCAAACCCAAACCAACCT	59.688	20	AGCTCCAAAACGCTGATGAT	59.843	20
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TTTGGTTCATGTAGCCGACC	60.894	20	TGGCATAACACTGAAGTGACA	59.245	22
AATTGAGAGGTGGGACGATG	59.927	20	GCCACAAAAACACTTAGGCAG	59.799	21
TCAACTTGGCGCACTGTATC	59.871	20	TCCAGTTAAACCAACCTCGC	60.11	20
CAATTTCTTTTTCCCCCTCC	59.75	20	AAAGAGAGAGAAAGGGGCGA	60.455	20
TGGTGCGAGAATGATTTGAA	60.197	20	TTCCATGCAACTTTCTACCAA	58.28	21
TCGTCACTTTCCTCTTCCTCA	59.974	21	CCATGCAAGGAATGGAAGAT	59.894	20
TCACGATAAAACAATTTTGGAAT	60.108	24	TCTGTGATGCAATGCGGTAT	60.104	20
GGACAGCGTAGGGAATGAAG	59.694	20	CCCGGGATTTCTAAATGGAT	59.978	20
GATGAATGGTTGGTCGCTTT	59.939	20	GAAGAAGAATCTGAGCCAGCA	59.708	21
AGATATGGAAGATGCGGTGG	59.917	20	GGCATCTGGAGGAAACAGAA	60.195	20
TGTAGCCGACCCCAATTTAT	59.297	20	AGGAAGTGAAGTCGGACGAA	59.844	20
CAGTTGCACCAAAATTTCCC	60.344	20	GGCGACTCACTTAAGGTTGTG	59.788	21
CAATCCGCCAATCCTCTTTA	60.031	20	TGTAGCACAATTGCCTCTGC	60.019	20
TGCCTGAGGTCTTACCCTTG	60.246	20	CCTAACTTTTATACCCGAAACA	58.616	24
CGTAATTTTCAACCCCAACC	59.178	20	TGCAAAACATTTCACCTAGCC	60.124	21
ATGGCAGTACATCGGAGCTT	59.723	20	ACACGATTAACTGCCTCGCT	59.904	20
GGCGTTTTCTAAGGCACAAG	59.883	20	CCCCAATTAGTCGTAGCCCT	60.332	20
ACCATGCGATGAACACGTTA	59.995	20	AATCCTTCGACGATGACTCG	60.218	20
AGTCACGGCCCCTTCTTAAT	59.962	20	CCTCAATTGCCACCAATTTC	60.309	20
TTCTCTGCCAACAATGAAATCT	58.836	22	AAAAAGTTTAGGGGCTCCAC	57.352	20
ATGTAGCCGACCCCAATTTA	59.297	20	CAACATGTGTGGAGTGGTCA	58.928	20
CATGCACCTCTTGAAGCAAA	59.988	20	ACGTCTCTCGCACTCCTCAT	60.017	20
ATGGAGAAACGAGCATTTGG	60.074	20	TGCAAATAGAAGGCCAGCTT	59.982	20
CCAATCAAATTGGGGTCAATA	59.511	21	TCCGGACCAAACTTTAATGTA	58.188	22
ATGAATATCCTTCGTCGCCA	60.435	20	GGATGAGCTGTTTGGAGGAA	60.195	20
ACTTGGGTTGTGCCAAAGTC	60.012	20	TTTCAAGCAAAATTTCAATTAA	58.814	24
CAAAACCAGGTCGCTCAAAT	60.11	20	CCAGTAATGGCATCCTTGGT	59.813	20
TCCGTTACCACTTCCTCCAG	60.103	20	CTTTGCTGCTGATGGTTCTG	59.591	20
CGAAAATAAGCCAACCGAAA	60.068	20	ATGTAGCCGACCCCAATTTA	59.297	20
CTGTTGCAGGGAAGGCTAAG	60.008	20	GTTAGGGGAGCTGCAACAAG	59.875	20
GTCTCAATGGGGACATCTGG	60.326	20	TCGTCTTAAAATGCAAACCTCA	59.758	22
TTTCCCATCCTTGTGATATGC	59.776	21	AATGACCGTCTTGATCGTCC	59.934	20
TGTCACCACTCCCAAACTCA	60.129	20	CCACCAGAAAAAGTGAGGGA	60.081	20
TGCCCTTCCCGATTATAGTG	59.916	20	TGTGACGTGAGGCTCCTATG	59.855	20
CCTCCGCTTAGGAACTCTCA	59.569	20	AAACCCATGCATTTGATTCC	59.628	20
TGCGATGGATTTTTCCTTTC	60.016	20	GAAGCCACATGGGAAAAAGA	60.051	20
AGGAGCTAGCACACCATCCC	61.585	20	CACTTTTCTCCCGGATACGA	60.066	20
AGGTGAAGCCCAGTCTGCTA	60.012	20	ATCAACTGTTGTTTCCCCCA	60.21	20
TGCCACCATTCTTTTGACAG	59.691	20	TGAGTTTTGGGAGCAAATTACA	59.625	22
GTGAAGATTAGCTCCGCCTG	59.978	20	CGGATTTACGGATTGGATCT	58.857	20
ATTCCACTTCATTGCACACG	59.572	20	CTGCCAACCAAAAACAAGGT	60.008	20
CTCTTCGAGCGAGTTCAAGC	60.419	20	ATCCTCAGCAGCCCAATATG	60.059	20
ATTGCCTGACGAATCGTTTT	59.574	20	AAGGGGAATGAAATGGAACC	59.996	20
ATGCTTTGTGTTTTCCTGCC	60.118	20	AAATGTAGCCAAACGCCTCC	61.357	20
GATTTATGTAGCCGACCCCA	59.784	20	CCGGTTCAGTGGTCATTTCT	59.966	20
AAACGGTTGGTCCAGAGATG	59.966	20	GCTGGCTGTGATAGGCTAGG	60	20
CTGCACTGTATCGGGAACCT	60.134	20	TGAGCAGGTGGAAAAGTGCT	60.975	20
TGTCAATGTTCTTCCCCTCC	59.903	20	ATTCTGTCTAGGCGCTGGAA	59.978	20
GTGAGCACCAAATTTATTATCGAA	59.44	24	TCAGCCCCAAATGAAGAATC	60.014	20
AAATGGTGTTGAATGGGGAG	59.647	20	AGTGGTCTTCCTAGGTGGCA	59.721	20
CTGCGGTACTTGCTCGGTAT	60.292	20	ATGGTTTGTGCCTGCAAACT	60.559	20
GACATGGTTGTGGTTTGTGC	59.862	20	TTAACATGGAGCAAATGGCA	60.073	20
AATTGCTTGTGTAGGGGTGG	59.853	20	TGTTCCTCATCATCCCGTTT	60.317	20
GGCTTGATCTTTGAGATGGG	59.629	20	AGTTGATTTGGATCAAGGCG	60.074	20
CCGCCATCATCTCCATAATC	60.26	20	GGAGCACTTCCGAGTTTTTG	59.853	20
GGAACCAACACAAACACACG	59.897	20	TCTTCTGGGTTGGACCATTC	59.903	20

TAATCTTGGCGCCTCACTTT	59.845	20	TGATGCTGCGGAGTCAATAG	59.972	20
GCCACATCACATCGAAAAGA	59.654	20	TGAATGTACATAAGCTAGATAA	57.484	27
CCACAGCTTCCCAAACAAAT	59.971	20	TCGGATGTCGTGTCCAATTA	59.924	20
TTGGAAACTCCGAAATCTTTG	59.188	21	CAAAAACGAAGAATGAGGCA	58.892	20
TCCATTTCGCACAAAAGACA	60.234	20	GACATCGCTTGCTTTCCATT	60.221	20
GGCATCCAATGCAACCTTAT	59.791	20	TATTTGAAATGCTGAGCCCC	60.038	20
ACGACGCCATTTACGTCTTC	60.14	20	AGACTGGTGTTGCTGCTGTG	60.096	20
CAATTTCGGGTGGTAAGAGC	59.569	20	AATCAATGGGCGGTGTAAAA	60.188	20
TGTTCATTCTCCCGAGTTGC	61.188	20	GGATACGCTGGAAATGTTGC	60.478	20
TTGTCCCGTCAAGAAAAAGG	60.081	20	TCAACTTGTTGGGTTGGGTT	60.246	20
TTCGCCACTGATGACAAATC	59.654	20	AAAACGTGGTCAAATTCAAGG	58.983	21
AAACGCGGTGATTTATCCAG	59.96	20	CCCAAGACCCCAATTTGATT	60.91	20
TCTGATCTCCGAAACCCATT	59.483	20	TCAACAACACATCGTCTTCCA	60.144	21
GGTCTTTCTGCATCTCCAGC	59.957	20	GGGTGACCCAGAAGTTTTGA	59.943	20
ATAGGGCTCCCTGCAAATCT	60.06	20	GCAATGGAGAAGCAGCAAAT	60.361	20
AGCAGGAGCAACTGTTGGAT	59.874	20	ATGGCCCTAAACACAGCAAG	60.132	20
CCCAAGACCCCAATTTGATT	60.91	20	AAGTGAAAGAATGGCGTGATG	60.125	21
CCCAAGACCCCAATTTGAT	59.59	19	TCTTTATCCCTGGTGTCGTC	57.58	20
CTCCACCACCACCACCTTAT	59.697	20	GGCGGTGGTGATTTGTAAAC	60.235	20
CAAAACCGAGAGCAGAGTCC	59.989	20	CAGGGAAATCCAATTCATGC	60.274	20
CTTGTTGCTCAGCACAGTGG	60.651	20	ATGTATTTGAATCGGCCAGC	59.929	20
TGGATTTGGGCAGAGAATTT	59.505	20	CGGGTTTGAAGGGGATTTAT	60.013	20
CAAGCCAACTTTGAGGAAACA	60.269	21	TGCAGTGAGATGCATAAGGATT	59.736	22
CCTTGCTAGGGCAGTACGAC	59.898	20	TGAAGGCTCATCCCAGATTC	60.158	20
TGGACATCCCGGATACTGAT	60.158	20	CCAGTCAGGCACTCCAAAAT	60.111	20
AAGCTCGAAAACAATGTCGG	60.249	20	GCATTCCTCAGAATAGCGGA	60.318	20
ATCTTCAGCAAACCATTCCG	60.074	20	GCCCATTAGCATTCCATCTG	60.435	20
TAAGAATTGAATCGCAGGGC	60.175	20	TGATTTCTCAGTTCCGGAGG	60.187	20
CTAGGTGTATGGCGGAGGAG	59.711	20	CGTTGAGTGTGTCTGGCAAC	60.357	20
CTTCTTCCCCTCCCAAACTT	59.548	20	ATTCCGATGTTTCACGGGTA	60.192	20
ACCTCTAGCCCGGTGAACTT	60.132	20	CTTCTTTTCAAGCACTGGGC	59.993	20
CCCAAGACCCCAATTTGATT	60.91	20	AAGGACACATGCTCGAAAGG	60.255	20
CGTTTTCTTTGATTTCCAAACAT	59.424	23	TGGGTAGGGAGTTTCACCAA	60.345	20
CCCAAGACCCCAATTTGATT	60.91	20	AGGGGAGCAAGAGGAAGAAA	60.319	20
AGCTCTCGACATCAAATCGG	60.362	20	CTCCTTGATTCTTGCACCGT	60.255	20
AAAGCAAAAGCATGGTTGGT	59.615	20	GTCAGGTTTCTGATCCGAGC	59.81	20
TGATGGAGATGAAAGTGGCA	60.201	20	TGCTCATCAACACTGCCTTC	59.992	20
CCGGATAAGCGATTTCTTTG	59.677	20	TGGAATAGGTTTCTTTGGAGAC	59.987	23
ACCCAACTTCCAAGGTTCAA	59.425	20	ACCAACATGATGAGTGACCC	58.186	20
GGGTACTCGTAGTCAACGCC	59.621	20	TCTTCGTCACTGCCGTCTC	60.13	19
GGGATGCATCAAAGTTGTCA	59.502	20	AACCATTGCACTCGAGATGAT	59.57	21
TTCCTTAGTCAAGGGGAAATGA	59.939	22	CTTGGTCATTTAATGGGATCA	57.415	21
GTGGCCATTCTGGAAAACAT	59.797	20	CCCAAGACCCCAATTTGATT	60.91	20
TTTGCGGAAAACTTTGAACC	60.089	20	TACAACCCAAAAACCTTCGC	59.975	20
CTCGGATTTAAACTCGACGG	59.702	20	AGTGCCAGACAATCCCAAAC	59.973	20
GGATCCTAAAATTTGAAGGGG	58.808	21	TTGGTTTATGTAGCCGACCC	59.823	20
TCCCTAGCAAAAGAGAGAGGG	59.963	21	GGGTTATCTATGGATCACTACC	57.813	23
CGAGCTGTAATTGAAAGGGC	59.845	20	GAGGAGGGGTGGTTTGAGAT	60.314	20
GCTATTGAGCAATATCAGAAACCA	59.67	24	TGTAGCCGACCCCAATTTAT	59.297	20
GCAACGAACCCCAAGTCTAA	60.11	20	TGCACATCATGATTTCGTTTC	59.538	21
GATTGCTCTCGCCTCAACTT	59.579	20	CCCCGTGTAAAATTCATTCG	60.181	20
ATGTAGCCGACCCCAATTTA	59.297	20	GCCCGAATGTAGATCTGCTC	59.803	20
TGATTCTAAAATGAATCCAATCCA	59.693	24	CTCGAATCAGTTACCATCACCA	59.993	22
GCCGACATGACCTTAGCAGT	60.285	20	AGAAAATCCGCATGCAAAAA	60.568	20
TGCACATTTCAACAGCAACA	59.877	20	AGCTTCTGGTGCAGCTCTTC	59.898	20
ATGGGCATGAACACATTCAA	59.781	20	ATCGCTCACCGTAGCCTCTA	60	20
TCGTTAATTGGTTCCATTTTGA	59.341	22	AAAATGATTGCTTGGCTTGA	58.361	20
CCATGTCTTGAGAGTGGGGT	59.962	20	TTTTCTTTTTCCTCTTGTCATCA	59.307	24

GTGGAGACTTAGGTGGGGG	59.365	19	CACCCAAAAATCCTCTTCCA	59.903	20
TGCAGCTTGCTGCTGTTACT	59.958	20	ATGAAATTGGGGTGACTGGA	60.173	20
GTCATGCTTCTTGTTGGGAAA	60.103	21	GACCCCACATAGTGGGAAAA	59.647	20
CCGAAACGCCATTATAATCAA	59.812	21	TCTCTCATTCTCCATTGCCA	59.322	20
TTGTCAAAGAACACGTTCACAT	58.187	22	GACGGCGTCGTTTTCTTG	60.39	18
TACGGAGTGGATGGTGGTTT	60.232	20	GACGGTGAAGCGTTTAGCAT	60.278	20
CATCGTCTGAATGAGTCATGTG	59.165	22	GGTAGCCGACCCCAATTTAT	60.041	20
CAACCGAAATTTTTGGAAGG	59.424	20	ATGCAAACCACCACGATTTT	60.235	20
TGATCATATTCGGAGCCACA	60.033	20	TTAATGATCGTTCTCGGATGC	60.052	21
TATCACTTGCCCAGGGATTC	59.894	20	CACAGTCTCCTCAATGGGGT	59.962	20
TACTCTGCCGCCAAAAGTCT	60.015	20	GTAATTTCAGCGGGGAACAA	59.938	20
TTGAGCCACTTATCATCTTTCAA	58.888	23	CATGTGACACCTCATGCGA	60.273	19
CGGAGGTAGTTGGCATTTGT	59.993	20	TAAATATCCGATTGGCCCAC	59.621	20
AATGTAGAGCAGAGAGGCGG	59.598	20	TTTTTAGGCGTTGAAATGGC	60.075	20
GACGTCTTGCAAGTGACGAA	60.032	20	TGCAGATGTAGTAGTGGCCG	59.888	20
TCTCGTCACCCTACAAGCATC	60.27	21	ATCCAAGTCCATCTCCTCCC	60.278	20
TTGGGGTCGGCTACATTAAC	59.823	20	ATCCATCCTCAAGGGGTTCT	59.755	20
CCCAAGACCCCAATTTGATT	60.91	20	AAGCAAAAACTTCGACCCCT	60.11	20
AATCTCAAACCCGACAATGC	59.939	20	AGGTTGCGTACATCTGACCC	59.997	20
GCTGATTCTGCAGGTTTTCC	59.82	20	ATGTAGCCGACCCCACATAG	59.836	20
CAGCAAGATTGGGGGTATTC	59.387	20	TGTTCACCGAGCTCAGATTG	59.984	20
ATTCATACCTGTCCCGACCA	60.195	20	CCCATGTGACACTTCAGCAG	60.309	20
TCCACATGCAGAATCGGATA	60.033	20	CATGACGGTGAAAAATAGCG	59.182	20
CAACGTTACCAGCTGCAGAG	59.658	20	CCCAAGACCCCAATTTGATT	60.91	20
TCCACTACTCCAATGTCTGCC	60.126	21	GTTTTTGGCTGGTTTTGAGG	59.587	20
TCGGGGTGGAGTGATTAAAA	60.301	20	CGCACCAAAAGTTGTTTGTC	59.22	20
TCAAGTTTGAGACGTTGCGA	60.574	20	TTCATTTCCTTTGACTTGCG	58.892	20
GCATGTCGGTCGAATTGTAA	59.548	20	TTTTCAATATTTAACTGAATTAA	58.651	27
GGTTGACTCACACGTGGAAA	59.571	20	AGAGGGCCACAAACCCTATT	59.827	20
TCCAGTAAATCAACGAAACGA	58.28	21	TCGAGAGTTCGGATTTTTGAA	59.809	21
AGCTCGACTGTCTTTGGACC	59.455	20	CCCAAGACCCCAATTTGATT	60.91	20
TGTAGCCGACCCCAATTTAT	59.297	20	AGCTACCGTATGAAAGGGGC	60.471	20
ATCAACCACCCATCAGCAAT	60.203	20	CCCAAGACCCCAATTTGATT	60.91	20
ATGTAGCCGACCCCAATTTA	59.297	20	GTCATGGGTATGCAGGGAAC	60.203	20
GGTGACAACCGCACGTAAAT	60.817	20	TTGTGTTTTGAGCACTTCGC	60.035	20
GAGTGCAAATCCCAGTGCTT	60.263	20	CCCAAGACCCCAATTTGATT	60.91	20
TGTTATTTTGTGGGTTTGCG	59.462	20	AATGGTGTCCACTTTCCACC	59.679	20
CTTTGGAATTGGAAGGACGA	60.044	20	TTTTTGAGAAGGTTCCTTAATT	59.227	26
GGGAGAAGAGGGTATAGCGG	60.053	20	GATTAGCAAATTTCGGGACG	59.547	20
CAACCACAAATTTTTCAGCG	59.202	20	AAGAGCGTGCTTCAATCGTT	60.022	20
TGTATCTTCTCACGAGCATTGG	60.27	22	CTCAAAAACCAATAAATGAAT	57.774	23
GAACTGACGGGCAAATGATTA	59.952	21	TGCTGACAATGATATGTGTTCA	58.039	23
TATGCTACGACATCGGGACA	60.096	20	TGGCATCCAATCAACAAGAA	60.049	20
ATTGTTTTAATGCATCGGCG	60.831	20	TGAAATTTCGAGTTGGACGTT	59.601	21
TGTAGCCGACCCCAATTTAT	59.297	20	TGGCCAAATACCCGAATTTAT	60.385	21
GAACCTTCGGATTGGTTCCT	60.306	20	ATGTAGCCGACCCCAATTTT	60.562	20
CCAAAAATGGTTGAGGGATG	60.162	20	TGGAAGTTTTACGAGAGCCG	60.378	20
ACTCTCCAAAATGGCATTGG	59.933	20	AACCCAGCGTAGAGGAGGTT	60.132	20
AATCATGAAAACCGAAACCA	57.916	20	TTCGCGACAGTCAAAGAAAA	59.585	20
ACTACCACGCCAATTATGCC	59.851	20	AGCCGACCTCACATAGTTGAA	59.749	21
AAAAGAAAGAACCGAACCCG	60.455	20	TTTCTGCCCGTGGACATAGT	60.517	20
TAGCTGACATTCTGGCTCCC	60.362	20	TAATCCCCCGAAATACCCTC	59.978	20
ATAACACTCGAACAAGCGGC	60.278	20	GAGGAGTGATGAGGGGTTGA	60.048	20
ATGCTCCTCAGTTGTGTCCC	60.12	20	TGGGGTGATTATGGTGGTTT	59.91	20
TGTACCACCAATCTCAATTACCA	59.257	23	ACACTTTCGAGATATAAATTCA	57.327	27
CCAGCAGTTGGCTCTATTTTT	58.528	21	TGTTTGATGTTATGTATTTCGTA	58.454	27
AGTTTTGGCCGGAATTGAAC	61.21	20	TGGTTGCAAGTCTTTGGTTG	59.734	20
CATTCGGGAAAAAGGATCAA	59.872	20	TTCATCGCCGTAGCTAATCC	60.196	20

ACGCGTTAGAAACGTACGAA	58.515	20	TTTCCTTTGACGTGGGAGTC	60.088	20
ATCCGAATGGATCAAAGCTG	60.036	20	TCCTCGCTCTCTCCTCTCAC	59.817	20
TGACACAATTCGTTCTGCAT	57.671	20	GCACGTGCGTAGAGGGTAGT	60.343	20
CACCCTGAGATGACGAACAA	59.676	20	AAAATGACATGCAAGGAAAAA	57.299	21
CCCAAGACCCCAATTTGATT	60.91	20	GCCGAACAAAGCAAAAAGAA	60.356	20
TGTCCGGCAGAATACAAGGT	60.517	20	GTCGATCTTTACGACCCCAA	59.933	20
TTCAGACGCAGCAGAACTTG	60.324	20	CCCAAGACCCCAATTTGATT	60.91	20
TGTTTTTCGGCAAGCAAAAT	60.599	20	ACTAACTGAGCTTGAGCGCC	59.786	20
AGCAAGAGGCATGTTTTATTTGA	60.141	23	TTTCACCTATGCATTTGCCA	60.073	20
TGAAATTTGGGGGTGTGTTT	60.066	20	ACATCATGGCCTCCAGATTC	59.893	20
ACTTTCTGCGGCAGTTCTGT	60.058	20	GGAATTCTCCAATGCCAAGA	60.014	20
TGTAGCCGACCCCAATTTAT	59.297	20	TAGTCACACCAGCATTCCCA	60.112	20
CGAAAACTCAATGGGGAAAA	59.91	20	TCGATTAACGAAGTCTCTCCC	58.398	21
TGGTGCTCCAAAAATTGTCA	60.088	20	ACCATCAGAGCACGACAAAA	59.293	20
CCGGAGCCATAATTAGCAAC	59.569	20	CAACAAAACCCCAACTCAGG	60.38	20
TGAGATCAAGAATTATGGCAAGA	58.844	23	TAGCACAACTCCGCAATCAC	59.871	20
TCGAAAGCTTCACAACATGC	59.995	20	CCCCATTAAAACAATGGTTACC	60.214	23
CTCGTAGCTTTGGCTGCTTT	59.791	20	GCCTCAGTTTTCAGCTTTGG	59.993	20
GCATATGGAAGAGCGGATTG	60.574	20	ACCTACTAAGGCCTTCCCCA	59.955	20
CTGAGGCAGCAACTTCAGTG	59.77	20	TCCGATACCCTTGGATCTTG	59.887	20
GTGTGGAAAAGGGAGTGCAT	59.973	20	CCAAAGACCTAAGGCACCAG	59.728	20
GAGTTGAAAGGCATGCAAGA	59.002	20	TGTAGCCGACCCCAATTTAT	59.297	20
TGTAGCCGACCCCAATTTAT	59.297	20	CAAGGCTCCCCTTCACAATA	60.066	20
TCCAAGCAAGCACATTTTTG	59.849	20	TGTAGCCGACCCCAATTTAT	59.297	20
ACCAACGAAGCCACCTATTG	59.993	20	CATACCCTTCACCGAGTGGT	59.844	20
TTGTTTGGTTCACGGTTTTG	59.459	20	TCCAATCTCAAGGGGATGAG	60.003	20
ATCACGAGTCAAGAATGGGC	60.081	20	TGCATGTTGATGTGTCTGCT	58.816	20
GGCTTAAAGACAACGGTGGA	60.11	20	CCGACCCATCTACCAAGAGA	60.065	20
CAGTCTCAGGTGCGTCAAAA	60.025	20	GGCTGATGGATACACCGAGT	59.957	20
GAAACATATGCACCTGCCCT	59.962	20	AAAATTTTACTGGGGCGGAG	60.305	20
CGAATGACCAGCCAAGAATC	60.603	20	ACCCTATGATTTCCATCCCC	59.843	20
TTAGCAGGTCGGGTTTTGAC	60.11	20	AATGCTCCACCCAATGACTC	59.934	20
GGTGAGGTCTGGTCAGGTGT	60.006	20	TGCATTTATTGGACGCAAAA	60.074	20
CACAGATGAGATGAGGCTGG	59.367	20	TTTTCCAAGATGGGTATTCG	57.551	20
TACCAGATCCCCCAGTCAGA	60.465	20	CGACAGGGAGTTCCACAGAT	60.112	20
CACGTGTACGTGCGTTCATA	59.226	20	ATTGGTTTGAAATTACGCGA	58.161	20
TTAAACCTCCACCAGTTGGC	59.971	20	CTCCACCTTTTCCCTCACAA	60.081	20
TGTGGCGTTGTAATAGGAGC	58.799	20	TTAACTGGCAGAGCAGCCTT	60.154	20
ATGTAGCCGACCCCAATTTA	59.297	20	ATCGACAAATGAATCCCCAA	60.133	20
AACGAATGTCACATCAACCG	59.42	20	ACGACCAATTGCTTCGTTTC	60.118	20
GCGTCCTGGCTTCTTTTATG	59.845	20	CAGCAAGATGAGATCACCGA	59.942	20
AGTTTACCGTCTTCCGAGCA	59.875	20	TTCACTACATCGCTGCATCC	59.83	20
GATCCTCTGGGCCAAATGTA	59.894	20	GCTCCATCAATGTGCTTCAA	59.805	20
GATCCGAAATGAAAACCCAA	59.739	20	CATCCCAGAACAAGGACCAC	60.363	20
ATCCACCAAAATCATCCACC	59.464	20	CCAGATCTACAAATCCCCCA	59.744	20
GGTCCTGGGTTTGGGACTAT	60.052	20	ATTGTCCTCACCTCCATTGC	59.934	20
TTCGATGTGCAGATGAGGAC	59.794	20	AAGGAAGGCCTTAGTTGGGA	60.068	20
TGCATAGTCACCACCCTTCA	60.112	20	CTGAGAGAAGTCTGGGAGCG	60.275	20
CTAATTAAATTCACGCGCCG	60.583	20	TGCCTAGCTTGTGTTAAATTGC	59.45	22
AACAGATGGCCAAAAGCATC	60.081	20	CACCGTCTCATCGACAAATG	60.112	20
TCAACTTTCTTTCGAGCTGC	58.379	20	CACATTTGGGGTTGTGAATG	59.667	20
ATGTAGCCGACCCCACAGTA	60.397	20	TGACAATTAGCAACCCACCA	59.964	20
TAATCACAGTCGAGTCCGCA	60.413	20	CGAACTTCGTGACGTGAACA	60.906	20
GGCAATTAGCCAAACCATGT	59.829	20	GTGTTGAGTAGGGTGGTGGG	60.275	20
TTGTAAAACACCCCAATTTGATT	59.528	23	GCACAACAATGATTTTTCAGTC	60.032	23
CGCCAACCCTCCTTCTTTAT	60.443	20	TGAATATTTAAAGGGATTGTTTA	60.006	26
CACCTTAGGTACCGCTCGTC	59.757	20	CAATGACAAAGGAAAACGATG	59.975	22
TCCAGCTGTTCTTCCGAAAT	59.813	20	ACCGTAAGGTTGCGAACATC	60	20

TCCAGGAGCCAAGAAAGATG	60.331	20	CCCACTTGCATTCTCCACTA	58.722	20
ATGAAATGAAGCTTCCACCG	60.074	20	GGACGGTGTTGTACGTGATG	59.88	20
GGAGAGAGAGTGGAGTGCGT	59.585	20	TAAAAGCAAAAAGGGCATGG	60.068	20
TAGAAGCCCATGGAGGAATG	60.029	20	CAAGATTGGTTTGTGCATACT	58.688	23
GTCGAATCCACAGGGATGAT	59.744	20	CCCAAGACCCCAATTTGATT	60.91	20
CTGTCACGTGTTGCAGTCCT	59.94	20	TCTAGGGGTGCTTCTGCTTC	59.574	20
CCAAGCCAGGTTTGTTCTGT	60.149	20	CAGTTCTTTGCCTTCCCTTG	59.846	20
AAACCTTAGGCTTCCTTGGC	59.725	20	TCCGATAGGGGGAGGATTAC	60.11	20
TCATGGAGAGAGGAGAGGGA	59.871	20	ATCATCAGCACCCACTGTGA	60.121	20
GGCTTAATACGTGTGTTGCG	59.254	20	GAAGGACCGAGTTGCAAGAA	60.375	20
GGTTCATTTAACCGACCCAA	59.662	20	CATGTTAAACAACCCCACCTT	58.73	21
GTGGGCAATCTTGTTGTGTG	60.008	20	CATGATCACCAATTTGCTCAAT	59.829	22
GGTAGCACTGCATCTGTCCA	59.862	20	TGGATTCAAACCCTCTCCAC	59.903	20
TCAAACAAACAAACCGGTCA	59.981	20	TGTGAAGAACATCGATTATCTA	58.142	26
CCCAAGACCCCAATTTGATT	60.91	20	ATGTTTCTGTTCAACCCCCA	60.21	20
CGTTTCTTCATCATCATCCG	59.075	20	GGAAAGATCAAATGGGCAAA	59.878	20
ACACCAAAATGCATGAGACG	59.572	20	TTCACGTGTGCTATTTCGGA	60.257	20
CACTGCTCTCACCACGATGT	59.897	20	AGCAGCAGCCTCTTCATCAT	60.127	20
CCCTTCTTTTCAAGCACTGG	59.846	20	ACCTCTAGCCCGGTGAACTT	60.132	20
TAGATTTGAACGACACCCCC	59.79	20	TTTAAAAATCGGACCGGAGA	59.52	20
GGCTGGTTGATCTTAGCACG	60.796	20	AAAAGCGAAGAGAGCGAATG	59.73	20
TTGCAGCAGTTCTTCTGGTG	60.175	20	ATCGAATTACCCGTTTGTGC	59.829	20
TGGAAGGAGAGACGGCTTAG	59.569	20	CAATCGGCCAAAATGTATCC	60.153	20
AAACGCCCTCCTTCTCTAGC	59.983	20	GAATTCTCCCACCATGCAAT	59.756	20
TTCGGTCCGATTAATCAAGAAT	59.808	22	AGCTGAATCCACGACAAGGT	59.727	20
AGGCAAAATGGTGATTAGCG	60.096	20	ATGGAACAGTGCGACAAATG	59.572	20
CTCGCATCTTCTACGCCAAT	60.374	20	CTGCTCGTGGAGAAATCCAT	60.218	20
TTTTCCGAGCTTGTGTTGTG	59.881	20	GCTCCTTGTCGTGAGCTTCT	59.751	20
TGCAAAATGGATTCAGGTCA	60.049	20	CGCATGAGGGATAAAATAATCA	58.96	22
TGTAGCCGACCCCAATTTAT	59.297	20	TCAAAAGGCAACATCCATGA	60.049	20
ACAAATGCGATTCAAGTGACC	59.992	21	TGGTGTAGATTAACACAACTTG	57.939	27
TTTCGGACCATTGATATCTTTTT	58.914	23	ATGTAGCCGACCCCAATTTA	59.297	20
ACAACAATATGGCCAAGGGA	60.192	20	TTATGGGAAGGAGATGCAGG	60.029	20
AAATGAACGTATGGCCTTGG	59.823	20	CTGTTTTAAGACAAGGGGCG	59.741	20
AGAGGAGGAGGCTAAGCGAC	60.117	20	TCTTCTTCCTGCCTCTCTGC	59.827	20
TGTTGATTGGGAATAATTGGG	59.511	21	CCACGGTCATTTCTAGGGAA	59.926	20
TGTGGATGAAGATGAAGATTTTG	59.077	23	CGCCCCTTGATTAACATCC	60.281	19
GATGGTGTGACTGAAAGCCA	59.682	20	CCCTACCCTGAATTTTTCCC	59.639	20
GTTGGCCCTCCAAACCTAAT	60.187	20	GGGTCTTGTGCCAGGTAGAC	59.579	20
ACACAACAAAAACAATAAAAGGC	59.856	24	TCAAAACAGGGGATTTGAAGA	59.532	21
ACTCAACACGGCCTGGATAC	59.997	20	AGAAGGGCCTTGTCTTCCTC	59.817	20
TCTCCTTCCAACACCCAAAC	59.943	20	TCGCCGGAGATCTTGTTAGT	59.836	20
CGTCGTCCTTTTCTTCAACC	59.711	20	GAATCCCTACCTCAAGGGGA	60.264	20
AAGGGGATGAAGCTGGAAGT	60.074	20	GAGCTGCAACTAAGGCCAAC	60.022	20
ACCCATCTGACGGACAAAAG	59.966	20	TTTTAATCACTATACCCGATTTC	58.455	24
AACGTCATTCTGGCTTGGTC	60.119	20	TCCAACGAGTGAATAAAGATG	59.229	22
TTACAGTGGGCAGCAGTTTG	59.904	20	TGGGACCAGAAAGATGAAGG	60.042	20
ATGTGGAGCCACACATACGA	59.992	20	AGAGAACAAGTGGGTGCTCG	60.444	20
ACCAGTTGTTGAGTCTGCCC	60.159	20	ACGATGATTCCTCCGATGAG	60.034	20
TTCAACACACCAAAACACCAA	59.889	21	CAATCTTGCACCACATTTGC	60.119	20
CTTTATTAAAATTTCTTTCACCAAA	57.99	27	CAATTCAATCAGGGTCAGGG	60.309	20
ATGTAGCCGACCCCAATTTA	59.297	20	CGAGTTTATGACCATCCGGT	59.813	20
CTATTGGGCCGTACCTCTCC	60.836	20	GGGTGAACCTTCCATCATTC	59.192	20
ACCATGCCAGACTTTGGTTC	59.973	20	GCACAGATTTCGAGGTAGCC	59.843	20
TTGCAAATACCTAAAGGTTGGG	60.225	22	CATAGTTGGCCTGGAAAACG	60.493	20
CCTACCCTCCTCAGGGTTAC	57.585	20	AACCGTCGGAATTACTGGTG	59.853	20
TTTTGCATATCTCCATTCGGT	59.424	21	GTTCACACCCGAATCCAAGT	59.827	20
GCTTTTCAGGGAGTTGGTCA	60.232	20	CCACATCATGCAAGGCTTTA	59.688	20

ACCCGCAAAAACACAAAAAG	60.011	20	ACTTGACATGATGGGGGAAG	59.779	20
TTTCAATCACTTTTTCTCGACG	59.379	22	TTTCACCCTCTGGAAACTCG	60.224	20
GCTCGAATATGCAACGACAA	59.839	20	GCGAATGCCCTTTGTAAAAC	59.592	20
GAAGGGAAGCATTCCAAACA	60.051	20	ACGCCTTTGCTGGTGTTTAT	59.637	20
ATGTAGCCGACCCCAATTTA	59.297	20	ACGGAGAATGGAGATTCACG	60.073	20
TTATGGGGGACCCTATCTCC	59.974	20	TTCTGCTGCTTCATCTGCAT	59.704	20
AACCGTTGATATTTGGCCTG	59.823	20	TCAGTTCTTGTGGTTGTCGG	59.72	20
AGTATGGGCATATGGCAAGG	59.807	20	CCAAAAAGAGAGGCCAACAA	60.22	20
TTGGGTGTGTGAGTGGTGTT	59.89	20	TGGGTTTATTGATGCACCTG	59.395	20
TCAAATAGCCGATTGCATCA	60.179	20	TCATCAAGAGATTACGTTTTAT	57.281	26
GTGAAGTTGTCAATTCCCCG	60.353	20	AGCTGATATCGGGCTTTGAG	59.434	20
CAATGTCTGGTTCGTGTTCG	60.152	20	TCGGAGGAAGAAGACGAGAA	60.065	20
CGATGGATAAGGCCACTTGT	59.955	20	AAAACAGTGGGGGAGAAACC	60.204	20
AGGTGGCGGTAGAGCTTTTT	60.262	20	CGCATGTCATCACTCGCTAT	59.854	20
ACCAGCATTTCCATCTCCTG	60.073	20	CCACTGTTGCTGCTGCTAGT	59.264	20
TGCGATCTAGAGTGTGGTGA	57.914	20	CTGGGTAAACCCACGGACT	59.829	19
CGGAAGACCAGAGGTGAGAG	59.978	20	CTCCAAATCCCACCAAGAAA	59.903	20
CGAGAATTTCCTCGGATTCA	60.148	20	TGATACGGGGGTGTTAGTTCA	60.234	21
TAGTTCAGGCGGCAATTCTT	59.845	20	TCCCTCGAAGGTAAGAGCAA	59.948	20
GACAGCATTGCTTTGCCTTT	60.395	20	CGCTTGGTCTTCTTGACCTT	59.473	20
TCAACTCATGCAAATGCAGC	60.969	20	ACGCACTTAGCAAGGAGGAA	60.015	20
AGCTCCGGAGTTTTGAATGA	59.813	20	AAAAATAAGCGCCACGTCAC	60.138	20
ACCTCACATGGTGGGAAAAA	60.21	20	TTGGAGAGAAGGAAGCAAGC	59.694	20
TCTCGAGCAGCTCACTGAAA	60.008	20	ATTGGAATGTGAGAAACGCC	59.939	20
TATTTTAACCACCGCACACG	59.486	20	TCCGTACACCTGGAATCCTC	59.927	20
AACAAAACCCGGATTGACAC	59.694	20	TCGTGCCTGTCCTAACAATG	59.716	20
CCCACTCCCACTTCTCAACT	59.149	20	CCAACACTTGTGCAAACTTCA	59.79	21
TTTATCGCAAGAGACCCACC	60.074	20	ATTCGATCGTAAAACAGCGG	60.096	20
TTGAATCCTCAGCGTGCATA	60.366	20	AGCCCTGTTACATATTTTCCCA	59.737	22
TGCAAGGGTTTGAATAAGCC	60.074	20	TGTTCCTCAAGTCGACAACG	59.873	20
CACAACTTGATCAAAATTGCAGA	60.159	23	CTTTCGCCCCCTATTTCTTC	60.034	20
TGTAGCCGACCCCAATTTAT	59.297	20	TCTGCTAAAAATATGATGAATG	60.008	25
GAGTCAGGGTGAGGTCGAAG	59.835	20	AATACGACGAGGCGGTTTTA	59.609	20
CCTGAAGCTGTCCCAGGTAA	60.246	20	CGAACAATTTTCAAACGGCT	60.11	20
ATCCAAAGGGCTTGCTTCTT	60.208	20	TGCAGGAACTGAAGCAGATG	60.136	20
TAGATGCCTGTTGGGGTCTT	59.55	20	GAGCAGTGCGACAAGCATTA	60.165	20
ATCCTGAGTTGCACACCCTT	59.579	20	AGTGATGGTGGTGGTGATGA	59.801	20
TTGATTTGAAATTCGTCGGG	60.807	20	AAATAGTACAGTGGGTTTTGCT	59.023	25
TGTAGCCGACCCCAATTTAT	59.297	20	TCCACTCCGTCTTCTTTTGG	60.224	20
CCTCTGGAATGGGAGTTTCA	60.042	20	TTTGATTGGGAATAATTGGGT	58.163	21
AAAGTTTAAAACCTGCCGGG	60.336	20	CTTCAACTTGGCGCACTGTA	60.05	20
TTCGTTTTCCCTCACAAACA	59.145	20	GCGACAGCAATCCTCTACCT	59.459	20
ATGTAGCCGACCCCAATTTA	59.297	20	CTAATGCAGGTCACCAGTCG	59.314	20
GATGGAATCCTGTCCTCTGG	59.46	20	CCAATTCAAGTCAGTGTTCCTT	59.552	23
GTTCCGGCCCTTCAATAATC	60.642	20	CAGATGTACGCAACATTTCCC	60.38	21
TTGGTATTTTGGCTACCAATTTC	59.306	23	AATGGGCCAACTACAGTGAA	58.076	20
TGCAGCTCTTAACTCTATCGGA	59.271	22	TGGCCGACGTTAAAATATGA	59.029	20
GCAATATCAATGTAAGATCATATT	57.778	27	AACATTCGTGGCATTTGGTT	60.235	20
TGTTCCCGTGGTATGTTTTT	57.85	20	TGTGGCAAGAGTCCATTGAA	60.24	20
TAAGGAGGCGAGAGAATGGA	59.91	20	ACCGGTTTGTGAGTGGTAGC	60.035	20
CATCTTAGGAAGTGCTCGGG	59.83	20	CTCCATCTCCATCCACGTCT	60.072	20
TGAATTTCTGAAGGTTGGTTG	57.715	21	AAAAAGTCCATCCCAAGAAAA	59.013	22
GAATTTGCTTTGTCATTGGGA	59.93	21	CCATCACTACCCACTGGAGG	60.377	20
TGCATTTCCAACACACACAA	59.563	20	ACCCTACGAAGGGGAGACAT	59.817	20
ACGATGCAACTGCACATAGC	59.902	20	TTTCTTGTCTGCATTCAGCG	60.134	20
TCCAATGCTTCCCTTCTTAATC	59.572	22	CTAATTTTACAAATTTAACGAG	57.347	27
GCACCCCTACAGCATTGTTT	60	20	TTGCTCGAATTCATCGTCTG	59.948	20
CTCCCTCCACTTTCTCACCA	60.229	20	ATTGGAAGATTTCGCTGTGG	60.074	20

GCATTGCTTGACTGAGTTGC	59.602	20	GTTCCTATGGTTGTTGGCGT	59.859	20
TTTTGTTACGGGAATAACCCA	59.218	21	GGAACCAAATTAATGGAGGAA	59.207	22
CCCAAGACCCCAATTTGATT	60.91	20	GCATTGAATCCCTACTTGGC	59.533	20
TGTCTCGACGGACTGACACT	59.442	20	CAACATCAAAAGTTTTCCAACA	59.793	24
GGAGACCTAAGGATGCACCA	60.073	20	ACTCGAGCGATTCAACTTGC	60.547	20
TTCAACAAGCCTTCAGTGGA	59.415	20	GCCTTCATCATCTTCTTCGC	59.923	20
TGGGTAGCTTACAAGTCCAGC	59.392	21	AGAGCGGAAACAGAGCACAT	60.02	20
TCATCATCTGGCTTTGTGGA	60.201	20	TTCTCCACTCTCCCCTTTTT	57.827	20
CCGCTACAATCTTTGGTGCT	60.27	20	AGGACAGTTCACATGCAACAAT	59.525	22
TGAATCAGAAGAGAGTTTGCCA	59.993	22	TGCACGATTTACGCATTGAT	60.103	20
ATTCAAAGCATATGCCCTCC	59.001	20	GCCATGAGGGGTAGAAATCA	59.894	20
CGTGTTTGAGTTTCTTGTTTGG	59.688	22	GTCCAATCATTACCCTTGGC	59.249	20
CCGTTTCTCCAGTTGACGTT	60.149	20	TCCTACGCACTCCCATTCTC	60.218	20
AACCTAATCCATCCCAACTTTT	57.96	22	ATGTAGCCGACCCCAATTTA	59.297	20
TAGAAGGAGATGGGTCCTGC	59.239	20	AGTGTGCAGGGAGACTGGAC	60.315	20
TGAGAGGTGACAAACAGCGA	60.593	20	TTCAAGTTTTGACAATGGGC	58.599	20
TAGCTCATCGCAGGTTGGAT	60.765	20	ACAGGAAAAGCAAAGCGAAA	59.996	20
GTTAGATTGGACCCCATCCC	60.388	20	GGTCCGTCTATGTTCGGAAA	59.933	20
TTGTCGAATAATTGACCGCA	60.073	20	AACGGCGTTTTGAATACTGG	59.996	20
GCTTTCGTGGTTTCGAGTCT	59.478	20	AAGGTCAAGTTCACACCAAACA	59.538	22
CGCAACTCAAACCCGTTTAT	59.996	20	GCGGAGAAATCTTCTTGTCG	59.955	20
GAATAGCCAGCAACTCCTGC	59.985	20	GCAAGAACACATGGGGAAGT	59.973	20
GCATTTCCGTGCAACAACTA	59.735	20	TGGGATTAAGGCTTTGGTGT	59.429	20
ATGTAGCCGACCCCAATTTA	59.297	20	ACACAATCAGCACAGTGCAA	58.871	20
CAAACCCACCAACAAACAAA	59.313	20	GTCTTCTGCGGTTTCTCTCG	60.134	20
GTGGCGTGTTTTCCAGAATC	60.504	20	AGACCTTGACTCGCAACACC	60.307	20
GTCTTTCCCACCCTCCATTT	60.169	20	AGGGAAGCTCTTCGTCATCA	59.95	20
ACATGAGAGCCTTGCATCCT	59.834	20	ACAATGCTTATGTTCCCTCCC	60.201	21
ACAAACGATTTCCCGTCTTG	59.971	20	TGGTTCCTATGTTGTCCCAA	58.821	20
TCACGACGGAAACATGTAGTG	59.624	21	GGGCTTTCAAGCTATTGCAG	59.982	20
AAGAGAAACTTGACGAGCGG	59.615	20	CCGTTTGGTCTTGGAAACAT	59.83	20
TCTTGATTGATCTTGGTGCG	59.799	20	ACGAGCCATTGTTGGATAGG	59.955	20
GGGAGTGGGTTATCGGTTTT	60.053	20	TCAATCGATGAATTATGCGG	59.478	20
GTGGGGGTGATTTGTAAACG	60.088	20	CACCGCCTCCTCCTTATGTA	60.088	20
AGGGAAGTGGAAATAAGCCC	59.42	20	CCATTTTGCCATTCAAGGTC	60.309	20
TGCGAACAATCTCTCCTCCT	59.95	20	AGAAGGTGCCCTGTTGAAGA	59.844	20
TTGGTTCATGTAGCCAACCTC	59.985	21	TGGATGAACCGAAACCTCTC	60.05	20
AAACAGCTCCCATCATCAGC	60.226	20	TGGAGGCATCAATCTTGTGT	59.09	20
GGGAAATGGCTTGCATAAAA	59.907	20	GCGTCAGCTTACATTGGGAG	60.796	20
GGGTACAGGTGGATGGTAAGA	58.778	21	GGAGCCATGAGACTAGACGG	59.827	20
TCCTGTGTGGTGTGTGGTTT	59.89	20	TTTTGCAATTTTCATTGGCTT	59.595	21
GCCCACACAAATTATCGAGG	60.331	20	TGTGATGTTTACAAAACGATAA	59.314	26
GAATTGGAGGCGGAGGAG	60.703	18	ACCTTGTCCTGAACCACCAC	59.859	20
GCTCCTCTGTCCAAGTAGCG	60.156	20	AGTTTGGGAGGTTGAATGGA	59.381	20
GATGTCATCACCAAGGTCCC	60.184	20	TCCTCCACCAGCTTCTGAAC	60.386	20
GCCGAGGGTGATGTATCAAT	59.78	20	CAAGTTAAATCCAAACGGGC	59.451	20
ACGCCTCATCGTCAAAACTC	60.263	20	TCTAGATCCCCCTGTCCCTT	59.89	20
CTTATGCCAGGTTTTCTGGG	59.564	20	AAGCGCAAATATATCCCGTG	59.95	20
TCGCGAGTAAAACAAAAACAA	58.53	21	TTTCCGCCATTCTTGACAGT	60.636	20
AAAATTGTGGTTATTCGCCG	59.832	20	TTGCTTCTTCTCCCTCCTCA	60.065	20
TTTGGAATCTTCCCTTCCCT	59.875	20	CGTCTACGAGGACGTGCTAA	59.097	20
CGAATAGAGGAGGGAAAGGG	60.025	20	TCCTTTGTCAGGTTTGGCTC	60.232	20
TCGGCAAAACCCTTTTATCA	60.427	20	GCAAATGTCGTGTTGAGTGG	60.16	20
CGAAGGGACCACAAAAGGTA	59.964	20	ACTCGAAGCCTTGACCTGAA	59.989	20
GAAGGCAGTGATGGATTTGC	60.613	20	AGGGCAAGAAACCAATCTCC	60.443	20
TGCCAAGCTTATATTATTGGTGC	60.349	23	TTTCCTTGGGTAAATTGCGT	59.451	20
GCTAACGACGTAAGGCAAATG	59.793	21	TCTTGCCGGTACATACATGG	59.42	20
ACACCGAGTGCAACTTCCTC	60.307	20	GTTCTTGGTTGGGAGGTGAA	59.943	20

TTCTTCCACAGTTGGCTCCT	59.844	20	TTCAAGCAATTTCTGCCAAA	59.42	20
TTCGCTCTGTGTTTTCCTCA	59.566	20	CATCTTTACTGCACCACCAGA	58.787	21
CAATGAACTCCAAGGGGAGA	60.042	20	GCCACCATCTTTCTTTCTCG	59.813	20
GGTAATGTCGAAGAGGCTCG	59.836	20	GAGTTCCATGGACGGAAGAA	60.05	20
ATGTAGCCGACCCCAATTTA	59.297	20	AGTCATTCATTTCCCGTGCT	59.556	20
CCCAGACTGAGTTATTATTTGATC	59.335	25	GTGGGAAGTGGGCAAAGATA	59.933	20
TAGGGAAACCCCCAAAGTTC	60.159	20	GAATTGGCCTTGCTTGCTTA	60.343	20
GAATAGTAGCGGCTGCAGGT	59.504	20	CAGCATACCTAAACCTCCCTG	58.73	21
TTGATGTTCTTTGGGTGCTG	59.691	20	TTTGGACCAAGTCACACGAA	60.128	20
AACAATAATATCGTCCGCCG	59.816	20	TGCAAGTTTGAGCGAGATTG	60.134	20
AGCCACTGCTTTTGTTGCTT	60.059	20	GGATCCATCAAGCGTCCTAA	60.036	20
TCATGCAAGAATGAATGTCCA	60.065	21	GCAGCGTGTTAAAGTTTACGA	59.489	22
GAGATACCGATGTCCGGATG	60.303	20	TCCAGTCCCCATTCGTATTC	59.75	20
GGTATTTTCATCCCGCTCAA	59.901	20	TAGGTTCTTCATTGCTTGCG	59.062	20
AAGGGTTTCTTCAACCAGCA	59.711	20	AATTGCCAATACCCAATCCA	60.016	20
CCACAAATTCTGAAACCGAAA	59.961	21	AAAATGACGTGAAGTATGAAG	59.557	23
TAAACCCACTGCGTCTCCTC	60.255	20	GGAACAAGAGATTTCGCAGC	59.962	20
AATATGGCATGAGACGAGGC	60.066	20	AATCTGCACGGGTTGAGTTC	60.119	20
GGATCGTGTGTGGGATCAAT	60.61	20	TGGCCACCTTTATTTTCCAC	59.801	20
TAACCGAAACCTCAACCAGC	60.11	20	GCTCTGACTTGTTCTTGGGC	59.997	20
TCTGAATCCCTTTTCATCCG	60.006	20	GAGCGGGGCATTTAGGTAAT	60.3	20
CAGCCTTCCAGTTGGGATAA	60.066	20	CTGGTCAAAGGAGAACGTGG	60.68	20
ATCTCCTGTTCACACCACCC	59.817	20	TGTTACCGTTGCCGTTGTTA	60.029	20
CCCAAGACCCCAATTTGATT	60.91	20	TGGTCGAAAAGTACGCAAAA	59.344	20
GCGCAGAAGGTGTAGTCGAT	60.428	20	AGGAATCCCTCTTTCTCCCA	60.008	20
AATGTATATTTCGTTCTTTCTTGTT	57.286	27	TGCTGAGCTTAGGCTTAGTGG	59.799	21
GAGCACGTTGTGTTCCACAG	60.357	20	GGCTGGTGCAGTATGAGGAT	60.104	20
GATGCAGGGATACTGATTCCA	59.909	21	AATTCGCCTGAACTCCAAGA	59.813	20
TGGCAAACAAAGGATGTCAG	59.691	20	GGGACTGCTAAAGGCAAAGA	59.452	20
TGAAAGGATCCCATAATTCCC	59.971	21	GAGAACATGTGCAGTGTCGG	60.319	20
TGCTCACCCACATTCACATT	59.967	20	GCCGTCAAGGAGTCAAAAAT	59.174	20
CCCCATATCTACCCCCTCAT	59.859	20	CCCTCCGAACGATATGAAGA	60.029	20
ATGTGGTCACCTGGGGAATA	60.05	20	TGGAAATGTGCTTTTGATCG	59.664	20
CCTCGGATGAGTCGCATATT	60.059	20	TGTTCGGGTTTCACAATTCA	59.941	20
AAAATCTTGCCGCCTTGTTA	59.72	20	TTTTTCGAAATCGTGCACCT	60.617	20
GCTCCAAGTTACTGGCCAAA	60.249	20	AGGCTTGTTGACCGCTTAGA	60.015	20
CTCCACGTTTTAACAACCGA	58.673	20	AAAGTGTAATGGCGGTGGAG	59.993	20
CATGAGATGAACAAGGTTTCG	58.215	21	GCGAGTTGATGGTTTTGGAT	59.939	20
GCGGGGATTATTGTTAGGGT	60.041	20	CGACCTCCACTCTTCTCCAG	59.978	20
GGCATTATCAGAATTTGGCG	60.424	20	GGTTTCTGTGAAGAGCGGAG	59.989	20
GCTGCATTGCTTGAAATGTCT	60.41	21	AGGGTCCCTTCGTTTTTGTC	60.34	20
CCCAAGACCCCAATTTGAT	59.59	19	TCATTTCAGTTTGCACTAAGCC	59.406	22
TCCTTGGAACTCTCAATCCAG	59.269	21	TGTTGGTTCAAAACTAATCCA	57.617	23
TTTAACTTGTCCCCGTTGGT	59.331	20	CCTAGGCTCTCAGACACACG	58.621	20
CACCTCATCTTGCTTCGTCA	59.984	20	TGAAGTGGGTATGAATGCCA	59.924	20
GCAACGAAAAATACAAGCCA	58.819	20	CCCTCATTTGGGATCTACCC	60.517	20
CACAACACCACTCATCCTCG	60.154	20	GCACTCGGGATTACTTGAGC	59.843	20
TATTGGAGAGGGAAGCAGGA	59.767	20	CTCTTGGTACGTCGATGGCT	60.277	20
CCCAAGACCCCAATTTGAT	59.59	19	TCTGAACATGGGGAAAGACC	59.903	20
ATCTCGGGGTGCATTGTAAC	59.82	20	TTCACGATTCATATGTGCTTCC	59.967	22
CGCCTCTTGAATAACCTCCA	60.206	20	TCAAGTGGGCAAAGAAAAGG	60.22	20
CAGTGGTGAAGTCCCACCTT	60.002	20	CCCACGTACGATCTCAGGTT	59.989	20
CGAGGAAGACGATGTAACCC	59.55	20	TTTCGATCCCATGGAAGAAG	60.006	20
TAGCCGACCCCAACTTATTG	59.953	20	GAGAAGCTGATTGTGACCCC	59.661	20
TTCGAAGGAAAAGAAACATAAAA	57.25	23	TGGTGTTGATAACGGCCATA	59.809	20
ACTCGAAGAGTAGCGGTTGC	59.644	20	GAGCTGGCCGTAGTTTCCTA	59.476	20
ATCGTGGGCAAATTTGAATC	59.768	20	TTTTGCATGTGAAAAATGGTTT	59.385	22
CCGTCATGGCCCTACATTAC	60.214	20	TGAGGAAAATGGGTGGAAAG	59.903	20

GATTCATGTAGCTGACCCCAA	59.947	21	GCAATCTCTACAAGCGGGAG	59.978	20
CGAAGGATCAACTTCATAGTCG	58.858	22	AGCTGTGCATTATCACCTACCT	59.693	23
CCCCCACAACGTTATTCATC	60.051	20	GCAAGCATTTTCACCACCTT	60.118	20
TCCCCTCAAAGTTCAATGGT	59.381	20	GCCTGAATAACGAATGTTGGA	59.952	21
GCTGGTATCAAAACGCCACT	60.14	20	AAAAACAACAAACAACCACTT	58.621	23
GGTCATCAATTCAGGAAGCC	59.488	20	GTGGAGGTCTTCAGAGCAGG	59.986	20
CACACTATCAACCGAACCGA	59.566	20	TAGAAATTGAAATGGCCGGT	59.411	20
GAACCATGATCTGCCTGGAT	59.893	20	AAATTCACAGGGCCAATGAC	59.797	20
GTTGAAGCCAAGCGTGCTAT	60.416	20	TGAAAAACAGAATGGAGGGC	60.051	20
TGACAAATAAAAACCTACAAAAT	59.231	26	ATTTTAAATTAAGAGCCACCCA	57.337	23
AGAGGAGGACGAGCATGAAA	59.95	20	CATGTTCCTCGGAATCACCT	59.927	20
CATAGGGCAAGTACGGGAAA	59.953	20	GGCATGTTGACACCCCTATT	59.676	20
CACCGGTTTTGGATTTGACT	59.83	20	AAAACCAACATTCACCACCTT	58.331	21
CAAATTTAAGTGAGCTTTGCTTGA	59.957	24	AAATTTATTGGGATTAAGGCTT	58.94	24
GAGCGAGTTCTTGATCGGAC	59.957	20	TCAAACCAGATGACCCAACA	59.935	20
CTGCACACTTTGGTCCATTG	60.152	20	ATGTAGCCGACCCCAATTTA	59.297	20
CCGGAACTCAATAACCAAAGA	59.074	21	TACTGCATTTACTGCGCTGC	60.185	20
CCAAAAGTTGGGGAAAATGA	59.772	20	TGGAGGATTTGTATGCGACA	60.073	20
CATTCATTTCCAGGCCACTT	59.933	20	GGTGAAGAAAGCACCGGTTA	60.11	20
TTGGAATCAAGAACCCCAAA	60.28	20	ACCACTGCACCCTAAGATGG	59.989	20
CACATAGTGGGAAACGGCTT	59.993	20	TGAGATCCAGAAGGTGTCCC	60.048	20
AAACAGCAAGGAGAGGCAAA	59.993	20	GCTAAGGCTGAAAGCAATGG	59.982	20
GAGAAATGTTTCCGGCGATA	60.038	20	ACTTCGCAGTGGACCAAATC	60.119	20
GTGCAGAAAGGCAAAGAAGG	59.993	20	TTACGCTAGTCCGTGGGTTT	59.632	20
CATCAACATTCCTGGGCTCT	60.073	20	TCCTGAGAAAGCCGATGTTC	60.34	20
TTCCATAGCTGCTCCCAATC	60.177	20	CTCCATTCCCATCTCTTCCA	60.003	20
TTTGGTTCATGTAGTCGACCC	59.845	21	ACAGGCATAACCATTGCCTC	59.962	20
TGCACCAGTATTGAACGAGC	59.871	20	CCTGGAACCTTCTTTTGTGC	59.711	20
CAACCATGGCAGTTGACAGT	59.597	20	GATGAAAGGGAGGTTCGTGA	60.05	20
ATGTCCTGTTGATTCCGAGG	59.927	20	ATGTAGCCGACCCCAATTTA	59.297	20
CGTACGTTGTACGGGTTCAT	58.432	20	CCCAAGACCCCAATTTGAT	59.59	19
GATTTTGTTAGTCGCGGAGG	59.708	20	TTGCCTCCTTACACTTATTTATC	59.631	26
TCATCGGGTCTAGGTGTTCC	59.927	20	AAAATCACGAAGCTGATGCC	60.221	20
AGGACAGAGCATCATCGCTT	59.981	20	CCGCCTCTCCTCCTCTCTAT	59.935	20
TATTTCCGACAATTCGGTCC	59.762	20	ATCCATATAGCCGACCCCAC	60.931	20
CATTTCAGTTTACTGGGATTAAGG	58.223	24	GCAACACGCTTCATTACCAA	59.735	20
AGTTGGAACCTCGAGCATTG	60.255	20	TTGCAAGCTGATAGGTGTTCAG	60.44	22
TGTGGCGACATGAATTTCC	60.474	19	GCTCTCATGCGTACAAGCCT	60.569	20
CACCTCCACGTGAATGATGT	59.393	20	GCTCCGTCACTGCTACATAGTG	59.965	22
CGACGAGCATCAAGAAAACA	59.988	20	TATGACGACGGCTCTGTCTG	60.008	20
ATCATACACGTGGACACCTCA	58.869	21	TGTGAACGGCACGACATATAA	60.006	21
AAACAGAAGCAGAGGGACGA	59.989	20	GGGCATTTTCACAGACGATT	59.939	20
CTTCGCTTTCCCTTTCACAC	59.853	20	AGCGGAAGTACAAATGGACG	60.132	20
GCATTTGGCTTGTTAGGAGG	59.708	20	GCAACATCATCCAGATTGGT	58.36	20
CGAGGGAGGTGAGGGACTAT	60.468	20	GGTTGCCAAAAGAGGTTGAA	60.088	20
TGAGCTTCAGGAATGTGTGG	59.831	20	AAATATTGCCGCTCATCAGG	60.06	20
TGTCTGAATTTGGTGGAGGAG	60.096	21	GTACAGGCTGGCATCCCTAA	60.096	20
CTGCCTCTCCTTCTTGTTGC	60.134	20	TGGCCTACGTTACTCAACCC	59.993	20
TCATCAAACCCAAACCAACC	60.594	20	TGCTATGCTTGGAAGTTATGTG	59.793	23
TAGGTCTGAGGGTTGGATGG	59.92	20	TGCAAGAGAGCTTTGTGGTG	60.175	20
CGTTAAATGTCACGCGAATG	60.133	20	TTCCCTTGATTTTTCCTGTG	57.643	20
TGATTGCACCCAGTCACCTA	60.112	20	CCCAAGACCCCAATTTGATT	60.91	20
TTCCTTTTCTTTTGCTACCCA	58.862	21	CAGCACAAAACAAAATGCTGA	59.903	21
TATGGTTTGGTCCGATGGAT	60.014	20	TTGCCCCTAAATCCTAGCCT	60.055	20
TGGGTGATTGAGTTTCCTCC	59.903	20	CCCAAGACCCCAATTTGAT	59.59	19
TGGCCTAATCGTTCCTCAAC	60.074	20	TCAATTCTTTGGTCGGGTTT	59.406	20
TCTAAAGCCTCCCACGAAGA	59.948	20	AGCTGCCCAGAGAACTTGAA	60.134	20
TGAAACCCTAGCGAACCAAC	60.11	20	CTCTCTCCTTCAATGCCTGG	59.943	20

TCGTTGTTCCACACTTCCAC	59.571	20	GAGGAGCACTGTGAGCTATGT	60.081	22
CTCTGTAGGCTTCTCCGCAT	59.598	20	ACCGCCTGATGATTTTGAAC	59.939	20
TCTTGGTGGTTCTGGTAGGG	59.959	20	GAGAGCAGAAGGTGTAGGCG	60.156	20
CTCAGCAACTACGTGCATCC	59.47	20	GTCATGCTGCGTTGTGAGAT	59.87	20
CGGGCTCTTAAATTCATTCG	59.677	20	TAGCCATTGAAGCTGGAACC	60.214	20
TAGGACTAGGGAAAACGGCA	59.702	20	GCTTTTCGGAGGAGGAAGAT	59.789	20
ACTCCAACAACTCGTCACCC	60.009	20	TTAACGTGGGCGTTTTTCTC	60.11	20
TGGAGCAACTTCTTCGATCA	59.522	20	CCTCTTGTTGAGCTTCCACC	59.844	20
TGATCCATATAGCCAACCTCA	58.052	21	ATGGACTGTGGTGCTGCATA	60.144	20
CTTACCCTTGTTTCCGTTGC	59.609	20	TGGGCTAATAATGGAGCTGG	60.053	20
TGTAGCCGACCCCAATTTAT	59.297	20	GAATTCGGTAATGGCTGCAT	59.929	20
TGTAGCCGACCCCAATTTAT	59.297	20	GGGAATTGGGATGAAAAGGT	59.996	20
GGTGCAAGAGATTGGGTTGA	61.046	20	CCCAAGACCCCAATTTGATT	60.91	20
GACAGAAGCAGAAATCGGGA	60.34	20	AAACACAACTGGCATCCCTC	59.973	20
CGAGGACCAGATTTGCATTT	60.074	20	TGAGAGTACGCACAGCAAGG	60.199	20
TTTTTGATTGGGAATAATTGGG	59.895	22	AAAATAAAATATATATGGGGT	58.563	27
TTTTCTTGCAAAACGTGAGC	59.087	20	TTTTTGGATGGAAAAATGGC	59.751	20
CGAAAAGATGTATGGCGAAAA	60.082	21	ATGTAGCCGACCCCAATTTA	59.297	20
GGATTCGTGACTTTCAGGGA	60.05	20	CTACCACCGTAACCACCACC	60.149	20
ATGTAGCCGACCCCAATTTA	59.297	20	TGCACCACAAGATGGTGAAT	59.967	20
CACCAAAGCAAAAACATCCC	60.344	20	TTTTGAGGTTAGTTTGGCCG	60.103	20
ACAATTTCGGTTTCGAGCTG	60.249	20	ACTGCACCCCGAAATGTTAG	59.993	20
GCCATGAAAAACAAGGAGGA	60.051	20	CTTGTCGTTTCCCTTTTGCT	59.355	20
ACTGACCTTGGACTTCGCTG	60.444	20	TTCAGATCATCCACCCACAA	59.893	20
GTGAAAATCCTCCCTCGTGA	60.05	20	GATCACCACAAACTCCCAGC	60.52	20
ATCCGATATTCCCGGCTAAC	60.137	20	GAAGGATGACGCGAGAGAAG	60.096	20
AAGCTGCTGTTGCCGTAGTC	60.602	20	CAAATTAATCAATCTCCTCCTC	58.164	23
TCAGAAAGAGGAGACGGAGG	59.525	20	AGGAAGCTTTGCACCTTGAA	59.993	20
TCACAAGAAACGACGCTTGA	60.574	20	CTGAATTACGGCGTGGATTT	59.96	20
GGGAAGGGGGTACATGCTAT	60.039	20	AAGCTTCTGACTGAGCTGGC	59.898	20
GCAGCAGCAAATACAGCATC	59.602	20	AAAACACGTGTGGAAGGAGG	60.005	20
ACGACGCTGACAAAACTTCC	60.299	20	TCCACGTTAATATGGATGCG	59.401	20
AGCTGTCGATTTCTGCCACT	60.02	20	CAAGGTTCAATTGACTGCACA	59.749	21
TCACTCAGGGGCTTTACCAC	60.111	20	GAGGAGACGAGAAGCTGGTG	60.135	20
ATTGAATGCCAAAAGCTTCG	60.209	20	TTCAGACAATGAGGGCTGTG	59.831	20
ATGTAGCCGACCCCAATTTA	59.297	20	GGGTCTTGGGGGTTAGATGT	60.052	20
CCTCATGAGCACAATTCCCT	60.073	20	TGAGGATTCCTACCCAGTCG	60.065	20
TTTGGCCTCTCATGGATCTC	60.158	20	CAGAAAGTCACAAATGCGCT	59.076	20
CTGCGTCCAGCATTCAATTA	59.833	20	ATGTTGCATGTGAGGTGCAT	59.999	20
TCCCTTTTCAGAAGTCGCAT	59.813	20	ATTGTGCATGCATGTGGTG	59.977	19
TGATGAATGAATGGTTCGACTC	59.939	22	CATGTGGAAGTGTGGAATGG	59.806	20
AACTGGACCATATTCGTCGC	59.962	20	TTGCAAAATGACACACGAAA	58.728	20
CCAATATGTGGGGAAGAACG	60.184	20	TGCCACCAAGGAGAGTACAA	59.288	20
ATTCTGGCAAATCATCGGAC	59.9	20	GGGGATCTCATGGACATTTG	60.135	20
CACCACCCTCTCATGTCCTT	59.962	20	TTGCATGTCTGGAGCAGTTC	59.992	20
GAGGAAATCACGACGGTGTT	59.973	20	CTCGTCACAATTTGCTTCCA	59.84	20
TTTTTCATATTGCCCACACG	59.42	20	CCCAAGACCCCAATTTGATT	60.91	20
GCAACTTTCAAGGAAGCCAA	60.365	20	CCTCAAGACCCCAATTTGAT	58.836	20
TGGAACGTGTACGACAGGAA	60.152	20	ATCAGAAGATCCAGCATGGG	60.034	20
GGTTCCCACGTCATCAAAAA	60.734	20	TGAATTTGCCTTAATAATTACC	58.893	24
CCCACTTCATGCAGTTTCCT	60.111	20	GGTTGCGTACATTTGACCCT	59.859	20
GTGTTGATGCATGGAGTTGG	59.967	20	CTCGGAAAATTCCAACGAAA	60.046	20
ATGGAGCTATTGGATGCTGG	60.059	20	AATGATTGATGAGAACCGCC	59.9	20
TTTTGGATTCGATATGGATTGA	59.259	22	TGCGTGCTCACCTTTTTACA	60.436	20
ACCCTCCAAACAAATACCCC	59.919	20	ACGGACATGATACGACACGA	59.992	20
ATGAGATGGGGACAGTCTGC	60.08	20	CTCAGCCCTATTGTAGGCCA	60.227	20
CAAGCAAACGCAAAAATCAA	59.858	20	GCATCAATGCCTTCTCCAGT	60.226	20
CAAATCCCACCAACACCTTC	60.21	20	ACCACAAGCTTCCACCAATC	59.973	20

ATGGAATAATGAGTGGGGCA	60.155	20	AGTGGAATGTGGGGAGAGTG	59.962	20
AACTCCCACCTTCCATCACA	60.363	20	AATGACATAGGGCACCCCTT	60.578	20
TCCAATTGTGCGTAGCCTTT	60.637	20	TTGATTCGTGAACATTAGGCTC	59.229	22
CCAATTTATTGGGATTAAGGC	57.539	21	AGGTGCTTATGGATTTCCCC	60.152	20
GAAAAAGAGTTCAAAGTTTGTGC	60.089	25	TTCCATTCGTAGATCCTATTAC	58.945	24
TGCCGAATAAAGCTAAATCCT	58.055	21	AACCTCCCGGACTGGTAGAC	60.371	20
TCAGCTCAATCCTTCGCTCT	60.24	20	GAATAAGGAATTCGCACCGA	60.038	20
CGTCGAATTTCGCTGATCTT	60.352	20	GTCGCCAGAGTTCTGAAACC	59.851	20
AAGTCAAGTGCCGCTCATTT	59.882	20	TGCATTAAGGGTTGGAGACA	59.123	20
TGACAATTCGAGCTTGATCCT	59.828	21	ATTCGAAACCACTCAACCCA	60.353	20
TAGGCGATGTACCTTGGGTC	59.955	20	AAAGGCATGGGCAACTTAGA	59.708	20
TTGGAATGCGACAGAGACAG	59.984	20	GGATAAGCCTGTGATTGGGA	59.894	20
GACACCATTGACTGTGCTGG	60.162	20	CGATCATGTCTTCCGGAGTT	60.073	20
ATGTAGCCGACCCCAATTTA	59.297	20	TCTTGGGAGTGCATTTTCCT	59.67	20
CAACAGGCACACTGGAATGA	60.722	20	TCGTCAAAATCTTGGAGGCT	59.813	20
GCAAACTCGAAGAATAGCGG	59.982	20	GACCGTTTAAACAGACCGGA	59.971	20
AGTTGCATGCAGAGCATTTG	60.019	20	TACTACCCCATCTTCGCACC	59.955	20
TGAAATGCCAAATCAGTTGC	59.67	20	ATCCTGGCATTGACTGTTCC	59.934	20
TTCCCACTTCAAGAATTCCG	60.044	20	CAAGAGCATCCCACTTCACA	59.831	20
AGATTGTCGTCGTTCCATTG	58.57	20	TGCCGATCGCAGTTATGTTA	60.237	20
GGGAACCTTCTCTGTTCCCT	59.534	20	TGAGGTCGCTCACAGACAAC	60.03	20
AAAAATCTCCAGTCCGGCTT	60.074	20	GACGGCTATTTTGTGAGGGA	60.074	20
ATGCGCTATTTATGGATGCC	59.92	20	TGCATATTAGTCTGCGGCTG	59.999	20
CCCAAGACCCCAATTTGATT	60.91	20	CTCTCCTCAAGCCAAGCTGT	59.745	20
GTTTCATACTCACCTCCGGC	59.556	20	TGAAGCTGATGTTGGCGTAG	60.011	20
TGCAGGAGAAGAGGTGGTCT	59.986	20	CAAATAATGGCTGCTGCAAA	59.842	20
CTGCCGATCAGATTGGTTTT	60.074	20	GGTCTCGTGGTGGCTAGAAG	59.867	20
AAGTGTGTCGAAATTGAGAAGAA	59.347	24	TTCCATGAAACATAAATCTTGC	60.194	23
CACAAAGGCAGCAGACGTTA	60.05	20	AGCTGCATGAGCAGGAATTT	59.985	20
CTGAGATGTCCCAGGTTCAA	58.641	20	GGCCATGGAGAAGAACAAGA	60.195	20
ATGTAGCCGACCCCAATTTA	59.297	20	TCCAGGTTATGTTCCACGGT	60.232	20
CCCGACCCAACTCAGTAGAA	60.103	20	GGAAGCTTGTGGAGTTGTGG	60.69	20
ATGTAGCCGACCCCAATTTA	59.297	20	TCACCATATGTTCAACCTGTCA	58.9	22
AAGGAAACCCTAGTTTCGTGTTC	59.928	23	AACGTAAATAGTTGCGCCTCA	59.793	21
AGGACAACTTGACTGCCTGG	60.298	20	GCTGATACCGGCTTCTCATC	59.803	20
CCATCTAGTTCCTCACCGGA	60.065	20	GGCCATCGGTACTTCACCTA	59.955	20
TAAAACCCCCTTCAAATCCC	59.992	20	CCGTTCCATCAAAGACCTGT	59.966	20
TCATCTCAAGACCACCCTCC	60.048	20	TCGGACCGTAAAGCTTCAAT	59.708	20
AGTGAAATGGGAAGGACTTCAT	58.967	22	CCTCCAGCATCCGAATATGT	59.917	20
CCACCTCCGTACCGTTACAC	60.291	20	GTGGTGGGGAAGAGTAGTGG	59.425	20
TGCTCGACAGGTCAAAAGTG	60.025	20	CATTGGTGAAGAATTTGGGG	60.162	20
ATTGCTCTTTTACCCAGCGA	59.845	20	TGCTTCAAAAATTCAGCCAA	59.42	20
TGCATATACACACATGTTGACCA	59.79	23	CGTGCGAGTTTGGAATTCTT	60.249	20
GGCTGGGTAATAGCCTTTCC	59.93	20	TACACGGAACAGACGCTTGA	60.449	20
AGCTTAGCACAGCAGCATCA	59.918	20	GGCGAATTTTGTGGTGAGAT	59.939	20
GAGCAAGTGTTGATGCGAAC	59.45	20	CTTCCAGGGTACAACTGCGT	60.171	20
AGATGGGCCGGCTAAATATC	60.267	20	GTGGGCTTATTGGGTGTGAA	60.755	20
TCTTTGTGTAGCACCCCCTC	60.111	20	TTTAACCCCTGCATCCTGAG	60.066	20
GTGGGGGCTGTTATTGAGAA	59.933	20	AAGGAAATGGAGACGAGCCT	60.212	20
AGGCATTGGATTCAGTGGTC	59.934	20	GTCCACACCTCCACCTCCTA	59.962	20
TGGGTCTCTGCCTTTTCAAT	59.67	20	CCCAAGACCCCAATTTGATT	60.91	20
TGAGGACTGGGCTGATCTTC	60.349	20	CACCTTAGTTGTCAGGGGGA	59.959	20
TTTCTTCAAACTCCCACCGT	59.569	20	AGGTTGCGTACATCTGACCC	59.997	20
TGATGGAACTTGTGTGCATGT	60.024	21	CCCGATATGGTAGACGGTTTT	60.082	21
CTCAGCTGCTGCTCTCAGTG	60.227	20	GGAGTTTTGGGACACTGCTC	59.703	20
TTCACACGCGAGAAGAGAGA	59.855	20	GACAGGGTTGCTGGTTTCAT	59.973	20
AAGATAAAGGACGGCCGAGT	60.096	20	AAACTACGGGTGGGGCTACT	59.886	20
GCTTCCAGCAGAAATCATCC	59.78	20	TGATCTGGTGGATCTTCGGT	60.475	20

AATGCAGTCCGGGTTCATAG	59.955	20	AGAGCAGAGGACGAGTTGGA	60.135	20
TGTAGCCGACCCCAATTTAT	59.297	20	TCCTCTGCAAATGAACATTGA	59.262	21
CCCAAGACCCCAATTTGATT	60.91	20	ACATGCAATAAGTTGAGAAAA	59.143	25
ATGTAGCCGACCCCAATTTA	59.297	20	TTCCAATTGCTTTCCTCACC	60.051	20
TCGGGTAAACCTTTGCTGTT	59.609	20	TCAAATTTCCCAGCAGGACT	59.67	20
AGTTCAGAGCTTGCTCAGCG	61.016	20	CAGAGAAGTGGAAAATCCCG	59.665	20
CATTCAATTCGAAATTATGCATGT	60.102	24	ATCCATGGTCGACGAGTTGT	60.395	20
CAGGGTTCCATTCGTCTCAC	60.51	20	TTGTGCCCTTACCCAGTAGG	59.986	20
GCAACCTGCAAGTCACATTC	59.297	20	AGATGTACTGACGGATCGGG	59.95	20
TAATGGGCCTTCACATCCTC	59.894	20	GCTGTTGATCAATGGGTGTG	59.967	20
GTTTTTGGACTAGCCCATCG	59.569	20	GACCACTACAATGTTCGCCA	59.572	20
GTTCAAATCCGGGTCTCTCA	60.05	20	TGGCAATGCTCATCAGGTTA	60.22	20
TTGTCGTGATGGGTGAATGT	59.812	20	ATGTAGCCGACCCCAATTTA	59.297	20
CGCATGACACTGATCTATCG	57.804	20	AATTTCCCACCCACTCATCA	60.173	20
CCCAAGACCCCAATTTGAT	59.59	19	TTGTGGGAAATGGTTGCATA	59.786	20
TAAAGAGAACCACCAACCCC	58.884	20	TGGTGGCTCTTTCAATTGCT	60.776	20
TTGGATTCTTGTTTTCCCTCA	59.532	21	GGGGAAATTCTGACAATGACA	61.08	22
TCCAGATTCAAGACCAAGCA	59.369	20	TTGGACGGAATCCAAGATTT	59.363	20
CGTCGCCAAAGTGTTCAATA	59.729	20	TGTGACGGCTAACATTCTGC	59.871	20
ACTCCAAACGTTTCCCACAA	60.388	20	AGCTTGTTCGCTTCGACAGT	60.201	20
TTGTATCGTGTTCGCCACAT	59.995	20	AGGCTTGCACCCTACTAAAGC	59.926	21
TCCCAGTTCGAACATCTCAA	59.215	20	CCCAAGACCCCAATTTGATT	60.91	20
ATCAAGCCAGGATGCAGAAC	60.226	20	TTGTCAATTTTGAGTCCCAGG	59.956	21
TTTTGGGTGGAGAAATGGAG	59.903	20	TTTTTATGCTGAAGCCCACC	60.074	20
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CCCATGCCGAATGTTATTCT	59.784	20	ATGTAGCCGACCCCAATTTA	59.297	20
CATTATACCACGGAGGAAGGAA	60.197	22	GTAAGGAGGGAGGGAGATGG	59.89	20
CTCTTCCCCCACACACTCAT	59.962	20	GCGTTTGGTGAAATCGTCAT	60.905	20
GTTGGGTTGGATTTGAGCAT	59.797	20	GGCAGCGGACTGTAAGTTTC	59.882	20
TGAAACATCCATTCTCCAAAGA	59.546	22	AGAATGACCCACAAGCAAGC	60.263	20
TAGATAACAGGCAATGCCGC	61.124	20	CATGTAGCCAACCCCAATTT	59.685	20
ACTCTTCAGCTCCCACTCCA	59.986	20	TGGAGCTCTTCGTCGAGATT	60.096	20
GTTCCTAGCTGTCGGCACTC	60.02	20	CGAATCTGCCAATGTAAGCA	59.833	20
GAGGGGGAAAAATTCGATCT	59.356	20	CAAAAATGGATTATGGGCAA	58.344	20
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CCTGATGAGGCTAAGGATGG	59.647	20	AGTTTGAAAGGCGTGGAGAA	59.853	20
CCGAAAATGTCCTTCATTGC	60.448	20	CCGATCTCCCCTCTTTTCTT	59.646	20
TTGAGGACCGGACTGACTTC	60.238	20	GCTAGGCATCAAGGCATCAT	60.207	20
CAGCATGAGGCAGATTGATG	60.376	20	CTCCAACAGGAGTTTGGGAA	60.081	20
CCGAATTCTGCTTCTTCCAG	59.948	20	CAGAAATCCGAAGCACGATA	58.869	20
CCCCTTGGGATATGTGTTTG	60.044	20	GCACGATGGTGATGAAGATG	60.08	20
AGATTTCGGAGCTTGTTGGA	59.813	20	CTCCCCTATCTCCGCATACA	60.051	20
TTGTCACTAAGCCAACACCAA	59.23	21	ACCATCATGCATTTTTCTTTCA	59.456	22
GGAAATGATTGTTCTCCTAGGTCT	59.073	24	AAGGGCCATAAATTGTGGAA	59.273	20
CCCCTTTTACCCATCCCTAA	60.007	20	TTTCTCTTTCAACGCACACG	60.027	20
GGCCTAAAGCTGATGGACCT	60.599	20	CTCCACAGTCTCAAAGTGCAA	59.071	21
TAGAAGGGCTTTGCTTCGTG	60.514	20	GTTGTACGTCGAGGCCGTAT	60.022	20
AGGGGACTCGTCAGGAAACT	60.111	20	TCAACAACACCAACACCCAC	60.309	20
TCTTTTTCCATTGCTCACGA	59.395	20	GCCTCTGTCTGCCTATTTGC	59.985	20
TACTGCATCGGTGTCTCACA	58.813	20	TGTAGCCGACCCCAATTTAT	59.297	20
GAAGGCAGCTTGATCGTAGG	59.978	20	TGTCACGGATTCTCTTCCCT	59.655	20
GGAGGAAGCATCTACGCAAC	59.843	20	GTGGGTTTCAATTGGTCCAC	60.073	20
CAATCAACGCTGTTTTTCCA	59.706	20	ATTCGTTGAAACCTGCTGCT	59.882	20
CAATAACGGCAACACAAACG	60.029	20	ATCTCCCCAGATTCAGGCTT	60.037	20
CAGCTCCTCTCTCCAGATCC	59.079	20	TCTGCGTCTGAAATGTACGC	60.019	20
GGAAGGTCACCGTGTTGTCT	60.009	20	AACCAAGACCCCAATTTGATT	59.563	21
AACAAAATCCCTCCCCATTC	59.996	20	CCTTGCTGGAGATACCGATG	60.615	20
TGCCTTAACACAAAGGGGAA	60.472	20	AAAACCAGCAACCTGGAATG	59.971	20

AGCTTTGGTTCATGTAGCCG	60.27	20	GTTGGGAGTCTCCTGCAATG	60.656	20
TACACGTTCAGACTGTGCCC	59.751	20	AAGGAGAAGCCAACATGACG	60.255	20
TGAAACTGGACCTGGTATCAA	58.062	21	ATTGTATCACCTCCGCCGTA	60.352	20
AATCTCGTTGCCGTTGGTAG	60.132	20	TTCCTGTGCGTGAATTTTGA	60.234	20
TGGCACCCTTACATCTCCTT	59.55	20	TTTCCTTCTTCCATGGTTGC	60.051	20
CGTTTTGCTTCTGCACTTCA	60.172	20	CCCACTTCCGTCATTGAGTT	59.966	20
GGGACAAGCTATCACACAGGA	60.126	21	TGTAGCCGACCCCAATTTAT	59.297	20
CAATGTACCATGGATCGCAA	60.343	20	AGACCATGCAAGTGGTTTGT	58.058	20
ATCATCAACTTCCGGTGGAG	59.927	20	GAAGATGGTGGCGGAGAG	59.291	18
GGGGGAGTTAAGTTTGTGACTG	59.901	22	CCCAAGACCCCAATTTGATT	60.91	20
GGCTTATGTCCAACTGCTCC	59.7	20	GCGTGGGCTGTTAGTTTTATG	59.661	21
CAGAGCGCACTCGAAGAGTA	59.49	20	TGAGGAAAACCAGGAGCTTG	60.366	20
TCTGGAAAAGAGAAGGCCAA	59.926	20	AGAAAACATTTGCAGCACCC	60.118	20
TGTGGGAAAAACATCGATCA	59.9	20	GGGTGAAAACTCCGTTCTGA	60.088	20
TTCGGCAACTTTTGGAAGAT	59.685	20	CACTTGTGGCTTTTGGAGGT	60.149	20
TACCTTTCTCGCCTAATGCC	59.32	20	TCACGAAATCGAAGTGAACAA	59.307	21
CGCGAACTAATCCGTCCTTA	60.223	20	CCTTCTTGGTCTGAACCTGC	59.844	20
CCCTCAATTTTGTACCCGAA	59.795	20	CATTTTGTGTCAATTGGTTTATT	57.181	24
CCCAAGACCCCAATTTGATT	60.91	20	AAAAAGATGCATGAGCCTCG	60.352	20
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CCACTGAATGTGAAGGCATTT	59.985	21	AGAGAGTCGATTGCTTGGGA	59.95	20
ATGACTTCCCTGCAACCAAC	59.973	20	ACTGATTGAGAGGGCACACA	59.261	20
GTCCTCCAGCTGTTCTTTCG	59.989	20	ACGTGAAGTGGGACTATCGG	59.989	20
GAGTGAACAGCATGGTCTGG	59.261	20	TGGAGAGTGCAGAGATGTCG	60.138	20
GATAAGGGGATTGATTGGCA	59.722	20	CACAAACGACACAAGTCCGT	59.641	20
AGCCACGAGAGAATTTGCAT	59.843	20	CCGACCTCACTTAGTGGGAA	60.103	20
TGCCCTCACAAACAAATTCA	60.088	20	TGTTTTGGGGGAAAATCAAA	60.138	20
CGAGACCTAAATTGGTTGTGG	59.48	21	AGGCTTGCCTTCACATCTCT	59.043	20
AAAAATCATTTATCCCCGGC	59.988	20	TGGGTTTTATCCTGTGAGGG	59.784	20
ATGCTGATCCACCCTTTGAA	60.461	20	CCCAAGACCCCAATTTGATT	60.91	20
GCAGCTGAGCTAGGTGCATT	60.709	20	CAGTCCGCATTCTCCATTTT	60.074	20
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TCAACATCTGCGATTGGAAG	59.799	20	TAAAGCCGTGTACCTCCACC	59.993	20
AAGGCAAAGAATTTCCAGCA	59.823	20	TGTCCTTTGGGTTCGTAAGG	59.964	20
AGTACCAGCCTGCCATCTTG	60.277	20	TCTGCAGAAGTCGTGAAACAA	59.624	21
ACGCCATAACAAAGGACTCG	60.132	20	CCCAAGACCCCAATTTGATT	60.91	20
ATGTAGCCGACCCCAATTTA	59.297	20	CGAGATAGCCAAAAGCGAAG	60.11	20
TCGGCATGTTGCTCTTTATG	59.833	20	ACAATCGCTTAGCATGCCTT	59.873	20
GCGCTGAAAGAGGATGAGAT	59.537	20	CCATTTGCTTGAAACGTCC	59.112	19
ACTTCCTCCTCGTCCTCCTC	59.807	20	TGATCCCTGCCCTAAATCTG	60.029	20
GCACTTGCACTCATTTTTGTG	59.381	21	TCGCTGTGTATGCATGAGTG	59.436	20
AATGCAAGATGTGCCCCTAT	59.415	20	TGGCGAGTTTTATGCTGAGA	59.566	20
GGACTATCCACCAACTCCGA	59.927	20	GCCAAAAACCCACAACCTTA	59.839	20
GTGCAGGCTTGCTTTTGTTA	59.111	20	AATGGGGAGGAGGACTTCAC	60.314	20
AATAAGATTTGCACGCTGGG	60.096	20	TCGAGAGCAAACTTTTTGGA	58.623	20
TGCTTGGCAATTCTACATGC	59.839	20	TGATTCAATATTAGCCGTCCC	58.912	21
GTGGATGGTGAAGGACCCTA	59.779	20	TGAAAACTTTGGGATGGGAG	59.903	20
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CTGAAAGGGAGTTGGAAGCA	60.366	20	GTGCAACCCTTCTCTCTCCA	60.386	20
CCCAAGACCCCAATTTGATT	60.91	20	TGCGGAACCGTCCTAGTTAC	60.132	20

ACGCCAATTTGGATTTTGAC	59.807	20	CTCATCATCAGCCAAACGGT	61.067	20
GGTCCTTCGTCGCATATGAA	61.003	20	AATGCGTTTTCCAGACCAAC	59.978	20
AAATGTCATATACCCGCCCA	60.038	20	AACAAGGGTAGGGGAAGACC	59.299	20
GGTGGTGAGAACCACGACTT	60.009	20	TTCGACAACAGAACCTGCAC	59.88	20
CCATCGGAAGTCTCAAGTCC	59.655	20	TGTGCAAGGTGGTCAAAGAA	60.278	20
TGTAGCCGACCCCAATTTAT	59.297	20	GCATGATACGAGCACGAGAA	59.979	20
GGGAGCCCTTGGATTTAGTT	59.42	20	AAAGGCTTTGCAGGACAAGA	59.993	20
GTTAATGTAGCCGACCCCAA	59.823	20	TGATTGTTTAGGCCAGGGTC	59.933	20
TGCACTTACAGCCAAGCAAC	60.058	20	TGAATTGAAAGCCACTGCAA	60.379	20
AATTGTGGGATAAAATCCCCTT	59.8	22	CCCAAGACCCCAATTTGATT	60.91	20
GAGTGTTCGCGCAGTTGATA	60.019	20	CCAATTTGATGACGACGATG	59.924	20
AAAAGGCCAGGAGAGCTAGG	59.976	20	TGAGGAGAGTGATGGTGGAA	59.18	20
GGATTCGAGCTCTTGTTTGC	59.962	20	AAACCACCATTGAAGGCTTG	59.971	20
GTTTATGTAGCCGACCCCAA	59.823	20	TGTTGCAATTTGAGGCTTTG	59.849	20
GATAAGCAGAGCTCCATCGC	60.088	20	AAAAACCCCTCGACCATCTC	60.306	20
TGGTGAAAAATCAAACACTTGG	59.876	22	CCTTTTAGTGGTCCGAGGC	59.679	19
TTTCTGTTTGGGCGATTTTC	60.053	20	CCAGATCCATCTTTCCTCCA	60.003	20
TTTGATTAAATCGGGCTATGA	57.306	21	CGAACCTCATTTCGAAGGAA	60.184	20
CTTCCTCCGACGACAACTTC	59.844	20	AGCAATAAGGCAGCAGCAAT	60.01	20
ATGCTTCTCCCCCTTGAAAT	59.903	20	TTTCCACGACTGCTTTGTTG	59.881	20
TCAGTTATAGCCGACCCCAC	59.955	20	CAGGGTGGCTGCTGATTTAT	60.096	20
AAGTCGTGCATTGACGTGAC	59.758	20	CCCAAGACCCCAATTTGAT	59.59	19
TCAACAGACATTGCAGCCTC	59.992	20	ATCTTGAATGGGCTTCTGGA	59.629	20
TGGAACAAACAAACAAGCACA	60.179	21	AGATTGGGTGGGTGCATTTA	60.192	20
TTTGGCGTTTGAGTGTTCAG	59.881	20	CCATGGATGCAACAATGACT	59.374	20
CCCATTTTGACGCTCTGATT	60.074	20	GACAACAACTTCCCACCACC	60.261	20
GATTGATTCCGGTAGGCAAA	59.901	20	GACTCACGGTGGAACCCTAA	59.966	20
TTTGACTCAGTTGAGCCCCT	59.844	20	TGATGTTTGCATTTTAAGATGA	59.143	25
GCATAACCCGAACCCAATAA	59.66	20	AAAGCATGGATGAATGGAGC	60.043	20
GGGAAGATTCGTGTTTCAGG	59.526	20	CTCCATTTTTGTTGAAGCCC	59.546	20
TGACAGATGAATGGACCAACA	59.951	21	TCTTCTTTATGGGGAGCTGG	59.264	20
CCCAAGACCCCAATTTGAT	59.59	19	AAGCATAAAAGGCATCGCTC	59.461	20
CATTAGCTCCGTGATGCAGA	59.972	20	TTGCAGTGTTCACTTACCGC	59.911	20
GACCCGGAAAGGAAATTTTG	60.644	20	GACCGCCGGTATAACTCTCA	60.096	20
TATCCAATATAGGGCACGGC	59.779	20	AAAGAGGCGGATTTGGAGTT	60.074	20
CGTTGATTCTTCAAAATCCCA	59.924	21	CCACGACTTATTCATTGCGA	59.688	20
GTATGTGGTAAGGCGAGGGA	59.955	20	TCCAGGATGGTGGAAATCAT	60.135	20
AGCCCGTTTCTGAAAGACTG	59.473	20	GAAGCGAAAAGCATTTGACC	59.829	20
CGAAGATACAGTCCCACCGT	59.989	20	GCCAAGATCAGCAGATCACA	59.95	20
TCCAGGCCTTTAGTCAGTGG	60.246	20	TGCAACATGGTCAAACTTGG	60.552	20
TTACCTCCGAAGGAACGAGA	59.807	20	AATCGACACTCCCACTTTCG	60.111	20
CCCAAGACCCCAATTTGATT	60.91	20	AAATGTGGCCAATCTTTTGTTT	59.758	22
CCATCACCATCACTTCCAGA	59.473	20	GCTGCCAAACTAACTGCAAA	59.111	20
GCGTACACGCGTATGACAAG	60.346	20	AGCAATACGCTGAATGCAAA	59.472	20
CCCAAGACCCCAATTTGATT	60.91	20	AATGGATGGTGCTTTTGCTC	60.081	20
TCTCCCTCCTCCTCCTCTTC	59.883	20	TGCATGTTTTGTGTGTGTGG	60.046	20
CCTCCCTCTAAAAACCCGAA	60.415	20	CATGAGAGAGGTGGTGCAGA	59.98	20
TCAGCTTCATGATACTTTGGGA	59.708	22	TTCAATTGGCTGGAAGAGTG	58.847	20
GCGTATTATTTTTCTCTCAATAGG	58.762	25	GACATCTGGTGAGGGGAGAG	59.638	20
AGATGGTCACGGTAGACATGA	58.014	21	CGGCATCCATCTCAATCTTT	60.036	20
ACAAATCGGAAAAGAGCAGC	59.457	20	CATCACTCCTCTCACTCGCA	60.138	20
TTCAACACTGCAGATGAACAGA	59.49	22	TGACAGCTGAATCAGTCGGA	60.557	20
TCGGAAGCTTCAAGTCCAAT	59.813	20	AAGCCCGTGAAAAAGGAAAT	59.945	20
TTTCCGCCATTTTTAGCATC	60.04	20	CTTCGCTTTTGGCTATCTCG	60.11	20
AGGCCGGTGTCGAAAATAAT	60.692	20	AGTAGACCCATCCTCCTCCC	59.372	20
AGATGCCGAGGACTTTTGTG	60.255	20	GGTAGCCGACCCCAATTTAT	60.041	20
AGAAGCAACCATCAACCGTC	60.119	20	CCCAAGACCCCAATTTGATT	60.91	20
TGCAGAATCAACTGCTTGGT	59.445	20	TTTCACGAATTTTTCATTCAGG	59.098	22

TTGGTTCATGTAGCCGACCT	60.517	20	TTTAGCAACACCAGCCACAG	59.904	20
TTCGTCCATATCAAGGCTCA	59.226	20	CATTCGCTTCCATTCATCTG	59.226	20
TCAAAAATGGATGGGGTGAT	59.991	20	CGCGAACAATGATATAGGGG	60.302	20
ACACCCGGACACAAGAATGT	60.284	20	ATGTAGCCGACCCCAATTTA	59.297	20
GAGTATTCTTGCCGTTGGGA	60.074	20	CAATGCTACGGGAAGACGAT	60.096	20
ATGTAGCCGACCCCAATTTA	59.297	20	TTTTTCAAGTGAAAGGTGCAA	58.451	21
TGGTGAACCCAAACTCTTCC	59.943	20	GTCTCCCTGCAGCAAAATTC	59.82	20
GGAGGAAATTGGCATCAGAA	60.014	20	ACCGAGAATGACACGACACA	60.162	20
AAACAGCTTCTCTCTCCGGG	60.892	20	GGCAAGGGACAAAGCAAATA	60.074	20
AAAATAATGATAACGGCGGC	58.963	20	GTGGTGATGGAGAGGCAGAT	60.08	20
TGGTGAGCTTGAGGAGGTCT	59.986	20	AACACAATAGGGATCGCTGC	60.103	20
TGTAGCCGACCCCAATTTAT	59.297	20	CAAATGGCAGACAAAAACGA	59.706	20
CCGAGACCCCAATTTGATT	59.735	19	TGATGGGTCTTCCCTGATTT	59.336	20
ATGTAGCCGACCCCAATAAA	59.297	20	AGACGACGACCAAAGGAATG	60.111	20
ATGTAGCCGACCCCAATTTA	59.297	20	TCAATGCAGCATCCTGAAAC	59.805	20
ATGTAGCCGACCCCAATTTA	59.297	20	GCACTTTGAGCTGCATTGAG	59.746	20
AACCATCTTTCCCCAAACCT	59.668	20	CCCAAGACCCCAATTTGATT	60.91	20
CCCAGTTTTTGTTGCACTGA	59.734	20	GGATAGCCTCCAGGAATCAA	59.08	20
CGATTTCTTCTACCTCCCAATG	59.96	22	TGGCATTTTAAGGCGTTTTC	60.075	20
GTCTCCCACATCCAGCTTTC	59.661	20	GGATTAATGGCCACGAAGAA	59.901	20
CAGTTTCAAGGGGAATCGAA	60.044	20	TGGTTTATGAAGCCAATCCC	59.762	20
AGGATGATGGTGGAGGTGAC	59.774	20	ATTGCACCGACAAAAGAACC	59.978	20
GAAGCTGCATGAGGTGATTG	59.399	20	CCGGAGAGGGCATCATAGTA	60.051	20
TCCTGCTTCCATTTTCTTGG	60.184	20	CCCAAGACCCCAATTTGATT	60.91	20
GTTCTCCTTCGGAGTTGCAG	59.989	20	CAGTACGCGCACTCACAAGT	60.12	20
AGCCGACTTCACATAGTGGG	60.134	20	AGCAACCTGCCTCGACATAG	60.419	20
ACGTTGTTGTTGATTGGGGT	60.134	20	GGTGATCGGGAGAGTCTTTG	59.655	20
AAATACAAAGCCAGCCAACG	60.131	20	CTGGCTACTCACCCTTCTGG	59.861	20
ATGTAGCCGACCCCAATTTA	59.297	20	CAGTCAGGGAATGAGCACAA	59.831	20
ACGTGTATTGGGTGGTCCAT	59.973	20	TCTTTTGGGCAAAGGATCAA	60.555	20
ACATGCAGAAGGCTCCACTC	60.418	20	TTTGTCTCCTGGTGTTTGGA	59.109	20
AACTTTTGCCTGAAACGCAT	59.752	20	TGTTGCTTGTTTCGATCTGG	59.84	20
CCAACTCCTCGCCGTATCTA	60.227	20	GGAAGATGCAGAAGCGAGAC	60.104	20
CGTTTTCTTTCTCGGTGCTC	59.993	20	CCGTACCCTCCTCCTAGACC	59.95	20
TTGGGATTAAGGCTTTGGTG	59.931	20	TGGAGTCGTGTAGCGGTATG	59.74	20
ATTTCTCATACGTGCCTGCC	60.103	20	TGAAAAACACGTGACATCAAG	59.22	22
TGCACATGGTTATTGGATGC	60.352	20	GAGAATTCCAGTACGGCGAG	59.836	20
GATGCGGGGGATTTAAAGTT	60.15	20	CGTGAAATTTTGGGGTGAGT	59.83	20
ATCATCACCGTGGATCATCA	59.724	20	CGCTTATGGTTGGAGTGTGA	59.716	20
AACTCTTACGAGGGACGGGT	59.994	20	AGGCCAACACTGAAAACCAC	60.012	20
AATAAAGTATGTGGGAAAGTCGA	57.317	24	ACAGCGAGTAAGCTGAGGGA	60.156	20
GAAACACCATCTTTCCCGGT	61.115	20	CTGTAGGCCCATAGCCACAT	59.978	20
ATGTAGCCGACCCCAATTTA	59.297	20	TTGCGTTCAACGATTTTCTG	59.849	20
GGGCTGTTATCGGATGCTAA	60.06	20	TGGAACAGCACAGACTGGAG	60.022	20
GATTCCCTATCTTGCTCCCC	59.866	20	ACCTGCTTTTTGTGATTGGG	59.971	20
ATGCAACTTGCCAACCTACC	60	20	TCCTTCACACCAAACTGCAA	60.278	20
CTTCCAATGCCGACGTTAAT	59.96	20	ACGCGGTGATAAAATCTTGG	59.96	20
GTGAAGAAAATGCCGTTGGT	59.978	20	CCTCCGTCCCTCTCTCTCTT	59.945	20
TGCGTACATTTGATTGGGAA	59.93	20	TTTGCATCATGGTGTGTGTG	60.003	20
CGGTGGTTCTCATGCCTAAT	59.955	20	ACAGCAGCAGCAATCATCAC	60.024	20
TTAGGCTCTCCAAAGGACGA	59.948	20	AGTGGTCATGACGAGCAGTG	59.897	20
CATTTCGACCTCCACATCCT	59.927	20	AACTCCGATGAACATCAGCC	60.081	20
TGGAAAGAGAAGTTGTGGGG	60.081	20	CCGAATCCATCACATTCAAA	59.325	20
GGGGTTTGGTCAGCATTTTT	61.08	20	ATTAACACCGGCATTGCTCT	59.597	20
CGGGTTCGAAGAAAACTTGA	60.22	20	AATCCCAATCCCAATCACAA	59.991	20
ATCGGCTGTTACTCCTTCCA	59.694	20	CCAATTTATTGGGATTAAGGC	57.539	21
AGGCTGAAAAGGATGCTCAA	59.955	20	TGCACCTTGAGTCATAACGG	59.716	20
GTGTAAGTCGCGGTCTCGAT	60.285	20	CCTTGTTTGAGCCTACTCCG	59.869	20

TCCATCAACCTAACAGCAACA	59.184	21	CTGTCACCGAACACAAGCAT	59.751	20
AAAAGGTGGCAACGAAAATG	59.975	20	TCCTAATACGACTGCCCACC	59.955	20
GGAGATCCCAATGAAGAGCA	60.158	20	TGAGAGAAGGCGAAGAGGAG	59.82	20
ATGTAGCCGACCCCAATTTA	59.297	20	TGCACATTTACAACCAACAAA	59.027	22
CTCATTGACGACATCCAACG	60.112	20	TTCCCTCTTTCGTCCTTGAA	59.784	20
AGCGGGATAATGGAACAGTG	59.955	20	TGTAGCCGACCCCAATTTAT	59.297	20
CTGCCTGCAAAAATATCCGT	60.096	20	AAGATTGGAAGGGTGGTTCC	60.169	20
TGCAACTTGAGGCTGAGAAA	59.716	20	TTCTTGGTAATGCCCTTTGG	59.931	20
GTTTATGTAGCCGACCCCAA	59.823	20	AAGAGAAAAGCCCAAGAGCC	59.962	20
GATGCTTAGTTGCCCATTCG	60.606	20	CCGTTGTTGCTGATCCTTTT	60.11	20
ATCCCCTAGTGGCTCTGGTT	59.957	20	TCCAAAGAAAAAGCAAAGGA	57.609	20
AGAAGGAGGGGATGGAGAGA	60.149	20	CGGAAGTAGGAAAACACCCA	59.964	20
TTAACTCCGCCTGTGAGTGTT	59.788	21	GCAGCAATATCAACCTGGCT	60.243	20
AAAATCCCAGAATTGGTTCG	58.879	20	AACCATGCTCTTTCCACCAG	60.111	20
TTACTTCGCCGTAGGTTTCG	60.257	20	CCACTTCCATTCTCTTCCCA	60.042	20
ATATATTCCCACAGACGGCG	59.807	20	GCCCAAGTGTAAGAGTCGGT	59.212	20
CAACTGCACTTGGATCCTGA	59.831	20	GATAGCTTACAGCGGCATCC	59.835	20
TGAGGTATGGATGATCGGAA	58.873	20	GAGGGAAGTGGAGGTGATGA	60.048	20
TCTCCTACCCAAAACTCCCA	59.521	20	TTGTTTGATTTGCTGATGCC	59.67	20
TCTGAAGCAGCTCCTGTGAA	59.855	20	TTGGACTAAGGACACCAGGG	59.959	20
GGGGATATCTTTTGGGGAAA	59.957	20	CCGACCCCAATTTATTTGAA	59.633	20
GGGGCCCTGTCTAAAAATTG	60.664	20	AGGTTGCGTACATCTGACCC	59.997	20
GCATACATCTGACCCCCAAG	60.34	20	TCAGTCAAACCACTCGGTCA	60.285	20
GCACGTAAAACCACCGAGAT	60	20	GTCGCAGAAGAAGGTCAAGC	60.142	20
AAGACAAATACGACGACGGC	60.14	20	AAAGTCTTTCATCTCCGCCA	59.813	20
TGTAGCCGACCCCAATTTAT	59.297	20	ATCCCATGTGCTGTGATGAA	59.925	20
CCCAAGACCCCAATTTGATT	60.91	20	AACGAGATGCTCTCGAATGA	58.544	20
ATGTAGCCGACCCCAATTTA	59.297	20	CTGGAGTAGGGGTCATTCCA	59.92	20
GCGGTGTTTGTGTGTGAGAG	60.357	20	AATGATAAGATCAAGGCCGA	57.244	20
TTTTTGGCGATTCTTGTTCC	60.053	20	GTTCTGCAAAAGAAAAGGCG	59.996	20
GGATCAGCCGAGTAATCCAA	60.036	20	TTCCATGTCGAGTTTGTTCG	59.691	20
ATTGGTATGCGCAACAATGA	59.96	20	AAAATCAACCATATTTTCGCC	58.005	21
TGGTCTCATAACAAACCTGACA	58.132	22	TTCTAAACAATTGGCTGCTGAA	59.89	22
GCCATGCGTAAACTAAAACCA	60.013	21	CGTAACATGCCACCAGTGAG	60.175	20
CACACCCTTACTTTCCCCAA	59.824	20	GGAGAATGCGAAGGAGAAGA	59.508	20
AAAAGTGGCATTTTGCCCTA	59.586	20	GAGGTGTGATGATGCTGACG	60.279	20
TGTGAATCCCAAATGCTTCA	60.049	20	AGAATGGCACCTCACGAAAC	60.119	20
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GCAAGACAAACAAAGTGCCA	59.888	20	TGTAGCCGACCCCAATTTAT	59.297	20
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GCATTTTCCTCAAAAAGGGA	59.135	20	TGAGTTGAGGTATGAGAAAG	59.658	26
GACGGAGTTGTGAAGGAATGA	60.104	21	CTTGAAGCATGCACGATGAC	60.423	20
CAATAGTCTAAGGGAGCACATGG	60.028	23	AATTCAATGCAGGATGATTGC	59.921	21
ATGTAGCCGACCCCAATTTA	59.297	20	ACTGTTGCGTTATCCAAGCC	60.14	20
TTGACCTTGTAAACCCCGTC	59.83	20	CTGCTTCACTAAATCCCCCA	60.066	20
CCGCGTTATTATTTGCAGGT	59.985	20	CTGGCTCCCCAAGAATTACA	60.066	20
AGCACACTCGAACAAAGCAA	59.64	20	ATCTCTGTCCCCCTCGTTCT	60.073	20
TTTTTCACGCACAACACACA	59.765	20	TTCTAGGGTCGCAAGCAAAC	60.386	20
TTCCTCTCTCTCTCCCTCCC	59.883	20	GTTCGCCACCTCCATTTCTA	60.074	20
CGTTGCCTGGCATTATTGAT	60.857	20	ACCAAACTCTCCTCCCGAAT	59.935	20
GGGGAGATATGTTGGGGATT	59.843	20	TCTTTCCACCCGAAATTGAC	59.91	20
CGTAAGAGCATTTTGGCTCC	59.845	20	AGACCAACAATTCCAGGTGC	59.973	20
GAGGTGGTCGGTTGGTAAGA	59.966	20	GGTGTGGCAGTTATAGCGGT	60.022	20
GAGCAAATGGCCTTGAGAAC	59.82	20	TCTGCTAGCACTGCCCTTTT	60.154	20

ATTGTGCAGTCCGGCTAAGT	59.763	20	CGACTAGCCACGTTCAATCA	59.864	20
TTTCGATGTCGAATTACAACAAA	59.524	23	CTTTTACCTTAATCTTCACCCTT	58.765	26
CGATTTTATCCCTCGCAAAT	59.035	20	AAAGAGGTTGTTTCCGTTGC	59.218	20
GGACATCATCCACCGAGAAC	60.335	20	ATCATCGCCACATCGTGTAA	59.955	20
AAGGGAGGGAATGAAGTGGT	59.795	20	CGTATCTGGTTGAAAGTTGTTG	59.187	23
GTAAAATTGCCCAAGTCCCA	59.801	20	TTGAACACGATGGGCATTTA	59.93	20
CAAAGAATTCCAACCCCAAA	59.772	20	TTGATTCCACCTCTTCACCC	59.903	20
GATTTGCAAGACATGCGAGA	59.955	20	CCCTACATAGGGGGAAAAGG	59.655	20
AGGGCATTACCTTTGCATCA	60.469	20	ATGGATGCACCGATTAGGAG	59.917	20
ATGTAGCCGACCCCAATTTA	59.297	20	GCTACTCCCGACCATTCAAA	60.074	20
TGTAAGCTCACCAGCATTCG	60.011	20	TTTGGCAGGAAATCACACAA	60.088	20
CAGCTTCAGGTTCTCTGTTGC	60.186	21	TCCAATAAAATTTTGCCCCA	60.123	20
GAGATTGACTCCCACCAGGA	60.048	20	TAATCACCATGGACTTCCCC	59.605	20
CCACTTATTTACTTCCGCCG	59.603	20	CTGGGGGTGAATTTTGGTTA	59.657	20
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GTTGGGAAGGTAATTGGGGT	59.919	20	CAAGTCACCTTTGACTCGCA	60.025	20
ACTATGCCTGATGGGATTGC	59.923	20	TCGAGAGCTCTGGTGTTTTG	59.161	20
TACATCGCACAAAATCACGG	60.523	20	ATTCTTGAACGCGAGGAGAA	59.955	20
TTATTTTGGGATTCACCCATT	58.163	21	ACCTACAAAATGGGTCTCTTTG	59.056	23
TCGTTAAATGCCACTGTGTTG	59.641	21	TCTTCAGAAGCTTGCTGTGC	59.47	20
CCCAAGACCCCAATTTGATT	60.91	20	CATGAGCAATCCGTGTTTTG	60.111	20
GGGATTAAGGCTTTGGTGGT	60.187	20	TCTGAGCAGCCACATAAGACA	59.606	21
AGCAAAAGAAGAGGTTGCCA	59.993	20	CATATTTTTCCGGCTGTTTCA	59.95	21
AAGAGGTGCATTTCAATCGG	60.074	20	CCTCTCAGTCCCAGACTTGC	59.986	20
GTTTACTTCCATTCCGCCAA	59.938	20	TGGTTCATGTAGCACATCCC	59.374	20
GGCGTCAGAGAGATCGAAAG	60.096	20	GATGCATCCTTCCATCTTGG	60.426	20
ATCAATGGGCATTGGATGAT	59.982	20	CACACAGCCAGACACACACA	60.426	20
AAGCCGTTAAAGCGTGAAGA	60.018	20	GGGATACAAATGAGTGTTTAG	58.944	23
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TGTCTCCGTTGGAACACTGA	60.285	20	GAGGTGGCTAAAGTGTGGGA	60.111	20
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CTTGAAATTTTTGTGTGGCAA	58.711	21	AAAGGAGGGGTGCTGAATTT	59.94	20
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AGCAATCTGGTGGATTCAGG	60.073	20	CTGCCAAATCTGGGACTGTT	60.111	20
TACCTTCTCCGGAATCATGC	60.036	20	TGGGTGAGGGGATGTCTATC	59.737	20
TCAATGGTTGGGCTACACTTC	59.985	21	GGTCGCATTGTGTCCAATAG	59.002	20
GACACAGTACGATCCCGACC	60.395	20	CGGTCTCTCAGTTAAGTCTATC	59.98	25
CCCAAGACCCCAATTTGATT	60.91	20	AATAATGCTACACGCCTCCC	59.07	20
CCGACCTCACATAGTGGGAA	60.913	20	CATTATGCAGGAACTCGCAA	59.833	20
ACCAATGCAAACAATCACCA	59.823	20	ATACGGGATGTGGAATTGGA	60.014	20
AGAATGCATTTGAGGACCCC	61.223	20	TTTTCGATTTCATCCTCATAGC	58.337	22
TGAAAATGGGGTGGTTGATT	60.029	20	AGGCTCGCAGACAACAGAAT	60.02	20
ATAATTCAGGAGGCACGCAT	59.556	20	GATCGATCAGCTCCGAGAAG	60.057	20
TCCCTTTCAATTACATCGCA	59.112	20	ACTTCAGGTTGAACACCCGT	59.474	20
AGGTCGGTTGAAAAGATGGA	59.526	20	GGATACGTGGATGGAGACAA	58.359	20
ATGGGTTTTGCCATCAATTT	59.138	20	TTGTTTGGTATGTGACCCCA	59.667	20
AAAGATCCAGTGTTGGCAGG	60.111	20	TGCACAAAGTTTTGTTTCCATT	59.536	22
ATAGTTCTCCGCCTGCTCAA	59.978	20	TAGGGCTACCGGACACTACG	60.147	20
CAAGTGTTCGAAGACGGGTT	60.149	20	GCTTACAAGCGAGACCCAAG	60.015	20
TTTGATTGGGAATAATTGGG	57.289	20	GAGTAACTTGGGCACCTCCA	60.111	20
GAGAAAAACAGAGGAGCAACAA	59.92	23	GTTTGGAGGAATGGGGAGAT	60.133	20
ATGCTGCATCAACCAGTCAC	59.714	20	CCCAAGACCCCAATTTGATT	60.91	20
TCAAGGTGTCCTCGATTTGA	59.215	20	GACACTCATCCACATGCTCG	60.279	20
TTCCAACATGCTGCCTAAAA	59.301	20	AGTCCTACACACCAAGTTCAT	58.639	23
AGAGGCCAACAAAGAGACGA	59.989	20	CTCATTGCCCATTTCATGTG	59.924	20
ATTTGGGATGCATGATGGTT	60.021	20	AGGATGGTACAGTTGGCTGG	59.989	20
ATGTAGCCGACCCCAATTTA	59.297	20	TGCCTCGAGAGTAAGAACCC	59.43	20

TGAGGGATTAAGAAAGACATTGG	59.489	23	CGAGCATAACAAGACTCGCA	60.157	20
TCCCATATTTGGAGTCCAGG	59.744	20	TGATGGTAGCAAGCAAAAGGT	59.761	21
GGATTTGCCAGTTTGAGGAA	60.051	20	CCCAAGACCCCAATTTGATT	60.91	20
TGTAGCCGACCCCAATTTAT	59.297	20	TTCAGTCCTGCAGCAAGAAG	59.314	20
GGGGTTGGGTTTTCGTATCT	60.053	20	TCCCTAACCATGTACCACCC	59.526	20
ATGTAGCCGACCCCAATTTA	59.297	20	TGGTGTAGATTGTGAATAAAA	60.155	26
AAGCCTTTCATGTCACCAGG	60.111	20	AGCAAAGAAATCAAAGGACC	59.585	21
TCCTACCTGATGGGCTATGG	59.91	20	TTGATCATTTGGGAACACCA	59.75	20
TGATCCATATAGCCAACCCC	59.605	20	CCATTTGCAATGGACAAAAA	59.396	20
GCTAAGGCCTGAACAACAGC	60.022	20	ATCATGGGTGGTGTCACCTT	60.096	20
TGTAGCCGACCCCAATTTAT	59.297	20	CCGCCCATCTCGAAGTAATA	60.053	20
CTCGAAAAAGTGCGTCATCA	59.988	20	CAGGAAGAAGGTGGGCAGTA	60.246	20
ACATATATCCCTGTGCGCGT	60.382	20	TCATTGAAACCTCCTCCTCG	60.187	20
CACCGCCGTTCAGTAAAGAT	60.132	20	GGACAAGAATTTCTGCAGGC	59.82	20
AGAAATCGGAAGATGCTCCA	59.773	20	ACTGAGTGCAAACAAGAGCG	59.239	20
TCTAACCCCACCATTTCTGC	59.933	20	GCATTTTGCATTTGTTGACG	60.118	20
TCCGTTGAAATAAGATCGGG	59.894	20	GCGGATTGTTGACTTCCATT	59.939	20
TGCTATGTGATGTTGGCTTGT	59.213	21	GTATTCACGGGCAGTGGAGT	59.997	20
TACTTCCACCCCTTTTTCCC	60.159	20	CCTCCGACGATCTCTGTGTC	60.829	20
ATGTAGCCGACCCCAATTTA	59.297	20	CGTTTCCTCTCATTTGCAGG	60.766	20
AACACCCAGTTTGAATTTTAGCA	59.926	23	GCTTGTTAGTTTGGTTATGTCG	60.076	23
GGTCCAAAAACTCAGGCAAG	59.711	20	TTGCAGTCAGCAGCAAAAGT	59.788	20
CGCCACGTAGAGGAAATTGT	60.132	20	TTCACCAGTCCCATCAAACA	59.935	20
ATGTAGCCGACCCCAATTTA	59.297	20	CGCCTTCCTTGCTCTTAGAA	59.724	20
AAAATTATGTAATAGTTTGCCGAC	59.748	25	ACACCATTTTGGAGGGAGAA	59.381	20
TCAAAGCGAGACCTAATGGC	60.352	20	CAACTAAATTGCCCCATGCT	59.96	20
ATATGTTTCGCCTCTCCCCT	59.925	20	TGTGAAGGTCAACGTGCTTC	59.88	20
CAACGTGATGTCGATGGAAG	60.112	20	CACCCAATTCTTCAGCCATT	59.933	20
GCCGGTCAGTTAATCTGCAT	60.103	20	CACGCTTTCACTGTTGTCGT	59.946	20
GAGACCAAATCCAGCCCATA	59.894	20	TCATTTCAATTCGAACGCAG	59.809	20
AAGCAGTGTCATTTGCTCCA	59.445	20	GCATGCCCTTACAACGAAGT	60.14	20
TCACATACCTGCAACCATGAA	59.98	21	GCTGTGAAAGTATGCCACCC	60.526	20
AATGCTCCAACTTCGACTGG	60.255	20	TCTAGAAACACCTTTGCGGC	60.386	20
ACCTGGATTCGAATGGTTTG	59.79	20	CAAGATAGGCCCGAAATCTG	59.662	20
GAGCCATCTTGTGACTGCAA	59.992	20	TGGGCCTTCAAAAGCATAAC	60.074	20
TGGGCCTTCAAAAGCATAAC	60.074	20	GAGCCATCTTGTGACTGCAA	59.992	20
ACAGATGTGCTGACTGGGTG	59.738	20	AAATCTCCAAGTCCCGTTCA	59.526	20
TTGTGGTCTCACTCCTCCAA	59.23	20	GCCACTGCTTCCACACATAA	59.722	20
TTGTGGTGTCTTGTGGTCTTG	59.626	21	ACGGCAAATTAAAATGCGTC	59.971	20
CGGCTGGTGCAGAGACTAAT	60.419	20	AAATTTGCCCTCTCCCTCTC	59.651	20
GATTGAGAATGACATGGGCA	59.456	20	AAGCTGGCTCAATTGCTGAT	59.985	20
GAGGAAGAGTTTCGGATGGA	59.213	20	AGATGAAGACTTGAAGTTGGT	59.668	23
CGGCAAATTAAAACAGACACG	60.525	21	CGGATCAAAAGTTGGATTTGA	59.924	21
TGGTGCATAATGGCTCTGAC	59.679	20	AATGCCTTTTTCTGCCATGA	60.585	20
TCCACACACGTCTTCACATTT	59.049	21	GAATCGAGCGGAAAGTTCAA	60.331	20
TCAGCATTATGTGCTCTGCC	59.979	20	ATGGTGCTTACAACGAAGGC	60.14	20
CAGCAGAGATCATCCACCAA	59.787	20	CTGGTCCGAATACCAACACC	60.232	20
GAAGCACAACCAACCAACCT	60.012	20	CAGAGAGAGAGAATGCCCCA	60.488	20
TTCGGTTTCATAAGGTTGTCG	59.982	21	GCTTCTTGATCAAATTCCGC	59.791	20
TCTACATTGTGCCTCCTCCC	60.073	20	AACCATCCGCGTGAAATTAT	59.301	20
CCACTCATTTTTCCACACGA	59.541	20	AATGCGGTTTTCCTCCTTTT	59.945	20
GGCTCGAGTTGATGATCTTTG	59.828	21	GGGAGGGAGTTTTTGTTTCC	59.783	20
TCGATTTCTTCGGAATCGTT	59.645	20	GCTGTTTGGTTTGGCAACTA	58.822	20
TATCGTTCCACATGCCTTCA	60.073	20	TTTGATGACCAAGGAGAGCC	60.195	20
CGAGATCCACGTGTCATTTG	60.112	20	GACAATGGCCTAGACCGAAG	59.694	20
AATTGTAGTCCTTAAATTCCCGA	58.165	23	TGTGGAAATACCCTAAATTGGT	57.44	22
CATCTGCCATGCACCATTTA	60.488	20	TCCTACCTTCACTAGTTTTCAT	58.759	24
TGTTCGGAGCTTGTGTTGAG	60.025	20	TGGCATACTTGCTGAAATGC	59.839	20

TCTCTCATTGGTGGCCCTTA	60.594	20	CGAAGGCCTTTTCGAAGTCT	60.865	20
ATGCATTAAAGCCGTGTGGT	60.395	20	TGAATCTGCAATTTTCTTGTTGA	59.75	23
TCCATGACACTGAATATCCCA	58.785	21	TGCAGAAGGTCAGAGGAGGT	59.986	20
AGAAATCCCGTGCGAGAGTA	59.836	20	CACACAAAATTGTGCCTTGC	60.157	20
CCCACTTGGTTTTGGACCTA	59.824	20	CGGTTGATTTTGAAGTGGCT	60.11	20
TTTCTGTTAGTCAAAATCGAGAGA	58.223	25	AACAATTATTTGAGGCGCAAT	58.643	21
CGTTGAACGCGTATTGTTGT	59.656	20	GGGATGGTGGAAGAGCAGTA	60.073	20
GGATTGTGTGGCTACTGGCT	60.142	20	TTGCTCTACATTCGGTGGAA	59.272	20
TGTCATGTCATCGTGTGCTTT	60.176	21	GTTCGGTTTTGTTCTCACCG	60.529	20
TCTCAGATATGGGCGTCACA	60.225	20	ACCCCGTATTTTCACAAATAAA	58.766	23
GCAGTTTTGGCACAGAATCA	59.847	20	TTGTTAATGGGGTGGGGATA	59.872	20
TGTGGTTTGCCTCACTCTTC	58.854	20	TATGGACGGTTCGGTCTAGG	59.948	20
TTATTTTTGGTACCCGGTGG	59.559	20	ATCCCGTATTTTCTTCGGGT	59.666	20
ATTGATTTGCAACTCCCTTTT	57.734	21	TGTTTATTTCCCCCATTCCA	59.988	20
TTCACTGCTCTTTTCAACCCT	58.969	21	TGGTGTTTGTGGGTGATGAA	60.829	20
GACGTGGAATGTGGATGATG	59.769	20	CATGGGGTTCGAGAATGAAA	60.832	20
TTTTCCGACTTTGGCAAATACT	60.004	22	CATATTCGTGATGGATTGGC	58.797	20
GTGGAATTGACGACTCCATTG	60.368	21	TGCAGTACAAATTTAGCTGGA	59.829	23
CAAATTAAAATGCGCCACG	60.081	19	ACGAAGAACGGCTTGAATGT	59.74	20
TGGGCGAAAATTCAATCTGT	60.448	20	CCCCCTGCCTTTCTTTCTAC	60.068	20
TGGCGAGAAAACTCAGATCC	60.34	20	ACGACGATCGACGGAATTTA	60.469	20
TAGAAACACACGCAGGCAGA	60.596	20	CGCAGTCTCCTTTTTCTTGG	59.986	20
TGAAGATTGCTTCCTTATGAATTG	59.644	24	GGCGTTGTTCTGTACTTGGG	60.55	20
TGCAGAGCAAATTCATGTCC	59.805	20	ATTCACAAGGAAATGGACGG	59.79	20
ATGTTGGAAGAAACAAAACTGGA	59.9	23	TCGGAGAGCTAACAGAGGGA	60.088	20
TCCAATCAAATCAAATGCGA	60.012	20	TGCGCGTATGCATAAGGTAG	59.886	20
GAGTCTTGGGAAGCGAAATG	59.813	20	CAGAGCGCACTCGAAGAGTA	59.49	20
TGTCGTGGTTCGGATATTCA	59.924	20	AAAACACCTGGGACCACAAT	59.162	20
TCTTGTTTTCTCCCCAAACC	59.003	20	TTGCCAAGAATTGAAAAGGC	60.188	20
TGGGCTTCTTCAGCTTCTTT	59.195	20	AACCACCTTGTCGTGGATTC	59.827	20
GCCTTCTTGGTTTGAGCTTG	59.993	20	TGATCATCCTCAGTTGTTGATT	59.985	23
GTTGCAATAATCAAGTTCAAGCA	59.311	23	TAGTTCCGAAATGATTGCCC	59.901	20
AGGAGCTTCTTTGGGGACAT	60.074	20	CCGCCCTCAAGCCTAGTTAT	60.593	20
CCCCTATAACTCTCGGGGTG	60.694	20	ATGTTTGAGGCTGCGCTAGA	61.071	20
CTCCATCGTCATCGAACTCA	59.787	20	GCCTTTCTCCTTTTCTTTAACCA	60.114	23
AATCGCAGAACATGAAACCC	59.939	20	TTCCGTAAAGCGAAGGAAAA	59.826	20
TCCCCTCATCTCTGCCTCTA	59.903	20	AATCATTCACCAACACGCAA	59.972	20
AGGCTGAAGCAAGAGAGACG	59.891	20	CCCGTTGAAAAAGTCTGGAA	60.081	20
TCATGGTGCAACACGATTTT	59.972	20	CCCGCCATACTGGTAAATGT	59.708	20
AGGAGGGTAGGTGGTCTGGT	59.848	20	CCTTTGGAGGTAGGTTGCAC	59.592	20
GAGAGGGGCCTTCTTTTCAC	60.19	20	ACGGTGTTGATTGTTCGTCA	60.008	20
AGAGGGACGAGGGACAATTT	59.935	20	CGGTCAACCGATTCCCTATT	61.061	20
GTCATTACACCCGGAAATGG	60.051	20	TTTGTGGACCTAACGCATGA	60.111	20
TACATGGCTGGCGTAGTTTG	59.752	20	TAGTGTGCACTCATCCACCC	59.551	20
ATGGGTGTTACCGTCTCTGG	59.844	20	AGGGACGGTGCTATTTAGGG	60.332	20
AAACAGTCGAAGTTCCCGTG	60.149	20	TCCGAGCCTGAGTCAATTCT	59.95	20
ACTTGGGCCCGATCTATTTT	59.799	20	AATTTGGTTGGGTGCTTCTG	59.971	20
AGGCATAAGAAAGGATGAATGTA	58.303	24	CGGATGAGATGCAAGAAAAA	58.843	20
TGGTATGGTGTGGAGAACCA	59.806	20	TATACTCGCTACGAGCCACG	59.111	20
TACGATGAAGGCTGCATTTG	59.833	20	TTCAGCAGGCGTAGACATTG	60.011	20
GGTGGTAAAGGTCCCCACTT	60.088	20	TTGCGGACGTCAAAATTCTA	59.301	20
GTTCAAATCCCACCAACGTC	60.218	20	AATGGGTTGTCCCCTTTTTC	60.032	20
GCCCGATATTTATCAAGGCA	59.892	20	TGTTGCACCCTGAGCAATAA	60.257	20
ACCCTAAGCAGAGGCTCACA	60.012	20	AGGTGCTTCTCCATCCTCCT	60.216	20
CACATGTCCCAAGTGATTTCAA	60.786	22	GCGAAACATGACGAGGCTAT	60.243	20
GCAACAAATGAATTGGGCTT	59.945	20	CATGTTGTTAGAGTGGCCGA	59.716	20
ATTTTTGGGAGGGAAAACGA	60.644	20	TTTGGGTCAATCATTTTGGTT	59.168	21
ACAGGCTAGTGTTTGGGCAC	60.179	20	CACGACCCAAATCAACTATTCA	59.861	22

TTTTTGGTACCAGAGCCACG	61.049	20	ACGTTGTCCTTTACAAGGCG	60.168	20
TTTGCCTATTTAAAGCCCCC	60.267	20	GAATTTGAGCAGGGAGCAAG	59.955	20
CGAAATTGATCGAAGGAAGC	59.784	20	CCTTGAATCTCAGCACCACA	59.831	20
AGTGGATACGAGCAAGGGTG	60.134	20	CTTTCGTTTCCAATGTCGGT	59.971	20
AGCAGACGATGATGCAGAGA	59.688	20	TCCGTGTGGCTAACAATTCA	60.111	20
AAGAAAAGGCGTGAATGTGG	60.11	20	TGGCATTCCTTTTTCAGCAT	60.585	20
TTAGGAAAGCAGGCAACCTT	58.973	20	ATGATTTTGGCCTTTCAGCA	60.585	20
CACTAGCACCTCATGGCTCA	60.008	20	GAGATTCTGGCACGAATGGT	60.081	20
GCCATTCACCATCTCTCGTT	60.081	20	CATCATGCGGGTAAGGAAAT	59.784	20
GGGGGAAACCATTAGGAGAA	60.124	20	TGCAATCTGCTCCATTTAACA	59.315	21
AAATCCAAATAATTGCCGGA	59.259	20	TCTCAAGTTCGCCCTTTTTC	59.429	20
CCCCCATGAAAAGTCAAAAA	59.772	20	TTGCTTCCAAATAATGGCTTC	59.202	21
CAAGTCAAATACCCGTGTCCA	60.791	21	ACATACATTTTATCATCCATTC	59.18	24
ATAGCTCACCACCGACCAAC	59.997	20	ATGTGAAGGTGTGCGTGTGT	60.08	20
CGTGTCATGTCGACTCGTG	59.868	19	TTTGGCATAATCTGGACTAAAC	58.687	23
CCTCCGTTTAAGGTGATGGA	59.926	20	ACCATTAACACGCAGGATAAC	57.713	22
TGAGAGCGAACTGCAATCCT	61.087	20	CGTCCCCTCTCTCCCTTAAC	60.067	20
TCTTTTGTTTCGGAAATCGG	60.046	20	AGAAAGGAAGAAACCGGCAA	61.088	20
GAGATTTGGTCAAGGGAGCA	60.195	20	TTGACAACAACTTTGCCAGC	59.888	20
GTCCAAGATGGGATTGGTTG	60.173	20	TAGAGAACACGTGCAGAGGC	59.191	20
CGGCATTTTCGGAATTAAAG	59.56	20	TGGGGAGAATGTAATAGCCG	59.916	20
GAGGAGCACCAGTCAACTCC	59.841	20	TGATGACCTGGAGTTGTGGA	60.088	20
TCCATTATCTGGCCCTTTTG	59.894	20	AGCAAATCGCACACATACCA	60.142	20
CTAAAAAGCCAGGGCCTACC	60.089	20	CACCATATTTGTGTTTCTCATT	60.625	24
TGCAACCCTAAGAAAAGGGA	59.679	20	CCATGATCAACCATGCCATA	60.159	20
AGCTAGTAGGGCAAAGTTGATTA	57.547	24	ACCCGGTGATCCGTATATCA	60.036	20
AAATTGATTGGAGCATTGCC	59.907	20	TTGAGATTGGTTGGTGCTGA	60.24	20
TGCAATTCCACCAACTTTGA	60.088	20	TGTGAACCTTTCGATGAGGC	61.188	20
CCGGAATCTGAGAGAGATCG	59.903	20	CCAGTTCCCTCCCTACTCACT	59.608	21
GCTTCTCTTCTGCCTGCATC	60.249	20	TAGTATTGTCCCTCCACCCG	59.807	20
CTTTGTCCCTAAACCCCCTC	59.799	20	TCATAAGGATTCGGCCAGAC	60.036	20
CACATTTGGCTGGAAGGACT	60.111	20	TGCCAAGCGAATGACATTTA	60.215	20
GGGAAAAGGACAATTCCTCG	60.797	20	CTCTTCAATGCCACAAGTGC	59.445	20
GAAGCATTTCACATGTAGAGTAT	57.987	27	CGTACCAAAATGTGCAACAAA	59.518	21
ATTCGAGCGAGGGTTTTCTT	60.208	20	TTTCCCCTTCATGTCCTACG	59.926	20
TAGCACTTGGGATGAAGCGT	60.796	20	AGGGTTAAAATTGGGAACGG	60.048	20
AGCAATTTCATTTAACAATCACG	59.91	24	TCATGGAATGAAGTTCTCAAG	59.316	22
ACTCTCCATGGACGTAGGTG	57.578	20	TGGAATTTTCCAAATCTGGCT	60.788	21
GTTTCGGAGGATTCGGATTT	60.265	20	TCCCATGTATGTAGATTGCTTC	60.218	23
TGAACTTGGGTTTGGTCCAT	60.21	20	TCTCGTCCTGACAAACTTCAA	58.483	21
TGTTTCTGCAGGTTGCAAAG	60.027	20	CCTCTTGCGAGAAGTTGGAG	60.126	20
GAAATATCCCCTGGAGCCAT	60.117	20	ATCGCCTTCAAGATCCACAT	59.513	20
GCCCTTTATTTCCGATGATG	59.369	20	TTCGAGTATTGGTTAATGGCA	58.174	21
TTGCAATTCCTAAACCAGCC	60.074	20	TCACCTTATTTCGCAATTTTCA	59.603	22
TCAATGTGCCATGATTTAGCA	60.088	21	TTAGCTCGCTAGGCTTCAGG	59.883	20
GTCAATCCGCACTTGGATTT	59.939	20	TGGACCCAAAATGCCTATTC	59.762	20
ACCCATTCCCAAGAGATGCT	60.853	20	TTGTACGGTAGCCAGTTCCC	59.993	20
TATTGCATTTCTCACACGGG	59.542	20	CCCATTTGAATCAACCCCTA	59.617	20
TTTATTCCTGTGCCAAGTTGAA	59.625	22	GGTTGTTCTCTGGAAACTGTTG	58.744	22
GTGGTATACCCAAAGCGCAC	60.395	20	ACAATGTCACATCCCAAGCA	59.967	20
CAACTCATGGTTGTCGGTTG	60.001	20	GGTTCATGATATTGGGGACG	60.014	20
ATGCTTTTGTCCATCTTCGC	60.221	20	CCCCAAAATTTCCCATTTCT	59.992	20
GTAATTGCTGGAGGCAAAGC	59.851	20	GGGGGAATTTATCCCGACTA	59.978	20
TGTTTATAGTCCCCCGGACC	60.929	20	ACCTCCGGTTTTCCATTTCT	59.805	20
GAAGTTTTGGGGATCCGAC	59.326	19	AATAGGCCGGACTTTCGACT	60.096	20
TTGAAGAAATCAAATCCCACAA	59.429	22	ATGTCGGTTTGGTTTAACGG	59.724	20
CCTGATTAGCCACAAGGGAA	60.066	20	ACCAAATCAAGGGGCTAACA	59.429	20
TTGTGCTCGTACACTCGACA	59.03	20	TGTCCCACATTGGAAAAACA	59.792	20

TTCTCATCATCATCAGCTCCA	59.337	21	AGGGACCTACAACTGGGAAA	58.498	20
TGTGTTTGCACAAGAGGAGG	59.873	20	TAAAGCGTTGTCTTTGAGCG	59.25	20
AGGGGTAGCGGTGTGTGTAG	60.051	20	AGGTTTGAGGGCCATGACTA	59.55	20
TTGCAGGCCATATGCTAGTG	59.856	20	GCTTGTTACACCACACTGGG	59.06	20
GAACGAGTTCGTTGACTAATTAAA	58.111	25	ACGCCCACGTGTAAAGACTC	60.179	20
CAGAGCGCACTCGAAGAGTA	59.49	20	ACTGAGGTGTCCCATACGGA	60.386	20
CAATCCTGTAATTCGCGTCT	57.849	20	TGTAGGCAATTCAAGAAGCA	57.1	20
TTTTGCACCCGAATGGTTAT	60.188	20	TGGTGAATTTCTTTTTGGCAC	59.967	21
TGGAATTTGTCCACCATAACA	58.733	21	GACCTCGAATGATGTCCGTT	59.934	20
GAGATATTTCCCGCTGTCCA	60.036	20	GCAAATATTGCAGTCAGCCA	59.839	20
GCAATGCATATTTAGGAAGTGG	58.654	22	GCGCCTCTTTTCCTTTCTCT	60.096	20
GCGAAACGAAATTTGGGA	59.598	18	TTCGAGTTTAGTTCTTCTGTAAT	58.63	27
AAGTGAGTTAAGTTTTGACCCAA	57.066	23	ATGGTTCGGTCTAACGGACA	60.375	20
GTCATTTCTCGTTTCGCGTT	60.257	20	TTCGGGACGAAATTTTTCAA	60.407	20
CCCATTCATCATGATTCCTTC	59.19	21	GGCGAATTAAAATACACCACG	59.376	21
TGGTGTCCTGTGAAAAACCA	59.976	20	GGGTTCCCGTGTCATAAAAA	59.662	20
ATGATGGCGTCATGTTTTCA	59.931	20	AAATCCTTGCACCTCCTCCT	60.074	20
GCAAATTAAAATGTGCCACG	59.077	20	TGAAGATCGCTTCCATCTTTG	60.337	21
GACTCGAACGAACACCCAAT	59.973	20	GGATCGAAAGGTTGTGGAAA	59.91	20
CACCCCGTATGGAAATTCAG	60.184	20	ATGGTGATTTTTGCCGTGAT	60.199	20
CCAATTTTTCAATCACCGGA	60.671	20	TTGCGGCCCATATAGTTGTA	59.053	20
GCCACGGATAAGTAACACCG	60.386	20	CCTCCTCCCCATTCTGATTT	60.264	20
AAGCTGACTCGCACATTCCT	60.02	20	AATGGTATGTTGGCCATTTGA	60.067	21
TCTCGTGGTGCAGTGGTAGA	60.463	20	AAATAGCAAGTTGATGGCGG	60.096	20
ACGCTCAAGCCATTCAAGTC	60.406	20	TCCATGTGCTTACAAGTTTTGG	60.032	22
TGACGTACGATCGAGTCCAG	59.855	20	CAGGAGGGTTTCTAATCCGA	59.122	20
TGGGAATTTAGGAATCGAGAGA	60.034	22	ATCTTCATCCGAGCCATGAT	59.469	20
CATCTTCAAGTCTGCAACGG	59.44	20	ATGGGTTGTTCCAAATCCAA	60.029	20
TATTTGTTGGTGGGTCGGTT	60.088	20	TGCCCATGTCTTAAATACTCTG	60.503	23
TTGATGGGAGGCAACTCATT	60.461	20	CAAGGTTTGGGAGAAAAGCA	60.22	20
AAGCACGTCAGCACAGACAC	60.104	20	CCCACTGACTCCTTCCATATC	58.46	21
ACTGCCCCCTTTCAATTCTT	59.94	20	AGGAAGGGGGAAAAGGAAAT	60.122	20
GACTATAATGGCCAGCACCG	60.49	20	TCAAACCCAGCAAGAAAACC	60.088	20
GGCCTGATTAATTGTGTGGG	60.192	20	AGAATCGACAGTTTGGACGG	60.111	20
AAAGGCTCAAGAACAATGCAA	59.875	21	GCAATTTTGTTGTTTTGTAAACT	59.539	25
CAGGCGGAACTAGAGAGGAA	59.569	20	TCAAACTCCTCCTCATGGCT	59.803	20
TGGTGGATTTTTATTTATGCAA	57.189	22	TGATTCAAAGCAGTTGATTGTT	60.159	23
TGAGCCCACCCAATTTAATC	59.762	20	TTTGTACGCAGCCATTACCA	60.133	20
ATAACGGGTAGGGCAGATCA	59.41	20	TTCCAGAAATTGTGTTGGCA	60.088	20
CGTCATGTCGTTCTTCCTCA	59.831	20	ATTGTCTCCCACCTGAGACG	60.112	20
GGCCCATTGCCAGACTACTA	60.096	20	CATGGCTAATGGACTTCACAA	58.637	21
GAGGCAGCTCCCACATACAT	60.104	20	GCTAGCAGCCTTGTCTGGAT	59.603	20
AATCAAGAAGCCTCTGCACG	60.538	20	AAGTCGCGTATTTTTCGTGA	58.439	20
CCTGCATATGCCCTTGTCTAA	60.103	21	TTGTGTGTAGGAGAATGCGG	59.716	20
GGTCGGCTACATGAACCAAA	60.894	20	CGTGTCATGCCAATTTCTTG	60.111	20
TTTTACTTTGTCGGCTCCGT	59.747	20	TCCAATTAATCCTAAACCACAT	57.985	24
CCTGGAAAAATGTGGGTGAA	60.724	20	TGGGGTCTTGGCGTACTAAC	59.993	20
TTATTGGCCGAAAATCCAAT	59.259	20	TTCTTTTTGACTTTTGAGCAGAT	59.933	24
ATTGGCTTTCCCGAGAACTT	60.074	20	CCAAACCCTCCATCTTTTCA	59.903	20
AGTCTTGTGGCCCAGAGAAA	59.844	20	CGATTTTTCACAGTAGCAGCAT	59.429	22
GCTAGTAGGGCAAAGTTGATTAGT	57.418	24	TCAGTGTTTGAATCACCTAATG	59.007	23
TTGTTTGCCACTTGCTTCAC	59.888	20	AGGGTGTGACAGAGGCAGAT	59.713	20
AGTGGGGAGTTTAGTTCCCG	60.353	20	TTGTTCCATGTTATTGCCAAA	58.922	21
GCTGCAGATGGACTCACAAA	59.992	20	GGCAACAGAAACTCCCACAT	59.973	20
TGTGTTATTTCATATCTTTGTGCTG	58.33	25	GAAGTTTTGGAGATCCGACG	59.67	20
ACTTCGTGGGCTTGGACTT	59.712	19	AGGGGCAATTTGTAGACACG	59.993	20
AAGTTTCTTTGGGACACCCC	60.204	20	TGCCACTGGAATTTTGTTCA	60.088	20
CGTGTGCTGGGCTATTTTCT	60.27	20	GGTCGAGCCTGCTACATAGG	59.859	20

ATGGGTTTGAACTGAAACTGC	59.091	21	TTAACGCGCGCCATATATTA	59.233	20
CGAGATTCAAAACGGTTGCT	60.249	20	AGTGAGACACTGAATGATATG	58.279	24
GTATGCAAAGGGAAAAGCGA	60.209	20	TGTGAATTCAATCGAGCCAA	60.197	20
AGATTGAAGAAAAAGGGGGC	59.532	20	GACCAGCACAGTGAAGACGA	60.03	20
AGACCAGACATCCACTTGCC	60.12	20	CAGCTGTTGATGGGATTGTG	60.112	20
GCTTCATGTATGCTTGGTCG	59.301	20	TTGTTATTTTCATTAAGTTATTA	57.628	27
ATTATTCCGACGATCTCCCC	60.117	20	TAGCCAGAAAACCCCAGATG	60.066	20
ACAATTTCCAGATGGAACGG	59.79	20	TCGTACACGAGGAGATGCTG	60.008	20
TGGTTTGACATGTGATGGGA	60.795	20	TGATCATGAGGAGCAACCAA	60.201	20
CGCAACAAGTTGTATGGAGC	59.347	20	TCTGCCATCATCCACCATTA	59.883	20
TAACCATAGCAAAACCCCCA	60.181	20	TTTCGGATGTAACACAGGCA	60.111	20
TTCCTAGCTCGATTTCTCCG	59.546	20	CCACCCTCTCTTTTTCCACA	60.081	20
GGATTTTCTTCCCATGTCCA	59.727	20	CTTCCCTCTGGATGGTGCTA	60.21	20
TCCAAAATCTGGTTGCTTGA	59.247	20	ATTAGGATAGGCAGCTCCGC	60.701	20
TGCTTCCATTTGTGAAGATATGA	59.6	23	TGGAATTAAAACCGAGCCAT	59.411	20
GGATGGATATGGTTTGGCTG	60.155	20	CAATCCAATTCCTGTATGGAAA	60.062	23
TGGAGGAAAGGAGCTGAAAA	59.926	20	TAGCAACTCGCTCTCCCAAT	59.978	20
AGTCTCCGGGGACAAATTCT	59.935	20	GACCGAGAAGGAAGATGACG	59.803	20
CGTGCTTGAACAAAAGCAAA	60.029	20	GCAAACACCCCAAGATTTCA	60.874	20
TTGGATGGACTAAAGGGCAG	60.066	20	TGTGGGATGCAATGAATCTG	60.481	20
TCCACCATGGAACACAGAAA	59.935	20	TGGGAAAGGAATTGCAACAT	60.309	20
TCTTCCACGAGAATTGGACC	60.05	20	TGATGGAATTAAGCTGCGAA	59.401	20
CGAGCTGAAAAAGACCAAGG	59.986	20	TGCTCCAATCTTCTCCACCT	59.803	20
TTGAACGAAAATTGATGGTCC	59.793	21	AAATCCCGGTGACAAGAAAA	59.406	20
GACGACCTGTGGACCTTCAT	59.969	20	GCAGGCATACACTCCCACTT	60.142	20
GCCGCAAAAGTTTCCATAAA	60.075	20	GTTGGCCCCCTTAGATCATT	60.152	20
CGGATTGCCAAGCCTATTT	60.045	19	TTTCTAATGGAGATCAAGTTCG	59.75	23
ATGGTGTCAAAGTTCACGCA	60.16	20	CCAATCAGAAAAGTCGGCTG	60.766	20
AAGGCAACAAGAGATGGGAA	59.67	20	TTGCTTAATTACCATAAATGCT	58.866	25
AATCATGCAACCACAACAATTA	57.953	22	TCCACTCCATTGGTTCTTTT	57.083	20
AACCTGCAAAATGCCAAAAG	60.11	20	CGGGTAGGAATCAGTTTTCG	59.564	20
GCATCGACCTTGGACAAAAT	59.939	20	AAAAATGTCAAATAAATTCTC	59.359	25
AATGGCTCAGTAAACAATGGG	58.962	21	CATTAACGCCCGTAGGCTAA	60.109	20
TCAAGCAAAAATATTCCGCC	60.04	20	CTTTCCAAATCCCTATGCGA	60.031	20
TTGCATCTTCATGTGCAATTC	59.685	21	CAACAATTCACCTCGCAACA	60.699	20
TGCTCCCTCCAATTAAGACG	60.206	20	TTTGCCCACCCCTAACAATA	60.181	20
GCGCCCATAAAAATGAAATG	60.282	20	TTAATCCCGACGTTTGAACC	59.801	20
GTCAGCCGACTTTTATGGCT	59.34	20	TTTCGTGTTTAGCCTTTCGC	60.376	20
GATGCGAATTGAATAAGGCAA	60.054	21	TTCCACCCTCTCCTTTTCTG	59.255	20
TTGGCAACAAACAGAATCCC	60.874	20	GGTTTCGCTGATTTTGTGGT	59.978	20
GAATGAAACGACACTGGGCT	60.119	20	CCAATGGTGGTATGGTGTGA	60.088	20
ATTTGGTTCGGTTCGGTTTT	60.573	20	TTGCTCCCCATTTTGTTTTC	59.916	20
GTATTCATTGTACACAATAAGGA	57.094	27	TCAATACCCGAGAATTGCAT	58.038	20
TTTGTCATGACTTCGGCTTG	59.84	20	ACTCCCACCGACAGTTTCAT	59.43	20
TTATCTAAAAACATGGGTAAAAA	57.432	26	ATGCAAAAATACGGAAACGC	59.971	20
TTTGAGGAGCTTTGCGTTTT	59.996	20	CGACTTGATTGCGAACCATA	59.688	20
AAAAGAGCAATGTGGCATCA	59.276	20	CCACTTTTGTGGGTTCTCGT	60.005	20
GGTTCTTCAATGGAGTCGTCA	60.104	21	ATCAAGTCAATCCGAGTCCG	60.073	20
ATGACAACCAAACATGCCCT	60.24	20	GCAGCCCGAGAATTGTCTAC	59.843	20
GGCGGAAGCCATAATATCCT	60.267	20	CCGAAAGAAACGGTGGTAAA	59.968	20
AAACGGGGTTGGGTTGTG	61.616	18	GAACCCACGCCATAAAACAC	60.235	20
AACGATAACGGTAACGATAACAA	57.743	23	TGGTTTCCTTCATGCTTTTTCT	60.109	22
GGAAGGAAAGCTAAAAAGGATT	57.242	22	AAGCCAAAATGATCGGCATA	60.424	20
TGCAAAAGCACTCTTCCTGA	59.716	20	AGGAGTGCAATCGAACAAAGA	59.867	21
GGCATGCGAGTGCTATTACA	59.862	20	GGGAGAGTGGATGTGTAGGC	59.535	20
GCAGACCATAATGCTTTTGTG	58.307	21	CCTTAGTGGATTTCATGGGC	59.387	20
GAAGAAGATGTCAAGCCGGA	60.34	20	TCCTAATCCGTGGAATGAAA	58.011	20
ACCAAGAGAGAGAAAGGGGC	59.817	20	TGTCCAATCAAGAGGCAACA	60.24	20

ACACTCATTCTGGGCCTCTG	60.261	20	TCGTTTCGACATCCGTTACA	60.111	20
GTTCGAACCGAACCATGAAC	60.362	20	TGAGTTCGGTGGGTATGGAT	60.195	20
TGCAACAATTTTTGGTATATATCTT	58.929	27	TGGCTTAACATTTCCCTCCA	60.439	20
TTATTGCACAGCTTCATGCC	59.839	20	CGCATGTTACGTAAATCGTTAA	60.289	24
AAAGCTTTGTCCCACATAGGAA	60.001	22	CCACAAAGCCCAATCTGAAT	59.933	20
CACTGCTGCTGAGGAGTTTG	59.77	20	ACCTTTCTTTTGACTGATGTGGA	60.026	23
AAACATACCAACTCACCACTCC	57.963	22	AAAGATGGGTGGAGTGAGAAA	59.976	22
GAGAAACTGCAGCAAAAGGC	60.14	20	ACCATCATCATCAGCAGCAG	59.819	20
AATTTCGTATCGAGTTGGCG	60.096	20	TCGCTATTGTATTTAGGCAGGT	58.007	22
GAGAGTTCAACTTGGCGGAT	59.288	20	CACCCTTGAGGTGTTCATCA	59.52	20
GGTCAGATCAAACCGAATCA	58.489	20	ATTAGCATTGGCGGTTGATG	60.857	20
AGACAATCCATCTCCATCTGGT	59.824	22	CATGCCTGATGACTCGAGAA	59.942	20
TCTGGTTTTGGGTTTTCTGC	60.088	20	TTGTGCCCCCAAGATTACAT	60.192	20
ATCCGATCGAATGGACCTTA	59.344	20	AAGTTCACCTTCGGAGATCG	59.284	20
CGCCTCGATTGAATCTTCTC	59.917	20	TCCACTCTCCCATTTTTCCA	60.43	20

PRODUCT2 size (bp)	start (bp)	end (bp)	FORWARD PRIMER3 (5'-3')	Tm(C°)	size
205	1435	1639	AACGAATTGAAATGAATTCTA	59.396	25
173	21	193	CGAACGCTCCAAATTAGAATG	59.728	21
118	241	358	CCAATTTAGGCACCTTCTGC	59.708	20
134	54	187	CTGAGCTTCAGAGCCCAGTT	59.745	20
228	599	826	TTGAATTCATAACCTTCCCATT	59.22	23
149	361	509	AGCTCCACCTCCAAACAAGA	59.844	20
275	14936	15210	TGCAGATGCTTCAGGTTTGT	59.445	20
187	19	205	TGTGTTGTGTGGAATAAAAG	60.217	25
114	667	780	AAGAGCAGTTTTGGCTGGAA	59.993	20
274	11	284	GCAGCAATGGTTGTGATTTG	60.119	20
228	82	309	GAGTCACGAGACACTTGGCA	60.03	20
175	20	194	CTCCCTCGACACACACTCAC	59.278	20
209	162	370	TAAATCATCAGCCCACGTCA	60.073	20
204	261	464	TCATTGTTTGGCCAGCAGTA	60.257	20
241	252	492	GACCGGAAGGTATGAACAAC	59.845	21
198	414	611	TCGCTGACATCATCTTATGGA	59.241	21
233	369	601	CTTGCTAGATGGCCGAAAAT	59.32	20
245	380	624	TCAAGCATTTGAGGGGTTTT	59.546	20
228	6	233	CGGGGACACATAAACCTCAC	60.232	20
262	15	276	TTCCCCTTTGCCCTCTATTT	59.903	20
151	13	163	CCCACTGATTTGTGTGAGGA	59.52	20
227	16	242	AGTTTTCATGGATGGATGCC	59.756	20
262	512	773	TCCAAGTTTTTACCCCACCA	60.198	20
214	28	241	ATGACCATATCTCGGTTTAGC	58.606	22
239	623	861	TTTTTAATGGGCGGTTATGG	59.669	20
117	200	316	GATTTCTTGGTTCGGGATGA	59.871	20
156	1	156	GGGTGGATGACTTTGGTGTT	59.679	20
208	8	215	TCTAACCCAAACCCAAACCC	60.938	20
276	14	289	TTTCGTCCCGAAATTTTGTT	59.429	20
243	81	323	AACCTTCGGCTTGAAAACAA	59.724	20
184	121	304	AACTTGGCCCCTAAGCTTGT	60.13	20
218	13	230	CCATCTATAGCGGTTAGCGTG	59.772	21
210	1	210	CCCACTTAGGAACATTTAGGG	57.624	21
206	252	457	TGATTTGCGATGATCTGCTC	59.914	20
266	214	479	GTTAGCGGAGTGAATGAGGG	59.694	20
214	66	279	AATTGATCATGGCTTCTGGC	60.043	20
175	133	307	GGGAGTTTGACACCTAAAGCC	59.99	21
275	219	493	AAGAAAAAGAGACACCCGCA	59.853	20
163	76	238	TGGTTATTACTGGAACGCGA	59.182	20
136	2141	2276	AAGGATCGAAAACGAGGGAG	60.569	20
230	2251	2480	GATGGGATCACCTTGATTGG	60.135	20
173	24	196	ATTTGACATCTAATACCCAACT	57.03	27
175	208	382	ACAAATTTATTGCAGGCGCT	59.748	20
147	28	174	GGATACCCTCTCAAACCCTAG	57.667	22
241	38	278	TGGTCATTTTCATTCACCCA	59.75	20
224	1023	1246	GAGGCTCGTCTGGTCCATAG	59.827	20
144	44	187	TGATTGGTGATGAAGGTCCA	59.893	20
274	28	301	AATTCTAACCATCTTCTTTTGC	57.932	23
163	132	294	ATCCTCCCACCCCACTTAAC	60.052	20
122	410	531	GAGGGAGAAAAGGGGAGAGA	59.749	20
215	30	244	GACTGTTCGAGCTTATCCGC	59.985	20
239	383	621	CACGTACTGGCCTAAATAATG	57.802	23
102	781	882	GAGAGCATGAAGAATGAACC	59.719	22
157	16	172	GGTGAGATTTGTGGTTTGGAA	59.822	21
227	16	242	TCGGTCGAAACCGAATAAAC	59.938	20

235	406	640	ATTACCGTGCACAGTCCCTC	59.997	20
163	0	162	CAATAATTTTGTTTCCCACCAA	58.76	22
211	74	284	CCCGGTGTAAAGAAATCGAA	59.931	20
270	952	1221	TTTCACAAACCACGTTGACA	58.57	20
274	137	410	GGATAGGCCCTAACTCGACC	59.925	20
166	1348	1513	TATAGAAGCAGGCCAGCACA	59.59	20
118	3198	3315	CGCTAAGATGGAGTTTTCGG	59.839	20
175	8	182	GGGATGCCATTCGTTAGTCC	61.606	20
198	915	1112	CAATTCGGGTTTTCCACGTA	60.722	20
154	0	153	CCCCTTTGTCAACTTAGGCA	60.103	20
278	421	698	CTAGGCGGCATTCTGTTGA	59.956	19
177	169	345	AGTCGGTGGAGTGGTTTCAC	60.009	20
251	1849	2099	TGTTCAGCAGAGGATCCAAA	59.369	20
102	0	101	GCTACCTTATTGATCCATTCCT	58.188	23
159	12	170	GCATGAAATTGTGTATTTTGGT	59.288	23
238	2598	2835	AATGAATGCCCAAAAATCCA	60.132	20
203	12	214	CTCTCTTTTTGGTTGGTGGAA	59.201	21
159	924	1082	TGGGTATGTGAATCATTTTCAT	59.504	24
164	648	811	TGCAATCTCAGCCACTCATT	59.399	20
184	4194	4377	TGGTCGTTGACACGACAGAT	60.162	20
212	302	513	ATGCAAGAATGGGTTTTTGA	58.066	20
236	51	286	TGCATGTTATTTTCGTGTTGC	59.622	21
264	59	322	GAGCACTCGAAAAGTAGCGG	60.154	20
184	61	244	CGAGGAGAACCTTGGAGTGA	60.377	20
165	25	189	TGAGTTTCAATTGCGTAGTCA	59.808	23
205	315	519	TCACAGACGGAGAGAGACAC	59.587	21
277	1138	1414	TTCGAACTTACCTAGGCCCAT	59.973	21
257	33	289	TATTTTGGACGATTTTGCCC	59.773	20
227	422	648	TCGTCCGCTGCAGTAATATG	59.856	20
202	473	674	TGTCTTGCAGGCAATTCATAA	59.315	21
235	446	680	TTCCTAATTTTTCGCTCCCA	59.655	20
264	189	452	CCGATCCCACCTTGTTTTTA	59.795	20
233	283	515	ATTTGCCTAAAATGCCCCTC	60.28	20
173	1217	1389	AAAAGGTGAACTCAAACGGC	59.218	20
270	1522	1791	CGTTGATCAAGCTGGAGGTAG	59.883	21
278	828	1105	TCTCTCCCTCTCAATGCACC	60.349	20
181	120	300	CGGATTCACCAGAACAAACC	60.353	20
113	1	113	AGACGATTTACACAAAATGCA	57.86	24
272	1394	1665	ATTGGACACAACCCACACCT	60.135	20
183	944	1126	TTCTCTCCCCCTCAACTCAA	59.773	20
269	2	270	GAAAAGGTGGTGGTGGTGTT	59.721	20
202	167	368	GTTCTGCCCTCCTTTTCCTC	60.19	20
261	293	553	TTCCCCCAAAACCGAATAAT	60.361	20
131	230	360	CTAGATCACTCGGCCAACCA	61.196	20
219	31	249	TGCTCTGCGGGATAAAATGT	60.606	20
108	40	147	TGACTATAAGGGGTGTTTTGA	60.052	25
188	14	201	TTGGGCTCGAGTGAAAAGAT	59.813	20
279	91	369	TCCCAAACTTCGTGTGTGTT	59.034	20
239	21	259	AAAGCTTGGCCATTCAACAA	60.617	20
205	684	888	CCCCCTTAATTACTTTGTCACG	59.767	22
144	1331	1474	GAAACCCGCTGTTTGGTTTA	59.975	20
161	10	170	TTTTGTTTGTTCCCAGGTTG	58.5	20
109	5018	5126	CCCATTATGGAATCTCACGG	60.148	20
127	325	451	GAATCACAGCCGTCCATCTC	60.633	20
157	26	182	AAACAACAATTCATCAAATAT	59.194	24
278	249	526	ACTTTGCATCCCAGTCAGGA	60.656	20
240	2148	2387	TCCCAGCTGAACTCCGATAC	60.218	20
202	510	711	CCTTGCAACAAACTCGGATT	60.11	20

190	43	232	CCTCGTCGACTACTTCCCAA	60.246	20
250	2098	2347	GCAAATGTAGCACGCAGAAA	60.021	20
278	650	927	TTGTGCACTTCATATCGCGT	60.288	20
186	8	193	GTGAGAATGATGAGGGCGAC	60.633	20
188	580	767	CTTCCTTTAGGCCATCCACA	60.066	20
153	48	200	CACTGACATCCATCCATTGC	59.925	20
226	620	845	GATAGTATGCCAATTTTTCGTG	58.212	23
119	315	433	TGGCACATTATTGGTCTCTCAT	59.457	22
217	100	316	ACGTACGTGTGTGTGTGCAT	58.491	20
219	902	1120	AGAAGAGCAAATGGTGGTGG	60.111	20
157	11	167	CGAATTTGGTGTTGGAATTG	58.866	20
150	368	517	CAACGGTTGTCATTGTTTCCT	59.883	21
254	881	1134	CATTTCGTGGCCTTGATTAAA	59.95	21
118	149	266	CGGCCGGAATATCTAAAGTG	59.564	20
206	70	275	GATGTCTTGCGGCTAGGATT	59.297	20
147	73	219	CGAAACTCGTGAACCAACAA	59.734	20
234	20	253	TTGCTTTCCAAAAAGTTGTACG	59.333	22
259	12	270	CGTGGTTCGGGTATTCACTT	59.853	20
193	1264	1456	TCGATTTTCATATTGCACGC	59.668	20
167	23	189	CATCCCAAACTCTCTCGCTC	59.95	20
266	58	323	CAACACCTGACCACCCCTAC	60.275	20
241	9	249	TCGTCGATCCTTCCTCATCT	59.761	20
280	207	486	TGCACTTGAGTTGCTTTTGC	60.18	20
204	29	232	CAATAACCCTTGGCTCGAAA	60.067	20
239	564	802	GCAGAATTCCTCCTCCTCCT	59.778	20
103	411	513	TCTTCCCCAAATTGGTTTCC	61.023	20
127	167	293	GCTTCGTTGTTTGCTTCCA	59.98	19
248	987	1234	AACGGACGTGTTTTGGCTAC	60.037	20
155	18	172	TCTGTGCTCTCTTTCTCAGTCG	59.93	22
136	178	313	TTCACCACCTAAAGAAGGGCT	60.116	21
159	6	164	TTGGGAGGATTTTCTCTTGC	59.244	20
115	312	426	TTCCTTCATCTGTCACGTCG	59.831	20
269	314	582	CGACGAGCATGGAAGAGTAA	59.024	20
202	572	773	GTGTTGACGAGAGCAGAGCA	60.343	20
269	8	276	TGTCCTGTTGAGGTGGAACA	60.129	20
275	1875	2149	TCCCACGTAACGAATTTTCC	59.801	20
230	1248	1477	ACAAAAAGCAGCACAACGTG	59.951	20
270	166	435	ACTGTCCTCTTAGACCGCCA	59.867	20
240	541	780	GCACGATAAGGACACGAACC	60.526	20
246	514	759	TAGTTTCCCACAATACCCCG	59.679	20
155	212	366	AAAACAATGTCGTTGCCACC	60.796	20
238	1548	1785	TCAATGTTTTGCGTTTCCAA	60.088	20
157	19	175	CAATGCAAGTGATATTCATCGT	57.66	22
126	96	221	GAGCTTGCACTCAGAGAGCTT	59.13	21
136	15	150	TGACCCTATGACGCCAAGTT	60.517	20
213	796	1008	TCCCGCTTCATAGCAAATTC	60.175	20
252	1799	2050	ATCCTCCGGTGGAGATTTTT	59.766	20
248	447	694	GCGAAACAAATTAGTGCGTG	59.373	20
255	407	661	TGGCGTTTGATATTTGAGAAGA	59.72	22
273	938	1210	TTTCCACACCACGTCAGCTA	60.301	20
271	498	768	AAAATGGCAGCGATGATAGG	60.06	20
250	221	470	CGTGTTCTTCACTCATCCCA	59.676	20
185	1192	1376	GCACTGAAACGCCAAAAGAT	60.257	20
267	19	285	CTAGCCCACTACTCCCCAAA	59.191	20
153	2178	2330	GATGAGTTCCGTGAGCATGA	59.794	20
272	860	1131	GGTGGCGAGAGAAGTGAGAG	60.135	20
114	17	130	TTGATGAACTCTCTTGGGTGG	60.096	21
157	2193	2349	AAGAATGGCACAGACTCCAGA	59.859	21

102	269	370	TGTGCCAACATTCCGACTTA	60.111	20
171	12	182	AAACCCAGAAGAAAGACAGC	58.969	21
214	561	774	AGACTCATGCGGCTCTTGAT	59.981	20
279	480	758	CTGTCGATCAACACCACAAAA	59.6	21
240	516	755	GTGAGCATTTTGGATGACGA	59.654	20
271	362	632	CCCCTCCTTCCATTCTTCTT	59.508	20
150	604	753	ACGAGGGAGAGAGACGATGA	59.945	20
249	0	248	TTCGTGCATTCCTACCCTATTT	59.864	22
157	81	237	CTCTCATTCACGCTTTTCAGC	60.147	21
167	2289	2455	AGGAGTCCTCTCAGTTTCATC	57.982	22
143	175	317	CCTTGAAGACAATGAAATTTT	59.865	23
164	19	182	TGTTATCCTTTGTGAGCCCC	59.933	20
184	61	244	GAGGAAATTCGTCATTCCCA	59.871	20
191	9	199	TGCACCTTCCACGAATCATA	60.073	20
196	82	277	AGTTGGTCGGAACACTTCGT	59.622	20
151	77	227	CGAAAATGCCCTTTTATGCT	59.212	20
273	11	283	TGTGGCATGAGAGAGAGGG	59.92	19
149	52	200	TCTCTCCCCCAAAGTTATGGT	59.813	21
185	73	257	AGTGCACGTCAGAGTTGGC	60.047	19
255	308	562	CAATCAATCTCAGCCGTTTG	59.272	20
234	76	309	AACATTTTACCACATGATTAA	57.587	25
255	291	545	CCCCAGCCATGTTAGAAGAA	60.066	20
233	1964	2196	ACACCAAACTGATTAAAATCC	59.638	23
245	20	264	GGTTTCACGTCGGAATATTGA	59.815	21
179	1421	1599	TCCGAATATGAAATCGGGTT	59.23	20
194	1073	1266	TCGAGAAGTTGTTTGTCTCAA	59.944	23
266	142	407	GGTCCCCTCCTAACTTTGCT	59.576	20
155	430	584	CCCCGAGGAAGCTAGAAAAA	60.674	20
128	49	176	ACTCCCACTTTCCGTAGCCT	60.132	20
185	14	198	CGGGCAGAGAGAGAGAACC	60.08	19
202	222	423	AGGGTGGGTTTGGAGAAGAG	60.48	20
119	338	456	TTAATGACGGAGCTAGGGGG	61.309	20
166	230	395	GTCACGTCAGCAAACCATTG	60.16	20
247	1094	1340	GGTTTTGGGAAAAAGGGAGA	60.271	20
279	48	326	CGTTGGACCTGAAAGAGCA	59.968	19
197	165	361	GGTAAACTAAGCACACCTGTA	59.035	26
178	7	184	TCCAACTCCATTTGCAATACT	57.23	21
199	15	213	AAAGCCTACCTTGCTTCCGT	60.262	20
120	92	211	GGAGAAACTTGCTTCTTGGCT	60.012	21
267	906	1172	TCGACGATTTATTTTCATGCC	59.921	21
221	545	765	AATAACAAATGGCCACGGAA	60.188	20
149	283	431	CGTTATCAAAGGAAGGGCAG	59.702	20
209	356	564	TGCATTCCTTTCCAGTCTCA	59.369	20
196	1126	1321	CCGTTCCGTTCCATAAATGA	60.692	20
175	782	956	CAGGCCAACTCCTATCTGGA	60.21	20
209	68	276	GGCGGAGGCAACTATAGAAA	59.32	20
256	561	816	TTTTAATTCATTACTCATATTT	57.16	27
101	20	120	CTCTCTCCTGCGTCTCTCTCA	60.018	21
255	689	943	TGCTATTGAAAATGATCCCAC	60.323	22
235	1842	2076	TCAAGACCTACCGAGCTTCTG	59.624	21
133	3643	3775	TCGAAGGGGATTTTATGTGG	59.756	20
239	73	311	ATGGGATACGGACGGTTATG	59.528	20
128	2608	2735	TTTGACAGACAAATCGCTCG	59.988	20
280	4	283	GCGCAGATCTAATGGTCCAG	60.765	20
190	10	199	CCATCCATTTCATGCATTTC	58.77	20
247	226	472	GGGAGAAAGATGACGACGAG	59.803	20
278	81	358	TTCGTCGTACAACTCGTCAA	57.897	20
272	428	699	GTTTAGGCTCATGCCCATTC	59.533	20

277	3	279	CGCCTTTTCACCTCAAATTC	59.685	20
252	16	267	GCTACTTCCGACTCTCTCGC	59.337	20
278	829	1106	CTTCCACGATCTCCCATACAC	59.42	21
200	0	199	TGCTAATCAGAAACTTGGAGC	60.018	22
270	6814	7083	TCTTACAACACAACCCCACAA	58.934	21
166	167	332	CAGTCAGTGGAAGGAGGTGG	60.702	20
261	311	571	ACGCAAGCGATATGGAAAAG	60.23	20
138	24	161	CATGGGTGGTATGGTGTGG	60.517	19
208	2	209	AGAGCTTGGTGTTGGTGCTT	59.914	20
192	1427	1618	GAGCAAAAATTAAGCCCACG	59.72	20
186	27	212	TTTACGTGTTAAGCCTTGGGA	59.634	21
129	114	242	ACATGCGTGTGTGTCTGCAT	61.271	20
149	0	148	CTTCTCTTCCACATCCGGTA	57.739	20
207	15	221	TTCGATGTTGTAACGGAGACA	59.184	21
221	23	243	TGGCTCTCACACTCACTCTCA	59.747	21
232	552	783	TCGATCGATAATAACGCTTTCA	59.717	22
254	160	413	ACATGTGTCCTATCCCGGTC	59.661	20
204	3492	3695	TCACAATCGCAACATCCAAT	59.931	20
187	516	702	GTGGGTGCAGTTGGATTACC	60.24	20
162	1574	1735	GCTGCGAAGAACACAATCAA	59.995	20
232	184	415	TGTGGAAACAAGTGCAGAGG	59.873	20
260	45	304	AACAGTTTTGCTCCCTCACG	60.291	20
167	28	194	GGGGCGTGACAATATCCTAA	59.784	20
205	0	204	TCGCTTGAATTGCGACATAA	60.356	20
135	175	309	ATGTGGTCCCAAACTCTCCA	60.363	20
260	689	948	TCAGCACGCGGACTATATGA	60.388	20
147	24	170	CACTCACTCTCACTAGCCGC	58.78	20
171	22	192	TACGCATTCAAAGCTGAAGA	57.257	20
225	3393	3617	CCTGTGGAGAAGAGGCTCAG	60.127	20
222	282	503	TTGGGAATTCAAAATGATTCG	59.759	21
260	90	349	TAAGCTTCCGGGAGGAAAAT	60.034	20
228	2995	3222	CACCAGCCTCTCCTTCAAAC	59.844	20
171	1473	1643	GCACTGTGAGACTGAGGCAG	59.764	20
164	25	188	AAGGCATCAAAGTTGTCGAT	57.265	20
198	2	199	CGAGGGCATTATGGGAAGT	59.902	19
230	96	325	AATGATAATCTTCGCCGTGG	59.923	20
253	55	307	AGCAATAAATCCACGTACAGG	59.912	23
166	200	365	AAACACCTCCTTAGGTGCAAA	58.754	21
139	22	160	AAAGGCCAAGTCAAGGATCA	59.67	20
202	267	468	CGAAGAACACACACTTTTGGG	60.568	21
212	26	237	CACCAACTGGCGAGAAATTA	58.771	20
275	315	589	TACCGACCTCACTAGTCCCG	60.126	20
197	44	240	CAAATGGCCAAGAAAGTTTAC	60.372	23
246	4	249	GGGGACTTTTCACTTTTGGC	60.836	20
266	69	334	TGAAGAATTCCCTTGGGTTG	59.903	20
233	148	380	TTTCTAACGATGATGGAAAAA	59.885	24
168	497	664	TCAATGGTTTTGGTTTGTTCC	59.693	21
277	2953	3229	ATTTTTGGCATTTCACCTGC	59.945	20
123	1146	1268	CAACATTTTGGCCTTTCTTGA	60.096	21
134	415	548	GCCTCGACAACATCATCGTA	59.679	20
277	6003	6279	ATTTCTCTTCACACGTTTGGAT	59.059	23
115	223	337	GACAAGAGCCGAAAAGTCGT	59.478	20
101	6	106	TCTATAGCAAGATCTCACGCA	59.284	23
219	3222	3440	TGATTCGTCGGGTCTTCATT	60.461	20
280	325	604	CACATTAAGAGGAGGTATCAT	59.814	26
194	186	379	AAGTTGGGCTAAGTGGAGGG	60.488	20
242	726	967	CGGTCGGGTGATCCTAATTT	61.061	20
273	456	728	CTGTTAGGCCCATGTCGTTT	59.993	20

270	616	885	TATGTTGGACCAAAAAGCCC	59.801	20
192	417	608	CGTTGTTTCCTCACACCCTT	60.005	20
154	19	172	CATTTCATTTCAGGAGCTTCG	59.831	21
122	270	391	CCATTTTTATCTTCTCTATCTTC	57.938	25
202	182	383	ACTCTGTGGTGACTGCCTCC	60.315	20
266	255	520	TCATCACGTAAACGGGGATT	60.192	20
238	203	440	ACAGCTTACACCGTTGAGCA	59.515	20
205	376	580	GGAGCAAGGAGAAGTTCGTG	59.989	20
194	919	1112	GGTGAACATTGGGAGCAAAT	59.797	20
234	239	472	TTTACCGATTGTTGCATTTTAA	58.315	23
210	728	937	TGATTTGGAAGAAAACGATGG	59.924	21
149	3	151	ACCCTACACTCTACACCTATTG	57.104	27
201	12	212	TGGTTCTGTAACCGAGTTGAA	59.649	22
192	1	192	CCCACTAACCCTTCATCACC	59.259	20
114	223	336	TGTGGAATATTGTCCCGGAT	60.014	20
158	62	219	TACAACCGCCAAGGCTTATC	60.096	20
274	0	273	TCCAAATGATAAAATCGTGGT	59.748	24
258	229	486	ACGGAGAGTCTTCACAAGCG	60.589	20
211	923	1133	TCAATTTGTGTCTTATAAATTA	57.208	27
220	56	275	CCTAGGATGAAAACTTGCATG	59.225	22
144	0	143	CGAACGGTTGGAATATCTAAA	58.643	23
229	662	890	CTTTCCTCTCACAATTCGCC	59.813	20
253	21	273	AGTAGTTATGCGTATTGTTACC	57.666	26
188	22	209	CTTTGCGACGTAATTCCCAT	59.96	20
121	437	557	TGTATCAGTCACCACCTCCAC	58.421	21
168	0	167	TGTGCCTTTTATTTGAGTAAGA	58.081	24
216	390	605	TTCAGCCTTTTTCATGTGGA	59.247	20
201	20	220	GCTTGTAATTTTTGGCTGGC	59.726	20
184	49	232	CGGGTTATTACCTGATTGCG	60.335	20
127	227	353	ACCAACCCATCAAGAATCCA	60.173	20
245	55	299	GAAAAGCAAACGAAAAAGCC	58.989	20
109	1	109	CAAGATGAGGAATGAAAAAG	58.929	24
274	18	291	GGAAATAAGGAGGTGTTATGA	60.434	25
222	15	236	GTGATGGTTGGTGTTGATGG	59.656	20
263	18	280	GAGGGGGAAGAGGTTGAAGA	60.565	20
238	130	367	TTTGATAGAGCCGGATTTGG	60.031	20
201	1821	2021	CAGTTTTTAAGTTTCGAAGTTT	58.659	24
279	410	688	TGAAGTGTCACTCAATGTGTC	59.794	22
116	24	139	TTGGTTACTGTTACGTATGCCA	59.74	24
137	537	673	TGAAACACGCTTACCGTTTC	58.822	20
195	1365	1559	ACCATCAAGGTCAAACCTGC	59.973	20
233	1409	1641	TTGCTGTTGTGTTGGCATTAG	59.784	21
100	303	402	GTCTCAATGGGGACATCTGG	60.326	20
277	44	320	GGAGGGAGAAGATGAGGAGG	60.149	20
229	3427	3655	AAGGCGAGGGAGGAGATAGA	60.306	20
230	3522	3751	GGGCCCACATTAGCTGTCT	60.088	19
280	5791	6070	AATTTAGTCGGCCGGATTTT	59.808	20
270	47	316	TTGAACCGTGTTACCCTTCC	59.83	20
273	317	589	TGTGCTCTCATTTGATTACACT	60.542	24
249	1995	2243	TTTTCCCCAAAACACCTCTG	59.942	20
237	810	1046	TCTTCTCCAACCCACAAACC	59.943	20
123	19	141	CCTAACAACAAAAGATAAAGT	58.045	26
247	147	393	ACCACCACCACCTCAACATT	60.135	20
231	32	262	TCTGCGGTACATCCAAATGA	60.073	20
275	176	450	TCACACTCACTCTCACTAGCT	59.871	23
190	395	584	GATGTTCCCAGAGTGGTGGT	59.817	20
226	375	600	GTAAACCCGAACCCTGTGC	60.368	19
224	1899	2122	TGGAAAATGGTGGAATGGTT	60.029	20

253	305	557	GCACCCCAAGATGGTAAACA	60.755	20
252	374	625	GCTTGCTGAGTTGGCATGTA	60.019	20
242	291	532	ATTTCGAAGATCAACGGACG	60.074	20
107	740	846	TAAAAATGTGCATGCAACTGA	57.86	21
205	23	227	TCTCTCTTTTTGGTTGGTGGA	59.697	21
230	21	250	ACATTGGGAGAGGTGGAGGT	60.77	20
225	695	919	TCAGTGCTGAACGTGTCAAA	59.002	20
182	196	377	CCGGAGTGATTTGTCAGGTC	60.51	20
119	20	138	AGTGTTTTGACATGATTACTC	57.373	24
191	1598	1788	AAATATCGGCCGTCAGATTG	59.923	20
273	72	344	CACTGCAGAAAAATTCACGC	59.469	20
125	47	171	AATCCCACTCTTGCTCCAAA	59.67	20
259	1139	1397	TTGTTCTCGTTCAAACCCCT	59.569	20
237	1	237	AAGAACACACACCAAGACAC	57.525	21
274	3165	3438	ATTTAATGTCCCACCCCGAG	60.929	20
243	2725	2967	CTCGCCGCTTAAAATTGTGT	60.264	20
277	47	323	TTCTTGGCATCCAGTTCCTT	59.67	20
247	24	270	AAGGGGGTTATTAGTGGATCA	57.425	21
261	841	1101	TTGGTGTTATGGATTGTGTGA	57.298	21
224	2	225	AATAGGCTTTTTGCCTTCCG	60.558	20
189	99	287	CTGAACATTGCCTGCTTGAA	59.988	20
256	478	733	TGTCCAGATAGCCTCACTGC	58.987	20
237	5	241	TGGGTATCGTCATTTATACAA	60.684	26
280	93	372	CCCCTCGTATGCACTCAACT	60.134	20
183	96	278	CACCATCATCCTCAGAGCAA	59.787	20
277	578	854	TGAAAGTGATTGCGTCTCCA	60.39	20
180	18	197	AGATTTGGGCAGTGTGGTGT	60.431	20
176	8	183	GCGAATCGAACGAATCTGA	59.899	19
272	2822	3093	CACCTCCTTATTTCCTAACTTC	57.086	24
154	187	340	TGCTCTCAGCTCTTTTGCCT	60.419	20
266	0	265	GACACAAGAGAGGAGAGGCG	60.135	20
179	15	193	TCGGAAAAGCTTGGATGAAA	60.692	20
237	18	254	TCTTTTGGTAGGTGAATGTATT	59.016	25
254	62	315	GGTCGTGTCAGAAATCGTCA	59.682	20
119	464	582	TCGCCTTGTTTAGGAGAGGA	59.948	20
258	2	259	TATGGCAATGGGACCAAGAT	60.155	20
280	220	499	TTCATCAACATGCAGCCATT	60.08	20
113	44	156	GGTGCTTGGTGAAGGAAGTG	60.69	20
222	245	466	TGCAGTTGAGATGTCCTTGC	59.992	20
242	2644	2885	ACATGGGCCAAATGAGAGAC	59.934	20
137	3118	3254	AAAATTTCGAGCACAGTGGC	60.257	20
256	246	501	TATGGATTATCACCGGATCG	58.255	20
201	61	261	TAAATGGCAGTGTGGGTTGA	59.964	20
200	107	306	TCGCTAATTTCCTAGATTTTCT	59.797	25
168	7	174	ACGGATTTAAGGGTTATTACC	57.667	23
214	105	318	AAAAATCATCACACGGGGAG	59.79	20
279	189	467	GGCGAATGATGTTTCTAGGG	59.528	20
234	201	434	CCCATTAATTTTTCCACCCA	59.497	20
279	1498	1776	TTTAACGGTTTGAGCCTATTG	59.687	23
239	379	617	CTTGGAAGAAAAACCCCACA	59.942	20
206	528	733	ACTATTCGAATGCGAGGGAA	59.668	20
275	1204	1478	CGTTGCACGGGATTAACTTC	60.502	20
149	1048	1196	ATGTCGCCATCATATTTTGC	58.458	20
153	609	761	GCTCATTCTGCTTCTTCCGT	59.579	20
269	988	1256	CGATCTGGAACCTCGAAAGA	60.331	20
191	1423	1613	GACCGCAAGAAAGGTTCTGA	60.375	20
252	1683	1934	TTCGGGCTAAACGAGTCAAT	59.708	20
262	450	711	GGGCACTCAACCCTTCAATA	59.933	20

230	18	247	AGGATGTAAATACGGTCTGTG	58.149	22
197	451	647	GACGTTCATTCGTATTGGGC	60.339	20
229	30	258	CGACTCACGACCCTACCAAC	60.567	20
213	1135	1347	TGATGTATGGTCTCCTTCCCTT	59.827	22
255	226	480	CTCCAACACCTCCAACTTGC	60.69	20
270	36	305	TGCTTCCTACTAAAGTTGAATT	59.05	24
183	29	211	AAAAATGGCGATGAAACCAG	59.938	20
122	0	121	GAGCTGTTATGCGTTTTGATGA	60.272	22
149	23	171	TCTTTGTCCACGGAGAGGTT	59.697	20
146	251	396	AAGCAATGAGCGAAAAGCAG	60.658	20
142	14	155	GTTAAGTAACCGGAGAGGCG	58.858	20
188	475	662	TCAGAAATTGTAGTCGCCCA	59.272	20
161	33	193	TTGGAACTTGAGCAACTGGAT	59.726	21
225	834	1058	TCTGGGGTTTCAGGTAGTCG	60.103	20
216	929	1144	CGCAGAAAATAAATCATGACC	59.964	22
137	25	161	GAGGTAGAAGCACTTGTGTGG	57.463	21
194	67	260	ATCGATTAGGGCAACATTCG	59.923	20
234	51	284	CGCACGTCGAGAATTGAATA	59.833	20
238	87	324	TCGGGTTTTAGTGGAGAACG	60.103	20
170	114	283	GCCACCCTTAAGTGATTTCG	59.569	20
130	487	616	ACCTTGACCATCAGATCCCA	60.326	20
279	1554	1832	GCTTACTCCCACCGATGTTC	59.556	20
260	250	509	CATGCATGCTCGTACTCACA	59.436	20
202	548	749	TCCTTTTTGTCTTTCATTCGGT	59.98	22
131	540	670	TTGCATTCCCACCCATTATC	60.532	20
104	607	710	GTGAAGGAGTCGAAGGCAAC	59.851	20
198	1900	2097	TGATCTTGCAACTTCATGCC	59.805	20
219	7	225	ACACTCGACAATTTGGGAGG	59.966	20
126	8	133	TGCTTTTCAACTTAGAATTCAA	59.363	25
258	101	358	TGAGCTGAAGCGAGCTGAT	59.983	19
277	28	304	AAAACTATAGGTGTTTGGTAAA	58.242	26
160	11	170	CAATTACAATGTTTATCCAATC	58.612	24
239	5	243	CAGGATCTCATCGGAACCAT	59.886	20
265	649	913	TTCCGATTCTCAATTCCCAT	59.32	20
181	750	930	TGAGATCCTGGCTGTGTGAC	59.827	20
259	390	648	TTGCGGAAGAAAACTAACCG	60.236	20
251	14	264	AATCTCACAAACCCACACCC	59.679	20
120	2	121	TGGTCACTTACACAGCAATCAA	59.245	22
135	181	315	GATCTGCACCCTCCATGAAT	59.893	20
200	28	227	TGCAGTAGGTTGTAGGTACTAA	57.062	27
174	20	193	GAATTTGGGTCATGAATTTTGT	59.135	23
253	877	1129	TGCCAGAAGTTCATCGTTCA	60.39	20
201	19	219	GGCTAGATGCAAGCCTTTGA	60.49	20
156	311	466	GGGCAGTAAGTTGAGTCCGA	60.255	20
167	281	447	TTGATTGGTTGTTGGGCATA	59.786	20
270	1268	1537	GGCTTACCCCTGCACTTATG	59.592	20
102	2	103	TCGCACTAAAGCAGAACGAA	59.752	20
219	690	908	ATTCTCGCTTCTTCGCTACG	59.752	20
210	7	216	CCCCTATTTTTGGAGGGAAA	60.116	20
280	3538	3817	GCACCACCATCTTCTTCGAT	60.081	20
270	1539	1808	CAGCAACCTGAAAGCATGTG	60.449	20
152	173	324	TTAAGGGGCGGTATCATTTG	59.789	20
243	839	1081	ACAAAAAGCAGACGAAGGGA	59.853	20
255	958	1212	CATGCAATGCGATGTGTTTT	60.532	20
268	1349	1616	GCCACCTCAGAAGATGGAAG	59.803	20
229	20	248	CAATTCATAAAATACATAGAAA	57.131	27
214	2	215	CCCCATCAACACACATACACA	60.144	21
276	10	285	CAAACCCCATCACCAACTCT	59.82	20

235	41	275	TCGGCCTTTTGAAACTTTTT	58.852	20
138	821	958	CATGCCTTGTTCAGGCAATA	59.688	20
100	6	105	GAAGAACAATTACAATGTTTA	57.771	26
223	610	832	TGTTTGCAATTATTTCGTGG	57.176	20
228	7	234	TGCATCAAGTTCTCTTCTCTAA	57.9	25
219	22	240	TTGAACCGATGAAACTAAAAT	59.885	24
201	217	417	GTTGGAAGTGCGAATGTTCA	59.697	20
111	2837	2947	GGGAAGCTCCAACTGCTTTA	59.452	20
251	66	316	AGTTGAACCTCGAACCGTTG	60.149	20
190	545	734	AATCATTGTGCGCATGTGTT	60.003	20
264	2110	2373	CACACCTACTAGGCCCAAGG	59.61	20
265	2049	2313	ACGTGTTCAAGGTTGAAGGG	60.005	20
237	263	499	AAAGGCATCTGAGCCGTTAC	59.34	20
136	106	241	TCGGCTGGGGTAGTAATTTG	59.953	20
207	97	303	GGAGCAAGCACTGCTCCTAA	60.678	20
258	201	458	AAACAATTTCAGCCGAGGG	60.059	19
278	1645	1922	TTCCCAAAGCCACAAAAATC	59.916	20
207	911	1117	AAAATGAGGAAATCCCTCGG	60.258	20
187	68	254	CTCCAACACCTCCAACTTGC	60.69	20
249	2127	2375	ATTTCCTGCCCCAAATTACC	60.02	20
198	95	292	TGAAACTCCATCAAAACCTCT	59.165	23
254	51	304	AGGCAGCAATCAATTGGAAA	60.585	20
128	1030	1157	AGATTGGAGCGAAGAGTGGA	59.95	20
187	6	192	TGTTTTGTAATTTCCCATGTTT	59.577	24
277	28	304	TGTCAATTTTCTCAAGAAACC	60.825	24
205	149	353	AGAAACGCATCGTTTTCTGG	60.249	20
102	8	109	TGATGATCAACGTTACCGATA	57.512	22
208	167	374	ATAACCCCACCATCCTAGCC	60.039	20
202	397	598	GTGAGAGGGGGTATCCAGGT	60.194	20
268	2628	2895	CGTTTCAGTTTCGCCATTTT	60.11	20
216	48	263	GATGTGAGACACGTGGCATT	59.557	20
214	1730	1943	ATGCAGTGGACCATAGCACA	60.144	20
269	435	703	AGGATGGTGATGTTGAAGCC	59.934	20
246	277	522	TTTTTCAAACCAAACCGACC	59.817	20
277	397	673	TTGTGCGTGTGTATGCTGAG	59.483	20
138	1426	1563	ATATCAGCGGCCAAAAATCA	60.424	20
249	69	317	CCTGCATGGTTTTTCCTTTG	60.472	20
208	224	431	CCCATGGAGTCCAATCTACC	59.213	20
202	229	430	TCATTGGTCAAAAGTGCAACA	60.142	21
183	20	202	TCATCATCTTCGTCCTAAAAA	59.617	23
197	679	875	GTCAGCTTGCAAAAGAGAGG	59.749	21
242	5	246	CACTCTCCCTCTTTCTCTCTCG	59.756	22
119	2	120	TCGAAATCGTAATAATCGGAC	59.455	22
272	129	400	CCCTTCCCCTTCTACCTCAA	60.426	20
262	2	263	TGTTCTCATTCGTTTGCTCTAA	57.719	22
189	29	217	TTGTCTGCGGTAATGCTTTG	59.872	20
100	453	552	GAAGCTTCAGCGAGGTTACG	60.154	20
124	26	149	TGGAGTTGGAGTTGAGAGGA	58.349	20
267	71	337	GCCTTCAATTTTATACCCGAG	59.483	22
106	402	507	CGAATCGCGAGTGCATATAA	59.825	20
239	68	306	AGCCTAACGTGGCTCTGATG	60.419	20
100	1	100	AGCCTTCTAGCATCTCTTGCT	57.618	21
274	796	1069	CATTCTCTGCCTGTGTCTGC	59.577	20
201	1036	1236	GGAACTATTGCCAATGCGAT	59.929	20
210	1075	1284	TTGTTCGCAAGAACAACGAC	59.888	20
236	220	455	AAAATTGATAAATAGTGCAAT	59.994	25
102	1	102	GATTGTCTAAAACGTAAAGCT	58.527	26
234	19	252	GGGACAAAAACCGAAGGAAT	60.166	20

155	967	1121	CCGTGTGAACACAGACCTTC	59.152	20
251	17	267	CAAATCTTGGGGAATGTGTG	58.821	20
263	3612	3874	TCCGTAGACCTTCCAACCAC	59.966	20
151	283	433	CATGGATATGTGGAAGCACG	59.948	20
270	1970	2239	GAACACACTTGGGCCTGTCT	60.159	20
246	150	395	GTGAAAGAAAGAGAAAAGGA	58.916	26
239	257	495	CAGTGGATCGTTCTGCTTCA	59.984	20
275	699	973	TTGATTGCAATAAGCAAATTTT	58.045	24
243	481	723	TCGCGGATATCAATTATCAAC	60.303	22
276	669	944	TTCTGTAATCGAGTTCAAGAG	60.076	26
267	43	309	GAAAGCAAGGTGAGGAAGGA	59.405	20
193	317	509	CGAGGAATGAAATCGATGGT	59.894	20
278	83	360	GCAAACCCGTGTTCTTCAAT	59.978	20
239	196	434	TTGCCTGCAGACAGACAAAC	60.032	20
244	124	367	TGCCATGGATATGATTGTTGA	59.76	21
258	494	751	GGCATAAATTCATCTGAACAA	59.857	23
276	171	446	GGATGAACGTCGGTCGTATT	59.82	20
117	1138	1254	GAATGTCATTGTTCGGACCC	60.181	20
150	667	816	CCGTCGTCGTCAACTACAAA	59.758	20
273	221	493	AAGCAAAAGAGTCAGCCGAA	60.132	20
261	252	512	CCGCATGTCATGTTATTGGA	60.343	20
212	979	1190	ATACCCCGAAAACCCTTTCA	60.534	20
142	4	145	AATCTCCCACTTGGGCAAC	59.918	19
200	214	413	GCTTTCTTTCTTCCGGGTTC	60.187	20
182	813	994	ATGCCAGTCTTGAGCCAGAT	59.834	20
187	1221	1407	GGTCTTTTACTTTTCAGACAAC	58.909	24
201	1057	1257	CACCTACACCCCTACTCCCA	59.837	20
219	846	1064	GAACTATCGTCTCGTGCCGT	60.285	20
112	286	397	CATTCATGCAGCATTCAACA	59.232	20
162	849	1010	GCGTCAGAAGAGAGAGCGAG	60.577	20
260	1220	1479	CTTCCCAAAGTCATTTCCCA	59.903	20
163	2290	2452	ACAGAGGCTGAAGCAAGGAG	59.745	20
255	98	352	GCCATATGTGGAAACCTTCCT	60.201	21
221	611	831	TCACGCCCCGACTATCTTAT	59.551	20
160	132	291	CCCAATTTGCCCTTATATGC	59.282	20
219	328	546	TACATCAACGCCGATGAAAA	60.073	20
253	593	845	TGGGGGTCTGTCAAAAATTC	59.767	20
178	788	965	ACATCGATTTCGTGGAGATTG	59.947	21
145	32	176	CAATTGGAGTGAAACGGAGG	60.486	20
176	2209	2384	CAACCATGACACACCCACAT	60.138	20
220	535	754	ATGGTTCGCCATAAAAATGC	59.801	20
268	143	410	GCTTGATAGTGGGTTGGGTG	60.375	20
121	18	138	CCCACTTTTGGGTTATTACCTG	59.641	22
190	2251	2440	TACGTGGATTTGACAGTGGC	59.572	20
222	396	617	GGGAGAGAGGAAGAGGGATG	60.149	20
220	117	336	TGTCCAAGCAAAATTGACGA	60.234	20
216	5	220	AAAGCTCAAAATGAAGAGGG	59.849	21
215	60	274	CGCGACACCTCTAGAACACA	60.049	20
219	971	1189	GTGGGGAGGAAATTTTGAGG	60.663	20
164	990	1153	AGAAACACGTGTCACTTGGAT	57.266	22
139	334	472	CCTACGAGCCCAAAGTTCAA	60.241	20
276	13	288	CCGAAAACCAAACCGAATTA	59.805	20
115	1	115	TTTTGGAGAATTTTCTCTTGCT	59.048	23
261	157	417	TGTTTGAGTTAGCAGCCAGG	59.072	20
186	510	695	TCCGAAAATCAAAAACCCAC	59.778	20
116	249	364	GCTGCATGGAGACTTGCAT	59.966	19
251	1258	1508	GCCAAATATGGTTGCAGCTT	60.103	20
221	344	564	CGCACCTGAGGAGGTGTTAT	60.134	20

138	209	346	CAATATCCCAATGTTTGAATC	59.963	23
126	220	345	TATCACCAAAAGGAGGGGTT	58.359	20
264	633	896	TTATTGTTTTGGGCCTGAATG	59.818	21
245	1073	1317	GGAGGAGATGGAGACAGTCG	59.792	20
275	82	356	ACGTCGTCTCAAAGGGTGTC	60.159	20
216	192	407	GCTGGATATTTGGGCTTGAAT	60.294	21
148	49	196	AAATGCTCGCTCTCACACCT	60.02	20
267	763	1029	CGCGTCCCTTTTTACATGAT	59.96	20
203	554	756	CTCCGTTGTCGACAGAATCC	60.656	20
273	0	272	TCAGATCTGCGCTGAAAATAA	59.985	22
246	1230	1475	CCTTTCAATTCCAATGCTTCA	60.06	21
226	579	804	ACCGTGTTGGAAATGGAAAC	59.694	20
138	2375	2512	TTTCTTGGCCAGCTCTAGGA	60.088	20
239	389	627	TGCTTTTGCATGGTAGTTGG	59.729	20
144	82	225	ACATTTTTCTTTTGGGCGAA	59.564	20
157	414	570	GACTTCGTGGCGGTATTCTC	59.7	20
153	46	198	TGTCTCCATTTGTGTGTGTGT	57.381	21
221	17	237	ACACCGACCTCCACTTCAAC	60.009	20
207	26	232	TTCTCAAAAGGTGGAAACCG	60.081	20
253	393	645	GTTGCTAACCAACTACGTTGA	58.511	23
211	3409	3619	GGAAGTCCAAAGATGACCCA	59.903	20
174	31	204	TATTTCTCATCCACACCCCC	59.605	20
104	25	128	GAACAATTACAATGTTTGTGA	60.394	27
280	270	549	TGTACCTCTCGCTGCTCTGA	59.88	20
151	6492	6642	CCACAACCCATTCTTCCATC	60.173	20
104	18	121	GGGTCCAGTCAATGAAACGA	60.903	20
167	1252	1418	CGGTGAAGATAAATTGCACG	59.182	20
210	780	989	TCGTTTGAAAATGGGGAAAA	60.273	20
275	8	282	TAGAAACACGCAACGCAAGT	59.536	20
260	227	486	ACACCATCCAGCGCTATAAAA	59.622	21
171	118	288	TGCCATTTTGAGACCAGACA	60.24	20
241	15	255	GGTTGTAATGAGGCTTTCGG	59.569	20
239	22	260	AAGGGGAGTATCACTTGAATG	59.487	22
242	2485	2726	CAATGCAAAATCAGTCCCCT	59.933	20
245	1975	2219	GGGCTACTTCCCAACACAAA	59.971	20
219	199	417	CACGAATGTGCTGATGATGG	61.12	20
215	790	1004	ACACACGGGTCTTCATCCAT	60.246	20
167	444	610	AGCAAGAGAAAATTCTCCCAA	59.372	22
150	1110	1259	TGAAAGTGCCAACTTACGGA	59.317	20
236	3441	3676	TTTTTGCCCCAATCCATTTA	60.123	20
251	873	1123	CCAACCTTGTCGGAACAGTC	60.545	20
128	444	571	TGCTCTTCTAGCGTTGTCCA	59.74	20
198	376	573	AAACCATACGCATGCAGGTT	60.395	20
199	20	218	TCATCATCTTCGTCCTAAAAA	59.617	23
103	209	311	GGCCAAACGTTATTGGAGAA	59.938	20
186	35	220	GACATCAACTCTGATGCGGA	59.794	20
140	48	187	TTATCTCATCAACCGCCAGG	60.992	20
182	32	213	CAATCCCAATTGTAGCCTGC	60.469	20
276	104	379	TGCTGAGACATAGCGGACAC	60.016	20
151	25	175	AAAGAAGAACTAAAGCTTCG	59.187	24
238	28	265	TGTGAACACAGCCTCACCTT	59.31	20
119	1832	1950	AAATTCGCAGATAAAGGCCA	59.682	20
186	24	209	TCAGAAAAGTTCGAGCGTGA	59.716	20
207	493	699	ATCACCAACTGGCGAGAAAT	59.556	20
162	17	178	CGTGGAACAATTACGACCCT	59.853	20
165	203	367	AAGGTGTAGATCTGGCGGTG	60.134	20
224	758	981	GTGAAAAGTCAAACCGGCAC	60.538	20
207	43	249	AAAAAGGGGTTGATGATCGTT	59.696	21

277	22	298	ACGACACGAACGGTTTTGA	60.144	19
224	6	229	TGCACAAATTCGTTTAGGCTT	59.772	21
160	3142	3301	CTTGCGATCGTTTCTGTCAC	59.445	20
279	98	376	TCTTTTGTCAATGGAGCATCTC	60.256	23
239	256	494	TGCAATAACAAATTTGGGAAA	58.074	21
245	2375	2619	CAGAAGACCGATGTTTGCCT	60.255	20
141	295	435	CCCATGTGTCCACAAAACAA	60.255	20
156	4224	4379	TCTGGGGCAATGAACTATCA	59.075	20
218	3134	3351	ATCAACTTTCTGCCCATCCA	60.461	20
129	64	192	AAGCACAAGAGACGAAGAGT	59.281	22
165	525	689	TCACCGGAATCCACTCTCTC	60.199	20
196	119	314	TACCCTTGCATGCACAACAT	59.995	20
277	321	597	GATGCATCAAGTCGACAATCA	59.67	21
160	1166	1325	GAACCCGTGATCTTTTGGTC	59.386	20
268	90	357	CCAAGGTGGAGTAGAATCCG	59.545	20
135	439	573	CACCTGAAGGCGAAAAAGAG	59.986	20
227	269	495	ACATACTCCACCAACTCGGC	59.997	20
134	16	149	ACATATTTCCAAGTCACCTTCC	59.755	23
280	236	515	CCAAAGGGGCTGCAATACTA	60.089	20
222	13	234	ACCATATTTAAGGGTTATCAC	57.552	24
148	93	240	AGCACGAATCACACAGCAAC	59.912	20
206	43	248	AGTCCCCATGTATATTGCCG	59.668	20
152	3	154	ACTGAGCCCTGATTTGGAAG	59.284	20
276	1417	1692	ATTTGGTATCAGAGCCACGG	59.955	20
217	2641	2857	GAATCCCAGCTGTGGAGAAG	59.803	20
246	687	932	GCTATCAAGCACCGGAAAAA	60.209	20
278	32	309	CAAAGCGCACTCGAAGAGTA	59.366	20
146	3	148	TTTTATCAAGCGCAACCTCC	60.209	20
264	7	270	TTGTCGTATGCTGTCCGAAA	60.257	20
267	644	910	ACGAAATTGCCCTTGTATGC	59.967	20
258	924	1181	CTGCAGCCTTCTTGTCTCCT	59.745	20
194	595	788	CAACCGCCTGATTTGTTTCT	60.11	20
273	755	1027	ACAAAGCATAAACATCCCAGC	59.104	21
143	378	520	GATGGCATTCATCGTCAGTG	60.08	20
158	22	179	ACGCCCCAGATTGTTTCTTA	59.569	20
107	209	315	CAATTGGGGAGATGTTCCTT	58.836	20
205	172	376	TTCACCTTTTTCTTCTCGGC	59.429	20
113	103	215	CATTCGTACCCCAAACTTGC	60.365	20
111	891	1001	GAGTTGAAACTCGACTGCCC	59.851	20
197	324	520	GCAACCGTTCATCACTCTGA	59.837	20
229	27	255	TCGTGCGGTCAATGATTTTA	60.073	20
247	15	261	GGATTCAGTTGCTTCAAGAGC	59.069	21
132	233	364	ACAATATTACAATGGGCAAGA	57.725	23
112	2989	3100	GGCATGTGCTTGTGTAGTGC	60.342	20
162	359	520	GATCGACGTCCCAGATTTGT	59.934	20
233	689	921	CTCGTCTCCTCCACTTCCTG	59.978	20
135	46	180	AAAGAACAAAATGACACGAA	57.978	23
255	575	829	TTGATTAATGGTTCGGTTCCA	60.174	21
238	10	247	TTTTGTGATTTCCCATGTTTGT	59.225	22
228	2706	2933	TCTCTCAACACTTCAACGGG	58.852	20
262	279	540	ATAGCATCCATTCATTCCCG	59.745	20
161	3162	3322	CTGCAACAGCATAGTGGCAT	59.895	20
243	313	555	AGGAAATTGGGGGAAAATTG	59.992	20
125	230	354	TCTTCCCATTTTCCCAACAG	59.903	20
277	7154	7430	CTCTCTCTGCAGGGGAGTCA	60.69	20
141	318	458	CGAAGGAGACTGGAACCGTA	60.246	20
277	224	500	GGGCCCCTAGTCTGTCTCTT	59.699	20
215	187	401	ACCTAAACCCAAAACCCCAC	59.955	20

271	83	353	TGTCAACATTCAATCACAGCC	59.562	21
176	87	262	TTTCCTTCTTCCCACCACTG	60.081	20
146	292	437	CCCATCGATCCATTTCTCTC	59.44	20
194	1050	1243	GGCTCTTCTCTGTCCGCTAA	59.717	20
229	2204	2432	GGTCACAGAGGTCGTCCCTA	60.112	20
197	1737	1933	GCAAGCTTGGTTTGCAGTCT	60.581	20
240	60	299	AACTCGTCCACCCCTTCTTC	60.489	20
237	662	898	TTCATTTTGATTGGTGTGCAA	59.961	21
147	11	157	TTCAAAAGCAAGAAAATGTGA	57.995	23
189	1498	1686	TTCAAATGCCCACTTTTTCC	59.916	20
277	28	304	TGAAAAATGACGAAGGAGGG	60.044	20
158	0	157	ATACCACTCGTTAATCCGGC	58.93	20
246	3447	3692	AACACCGGAGAGGGAGTTTC	60.489	20
170	359	528	TGGTTCAATGGGTTATTCGAC	59.677	21
127	78	204	GTGCATCAACTTATGCCAAA	57.223	20
181	62	242	TGAAGTTAGGAAATAAGGAG	57.525	24
278	450	727	ACGCGATTTCACTCACAACA	60.31	20
265	6	270	ATGATGGGCACATGGATTTT	60.021	20
126	103	228	GGTGTTGGATGGAAAATGCT	59.797	20
242	56	297	CGCTTTGGGACAGCAATTAG	60.762	20
115	301	415	TCGAACAATCAAACTCGTCG	59.84	20
272	1443	1714	ATCCGCCATTGTTGAAACTC	59.939	20
117	4	120	GGCCACCACAAAGGAATAAA	59.801	20
146	539	684	TTTCCCTCTCCTCCTCCATT	60.008	20
181	1525	1705	GACCAATTCGGTTTGGTGAC	60.218	20
239	2810	3048	CACGTGTCATCTTCTTCAGCA	60.04	21
244	684	927	GTGGATGCATTCCATTTGTG	59.781	20
121	65	185	GGGCTCTTGTTGATCCTTCA	60.195	20
200	1162	1361	AGATTGTCCCTCACATGCAA	59.09	20
185	432	616	GCTGGAGCAGGTCTCTTGTC	60.143	20
109	155	263	GGGGAAGTGTGATGTTTGGT	59.679	20
220	417	636	TAGGGTTGGGGTGCATATTT	59.158	20
223	889	1111	TTATATGGGTTGGGTACGGG	59.406	20
279	278	556	TTGAAAATAAAAATGGAGTGA	59.343	25
165	25	189	TTTTACGAGATGGAAGAAGCT	59.445	23
201	5	205	GCGAAATTCATGTTGACCCT	59.939	20
222	307	528	ATGCAAGGATTTCCCAAAAA	59.388	20
168	2	169	GGCATTGCTAGAGCCATTGA	61.278	20
272	92	363	CCCTCGGATGCTAGTGTTTC	59.694	20
256	183	438	CTCCCCTTCCCATGCTAACT	60.455	20
269	12	280	GTCTCTTCCTGGGAGGGTTC	60.05	20
174	657	830	GATGGGAATGGGAGGTATGA	59.563	20
107	61	167	GCAGTGGAGTGGAGGAGAAG	59.986	20
144	1886	2029	TATTGGCTCGGTTTCTTGCT	59.845	20
230	362	591	AGGATTCCAGCCACATGAAC	59.934	20
246	143	388	TGGGCTAATCATTCTCAGCA	59.375	20
106	2157	2262	TTGTCCTCTTTCTTCGCCTC	59.55	20
198	667	864	ATCTGTTCCGAATGCGAGTT	59.7	20
237	25	261	TCTTAAAGCATCAACCGCCT	59.845	20
156	34	189	GTCACTTCAGCCGTGTTCTG	59.467	20
167	5	171	TTGGTGCGATATTTTGTTCG	59.562	20
280	67	346	CAATCTCAACCCAAACCCAT	59.647	20
259	12	270	GAAAAGCTTGGCCATTCAAC	59.691	20
156	1485	1640	TGCCCCTTTACTGCCTATGT	59.592	20
116	349	464	GTTTTTCCACCGAATCAAGC	59.551	20
269	344	612	TGCTGCTAATTATCCCTCCAA	59.69	21
209	72	280	ATGATTGGCTAGACATCGCC	60.066	20
136	31	166	TCATCCATTTTGCACCTGAA	60.049	20

275	27	301	ACCCATTTTGATCCTTGTGG	59.647	20
161	573	733	CGACGATGGGAAGATGGTAG	60.474	20
159	586	744	TGGATGGCTAAGACAACAACA	60.534	22
132	187	318	TCGTGAGCTTCTCGATACCA	59.547	20
229	1428	1656	CCTACAGCTCTATCCCGTCG	59.853	20
129	34	162	TTTGCAAGTTCCAGCGATTT	60.752	20
111	985	1095	GTCGAGGCGTAAGTTTGAGC	60.022	20
200	31	230	AGCCAGGGCTTTTATCATGT	58.672	20
204	2496	2699	GAGACAACGGAGTGGAAGGA	60.238	20
246	60	305	GCTTCATAGCATCTCTTGCTCA	59.758	22
221	22	242	TCTTGGTAAGCAGACTGCCA	59.591	20
109	2666	2774	GGCTGAATTTGACGATGCTC	60.754	20
189	12	200	GCACACAAGTTATTGGTTTCTA	60.209	26
161	786	946	GACCACGGGCGATAGTAAGA	60.096	20
126	151	276	ATTTCGAAGATCAACGGACG	60.074	20
111	80	190	CCCCTTACTCAATTTTAATTTGT	57.012	24
262	2704	2965	GTTACCGCTTGCTCCTTGAC	59.882	20
191	169	359	TGCGATGTCTATGTGACGGT	60.144	20
203	91	293	AAGTCGGACTCTTGTTCGGA	59.844	20
147	94	240	TTCATCCTCCCTCATTTTCG	60.006	20
257	1455	1711	TGGTGTCTACACGGTCCTCC	60.987	20
204	670	873	AGAAGAAAGGTGGGCATGAA	59.67	20
233	1745	1977	ACATCCATCTCAAAACAATATC	57.575	24
212	3056	3267	GCAGTTTGGCATCAGAGTCA	59.992	20
194	1145	1338	TGTGACAGAGCTGAAATGGG	59.831	20
257	148	404	TTTTGTTTCGTTTTGTTGCG	59.758	20
262	607	868	AACCTGCATTCCCAATTCAC	59.797	20
126	98	223	GAGTGAAGATGAAGTGGGGG	59.505	20
235	1914	2148	CCCCCTAACATTTTCCCACT	60.046	20
156	132	287	CAGCCCGGTACAGAAGGTAA	60.125	20
265	194	458	AATTCATGCCAATTTCTGCC	59.907	20
194	765	958	TGTTTTCTCTTTTGCATAATCAA	57.152	24
248	136	383	CGTTACAGCATCACTCGGAC	59.318	20
260	312	571	TATGAGCCCGCACATTATCA	60.058	20
275	1281	1555	TTTTGTGCCTTCATTATGCC	58.627	20
279	845	1123	TGGAAGGTATGTGAAATTTGG	57.474	21
117	92	208	TCTTGGCAAGGCTCTGAAAT	59.955	20
146	42	187	TGTTACTCTATCTGCATGCTCT	57.376	23
161	177	337	AAAGGGAGTTGCAGTCAGGA	59.844	20
152	206	357	TTCTCCCCCTCTCTCTCGAT	60.292	20
235	8	242	CACATACTCACGCATTCCCA	60.539	20
162	31	192	GCCTACCTTGCTTCCGTAGA	59.476	20
173	92	264	GGTGCTTTCTGGTTCATCGT	60.119	20
229	179	407	AGACCGAACCGAAACTGGTA	59.592	20
179	8	186	TGCAAGATCCAAGGGATGTA	59.075	20
277	449	725	CAAACATTTATCTTGCACTTGG	57.4	22
118	74	191	ACAGCAGGGTGTTTGTGTGA	60.203	20
268	796	1063	CTCGCGTCTCTCATCCATTT	60.362	20
236	761	996	GGGGAGTATCACTGGAATGC	59.366	20
258	225	482	ACGACGCATAAAGAGGCAAA	60.772	20
153	233	385	CGCTGTTTCACCATTGGATT	60.894	20
254	406	659	GCCCAAGTCCTCATCTTCAA	60.195	20
177	142	318	AAAGGTTCACCAAACTACGCA	59.663	21
231	311	541	CCTAGTCGCTCGTGGTTCA	59.992	19
279	820	1098	GCGCGCTAAATCAGATCAAT	60.339	20
195	26	220	CCAGAGGAGAAATAGGGAGA	58.845	22
250	11	260	TGACCACTTTTTACGGATTTGA	59.492	22
202	578	779	TTCTTTTGAACCAGGCAACC	60.088	20

216	3573	3788	CCAATCATGCTGGTTTTTCA	59.518	20
186	592	777	ATGCAACCAGATTCAAAGGG	59.933	20
273	470	742	AATTGCAAAACCCAACTAAGC	58.311	21
245	3	247	GGTTTGGCTTGACCTTGATT	59.031	20
138	88	225	GGAAATGACACCCAAACCAC	60.073	20
136	93	228	TCCACTCTCTTCTCTCTCCCTTT	60.006	23
154	18	171	ACCATATTTAAGGGTTATCACC	57.552	24
276	71	346	TAACTCAAAATCTTGCCCCG	60.067	20
167	241	407	CGAAGCAAACCTATTTCCCC	60.792	20
136	327	462	AAAAACTCACTGGTCGTCGC	60.299	20
272	3	274	AAAAATGGGGGAAATTTGATT	58.593	21
146	1565	1710	CGTCCAAAATCGTATCCGTTA	59.84	21
147	1451	1597	ATTCTTCAGGCTGCTGCTGT	60.164	20
269	1530	1798	CGTTTCGCAAATTAATCGGT	59.964	20
155	49	203	GGGCTCAATCTTGCTGCTAA	60.49	20
156	1160	1315	CAATGAAACCAAACCATCCA	59.222	20
275	5583	5857	GAACAGGCTGTGCCATTTCT	60.263	20
169	306	474	GAGGTGGTTGCACCATAACG	61.355	20
268	142	409	TCGAAAATCAAAGGCACACA	60.234	20
273	4676	4948	GATCGGAACGCTCATCAAAT	60.043	20
217	661	877	GCATTTGTCCCGTATGGCTA	60.857	20
252	1020	1271	CCCTCTTGATGGATTTTTGAC	58.491	21
216	1765	1980	TTGGCAGACTACTTTGTGGG	58.773	20
165	549	713	CATTTATTTCTGCCCCTCCA	59.894	20
273	354	626	CCAGCACGATAGATACAAATC	59.536	23
275	545	819	TCGCTGGTTTTGTAGTCGTG	59.904	20
110	8	117	ATTCTGTCGGATAGGTGCGT	59.579	20
122	1666	1787	CTTGCATTAATGAGCCGTCA	59.833	20
146	0	145	GCGTTTTGACGATATATAGTGT	60.194	26
279	104	382	AATCAATCTTTGAAACCGGC	59.022	20
249	194	442	ACAAATGCCAGCCGTTAGAT	59.597	20
207	194	400	CTATCCATTTAGTTCGCGGG	59.564	20
152	138	289	TCTGCTTCACTCACTCACGC	60.343	20
270	2030	2299	CACTGCTCTCTTTTCCTCGG	60.126	20
263	232	494	GATTTCGATGGTTTTGGGTG	60.17	20
180	718	897	GGCACACCTGTATACCCCAC	60.119	20
269	1279	1547	TGCATCTTTGGGGATGAGAT	60.426	20
258	93	350	AAAATCGACCGCACATTTTA	58.161	20
260	596	855	GATAGGCCCTAACTCGACCC	59.925	20
219	89	307	ACGTTGTCCTGAGCACGTTA	59.365	20
275	557	831	AGAGGGAGATCGTGGGAGAG	60.748	20
235	687	921	CCATGATATTGTTCCTTCGGA	59.77	21
219	23	241	TGATGAAGTTGGGTGTTGGA	59.935	20
197	57	253	CCTAAAATTGAACGAAACTCG	59.667	23
155	184	338	TAGCCCCTTTGAGACCATTG	60.066	20
134	589	722	CGTATGACGTATTTTGGGGG	60.067	20
251	226	476	TTCCGATGGAATGCATTTTT	60.268	20
203	67	269	CTGCACGGACACAGAAACAC	60.357	20
155	24	178	TCCCAGTTCAACTCTTTCTCG	59.458	21
123	274	396	GTGTGGGTTCCTCTCGTGTT	60.009	20
176	231	406	TCCACTAGGGGTACCAAAATG	58.82	21
195	19	213	AAAGCCAATCGAGTCTTGGA	59.813	20
207	15	221	AGAGATTTGAGCTTGGTGGG	59.284	20
190	170	359	TTTAACCCCGGAAACGTAGA	59.447	20
188	0	187	CGAATAGAGTGATGAGCCAAC	57.436	21
174	65	238	GCAACGGAATACCACTCGTT	60	20
176	2657	2832	ACACCATACCCAAAAGCCTG	59.853	20
278	396	673	TCTCAATCATGCGATCCAAA	60.159	20

227	147	373	GGAAGCGCAATTAATACGGA	60.061	20
197	68	264	ACGATTTTGCCCTTGTATGC	59.967	20
278	150	427	CACGATAAGGGATGGATTCAC	59.259	21
276	1089	1364	ATTAATGAGCCGACTCGCAT	59.696	20
174	44	217	TGTTCAAATGATTTTGGGGG	60.535	20
158	48	205	CACGCACGCATTCTTCTTT	60.003	19
270	1589	1858	TTAAGTCCTACCGCGCCTT	59.853	19
272	27	298	AATCGTTGCTGGAGCGTC	59.95	18
177	75	251	AGCCATCGCTCAACCTACAC	60.285	20
217	163	379	TCATGGGATCAGTTTCAATCC	59.741	21
270	105	374	ACTGTGCTGCTGGAAAATTG	58.926	20
210	53	262	ACAAATGACCAAGGAGGAGTT	57.626	21
255	156	410	TGGATTGTATGTGTCCCCAG	59.215	20
246	123	368	GTTATGTGGCCCGAATGACT	59.82	20
176	4	179	CCCATGTTTGTAATTATTGTAG	58.675	24
261	3368	3628	TTGAAATTTTGGGGGAAAAA	59.251	20
115	549	663	GAGCTTGGCAGAACGAGAAC	60.142	20
232	429	660	GCCTTATTTGATGCACGGAC	60.478	20
204	314	517	GGTTTTGTTTCAGAGGCCAG	59.711	20
191	226	416	GGAGGAGTTCTCTGTGTCGG	59.835	20
274	429	702	GCGTGACGCACAGTTTCTTA	60.058	20
208	681	888	CTGATGTCAATTTCCATATCCA	57.427	22
171	936	1106	CCTGATAAATGGCACCCACT	59.813	20
258	3975	4232	AAAGGGGTTTGGTTGGAGAC	60.204	20
157	99	255	TCGTCAAACCTCCCAAACTT	59.569	20
112	7	118	GGCAACGGAATACCATTTGT	59.691	20
261	1647	1907	CTCCCTCTCCCATCTCCAAT	60.412	20
186	2272	2457	TCCAAGGGAAAGTGTTCAAGA	59.697	21
278	1042	1319	GGAGGGGCAAAGAAAAGACT	59.691	20
235	53	287	CGAAGTTTCGTAGAATTCGGA	59.348	21
261	35	295	AACAAACACCTGGGACCACT	59.325	20
214	169	382	TGTGAAGAGTACAACTTACAC	59.494	24
180	446	625	CGAAAGCTGAAGAGCGAGAT	59.859	20
276	380	655	GGTCGGGGAACAAAGTACAA	59.83	20
208	20	227	CAATTTCTCTTCATGTGGCCT	59.184	21
265	327	591	CAAACGCTTTGTTTTCCGTT	60.145	20
190	389	578	CGTATTCATTGTTTTCGGCA	59.562	20
279	70	348	CAATCTCAACCCAAACCCATA	59.671	21
122	2	123	TTGGTTCACACAACCACTCC	59.415	20
179	62	240	CTCCCACTAAAATTTTCCCGT	59.359	21
273	1346	1618	GTGAGTGCCTGTGTGTGGTC	60.216	20
132	51	182	GCATGCTAGTGCCTGTTGTG	60.481	20
277	707	983	GCTCTCAAGGAGGAGAGCAA	59.827	20
204	325	528	TCACAACAGGATTCAGGCAG	59.831	20
250	98	347	TTCACAAAAGATTCGATTCGG	60.06	21
276	573	848	GGACTGCTGCTCCTCTAACC	59.043	20
231	27	257	AGTGAGGAGTTCACGGAGGA	59.835	20
240	2016	2255	TCTCAAAACCACAACAAACCC	59.861	21
280	402	681	CGACTACTCAATCATCCAACCA	60.787	23
256	553	808	AAGGGAGGAAAACGTAACCC	59.326	20
271	29	299	TCCGTGACATCAAACACTCC	59.525	20
187	2314	2500	AGACCGTGGTTGATCCAGAG	60.112	20
211	40	250	GGGGAAAATTTGCAAGATGA	59.878	20
192	4158	4349	CCCCATGTGATTGATGATGA	60.137	20
276	289	564	TTCATCTGCTGAAAGGAGGG	60.331	20
170	75	244	AAATCGGCGAATTTATCTGC	59.174	20
247	502	748	CAGGTGCAGGGAAGAAATGT	60.111	20
233	1762	1994	TAAGCAATTGATTGTCCGCA	60.215	20

145	12	156	ATGGCCACAAATGGTTCCTA	60.192	20
193	309	501	CTCTCCGAACAAATGTGCAA	59.84	20
212	138	349	TTAGGGTTTAAAATCGCGCA	60.564	20
162	22	183	CGTTGAGCCGAATGTGTTTA	59.729	20
222	1022	1243	ATTCACGTCCACGTTTCTCC	59.973	20
168	10	177	CCTTTCCTAACAGTTTGGCATC	60.001	22
130	43	172	CGCCATTCTCTCTCCACTCT	59.555	20
253	212	464	TGCGTGTTCTTGGTGTTCTT	59.339	20
129	160	288	ATCCCAAGTCATCACCGCTA	60.483	20
133	99	231	GAGTGAAGATGAAGTGGGGG	59.505	20
260	869	1128	TTTCCGACACCCAATCCTAC	59.79	20
141	2556	2696	CCACCTGGAAATCTCCTTCC	60.822	20
218	19	236	GATATTGACGGTTGGTTGGC	60.199	20
269	34	302	AATGAACCAAGTCATTGCAGC	60.133	21
182	89	270	AAGCCAAAAGATACGTCGGA	59.708	20
262	398	659	AGGTTGGAGGGAATGGAGAG	60.447	20
115	14	128	AAAATACCATTTCATTTTGTAA	57.172	27
154	3562	3715	ACTGAAAACAGCTTCCGTGG	60.291	20
190	2	191	CACGAGTGAAGAAAGGGAGA	59.072	21
251	882	1132	TGCATTGATTGATCGACAGC	60.79	20
244	1024	1267	TGGGATTAATTTCCACCATGA	60.002	21
243	28	270	TCAAATCATAGTCTTTCCTCGT	60.02	25
201	3	203	TGAAGTTAGGAAATAAGGAGG	58.743	25
232	749	980	TTTTCTCTCTCCGTCTCCCA	59.92	20
106	183	288	GAAATTTCGCTAAGTCGAGAA	58.255	24
256	2225	2480	AGGGACAGCTGTGGACTCTG	60.458	20
276	188	463	TGTGGTATCAGAGCCACGAC	59.707	20
200	44	243	GCATTTATGTGTCAGCCCCT	59.962	20
186	334	519	TGGTGAACGTGTTTTGTTGC	60.596	20
192	16	207	TTCACCACCACCATCTTCAA	59.935	20
274	5	278	GTGTTCGTTGGTGGAGTTGA	59.571	20
276	109	384	CATCCTAAAGATAAGAATGGT	57.108	26
202	155	356	GGCAAACATGAATTCGTTCC	60.318	20
171	30	200	GGGAGAAGTTGGTGAATTTGA	59.017	21
216	179	394	CCTTTCTCCCCCGTAAATTC	59.772	20
276	18	293	ATCGATTATTACCGGATCGC	58.88	20
204	70	273	CACACGCATTCTTTCTCCCT	60.255	20
173	268	440	TGAGTTTTGAATTCGGACCC	59.91	20
201	579	779	AGACAGCAATACCAGGGGTG	59.989	20
144	2350	2493	GTCGTGGCTCATTTTGAGGT	60.119	20
171	363	533	ACCGACTTCTGCACCATTTC	60.119	20
247	18	264	TCGGTTCTTGCTCCATTACC	60.074	20
174	16	189	TTTTTCTTTCCACAAACCCCT	59.837	21
116	62	177	CAGGAAGGGAAAAGCATCTG	59.807	20
177	577	753	TGTAAAGGTAGGAAATTTTTGC	58.665	23
229	2043	2271	GGGTTTGAAATTTTGAATGCT	58.1	21
248	481	728	TTGAAAATCTGAGCGTCCAA	59.395	20
271	102	372	GATTTGGCTAGGAATGGCAA	60.038	20
132	264	395	TCGTCCGAACACATTGAAGA	60.24	20
192	6	197	GTACTCGGACGGGATCTTGA	60.073	20
273	1848	2120	AGGGGAGGTGTTATTCAGGG	60.183	20
209	77	285	TGTTTCTTCCACCTCCTGCT	59.844	20
212	6	217	CGAGTGGTTGTGAGGTGAGT	58.725	20
229	430	658	TCGCACAAATGATAGCGAAT	59.285	20
251	1216	1466	TGAACCACCTCTGCAAACAA	60.278	20
188	151	338	TGCATAAGACACCTAGCCCA	59.297	20
250	274	523	TGATGACTGGGCAACTCAAG	59.831	20
236	606	841	TCATCTCCATCCCCCAATAA	60.088	20

233	465	697	GAAAAGCGAAGTGAAGCGAG	60.27	20
277	399	675	GCAAATCTGGATCCTTCGTT	59.129	20
253	114	366	AAACTTGAGCAGTCAGTTCGA	59.468	23
240	18	257	CTCCACCAGATCATCACCAA	59.473	20
212	3087	3298	CCAACCTCCCTGTACTGCAC	60.567	20
229	1723	1951	TAGTTGGAGGGAATGCTTCG	60.206	20
221	225	445	TGGCTCCTGAATCTCACAGA	59.499	20
219	76	294	TCACACAGAATCCCTGTTGC	59.682	20
147	27	173	ATAAATATCAGGTGTTTTCTGA	57.122	26
177	0	176	CCCTTTTAGGCTCAAATCTCTT	58.117	22
178	220	397	TTTTTCGCCTCCCACTAAAA	59.693	20
146	222	367	TTTTTGCCACCTATGCACAA	60.111	20
189	36	224	TCGGCCAGAGAGAAAAAGAA	60.066	20
265	106	370	AGTGCGTTTGCAGAGCTTTT	60.197	20
124	97	220	CATGATATTTTTCCTAAATTTT	58.561	27
185	105	289	CTCACCGTGGACGTAGATCA	59.701	20
269	1205	1473	TTGTTTAGAACAGCGGCAGA	59.609	20
238	332	569	AGGGTACCGGAGATGAGGAT	59.778	20
174	1	174	CCACAAACCGAGCTCACC	60.246	18
117	194	310	TCATGGATAGAGCGTGCAAT	59.256	20
278	21	298	TCGGTGATTCAAGAGTGGAG	58.8	20
243	47	289	CGGGCTGAGATAGTTGTTGA	58.874	20
100	1	100	AAGGAACAAATGAGAATGTTA	59.957	25
196	5	200	AGGGATTTGGGACGATTTTC	60.131	20
262	500	761	ATGCTACTTGGGCGTACACA	59.224	20
164	3	166	GGTGTTCTTGGCAACAGGTC	60.555	20
178	26	203	TCAGTTTCGAGTTATGAAGTTA	59.749	26
176	1840	2015	TGGATTGAAGCATGAGCCTA	59.375	20
114	170	283	ATGGGGCTGTGGTTGTAGAG	59.989	20
267	247	513	CAGTGACTCACCTGAAACGC	59.467	20
197	492	688	CACCTGCAACAGAGGAGTCA	60.022	20
170	89	258	TCACATCAATTTTCACACCCA	59.808	21
187	173	359	CATGATTGCCTGCTGAGTGT	59.862	20
181	390	570	TGCAAGCATCAAACAACACA	59.877	20
238	53	290	GATTTGTGTAATGCCCCGAT	59.651	20
127	392	518	ACCTTACCCAACCCACTTCC	60.088	20
237	541	777	ATCGAAGAGAATGTCGACGG	60.218	20
182	17	198	ACGTCTTGATGTCGAAACCC	59.973	20
279	763	1041	TAGGGTTAGCATGCTTGGGA	60.597	20
177	249	425	CATCAACCGCCAGGATTATT	59.784	20
219	193	411	GATGGAATGGGGATTTGTCA	60.526	20
229	83	311	ACCCCACCTTTCTTGGATTC	60.169	20
225	363	587	AACGTGAATCTCGGATCAGC	60.226	20
103	591	693	GCGTACATTTGCCCCTAAGA	60.096	20
211	177	387	CATCCAGGTTCGGTTTCAAT	59.79	20
214	206	419	ATTGACTTGGGCTTTGCATT	59.574	20
203	164	366	CTCTTGTAACAAAACCCCATG	58.035	22
252	93	344	GTGGGCTAAGTGAGGTGGAG	59.721	20
242	338	579	TCCAATGGAGAACCCTTTGT	59.381	20
204	3744	3947	ACCAAGTCAATTCCTAGTGCG	59.252	21
170	392	561	TTGACTTGTGACCCTCTCCC	60.088	20
277	1	277	CATACCAAGTCCCAGGGAGA	59.92	20
215	278	492	TGAGACTGCCTTCGTCACAC	60.03	20
222	490	711	TTTCAATGGGTAGCTCAGGG	60.066	20
102	50	151	CAAATGGCCGAGAGAGAGTT	59.43	20
235	953	1187	CCCCACAGATATCCCACCTA	59.623	20
183	646	828	TCATCATTCGACTTCCATGC	59.61	20
162	2	163	AATCTCCATGTTCAGGACTTCA	58.646	22

168	3636	3803	TGTGACACCAATGTGATGGA	59.325	20
223	364	586	GCAAAGTGTGCGGTCAAAT	59.713	19
164	44	207	AGAGGAGCCCAGCTTCTTTC	60.096	20
257	88	344	AATCTTCATAAGTGGAGGGGC	59.433	21
266	836	1101	CAAAACGTCCGTATCGACAA	59.585	20
183	103	285	CTTGAAGATTTTCATGGTGGA	57.657	21
208	453	660	ATGTTTCAATGACACGTGGG	59.267	20
167	158	324	CTGGGTCTGGTGTTGTTGTG	60.039	20
217	1291	1507	TTTACATTTTTCTGGCTCCCA	59.573	21
163	3	165	TGAAGTTAGGAAATAAGGAG	58.743	25
261	4160	4420	TCATCATCGTGCTTTCCTTG	59.799	20
162	136	297	TGCATGCACACTTGTAACCA	59.746	20
129	2508	2636	GGAAGAATGCGTGTGTGTTG	60.16	20
268	1303	1570	ATGCTGAGGTGTTGTCGGTC	61.146	20
201	1628	1828	GGCTGAACCATTCACCTGAT	59.934	20
252	1109	1360	GATCAGGTGGAATCAGGGAA	59.862	20
276	260	535	TGCACGTAGGCATGTTCAAT	60.142	20
147	585	731	AGCTTGGAATTGGTGACGAG	60.255	20
173	1	173	TGCAATTAGTGCATACAATGA	57.43	24
205	52	256	ATCGCAAATAAAACAACCGC	59.971	20
118	1950	2067	TCCACCGATCAAAGAGTTCC	60.05	20
173	31	203	CTGATTCGCACAAATGATCG	60.22	20
248	88	335	ACGTGTGTGTGATTGAGGGA	60.005	20
208	393	600	TGGTTATTACTCGAACGCGA	59.325	20
241	145	385	GACCGTGTAGGAAGGCTGAG	59.867	20
126	233	358	TTCTAGGCACAAAACCCACC	59.971	20
232	95	326	TCTGAGGATCCGAGCTCATT	59.91	20
277	319	595	CCCCAAATCATTACCGAGAA	59.756	20
177	795	971	GTTCAAGAAAGCCGTGGAAG	59.853	20
276	148	423	CATCCTCATAACCCCCACAC	60.05	20
229	2166	2394	CTTAAGACCCGATGCCTTTG	59.702	20
245	985	1229	TTCTCTATCAATCGGCTGGG	60.17	20
167	418	584	AAACCACCCCGTCTTTTCTT	59.842	20
242	175	416	TCCTTTCCATCTTCCCTCCT	60.008	20
251	1823	2073	AAATGAGACAAATGTGGGGG	59.647	20
256	950	1205	GCACTGTGTGCCAAGAGAGA	60.187	20
280	1247	1526	ATCCTTGATTTCTCGGAGGG	60.401	20
257	336	592	GTTTTCGTCCGTCCCATAAA	59.801	20
226	4330	4555	CACGTCCGTACAACTAACATC	59.424	22
267	82	348	GTGGAGTGCCACAACTAGCA	59.905	20
267	625	891	ACCCTCAAGCATCAGCATTC	60.226	20
224	1929	2152	AGCCTGTGCGAGTCTCACTT	60.205	20
185	235	419	CGGACACATAGTTGTGCGAG	60.324	20
220	275	494	TGAAAATGGGTACCACACACA	59.725	21
147	1404	1550	TGCAATTCATCAGTCTTGTGC	59.862	21
280	247	526	GCAGGTTCGAAGTAGGGTGT	59.212	20
133	3837	3969	TAATCTTTTGCGATGCCTCA	59.401	20
212	248	459	GTTTTAAGTTTGGGGGTGGG	60.435	20
217	41	257	CGATTGGGCCTATCCTATCA	59.878	20
132	52	183	CGCTCTTCTTTCGTTTTGAGA	59.755	21
280	287	566	GCGAAACAATGATCGCATTA	59.668	20
279	337	615	CTTTTTCGGGTTTGGACGTA	59.968	20
102	38	139	CAATACAACTGTCGAGCTGAA	58.464	23
152	239	390	AAAGGCCCACGATGGTTATT	60.562	20
255	260	514	TGGAATTCAATGGCAGATGA	60.009	20
180	286	465	AACCGTGTGTACAACAATAGC	59.499	23
199	28	226	CCTCTCCTCTCAACTTGCTTG	59.218	21
159	6	164	ATTGGCCCTTGATCTCCATA	59.344	20

225	75	299	GCATCTCTTGCTCTCTCGTTG	60.292	21
245	1544	1788	GCAGAAGGAACTGATGGCTC	59.957	20
154	593	746	ACTGTCGGAAAGGTCGAGAA	59.844	20
178	420	597	CAGCAGAGCATACTGCCAAG	59.764	20
215	105	319	TTCGGTCCTTCTTCTCCTCA	59.92	20
181	232	412	CCTTATGAAAAACGTTGGGG	59.311	20
170	2	171	AGCCTCGGATTTCCTGTTTC	60.578	20
279	83	361	TAGGGTTAGCATGCTTGGGA	60.597	20
195	100	294	TTACGGATGCATTCGACATT	58.994	20
125	47	171	TGGGGTTGTTGGAAGAAAAA	60.314	20
118	205	322	GGATTGGGCTTTGAGAATGA	60.014	20
173	203	375	CCGAAAATCCTTTCACCCTT	60.291	20
209	18	226	CAGAAATTGCCTTGGTTGTTC	59.601	21
135	293	427	TGACGCTGAAGTTAATGCAAG	59.122	21
105	102	206	TTTGGTCTTCTAGCCTCTCTCG	60.144	22
220	241	460	ATCGCATTGCTATCATCCAA	59.094	20
148	77	224	TCATATGATGACAGCCAGCC	59.635	20
232	296	527	GAAACACTTTCACCTCCCCA	59.943	20
275	69	343	GTTGGCAAACAGGTCCCTAA	59.971	20
156	1298	1453	ATGGGATAGCACTTTTGCCA	60.469	20
190	10	199	ACGGATTTAAGGGTTATTACCT	57.667	23
155	495	649	TTCTCCTCCCCTTAGCTTCC	59.783	20
150	132	281	CGTCGAAAGGGAAAGAAACA	60.22	20
227	163	389	GTTTTGGGGTACATGCCACT	59.717	20
158	615	772	CACAAAATGGATCGAAACGA	59.518	20
238	619	856	GCGTCGAGTACCACTTTTCC	59.74	20
173	73	245	TCCACAACTGCAATTTACTGTG	58.75	22
215	201	415	TTAGGATTGGAAGCAGTGCC	60.214	20
263	2897	3159	CAGGGTGGATGTACAAAGGC	60.375	20
213	2104	2316	CACAACAGGAGGAGGCACTT	60.298	20
206	944	1149	CCAAGATTGAGGTCCGTTTC	59.526	20
272	3927	4198	TATTCCCAATCTGGGCACTC	59.894	20
249	225	473	GGACGCACCAGATTGTTTTT	59.978	20
235	102	336	TTTGACATCAACGGATGGAA	59.9	20
225	0	224	GAAAGTGGCTTTGATGGAGAT	58.254	21
174	88	261	TGCAATATGTTTATTTCGGGA	58.048	21
262	86	347	TTGCGATTTTCGTTTTCCTT	59.699	20
127	87	213	GCCTGAATGTAATGCCGAAA	60.971	20
108	32	139	GCAATGGAATACCGTTGGTT	59.691	20
166	735	900	ATTTCCAGCTTTCGGCTTCT	60.34	20
257	42	298	TGGGAGCAAAAGGATGGTAA	60.439	20
239	2172	2410	TTGGGAAAGGGGGAGTAAAT	59.639	20
269	948	1216	ATGATATGCAAGAATTGTCAC	60.095	23
219	659	877	ATGAGTTTAGGGAGGTCGGC	60.464	20
100	272	371	CGTGCGACCAAATGTGACT	60.739	19
242	4467	4708	TGTAGGCTTTGGTTTCCATTG	59.982	21
258	650	907	GGAGCCATGTTTTGGTGTCT	59.973	20
102	1	102	GAAGATGGAGTAGAGAGAGA	59.94	27
189	365	553	CATTTCAACCCACCATCTCC	60.173	20
234	71	304	AGAACCGGATTTAGAGCAATC	60.095	22
257	568	824	GAACAAATCTGGGCCATCAG	60.461	20
171	257	427	GGTGTGGTGGGGACATTTTA	60.474	20
192	1498	1689	AGACACCCATTGCTGTGTGA	60.162	20
248	1385	1632	ATCCAACACCGCATCTTCTC	60.081	20
189	64	252	CAGACTAGAACGTAGACCTGG	60.845	23
279	69	347	AATAGCCCGAGCCAAAATG	60.045	19
172	4560	4731	AAAACGATGGTCGGTGTCTC	59.973	20
210	722	931	GCCTTCAGTTTGATTTCGTTTC	60.116	22

234	276	509	TGGGTATCCCAAAATTTCTCC	60.006	21
235	110	344	AATCTAACTAATGGCGCGGA	59.704	20
158	383	540	CGGAAAATTGTTGTCGGAAA	60.836	20
162	65	226	CTGATTTCAGCAGTGCTTGG	59.591	20
205	71	275	GAAACGACGGGAAGATGAAA	60.051	20
232	84	315	CTGCGCAGATCTAATGGTCC	60.765	20
158	2936	3093	CTACCGGAGAGTGGTGGTGT	60.026	20
257	101	357	TCCATTCCGAAAATCAAAGG	59.872	20
176	10	185	TGTTTACATTCAGGCCTTTTGA	59.625	22
149	36	184	TTCTAACTCCATTTGTAATAGT	57.769	27
235	16	250	GAAAGGAGATGGAGCGTGAT	59.243	20
199	109	307	GGGTGATGAGGCTTGAAGAA	60.195	20
185	2379	2563	CATGCATGCAAAACTGAGGT	59.722	20
231	1071	1301	TGGGTGGAACTTCTTGCTTT	59.711	20
234	1550	1783	CAAACGAATTGCAGCAGAGA	60.134	20
264	2202	2465	AGCTGGTAGCCATTCTCCTG	59.454	20
244	265	508	TGCCTGAAAATGTCTGCAAG	59.988	20
268	76	343	CTCGTTCCCAAGCCTCCTAT	60.59	20
171	2554	2724	CTACGACTACGGCTATGGGC	59.752	20
165	683	847	AGCTGAGATTAAATCCCCCG	60.411	20
186	286	471	GGGATATCGTCTAACCAGCAA	59.057	21
145	17	161	CCAAAATGCAAATCCCAAAA	60.652	20
153	350	502	CACAAGCACATTTGGGAGAA	59.691	20
205	222	426	GGTTACTGTTCCTCAGCCCA	60.111	20
179	230	408	ACCAACCCAACCCATTATCA	59.91	20
127	1096	1222	GGCAGGTCATGTGTATGTGG	59.837	20
205	10	214	CCTTTGTCAACTTGGGCAGT	60.149	20
154	165	318	AAGTGCAGGCAACAGTTTGA	59.49	20
213	50	262	GCTTCAAGACATAGCAGCCA	59.178	20
274	46	319	CCAGGTGAGCTAGCCCATAA	60.227	20
247	457	703	GGTGTGTGGAAGGAAGGTGT	59.859	20
147	167	313	GAGGGACGAGTCCTAAAGGG	60.067	20
207	245	451	GTGAGAGTGTGTGTCGTGGG	60.207	20
169	1909	2077	GGGATTTCAGCGACGATTTA	60.038	20
263	180	442	AGAGGAGGGCTTCAACATGA	59.803	20
163	67	229	TTGGCTAACAGGTCCCTGAA	60.626	20
265	203	467	TAATGTGGAACCATAGGGGC	59.645	20
229	0	228	GTTTCAAGGGTTTGATCGGA	59.91	20
254	3	256	GCCTCTTCTCTGCTAAAAGCC	59.76	21
256	140	395	TGAAAAGATTTGAAAAACATT	58.686	25
187	108	294	GTCCTTCTCTCCGAATTCCA	59.213	20
214	187	400	TAGGCATGGCCTCAACTACC	60.096	20
158	7	164	GATGGAACGGGGATTTGTTA	59.622	20
100	430	529	CTCGAGCATAAACACATCCC	58.173	20
127	29	155	AGCTACACTCACCGTCTGAGA	59.161	22
201	865	1065	TCTCGATTGCTCTCCGATCT	60.057	20
261	108	368	GCAAGACATGCAAGGCAGT	60.008	19
194	215	408	GCAGCAAAAATGCTGACTGA	60.142	20
158	283	440	GCAAAGTGCTAAATGGTTCAA	59.298	22
186	98	283	TTGGTGGTTTGTATGCTATCG	58.57	21
273	4087	4359	GCCCCTCCTAGCAATTTGAA	61.432	20
198	5	202	ACCCTCGGGGAAGTTACAAT	59.691	20
212	33	244	TTGGGATTAAGGCTTTGGTG	59.931	20
205	2	206	AACAACGAATCCATTAAGTGA	57.396	23
223	329	551	CTTTCGGGACACGTTCTCTC	59.844	20
127	254	380	AATTGCCCCCTCATTTTCAT	60.511	20
127	2520	2646	AAGGCTCGATTAACTGCGAA	59.982	20
119	1687	1805	AATGCCCCTATTTTTGGAGG	60.143	20

168	178	345	GTAGCTCAAGGGTTTTCGCA	60.386	20
272	42	313	CACAATGGGGGTATTTGCTT	59.685	20
241	829	1069	GGATAGGCCCTAACTCGACC	59.925	20
245	1180	1424	TGCGAGATGAGATCAACCTG	59.942	20
198	38	235	GGCTCAAAAGACAAGTCCCA	60.232	20
218	467	684	TGTTAATTTGGTTGGCCCAT	60.053	20
158	39	196	CCATTTGCAATACTAAGGCTTT	60.354	24
157	831	987	TTTCAAGAAAAGGGTGCCAT	59.546	20
267	106	372	ACGTCGGTTTGGTTTAAAGG	58.994	20
223	1	223	CATTTAGAACCCACGTTCAGG	59.48	21
176	95	270	TGGAACAATTTTTGCCACAT	58.869	20
262	98	359	GAAAAACGACGTGAGGGAGA	60.232	20
202	34	235	GTTTTGGAGTATTCCGTGCC	59.434	20
193	590	782	CACTTGACGAGGTCACTGGA	59.864	20
257	237	493	TATTTCATTCATGCCACGCC	61.761	20
278	1570	1847	GCAGCAGATTCGATGAGGTT	60.37	20
243	45	287	ACGTAAAAACCCTTCCACCC	60.089	20
100	163	262	TCCTGATTTGGTGGAATGTG	59.343	20
268	39	306	ACGGATATGCCCTTGTATGC	59.813	20
241	25	265	ATGATGCTTACCTGAACAGCA	59.27	22
137	30	166	ACAAGGATTGCGAACTCAGC	60.406	20
106	73	178	CCCCTCTCAACAACCACAAT	59.82	20
279	4548	4826	AGAAATTGCCTGCTTCCAAA	59.823	20
245	185	429	AGTCTCTGGAGCTCTTCCCC	59.952	20
198	3585	3782	CCACTTCCTAGGCAAACACC	59.592	20
273	63	335	AAATTTTGAATGGTTCCCCC	59.867	20
221	571	791	TCTCGTGGTGCAGTGGTAGA	60.463	20
132	316	447	TTGACCACAATCAAACACCAA	59.849	21
125	543	667	AAATTGATTTCCCACCACCA	60.029	20
104	20	123	GGTGGTGTGGAGGAGAGAAG	59.682	20
194	727	920	TTTCCATTATTTTCGTTGGAGA	59.838	23
254	2320	2573	TAATGCTTTGAAGGGGTGCT	59.708	20
151	569	719	AGATCACAAATCCCACCTGC	59.934	20
175	48	222	TATTTCGGTCCGCCAATTTA	60.275	20
218	141	358	CCCAAAAATTTAACGACCCA	59.671	20
135	275	409	CCAACACAACACAGGTTCTCA	59.626	21
155	5	159	TTTCCCATGTTGTTTGTAATTAT	59.147	25
166	610	775	ATTTGGAAACCTCCCACTCC	60.169	20
162	214	375	CGCTTGTTTCTCTCGCTAGG	60.284	20
175	103	277	GGTCAACTGCGGATCAATTT	59.939	20
274	52	325	GGGAGTGATTGAGGGAGTGA	60.048	20
238	1935	2172	GCAACAAAGAACCAACATCC	60.919	21
218	283	500	GAATTCCCCCAACACAAAAA	59.64	20
264	275	538	CTTCGCTATGAGTCACGGGT	60.277	20
226	210	435	TGAAACAATGCCTGGAAACA	60.088	20
143	88	230	GCAACTGTACACGTGTGGCT	59.826	20
278	215	492	CGAAGAATTTTGTGCCATGA	59.664	20
207	442	648	TTGTTGAACGCATAATTCGAT	58.25	22
274	41	314	CGTTCCTCAGAGTTTCCAGC	59.989	20
104	19	122	CAAACTTTCTGGATTGACTTTG	58.414	23
246	13	258	TCAACACTCTGTTTTTCTCTCA	59.074	24
209	461	669	CGTGTCCTCCTCAAACTGGT	60.151	20
204	1	204	TCTATTATATGTCATGTTTTGC	57.462	27
201	45	245	CCCATCCCTTAATCAACCCT	60.011	20
118	0	117	ACGCGAGATTTACGTGGTTC	60.14	20
227	309	535	GTTTCATGTTTAGCATTTGCG	58.368	21
263	72	334	TCGGGGTAGTATTGAGTCCG	59.948	20
178	441	618	GGTCCTTTGCGACGTAATTC	59.574	20

214	1225	1438	GCAGGAAGTCATGGTTGCTT	60.263	20
129	1214	1342	TTTAATCACGTGCAACGCA	59.852	19
189	999	1187	CATCCAATAGCCGAACAAAA	59.95	21
173	1488	1660	GCGATGCTCCAAAAGTGAAT	60.221	20
231	431	661	CCTTTGCTGAGGATTTGAGG	59.807	20
246	6	251	TTAGCACAATACAAACATGTC	58.162	23
228	78	305	TTGTGTGTTATACGTGTGGGT	60.124	23
240	136	375	TTTCAAGGTCTTCGCTGGTT	59.853	20
225	228	452	TATATGATGTAGGCCGCGTG	59.567	20
243	968	1210	TGGACATGGCAATTATTCTTG	60.323	22
254	442	695	ATGGGTTCCTTACCCCTTTG	60.046	20
223	188	410	AGCAGGAGGACTGAGGTTGA	59.986	20
230	287	516	CCTTTCTCCAAGTCTCACCTAC	59.797	23
250	27	276	GCAAGGGAAACTGATGGTGT	59.973	20
114	13	126	CGGATTTAGCGGTTATTACCT	61.448	23
116	1093	1208	GCCGTGACAATCATTCAAAA	59.523	20
117	97	213	GTGGCAGCTTTTCATCCATT	60.081	20
200	31	230	TTTGAGATCGGAGTGGCTCT	59.95	20
208	563	770	AAATCCGACGGTTGTAGTGG	59.853	20
253	3929	4181	TTCAACCGTGCGTGTATGTT	60.035	20
225	139	363	AAGATGATGGTGAAAGGGGA	59.336	20
256	38	293	TCACTTAGGGATATATTTAGG	57.128	26
242	188	429	AAGACATGCATCGTTTGTACT	59.265	24
247	714	960	TTCAACAACTTTCAGCCCAA	59.293	20
238	241	478	TCAACGCCCCATATTGTTTC	60.701	20
252	2235	2486	ATGAAACGCCCATTTTCTCA	60.448	20
267	162	428	TCCTCGAAGAACCTTATCGC	59.41	20
191	3	193	GGCAGTACTCCAAAATCACCA	59.985	21
233	51	283	AAATGAAGGGTTGAGCATCG	60.074	20
246	78	323	CGTTGGGAGGGAAGTTATCA	59.926	20
100	752	851	CTGAACCTGAACCACCAACC	60.399	20
186	314	499	GTTGATAAATTACAAAAATTT	58.406	27
221	515	735	TCCGATAAACACCAACCCAT	60.051	20
275	43	317	CAAGGATTCATGAAGAAGTGT	57.475	23
159	19	177	AGGGGAGTTATCACTGGATCA	58.46	21
106	1362	1467	TTTGGGCTTTCAAATGAACC	59.916	20
116	713	828	GTCCCCAGCCTCAGATACAA	60.073	20
238	964	1201	ACAACACCTGAGATGCCCTC	60.12	20
232	6019	6250	GTTTTTGCACGTCTTCGGTT	60.154	20
265	93	357	TACGTGTTACCCTCTCAATTTA	59.038	25
244	499	742	TTTAGGCATTCCCACCTTTG	59.931	20
142	138	279	CCCAACTCTTCGGCTCAATA	60.206	20
165	24	188	GTCTGCAAGAAAATGGGTGG	60.495	20
153	103	255	CCTTGTAGAGATTGTGGGGC	59.55	20
124	346	469	CCAACCCAAACCCACTTTC	60.195	19
222	49	270	AGCATCTCTCTCTTGCTGTCAT	59.679	23
122	221	342	CATTTTGACATGATCGACGG	59.924	20
243	655	897	TCGAACGATTATTTGGTTTGA	59.472	22
110	387	496	TTTCAAGGCATGGGAGGATA	60.405	20
243	775	1017	GATAGAGGCAGACGAACCCA	60.218	20
258	81	338	ACATTAAAGGTGGCTGGCAT	59.457	20
279	543	821	GAACGGTTCTCCACACACCT	60.009	20
280	1337	1616	GCGGGCTTAAACACAATTTTT	60.349	21
144	497	640	CTGTCTCCGGTCCATGAAAT	59.927	20
136	701	836	GCGAAAACAACAGACAGCAA	60.035	20
187	5643	5829	GGCTTGTGTGCATCTTCTTTC	59.874	21
255	58	312	GTATCACAGAGCCACGACGA	59.862	20
101	2077	2177	AGACATATTTTTCCCCTTTCCA	58.864	22

209	2536	2744	AGGCAAAGCACAAGATGAGG	60.397	20
260	218	477	TCGCCATTTCCCTGTCTTAC	60.074	20
160	0	159	CGTGATATTGGGAAACAATGA	58.348	21
257	319	575	GCATTAAAATTGTTGGTCCCT	57.987	21
198	65	262	TCCCTTTTCAGGTCCAAGTG	60.081	20
279	491	769	GCGGATTTTATTCTCGTTCAA	59.202	21
101	343	443	TGGAAAAGGTAGGGACAAAAT	57.596	21
156	318	473	CAAGCAACAAGCCAATAGCA	60.014	20
255	149	403	AGTTATCAAGATGGCCACGG	59.955	20
144	45	188	TTACCCAAAACACCCCTGAC	59.688	20
243	104	346	TTTTTGGGAAATCCTTGCAC	59.916	20
279	469	747	CCAACCACTTTCACTGGAGC	60.69	20
200	305	504	GAATACACCAACAGCCCCAG	60.375	20
269	0	268	TGCTCCTAGTTAGCACACAACT	58.288	23
269	1	269	TGAAGTTAGGAAATAAGGAG	58.743	25
229	2112	2340	GCCCCATTTTCTTAGGGTTT	59.311	20
268	2096	2363	TTGGAGGCTCAGAGGTTTGT	59.844	20
215	2457	2671	TCTACGGGTCACTCATTGGA	59.086	20
194	230	423	AGGTGTGCTTTTAGCTTGGG	59.378	20
179	166	344	CACGAACGGCTGGAATATCT	60.096	20
270	45	314	TAATAGGTGCGGGTTTGAGG	59.953	20
106	10	115	GGAGGAATGAAGGTGAAGGG	60.822	20
213	477	689	AGAGGGAGGGAGAAAAGGTG	59.671	20
256	5	260	CCCTTGGTATTCTCCCTGTG	59.401	20
245	390	634	TGTGGCAATATGATGCTTTGA	60.088	21
280	5594	5873	TGACATACATGGTTTGGGGA	59.623	20
160	579	738	GCTAATGCTTCAGCACCACA	60.019	20
258	236	493	ACACACCCACACCATTGAAA	59.701	20
101	384	484	TAAGGAGATGTGTGCATGGG	59.522	20
170	659	828	CACCTCACTTTCAATGCTCG	59.44	20
170	37	206	CCAAAACTCCACCTTCAACTG	59.619	21
167	177	343	AAGTCCGGCCATCTCTCTCT	60.358	20
255	459	713	ATCATGGGGAAAAGAGTTATC	57.552	22
197	2	198	TTGATTCATACAAGTCATCTTTA	57.459	27
243	0	242	GGAAATAAGGAGGTGTTATGA	57.235	25
270	1022	1291	TGCGATAGTTGGTTCTGCAA	60.401	20
277	107	383	AAAATGAACCGTAACCGGC	59.815	19
279	996	1274	GAGTGAGAGGAAGACAGGCG	60.135	20
255	35	289	AATGCAACTCAAAGGGAGGA	59.67	20
115	43	157	TCAATGGCCACAAATGGTTA	59.786	20
173	5	177	GGTGTGTTGGCATTGCTAGA	59.722	20
107	456	562	CATAAAACATACCTCGGCATCA	59.853	22
168	361	528	CAATTCCGAACCGAATAAGC	59.547	20
151	598	748	TGCCACTATAATTGTATGGTCT	60.27	24
150	169	318	CACCTTACCCACCCAACCTA	59.705	20
197	12	208	CACAAACACACTTGGGAGGA	59.565	20
245	812	1056	GCATATTGCGACAAATAGCC	58.279	20
278	362	639	TGTGCTGGTGCTGATTTTTC	59.847	20
255	104	358	ACGTTTTTGTAAACGTTGTCCT	57.794	22
143	334	476	AAACATGATGCCAATCCAGC	60.874	20
173	12	184	GTGCATGCAGTCAAATCGTT	59.728	20
110	382	491	TGGCACCTAAACCATAAGGC	59.96	20
102	9	110	CATTTAGGATATTTTCTATTCTT	57.631	27
212	435	646	AGGATACCGGAGTGTTCACG	59.989	20
179	688	866	CTCCGCCCAGTTGGATACTA	60.088	20
279	180	458	CATCCACCACCTGTCCACTC	61.434	20
137	0	136	TTACTCACACGCACACCCAC	60.639	20
258	585	842	GCTAGGGCCAAGGAGTTAGG	60.221	20

109	358	466	TAATCACGTCCTTATTAACCA	57.462	25
122	519	640	GTGATGCATGATGGGTATCG	59.763	20
166	148	313	GGTCTCCGGTCCATGAAATA	59.75	20
261	77	337	GAATAGCCGTTGAGGCATGT	60.103	20
273	774	1046	GTCACATATAAGAATGTCTCC	58.479	24
235	221	455	ACAGAAACATTGACTCCGGG	59.966	20
270	172	441	CATTGTGCGAACCATGAAAA	60.501	20
199	105	303	GCGTCTGAGCAGAGGAAAAT	59.579	20
274	19	292	TGGCATCATAATCAACCATCC	60.547	21
214	75	288	CCCCAACTAGGGGATGAGTA	58.859	20
224	844	1067	TGTTACCCCCACTTCATTCAC	59.703	21
161	102	262	CGTTTCCATTGTTTAGCCGT	59.996	20
116	135	250	ATTGGTCGAGAGAAAGGGCT	60.212	20
211	13	223	AAGTGATCTACGTCCACGGG	59.989	20
225	613	837	TCCTCCCAAAAACATCCAAC	59.767	20
187	6253	6439	ATTGCACAAGTTTGGCCTTC	60.118	20
175	162	336	CACACAAATGGATCGAAACG	59.964	20
253	1546	1798	TTCAACACACGACATGGGAC	60.426	20
224	1019	1242	TAAATAATGATTGGGGGCCA	59.976	20
239	8	246	AGCATCTATTTTCGACCACTG	58.861	22
278	160	437	CGTTTGGATCCGATTTGGTA	60.692	20
241	368	608	CCGCGGTTGAGGATAGATAG	59.685	20
279	148	426	TTTGCTGAGAAATCTAATGCG	58.2	21
102	191	292	CAACCCATTATCAAAACCCAC	59.054	21
238	45	282	CCACCTTGAGTTACATGCTCC	59.607	21
267	453	719	TGACGAATTCTCAAGTTTGTC	59.276	23
275	434	708	TTCAGAAGCCCCTGAACAAC	60.232	20
271	2174	2444	AGAGAGAGTCGGCAATTCGT	59.043	20
239	41	279	CACAAGGACCATTCCAGCTT	60.111	20
207	203	409	TACGATGGGCTTTAAGCAGG	60.223	20
263	87	349	AGTTTCTGCATTGTTGCATAG	59.433	22
156	273	428	CCCAAAACCTCAAATCGTTG	60.336	20
263	2280	2542	GTGAGTGCGCATTGATGTTC	60.281	20
279	1312	1590	AATGGTCCGGGGTGATTT	59.987	18
253	32	284	TCACAGGCATTGTCAGTGTGT	60.219	21
127	164	290	TGTGCCAAGAACAACTCCTC	58.854	20
233	210	442	TAGGGATTGAGGGTGATTGG	59.744	20
101	107	207	TGGATAGACTCATAGCCCGTG	60.103	21
204	37	240	TGACATTGCCTAGAAAGTGGG	60.118	21
278	5	282	GGCTGAGTACACGAATGCAC	59.323	20
181	329	509	AAAGAACACACAATTCATGTG	59.392	23
170	341	510	TGGATGTCTTTGATTTGCGA	60.197	20
237	92	328	CTATAGCCCCCGATTCACAA	59.916	20
170	584	753	ATTGGGAGAAAAGAGGGGAA	59.875	20
222	34	255	AGAGGGTTGATGGGTGATTAA	59.704	22
169	92	260	TTTTGCCCTCGAATGCTATC	60.175	20
268	579	846	TCTAAATGAAACATCAACAAT	58.543	24
173	460	632	GCTGCTGACTACCCACACAA	59.905	20
265	3	267	AAAATCAAAGGCCCACAATG	59.801	20
112	420	531	CCGAAAGATTTCTTAAGCCTT	59.354	23
255	837	1091	AATCCATGATCCGAAAATGC	59.728	20
158	56	213	CTCCAATGGAACAGTAGCCG	60.647	20
100	311	410	AACACAGAGACAAGCACCCC	60.159	20
181	8	188	TTGTGAGTGACTGCGTGTGA	60.07	20
149	332	480	ACACGGTCGAGAAAGAGTCG	60.444	20
151	263	413	TGCCAGAAGAAAGCATCAAA	59.542	20
204	1469	1672	CCCATCCTCATTTTTCTTTCAA	60.285	22
246	53	298	TAAGGTGGCTGGGGTGATTA	60.323	20

204	64	267	TCTTGTTGGAATTTTTCGGG	59.91	20
247	6	252	CCCATGTTGTAATTAATGTAG	60.228	25
278	18	295	ATCAATCCCAGCCACACAAT	60.203	20
219	846	1064	GCACATGAAATCAGGCACAC	60.128	20
103	158	260	GGTTACTGTTCCTCAGCCCA	60.111	20
185	491	675	AATTCTCAGTTCTCCCCTCAA	59.213	22
162	58	219	TTCACGTGGACTGCTTTCAG	60.025	20
246	41	286	CGTGTTCACCGTAGGGGTAG	60.423	20
235	128	362	CGAAAGAATTAGAACCGGCA	60.202	20
217	1	217	GTCCACGGTGGTTTGAGAGT	60.009	20
269	545	813	AAGCGCAGAAAATATGGGAA	59.682	20
187	247	433	TATATTGTGGGGTGGATGGG	60.266	20
110	705	814	TCTTATAGCATCAACCGCCA	59.281	20
133	29	161	GATCCCTTGGAGCTCAACAT	59.094	20
169	301	469	CCTTGATACATATGCGGTTTTC	58.521	22
238	76	313	CCAATCTAGGGTTCATCACCA	59.799	21
159	339	497	CGAACGAATATGTTGCATCC	58.994	20
148	73	220	ACTACGAGCATCATCATGTGT	58.667	23
144	63	206	TGCCAATGAAATGAACCAAA	59.907	20
130	699	828	GATTGGATGAGAAGAACCGC	59.635	20
279	9	287	TTGTCGGGTCATTACTATTAC	58.578	23
271	79	349	AGATCATCTCGGGTCCAAGG	61.391	20
253	2780	3032	AACCGGTTAAAAATCGGACC	60.055	20
166	25	190	AACCATGTTTCCATCGGTTG	60.615	20
223	80	302	TCTCTCTCAAACGCATGTGG	59.984	20
216	1	216	TCTCTGACGCCATTCAATCA	60.353	20
116	5	120	TGAGTAAAACGTGTTTGTCAG	57.555	23
108	87	194	GGGTTGTTGGCTAACACAGG	60.41	20
157	74	230	TGTCGGTTGTCTGCTACACC	59.751	20
203	82	284	GAAAAGCTGCCACATCACAA	59.847	20
190	510	699	GCCTTCAGATCCCCTGTTTT	60.443	20
256	396	651	TGCAAAATACCTTTTGTCGGT	59.505	21
280	2976	3255	TGGAGTCCTAAACTAAACCTC	58.484	27
180	138	317	GCTGCAATTCCTATTCAGCA	59.019	20
240	6511	6750	AGCCCGTCACCAAGATTATG	59.955	20
174	10	183	TCTTGATAGTACTTTTCATGGA	58.093	27
164	4061	4224	GTTTGCCTCCATTGTTGCTT	60.118	20
112	7	118	TTTTATTTTTGTGTGGTTTTGAT	58.124	25
178	233	410	AGAGGAAGCAGAGATCGACG	59.703	20
233	1114	1346	TTTTCGACCAATAGGAACGG	59.931	20
180	10	189	AAATGCAGGGAAGATTGTGG	59.933	20
179	748	926	ACCATGGAACATGTGTGTGC	60.304	20
163	64	226	CCGAGATGGCTGCATTAAA	59.777	19
243	1009	1251	TCGGATTAGCGTGTCGTGTA	60.28	20
196	0	195	TTGCACAGTACATGCGTTCA	59.902	20
266	972	1237	ATTCTGAGCTGGCGTGAAAG	60.538	20
183	58	240	GGTGGAGTTGGTTCGAAGTT	59.04	20
191	96	286	GAGAACAGAAAGAAGCGGAA	58.707	21
175	0	174	GATGCCATTCGTAAGTCCG	59.09	19
178	85	262	CGCTAAATTTGATCGTCTTCC	58.844	21
177	6	182	GGATTGATTCCACCAACCAT	59.464	20
254	71	324	GTTAGAAGGCAGATGGACGG	59.694	20
275	409	683	CCTTCTTTGAATAGCGTGCC	59.845	20
164	298	461	CCCTCCAACCATGCATAATC	60.155	20
177	1527	1703	CGATGATATTTCTGGGGTGC	60.296	20
151	1046	1196	TCTCTTGTTGCCCTCCAACT	59.844	20
159	1062	1220	CACTGATCTTGCCAAGTTTCC	59.726	21
244	668	911	TGCAATTAGGGTTTGGGGTA	60.181	20

149	43	191	CACTCGCCACAATGTCAGC	61.494	19
212	688	899	CCCTTCTTCAAAAAGTCCGA	59.284	20
159	70	228	TTTTTGAGATTAGGCTATAAG	57.497	27
204	278	481	AGTTTTCTCCCCTTCGTTGC	60.61	20
246	494	739	TTGGGTGGTCGTATCCACTT	60.232	20
226	249	474	TGAGACACCCCCATCTCTTC	60.048	20
108	302	409	CACGAGATTTACGTGGTTCG	59.195	20
127	305	431	CGATGTCGGTAAAGGCAGTT	60.132	20
214	741	954	TCTGTACGTGTGTGAATGGC	58.111	20
280	95	374	TTGGTGGGGTTACATTGGAG	60.605	20
203	898	1100	TATTACAGAATGCACCGCCA	60.096	20
277	1571	1847	TGTAGACGATGCATGGGAAA	60.073	20
109	42	150	AAACACGCAACACAAAGCAG	59.951	20
228	13	240	ACCATCCCACCAGCATTTAG	59.813	20
148	319	466	CCTTCGAGCCTCTGCTATTG	60.11	20
259	2450	2708	CCAGCCAATGGAGATTACAA	59.946	21
133	329	461	AGGATAGGAGCCCACCTTGT	59.957	20
273	86	358	TGAACATGCTCCTATTTTAATA	59.731	26
242	496	737	AAAATGCCCTTGTATGCTGC	60.103	20
261	292	552	AGTTCCGACGTTGAACAGTG	58.777	20
177	332	508	CCAACGCTACTTGGCCTTAC	59.769	20
252	15	266	GCATTCTTGAAAGCTGGTGA	59.002	20
176	883	1058	GTAAGAACGAAAGCAGGCCA	60.386	20
216	325	540	CACTCACCAGTCCCCACTCT	60.153	20
146	318	463	TGACATCTTTTGATTTGTTTTG	59.156	23
280	211	490	ATAGTGGTATGGTGTGGGGG	59.405	20
115	3602	3716	ACCCACTGACCTTGGATGAG	59.962	20
251	205	455	GCATGCTTCTGACCAATTCA	59.805	20
134	45	178	ATTACAAATGGCCAAGAGGG	58.903	20
125	545	669	TCCGAAGTTATCTCCAACGC	60.214	20
141	475	615	GAGAAAGCATGTTCTGCACG	59.596	20
102	106	207	GACTAGTTGGGCTTAGTGGGG	60.005	21
233	6	238	CGTCTCGTGTATGCCATCTG	60.287	20
173	1235	1407	GCTGAGAGCCTGAAACTGGA	60.678	20
238	28	265	CAATATGAGAATGGCCGAGA	59.677	21
247	330	576	ATCCTCTCAACGCTTGGCTA	59.978	20
166	107	272	TCTTTGTCCGTTTTTCGTGA	59.293	20
155	33	187	AGTGGATTGTGATGAGGGGT	59.232	20
261	31	291	GTGCCGTAATAAATTGGATCA	57.53	21
268	41	308	CGTTAATGCACACAGCTTCAA	59.926	21
214	165	378	TTTGGGGTTCGGTATTGATG	60.555	20
146	36	181	CACCAAAAACACACATTGGA	57.837	20
279	73	351	GTCAACTTTGGCAACGGAAT	59.978	20
255	114	368	TCCCATAGCATCTTTTGCTC	57.915	20
217	446	662	GAATATGCTGATGCTGGCTG	59.405	20
271	1493	1763	ACACCGCCATATTTGGTTGA	61.149	20
280	1467	1746	TCCTAATCTTTGTGGGCTAAT	59.977	23
245	39	283	TTTGGTACAAAATTTAGGGTT	58.49	27
274	331	604	TTTTCTGAGATTGACGGCTG	58.999	20
150	980	1129	GTCACCATCCGCCTTGTTAT	59.82	20
212	299	510	ACATGCAATTATGCACTCGC	59.724	20
156	28	183	TACCAACCCAACCCACTCAT	60.088	20
250	1082	1331	CGATTCGAAGAAATGCATCA	59.769	20
201	20	220	ATTCTCCCACACGATCAACC	59.786	20
177	338	514	TCATTCTCAAGCCACTCCCT	59.803	20
271	0	270	TGGGTGAGAAAGAGAGATAG	57.301	23
195	213	407	GCAAAAGTAATAAAGAGCGA	59.861	24
219	21	239	GGAAATTTTCTTTCTTCCTCAC	60.441	23

129	1549	1677	TGTGCGAGAAAGTACAAGGG	58.923	20
208	824	1031	GCTCAGGACCGATGAATGAT	60.042	20
216	78	293	GTGTAGCCGGAATATGAGCC	59.556	20
236	2510	2745	GTGGACTGTGGGAATACTGGA	59.835	21
254	26	279	TCGATGATAACTATGGTTTTG	57.589	23
166	51	216	AAGTCGAAATTTGGCAAACAA	59.617	21
237	561	797	CTGCCTATCCGTTACCCTCC	60.836	20
232	5236	5467	CGGTTCGGATTACGGTTTTA	59.826	20
141	1102	1242	CCATTGTTTGTGTGTCGGAG	60.001	20
109	18	126	ATCGGTTATTACCGGATCGC	61.031	20
121	4	124	TTGAATTAATGATGTCAGATAT	58.51	27
220	66	285	AATTTTCTACAAAACAAGACC	57.963	26
171	233	403	TTGCTCTAAGCTTCATCCGC	60.626	20
255	142	396	CCTCCGATTTCGTCTTCAAA	60.184	20
184	19	202	TCCGAAAATCGGTCAAAAAC	59.916	20
146	272	417	TGCTCTTATGCTTTGTTAAATT	58.961	26
135	1118	1252	ACAAGCTATTTCGAGGCAACA	59.897	21
203	15	217	TGAAAGTAGCCGAGAGTTTAC	58.273	23
127	295	421	CGTTGCATCTGTGAGCTTTT	59.076	20
207	81	287	TCGAGAAATGCCACATGCTA	60.366	20
103	757	859	AATTGCTCCGACGACTATGG	60.096	20
219	6	224	ACCATATTTAAGGGTTATCAC	57.552	24
225	290	514	CTCGAACTCGGTCGAGAAAG	60.126	20
257	155	411	TGCCAAGTCTAAAGCCACTG	59.072	20
185	261	445	ACTTGTTCCCTCATTTGCTCA	59.726	21
120	56	175	ACAATATTTAACGCAGCTAAA	57.734	23
177	2324	2500	AGGCCTACCGATCCAAACTT	59.962	20
245	387	631	ATCAAACTCGGCCTCTCTCC	60.735	20
177	98	274	GGATGGAAATGATGTTGGTAG	58.765	22
277	10	286	CCCTAAATTTTGTATCCGAATG	58.395	23
103	1413	1515	TTTTAGAAGTAAGTGGTGTTCG	59.561	25
164	1284	1447	TGCAGGAATTTTCACCAAAG	58.745	20
195	17	211	AGCATCTCTTGCTCTCTCATTG	58.842	22
193	201	393	ACAAACCCAAGCAGACATCC	59.973	20
246	357	602	GGCGGGGGAGATATAGAGAG	60.017	20
267	76	342	GCATGCTCTATCTGTTACAGG	58.885	22
130	4	133	GATTGCCCAAGATCTACGGTT	60.334	21
273	626	898	CACACAGACACGGTGGAAAA	60.606	20
238	246	483	TGCCATCTCGAAAAACAATG	59.664	20
188	36	223	TGGAATCCGAGAAATTCAGG	60.006	20
280	8	287	GACTTAAATTGCTGCAGACGC	60.039	21
216	192	407	GCACTAACCACCCTTGATTTG	59.485	21
208	994	1201	GGGAATTAGGGTTGAGGTTGA	60.173	21
209	2	210	CCAAGCCATACAAACTGCAA	59.729	20
140	328	467	GAATGCTGGGCTGATAAGGA	60.177	20
169	133	301	TCTCTCTGGTTGGCTGCTTT	60.134	20
149	1595	1743	TGGCAATGGAAAGAAACACA	60.088	20
149	2	150	GGCAACGGAATACCATTTGT	59.691	20
211	3424	3634	CACAACCATCCAACCACAAC	59.701	20
254	440	693	TCCAAGATTCATGTCGCAGA	60.353	20
279	45	323	GCAACCTCAATGCTTCTCAAA	60.38	21
194	790	983	TGAATCCGTATCCTTATTGTTG	60.214	23
201	86	286	GTCAACATTTTGTGCATTGGA	59.435	21
255	1	255	TGATTGGTCAGTTTGTCCGA	60.088	20
237	100	336	CCCAGCTCTCTCACTCTGCT	59.883	20
197	1857	2053	TATGGAGTGGAGCAAAACGG	61.021	20
197	246	442	TTTAAACCCTAAAACGCGCA	60.593	20
261	2347	2607	TCACCTAATTGCATCCCCAT	60.155	20

274	1275	1548	AGAGAGAGGCGATGCAAAAA	60.096	20
104	684	787	AGACAAAACTAATTGGGGAG	60.001	22
219	3355	3573	TATAGCTCCGGCAGCATTTT	59.838	20
265	907	1171	CATTCATCATCATCAATATCA	59.64	26
174	12	185	GATTCTTCCAATCTGACGGC	59.635	20
185	1009	1193	GAACAAATCTGGGCCATCAG	60.461	20
162	27	188	CCCAACTAACCACCCCACTA	59.705	20
208	51	258	TTAGCCCTTAATGGCCTGC	60.181	19
214	815	1028	TGGTGACTTTGAGGAGGGAG	60.229	20
212	830	1041	CACAGTGAGGCCCCTTTTAC	59.592	20
135	12	146	ATTGAAATAAAGGCGCCAGA	59.682	20
187	962	1148	AATCGTGGTTCAAAAATCGG	59.801	20
278	194	471	TTCGGTTGCAATTTTAGTTGTT	59.931	23
224	889	1112	ACAGGGGCATATGTGTCAAA	58.85	20
280	68	347	GCCCAAATAAGTTGGAGTGG	59.429	20
252	109	360	AATTTGAAACCGGACCGAAC	61.08	20
168	89	256	TGGTCCATTGGTCTTTTGTATT	58.353	22
178	697	874	TCGGCTCAGATACGACCTGT	60.823	20
171	3	173	TTCATGGGGCAATGGGATA	62.008	19
179	2171	2349	GTGGTGGAAGAGGCAATGTT	59.973	20
245	466	710	ATAGGTCCATCCCTGCCTTC	60.293	20
221	326	546	TTTAAAAGGAGTTTTGACGGG	59.978	22
242	168	409	GATCGTAAATAAGGCGGTGG	59.433	20
188	11	198	AAAAGTAATGCATATGTTTTC	57.308	27
234	26	259	CATGCACCTGAACATGCC	59.61	18
265	275	539	GGTTGAATTTCGTACCCGTC	59.292	20
175	23	197	CTAAACCAAACCCACCCCTC	60.581	20
240	94	333	CAACCAAACACCCCCTTAGA	59.824	20
217	476	692	CGTTCCCTTCGTCTTGACTC	59.844	20
237	191	427	ATAAATGTTCAAACCGGCCA	60.188	20
271	275	545	TGCACGTAGGCATGTTCAAT	60.142	20
190	195	384	CAAAGAAGAGTGGGCTTTGG	59.846	20
182	2116	2297	GGACGCCCGAGATTATTTCT	60.419	20
227	104	330	CCTCTCGCATTTCTCTTGCT	59.717	20
275	54	328	CACATCAACACCTCAGCCC	60.105	19
276	178	453	GGGGGAGAGACAAAGGAGA	60.565	20
197	581	777	CATTGTTTAACCGTCTGCCC	60.365	20
265	1890	2154	TCTTCTTTTCATCATCGCCC	60.155	20
134	2181	2314	ACTAGAGGGGTCAGCCCATT	59.957	20
101	373	473	CAACCACATTAGGCCATGC	59.94	19
258	383	640	AGGGTTGGATAACTCCATCG	58.861	20
178	67	244	TATGCATTTGCACCTGAGGA	60.22	20
244	487	730	AGGGGTGTAGGCAAAAGACC	60.361	20
242	2567	2808	GCAATTGGTAGGTTCGTTGG	60.365	20
245	531	775	CTTCCAGAGTCAATCCAGGC	59.803	20
172	53	224	GCTTCCAAAAGAAAGAGCCC	60.32	20
264	243	506	TGTTTCCCGTTTTATCAGCA	59.157	20
172	10	181	TCATTTATGAAGCAAGGGGG	59.894	20
266	179	444	TGATGAGGCCATAACTGTGC	59.679	20
228	9	236	CAACCCTACCTCCTTCTCCC	59.928	20
180	2102	2281	GTGGGAATACCTGCAACACC	60.24	20
156	2634	2789	CGGAAATGATAACAGCGGAT	59.923	20
242	632	873	TGGTGAAGATGTGGGTTGAG	59.52	20
265	1365	1629	GCACGTAACATACATTGCCC	58.923	20
178	632	809	GGCTCACTGCTTCTTTCTCG	60.277	20
236	35	270	ACAATTGGTAGCAAACCATGA	59.384	22
260	23	282	CCCCATTTCGTCAGTTTCAT	59.79	20
278	10	287	CCCAAAAATGGGTTATTATTT	59.047	23

167	342	508	CCGTTGTCTTTAAGCCGTTG	60.659	20
258	770	1027	GCTGATCTCCATCTCCAAGC	59.917	20
172	236	407	TGGGAAAAATAAAGAGGAAA	58.542	22
273	172	444	TTCTCATTTTCCCCGTCATC	59.871	20
280	785	1064	TCCCCACTGCATCTTAGAATTT	59.966	22
201	401	601	TCCCTCCCTCTCTCTTTTCG	60.832	20
213	1637	1849	TCCTAATTTGGAAAGTACTGG	59.36	24
222	99	320	CGTCCCTCGAGTTTCGTAGA	60.388	20
117	7	123	TGGCTGGATCTCCTGAAAAT	59.629	20
218	134	351	TCATTCCGAAAATCAAAGGC	60.016	20
275	6	280	CTTTTGTAAAGTAGCCGCCC	58.899	20
272	291	562	TGCACGTTTCAAAGCATAGG	59.872	20
222	389	610	TCAGAATCCCATTAGAAGGGT	57.599	21
204	262	465	GAAATTGAAGGGATAAGAATT	58.995	25
275	234	508	ACCTGATTCCAGTTGGATGG	59.779	20
193	2962	3154	ACCGATCTTTTGGCATTCAA	60.448	20
186	466	651	AAATCCTATCCGGTCAACCC	60.017	20
274	142	415	GAGGGTGAAAGGAGAGGGAG	60.186	20
191	2888	3078	TCGTGCTCAAGCATATGGAC	59.83	20
207	792	998	CCCATACACAATTTGGGGTC	59.91	20
238	43	280	ATCTCGGCTACGAAGTGCAT	59.866	20
143	314	456	TGACGATTGCAACCTTTGTC	59.697	20
229	0	228	GTCCTCCGAACTCATGGTGT	59.969	20
223	352	574	TTACCCGGACAATAAATCCG	59.655	20
134	1189	1322	TCTTTCGCTCAACCTCCATT	59.813	20
239	896	1134	TCCCATTCAACCATTTTCAA	58.792	20
210	138	347	CAACGCACGGGTAAAAGACT	60.168	20
148	667	814	AAGAGCATTTTCATGCCATTTT	59.976	22
221	14	234	TTGGTTTTTAGTTAGCACACAA	58.49	25
166	97	262	ATTTCATGCGTGTCAAACCA	59.972	20
166	175	340	AAAATTGTGGAGTTGCCGTT	59.476	20
111	30	140	ACCAATTTGATGAGGGTCCA	60.173	20
180	30	209	GATTCTGGATTATCCTGCGG	59.486	20
187	172	358	ATGTGTCGGGGGTACAAAAG	59.711	20
101	18	118	AAATTATATTCTCGCTTCTTCG	59.067	24
183	39	221	GCCTACCTTGCTTCCGTAGA	59.476	20
134	231	364	GAACATGTGTCGGAAGCTCA	59.837	20
236	41	276	GCGCTTTTTGCCTGATATTT	59.349	20
267	210	476	AAGGTGGGAAAGAATTTGGC	60.299	20
123	307	429	CGAAATTGAATGGCAAGGAT	59.901	20
248	187	434	CGAGGCGTGACATCTACCTT	60.277	20
213	36	248	CGGAAGAATAAGAAACGGCA	60.202	20
185	150	334	TCAAAAGTGCAACAAATCTGC	58.956	21
231	571	801	GGAATGTAGTGTGCGCAAGA	59.871	20
246	116	361	TGAGCTCGGACCTCCAGTAT	59.827	20
266	30	295	GCAACGAACAAATCTCATTGG	60.496	21
129	680	808	CGTCAATCAATGATGCGATTA	59.534	21
119	2234	2352	CATGAGGCCGGTTAGGATAA	59.916	20
236	774	1009	TAATGATCCAACACCCACCA	59.623	20
183	35	217	GCACTCGGAACAACGAAAAT	60.118	20
247	122	368	GCGCAGATCTAATGGACCAG	60.765	20
130	242	371	TCCATTTCAGACCCAAAAGA	58.117	20
250	2095	2344	CGAAAATTGAAAATTTATTCC	59.921	23
240	1258	1497	TGGACCTCATATGTCATAACC	58.709	23
117	178	294	TTGCGGGGTTGTTAAAGAAT	59.451	20
218	35	252	AAGTCTCTCACCCTTCGCAA	59.989	20
223	48	270	TCGATGTTGTAATTCATCCGAG	59.96	22
233	1131	1363	ATGAACTATGCCCATGGAGG	59.773	20

220	1164	1383	AAGAGCAAAACAATAACAAA	59.732	23
271	103	373	ACCCATGTGTCCACAAAACA	59.701	20
156	245	400	CCTCTCATGGATTCGGGTAA	59.887	20
241	3	243	AATTTACTAATTTATCCACCTC	57.088	26
194	107	300	CAACGATGAGGTGGCATGTA	60.539	20
195	291	485	CTCCTTCTCTCCCCCATTTT	59.508	20
254	1001	1254	ACGTTTATCCATTTGCCGAC	59.829	20
209	189	397	ATAAAGTGCAGCAGACGGGA	60.796	20
241	7	247	GCTCTTCGAATTCTCCTCCC	60.293	20
229	9	237	TTTAAAACCGTTCTCACCCC	58.925	20
239	4	242	TCAGCACGCGCATTACATA	59.986	19
171	97	267	ACTTCAATTTTCGAGCCCAA	59.685	20
115	0	114	CATGTTAAATAATCGTCAAGT	57.898	26
188	278	465	TTTACCAAAACTGCCATCCAC	59.853	21
115	193	307	TTTTCTTTTTCCCGGTGATG	59.91	20
218	87	304	TTCGTGTCTATCCTCACCCC	59.927	20
158	657	814	TGATCGTTCTTCACTCTCTTGC	59.621	22
156	693	848	CCAGATCGCGACCCTATAGAT	60.445	21
249	124	372	CAAAGGCCCACAATGGTTAT	59.685	20
243	132	374	GTCATTAGCAGCTGGGGATT	59.154	20
217	47	263	CTCATAGTTGACGCCCTTCC	59.694	20
213	67	279	AATTTGGGTCAAACCCCTTT	59.549	20
263	292	554	TTTTTACCAATTTGCCCTCG	59.937	20
277	248	524	GAGCTGTTACCTCCGTGGAC	59.727	20
216	244	459	AGACATGGCGATACGACGTT	60.547	20
144	88	231	TGTGTGTCCAACATCCCATT	59.656	20
192	33	224	GCATCTCTTGCTCTCTCATTGT	58.699	22
222	87	308	CGATTTTGCCCTTTTATGCT	59.212	20
272	29	300	TTTGTTGTTTCCCAAGTTGCT	59.64	21
170	10	179	ATTTGCTTGATCCAATGGTG	58.423	20
184	3	186	TGCGTGATGCAGACATATTG	59.259	20
143	1642	1784	TGTCCCCATCTCGTGTTGTA	59.96	20
275	339	613	CATGCAGTCATGCACAATCA	60.282	20
261	495	755	CTTTTGACCTTGCATTGCTG	59.464	20
146	145	290	AAATAAGGAGGTGTTATGAAG	59.323	24
252	49	300	AATTGATGGAAGAAGGCACG	60.074	20
192	98	289	CGAGAGAAAAAGAAAGGCGA	59.702	20
101	154	254	GTGCGTGTGTATGCTGAGGT	59.783	20
254	213	466	TGATGTTTGCATTTTAAGAGG	57.459	22
240	14	253	ATCTCTACCGGACTGCGAAA	59.836	20
150	1	150	TTCAACCAGGCAAAGACCAC	61.075	20
231	465	695	GGAAGGAATATTTCATCACAC	59.635	24
148	47	194	TCGATAATGCACTTTATCAGA	57.221	24
251	243	493	GGTTGGTGAGTTGGCATGTA	59.42	20
116	570	685	AGATGATCACGATGAAGCCA	59.197	20
237	576	812	CATGCACGGAAAACTTGAAA	59.706	20
208	773	980	ACCGATGAGTCGGTTTGTGT	60.431	20
273	1770	2042	CATTGCGTTTTACAGCCAAA	59.742	20
164	480	643	TGATTTCCCTGAGAAGGGTG	60.042	20
232	29	260	TTGGTGTATACTTTTGTAGTGA	58.276	27
235	9	243	ACCCGAATTTTTCGGATACC	60.02	20
189	2	190	GAGAATAGATAGTTAGAGAG	58.82	27
275	65	339	CTTCTCACCGTCGACCAAAT	60.111	20
237	103	339	TTCTCAGCATATGGGAAGGG	60.029	20
267	1395	1661	GCTGACTGGACTGCCTTTTT	59.478	20
262	67	328	TGAGCCTATCTTGGAGCACA	59.547	20
280	65	344	TCTTTGAATCATCTTCCACCTT	57.786	22
227	81	307	CACCATCTTCCCCTTCTGAG	59.649	20

247	10	256	CAAAAATGGCCAAAATCGTC	60.302	20
212	389	600	CACATGTTGCCATCTCCAAG	60.112	20
205	25	229	CTTTTTAGCATGCGAGAGGA	58.267	20
189	34	222	TCAACAACATGCAAGCATCA	59.833	20
197	402	598	CGCTGCACCTACAAATGAAA	59.872	20
228	1213	1440	CCATTTCTTTGGCAAGTTGA	58.745	20
167	447	613	AAGTAGCAGCACCGCAAACT	60.081	20
203	623	825	TGCATCTCTCTCTCATCCGA	59.611	20
240	2392	2631	TGATCATCGAGGCAGAGAAA	59.476	20
184	32	215	GGGCAAAACTTGAACAGCTC	59.859	20
187	816	1002	GGATCGGAGTTGCCTAAGTG	59.694	20
130	4	133	GCACAACCACTCCACAAAGA	59.726	20
204	585	788	ATAATTTCGGCCATCACCCT	60.531	20
151	254	404	TGTAACGGTTCGATCTCACG	59.716	20
243	243	485	TCGAAGGTGAACTCGGTCTT	59.844	20
218	446	663	GGATAGGCCCTAACTCGACC	59.925	20
220	3	222	AGAGTTCACCAAGGTACTTTA	57.201	27
218	1371	1588	TGGGCACATTTGAATCTTGA	60.049	20
267	837	1103	CCAAACGAAGTGACTTGCAG	59.485	20
178	224	401	TGTAGGCATGCTCAATTTGG	59.688	20
253	396	648	ACACACACTCACTCACTCCCA	59.181	21
158	71	228	GTTCGTGGTTCGGGTATTCA	60.755	20
116	14	129	AAGGGTTATCACCTGATTTTCT	57.73	23
166	631	796	AAGGATCTTGTTACGGGCCT	59.962	20
172	1757	1928	TTGACTGATTGGAGCAGTGG	59.831	20
236	24	259	TCAAATCTTCAACATGCAAGC	58.909	21
264	242	505	TACGAGACTTTTGGGGGACA	60.486	20
248	214	461	CACGTGCGTCAACTCCTTTA	59.904	20
243	44	286	AAACACGCAACACAAAGCAG	59.951	20
232	648	879	AGCCCTGTAGAGGAGCATCA	59.973	20
158	313	470	TTTATTGGACGAAAATGCCC	59.773	20
195	432	626	TAAACCGTTGTTTTGGCTCC	59.975	20
278	26	303	CAGTAACAAAGTAAGACATGA	58.534	26
132	283	414	TTGCTTGAAACCAACTGTCG	59.881	20
277	359	635	CCCGATTATCGCAAGAACAT	59.923	20
249	252	500	CGCACAAGCTGAGTGAGTGT	60.251	20
212	76	287	GTTGTGCTTTGTGCTTTGCT	59.126	20
142	71	212	TCCTCTTCCCATTCTCTCCA	59.731	20
103	19	121	ACACGAGTGAAGAAAGGGAG	58.929	21
273	79	351	AATACTTTCCGTCACCGTCG	59.993	20
230	1103	1332	CCCATTCACAAGACCTCCTC	59.505	20
237	346	582	TGAATGAGGAAGATAAATGTG	60.19	23
147	193	339	TTCATTCCTTCGGCTGACTT	59.813	20
245	679	923	AAGGGGAAGTTCTGCATGTG	60.111	20
280	0	279	CGTCAGAAACCTCTCGCATT	60.397	20
191	294	484	GACCGCCAACTTTTCTTGAG	59.853	20
211	101	311	AAAGGATCGAAACGAGGGAG	60.569	20
196	9	204	TGTGTTGTCTTTTAGATCAATG	59.53	26
171	4755	4925	TCAAGGGTAATTTTTCAGGCA	59.573	21
137	259	395	TAGTTAGCATGGGGGAATGC	59.923	20
272	83	354	TTTAATTTGGCCGGATTGTC	59.773	20
185	1778	1962	AAAACTGATATGCGCGTTGA	59.329	20
267	929	1195	ACTGCCTCCAAGCACAGGTA	60.854	20
272	89	360	CCACTTAGGAATTTCATCAAAT	60.339	27
180	364	543	TGGACACAAGTATGGCTCTCA	59.303	21
195	871	1065	TGCTGATGAAGAATCGGATG	59.756	20
174	1024	1197	GAAATCAACCGCGGAGTAAG	59.708	20
123	637	759	GTGAACAACAATCCCCACCT	59.679	20

226	20	245	ACTGAAATTGGGATTTGTGGC	61.095	21
218	13	230	TGTAATGCTACAGTTCTTAATT	57.643	26
275	2128	2402	AAAACCCAACGACCGGTTA	60.213	19
140	246	385	AGCCCGATCTCAAACTCCTC	60.735	20
226	484	709	GCAAACTGATTGACCCGAAT	59.939	20
106	20	125	AGCTTAAACAAAATGGCATTA	59.54	25
192	2	193	ACGGTTAAGATTCAGCACGC	60.278	20
201	29	229	CTCACGAAAACACACGCACT	59.946	20
149	705	853	AAAAATTGGGCATTTTGACG	59.81	20
141	69	209	CAGTTATCACCGGATCACGA	59.522	20
243	16	258	CTCAACGGTATGCTCGGATT	60.096	20
268	241	508	GCACCCCGTATTTTAGGACC	60.562	20
178	1180	1357	AGCTATGCTGCAGGTTCCAC	60.428	20
151	66	216	AGTTTTCTCTATTGGGGTGGC	59.473	21
173	76	248	CAACCTATAAATAAGATCTCA	57.587	27
138	727	864	CCTGCTGGTTCTTGCTTCTC	60.134	20
179	364	542	CATTTCGCACACAGAGATGC	60.423	20
185	478	662	CGTATATGTCGCCGGAAAGT	59.982	20
134	230	363	ACCAATAGGTCATGGGTTCG	59.67	20
238	646	883	CGGTTAGAAACCAGACCGAA	60.103	20
172	1167	1338	AAAAATTTCGATCGTTTCGG	59.055	20
278	145	422	ACCCTTTTCGGGGCATAAAT	61.703	20
258	30	287	TTAAACCTTTGTGCGGTTGC	61.027	20
268	486	753	TTCTGGTCCAAACCCAATCT	59.381	20
228	613	840	CCACCCACTTTCTCTTGTCC	59.549	20
208	656	863	ATGGAAAAAGGCCGAGAAAT	59.909	20
201	884	1084	CCAGTGTAAAAAGATCGAGC	58.041	21
198	1004	1201	GAAACGAAGATGGTTTCGTG	58.201	20
270	587	856	TGTTATGGGTTTTTGCCGTT	60.223	20
161	2090	2250	GGAAAAGAACCTGAATGCGA	60.192	20
207	215	421	CACGTGTTCTTGCTCGTACC	59.365	20
180	49	228	ACCAACATCACCAAAAACCC	59.55	20
274	0	273	GCACACTCAGATCACACAGG	59.888	21
213	31	243	ACCAAGATTTGATCATGGGC	59.756	20
253	204	456	AATGGAGGCAAGCTACTCGAT	60.243	21
165	2796	2960	CGGGAAACATGATCCGAATA	60.66	20
126	75	200	AATATTGCAAATGGCCGAGA	60.424	20
243	261	503	TACGATACGAGGAGGGGTGT	59.43	20
261	3292	3552	AGGATCATGGCCACGTAGAG	60.096	20
132	400	531	GAAGGAGGTTGGGAGGAATG	60.822	20
272	1179	1450	TCCACCTCACTTTTCCCTTG	60.081	20
232	248	479	CAGCTCTTCAAACTGGACACA	60.465	22
201	1102	1302	AACCGGTTAAAAATCGGACC	60.055	20
180	28	207	AACAAACACCTGGGACCTCA	60.399	20
249	6	254	CAACCCTACCTCCTTCTCCC	59.928	20
169	287	455	CAACTGTTCTGAATGCGAGC	59.596	20
174	1771	1944	TTCATTCAATTTGCTCCTGG	58.695	20
261	40	300	GACATTGCCTAGAAAGTGGG	59.184	21
229	100	328	TGTTGCCAATTAAGATTGCG	59.702	20
266	48	313	CATTCACATCGTCTCTGCAA	58.352	20
120	690	809	GGCATTGTATATGGAGGGCA	60.69	20
279	1191	1469	GTGGCCGCATTGTATGAAAA	61.783	20
199	400	598	GGAGAACCGTCGACATGATT	59.934	20
156	263	418	CCAAAACCGACACTCCCTTA	59.964	20
211	11	221	CCATAGAAAATGTTGTTAGCA	59.577	24
108	103	210	CAGATTTTGAAACCTGTAAGT	57.574	24
277	130	406	TCAATTCATAAATATGTCGAA	59.021	26
195	710	904	TTGCGAATTGTTGCAAATCT	59.305	20

272	1566	1837	TGCTGCAAGCATGTATTTGTC	59.894	21
276	955	1230	AACTCAAGTTCCGATCGTGC	60.263	20
138	304	441	TAATATTTGCCGCCCAAGAC	59.928	20
279	90	368	TTCTGACGAAATTGCCCTTC	60.192	20
148	440	587	TTCTTTGTCCCTCTCCTTGC	59.405	20
245	3281	3525	CGCCATATCGGACAAACTCT	60.096	20
163	941	1103	CGTCCAACGAATCAAGACAA	59.691	20
105	9	113	GGAGCCTCCGAACTTTGAA	60.324	19
181	1608	1788	TTGTGTACCAAGACATTTGTGT	59.374	24
189	63	251	CGACTATCTGCAGGAGGCAT	60.384	20
181	314	494	GAACACCGGATTTACGTGGT	59.717	20
117	14	130	TGGATAAGTCTATCAAGATTTA	58.272	27
273	14	286	CACCGTTTATTCCCCATGTC	60.051	20
230	418	647	ACTTTTGTGGAAAAGTGGCG	60.147	20
104	23	126	TTGATCATAACTCTCTCTCGCG	60.407	23
126	90	215	TTGTGAGTCGTTTGTTCTTGG	58.811	21
267	425	691	TGACCACCCAACCACACTAA	59.848	20
280	146	425	TCCCCGGAATAATTGTTATTTC	59.945	24
221	201	421	GGTGTCCAAATGTTGGGTCT	59.679	20
195	39	233	CAAGAACTTTAATTGTTCATTG	59.944	26
173	386	558	TGTTGAGGGTTGTTTATTATGG	59.991	23
257	1089	1345	TTAATGGTGGGGACATGCTT	60.192	20
139	489	627	AAACCCACTAACCCAAACCC	59.955	20
267	483	749	AAAACCCTTCCACCCATTTT	59.549	20
264	932	1195	TGTGTGATGTGTGTGTGTCGT	59.499	21
280	30	309	TGCAAGCATTGAAGTTGAAA	58.046	20
208	2825	3032	GTTCCAGAACTCCGTCTCCA	60.238	20
247	150	396	CGGACGGTCGAATCAATTA	59.484	19
105	212	316	TTCTCGTGTTTATCCTCGCC	60.214	20
182	24	205	AGGGAAACAATGGATACTCCT	59.734	23
227	3	229	CATAAATGCGGTGGAGATGTA	58.52	21
267	16	282	TTGCGTACCAAGTTTTTGGC	61.027	20
277	620	896	TTGGTAGCCTGGATAGCACC	60.096	20
273	60	332	GTTTTCGGGAGGGAAATGTT	60.166	20
268	124	391	CAAACCCTAGCCCAAGAACA	60.103	20
185	50	234	TCTTTCCCATTTTGCCCTTA	59.52	20
178	295	472	CGCCCAAAAATCTAACATTCC	60.659	21
124	2368	2491	GTCCCAAGCACCTTTCTTGA	60.232	20
128	417	544	AAAGGGCGGTATCATTTGAA	59.411	20
249	11	259	AGATGACAACCTTCGGCTTG	60.255	20
266	225	490	CTAGCTTCGGTACAAACCGC	59.904	20
187	212	398	ATGGGATATGATTCCGGTCA	59.975	20
217	327	543	AAACACCAGTGAAGCAAGCA	59.49	20
244	298	541	TAGCAGGCTGACCGTAGTGC	61.532	20
269	227	495	GTGTGGTCTGAAAACTCGCC	60.7	20
266	100	365	ATATTCTCGCTTCTTCGCCA	59.945	20
140	393	532	ACCCTCCTTCAGCCAAAAAT	59.94	20
188	169	356	CGTTTCTCGGAGGTTTCAGA	60.366	20
126	189	314	CCTTCGTCAACTTTGGCAAT	60.11	20
166	237	402	TGCCAACCTCCAAAATCTGT	60.495	20
170	57	226	ATGGTAGCTTTGAGACACGATT	57.892	22
225	21	245	ATCGTGATTCGCAACTCTGA	59.399	20
266	39	304	TTTTTCGATTGTGCTTGCTG	59.992	20
209	302	510	TTGATGGTGAACAAACGGAA	59.941	20
169	60	228	ATGCGTGGAAGAAAAGATCC	59.129	20
114	132	245	CCCATTTCTAACTACCCAAATC	59.962	23
208	1007	1214	CTGAAACATGGATTGCCACA	60.517	20
200	698	897	CGAGTATGCTGACGGGAAAT	60.096	20

231	303	533	TGTTAACCAAAAAGAAGAATC	57.104	23
154	209	362	ATGCCCTTCTATGCTGAGGA	59.797	20
260	2165	2424	GACCGGGCTGTATTTTAACG	59.474	20
181	49	229	TCCATTTGCAATACTATGGCTT	58.654	22
103	23	125	AAATGGGCGAGAGTTTTCAA	59.685	20
207	17	223	AGGTGTCCGAACTTTATATGG	59.398	22
166	41	206	AGATGACAACCTTCGGCTTG	60.255	20
194	171	364	CTCTGCCTCGTCTGGCTAGT	59.769	20
216	86	301	CGAGCCGGTAAATTTTCACT	59.225	20
231	1350	1580	AGCAAATAAAAATTATGGTTTT	60.61	25
279	17	295	TAAAGTGTCGCGGACGGTAT	60.523	20
121	3	123	AGGAAAATATCAAGTCAACAC	58.257	25
174	643	816	TTTTTACCATTTTGCCCTGG	59.805	20
275	295	569	GGGACAATGGAGTTCACGTT	59.827	20
184	1630	1813	TTAATTGGACGGATATGCCC	59.621	20
259	76	334	AAGTGACCGTTGGCTTCATT	59.598	20
132	808	939	TTGTCGCCATATACGATCAC	57.029	20
145	63	207	TCTGCTTCAGCTCAGTGTGG	60.333	20
175	212	386	TAGGGGTTATCACCGGATCA	60.148	20
132	53	184	CCGAAAATTCAATCCTCGAT	58.974	20
196	4	199	TCCCAACTAAAATATGCTGCA	59.624	22
243	244	486	TCCTGACAGTTTGGCATCAG	59.831	20
106	53	158	TTGCAGAAAATGGAGAGGAG	59.94	21
178	1330	1507	TGTCGCGAACGGTATAGGAT	60.49	20
108	308	415	TTAATAGGCTGCCCTCCTCC	60.542	20
279	828	1106	AGGGCTGAGCAAAAATCAAA	59.823	20
184	11	194	CAACAATACCACACAGGTTCA	58.458	22
227	797	1023	AGATGGCCTAAGACGGTGAT	58.622	20
261	148	408	GCTCCAAATCAAAATCCCCT	60.265	20
170	1	170	TTGTTCCTACTCACTCACATTA	57.186	25
101	93	193	TGTTGAATTAACTTCCCAAAA	60.25	23
242	108	349	CAGACATTGAGGTTTGGATGG	60.36	21
271	232	502	GTGGGTCGAATTTCGTGAAC	60.362	20
273	88	360	GGAACCTATGTGACATCCAGC	59.425	21
129	29	157	ATTATCCGATTACCCGACCC	59.873	20
267	1015	1281	ATGCACATGTTTATCGCACG	60.554	20
215	219	433	TCGCTCATCCAAGTAAGTCG	59.024	20
204	363	566	AGATGAAGACGCATGCCAG	59.959	19
144	752	895	TTAACAATGGTGGCCGAAAT	60.188	20
248	2	249	TTATCAGCATTTGGGAAGGG	59.894	20
126	50	175	ATGTGCGCCTTTTAACCTTG	60.131	20
275	70	344	AAATACGGTCCGTGCATGTT	60.257	20
119	67	185	AGAACAAGCTAAGGCACCCA	59.875	20
274	539	812	CCTCCAAGTCTAAGCAGCCT	58.695	20
160	92	251	AGCACTTGCTTGGATTGTCA	59.445	20
221	52	272	TCGTTGATTGCATAGTGGGA	60.073	20
247	1071	1317	TTGGGATCTGCCTCTTCCTA	59.767	20
225	222	446	TCCTCCCCAATTTTGTGTGT	60.21	20
280	551	830	ATGTAGCAGGTTTTGTCGCC	60.14	20
179	642	820	TGAGTGTATGGAGCCCATGT	58.96	20
127	385	511	CAAAGGCCCACAATGGTTAT	59.685	20
256	6	261	GAGTCACACAGTTTGGCACTT	57.845	21
272	67	338	GCCTTAAAAGGTGGTGTGGA	59.971	20
154	923	1076	TGCAACACAACCAAAGCAAT	60.157	20
101	13	113	CTTGCTGTGTTGGATGGAAA	59.691	20
122	339	460	ATGAGCCACAGTTCCAATCC	59.934	20
158	191	348	GTCCGTGAAGTTTAGCGACC	59.74	20
225	171	395	TCTTCCGCTGGTTTTCTTGT	59.853	20

269	225	493	AATGAATGCACCGGATTAGC	59.929	20
211	341	551	GCAATGTGGGCTGAAATCTT	60.081	20
199	1143	1341	ATTCGTCATCAAATTAAAGCCT	57.001	22
277	390	666	GGCGAGAATGGAGGAGAAA	60.288	19
155	760	914	CTCAAGATCCCAACCGACTC	59.655	20
210	76	285	TCGAATTCGGGATACCAGAG	60.029	20
251	108	358	CCTAATAGGGTTGTGTGCCC	59.312	20
112	95	206	GAGACGAGAGAAAAGAGTGC	59.367	21
169	705	873	CGATTTGTATATTTTCCGAAAG	59.092	23
220	18	237	CACCGTTGTCTTTAAGCCGT	60.168	20
106	111	216	GTCGCAGTGATGTCCTTCCT	60.269	20
190	39	228	TCCTCGTATCCGTTCTCCAC	60.073	20
200	1932	2131	CGCCTACAAACACGCCTAAC	60.689	20
252	1478	1729	ATGCCCGTTTGCAATATGA	59.906	19
118	545	662	GCTATGGTGGTTTTGTAAACGT	60.667	23
216	7	222	AACACCTGTGAAAGGGATCG	59.966	20
234	340	573	TTTGTGTTGGCAAACAGGTC	59.591	20
213	23	235	TTCGGAGTTATGAAGTTAGCA	59.68	23
184	184	367	GATTAGCAAATTTCGGGACG	59.547	20
269	1372	1640	CGACCATAACAAAGAAAACA	59.553	22
265	336	600	CGCAGATCTGATGGTCCAG	60.371	19
242	52	293	ATTTAAAACCGATCCCACCC	59.888	20
226	326	551	AGGTGCTCAAAAATCCGAAA	59.685	20
101	216	316	TGAGATAAGGGGGTGTTTGC	59.933	20
176	77	252	CCTCCTTCAGCCAAAAATGA	60.184	20
261	200	460	TCCCTATTTTTCGTCTCCCAC	60.305	21
174	274	447	CGAAGAGTGTGGAATCAAACC	59.583	21
272	388	659	TCACACAGATTTGACATCGAA	60.161	23
271	512	782	TGATTTAAGGGGGTGTTTGC	59.801	20
264	17	280	TGATTAGTACCGATGAATCAA	60.595	24
119	11	129	TATGACCTATGGAAGCCCCA	60.288	20
193	3696	3888	GATTCGGTGGGAGAACAAAA	59.91	20
259	171	429	TCAACATGCAACCAACAAAAA	59.999	21
277	97	373	CAGGAACCCTTTCTCTCATCC	60.059	21
264	890	1153	TGCCAATGCTTGTCATAGGTT	60.517	21
202	267	468	GTCTCAACCCTTGATTGCGT	60.119	20
216	1962	2177	AGTGGCTCTTGTCTTCCTGC	59.604	20
256	135	390	TCCTTTCCCTTTCCTTTCCT	59.144	20
106	15	120	ACCGTAGGCATGGTTTGTTC	59.859	20
222	0	221	TCGATAAAGGGTGAGGAGGA	59.623	20
257	317	573	CCTTCCCATTTCCTCTCTCC	60.008	20
117	129	245	CATTGGCATTGTAAGCTTCG	59.325	20
278	4	281	TATCCTCCTCCCAATCGAAA	59.458	20
222	20	241	TTGTTGATGATGGAGGACGA	60.048	20
155	148	302	TCACTAACGGCCGGAATATC	59.923	20
161	632	792	AAGGGGTGTTGTGTTGTGCT	60.466	20
133	50	182	GCTACGCCTAATTGCTTGCT	59.658	20
138	922	1059	AAGCATGCATATCGCAGAGA	59.553	20
148	107	254	CGTTGGAGCTGCTAGGATTC	59.978	20
234	305	538	TTTTGTTATTATAGGATCAAAC	58.722	25
195	1493	1687	TACCACCACATGTCCCTTGA	59.806	20
132	1	132	AGTTTTGACAATATTTAGGTGT	58.65	27
260	122	381	AACGACTCCCAATCAGCAAA	60.636	20
269	210	478	TCTCTCTCGACGGTGAAGGT	59.986	20
195	15	209	AACTCCATTTGTAATAGTAAG	58.438	27
113	81	193	CGGCCGGAATATCTAAAGTG	59.564	20
246	866	1111	CGATTTCGGTTCAATTTTGC	60.436	20
263	99	361	TGGTGGCCATATATACGCAAT	60.075	21

111	1	111	CTTTGGCAACGGAATACCAC	60.365	20
203	829	1031	TCCAAATACCCAGTCCCAAA	60.162	20
161	38	198	TCTCTATCTTCGGCCCCTTT	60.166	20
243	393	635	GCGAAGCTTTTCCAACTCAC	60	20
121	646	766	CGAATAGCGGTTGCTGATTT	60.23	20
114	355	468	TCCGAACCAAGTTTTTGTCA	59.145	20
208	779	986	AAATTCACATGCGACATCCA	59.931	20
174	211	384	ATGGGTTATTACCGGATCGC	60.903	20
247	1884	2130	AAAACTTCAAACCACGGGAT	58.411	20
226	1109	1334	ATCACAAGCATGCAAGATAAG	59.252	22
258	82	339	GGATGGACCGGATGTTAGAA	59.75	20
249	109	357	AAGTCGCCAGAAAAGTGTCG	60.431	20
168	0	167	ACAAGCACGAACACACACAC	58.155	20
185	3948	4132	AAGCTAAGGATTGAAGCGCA	60.117	20
272	769	1040	ATCAATCGGAGAACGTCGAG	60.218	20
155	43	197	CCCATGCATGTAACAAACCA	60.234	20
251	691	941	GCTGGCTTTTCTCTTGGACA	60.517	20
258	27	284	AAAATGCCCTTGTATGCTGC	60.103	20
228	111	338	TTGGATTCAGATCGTGGAAA	59.049	20
100	9	108	TTAAATTTTCGAACGCCTGC	60.205	20
133	113	245	TCACCATAACGCACCCCTAT	60.214	20
235	838	1072	TTCGGGGTTGCACTGTATTT	60.365	20
212	587	798	TAGTTTCGCCCCTGCTTATG	60.223	20
155	809	963	TGAAGGGGATAGCATTTTGG	59.894	20
274	431	704	TTCTAGCAATTGACCCACCC	59.933	20
233	86	318	CACCTGATTTGCTGGCTAGA	59.024	20
278	1216	1493	ACACTTCCATCACTGCACCA	60.162	20
234	66	299	TCATGCAGGTTAGCAAGGAG	59.024	20
279	46	324	CAAACAAAGGGGACCACAAA	60.756	20
123	75	197	TCTACGTCCACGGAGAGGTT	59.721	20
239	521	759	TTAACGGGGATACAGGATGG	59.64	20
134	1	134	ATGAAGTTAAGAAATAAGGAG	57.239	26
250	3	252	CGGTACCATCGTCTCTCGTT	60.134	20
269	1337	1605	CAAGTTCCACCCAGGTGTCT	60.002	20
277	250	526	TGCATAGGCTGTCTCTTGGA	59.547	20
267	320	586	CCCTTGTATGCAGCCATTTT	59.96	20
135	483	617	TTCGAGTCATACGGAGGAGG	60.21	20
158	55	212	TGGGCATCACAAATAGACGA	60.073	20
278	637	914	AGTTGAGCCCACCCAATTTT	60.723	20
275	146	420	TGTCCTTTCGTTTAACTCCTCC	59.631	22
188	60	247	GCAAGGCTTCCATATGCACT	60.243	20
273	818	1090	TATGCGGTGTTTTGGTTTGA	59.969	20
225	605	829	ATCTTGACCGCTGATTTTGG	60.074	20
260	398	657	GGATCCCACTGAATTGTGCT	59.934	20
147	373	519	GAGGAATTGAACCCAGGATCT	59.387	21
262	84	345	AGGCAATTAAGATTCGCCCT	60.061	20
107	14	120	GGGGGTGAATAGCCTCACTT	60.328	20
164	326	489	GCCCATTTGAGCCAATCTAA	60.038	20
171	87	257	ATTGCCCCTCATATGCAGTC	59.923	20
274	592	865	TACGGCTAATTTGATGCACG	59.725	20
151	98	248	AAAAATCACGCCACCATTAG	57.635	20
153	70	222	TGGATCAAATGTTTGGTTGC	59.375	20
257	81	337	AAGCAGCCATTAAGAGTCGG	59.476	20
243	15	257	AATAAACTCCGACGCCTGAA	59.708	20
207	111	317	CCCTAGATGACAACCTTCGG	59.545	20
159	269	427	TGCCCTCAATCTCGAAAAAT	59.645	20
280	1698	1977	AGCGGTTAGGCTTCCACCTA	61.125	20
168	12	179	AAACTCCTCCAAACTTCCTCCT	59.637	22

255	23	277	TCTCCTTACATAATTTGCCCTC	59.977	23
209	57	265	TCCTCACTCTCACTAGCCGC	60.7	20
261	1415	1675	GTTTGCAAGCAGTTACGGGT	60.176	20
190	36	225	GCAGCCCTCTACCCTTCTTC	60.349	20
219	159	377	TTGATGTCCCTTCTCCTTGC	60.195	20
254	395	648	ACTGTTCACGGGAGCTTTGA	60.833	20
277	441	717	CGAGTGCATGAGCTTGAGAG	59.88	20
176	5004	5179	TGGTGATGGTGATGAATGTTTT	60.096	22
262	47	308	TGGAAAACAAAACACCCCAT	60.066	20
235	794	1028	AGCTGAACAGGAATGTGTGC	58.884	20
257	11	267	GTGTGTAGAAGTTGGCACGC	59.369	20
182	1286	1467	TCCGATTTCAAACCCAAAAA	60.273	20
277	96	372	372	372	372
266	999	1264	ATGCTGTGAGATTCGCATGA	60.386	20
278	58	335	TTCAAGCTGAGATCGACGAA	59.673	20
172	184	355	ATGCGAAAAACATGGAAAGA	58.214	20
133	58	190	TTAGATGATCTCATGAAGTGA	57.71	26
220	150	369	TTCTCCCAACCAGAATCACC	59.903	20
221	340	560	TCGGCAGTAGGAGATGGAGT	59.827	20
268	112	379	CTCATGCAATGAAATCCGAA	59.622	20
203	5	207	ATATCTGGAGGCGGGAACTT	59.925	20
229	26	254	ACCAACCTAGCCCACTACCC	60.247	20
181	96	276	GCACTCACTGAGGAACCCTT	59.305	20
118	171	288	GTGAGGTGGGGTGTTAGGAG	59.425	20
175	352	526	CGACTCATGTTGTTCCATGC	60.12	20
231	3484	3714	TCCTCTAATGGCCGAAAATG	60.031	20
104	108	211	TAGATGGGCTAAGTGGGGTG	59.948	20
255	18	272	GAAAGTCTCACTCGCAAGGC	60.142	20
272	1072	1343	TGCGGTATCATGGTGATGAA	60.905	20
204	611	814	CCAGTCACGTTTCACAAGTCA	59.779	21
136	14	149	ATCTCGCCTCAACGAGAAGA	60.096	20
174	192	365	AAATCAAAAGCCCACAATGG	59.801	20
258	253	510	GTAATGCTAGCCGGAAAACG	59.742	20
126	805	930	CACACCCTCTCCCACTCTCT	59.27	20
226	106	331	ATGCTGTCAATTAGTGGGGG	59.813	20
158	0	157	AATTTTCTGGCAGCCTTTGA	59.823	20
179	68	246	CGAAAATTTGGTTGTTTTCCA	59.834	21
230	417	646	CTTCGAACCGCGAAAGAGTA	60.514	20
225	106	330	TTCAATTTCTTGGCTCAGGG	60.184	20
216	274	489	CGTTGTCTATGCACGCATTT	59.759	20
245	86	330	GGCTTGTTGCTTGTTGGTTT	60.154	20
224	149	372	AAATATACCCCCGCATGCTA	59.304	20
205	66	270	TTCAACATGCAACCATCAAAA	59.961	21
221	50	270	GATTCGCACAAATGATCGTG	60.08	20
277	4	280	AAGGCTTTCTTAACTTGTTGGA	57.273	22
137	304	440	CCGTTGGAGTTAGTTTGAGCA	60.29	21
259	346	604	TATCACAGTTCACACCCCCA	59.806	20
187	56	242	CAAGGGGCAGAAGGATTTTT	60.423	20
199	384	582	AGAGATCCGAAGCCAAGGA	59.895	19
123	111	233	CACCCGTGGACGTAGATCAT	60.801	20
254	263	516	AGCAAGGTAGGCTTTCGAACT	59.556	21
261	1150	1410	GTCATGCAGTGCTTCGGATA	59.83	20
279	5	283	GGGGAGGGTGGTTAGGTTAG	59.685	20
140	300	439	CATCGGAGCGATAAGGAGTC	59.797	20
118	522	639	TGGTGGGTTTCGTCATAGGT	60.232	20
161	122	282	AAGGTGGGAAAGAATTTGGC	60.299	20
129	1529	1657	TTTTCCAGCCTTTGTTGACC	60.088	20
209	30	238	TTTGTTGTTTCCCAAGTTGC	58.649	20

270	789	1058	TCGGATGCTATGGTTGAATG	59.499	20
275	506	780	TCAAGGACTTACCGCTGGAC	60.255	20
248	1297	1544	AAGAAAAAGGTTCCCCTCCA	59.912	20
256	1078	1333	TGCTCGAGCTGGATGAGAAT	61.058	20
276	91	366	CGTTGCCGGATAATTCAAAC	60.323	20
237	3	239	GTCGCTTGAATTGCGACATA	59.839	20
174	153	326	TATGGGTTAGCGTGTGATCG	59.566	20
259	4025	4283	TTCACTCGTCAAAGAACCCC	60.088	20
261	685	945	GGGAAAATGTCTTGTGGTCC	59.239	20
193	207	399	TCGGACTTATGAAGTTAGCAC	58.403	22
269	23	291	GGCTGTGAGATCTAGCGTGA	59.143	20
158	27	184	TGATCTATGGAAGCCCCAAA	60.405	20
134	31	164	CCCATGTTGTAATTAATGTAG	59.089	24
269	425	693	CGAAATAAAAACCGAACCGA	59.937	20
141	63	203	TCCATGAAAGCTCACCCTCT	59.803	20
115	685	799	ATGGAATTGGGTGTTGGATG	60.439	20
196	458	653	TTCACCGCCTGCTCTTATCT	59.978	20
280	138	417	CGCTCAAATCACAAACCCTT	60.11	20
245	2898	3142	CTGGTGAAGGTTTGCCTTGT	60.149	20
227	307	533	GGACACCCCCATTCCTTAAT	59.881	20
219	351	569	GTACCGAATGCGAGCAAGTT	60.278	20
239	558	796	GAGCTGAATTGGTTCGCTTC	59.962	20
107	77	183	GACAAATCAGGGGGTTTGG	60.157	19
252	1121	1372	GCAAGTTTCCGTAGCTGGAG	60.015	20
245	216	460	ACACAGATCATCTCGGGTCC	59.928	20
222	360	581	TTGCTCCGATCTCCATTTTC	60.155	20
177	1073	1249	AAGAGATGGTTCCGCTCTGA	59.95	20
220	162	381	GGAGGTTCGACGTGGTTTC	60.504	19
252	72	323	TCACACCACATCTCAAATGAC	60.028	23
149	331	479	GCTCGGAATTCATGTCCTCT	59.243	20
187	197	383	AACTCAGGCCTCACTCCCTT	60.252	20
159	147	305	AGAATCACGGCCATTTTCAA	60.448	20
216	13	228	CGAGATGTCCGAGATGATCC	60.588	20
111	1	111	GGGTTGTCGGCATAGAGAGA	60.218	20
277	680	956	AAAAGTCTAATCGCCTGGCA	59.845	20
275	12	286	GGTCCTCCCACCCTAGAAAC	59.795	20
119	102	220	CTTATCTCAGGAACGACGGC	59.836	20
204	10	213	ATTACCATATTTAAGGGTTATC	57.31	27
153	377	529	ATTTTTCCTCTTTCCCCACG	60.291	20
149	2858	3006	AAGGCGTCTCGAGTGAAAAA	59.993	20
229	47	275	GACACCGAAAGGGAGGAAAC	60.862	20
153	999	1151	AAGGAGAGTGACAGCGAGGA	60.135	20
280	710	989	TGGCCGGCAGTTTATATAGG	59.943	20
129	176	304	TGACACCTAGCCCAAACCTC	60.111	20
175	4	178	TCTGAGACGACGGTGATACAA	59.303	21
135	1091	1225	CCTCGCACATTCAATTTCCT	60.074	20
172	6	177	GAAAAAGTCAGCCGAGAGAA	60.001	22
256	249	504	TGATGTTGATTTGGGTTCAAGT	59.336	22
228	25	252	CACTCACTCTCACTAGCCGC	58.78	20
152	41	192	TGATTTTCTGAAATCGCACG	59.809	20
243	1124	1366	GGCTCAAATCCGATGATTCTT	60.413	21
243	621	863	ACCACGGAAATTACGGAAAA	59.315	20
211	494	704	TCTGCTAGGGTTGGGAGAGA	59.943	20
139	51	189	TTTGGACGATTTTTCCCTTTT	59.81	21
166	480	645	TTTGCAAACATCCAACTACGA	60.166	22
182	224	405	CTTCGGAACTCTATCCACCG	59.688	20
280	228	507	CCCCAATTTTGTACCCGAA	60.54	19
225	518	742	GGTTAGGTCTCACGGGGAAT	60.19	20

257	210	466	ATGGGGATGAAATTCAGGTG	59.605	20
190	306	495	TGAAACTAGGAACGAAAACTG	58.114	23
117	2926	3042	GACACTGCAAGGTGCTTTGA	60.032	20
266	143	408	ATTCCAGGAGATCGAACGAA	59.629	20
220	88	307	TTTGTCAACTTTGGCAATGG	59.561	20
202	269	470	CTGGACGCCTTTAAATCAGG	59.702	20
246	1175	1420	CGCTACAGTTCACACGTTCG	60.507	20
195	26	220	TCAAAATTTCCAAAAATCAAA	59.509	23
176	14	189	CTCAGGTTCCGACCTCAAAC	59.697	20
141	43	183	TTCAAGGCATTTATCTGGGC	60.038	20
110	216	325	GCCCCTTGAAGTTTCGTAGA	59.312	20
240	2179	2418	TTTTCCTTGGGACACAATCC	59.767	20
280	928	1207	GGGCTAGTCCTGCAACACAT	60.142	20
270	405	674	CCCGATTTGTAAGGTTCCATT	60.061	21
188	6	193	GCTCTACAATATTACAATGGG	58.236	23
249	99	347	TGTGATAGGATAGGGCCAGC	60.059	20
274	25	298	ACCTGAAGGGGGACTTTTTG	60.332	20
235	845	1079	GCTTGAAAAGCCATGCAAAT	60.217	20
196	520	715	TCCGTCCGTTTTCATGATTT	60.309	20
265	1465	1729	CCAAGTGAAGGCTGGTGATA	58.722	20
278	485	762	TTGTCATTGTTAATCCCAAAAC	59.262	23
203	254	456	CAACGTCGAGTCGAGGAAGT	60.444	20
214	124	337	AGCACGGCTTGTGCTATCTT	60.044	20
209	2473	2681	ATGAATCGGGTGATGATGCT	60.312	20
149	261	409	TATAACGACACGGCCATTGA	59.953	20
213	32	244	GAAATCCTTGAACCATTCCA	57.426	20
231	659	889	AGAATTCGTGCCCCTCATTA	59.528	20
274	79	352	CTGGATCAAATCCCCAACAC	60.173	20
177	752	928	CCCGGTATGCTGACGATAAC	60.352	20
269	53	321	TGAGGTTGGAGTGTGTGGAA	60.129	20
119	2	120	GGGGAGGGAGGGAGAGATAG	61.291	20
102	1	102	GGAAGAATGATGGAATTGGG	59.175	20
220	873	1092	TGAACAATTGAACACCGGAA	59.941	20
263	223	485	CCTCACAAAATGACACGCAT	59.572	20
135	294	428	ATCACAATAGGGCATGGGAC	59.635	20
176	38	213	CACTCACACTTTGCACACTGA	59.986	22
269	218	486	GGCAGATGCCTTTGAAGAAC	59.82	20
232	255	486	TTAAAACAAGAAAGCCCACCA	59.612	21
277	351	627	TCATCAAATCTCTAATTGCACC	60.326	23
103	173	275	TGAAAGAGCCATCAGCCAAT	60.744	20
172	962	1133	GGGGAGATGATGAACGGATA	59.709	20
222	135	356	TGTCCATTCAAGTCGTGGTC	59.525	20
271	95	365	AAAAACATTTTCTCTTGAACGC	59.194	23
168	44	211	ACACAACAATACCACGCAGG	59.49	20
231	61	291	TTGTTGCCGTTAAAGTGTGG	59.627	20
236	95	330	GGGAGAGAAGGGAGGAGAGA	59.883	20
257	53	309	GGATTTGTCAACCGGAAAAC	59.269	20
183	825	1007	CCAGCTCACCATTTCATGTG	60.112	20
203	35	237	TGCAAACACCACAACAATCA	59.563	20
248	169	416	CACCCCTCCACTCTCTCATT	59.101	20
191	57	247	GACAACAGAAAAACCACGCA	59.74	20
214	380	593	GCACCAACATCATCGAACAG	60.12	20
217	1570	1786	TGTTGTCACATACACGTTGGG	60.331	21
265	52	316	CACCACAATGAAGTGGATGC	59.967	20
246	91	336	ACAACAATGTCGCGAAACAA	60.157	20
248	66	313	TCGTGCTCACTGATCTCTCTTC	59.751	22
220	522	741	TCAAAAGCAATCAAATATCCC	59.433	22
156	384	539	CAAAAGATCGGCTATTTGGTG	59.595	21

110	342	451	TGGATGCCTTTCATTTAGGTG	59.946	21
156	602	757	AAACCGAATCTTTTCGTGGA	59.546	20
275	81	355	CTTGGCAAAAAGCACAAAAA	58.979	20
252	389	640	CGGAACCCTAACTAACGCAC	59.632	20
211	313	523	CAATAGAAAATGAGTTTGAGT	58.504	25
109	224	332	ATGCATCCTGGCCTTGTTTA	60.469	20
249	2030	2278	GAATGATGAACCCCTTCCCT	60.133	20
121	579	699	GTTCTTGCTTGCTGTCCCTC	59.997	20
261	180	440	CAAGCTGTCAACCCAAAACA	59.734	20
214	355	568	GTCGGCAAACCAGAGCTAAC	59.882	20
272	87	358	TCTCCCAATTTTACCCTCCC	60.124	20
226	171	396	CCAGGTTCAACTCTCTTCCG	59.837	20
100	27	126	CCATTTGCAATACTAAGGCTT	60.047	24
273	1060	1332	AGGAATAGGGCCGAGAAAAA	60.034	20
206	2083	2288	ATCAACTAAATTTGGCGCGT	59.614	20
261	2336	2596	GACATTGGCATTTTCTGCAA	59.67	20
147	21	167	TCTTGGATGATGAGGCTTGA	59.322	20
229	1435	1663	TTCTCCTTGTAGCGTGGGAG	60.388	20
276	157	432	TCGTCAAAAACTAATTAAGGC	60.013	23
102	18	119	TGAATTACTTGAAGAATGATG	58.528	26
207	36	242	CCAAACCCCCAATTTCAATA	59.497	20
248	845	1092	CAGGAAGCTTCAACTCCAGG	59.982	20
196	15	210	TTTTGAAATGGGGAAAGACG	59.91	20
155	2183	2337	TGGAGTGTAGTTCCCCCAAC	59.82	20
191	490	680	TCAATGCAACTCAAATCCCA	60.049	20
232	418	649	TGTGTGCAATGTGTGTGTGTT	59.523	21
223	68	290	GGGGAAGGAAAAACACAACA	59.807	20
159	3649	3807	CGACTACAGGAACTGAGGGG	59.715	20
225	2381	2605	CACTTCTGCGGCTGAAAAAT	60.386	20
213	1034	1246	GCCCGTGAAGATCTCGTTTA	60.214	20
195	36	230	CAGATACGCGGGTTCATTCT	60.096	20
100	31	130	CTCTGTGCTCTCTTTCTCAGTC	60.871	23
270	5	274	ATGAAGTTAGAAAATAAGGA	57.239	26
187	205	391	AAACTGCCCTCCAATGCTAA	59.708	20
229	68	296	CACAGAAATCACGTTGCAAAA	59.761	21
169	70	238	TTGCCCATTTTGCCCTAATA	60.275	20
241	80	320	ACCTCCCCTGCTCCATACTT	59.957	20
272	646	917	CTACAGCAATTGGGCCATTC	60.469	20
106	3	108	CTTGCCGATTAGGATTTCGT	59.182	20
186	4	189	CAAGCACTATGAAAGCTAAAT	58.302	27
249	96	344	ACGCTTGTCCCCTTAATCCT	59.962	20
212	214	425	TTTACCATTTTGCCCTCGAA	60.427	20
106	778	883	TCGTGTGTGTGAGTGAACCA	59.737	20
148	261	408	TTCTCCAAACAAGGAAGGGA	59.641	20
230	53	282	ACCGTAGGCTTGCTTCTGAC	59.501	20
273	1242	1514	TCCAGTGACAAAAACCGACA	60.128	20
209	1737	1945	CAGACAGAGAGATGCCACCA	59.98	20
234	104	337	CCAATTGATCGGGAATTGAT	59.581	20
217	546	762	ACATGATTTGGAGCTTGCTG	58.877	20
249	71	319	TTCTTCGCCAAAACCTTGAT	59.685	20
107	39	145	ATCCATCCTGTTTCTCCCCT	59.755	20
233	809	1041	GGGTATCTAATTTGCTCTCAT	59.029	23
211	532	742	AACCCAACCCACAATAAACG	59.587	20
210	86	295	AGCACCACATGCATTCAAAA	60.119	20
159	50	208	AGTTGGGCTTAATGGTGTGG	59.853	20
105	76	180	AGGAGATGGAGAGAAAGTGT	59.878	22
271	73	343	CTCGGAATCAACTCCAATCC	59.483	20
217	433	649	AAGGGGTTTTCTCTGGATCG	60.434	20

250	442	691	AATGGGACCTCCTTTACGCT	59.962	20
102	24	125	AGTCCGCTGTTGTGGATGAT	60.542	20
265	484	748	TACTGCTCTTGAACTCGCCA	59.74	20
234	11	244	ACAATGGCCAAGAGGATTACT	57.681	21
256	69	324	GAGAGTTGGTCATTTGAAGCG	59.867	21
233	37	269	TTTTGTTTGTTCCCAGGTTG	58.5	20
115	180	294	TTCTTCCTCTCCCTTCCGTT	60.183	20
173	376	548	GATTTGAACTTGGAGGGCAG	59.67	20
156	40	195	TGCATGGTTAATGTTGTAAGG	59.758	22
212	49	260	TGCGTCGTGTTCTGATTTTC	59.847	20
265	2	266	AGGGCTGAGTACACGAATGC	60.285	20
277	70	346	GCTTTCAAGGAGTGAGGCAC	59.997	20
220	141	360	GTTGGGATCTAGGCAATCCA	59.894	20
197	3313	3509	TCCAGTTTTCAATGGTGCAA	60.088	20
149	131	279	TTCTCACATCCTTCTCGCCT	59.95	20
161	479	639	CATTTATGTATTGCATGCCAC	60.102	22
189	5823	6011	ACTGGCCGGCTAAGTTGATA	59.73	20
102	10	111	GAATACCGCTCGTAAGTCCG	59.73	20
243	222	464	TGATTTTGGTGTGTTGGCAT	59.823	20
246	1390	1635	GTCGACCCGGACAATCTCTA	60.073	20
244	390	633	CATATGGCGCTCCACCTACT	60.118	20
219	71	289	ATGCATGATGTGATGCCAAT	59.77	20
231	29	259	TGCCCATACGGTTGTATGAA	59.809	20
239	24	262	TTTTATCTGAATGCTAGATGTT	58.809	25
212	157	368	GGAAAAATAGCATGCCTTCG	59.682	20
256	243	498	CGAATGCGAAATTGAAGTTG	59.301	20
248	23	270	TGTGTACTTCCCTACTCATAAG	59.296	25
147	168	314	AATGAACGGAGAACAGACCG	60.111	20
179	905	1083	GAAAATGAAAATTGGGGGCT	60.13	20
229	3330	3558	TCACATCACCGGCGTATAAA	59.953	20
270	146	415	ATGATGGGAAGGGTGGGTAT	60.272	20
254	20	273	TTCCACTCACGAAAACACGA	60.278	20
213	399	611	GGTGGGAGCAGACAGAAAAG	59.844	20
169	366	534	AAAATCCAGAAAGAAGCGCA	59.96	20
277	13	289	TTGCTTACTCATTGTAATCTCT	59.404	26
183	21	203	GCCACCTTACACCATCATCA	59.374	20
264	168	431	ACACTAAACCCGCGTATTGC	60.025	20
230	244	473	GGATACCCTCCCAAACCCTA	60.011	20
266	198	463	CGAGCCTCGAGGTAGCTG	59.831	18
278	2	279	CGGTGGTTTGAGAGTGATTG	59.135	20
219	537	755	TGAAGAGTCCGAATGGGAGA	60.737	20
136	19	154	ACAATTACAATGTTTATGAAA	57.992	26
202	249	450	GTTCCGACCTCGAACACTTG	60.69	20
236	29	264	TCCTCACTCTCACTAGCCGC	60.7	20
254	102	355	TTTTATCGTCACCCCGTTTC	59.801	20
177	5	181	CATCAACTCACCCTCACATTT	59.454	22
234	613	846	TCCAAGAAACTACGCCAACA	59.317	20
234	51	284	TTGGAGTTTAAATGTAGAGGC	60.134	23
117	20	136	TTTAGTGTTTTGACATGATTAC	57.557	25
186	249	434	TAGCTGGTTTGTAGCGGGTT	59.769	20
238	1551	1788	ATTGCATTAGCAAATCCCGA	60.424	20
149	121	269	ATGTTCGAAGCAGCCAAACT	59.882	20
278	153	430	ATAGTCGTCGTGTTCCGGTC	59.997	20
183	3	185	TCCTTCTTAAAGGTCTTAATCG	59.658	24
216	416	631	TTGGGGGTTTAGGGTTCTCT	59.799	20
184	2834	3017	TACGGCAACTGTGGTTTCAA	60.149	20
278	235	512	TTTGTGTTTGCAGAAATCGC	59.856	20
115	172	286	TCATTTTAACCCAAACCCCA	60.024	20

280	2128	2407	AACGATCCTACACAATGGCG	60.914	20
125	74	198	GATTGGGGACTGACCTTTGA	59.903	20
179	164	342	TGGCAACAAACAAAGCTGAG	60.027	20
256	45	300	TATCGACGTGATGGGTGATG	60.353	20
245	83	327	GATCCAAGGATCACAAGTGGA	59.918	21
230	146	375	TTTTGTCGGCCATTTTCTTT	59.564	20
190	21	210	AACTGCAAAAGAGATTTGATG	58.4	24
102	27	128	TTCACGAATAAACATGTTCCAC	59.505	23
269	3	271	CGCCCACAATCCTGATATTT	59.784	20
274	195	468	CGCACCTATTAGGGTCGGAT	61.21	20
220	507	726	TAACGAGAAAATTCGGCCAC	60.074	20
209	6	214	CCGAGGTGGAGTAGTATCCG	59.569	20
248	1996	2243	TGCATTTACCTAGAACCCCC	58.903	20
248	345	592	AGGAGCAGATGGAAAGACCA	59.803	20
250	78	327	TTTTCGCAAGCCACTAAAAA	58.608	20
251	2252	2502	CAGGAAAGAAATGGGCTTCA	60.184	20
158	23	180	AAGCGAAACTGTTGTATGCTG	58.121	21
126	65	190	TGTTTTCGAGCTGTTATGCG	60.014	20
143	21	163	TAACCCGAGTTGAGGTCCTG	60.103	20
200	106	305	ACTTGTCATCTCCACCGCTT	59.727	20
263	90	352	GGAAGATGGAGAAATAAGGCA	59.572	22
262	1982	2243	TGGTTTGGTTGTCACTTTCTTG	60.045	22
172	126	297	TTAGTTAGCAAGGGGGAGGG	60.435	20
100	427	526	AACCCATACTTAATTCATAACC	59.053	25
243	9	251	ATGATGTGGAGAAAGTCCCG	59.927	20
217	31	247	TTCGATGATAACTATGGGTTTT	58.079	23
164	272	435	AATGCTATGGACAAACCCGA	60.331	20
260	290	549	TGGAGAAGTTACGATGGCAAA	60.623	21
100	8	107	GAGGTTTTGACATAACTTAGGT	58.286	26
268	317	584	GACTTCCCGTTGTGGCTAAA	60.11	20
150	540	689	TTGTGTAAAAGCCGATCGAA	59.301	20
198	1708	1905	TGCTCCGAGACCTTAGACTCA	60.141	21
234	64	297	AGAATCCCGAGATTTCATGC	59.083	20
127	94	220	AGCTGGAAGATAAGATGTGAA	59.797	23
228	245	472	GGTGCTCCCATCATCTCTTC	59.617	20
257	1136	1392	GTCCAAAATTGTGTTACGGG	57.85	20
280	733	1012	AACCTTTTGACTGGCCTTCC	60.476	20
119	35	153	GTGGGTTAGCACGTGATCG	60.128	19
266	3628	3893	GGGATTTAGGCCAAACGATTA	60.155	21
273	1606	1878	CGGAAATACCTCGCCTCATA	60.053	20
193	393	585	AGCCATGATCTCATGATTCAAA	59.533	22
248	186	433	TTCGGTTAATCCAAAGGTCAA	59.438	21
227	20	246	ATTGAATGGCAAGGATTGGT	59.249	20
224	592	815	AGTGTAATAGTACATACAATGC	59.374	27
176	1	176	AGCCCCAAACTTTGCTGAAT	60.987	20
270	73	342	GATGTGGAGATGGGCTGACT	60.08	20
160	64	223	CGCGCACAAAGAACTTTACA	60.052	20
183	8	190	CCTGAAAAGGGACTTTTGGA	59.143	20
222	3460	3681	GCCTTTTGGCATGCAGTATT	60.103	20
253	320	572	CGTGCAAGCATGAATCACTC	60.423	20
262	371	632	GGAATGCGAGATGGAAGAAA	60.155	20
126	441	566	TGTCTCGGTGTTCATGGATT	58.933	20
275	378	652	AGAAAATTGGTTGTTATCCACA	58.549	24
181	44	224	CAATACCGTGACATGCCTTG	59.988	20
278	4168	4445	CAAGAAAATCCCACCTCCAA	59.903	20
142	143	284	ATGAGAAGCGTGGATTTGGT	59.556	20
101	17	117	GCCACCACACGAGTATATCAA	58.516	21
162	2772	2933	CCTCCTCTTTCTTTTTGCGA	59.564	20

269	297	565	CATGTAGGCGCCTCTGATCT	60.384	20
227	81	307	ATCTCGCGTTCGACTCCTTA	59.978	20
151	73	223	TGCTCTCTTTGTAATCTCTCCC	60.379	23
183	530	712	AGCAGAGGAGGAGTTGCTGA	60.284	20
267	110	376	GTCGCGAAATCAAAGAATCC	59.651	20
233	588	820	TTGGCAGAAACATGGAAACA	60.088	20
143	484	626	AAGATGAGCCCACCCACTTT	60.883	20
106	346	451	TATGATGGGAAGGGTGGGTA	60.006	20
236	179	414	GAAATGAAATCCTGGCTTCG	59.645	20
279	1	279	TCAGAAACTTGGAGCAGAAG	59.238	22
115	71	185	TTGGGCTATGGTTTGGAGTT	59.429	20
212	824	1035	TCTTTTCAATATTTATACCAAC	58.178	25
223	1767	1989	AACCCCCAAACATCACACAC	60.533	20
236	68	303	CCCCAAACAACGAAATGAAT	59.662	20
273	305	577	GCTCCCGAGCTCAATATCAA	60.318	20
262	574	835	TCGACATCCCCAATTCTAGG	59.887	20
279	229	507	TTGACATGATTTGTTAACGGG	58.4	21
135	53	187	TGTTTTTCATCCCGTTTCATC	59.793	21
238	32	269	GAGGACACGTTGGACCTGAT	59.969	20
240	24	263	CTCACTCTCACTAGCCGCAG	58.932	20
237	38	274	CAATCATCTAGCCCTCTAACA	59.682	25
191	658	848	TTCTCTGTCGCCAGATCCTT	59.95	20
178	21	198	GAGCCACGTTAGGCTCAAGA	60.538	20
176	233	408	CCCATTTAAAACCCTACGGA	58.805	20
271	829	1099	GATATGGAAGAGTGGCACCG	60.483	20
247	320	566	CCGGCTACTTGTGAATTCCT	59.195	20
278	535	812	ATGTCGATGAACACGGATGA	59.925	20
262	1266	1527	ATTTTAGAACGGGGGTGGAC	60.053	20
221	105	325	TGGTTGGAGGAAAATCTTGTG	59.956	21
231	40	270	CACCTCTCGCCACTACCACT	60.321	20
222	37	258	TTGTTCCAGCTTTCTCTCCC	59.405	20
207	421	627	GAGGGACAAAGCAAAACGAA	60.227	20
215	154	368	CATCAGAGCCACGTTAGGC	59.41	19
154	312	465	TGAACGGTTGAAATTTGCTCT	59.738	21
216	1070	1285	TAACCGAAAACCTTGAGAGC	57.096	20
141	614	754	AGGGTCCTCTAGCCTGCATT	60.233	20
211	2186	2396	GGGGAAAAGAAGAGTGGGAC	59.912	20
257	681	937	CTCCATTTGCATATTATTTTTG	57.819	23
177	1163	1339	TCAAGAGCCTCCGACTTTTC	59.55	20
271	202	472	TGAGGGTTTTGGAATCGAAG	60.044	20
124	4	127	CAAATGGCCAAGAGAGTTTAC	59.267	22
179	480	658	GCCTGAATCGACGACAAACT	60.263	20
202	104	305	CGATTTGGATTCGAATTCTGT	59.033	21
267	712	978	ACAAAGAACGTGCACACACA	58.761	20
198	387	584	TGGAAGGATGTGAGATGGTG	59.473	20
209	2035	2243	GATGAAAAGGAACAGCGGAA	60.192	20
253	202	454	TTTGAAATGGATGGTGGTGA	59.75	20
124	228	351	AGGGGCTTAAGATCCCAGAA	60.032	20
112	101	212	CTTCCGCCCTTCCCTACA	61.135	18
241	234	474	CTACTCTCAATTCCCGTCGC	59.836	20
224	399	622	CGCACCGATATGATAGACCA	59.523	20
247	103	349	CCCTAAGATAATGCCACCCA	59.778	20
213	184	396	TAGGCCCTAACTTGACCCAG	59.191	20
203	13	215	AACAAAGCTTGTCACACGGG	61.124	20
255	583	837	CCCAGACTCGATAACTGGCT	59.308	20
228	245	472	TTGGCTGTGGACTCAGTTGT	59.31	20
233	108	340	CCAAAAGACGATCTGGGATG	60.452	20
149	255	403	GGGTAGGGGTTCAAGTCCTC	59.795	20

234	213	446	TGCGAGCCATCAACATGTAA	61.225	20
242	3247	3488	CATGCACGAAACTCTTGGAG	59.44	20
245	215	459	ATGTATTCCTTGAATATGAGA	57.831	27
169	415	583	TGCAACAAGCTCAAAAGTATG	60.437	22
110	362	471	GCCCATTATTTTCCACCAAC	59.138	20
190	98	287	GGATTTTGTGAATCACGGGT	59.653	20
110	4452	4561	TTTTCTTGGCCATAGGCATC	60.038	20
260	1120	1379	GCATGCATCCACCACTCTAC	59.12	20
193	90	282	CGAGGGTTCGAGTTCACATT	60.111	20
277	946	1222	TTTTCCTCAATCATTCCCCC	60.995	20
272	3151	3422	CAACACATCGCTATCGTCCA	60.687	20
208	25	232	GGTTATTTAAATGCACACCCC	58.238	21
198	36	233	GACACGACAACAACAACATC	60.064	21
123	147	269	GAGAGAGTTGATTGTGGGGG	59.505	20
261	91	351	GTTGGAATCAGTAATGGCGG	60.331	20
101	59	159	GGACCGCGAAGTATCTGTTA	57.849	20
141	96	236	CAAAGACAAACCAGCAGAGC	58.65	20
131	150	280	AAATGTTTCAGCCCATAGAAT	58.165	23
138	47	184	GCTCACGGTGGAAGAAGAAA	60.375	20
142	96	237	TCTTCTTCCCAAATTGCCCT	60.929	20
248	1247	1494	CATAATGAGAGGCGGTTGGT	59.955	20
261	166	426	TGTATGCACCTGAACATGCC	60.549	20
179	177	355	TCAAGAGTCCCCTTGGTCTG	60.229	20
265	735	999	TTACCCCCATATGCAGTGGA	61.11	20
273	104	376	CAACGGAATTCGATTTTTGG	60.294	20
211	330	540	CCCAGCTATATTGCATTCACA	58.664	21
110	373	482	AGAGGGGGCTTTTCTTTTCA	60.18	20
172	97	268	CCAAAAAGCAAGGGATTTATA	58.968	23
175	304	478	CCATTTTGCCCTTCGTATGT	59.823	20
280	287	566	TGCGCACGTTGAAATAAAAA	60.246	20
221	9	229	TCGGCTGTCAAAGACAAAAA	59.439	20
250	590	839	TGGTATCTGGCCAATTGTGA	59.924	20
168	684	851	GCCCCACCCTTCTATCTCTC	60.037	20
193	13	205	GGCTTTCTTAACTTGTTGGAA	60.376	23
102	512	613	AGATGATGGAATTTGGGTGC	59.756	20
214	1694	1907	GAACGGGGCCATTATCTTTT	60.15	20
263	234	496	TTTCTGGGGGAGATTTGTTG	59.903	20
247	66	312	CTCTCACGCACCTTCACTCA	60.178	20
224	9	232	CAGATTTAAACAGTGGCTGCG	60.807	21
190	106	295	GTTCGAAAGCCTACCTCGCT	60.894	20
216	59	274	TGTTGGGAATAGAGCCCAAG	60.066	20
257	1324	1580	TGGTTAGTATTGGAACGCGAC	60.011	21
210	249	458	GTTATGCGATCTGCTCGTGA	59.979	20
216	1028	1243	CTCTGATTCGGGAAAACATGA	60.059	21
210	1445	1654	TGATTGGTTTGCAGGTACGA	60.111	20
251	2133	2383	AAAACTGGCCCCAAAATGAT	60.542	20
265	30	294	AAGGAAGCGAGGTAGGCTTT	59.504	20
143	4437	4579	ATACGATCTGTCCCTCGTGC	60.104	20
267	3	269	TCGAATTCGCATTCAAAATAA	58.301	21
170	364	533	AGGATTGGGCAATTATCGTC	58.86	20
166	236	401	TTGAGATCCCTTTTGTGGGA	60.43	20
247	533	779	GGGAAGAGGGGACTGAAAGT	59.534	20
230	22	251	GAATTGGTGGAATGATTAGAG	58.224	24
149	242	390	TTCGAGTTATGAAGTTTGCAC	59.271	22
167	111	277	CCTCCGTGGACGTAGATCAT	59.95	20
263	23	285	TAACGTCCCAGATTTGCTCC	60.074	20
136	5527	5662	TCTCGTAAACTCCCCCTCAA	59.665	20
250	284	533	GGGACCTCCCTTGTATAGGC	59.789	20

264	5399	5662	TGCAGGTTTGTTGAATTTCG	59.706	20
149	6	154	CACGAGAGTTGAAAGGGAGC	59.989	20
273	100	372	CAAATGGAGGTGAGAGGTTTG	59.578	21
194	42	235	TCCTCCCTCTCTCCTTTTCC	59.749	20
163	689	851	TTTCCTGAGTGGCGATAAAGA	59.831	21
147	88	234	AATAGAGCAGCAGACGCGAT	60.147	20
142	4	145	ATGAGGCGGTTAAAGAAACG	59.225	20
179	30	208	GATGAAGCTGAACCGGCTAC	59.843	20
151	175	325	GTCGTATACTGCCGCCACTT	60.162	20
258	20	277	GGAGAGGAATCAAGTCGACA	59.274	21
221	55	275	AATGAGGGATATGGTGGGTG	59.483	20
147	1486	1632	CGTGTTTATCCTCACCCGTT	59.853	20
215	777	991	AAGGCTAGCACAAGAATGGC	59.481	20
163	39	201	CAAATGGCCAAGAGAGTTTAC	59.267	22
119	104	222	ACAAACATAGAAACATGGAC	59.024	22
178	294	471	ATTCATACCTTTCTGCCCCC	60.152	20
233	915	1147	AAATGCATGCACCTGATTACA	59.055	21
125	222	346	AAGCTTGTCAACCCCTTTCA	59.711	20
182	1834	2015	AGCGAGTTCCGAAATGAAGA	59.955	20
101	28	128	TCTGTCTTGGATGATGAGGC	58.749	20
236	149	384	TTATGTTGGAGGTGGAGGGA	60.309	20
184	31	214	CCTCACCTTCTCTCCACTCTC	58.046	21
247	18	264	CCCGGTGTAAAGAAATCGAA	59.931	20
258	196	453	TTTGTCCCATAAAACTCGCC	59.938	20
195	122	316	CTAGGGGAGACAGGGGGTAA	60.311	20
118	132	249	GGGGTTGAAGTAAATGAGGTG	58.423	21
114	201	314	TCGGACTGATTTACCCTTACA	57.234	21
186	676	861	ACCATACTCATGGACTCCGC	59.957	20
211	53	263	CCTAAGTGCCTACGTGTTGGA	60.175	21
280	66	345	CCAGATGCCTTCATTTTTCA	58.695	20
250	987	1236	CGACGAGGCTTGGATTTCTA	60.344	20
155	890	1044	TGGCTCTTTTCCAGAGCAG	59.252	19
106	148	253	TTTTGATCAATTTTCACTCGTA	59.898	25
157	107	263	TGCATGCAATCCTAACTCCA	60.22	20
185	4388	4572	CATGAGTCCATGACCCTTCA	59.473	20
105	503	607	TCTCGATCTTGCAATCCAAA	59.35	20
219	573	791	CCCTTGAAACCACGGATCTA	59.926	20
116	11	126	GGAGAAAAAGAGATTGAGAG	60.189	23
216	26	241	AATGCCCCCAACTGCTAAC	59.947	19
277	322	598	AGTTTTCAGTTCGGGCGATT	60.987	20
104	25	128	TACGTTGGACCTGAAAAGGG	59.964	20
215	198	412	CTGCCTTCAGGGCATTTATC	59.668	20
204	49	252	TCAACAATCCGACTTCATCG	59.648	20
178	248	425	CCTTGGCGGATCATATCACT	59.917	20
246	1053	1298	ATGCATTAATGGACGTCGTG	59.425	20
236	79	314	TTGGCATCACAATCAACCAT	59.781	20
194	887	1080	TAAAAGCCCAGTTCAGGTCG	60.241	20
218	18	235	AGCTGTTAGGGTTGTATAGTG	57.436	27
196	107	302	CCCCAGTAGTTCCCATCAAA	59.784	20
103	27	129	TACCCAACCCACTAACCCAA	60.081	20
169	1151	1319	AATGGCAGAAGCAAAGAGGA	59.955	20
197	9	205	CAATGTTACAAAATGGGCGA	59.42	20
276	822	1097	CATTTGATAGTTGTTTTTGTGG	58.526	24
204	4	207	TGACTTATGGGGGCTCAAAC	59.933	20
258	56	313	GTGTGGCGTAAGACCCGATA	60.914	20
107	1219	1325	TGGATTGATTATGCTTTGCCT	59.561	21
180	495	674	CCCAGACACCGTAAGGAAAA	59.964	20
151	56	206	GAGTCGTAGTTGACGCCCTT	59.357	20

194	83	276	TTCTTTACCCTTTTGTAACATAA	57.251	27
190	47	236	CGATAAGTCCCAACCACTTTC	58.566	21
184	470	653	CAATCTACTCCCCTGGCCTA	59.146	20
158	58	215	ATTGCCCACGAGAGAGATTG	60.218	20
100	3	102	TCAACAGAGAATGCAAGCAAA	59.6	21
215	46	260	TATGCGGGCTGGAAGACTAC	60.235	20
261	1935	2195	GAAAAGCACCACACTGCAAA	59.888	20
209	38	246	CCTTTGTCAACTTGGGCAGT	60.149	20
190	74	263	CACCTTCTTTCCTTTCACCG	59.705	20
272	4084	4355	CGCTGCCGTTACCTGATAAT	60.117	20
149	92	240	AGGGGAAGATGAATTGAGGT	57.494	20
246	128	373	CGTGGTTCGATCGTAATTGA	59.542	20
171	111	281	TATTGAGTTCGGGGTGATGC	60.864	20
214	1380	1593	TGGAGAAATCAAGAGGAGGG	59.209	20
261	87	347	TTTTGTGGTTCGATCGTAATTG	59.868	22
119	38	156	TCACAGGAGGGTTCACACAA	60.129	20
257	294	550	GCAATTGAGAGTGAGTGCGA	60.144	20
152	379	530	ACCCTCTCTGGTTCACGAAA	59.697	20
270	112	381	TCCATTCCGAAAATCAAAGG	59.872	20
232	1259	1490	AGGACACGGTTTCTAATGTTTT	59.462	23
216	200	415	CCTTTCATGTTATTCTTTTCTCA	59.472	25
149	95	243	GAAATGATGATTTGACATTGC	59.281	22
189	442	630	GAACCAAAGTGAGCCCGATA	60.074	20
271	226	496	CGAGGTGATGAGTGACATGG	60.113	20
218	33	250	ATCACAAGCCCTAGCTTTGC	59.481	20
130	59	188	TTAGCTGCTTGGTTGGGAAG	60.378	20
256	18	273	GGTAACCGATTCCCATACCA	59.505	20
279	276	554	ATCCTTGACGACTGTTTGGC	60.119	20
243	763	1005	TGCCAATTTGATAGAAGCCC	60.038	20
233	367	599	CGTGGAAATTCCTTTAATGTG	57.185	21
165	335	499	TTAGCACCCGAACCAATTTC	59.938	20
218	78	295	CGGAGTGTATTGCGAACTCA	59.864	20
152	38	189	GTTCTCTCTCTCGCTGCACA	59.446	20
272	136	407	TCCAACAGTCACCCTCATCA	60.088	20
144	1364	1507	ACACTCCCCTTAACCCGAAC	60.225	20
246	268	513	CAGGTGAGGGACAAGAATGA	59.706	21
157	2138	2294	CCAAGAATGAGTTTTTGAAGG	59.974	22
180	203	382	CCTCCTATAATCCGCTGCAC	59.691	20
242	20	261	CAGCCTTTCCTGGGAACATA	60.066	20
256	8	263	ACCCACACCAGACCAACATA	58.697	20
238	1895	2132	CACCTGAAAGGAAGGCAAAA	60.22	20
209	19	227	CGGTCTCCCACTTCAAAATC	59.526	20
235	44	278	TAAACAGCATCGCGTTTCAA	60.39	20
198	126	323	CCGCCATAACCTGTTCAACT	59.993	20
165	149	313	ATTGGTCGAGAGAAAGGGCT	60.212	20
275	713	987	CCATGGGAAATGGTTAGTTGA	59.671	21
213	32	244	CTTGAATGGAAATACCCTCTTA	59.44	24
238	272	509	AGGGTACAACCGTGCAAGAC	60.035	20
243	1669	1911	TGTTTTGTAGGCCTGCCTTT	59.747	20
147	64	210	GTTGCTCGGAATTCATGCTT	60.221	20
278	402	679	TGACCAAAATTTAGCGAGGG	60.067	20
239	92	330	GAATTACCGGCTTCAACAGC	59.713	20
216	1	216	TGAATCTTGTCACATTTACCAA	59.961	27
199	3196	3394	CGATACCCGAACCGTATCAC	60.214	20
147	66	212	TGCACAAGTGCCAAAGAGTC	60.032	20
156	1715	1870	CAAGGGTACCATCCTGTGTGT	59.754	21
202	1585	1786	CTTCTCAAGCTCCTCCAACG	60.126	20
217	281	497	CAAGGTACTCGGTGAACACG	59.209	20

125	207	331	TCAAGGTGCTGTAAGGGGAG	60.246	20
280	1131	1410	TCACATTCTGCGATTGCTAA	58.017	20
123	105	227	AATGACAAGCGGAAAGGGTA	59.569	20
102	29	130	GACCGGTTAGACCGGATTTT	60.187	20
279	36	314	CTCACACACCTCTCGCTCAC	59.603	20
215	216	430	TGACGAATTCTCAAGTTCCTCA	60.655	23
103	39	141	AGCTGCTCCTTTCCACAGAA	60.134	20
118	2053	2170	ACAAGTTGAAGGATGGCCTG	60.111	20
236	239	474	AGCCAAGGTATGGTAGCCCT	59.983	20
204	1	204	GAGAGAAAAGGTGGCAGGTG	59.844	20
230	34	263	CATAGGCCAAAGCCCAAATA	59.922	20
238	667	904	TGGCCTGGCTTAGTTGTATTG	60.138	21
214	18	231	TCTTCTCCGCCTTTGTGTG	59.968	19
275	312	586	ACGTCAGCATCTACCCCAAC	59.997	20
259	4	262	ACAACACATTCAATACATTCT	59.7	25
239	393	631	AATGTTTGATGCATTTCGCA	60.081	20
165	1887	2051	CTCTCTCGCCTCGCTTTCTA	59.993	20
275	178	452	GACGAGATTGTCGAGTGCAA	59.992	20
232	1122	1353	CGACGAGAAAGTCGTGTCAA	60.025	20
107	64	170	TCATGTAAATTCTTGGTCATTC	59.891	25
145	17	161	CCCAAGCTATCACTCATCACC	59.565	21
184	419	602	TGTTTTCGCGTTTCCTCTCT	59.993	20
140	70	209	GCAACGGAATACCACTCGTT	60	20
194	17	210	GAGAGAAGGGGGAGGAGAGA	59.883	20
195	190	384	AGGCATGTTCAATTGGGAAA	60.309	20
211	106	316	AGCATTCAAGGGGCATTTTT	60.802	20
236	375	610	GCAAAACCAAAGTACCACCG	60.399	20
101	2	102	ATGGAGGGTTTTAGCGTGAT	58.53	20
225	52	276	ACCCACCTCACCAACATCAT	60.096	20
274	60	333	GCATTTGGAGCAAGGCTAAG	59.982	20
181	44	224	CGCCGCCAGCTTTAATTC	61.765	18
248	47	294	GCCCTCATGACTCTCACCAT	60.08	20
280	309	588	ACATAAAATGAACATGCTCCA	57.194	22
157	43	199	AGAGCCAAAAAGCTGTGACG	60.571	20
214	3	216	TCACACAAATAAGCAAGGCAA	59.359	21
200	13	212	ACAATATTACAATGGCCAAGA	57.725	23
211	58	268	GTCCGCGAAGAAACATTCAG	60.776	20
218	53	270	TTGCCATATTTAAGCCGAGG	60.054	20
162	18	179	TGTCTTTTCGTGTTGAGTCG	57.44	20
150	839	988	CATGATTTTGCAACTTACCATT	59.788	24
178	33	210	CCCTCAACAATGCAAAAAGC	60.617	20
125	570	694	TTTTCGGCCAAAAGAAAAGA	59.805	20
215	1179	1393	AGTCGTCACCCCGAACATAG	59.989	20
278	280	557	AATGAGAAGCCCAATGGAGA	59.629	20
109	403	511	CCGTTGCCTCTTTTGAACTC	59.853	20
151	18	168	GCCGGAGGTTTGATATGGT	59.765	19
234	1483	1716	ATGGAGGATTCTTTCCCCTG	60.264	20
137	76	212	TGGCATGGGGAAGCTACTAT	59.551	20
189	43	231	CACTGTGTAGAAACATAAACT	59.708	25
276	1050	1325	AGAAGCCGTGGGACATAAGA	59.694	20
272	132	403	GGGTTTTGCAGGATTGTGAT	59.797	20
230	684	913	TTGTGTTACAATGATGGGGG	59.097	20
199	340	538	AGGCGAAAGCACAAGGACTA	60.015	20
128	87	214	AGGGGTGTTTTGACCTAATCG	60.228	21
228	3663	3890	CGAAATAGGGTTGGTGAAGC	59.569	20
206	355	560	CGGAACCCTCTCTCTTACCC	60.067	20
247	338	584	GAAAACGACGAAGAAATGGC	59.691	20
220	377	596	AAGTGAAAATGGCAACCACC	59.836	20

146	111	256	GTTCCGAAATGGAGATCAGG	59.483	20
198	2063	2260	ACCGAAGTTCCTGCTCACAG	60.444	20
219	59	277	CCAAACGCATCAAATTCTCA	59.664	20
229	1428	1656	GCGTAGGCGTAAATTCAGGT	59.252	20
261	0	260	AACAGTCTTCGGGACACCAA	60.545	20
248	795	1042	TCTACGTCCACGGAGAGGTT	59.721	20
105	659	763	AAACCGAACTTTTGGCCTTC	60.463	20
246	2938	3183	AACTTCTCCTCCCAATCGCT	60.212	20
112	65	176	TACGATACCCTCCCAAACCC	60.929	20
238	2146	2383	TCTGCATGCAAGATAGTACGG	59.797	22
275	414	688	ATTGCCATCACCTTCTCCAC	59.934	20
191	696	886	TTTGAAACGGGTGGTTATGA	58.866	20
278	213	490	ATCTGGGTATTTGACTGGGC	58.864	20
270	228	497	GTCTGTGAGGTGGGCTGAGT	60.315	20
159	561	719	GGGGTCCCAGAAAACTGATT	60.169	20
185	0	184	ATATTCTCGCTTCTTCGCCA	59.945	20
262	367	628	AAGTTCGTTTTTGCCTCTCG	59.494	20
124	267	390	TCACCACGAAGTCTACAAAAA	59.968	24
223	4	226	CGCGCCTACAATTCAAAGTA	58.982	20
141	365	505	TGTGGGACAGCTGCTAATTG	59.864	20
256	504	759	ACTTCCCATAATGCCCTCG	59.902	19
190	223	412	TGGTATATGGAGGAATGCCC	59.605	20
193	2674	2866	CTGGTTCTGGTGGCAATGTA	59.566	20
268	10	277	CACATCAACACACCCACACA	59.878	20
274	1393	1666	GACCGATCGAAACACACTGA	59.682	20
168	1429	1596	CGGTTTCCACAACAATAGCC	60.365	20
121	51	171	GTCAACTTCGGCAATGGAAT	59.939	20
182	189	370	GGAAATTGATGGATTTGGGA	59.558	20
197	106	302	GGAATGCGTCGAGTACCACT	60.142	20
222	25	246	CCCATGTTGTAATTAATGTAG	59.089	24
167	869	1035	ATTCTGACTTGAATTCGCGG	60.214	20
278	27	304	TCCCCTCCTAACTTTGCTGC	61.633	20
162	66	227	CCCCTTGAACGACTATCCAA	59.926	20
116	657	772	GTCCCACAAAAGCTCAGAGG	59.844	20
204	31	234	CTCAGCATTTGGGAAGGGTA	60.066	20
110	704	813	CGGAAGCAATTTTATCATAGA	58.879	24
149	89	237	TTGATGTCCCTTCTCCTTGC	60.195	20
108	1001	1108	ATCAACCACCACCTTCGTTC	59.827	20
214	179	392	TCTGTGCCGCATTTATGATT	59.14	20
196	27	222	TTTTCGAGTTATGAAGTTAGCA	59.761	25
186	2	187	ACCCAAGGTCAGTGGAACAA	60.399	20
220	343	562	TAGCAATTTTCGGGGTGAAA	60.427	20
176	1244	1419	CTTTCTTTCACACCGAAAACG	59.771	21
278	375	652	AGTCGTCACCTTAGTGACCCA	59.631	21
261	1352	1612	CTTCAATGGACCAGCACCTT	60.111	20
245	29	273	CCTGCACGAAGAAAGGATTC	59.813	20
255	5	259	TTGGTTCACACAACCACTCC	59.415	20
249	42	290	TGAATGATTTAATAACCTATG	58.467	25
273	202	474	CAATTTTTCGTCGTGCTCAA	59.849	20
152	50	201	ACAATGTGAAATGGGCAAGA	59.985	21
238	19	256	ACAGATCTTTCCACGACCGA	60.656	20
202	696	897	TGCAAGAAAATCCAGCTTCA	59.542	20
280	138	417	TGCAATTCCAAGCTACAACG	59.872	20
148	1149	1296	CTCCGAATTCAAAATCTCCG	59.64	20
225	400	624	TAGCGTGATTTGTGGACGAG	59.864	20
243	29	271	CACTCACTCTCACTAGCCGC	58.78	20
127	239	365	TGAGCAAAGCATTTTGGATG	59.809	20
174	19	192	CCATTTGCAATACTAAGGCTTT	59.224	23

278	790	1067	GAGCAATAGCAGGTTCGGAG	59.978	20
232	69	300	CAAGCATATTGGCAAGAAACA	60.13	22
251	36	286	TTGGGGCTTGATTGATGTTT	60.309	20
201	261	461	CCACAATCATTCAAGCAAACC	60.359	21
142	71	212	GAGATTTCACATGGCAACACA	59.562	21
197	102	298	ACTCCTCCGGGAGACTCCTA	60.208	20
250	1919	2168	AATTCATTTCCCCTCGACCT	59.766	20
228	296	523	GGTCCATTGGTCTTTTGTATTG	60.102	23
222	1	222	TGATTGCATCACGTCTCCTC	59.794	20
259	326	584	CATGGACTCACGCTCTCTCA	60.138	20
223	194	416	CACCCAACCATCAAATCACA	60.216	20
144	965	1108	TCAATCCCAGCCATTCATTT	60.274	20
111	4	114	CTCATTCTCTTCTCTATCTCTCT	59.741	27
242	836	1077	TGGGTGAGGTGGAGGAAATA	60.309	20
200	202	401	CCCCTAGCATACGAAGGACA	60.088	20
245	157	401	AATTAATGTGGCATGGGGAA	60.016	20
242	13	254	TTACAGTAGGGTGGAAAACAA	59.044	24
221	23	243	AAACATGCATTTTCTTCTTTCTT	59.959	26
279	38	316	TGAGTGTTGTCTTGTGTTTTTG	60.096	23
110	5	114	CAGATGGAGGGTGTGTGAAA	59.52	20
266	436	701	CGTTTAGCCGCAAGTTTCTC	60.018	20
239	193	431	CGAATTTTGTGTGGACCGTA	59.439	20
258	98	355	TTAAAAGGCCAAGCAAGGAA	59.826	20
145	66	210	TGGCTTCTCTTGCTCTCTCA	58.984	20
188	567	754	TGCCGAGTCTTGTTGATGAT	59.245	20
112	710	821	ATTGAGTCAAGGGCGGATAC	59.009	20
230	145	374	TTGTAATGTGGCATGCGTTT	59.999	20
176	262	437	AGGTGGCACGCATCTGTAA	60.279	19
237	167	403	TTGATGTTTAAAGTCGTCGGC	60.124	21
233	719	951	TTTCCACTGTTATGCTGCGT	59.347	20
269	834	1102	TGCAAGCCTATGGTGGGTAT	60.352	20
210	0	209	GCCGAGAGAGATGAGGAGTG	60.096	20
238	2987	3224	GGCCCTGATCAGAATCAAAA	60.014	20
179	75	253	GGGAAAAGGGAAGAACAAGG	59.912	20
192	2566	2757	GAGGGGACCTTCCTTTTCTG	60.045	20
237	2012	2248	CACTGCAAAAGCTTAGGTGG	58.579	20
268	1054	1321	TGATTGCTTTGGCCCTACTC	60.214	20
192	23	214	TGACGTCTTGTGGGAGTGAC	59.712	20
164	402	565	TACCGATTTTCGTCGCTCTC	60.352	20
268	329	596	ACCCCAATCTCCGTTCTTCT	59.935	20
154	9043	9196	TTTCGTCCTGCTATTTGCCT	59.845	20
248	1	248	CGGAATTCACTTCTTTGCTG	58.501	20
205	335	539	GGTTTCGGTTGTTTGTCCAC	60.255	20
101	30	130	TGTGGGACTTTGAAAGAGGAG	59.314	21
245	918	1162	CTCAACGGTATGCTCGGATT	60.096	20
174	6	179	GCTCAAGCTTGCTGTTTTCC	60.14	20
266	7	272	GGTTGTAATGAGGCTTTCGG	59.569	20
166	552	717	CATCCAATTCCAATCCCACT	59.605	20
185	152	336	GGTGTGGCTCTGTGGATTCT	60.12	20
245	781	1025	ACTGCTGCAGGGCATAATGT	60.688	20
218	412	629	TCTATCGGCCGAGATTTGTT	59.668	20
269	322	590	ATCACGAACAACACACTGCC	59.603	20
229	1128	1356	CACACCTCTTTGCTTTGTGC	59.49	20
148	397	544	CAGGTGGTCGTAAAGCCAAC	60.55	20
208	136	343	TCGAAGAGGAAAATAAAATAA	60.055	25
230	2550	2779	GGGCACTGCAGGTGACTAAT	60.142	20
169	143	311	CGTCTAATCCACCGCCTAAA	60.089	20
185	217	401	TCTGCTCTTCGATGTTGCTG	60.287	20

163	399	561	AATGGCTGCAATTATCCCTG	59.923	20
273	34	306	CATGATCAAATCTTGGTGCG	60.073	20
226	42	267	CAAATGCCCAAGAGGGTTTA	59.931	20
209	152	360	GGCTGTACCATAAAAGCCCA	59.96	20
194	161	354	CCGAATTTTCCACTCCAGAA	60.044	20
190	2311	2500	TTGCCCAAACAAATGAAAAAG	59.965	21
272	105	376	CGATCAATAAAGCTGCACACA	59.887	21
260	191	450	ACTTGGACCTGAAAGGGGAC	60.349	20
168	78	245	TCGACCGAAGAGCTATCCAT	59.797	20
178	48	225	TGAAAAAGGACTCTTGGGCA	60.745	20
163	625	787	AGAGGTAGCCATTTACGCGA	59.867	20
138	31	168	TAGGCAATGGAATACCTCCG	59.916	20
262	100	361	CCACCACCTCACTGTCACAC	60.045	20
148	464	611	AATTCTTGATTCGCCACCAA	60.448	20
269	907	1175	CCACAATGGTTGCTCTCCTT	60.111	20
201	1997	2197	CCTGGCTCGTTAGCTGATCT	59.598	20
266	1323	1588	TTCCAAAGCAACGTAACATGA	59.216	21
225	542	766	AGGTCGTGGTGAAAAAGGG	59.951	19
133	53	185	CTGCATGCTCTATGCAAGAAT	58.16	21
271	4	274	CAATGATTGTCAAAATTAGAG	58.718	26
218	76	293	TAGGATACCCTCCCAAACCC	60.011	20
193	329	521	AAAAGGGGCATTTTGCACTA	59.586	20
234	100	333	TGCACAGCATATGCCTTCAT	60.251	20
239	252	490	GCTCCTCCTTGGTACTCACAA	59.343	21
251	87	337	CGAGATGTCTTCAGGGCATT	60.218	20
197	56	252	CTCCTTCTATCTCCCCTGCC	60.169	20
208	238	445	AGAGCGAAAACGCTCTTGAA	60.27	20
187	56	242	TCTCTCACCTCCCCAAACCT	61.021	20
163	81	243	GAAAAGGTTAGTGGGCTGAG	60.116	21
258	173	430	TGAGCTAGCTTTTGTGGTGG	59.072	20
155	356	510	CTCGGACAAAATTCACCTCG	60.626	20
265	511	775	GCCTTGGTCATGCCATTTAT	59.791	20
255	63	317	GACGATTGACCCAAAACTCG	60.495	20
202	4	205	CCGTCCAATAAACCGAAGAG	59.564	20
156	184	339	TCCATTCCGAAAATCAAAGG	59.872	20
218	225	442	CCCGTGCAAGGCAATATCTA	60.98	20
161	438	598	TCGTCGTTGTTACTGGCCTA	59.342	20
266	717	982	TCTGATAAGGTTCGAATTCAC	59.225	22
221	975	1195	TGTTATGATTGGATCGCACC	59.355	20
147	375	521	TGGGTTTTGGGCATTATGTT	60.053	20
268	428	695	TGGTAGTGTTGAGTTGGCGA	60.301	20
273	450	722	GTGCTTTCAATGTCCACTGC	59.297	20
223	23	245	CAAGATTCGAAATCACATTCA	60.336	24
223	41	263	GTCCACGGTGGTGCTAGAGT	60.182	20
195	1109	1303	ATTCTTCTTCAACCTCCGCC	60.578	20
206	214	419	TGCCCTTAAGTTAGGACACTA	57.268	23
131	219	349	TTTTAGGGGTGCGAAAGTTG	60.103	20
103	19	121	ATCTTGGCATGGTCAAAGGT	59.41	20
279	48	326	CCTAGTTCCTACCGCGTGTC	59.757	20
259	91	349	ACTTGAGCGTAACCACGTCC	60.179	20
177	6	182	CTGCTTAAAGCCCAGTCCAG	60.008	20
126	185	310	AGGGCATTATTTTAACCCCG	60.036	20
224	298	521	CCGAAATTTTACGTGGTTCG	60.348	20
108	3	110	GAGTTTAGAGAGAGGAAATG	57.33	26
163	1964	2126	CGTAAACCATTCGAAATCCC	59.273	20
257	2217	2473	TGACAACCATCACCTCGAAA	60.088	20
168	4	171	TCTCTCCCTTTCCACACTCG	60.377	20
141	622	762	GACACCAAAACGGAGGAAAA	59.948	20

208	285	492	GCCAACACTCCAAAGAAATGA	60.103	21
161	22	182	TCCTCCTCAATATTTTCAACAC	58.616	23
280	46	325	CAAGCCATGAAACAACACGA	60.699	20
203	201	403	ATGCGTGTGGAAGAGGACA	60.263	19
156	2886	3041	CAGCATTCAAATGCGAACAG	60.401	20
276	157	432	TGCAATGCATGGAGGAAATA	60.035	20
109	25	133	TCCATTCCGAAAATCAAAGG	59.872	20
103	289	391	ATCTGGAAATGGGGAAAACA	59.22	20
215	162	376	CCAATCTTGACCGCTGATTT	60.074	20
153	45	197	GTTGTCTGAAACCCTTCCCA	59.943	20
251	298	548	AAGACACCTATTTGCCCCCT	59.827	20
277	599	875	CCACCATCTCTCATCCCTCT	59.052	20
167	1563	1729	ACCCGAAATTCTCCCAACTC	60.306	20
259	1211	1469	AAACCTTACTGTCACGCGCT	59.943	20
186	528	713	TGTCTCTCTTCTCTCCCCCA	59.913	20
197	1	197	CTCTATATACAACTCGCATAC	59.859	26
135	320	454	CATGATTTCAGAATCGTGCG	60.22	20
249	351	599	CTGAGCAGACCAGTCCAACA	60.022	20
174	177	350	GTCTCGTCCCTTTGTGCTTG	60.833	20
251	15	265	AAAGGTATGGGGAAAATGCC	60.02	20
163	143	305	ACTGGGAGTCTGAGAGACGG	59.425	20
202	5	206	TCTCATGTTGTAATTAATGTAG	58.177	26
214	19	232	AGCCACTTTCCTTAAACCAAAA	59.203	22
106	4	109	TGTCCTCACTCGTTTCCTCT	57.416	20
256	555	810	AGATGTGAACCAAGAACCCG	59.966	20
178	9	186	CTAACCTTGGGCTCTGATGC	59.836	20
154	42	195	GCATCAGAGCCCAAGGTTAG	59.836	20
268	189	456	TGAGGAATCGAACAAGGACA	59.215	20
261	4527	4787	GGAATTTGATCCCCACACAC	60.034	20
192	195	386	ATCACCTCCATTTTCCCACA	60.173	20
144	350	493	GCAGGTAACCAGGTCGTTTT	59.101	20
131	93	223	ATAAACTGTTACTCCTGGGTG	57.318	22
235	1358	1592	TCGAACCATTCACATCCTGA	60.048	20
246	136	381	TGTGCCATAAAAATGGTTCAT	57.885	21
223	164	386	GGGGTGGTAACCGATGTATG	59.933	20
223	212	434	ACAGCCTTCAATCCTTGCAT	59.7	20
214	1	214	TGTTGCGCGTGCTTTAAATA	60.401	20
265	1453	1717	TATTATGATTCCGGGTTCCG	59.616	20
191	134	324	TTGTGCTTCCACCAAATCAG	59.691	20
220	7	226	GGCTCTTTTGATCGATCTGC	59.923	20
174	354	527	ACGCATGAATTCTGTTGGAA	59.127	20
145	1051	1195	CCCACCCCAGATCATAGAAA	59.744	20
250	389	638	TTGAGCATTGAGGTTGCTTG	59.988	20
279	89	367	TAACAGCATTACAGCCGTGG	59.752	20
129	2	130	GAATGAGGGAGGGAGGAGAA	60.532	20
250	387	636	GGAAGCCCGACTTTTAGTCA	59.312	20
117	325	441	TGTGTTGTGTGGACTCTCCC	59.55	20
191	179	369	TCACAAATCGATGGTCTGGA	60.048	20
139	106	244	GAGTGCCATTCTGACAGTGC	59.425	20
277	0	276	GAACCAACTCTGTGAGAACCA	59.232	22
174	44	217	TCATCGTGTTCTTCGCTCAC	59.992	20
204	253	456	AACTTCGACAGCTCCTGCAT	60.02	20
157	394	550	ACGGAACGCTTAATGCAAAA	60.619	20
161	238	398	CGTCTCTCACAACTCCACCA	59.864	20
273	130	402	TCCACGGAGAGGTAAAAAGC	59.312	20
216	77	292	CAATAGTTTTTGGCAGCGGT	60.131	20
280	793	1072	GCATTTGCCTTTAGGAGCTG	59.982	20
246	37	282	AATGCGCAATTTTAAACCCT	58.631	20

238	34	271	CCGAAATCTGTAAATCCTAGC	59.145	22
167	5	171	TGTTTTGTAATTTCCCATGTTT	59.577	24
268	2749	3016	ACCGTGTGGCATTTGACAT	59.828	19
107	1391	1497	TGCCAATGATCACCAAACC	60.322	19
140	4	143	TTCAAATGCACGTGTTGGAT	59.972	20
158	14	171	GCTGATGCACCGAGCTAGTA	59.203	20
146	323	468	TGTGTCCAGCAGCAACTTTT	59.49	20
165	4291	4455	CCTCAAGCAACGTATATCGTC	60.152	22
144	254	397	ATTCATTCTGCCACCTCTGG	60.073	20
217	109	325	CATTCAAGGGGCATTTTTGT	59.801	20
231	102	332	GAACACCTCACCCCTGTCAC	60.421	20
181	32	212	TCTGTTGGCAAATAGGCACA	60.257	20
175	268	442	TTTCTCTCGATGCACTCTCG	59.267	20
201	18	218	TTCGATGATAACTATGGGTTT	57.589	23
271	235	505	TAGGCAAAAACTTCCGTCCA	60.608	20
274	102	375	ATGAAAATGCCACGTCTGAA	59.127	20
154	68	221	GGGTGGAGAGAAAAAGAGGG	60.045	20
197	331	527	ACCACATTTTTCCCGACTGT	59.308	20
176	2	177	TCACGCTCCATCTCCTTTCT	59.95	20
261	97	357	GGGCATTTGTATACCCGTTG	60.074	20
112	85	196	CCGAGGTGGAGTAGTATCCG	59.569	20
277	0	276	CGAGTGAGAGAGTGAGTGCG	59.915	20
184	199	382	TCACACAGCACCTGATCACA	59.858	20
250	666	915	TACGATCCGAGTGCCTCTTT	59.836	20
279	589	867	CTAGGTGAGCCATTCGATTTC	58.801	21
174	1617	1790	ACATGTGTGTGGCATCACCT	59.879	20
122	41	162	TCCACAAAGATCTCGCACAG	59.984	20
258	299	556	TTGTCCACACTTGGCACTTT	59.187	20
207	92	298	GCATGCAGACATGGGAGTTT	61.078	20
261	558	818	GTGGACGTCCCAGATTGTTT	59.827	20
171	53	223	CGCGAACTTAGATGGGCTAC	59.867	20
240	1627	1866	CGAAAACTCAATTTAAAAGGC	60.47	24
277	453	729	AAAGTGTTCACGAACCATAAA	58.912	24
134	441	574	GCTCATCGTCATTCTCCACC	60.633	20
195	1001	1195	TATAATGGGAGGAGAGGGGG	60.103	20
188	596	783	ATAAGCTGAAGATGGGGCCT	60.06	20
249	28	276	ACACGCTATCTCGTTGCTCTC	59.659	21
221	3800	4020	ACAAGGGCAATCGTATGAGG	59.955	20
274	1748	2021	TTTTTGCGGTGTGCATTTAG	59.742	20
248	877	1124	CAATCTCTAGTTGCAGGCCC	59.836	20
109	746	854	TCATGCACAAAATAAAAAGG	59.741	23
233	9	241	TCTCACACACGTTTACACCCA	60.057	21
110	1355	1464	GCCATCTTCTTTCCCCATTT	60.265	20
141	383	523	CGCACCCTCTGTTCTCTCTC	60.135	20
126	1547	1672	TGTAGCCATGTAGGTGCCTG	59.74	20
132	346	477	CGTCCTCTCCATCACTCTCC	59.792	20
258	286	543	CAAGACCAGTTTTTCAGGGG	59.563	20
264	356	619	ATCGGATCGGATACCCAAAT	60.366	20
125	269	393	TTTTCCACGGAAGGAACTGA	60.605	20
233	25	257	TGACAGGTTCAGAGGCAATG	59.831	20
104	41	144	GTGCTGCCGCTATTGAGAGT	60.569	20
250	56	305	CTTCTCCATCACCACCTTGC	60.656	20
125	893	1017	AGTGACCCAAATCATGAGCC	59.934	20
270	9	278	CCGGTCTAAACCCGGAATA	59.764	19
167	765	931	AACACAAACGCTAAACCCGT	59.54	20
268	1126	1393	TGTAGTCATCCATGGGGGTT	60.05	20
171	180	350	AGGGATGTTGAAACACTTTGC	59.091	21
213	98	310	GGTTATCACCTGATTTTCTCCC	59.734	23

280	915	1194	TGCCGAAGATTTACTCCTAATT	59.188	25
264	139	402	TGATGGATTTGACGTTGCAT	59.931	20
190	3	192	TCAAATCTTCGAGTACAGAAA	59.667	24
235	784	1018	CAGCTGATGCACATATTCCAG	59.312	21
249	104	352	CTTCACTTGAATTGAGGGGG	59.521	20
280	99	378	TTATTTTCTTGGGTCGCTGG	60.067	20
242	108	349	AATGCGCGTTTTTAGGGTTT	60.825	20
200	34	233	CAATAAACCCACCGAATGCT	59.823	20
266	7	272	TTTTGTGAAACAATAATGACTT	57.874	25
271	678	948	TCCAGCTAATCTGGTCCGTT	59.694	20
178	427	604	CTCCACTCTCTCACACGCAG	59.757	20
238	377	614	GCAAAAGGCAGCCTAAAGAG	60.035	21
274	1896	2169	GAGGGGGAGACATATGCTTG	59.508	20
150	802	951	GGCATCGTGAGGAGTGTTG	60.263	19
254	851	1104	TCACGCCCTACAAAACAATG	59.585	20
115	243	357	TTGGTGCATGCCTTTTGTTA	60.111	20
251	2141	2391	TGAAAAACAAGCGAGCAACA	60.557	20
142	433	574	GGCGAATGCTATGCATTTTT	60.068	20
107	191	297	CAACACACATCCTTCATGCAC	60.024	21
191	1760	1950	TTGATGGTGTTCCCCTTGTT	60.21	20
265	1868	2132	CACGAAGTCGTCATTAATTCC	59.996	22
247	17	263	CATTCCCAGGTGTGAATAGCA	60.899	21
161	389	549	AGGAAATGATCACAGGCCAT	59.366	20
231	0	230	AGCGGTTATTACCGGATCG	59.93	19
270	734	1003	GCCGTCCTTTCAATCTCTTG	59.813	20
126	73	198	GCAAAGAGGATGAATCTGGG	59.629	20
268	530	797	TGGGCAAACCAAGATACACA	59.964	20
207	671	877	TCCTTAAACATAACGAGATCA	58.388	25
175	189	363	TCGTATGCTGCCCCTAAAAC	60.096	20
255	17	271	CTCTTTCTCTCTCCGCCCTT	60.088	20
157	447	603	AAATCCACCAGAAACCCACA	60.21	20
265	155	419	GAATTCCCATTGCAATCACC	60.141	20
261	396	656	ATTACGGCCACGCTAAGTTG	60.152	20
111	431	541	CCCCTCTCATTCAACACCC	60.31	19
101	106	206	CCTACTGCCGTGTTCGATTC	60.657	20
280	23	302	TCATGAATGGATGTGTTTTGTT	57.849	22
190	1	190	ATTTAGTGTTTTGACATGATTA	57.898	26
254	44	297	GCTGACAGGGGAATTGTGAC	60.52	20
220	661	880	TCTACCCTTCATTGTCATTCTC	58.707	23
227	1855	2081	TGACCATTTTGCAACTCTCC	58.697	20
202	24	225	TGAATGGCCGTGAATGTATG	60.343	20
164	71	234	ATGAAGAAAATAGGACTAATG	58.32	26
227	210	436	ATCGTGAGAAGCGTCGATCT	59.981	20
169	482	650	GCCAGATTCTCTTGGTGGAG	59.803	20
248	14	261	ATCCTCGGAATCCATACCCT	59.611	20
253	563	815	CCAAATGCATGCAGCTTCTA	59.976	20
264	133	396	CCTGTAGACGGCCAAATGTT	59.993	20
253	266	518	TGGAAGCCATGCAAAATAAA	59.146	20
161	1339	1499	GAAATTGGACACAGAATGCG	59.127	20
264	2148	2411	TTTCTTTTGTGACGCAATCG	59.849	20
169	4809	4977	ATAGTGGAGGGATGTGGCTG	59.95	20
126	4	129	CAAATGGCCAAGAGAGTTTAC	59.267	22
255	322	576	GGAATGGGGGAAATTTGATT	59.83	20
253	6304	6556	TCTCACGCGGGTAAGTGATA	59.297	20
154	39	192	CTATCGTTCGATTTGCCGTT	60.096	20
127	1133	1259	TTGCAAGAAAAATAAAGGGC	59.719	21
181	195	375	ATCAGACGGGCAGTTGAGTT	59.727	20
153	1170	1322	TTAGGGTTTAAAATCGCGCA	60.564	20

215	2	216	AGAGGACACTTGGACCTGAAA	60.146	22
118	574	691	AATCCTCGCAGGAGTTCAGA	59.95	20
271	385	655	CCGTGATTTAAGGAGTCGGT	59.052	20
160	14	173	AGCTGTTAGGGTTGTATAGTGA	57.436	27
200	38	237	TGATGTGGTGTTGGAACATT	57.17	20
226	2483	2708	CACCAAGTCCAGCCTTCTTC	59.844	20
269	451	719	CACGTGGAGGATCGTTTTCT	60.111	20
266	96	361	CTGAAGGTCCCGTCATCATC	60.475	20
271	1310	1580	TTTTGTGAGAGGCGAGAGGT	59.989	20
106	201	306	GCGTACATGAGTCCAGCAAG	59.47	20
241	216	456	TGCATGTTGCGATTTCATTT	60.081	20
198	4000	4197	TCTACCTGTTGCTGTGTGCC	59.905	20
126	49	174	TCAAATGAACATAATCCTGTAA	59.33	25
149	616	764	CCCAAATCATTGTATTTCATGT	57.81	23
213	553	765	CACCAAATTTCATCATTTTCAA	57.548	22
134	1756	1889	AGCTTTATGCGTTTGCAGGT	59.911	20
209	234	442	CATCAACATGCAACCAACAA	58.966	20
198	1103	1300	CATTATTATCAACGGCTGCAAA	59.989	22
244	2874	3117	TCGTAGCCTGCTTTCTCTCC	59.717	20
115	9	123	TGAGAGGAAGAAAGAAGATG	59.111	23
280	646	925	TCTAAAGAAAACAAAAGAAGT	57.236	26
249	247	495	TGGAGCAACAAAGATGGAAA	59.247	20
144	400	543	TCCTAACAAAGAAAGGCGGA	59.817	20
278	523	800	ATCCCTTTTGCTTTTGCTGA	59.823	20
158	1579	1736	TGATCCTTGCTCTCTTGCCT	60.096	20
210	967	1176	AACGCAAGATGGGAAAAATG	59.938	20
270	205	474	ACAAGCAGGTAAATATCAGTT	59.974	25
200	433	632	AGGATCCCAAATCACCAACA	60.173	20
280	636	915	TCCTCAAAACCACCAACTCC	59.943	20
137	247	383	ATAACCGACCACGACACCAT	60.119	20
214	27	240	GGTTATCACCGGATCACGAC	60.203	20
144	44	187	GCGGTAGGAGTTGATGATGG	60.483	20
203	756	958	CGGAATGTGATCGAATAGCA	59.646	20
174	2630	2803	CTTTTTGCCATGTCAGCGT	59.856	19
224	1036	1259	TGTCGAATGCAGGGTTGATA	60.073	20
243	186	428	TCAAGAAACGCGCCATGTAT	61.554	20
235	2257	2491	TCAGGAAGATCATCTGCGG	59.884	19
233	567	799	AGCAGCAATTTCCGAAAAGA	59.96	20
148	45	192	CATCCAACAGGTCAAGCAGA	59.831	20
141	148	288	CAGACGAGCAGTTGAGTTCG	59.77	20
160	325	484	TCCAGTGTCTCCATCTCGTG	59.82	20
179	1622	1800	GCCACATTCTTGCTTCTGCT	60.547	20
206	21	226	CAACAAAGCAACAAAACATTG	60.062	23
245	98	342	TAGGCTTGAGCATGTGGAGA	59.547	20
205	1	205	TTTTGAATGGCACAGATTGG	59.518	20
280	302	581	AGATGCTGGTAGAGGCGAAG	59.598	20
223	54	276	ACCATAAACACCGTGTCCAAA	60.139	21
253	354	606	TAGGTCTTTGGCGGTCTTGT	59.734	20
278	182	459	AAAATGGTGCACAAACCCAT	60.096	20
174	3449	3622	GGAATGTGCAACAGGATGTG	59.967	20
261	1212	1472	TTTTATTGCAGCTGTCACGC	60.021	20
194	90	283	GCGCATTTTCCTTTTTGTTC	59.704	20
251	2990	3240	GTGTCTTCTTCGGCGTTTTC	59.859	20
160	87	246	TTGAAGGTTCTGGAGTTGGC	60.232	20
153	7	159	CTACCCCCTCTCGCATTTCT	60.59	20
208	193	400	CCAAAGTGCCCTTTTATGCT	59.225	20
200	39	238	CCGCACATGTTTCTCTCTCA	59.984	20
116	1020	1135	TCTACGAGATTTGCTCCCAA	58.449	20

252	385	636	TGAAGCGTGAAAGTCAATCG	59.988	20
177	1067	1243	TGAAATTATACGAAGCCGGAA	59.573	21
208	35	242	GATGCAGTGGGGTTTTGTTC	60.362	20
191	992	1182	TTTCCATTTTCCACCACTCA	58.947	20
204	206	409	CATTGCCACCCTTATCCACT	59.813	20
188	221	408	TTCCCTTCTCATTTCCATGC	60.014	20
240	58	297	AAGGCAACATCTATCGAGGG	59.15	20
279	144	422	AGTACTGCAATTCTGCCCGT	59.763	20
249	189	437	TGGTTGGAGATCTTTGGAGG	60.042	20
192	247	438	GGGTGGTTATGGGTTTTAGG	58.162	20
130	163	292	GGATTGCTGAAAACTGGCTC	59.82	20
213	61	273	AGCAGCGAAGGAAAAACTTG	59.632	20
252	419	670	TCTCTCCGACCACATTCCTC	60.199	20
146	586	731	GGAGATGGGGAATTTTGACA	59.727	20
224	158	381	TGGAACCATGTTCAATCCCT	60.173	20
219	601	819	CTTGACAAGGCAGTACCCGT	60.171	20
253	565	817	GCCCACCTGATTTTCTTCAA	60.051	20
279	30	308	GAGAATCCACCCACCAAGTG	60.363	20
192	308	499	AAGGGTTGGTATCATTTGAAC	59.168	23
197	14	210	CCGGGTATCGGAAATTAGGT	60.034	20
217	14	230	GTGAAACCCCCAATTGTGTC	60.073	20
274	67	340	TGCGTTTAAACAACCCAAAA	59.094	20
273	20	292	TTTATTTTTCTCAAATGCTATG	59.274	25
158	71	228	CCAAACGAACTCACGGGATA	60.883	20
189	136	324	CTTGGGAGAATTTGTGGGAG	59.521	20
276	588	863	CATGTCGATCAACACCACAA	58.921	20
248	84	331	AGCATAACAGCTGGCAAACA	59.493	20
252	298	549	TTAGCTCTGGTTTGGTTCCG	60.241	20
213	368	580	CAGATTACTGTGTGCGGCTG	60.472	20
276	1632	1907	CTTCCGAATTCCAATTACCA	57.551	20
149	199	347	TGAGCTCATTCCGCATTAAA	59.401	20
140	14	153	CTTGCCCCTTCACTCTCATC	59.803	20
186	414	599	TTGGAGTTGTCAGTTCCTTCC	59.173	21
122	87	208	TTGACCAAGGTGAGAATTTGA	59.587	22
176	51	226	CTTTTTCCTATGTGTGACAAAG	58.003	23
252	200	451	CAGAGCATTTACCTGGGCAT	60.096	20
256	21	276	GCTCCGAAACATGAAAAATCA	60.067	21
171	262	432	ATCTCGGTGACGAAGTGGAG	60.261	20
121	1375	1495	CGCACTGATCCAACTTTTCA	59.84	20
165	47	211	TGGGCATATTAGCCTTGACC	59.923	20
217	211	427	TCCACCCTCTCACTTCCACT	59.682	20
268	71	338	ATGTCGCCGAAAATCAGTTC	60.081	20
192	3440	3631	TTGGTCGTTGGTTCATGTGT	59.855	20
208	0	207	TCTGTCCCGTTTTCTTCGTT	59.711	20
136	638	773	CGGTGTGCTTTTCTTTCTCC	59.853	20
172	188	359	CGATGGCCAAGATTGCTCTA	61.266	20
138	71	208	TCCTTTTCTTTTTCTGAGCACC	59.871	22
274	269	542	ATTGAGACTGGCTTCCATGC	60.226	20
280	161	440	TACCGGACCTTGGTCTGAAC	59.966	20
280	442	721	TTCCTACCAAATCTCCCCATT	59.652	21
146	3416	3561	TGGATCTCGGAATATCCAGC	59.998	20
131	636	766	CCTACCTGTTGCCACTCCAC	60.567	20
270	428	697	ATGCGTAGAGCACCCTCATT	59.723	20
177	299	475	CACGCAGACAACACACACAC	59.818	20
126	260	385	GTGGAAAAGAAGATGCTCGG	59.813	20
163	69	231	GCCGTGAATGAAGGGATTT	59.886	19
122	7	128	GCGAAGCACCGAGACTACTG	61.136	20
239	208	446	TCAAATCGCCTGAGAAGGAG	60.474	20

182	255	436	AATGCACTGACTTGGCATGA	60.272	20
278	29	306	TGATCGATTTTCAGCCATGA	60.159	20
170	46	215	ATTTTCAAGCGGCACATGAT	60.478	20
161	14	174	CGAACTCAATTTGATCCGAAA	60.06	21
277	67	343	CCACTTTGGTGACTAACGCA	59.758	20
185	287	471	TATTTCCGGTTCAAACTCCG	59.931	20
154	25	178	TACCCAACCCACTAACCCAA	60.081	20
238	260	497	GACACACGAGCAAGCAAATG	60.459	20
239	370	608	GGTGAAGACGGATCGTCAAT	59.934	20
269	247	515	CGAATCCGTTTTCCAACAGT	59.971	20
207	3	209	TTGATTCAAAGGCTGATAATG	59.857	23
117	136	252	TGTGATCGACGATTGGAAAG	59.648	20
263	0	262	GGAAATTATTGGGAGGGAATG	59.499	21
276	29	304	CACGCACAAAGAAGATCTCTA	59.571	23
139	90	228	AAATCGTGCAGCAAACATTG	59.735	20
272	1475	1746	CTTCAGCCTGTATGTTGGGG	60.508	20
188	11	198	TTTCCTCCCAGCTTCTACCA	59.807	20
226	379	604	TCCCACTTTGTCTCCCAATC	59.903	20
228	106	333	GTAAGAACCGGGCACTGAAA	60.11	20
233	2968	3200	ATTAAGGGGGAGTGTTTCGG	60.18	20
191	77	267	TTGCCTTGTGCAGGTTACAG	59.904	20
170	650	819	CCACCCCAAATTTTCCATAA	59.497	20
264	509	772	TTGTTGTTTCACAAAATTTAAG	59.653	25
258	188	445	TGGCATAAAATCCAACCATT	57.817	20
171	38	208	CTTTATCCACGTCTCGCACA	59.864	20
227	32	258	CAATTACAATGTTTATCCAATC	58.177	26
122	554	675	CCACGTCAGCATCTACCTCA	59.855	20
278	140	417	AGCTCGAGCCAAGAAGTTCA	60.277	20
146	40	185	TGCATGCACCTGATTACAAA	58.703	20
279	425	703	GGATGATTCCGACGAGAAGA	60.158	20
276	407	682	ACGAACCACTGGCTGAAATC	60.119	20
151	5	155	TGAAGTGTTATGCGTTTTGACA	59.274	22
274	339	612	CAACTCCGAAAGGCATTCTT	59.312	20
183	42	224	CAAATGATCTTACGCGCACA	60.807	20
261	379	639	GAAGAGACCAGAAGTCCCCC	60.05	20
256	139	394	AGAGTTCGAGGTGGGCTTTT	60.247	20
126	154	279	CCCCAAATGAGGAACTTTGA	59.903	20
126	166	291	CACACATGCGTTCATTCACA	60.164	20
205	88	292	TGCACGTAGGCATGTTCAAT	60.142	20
245	602	846	TTCGAGTTTGATTCCATCCA	59.049	20
219	491	709	GATTTTCCTGTCTCCTTTCTCAA	59.777	24
138	106	243	TTTTGCCCTCGAATGCTATC	60.175	20
215	2	216	AACACCTGTGAAAGGGATCG	59.966	20
210	262	471	CGGAATTTTACGTGGTTTGA	58.531	20
118	102	219	TCGAACGACATGAAAATTCG	59.664	20
254	9	262	AGTGGGCTTTGGCACAAGTA	60.689	20
276	278	553	GAGCTGGTTTGAGGGAGATG	59.803	20
237	298	534	ATGAAAACCGAAAATGGTGG	59.662	20
120	184	303	ACGACCCTCATCAACTTCCTT	59.987	21
129	280	408	CACTCATGTGGGGGATTGTT	60.634	20
233	48	280	CGGAAATGACCCCATAATGA	60.523	20
149	55	203	CAGAAATGGCATTGGTTGTTC	60.359	21
263	581	843	CGCATGATGTAACGTGAAGG	60.134	20
107	376	482	TTGATTATTCCGCTTACGTTTT	57.918	22
171	35	205	TCACATCCTCAGCACAAACC	59.682	20
165	502	666	TTTTGACGAGCCTATGTGGA	59.272	20
200	1	200	ACAGAATTAGCCTTACCAAGA	59.926	24
247	39	285	CTCTCTCCTACCTGCGTGCT	59.769	20

193	348	540	AAGAGTTATCACCGGATCGC	59.154	20
212	19	230	TTTGATCCTTGCTTTGCCTT	59.823	20
213	645	857	GAGACCGACGCCTTAACATC	59.7	20
196	298	493	TGGGGTTGGAGGTTTTTGTA	60.198	20
231	767	997	ACACTAACGCTCGACCTCGT	59.937	20
280	2118	2397	GCGGATTATCACATTGAGGA	58.521	20
253	4	256	AATACCCTTCGCATCCACTG	59.955	20
255	56	310	CGCCGGACTATTCTCTGAAG	59.971	20
187	650	836	GAACCCTTTTTGGTTTCCGT	60.2	20
276	443	718	TCAATCAAATTTTATCAAACAA	57.101	25
146	394	539	AAACAACCCCGGACTATCG	59.799	19
232	106	337	CAAAAGATTACTCATGTGATAT	61.041	26
113	98	210	CGTTGCCGGATAATTCAAAC	60.323	20
234	1735	1968	TGGATGGGGACAAGACAACT	60.363	20
257	2822	3078	TGGTTTTCGTACACAATTCGAG	60.032	22
252	5328	5579	TGGAACCAAGACATATGGGAA	60.177	21
184	96	279	TACGTGATCGGACACGAGAA	60.263	20
275	4639	4913	CTCCTTGCTTCCTCCATCAC	59.803	20
172	898	1069	CAATCATGGAATCGTTCGC	60.025	19
280	68	347	CTTATGTCCCAAATCGCCAC	60.331	20
234	72	305	AAAATCAAACCTCAACCCGTC	60.214	21
260	4182	4441	GGTAGAGGAGCTGATGTGGC	59.834	20
172	446	617	CCCCTTACTGCTAACACCGA	60.125	20
219	1009	1227	TCAGTTTTGCAAGGATTGAGA	58.488	21
250	174	423	GTGGTGGGAAACAAGAACCT	58.891	20
152	599	750	AGGAATGGGCTCGTAGGTTT	59.962	20
245	527	771	TGCTCTCCACTTTGATCCCT	59.803	20
217	2641	2857	AAATGCTCCTGCACTTCTCG	60.538	20
219	381	599	GTGTCAATTCCTGGGCTTCT	59.141	20
169	1832	2000	CTCACCAATTCCATCAGCCT	60.073	20
232	1305	1536	AATAATCGGTTGCAAGTTTGG	59	21
221	49	269	ATACCCCCGCGAAAAGTAAA	60.664	20
119	256	374	GGCTTAATGGGGTGGAAAAT	60.02	20
241	112	352	ACGAAAAACGAAGGAGACGA	59.853	20
276	488	763	TGATTTTAAGAGGTGATATGAT	58.255	26
219	63	281	GCAGAAATTCTTTCTTCTGTTTT	60.17	26
185	321	505	GTTTTTGTACATCGGCGGAG	60.502	20
197	41	237	ACAAATGGCCAAGAGAGAGTT	57.922	21
255	527	781	GGAGGTGCGGTGTTAGAGAG	59.867	20
236	1630	1865	TATCAAGCCCACCGTAAGTG	58.649	20
134	331	464	ACAACCCGTTTTAAAGCTCA	57.426	20
182	10	191	TGAATTCATGTACACATTTGGA	57.94	23
101	200	300	GAGATATACGCAGGGGACGA	60.059	20
262	247	508	GGCCGATATTTGTTATGCGT	59.822	20
247	2	248	CGGAAGAAACAAACTAGAAAC	60.193	25
247	53	299	GCGATGAAATGTACGTTAGAG	58.783	24
146	279	424	GCTACTAACTTGATGCGGGG	59.73	20
114	8	121	GGAGGGATGATGAAGATGGA	59.821	20
257	168	424	CCAGATGTCGTGGATTTTTG	58.973	20
181	1118	1298	TGAATGGATTTTTGGCATGTT	60.181	21
245	31	275	TGTTTTATTAACCTCAATTGTGA	57.051	25
273	1244	1516	GTTGAAGATGGGAAACCCCT	60.169	20
149	987	1135	CCGAAATTTTACGTGGTTCG	60.348	20
102	171	272	GATGCATGCACGTGAATAAGA	59.709	21
209	251	459	CAATCGTTGCGACAAAAAGA	59.849	20
262	61	322	GCTCTGATGCCAAACTGTTG	59.445	20
226	313	538	GCGATTCTTCCGTATGCTGT	60.243	20
182	28	209	TGGTTTGGTGGAAGAAATGA	58.947	20

272	29	300	TTTGCATACTGCATGGGCTA	60.237	20
185	5	189	GGCAACGGAATACCATTTGT	59.691	20
216	240	455	CAAAGCCGCTCCTAATGAAA	60.335	20
235	8	242	GCTTAAAACAATTATTGAACC	60.546	24
264	83	346	CCAGTTCGGCGATATATGGTA	59.824	21
239	1619	1857	GAAGGGAAGGGAAAGAATGG	59.875	20
235	40	274	TGCCTATCAACCCACCAAGT	60.375	20
165	1422	1586	CATGTGAGAAACGTCCCCTT	59.966	20
227	34	260	CAAAATTTAAGGTTATTATTG	59.806	27
137	2602	2738	CCCCTCATTTTTCGTTTTCA	59.91	20
277	110	386	TCAGTTTCCACACGCCAATA	60.111	20
187	16	202	TCATCATGAAACACCCTAGAA	58.616	23
260	137	396	TTGACCCACCTTTGACCAAT	60.21	20
191	195	385	ATCGTAGTGAAGTAGCCGCC	59.364	20
158	36	193	GAGTTGGTGAGGCAAAGAGG	59.844	20
179	47	225	GGAGGTTCTGATTGCTCCCT	60.596	20
279	64	342	TGGAGTAGGGAGCCTCGTAA	59.83	20
236	15	250	TGGTTATTACCTGATCACCATC	59.959	23
174	158	331	GTGCTCAGTGGACACATTGC	60.328	20
277	343	619	TTTAATGGACACCTCTGCGG	61.021	20
184	161	344	GTTTTGTTTCCTGGGTTTGG	59.308	20
241	228	468	AATACATCCAGTCATCCCGC	59.78	20
143	1016	1158	CCACTCGTGCATCACTCAAG	60.463	20
182	865	1046	AGTCAAATTGGCATTACGGG	59.823	20
174	2951	3124	CCCTTCCCTTCCATTTTGTT	60.159	20
251	2642	2892	AGGGGCTTTGAATCTACCAAA	59.952	21
210	37	246	ATCCATCTCATGTTGGGCAC	60.758	20
186	2253	2438	AATAGAGGGAGGGGAGGGTT	60.144	20
204	41	244	TGAACTAAGGAGGTGTTATGA	59.249	25
214	43	256	AAACAAACCGTGTTAACATCC	60.021	22
127	17	143	CTCATCTCTCGCTCTCCCTC	59.232	20
233	31	263	TCGATTCAGTTTCCCCACTC	60.05	20
127	920	1046	TGCTTGGAAAGACAATTGAAT	60.11	22
165	446	610	CATCACCAGATCATTTCGGA	59.451	20
245	1046	1290	CGAAGGTTGGGTGGTAGAGA	60.103	20
260	25	284	AATACAACTGCCGAGCTGAAA	59.897	21
215	50	264	GCCGAAATCTGGCCTTCTAT	60.551	20
269	966	1234	CCCAAATCCGTGGATAAAAA	59.633	20
165	232	396	CTTTCTCAACCGAGCTCACC	59.989	20
221	624	844	TAATGGCCACCAAGCTTTTC	60.074	20
275	1320	1594	AACGACGGAAATATGGAGCA	60.469	20
197	434	630	GTAACCAGCGCTACTTTCGC	60.046	20
117	2	118	TGATGGTTGTGATTTGTTAGAG	59.007	23
109	724	832	GAGGAGCAGATGGTGTCGAT	60.231	20
105	466	570	TCGGGTTTGAACCCTCAATA	60.301	20
230	448	677	GTCGACCGGCTTAGAAATGA	60.214	20
260	26	285	AAGGGCGGTATCACCTGAA	60.467	19
238	928	1165	CCAACACTCTGCTCTCTCCC	59.986	20
214	865	1078	ACGTAAACCCCTGGTCAAAA	59.331	20
174	294	467	TCCCAAATTATATCCTCTCCCA	59.637	22
271	118	388	AAATCAAGTTTAGGTGCGTCA	57.439	21
280	15	294	TCCATTCCGAAAATCGAAAG	60.009	20
233	67	299	GTCGTTGGTTCTTCGTGCTT	60.299	20
192	449	640	CCACTGATGTGAGCCAACTG	60.309	20
139	422	560	CTTGCCGATGTTTACCGTTT	59.996	20
275	110	384	TGACTCTCAATGCCTTCTACCC	60.63	22
251	1868	2118	TCAAAGAATCCACCATGCAA	60.049	20
172	18	189	AGCTGTTAGGGTTGTATAGTG	57.436	27

257	61	317	AATTTCGACAAACAAACGGC	59.982	20
276	10	285	GCGGTGGTAGGAAGAAACTG	59.734	20
185	61	245	GGGCATGTTTAATTGGGAAA	59.638	20
176	197	372	ATTTTATGGGACGGAGGGAG	60.145	20
184	1277	1460	GGAATTGAATGTGGGAGTGC	60.326	20
120	2815	2934	GTTGGTGCTGGCGTTTAACT	60.176	20
274	148	421	CCAGTACCCCTCTTTGGACC	60.736	20
257	0	256	AAAAATGCAGATTATGCTCCA	58.275	22
255	590	844	TCAATATCATCGCCATTTTGAA	60.282	22
263	637	899	TTTTGGCATTTAACGTTTTCG	59.989	21
261	260	520	GTGAGTATGCAGGCGACAAA	59.871	20
245	712	956	TTCGGTTTTGAACCTTGGAG	60.081	20
260	12	271	TGCACAATATGTTGGGAGGA	59.924	20
280	80	359	AGCCTAACTAATGGCACGGA	59.73	20
264	229	492	TTATCATGGGAAGGGGAGGT	60.517	20
211	72	282	CAAACGAGGAGCAAAAATCA	58.892	20
194	380	573	CTTTGTCCAAACAAATGAAAA	59.062	23
125	13	137	GTGAGGGATGGACGAGAGAG	59.792	20
252	2566	2817	GCCTCTTGGGGTCTTAATCA	59.126	20
226	94	319	AGCCACGATTCCTGATTTTG	60.074	20
214	17	230	AAACACGCAACACAAAGCAG	59.951	20
158	652	809	GTTCCTCATGCACCTTGGAT	59.934	20
152	80	231	ATCATCGGGGTGTAACGAGA	60.34	20
207	770	976	CACTGCCAGCAGTCGATAAA	60.011	20
159	0	158	AATGGATGGTTGTGATTGAGTT	58.293	22
207	429	635	GTCCACGTGCTTTCCTCTGT	60.307	20
271	6	276	AGTCGAAGGTCGCGTGTAAT	59.763	20
186	821	1006	AGCTGGCAATCCTTTCTTCC	60.713	20
202	23	224	TTTTGCCCTCGAATGCTATC	60.175	20
199	39	237	TCCCACATTGCATGAGAGAG	59.787	20
120	1	120	CATTGTGTTTTCTCCATATTTT	59.016	25
216	646	861	CAATGGTGATGGCAGAAGTG	60.112	20
234	4	237	TGTTTGAGTGGTTTTTCCTTGA	59.626	22
104	2	105	CTCACTCCCACTCCATCACC	60.527	20
130	1	130	ACCTGAAACTCCAAATATTCTT	60.267	26
180	631	810	TCTTGCCTTACATCAGCCCT	59.836	20
182	371	552	CTCCGGTGAACTTCTCCAAC	59.697	20
191	50	240	GGACGGAGGGAGTACGTCTT	60.511	20
237	67	303	GAAACCTAATGCCATGGTTCA	59.815	21
176	253	428	AAAAGGAAGGAGGGAGCTAA	57.181	20
179	86	264	TTGTAAAACATGTATGGGATT	58.355	24
132	3813	3944	CTGTGGTTGCGTCCTTATGA	59.716	20
216	1760	1975	CAAACATGGAGGGGTCAAAC	60.21	20
248	472	719	GCATCCTGAGTGGCGTAGAT	60.249	20
214	9	222	TAGGATACCCTCCCAAACCC	60.011	20
179	71	249	TCTCATTCACGCTTTTCAGC	59.152	20
267	1002	1268	GTCGCTTTCGATTTTTGAGC	59.967	20
182	73	254	GTTCTGGTGAAAAATTATGAA	57.752	23
271	1539	1809	GGGGTGGTTAAGTTGTGGTG	60.126	20
104	291	394	TTTTTGCTAGGGACCGAAAC	59.202	20
242	350	591	TTTGCCTATTTTGCCCATGT	60.323	20
150	85	234	CTTGGGCTAAAATCCCAACA	59.931	20
188	1689	1876	GGTTGATTGGTTTTCATGGC	60.177	20
100	8	107	CAAATATTTTGTAGTTTCCCAT	59.948	26
241	4198	4438	GGCGAAACATATCCGGTAGA	59.923	20
223	187	409	TGGGGTTGGAGATTTTGAAG	59.903	20
221	35	255	GGATTTTCGAAATTTTCTCGC	60.035	21
274	1208	1481	TCGCTCAAAACACAAACACC	59.74	20

248	21	268	CGTGGTTCGATCGTAATTGA	59.542	20
168	949	1116	TTTCTTTAATCACCGCACCA	59.157	20
271	254	524	GTAGCTTGCGAACGGGTAAC	59.775	20
278	20	297	TTGTGATTTGTTCCCACAAGA	60.378	22
203	23	225	GCACTGTGTTACGCCGATTA	59.759	20
265	239	503	AAAAGAAAAAGTGAAGGGCT	59.411	22
249	635	883	CAGAGCTAATTCAAACCCCG	59.702	20
115	5	119	GAAGAACAATTACAATGTTTA	58.084	27
253	2291	2543	CTGCAGAGCTCCATGACAGA	60.294	20
112	21	132	CAACAGAGAATGCAAGCAAA	59.097	21
271	84	354	AACATGATTTGATGGTGCCTC	59.811	21
111	1	111	TGCGTTTTGACAATATATAGG	60.083	26
215	27	241	CTTCCCAGGATCGATTTGAA	60.006	20
214	549	762	TGAGGCCGCTTCTTATTTTT	58.966	20
108	0	107	TTGGTGGAAAAAGGTTAACGA	59.478	21
253	15	267	TGACGAGAGAGAAAAGCGAA	58.874	20
107	17	123	AAGGGGGTTATTAGTGGATCA	57.425	21
160	50	209	TGTGCGTGTATGCAATGTGT	59.621	20
156	953	1108	TGACATGGAACGTTGATTGC	60.526	20
211	46	256	TTCCGGTCTGGTCGTCTTTA	60.626	20
187	35	221	ATCTCGACTAATTATTATGCCT	58.678	26
255	43	297	AATTAAAATTTGGGGAGGGG	59.034	20
184	981	1164	CAGACCGTCGAATTTAGACCA	60.118	21
250	0	249	TTTGGGACGATTTTCTCTCTAT	59.617	23
266	898	1163	TGCTGCAGAGAAGGTAGGGT	60.012	20
235	65	299	CTCGTTTGTGTGTTCTTCGTG	59.395	21
265	229	493	TTGGTTGTTTTAATTTGCTCCC	60.213	22
210	535	744	TCCTTTACACCACAAGGAAAC	59.512	22
271	6	276	TCAATGGCTCAAAAAGTTTCA	58.4	21
257	32	288	AAATGAAATAGAATTCGCGAG	59.608	22
275	30	304	CACACACATTACATTAAACCG	59.229	24
276	442	717	TCGCATGTTCGATCTTCAGT	59.399	20
204	22	225	CACATCCCACCCAACTCTCT	59.962	20
233	488	720	TGGACGTAAATACCCTTTTAC	59.667	23
196	188	383	AGCCCAAACCTCAATCAACA	60.495	20
225	565	789	ATCCAACCACCCACGAACTA	60.232	20
240	2379	2618	CTCGGAAAAGTCTACCGGC	59.822	19
248	700	947	AGTGAGCCTACACCACCACC	60.033	20
188	114	301	CCCCAATGCTATGGACAAAC	60.192	20
170	97	266	CGTCTGAGCTCGGTAGAAGC	60.299	20
123	270	392	AGATCCGATGTCCCAAACAC	59.786	20
237	2945	3181	ATGTGCTCTTCATGGGGAAG	60.073	20
222	23	244	CATCCCAACCACTCATTTCG	61.296	20
255	1892	2146	GGTATGTGCGTGTGGATTGA	60.399	20
222	18	239	GGTTAATCTCTCTATCTCTCTC	58.624	27
160	67	226	GCAGTGTAGTTAGGCGGTTTG	59.821	21
125	816	940	TTGTCGGTCATTGAATTGTGA	59.956	21
197	56	252	GTTTTCATTTGATCACCTCCC	58.347	21
177	147	323	GATCTGCGAAATGCTTAGCC	59.951	20
254	585	838	TCATCTTCCTTACGCGGACT	59.836	20
165	113	277	ACTGGAACAACAGCTACGCT	59.558	21
220	448	667	AGTGCTCACAGATCCCACCT	59.713	20
110	10	119	GAAATAAGGAGGTGTTATGA	59.323	24
194	19	212	CCCCTGTATGCACCTCATTT	59.813	20
191	470	660	AGTAGTGAAGGCAGCCCGTA	59.898	20
245	241	485	GCACTGAGTACCCATTTTGC	58.229	20
205	10	214	CCAGGTCTCAATCTTTTTGGTT	59.499	22
272	73	344	TGCTGCTATTGAAGCCATTG	59.976	20

150	1389	1538	GAAGGTGAACGTCGGTAGGA	60.111	20
210	357	566	TGAGGTTAAGGTGTGACAAAC	60.067	22
174	299	472	ACACGCATCTCTCTCTTCCC	59.41	20
279	761	1039	TGAGGCTCCAGATTTGCTCT	60.096	20
122	74	195	GGCCTACTTCCTGGATCACC	60.853	20
167	122	288	GGAGTTTCTATCCGCCCTTC	60.039	20
202	55	256	CGATGGTCTGAGTTATCCTCT	59.652	23
121	38	158	ATCGTGTGTAGGAAAAACATC	59.02	22
178	0	177	GTTTTCCAGTTCCCGATCAC	59.386	20
278	193	470	GCTGGACAAATCTGGATGCT	60.226	20
279	11	289	GCGGTTTGAGCCTAATTTTG	59.72	20
277	79	355	GCATACACCGATAGCATTTTG	59.992	22
110	360	469	AGAGTGCTGCAGCGTATGTG	60.23	20
230	410	639	CCGGAGTATGCTATAAACGAA	58.355	22
225	80	304	CCCGATGTCTGAAACTTGCT	60.255	20
207	47	253	TTCTTCCTCAATTTCAGTGTGG	59.215	22
231	75	305	CACGGGGTTTCCAGACTTTA	59.964	20
186	43	228	AAATTAAGTGGGGGTGGAGG	60.046	20
233	115	347	GAGACACCTGGCAAACATGA	59.682	20
264	1341	1604	CGATACGAATTTTCATACCAT	59.213	25
128	59	186	GATTTTGGGACGATTTTCTCTC	59.965	23
225	1	225	GCGAGTGTCGCCTAGTGTAG	58.703	20
280	308	587	TGAGCACGTATGGACACGAT	60.144	20
150	2538	2687	CTCCTGCGTAATATCGGAGC	59.829	20
171	485	655	TTGAATCCAGGATCTTGAGC	57.804	20
172	81	252	GGGAGAGATGGATCGACAGA	60.16	20
102	5	106	GATTTGCTAGAGGTTTTGACG	58.516	22
180	2346	2525	GGATCTCGTGATGCCACTG	60.222	19
279	2253	2531	CATTCACTTGAGGAATGGGG	60.309	20
242	1654	1895	ATCCCGTCTGCGTTTATCAC	59.962	20
147	2434	2580	TTCAAACGTGGCACCAATTA	59.969	20
239	14	252	CACAAGATTTATGGGTTATCA	58.787	25
172	316	487	AAAAGGTTAAGGGTGGGGTG	60.082	20
188	165	352	TTCCCATCAGTCAAGATCTAC	58.121	22
243	509	751	TCCTCGACTGTTTTTCCCAC	60.088	20
273	1439	1711	GCAATGGTGTTGCATATGTGT	59.341	21
277	2078	2354	GCTACGAAGACATCCACCAA	60.125	21
105	212	316	TGCCTCCTTTTCTTTTTCTCG	60.826	21
116	13	128	TGGGAGAATTTTCTGCTCTTG	59.438	21
183	3	185	CCTCCCAACCCCAAATTTAT	59.882	20
146	18	163	ATCGGTTATTACCGGATCGC	61.031	20
266	709	974	ACTTAAATCCACCGCCATTG	59.823	20
206	1156	1361	TGAGGGACTTGGGTAGTTGC	60.111	20
235	1135	1369	GACAGAAGAACGGGCTTTGA	60.375	20
146	622	767	TTTTTAATTCATCTTAACTGAT	58.447	26
147	335	481	GCGCAAAAATACTCGCTTTC	59.992	20
124	172	295	ATCTACCCCTCATTCCCGAC	60.154	20
195	13	207	GATCTTTCCACAAACCGAGC	59.676	20
203	91	293	TAAAACATTTTCGGCCATGA	59.004	20
230	295	524	AGCTCACGTTTTTCCCTCAA	59.853	20
240	1102	1341	CCAATTCGAAAACCGGTAAA	59.805	20
265	4	268	AGGGCTAAGTGTTGAGATTGG	58.331	21
145	690	834	TGCGTTTGATCGTTAGCTGT	59.493	20
205	78	282	TGCACGTAGGCATGTTCAAT	60.142	20
179	954	1132	CCATCCATGCCTTGGTACTT	59.813	20
259	23	281	TGACATCTTCGAGTGATCGTG	59.846	21
197	153	349	GCGAAGAAACATTCAGGGAA	60.192	20
252	554	805	GCGGCCAAAAGTAATTCAAA	60.075	20

144	44	187	ATGCATGTGTGCCAAGTGTC	60.614	20
237	1824	2060	CAAAATGTCGAAAAATTCGC	58.278	20
242	18	259	TATCCATGGAATGCCCAAAT	59.979	20
178	837	1014	GTTACATGGATGGATGGGTTG	59.925	21
172	0	171	GCAAACCAAACATGTATCAAA	57.628	22
128	223	350	TGAATCCATTTTGTGTTGGG	59.222	20
260	4163	4422	TCTGGACCTTTCGGTTCTTG	60.224	20
261	28	288	AAGCAGGAGGTCCACAGTTG	60.298	20
247	767	1013	TTGGAGGTGCTCTCAAGGTT	59.844	20
242	361	602	GCTGGTGCATCCTCTTCCTA	60.362	20
260	320	579	TGCGTTGGATCAATTTGTGT	59.972	20
122	585	706	ATCGCACGTGCTAGATCCTT	59.866	20
229	1197	1425	GCAATCCGGATCAAAAGTTG	60.448	20
176	1276	1451	CCTGGTCAATCGGTTGTTTT	59.83	20
130	41	170	TGAGCAAAAGTAATAAGAGC	60.422	24
193	3	195	TTGTAATTATTGTAGGGAATA	57.858	27
237	149	385	ATCTCAGTGCGTGTGAGTGC	60.063	20
114	444	557	TAGACGCCCCAGACTGTTTC	60.255	20
274	18	291	AAGGGTTATCACCTGATTTTC	57.73	23
209	283	491	GGTAGCTGTCGTCGATGTGA	59.862	20
239	82	320	CACTACTAGGGTTTGGGAGG	59.866	21
244	177	420	AACGGCTATAGCAAGGGTCA	59.73	20
118	71	188	AAAGCTATCCACGATGGACG	60.096	20
128	693	820	TGGCTGTGAATCATTGTTCG	60.665	20
238	109	346	AATGCGCAATTTTAAACCCT	58.631	20
228	167	394	CGGCACCAATTTATTGTGAA	59.42	20
154	58	211	GGTTGGTCCACAAGATTTACA	58.486	22
244	159	402	TGTTGGCATCAAAATCAACAA	59.961	21
196	466	661	TCCGAAATTTAAGGAGTCGGT	59.952	21
254	23	276	AAGGAGATCATGGGATCGTG	59.886	20
169	44	212	TCCCCAAAATATCAGCCTTG	59.894	20
265	1237	1501	CTCATTTTGCACGTCTTCCA	59.84	20
213	62	274	CAGAAACGTTTTCCCTGAGC	59.853	20
118	785	902	AATGGTGGTGCACTTTTGGT	60.277	20
151	83	233	CCGGGGTATGCTATAAACGA	59.81	20
270	23	292	CCCACAAATGAATGGTTGTG	59.667	20
225	230	454	TTCTCACAAGCAAAGACCCA	59.415	20
246	1984	2229	GAGCGTAATATCAAATTTTTG	58.97	23
229	51	279	TCGAAAATCAAAGAGCCTCAA	59.946	21
124	1	124	TTCTTAATTTGCATGTTCGTTA	59.109	26
225	0	224	GGTGCAAGTGTCAATAGAAGA	57.558	23
198	22	219	AGAAACTTGACGTGTGCGTG	59.946	20
277	488	764	TGAGACCCAGTTAAGCACCA	59.288	20
215	185	399	CCTGGCAATGAAGACAGGTT	60.111	20
195	39	233	ATTCTCAAGCCACTCCCTCC	60.596	20
217	274	490	TGGCCTCAAACTGCTTCTTT	59.993	20
234	43	276	CGAGATTCGGGAAGACAGAG	59.943	20
256	2436	2691	TTTGGTAAAGTTTTGAGATTCC	57.863	23
217	820	1036	GGGGCATCCAGATAGTTCAA	59.894	20
232	329	560	CTTCAACCTTTTCCTTGTCTCC	59.255	22
111	4	114	GGGACCACAAAATTATCCCC	60.245	20
103	105	207	TGGTTGAAAATCATTGTGGG	59.222	20
224	513	736	AAGGGAATTTTGTCAACTGGA	58.54	21
246	1782	2027	TGGAGCCTACCATGACCATT	60.34	20
130	1119	1248	AACGCGAAGAACACAAGAGG	60.431	20
198	235	432	ACACGTGCCTCGTTTGAAAT	60.559	20
274	5744	6017	CAGCAGCAAAGCTTCGAAAT	60.658	20
239	778	1016	GGCCAACATATGGGATTTTG	60.016	20

166	389	554	CCTCCACAAGTCGGATATGG	60.331	20
187	5	191	CGACGTTGTCTTAACCTTGGA	60.154	21
111	2108	2218	TAGTTAAACTCACGCACGGC	58.992	20
249	284	532	TTTCCCTTCTTTTGGGAGGT	59.912	20
206	30	235	GTTGGAGGAGAGCTGTAGCG	60.156	20
197	12	208	CACCCAAAATGGGTTATTATTT	59.404	23
249	87	335	GCACGTTTTTGGCCTGATA	59.679	19
213	31	243	GCGGGGTTGTTGAAGAATTA	59.938	20
203	258	460	GCATGGACTGGGGAAATGTA	60.723	20
189	8	196	GGTATTCGTGATCGTGATTCCT	60.215	22
187	5	191	GGGTTCGTAACCTAGGAGCTG	60.137	21
271	98	368	CAAGCGGAACAAACAAACAA	59.746	20
239	12	250	GGGACGAATATACCCTCGCT	60.307	20
187	801	987	AAACACCCTTTTATTGGTTCTTT	57.427	24
161	2903	3063	TACCTGGGCTGTTCAGCAAT	60.657	20
214	19	232	CGGATTTAAGGGTTATTACATC	57.222	23
188	204	391	CATTTTTCCACCTTGTGCCT	59.971	20
136	202	337	GGAGGGCTGTGTGATTGATT	59.934	20
265	15	279	ATCGTCGCCTCTAGCCACTA	60	20
191	34	224	GGTTTTACGAACCACAATCCA	59.716	21
143	82	224	TTTGCACCTGAGGAGGTGTT	60.69	20
261	941	1201	TTGCATCTAAGGCACTCAGC	59.178	20
279	497	775	TTCTCCTATCTTCCCCAGCC	60.537	20
172	338	509	AACTGGCATCCATACGAAGC	60.103	20
233	772	1004	CAAATCTCTCAATCGGCACA	59.799	20
154	74	227	AGGGTTTAAAATCGCGCATA	59.586	20
217	370	586	TCCCATTGGTTATGGGAAGA	60.126	20
266	471	736	GCGGATTCAACAAGTTCACA	59.697	20
209	94	302	ACACCCACAAATCAACCACA	59.701	20
255	395	649	CAAACCAAGGTCGAGAGTTGA	60.275	21
238	7	244	CCAGCTCAGTGTGGGAAAAT	60.111	20
252	370	621	AGGTGATTTGGCATTAAGGGT	59.717	21
234	338	571	AAAAGCAATTTCAACATAGGT	60.281	24
253	13	265	TCGGCTCGAAATCAGAAAAT	59.784	20
209	260	468	CTGTAGTCGTGGTGGGCTTT	60.171	20
240	500	739	TCACAAACCCAGATATCATAAT	58.386	24
162	1275	1436	CTTCTAAAGAACCCTCCCCG	60.061	20
106	176	281	TAGACCTCCAACGAAGCACC	60.255	20
121	15	135	ATGTGATGTTGTATTTTGGTAC	59.499	26
112	174	285	CAAACGGTAATTCCCCTCCT	60.18	20
212	41	252	ATCATAGTTGACGCCCTTCG	60.096	20
117	229	345	TGCTATTGCATGCTAAGAAGTC	60.055	23
279	305	583	TGTGGAATGGGAGATAACAGA	59.429	22
112	21	132	GTGTTGGACGCATCAGGTAT	58.444	20
206	408	613	ACAACAATCCGGAGGTGAAG	59.966	20
247	1	247	ATGATCAAATCTTGGTGCGG	60.864	20
147	50	196	TTACCTTTCTCGATCGGGTG	60.066	20
150	264	413	CGCTTAATTGGTGATTGTGAAA	60	22
153	227	379	ATTTTTCGGCGAGATTGCTA	59.816	20
262	10	271	TCAATCAATTAGATTTTCGGCT	59.601	23
128	81	208	AACAGCAGGTGAGTTGGAGG	60.298	20
217	1781	1997	TTTCACTGTTTCCACACATGC	59.606	21
163	297	459	GCCTGAAGGACCGTATCCTA	59.15	20
101	1105	1205	GTTGGATGGCTGGTTTCTGT	59.973	20
205	5	209	CTTCTTTTCTCTCCCTCCCC	59.252	20
231	820	1050	TTCTATCGCGCTCTCTCTCA	59.002	20
106	4	109	TGTTCTTCGTGTTCTATATTTCT	58.935	25
202	10614	10815	TCAACTCCAACTGATGCCTG	59.831	20

220	883	1102	CATGTTCAGTTTTTGGGGCT	59.971	20
272	0	271	TATCAAAACAACCCCCGGAC	61.84	20
165	110	274	AGCACAACACACACCCTCAC	59.63	20
168	249	416	CAAGTCAAGCAAGGTGGACA	59.873	20
255	17	271	GCGACAAGTCTGCGTGTTAT	58.955	20
208	217	424	CCCTCATCGACTACTTCCCA	60.065	20
249	70	318	TAACATGGAGGACAGGGGTC	59.779	20
276	326	601	GGATTGCATTTGTGTAGTCTG	59.499	22
277	412	688	CCAGACCAGTTGGTGATCAGT	60.018	21
254	5310	5563	ATGCCTCTGGTTGTTGGAAT	59.41	20
219	373	591	CAAAGAAGGCAATCTATCCCA	59.168	21
252	215	466	CAATTTCCCAACCTCTTCCA	59.903	20
254	2270	2523	TTCCGCGCTTTTTACTATGC	60.355	20
237	116	352	AGCTCACCCTTGTCATCACC	60.12	20
154	240	393	CGCACTCACACACTCTGACA	59.624	20
241	301	541	TTCGGTAAAATCAACGTGAAA	59.511	22
219	659	877	ATTGCTAGGGTAGCCTCCTT	57.088	20
163	1499	1661	AAACGCCATGCAAAAATACG	60.859	20
239	49	287	AAGCTGCACGTGTTACACCTA	59.872	22
266	88	353	AAATAAAAGAGGAAGGCTGA	59.17	24
191	2854	3044	TCTTTCCCACTTCCCACATC	59.903	20
194	69	262	ACAGTCACTCTCACTAGCCGC	59.685	21
245	82	326	GGGCTTAGAATGCAATCCCT	60.419	20
151	585	735	CGCGCACACACTTACAAACT	59.974	20
263	583	845	TCTTCTCCCTCTCTCCCTCC	59.883	20
213	535	747	TGCCCACAAAGATTTCATCA	60.049	20
107	1	107	GCATCTCTTGCTCTCTCGTTG	60.292	21
267	51	317	AGGCATCCATCCTTTACTGC	59.154	20
152	1260	1411	GGGATAGAGAAACTGAATGA	59.526	24
195	16	210	TCCACCGTTGTCTTTAAGTCG	60.154	21
207	319	525	GCCTAGGGGGAAAGTATGGA	60.278	20
236	1012	1247	GGCAGTGAAGGACCAACAGT	60.159	20
171	74	244	GCATCTCTTGCTCTCTCATTG	57.78	21
143	169	311	TCAAAACCCAAATCCGACTC	59.91	20
215	572	786	AGCACCAAGACAATGCCCTA	60.657	20
221	42	262	CGTGTTTTACCGAAATGCGT	60.915	20
188	13	200	TCCTTTGAGTATGGATTGATGA	57.155	22
253	960	1212	CGATCCGTCGACTAAACCAT	59.955	20
230	1111	1340	ATGCGAGAACGGAAAGAAAA	59.823	20
280	264	543	CCTATGCCGCTTACCTTTTT	58.409	20
258	450	707	CCAACTACTGATGGTCCAAGC	59.607	21
280	130	409	TTGGATCCGTTTTATAATCGTG	58.871	22
190	1184	1373	TCTAACACGCGAATCTGACG	60.011	20
146	73	218	TCGTGAATGGCATGACTGAT	60.08	20
142	6	147	GAGGTACGGTGATATCATGCT	59.843	25
111	1901	2011	ATGGGGAGTTCAATGTCGTC	59.786	20
264	147	410	CCACGAAACATCAGCATACG	60.134	20
278	174	451	GGCCCAGATTTGTTCCTACTC	59.954	21
205	476	680	GGACGCCCAATATTGTTTCT	58.906	20
167	178	344	TGTAGAGGAAGTTGGGGGTG	59.959	20
271	29	299	CCGTCCATCACTCCTTTTGT	59.966	20
113	387	499	CATCTCATTGACCGATCCCT	59.886	20
201	516	716	ATCAGCATCTTTACCGCCAC	60.103	20
276	995	1270	TGGCAGATTGTTCAAGCAAC	59.847	20
271	72	342	ACGCACACTTACGCATTCAG	59.935	20
212	152	363	AGTTGGAATGAGCAACATGC	58.726	20
224	257	480	AATCATCTCCTCACTAATTCCA	57.69	24
191	1228	1418	TACGTGTGTGCAGTTGCTGA	60.096	20

157	35	191	GACCGCAGGATAATCCAGAA	60.036	20
217	693	909	TTGGACTTTTCGAAGAGCAT	57.546	20
264	81	344	CCCGATTTCCATGCTTAAAA	59.901	20
262	384	645	GTCAAGGAAGGCATCCACAT	59.934	20
278	2039	2316	GGCCGTATCTCCGATTGTTA	59.923	20
168	160	327	GTATCTTCTGTTGGGGCGAA	60.074	20
164	26	189	CTGCCTTGCCAATTGACTTC	60.776	20
259	140	398	AGACCATGGTTCGGAGAGTG	60.112	20
249	2022	2270	TAGCTCACAGTGCACAAGGC	60.207	20
257	377	633	TCACGTTATGGGGAGAATCC	59.75	20
159	1163	1321	CAACGATGGTTGTTGAAACG	60.004	20
180	5	184	TGCGTTTTGACAATATATAGGT	60.083	26
258	219	476	TTCAGTGGAACATGGTTTGC	59.547	20
154	231	384	TTGGAGTCGGAAAAACGAAG	60.22	20
234	414	647	GCATGCATCAACTGCAAATC	60.237	20
224	5	228	CTTTAGGGCCCTTGATTTCC	59.903	20
203	332	534	GTTGCTTCCATCGTCACCTT	60.119	20
208	174	381	TGGTTGTGATTGTAAAGGGGA	60.213	21
275	231	505	CTCGTCTCCCTTGTTTGCTC	59.989	20
264	0	263	GGGTGCTTGAAGATAAACATG	59.091	22
233	438	670	CGCATGGGAAGGATGTTAAT	59.784	20
267	26	292	CGCGAAGAACACAAGAGGAT	60.397	20
167	218	384	CGCGAACTCAAATACCCTTC	59.708	20
177	197	373	CTATTCCGAACGCAGGTACG	60.648	20
251	618	868	CCAAAGACAACGAACATCCA	59.541	20
270	382	651	ATTGTGTCACCGTCGTCTCA	60.162	20
272	1550	1821	TTCATGCCCGTTTTATTTGAC	59.824	21
232	88	319	TCCGATCCGATTCCTTAAAA	59.479	20
156	9	164	TGCTCTCATTGTAATCTCTCTC	58.289	24
276	316	591	TGCTTAGGTGGATTTCCCAT	59.387	20
135	66	200	TTCACCATAATTTGACACACA	58.859	23
182	25	206	GCATATGATGTGCATATACGA	57.665	23
261	289	549	TTATCCCTTCACCGTTCACC	59.79	20
279	195	473	TTCGAAATGTGAAGCGTTTG	59.849	20
134	292	425	TGAACTCACCACGTGAAGGA	60.285	20
196	2813	3008	GCAGCGATAGCTGGAGACTT	59.746	20
276	93	368	GGGGTAAAGTAGTCATTGTCG	59.812	23
220	313	532	AGCGTACATGGAATCCCAAC	59.82	20
229	95	323	TCTGTCACGTCATTGTGTCG	59.265	20
243	9	251	GGTGGTGCGAGAGTGATTGT	61.146	20
135	73	207	ACTCACTAGCCGCAGCTCTC	59.921	20
164	74	237	TCTCACCCTTCACCCAAAAC	59.943	20
228	9	236	TTTATAGTTTTGTGGGGTTATT	58.102	25
242	1	242	CGGTTGTATGAAACCGTTAGT	60.658	23
118	10	127	TCGGAGCTAAAACGGAGAAA	59.953	20
238	104	341	TGAGCATGTGGAGAGCAAAG	60.136	20
215	49	263	CCTTCCAACAGAACAAACTCG	59.76	21
271	166	436	ATGCGCGTTTTTAGGGTTTA	59.624	20
184	1861	2044	TGCTCTTTGACCAGCTGTTTT	60.045	21
250	89	338	GGTACATTCTCCGGTGACCA	60.78	20
237	17	253	TTGGGGGAATGGAGAGAAAT	60.632	20
274	0	273	CAATTAACGGTAGCCATCACA	59.89	22
233	106	338	ACGACTGTCGATCCACACAA	60.162	20
253	2263	2515	TCGAAACAGATCAAAACTGCC	60.242	21
121	78	198	AGTCCCAACTTGCTCATTTCA	59.726	21
203	1791	1993	CATCGCCTCTTCCTTAGCAG	60.11	20
185	22	206	AGTTGTCGAGCAGCTTACTTT	58.861	22
214	36	249	GTTGGACTCAAGTCATGCGA	59.837	20

178	85	262	GATAGCGTCATTGTTTGGCA	59.694	20
137	1884	2020	GTTTCTTCTGCCAGCACCTC	59.997	20
258	2368	2625	TGTTTACGGCTGCAAATTCA	60.251	20
131	2	132	CGTGGTTCGATCGTAATTGA	59.542	20
227	328	554	ATGCACGTAGGCATGTTCAA	60.142	20
272	227	498	TGCATCTTTGTACTCAGCCC	58.877	20
256	190	445	GCCGAGTGTCACCCATATCT	59.957	20
175	37	211	TTAAAGCTCGGTTCAATTTCA	57.589	21
221	33	253	AAATCAATCCCCACCATTCA	59.991	20
199	0	198	TTGATCCAAGGGTGTATAATG	58.694	22
262	550	811	TCATGACTCCATCCTTCACTTC	60.125	23
251	13	263	GTTGACAACTTGACATCAAAT	57.197	25
234	47	280	GTTGGACCTGAAAGGGGACT	60.349	20
177	440	616	TGTAGTCAATGCTTTTGAGATT	58.415	26
266	367	632	CGGATTTAATCGTGGCTGTT	59.96	20
238	615	852	TTCAACCCGAACAACAATGA	59.941	20
117	55	171	TCTTTCAATTTTCAGCCCTCA	59.809	21
238	3032	3269	TGCTTGCATTTGAAGTAGCG	60.155	20
256	98	353	TGGTGTTCTTGGTGTTTTGG	59.435	20
173	174	346	CACGTGTCACCTTATCAACGA	59.624	21
216	90	305	TGGAAATTTTCGGGGAATAA	59.233	20
193	434	626	GTGCCTATTGCCGACGTAGT	60.162	20
245	66	310	TGCTTTGCGATAAGCATGAG	60.118	20
278	267	544	ATCACTTCGATTCGACGCTT	59.843	20
232	28	259	CGCCCCATGGAGAAGTTTAT	61.191	20
215	650	864	ACGTGTCATAGGAAAACGAG	59.256	21
105	1929	2033	GGTTGATCTGCAGGGAAGAA	60.195	20
215	400	614	GCGCAAGTTACGTGTTACCC	60.564	20
154	962	1115	GTCATTCCGGTTGTTTCAGG	60.353	20
248	428	675	GATACAAAGTCCCACGACCG	60.375	20
265	219	483	ACTTGCTTGACTTGCAACGA	59.64	20
267	258	524	ACGCTTTGGATGTGCTTTG	59.856	19
128	293	420	CGCCGAGTTGGTTCTCTCTA	60.529	20
241	3768	4008	TTTCCTAGAAAGATCGGGCA	59.778	20
270	560	829	TCAGGATAAATATCAGTTTCA	57.252	24
131	85	215	TGCAATCACACAATAACAAGC	60.177	22
275	281	555	TGAATGGATGTGATTTGTTTG	58.869	22
101	7	107	TCCGGAGTAAGTTCGAGGAT	58.741	20
123	275	397	GGGCGAGAGAGGGAGTATTT	59.674	20
107	554	660	AAAAAGGAGGCATTCGATCC	60.399	20
180	2073	2252	AACCGAAACCGTGTTCTTCA	60.529	20
139	330	468	CAACGGCTCTTTTCTCCAAC	59.853	20
161	323	483	GCATTGTTTTTGTCGGCTTT	60.117	20
276	432	707	TCTGGGGGTTAGGTTGGTTT	60.581	20
198	66	263	ACCTAAACCATGAGAGGCCC	60.328	20
204	1291	1494	CCTTTCTTGAGTTTCAACCCC	59.963	21
278	1437	1714	ATTCACAAGCGGCACTTCTT	59.882	20
275	2252	2526	CTGAGGCAGTTTTCAGAGCC	60.134	20
146	281	426	TGGCATAGTTTGGTTGTGGA	59.964	20
277	1139	1415	CTATTGACGAATCCATCGGC	60.435	20
188	444	631	ATTGGTCTCGGTTGCTGAAT	59.556	20
232	1097	1328	TGCAAGGAAGAAAAACAAAC	58.451	21
142	363	504	GCTTGCTGTGTTTTCTGTCG	59.64	20
194	27	220	TCCCATGTTGTAATTAATGTAA	59.917	26
199	48	246	TGAGAATGGCCGAGAGTTTT	59.813	20
205	4615	4819	TGCAAACATCAGCCATTTTC	59.67	20
266	4453	4718	TGGGAAGAGGAAATGGACAG	60.042	20
202	37	238	GAATCAGGGGAGGGAGAGAG	60.149	20

238	2162	2399	TTCATACACACCCTTGCAGC	59.722	20
251	213	463	TCCAGGAGTCGTGCTTGTC	59.971	19
190	0	189	TTGGTCCCTCAACAAATAATA	57.644	23
130	343	472	GTTCCTGTGCTTTCAATTTGG	59.601	21
230	911	1140	AGTCCCTGATTCTTCCCTCG	60.586	20
173	15	187	CTCCTTCAGCTTCAGCCATC	60.096	20
117	15	131	TCGGAGCTTCCGAACTTATG	60.344	20
244	1470	1713	GATAATGAAGGCGCGAAAAA	60.172	20
206	55	260	ATTTCCGGCTTCCTAGCTGT	60.228	20
263	82	344	CATGTAGTCCGCTTTGCTGA	60.011	20
215	375	589	AGTCCTAGAAGGCGACACCA	59.867	20
118	816	933	ACTCACACACGCTCAAGCAC	60.104	20
185	9126	9310	GCGAACATCATGAGGAGCTT	60.37	20
193	3	195	GAGGAACTTGGGACGATTTTC	59.933	21
272	5397	5668	CCATGAAGAGGCTCGGTAGA	60.353	20
222	97	318	GACAACAGAAAAACCACGCA	59.74	20
122	700	821	TGGCAGGTTGGAGACACATA	60.112	20
237	1104	1340	TGCCTGCCCCTACTAGAAAA	59.839	20
170	3	172	TGTGCACTGTTTCTCTCTCTCA	60.222	23
145	4091	4235	CGGTGGCTGAAAGAAAACAG	60.796	20
176	98	273	TCACCACTCACCAAGCATGT	60.162	20
111	24	134	TTTGATGTCCAAAGTGGCTG	59.691	20
269	59	327	GTCGATTGTGTAGTTGTGGGT	57.431	21
217	634	850	TGGTTCTAAATTCATGTTTCTT	59.432	24
141	1314	1454	TGTGAGAGGTGTGAAGCAGG	60.022	20
172	225	396	CTCTCTTGCCTTCCTCCTCC	60.468	20
140	532	671	CCCTCATCCCTCAATTTCCT	60.264	20
245	2185	2429	GGCTGACAGTCAAGGAGAGG	59.986	20
208	702	909	TGGCTTCTCTTTGCAAAACC	60.365	20
201	9	209	TCACGTTAAAGGAGGGTATCA	60.126	24
144	1251	1394	AAATTTCACTCTAGCGGGGC	60.582	20
277	233	509	GGCGCAGCATATATACACGA	59.714	20
161	176	336	AATTGCCATCCCTCACACTC	59.934	20
169	1948	2116	ACGTTTTTCCTGAGCACGTT	59.78	20
212	333	544	TCGACTCCATAGTAGCCGAG	58.076	20
188	444	631	CCTTTTATATGGCGACCGAA	59.922	20
256	334	589	ATTTTGGTCGAAACCGAATG	59.801	20
266	301	566	GACAGAAATTCTCCACCACGA	60.104	21
243	1013	1255	TTGGCAGGTTGATCATAAATT	59.832	22
211	7626	7836	TGAAGTGGCCTAATCCAAGC	60.214	20
233	187	419	AGAGGAGGTGCAAGAATTTC	59.705	21
195	0	194	CCCTTTTATGCTCACATCTCTT	60.026	24
217	649	865	TTACGTGCCTGGCTTAGGTT	59.769	20
272	1064	1335	TGCTTCATTATTGCGTCACC	59.694	20
280	2	281	ATTTTAACATTGTTGGCGGC	59.838	20
179	1447	1625	TGATGAACTGGTTGCGTGAT	60.12	20
217	924	1140	TGAACTGTTTGGTTTCTGCG	59.881	20
181	54	234	CGATTTGCAAGTCTATGGCA	59.833	20
115	24	138	CATTGGTTAGCACTTGAATGA	59.28	23
247	76	322	TGCACCATAACAATATTCGAC	60.252	23
257	1280	1536	ATCGAAGCAAATGGAGGAAA	59.645	20
227	1073	1299	GGGATTCCAATCCGAAATCT	60.096	20
184	21	204	ATAGTGGTATGGTGTGGGGG	59.405	20
241	644	884	TTGCAGATGGGACTATGCAG	59.823	20
206	297	502	CCTTGTGCAAATTAATCCCG	60.315	20
213	711	923	TCCTTGATGAACTGTGGGTG	59.52	20
280	526	805	CGACGTGCATCATTTCTCAT	59.679	20
261	986	1246	CATTTCAGGCCAAATCCTGT	59.933	20

181	485	665	CCTTCTTCTTGGCGTCAACT	59.473	20
275	82	356	TCTACGGAGGACGAGCTGTT	60.012	20
266	214	479	CGACATGGCTACTGTTCTCG	59.465	20
280	1240	1519	GCGCCACATCTTGTTGAATA	59.694	20
175	44	218	TGTGATCAGGTGCTGTGTGA	59.858	20
198	514	711	TTCTCAGCATATGGGAAGGG	60.029	20
253	324	576	ATGCATGTGTGCAGGTGTTT	60.04	20
170	467	636	TCGTTGACCGTATGGGATTT	60.192	20
152	166	317	CAAACAAAGTCTGCAACCCC	60.529	20
276	676	951	TTGATGAATCATGTTTTGCGA	60.066	21
279	14	292	ACGGATTTAAGGGTTATTACCT	59.498	25
192	991	1182	CCTGCCCTCCAAGATCATAA	60.029	20
273	11	283	ATTTCTCACGCTGAAATGCC	60.221	20
101	29	129	ACAATGGCCAAGAACGTAAC	57.604	20
198	1217	1414	TTTCCTTTTGCAGCTGGAGT	59.993	20
280	5	284	CCAATTTGAATGGTTATCACCT	60.457	23
233	216	448	CATGAAGATACATGCACGGG	59.948	20
225	32	256	AACAATTGCACCTTTAATAGCA	57.978	23
196	5	200	ATTCCGATCAGCTTCAGCAT	59.803	20
152	229	380	TGGTTTCTCGATGGCTTTCT	59.813	20
172	2734	2905	GCTTTTATCAATGCCCTCCA	60.038	20
188	21	208	GTTATCACCGGATCGCAAC	58.941	19
265	776	1040	CCACATTAATTTCGGGCCTA	59.789	20
238	6804	7041	AGCTCCACTCAAGCAATGGT	59.874	20
262	3221	3482	TGATGTTTTCCCCATTTTTG	58.308	20
271	228	498	CCTTCAAAATTGGGATGAGG	59.359	20
217	908	1124	TATTTTTGGGTTTGGGGTCA	60.024	20
175	1078	1252	GCACCCTTTTGGTGGTAGAA	59.971	20
213	6	218	TGTGTCATTCCTTCCACTGC	59.682	20
226	380	605	TCATTTAATATGGTCTGTGCGA	59.507	23
152	115	266	TTAGGGTTTAAAATCGCGCA	60.564	20
230	1336	1565	TGGGTTAGCCCAAAAATGAG	59.931	20
168	34	201	TTGTATTAGATTGTGGCTCCGT	58.653	22
202	32	233	ACACTCACTCTCACTAGCCGC	59.685	21
216	938	1153	AAGCAATGGTGGTCTTCTCG	60.255	20
198	75	272	TCCTCACACACCCACTTTCA	60.129	20
158	488	645	TCTGCCTGTCGATCTCACAC	59.988	20
271	312	582	AGCATTGGTAAAACCGGGAT	60.562	20
192	33	224	ATGGTTATTACCTGAATACTCC	57.944	24
175	70	244	CATGGTCGTCCAAATCTCCT	59.927	20
279	224	502	GGATATAACCACCTCACCCAA	59.945	22
194	241	434	ATCGTAGTTGATGCCCTTCG	60.096	20
202	16	217	GCGAAACCGAAGAGAAGAAG	59.195	20
150	17	166	GAATAGTAGCGACTGCGGGT	59.364	20
234	35	268	TAGTCATTCGGGCCACATAA	58.991	20
153	215	367	CTGAGCACGTACAGATAAAAG	60.188	23
254	794	1047	CTTCCTTCCACGCCACATAC	60.517	20
147	28	174	ATGCTCATCAAGGTCTGGCT	59.834	20
198	27	224	CGTGGCAGGCTAATATCCAT	59.945	20
139	11	149	ATTGTTCGATGTCAGCTTCG	58.877	20
171	1213	1383	ATCGACATTCTTCTGCAGGC	60.37	20
201	10	210	TCATTATTTCTCACTCACCAAG	57.94	24
115	80	194	TCTCTCGGTGGTGATGTTGA	60.246	20
225	883	1107	ACTTAGGACCAAAGCCCGAT	59.962	20
240	741	980	GTGGATTTTAGGGCTCATGC	59.533	20
152	3147	3298	CCATTCGGAATTGGTTCTGT	59.79	20
260	1306	1565	CAGTTTCACCAAGTCACCCA	59.565	20
214	12	225	AAAATCAAAGGCCCACAATG	59.801	20

227	221	447	CCGTGTCCAGTCTGTGTTTG	60.194	20
146	367	512	GAATTACACAATCCTCGTGGG	59.302	21
218	1095	1312	GCCTAATGTCATTGCCTGCT	60.243	20
260	368	627	ACACATGTGCGACACATCAA	59.575	20
192	65	256	TGGGGGTAAAACTGTCCAAA	60.198	20
267	67	333	ATTGTTGGGTATTGTTGGCG	60.617	20
162	879	1040	GAGTTAGGCGAGAAGAGGGG	60.34	20
104	22	125	CGGATTTATTGGTTATTACATG	57.538	25
141	0	140	CTTCGGAACTCTATCCGCC	59.782	19
269	105	373	GCAGATCCAGATGCTCCAAT	60.189	20
148	230	377	GCAACCCAATTCACCATTTT	59.668	20
273	1246	1518	TTGCCTTCGTTCCAAGTTTT	59.724	20
278	24	301	ATCCTAAGTTCGCCCCTGAT	59.925	20
277	38	314	CGAAATTGAATGGCAAGGAT	59.901	20
261	565	825	GCAGGTTAACTCTAATTAATCC	60.196	27
259	867	1125	TTCCCCCACATTCAAAAGAG	59.903	20
157	1039	1195	ACGGATGAAGAGAAATGGCA	60.603	20
167	365	531	CCCCGGTTTCATTTATAGCA	59.789	20
236	25	260	CTCCGGTGAACTTCTCCAAC	59.697	20
185	498	682	CCCTTGTATGCTGCGTTTTT	60.131	20
268	30	297	CCCATGTTGTAATTAATGTAGG	59.089	24
153	69	221	CCGTGCATCCTATCCTGTTT	59.955	20
138	170	307	TTCAATCGCAACCATCAATTT	60.316	21
260	248	507	GGCCGATATTTGCTCGTAGTT	60.473	21
141	236	376	TGCAAAAATGGTGAGAGTGG	59.691	20
227	35	261	AGATCTACCTTTGGGTAACCG	57.252	21
239	115	353	ATCATTGTTTCCCCGAACAG	59.79	20
279	57	335	GCACGTGTGTGTGTGAAAAA	59.191	20
214	2782	2995	CACTGGTGTTCTCTCCCCTC	59.682	20
157	179	335	CGACACACCTCCTCAACCTT	60.151	20
116	252	367	GGACTGGTTTGACACCTTTGA	59.997	21
275	101	375	CCCATTACTCCAAACCCAAA	59.657	20
234	2213	2446	ACGATCCATGAAAGCAAACA	59.127	20
279	2	280	TTGCTCAAACTTGAACTTGAAT	59.65	26
205	183	387	ATGCCTTGGTCTTCCTCATC	59.094	20
208	84	291	TGATGAATGAAAGATGAAATG	59.402	23
169	351	519	TCTTTCACCCGCTTTAGGTG	60.241	20
229	77	305	GGAGAAGAGGGAGGATCGAG	60.292	20
144	113	256	CATTCAAGGGGCATTTTTGT	59.801	20
247	449	695	TGGAAAACCAAAGCAAAACA	59.178	20
260	309	568	CCCTCCCTCATCTCTCCAAT	60.412	20
256	324	579	CGAGCTGGCTTGAGCTACTT	59.92	20
143	460	602	CTTCTCTCCTCCATTTCCCC	60.008	20
273	206	478	TAATGGGTGTTTGTGCGAAG	59.585	20
262	142	403	TTCCACCGGTAGTCATCACA	59.96	20
252	4225	4476	GGGGTAAATATTTTGGGAGGG	60.58	21
163	2598	2760	GCGGGACAACTACCAACAGT	60.035	20
246	2315	2560	GCTTCCCCCTAGTGAACACA	60.111	20
223	19	241	AATTTGTGCCAGTGTCCTTG	58.623	20
198	445	642	TTAGGGTTTAAAATCGCGCA	60.564	20
275	596	870	GCAACAAGCGATTGAAGGTT	60.257	20
163	2	164	ATACCCCTCTTTAATCCGGC	59.292	20
225	1380	1604	ACTTTGGTTGCTGGTGTGGT	60.466	20
105	352	456	ATTGCTCAAAAGGTGATGGG	59.933	20
280	164	443	GTGACCAAAATTCAGTAAGGG	57.148	22
226	44	269	GGTTATCACTTGATCATCCCC	58.174	21
152	39	190	GAAGTTCGGCCATTCTTACG	59.708	20
255	591	845	GGTGGATTTTTGGAATGTCA	58.243	20

239	358	596	CCATAGCTCGATCAGTCGGT	60.24	20
172	85	256	TGGGCTTTGATTCTTGCTTT	59.823	20
172	27	198	CAGAAATTGCCTTGGTTGTTC	59.601	21
237	50	286	ACGACTTGTCGTGGTTAGGG	60.028	20
166	45	210	CCTCGGATAAATTATGGGAAA	59.213	22
191	19	209	TGTGCAAGGTTGAACCAAGA	60.278	20
112	87	198	CTTGCCATTGATTTTGGTGA	59.518	20
106	90	195	ACGTTTTTGTGAATGTTGCC	58.529	20
256	632	887	ACAAGGTGTAGATCTGGCGG	60.134	20
255	79	333	TTTTGAGAATGGGGAGGTGA	60.43	20
198	575	772	AACAGTTTCAATTCGCCACC	59.978	20
179	299	477	TTTTTACGAATTTGCCCTCG	60.068	20
235	155	389	AGTTCGTCAAACCTCCCAAA	59.569	20
233	1	233	TTGTTCCTACTCACTCACATTA	57.23	25
113	29	141	AGAGGAGAGTTGATGGTGAG	60.252	22
279	16	294	GCCATCAAGGAAATAAAGAA	59.254	22
232	115	346	GTTGGACCAAAAAGCCCTTA	59.064	20
257	365	621	TTACCCAGAGCACACTCGAA	59.44	20
259	383	641	ACAATGGAGGCTGGAGGAG	60.207	19
212	0	211	TGAGAAATGCTCCAAAGCCT	59.955	20
167	270	436	GTTCTCGCTTCATTGGCACT	60.406	20
187	116	302	CCGCCTTAAATATGCGTAGC	59.738	20
172	284	455	GTTGTCACGGCGTGTGATAG	60.183	20
226	392	617	GAGTAGGTGGATGGAACCCA	59.779	20
208	180	387	TTGAGTGGTTTGGTTGGAGA	59.109	20
209	33	241	TTCCTCAATTTTCGAATTCTCC	59.55	22
238	513	750	GGGGCGAGTCTCTCAAGTTA	59.43	20
236	1908	2143	ATTGTGAGGTCCCATTCACC	59.636	20
200	82	281	GAATGCTTAATGGGAAGCCA	60.038	20
271	110	380	TCAAGTTGAGCCTCCAAATCT	60.242	22
181	89	269	GCAATAAATGCGTTCACACC	59.044	20
194	114	307	TCCCTTTATGATCATTCGGC	59.862	20
256	158	413	AAATGTGATGTGGGTTGGGT	59.95	20
181	245	425	AAAGAATGGTGGAGGTGCAA	60.495	20
254	2570	2823	ACCACAAGCAAGCATTTCCT	59.74	20
191	482	672	GATCGGACGTCGAACAAGAT	60.081	20
267	104	370	TGTGCTTCTTTTCTCCCCTC	59.405	20
197	435	631	TGGTTTAAACAAATCGTGTTCC	59.904	22
214	2688	2901	TCTTTCGATTCTTGGTTCCG	60.184	20
146	194	339	GGTTGCTCTAAGGTGCCAAA	60.249	20
228	24	251	TGGTTATTACTGGAACGCGA	59.182	20
277	23	299	GGGGTTATCACTGGATCACG	60.195	20
265	2189	2453	CCCTAACTCGACCCAGATCA	60.065	20
222	176	397	GAGTGGGTATGAGGGGAACA	59.779	20
267	32	298	CGAACGACAATGGTTTGAGA	59.691	20
188	385	572	AGGGACGAACATCACCATTC	59.786	20
251	445	695	GCAGATTCCCAAATCCAAAA	59.878	20
278	88	365	TCACGCATTCTCTCTTCGACT	60.149	21
206	655	860	TATTCGGGGAAGTTATTGCG	59.922	20
168	199	366	TGATGCACGATGTATGTCGAT	59.971	21
221	3067	3287	GGGGAGAAGGAAGGAGAGA	59.749	20
165	120	284	CCTGCATGGACAACAGAAAA	59.691	20
158	394	551	TGGTTGGGCATTCCATTATT	60.016	20
193	1104	1296	AAACTCATATTCCATCCAAAG	57.972	23
102	23	124	ACAATATTACAAATGGCCAAG	58.988	24
274	311	584	TAGTGCTTTGGAAAACTCATG	59.406	22
242	94	335	GGGAAGAAAACGCAACACAT	59.978	20
121	2321	2441	GTTGGAAGGGGGCTAATCAT	60.152	20

270	158	427	CGTGGTTCGATCGTAATTGA	59.542	20
182	239	420	ATCACATGAATGGACCCCTAT	59.91	22
247	19	265	AGGGATTTGGGACGATTTTC	60.131	20
233	2263	2495	TGCGGTTGTTTGTGTTTGTT	60.05	20
272	265	536	GCCTCAATAACATGAGGCGT	60.103	20
266	1282	1547	GGTCGATGATTCGGCTAGAG	59.797	20
222	321	542	TAACAATCGCAATGCCAAGA	60.215	20
102	150	251	AAACATCGATCAGTTATCATG	60.089	23
175	0	174	CAACCGAGTACCTAACCACAA	58.56	22
270	555	824	AGGATAGGGAATAGCGTCCC	59.402	20
225	400	624	GATCGGGGCGTTACATTAAA	59.795	20
209	54	262	TGCAGACGAAACGTTACTGG	59.904	20
105	619	723	TCCAGGCAGGTTTTAATTGTG	59.982	21
197	3383	3579	CCTTCTCCATCAACTGTGGG	60.501	20
131	77	207	TCCATTTTCAGGTCCTCACC	59.903	20
101	367	467	TAGCCGATAAAAATGGCACC	59.928	20
177	100	276	AGCTCACCCTTGTCATCACC	60.12	20
147	294	440	ATTTTGAATCTCACCGTGGC	59.939	20
160	7	166	TATGCAGTGGGTTTTTGGTG	59.439	20
184	74	257	TAGGACCACATTTTGTCGCC	60.894	20
198	1053	1250	CAGATGGTGGTGTACGGTTG	59.873	20
280	362	641	ACCGAGTTGACAGCGAAAGT	59.914	20
253	737	989	TTTCATCCGCCTTTCTTTTG	60.181	20
247	507	753	AAAGATGAATTGGGGGAGGT	59.629	20
168	302	469	TTTGAGGGACAAAATCGACA	59.097	20
277	294	570	TCAGAACCGTTGTCTTTCAGC	60.425	21
270	64	333	TGATCCCTAAATTGCCCTTCT	59.917	21
204	40	243	TGCATAGTTCGACGATGTAAG	59.307	23
118	17	134	AGGCTGATATCACCATAACGC	59.084	21
111	3	113	CGTTTATTCGAGACACACACG	61.108	22
246	27	272	ATATTCTCGCTTCTTCGCCA	59.945	20
131	3669	3799	ATCGGAAGGAGCCTTGTTCT	60.212	20
235	1056	1290	GCCATTATGCACTTCCCAAT	59.791	20
152	695	846	GTTTTGGGCGAAACAAGAGA	60.227	20
193	732	924	AGTGACAGTTTCACCTGCGA	59.467	20
165	826	990	TTCTGTGATCGCAAAAGGTG	59.84	20
209	0	208	TGACAAATAAATGAAATACAA	57.062	26
178	65	242	CTTTCATGGGTGATGGAAGC	60.461	20
273	2754	3026	CATATCAAGTTCCCGCCATC	60.296	20
102	13	114	CGGTTGACTCTTTTACTTTAGC	58.582	23
227	250	476	TTGAGCCAGTTTGTGTCCTT	58.342	20
169	11	179	AGATCTAGGAGAAAAGTGACA	59.765	27
239	773	1011	GCACGTTACAACACCGACAA	60.618	20
196	583	778	CTTGCCGAATGTTTGTCTCC	60.636	20
267	772	1038	CATGGGGAATATGCATCCAC	60.953	20
279	208	486	GCTTGGTCCGAAAATTTCAA	60.053	20
246	229	474	TTCGTTTCGCGTGCTAATTT	60.749	20
255	103	357	TCGTCGCGTTGGATTAATTT	60.456	20
199	533	731	TGCTTGTGGGTTTTGTTTTG	59.603	20
226	76	301	CCGGACAGTGTACACCCCTA	60.822	20
278	48	325	CAGAGGAGATGGGAATGGAA	60.003	20
241	344	584	GGACAAGCTGTCGGATAAGC	59.843	20
270	4473	4742	GGGTGGATGTACAGTAAAGG	59.415	22
272	645	916	TCCGATGATCAAGTCAGTGC	59.794	20
226	65	290	CCATCAAAAAATTCCTCCCCT	60.124	20
118	68	185	CAACGGACGCTATCGGTTAT	59.982	20
125	7	131	TCAATCCCGTCACCTTCATT	60.317	20
226	103	328	GGGGGATGCCACTGTAGATA	59.773	20

223	343	565	GGAGAATTCGAGAGATTGCG	59.917	20
235	198	432	TTCGTACAGCCGTTTGATGA	60.257	20
259	7	265	TAGATGCACCGGTTAGGAGG	60.088	20
130	592	721	TCTTGCTCCACTGTTGTTGG	59.873	20
119	571	689	ATGCCATTTTCTTCACTCGC	60.221	20
210	609	818	CCTTTTTCTTTCCTGCACCA	60.22	20
247	3	249	GTTCAACCTGATTTTCCCCA	59.767	20
124	0	123	TGTGCGTAAATTAGCGTTCG	59.902	20
216	162	377	GTTATGCGTTTTGACGGGAT	59.829	20
215	298	512	GCTCATAGAGCTGGAAGGCA	60.646	20
183	1027	1209	TATTGGTTGGGTACGGGTTG	60.472	20
165	6	170	TTCTCATGTTGTAATTAATGTA	59.318	27
264	388	651	AGAGAATGTTGTCGCGGACT	59.874	20
125	769	893	GGAACAAATGAGACTGTTTCT	60.165	23
154	244	397	CGCTAACATTCCCTTTCTTCC	60.082	21
271	271	541	TTTCTTCTATCTTTTGATTACCG	59.171	27
194	187	380	CAACCGACATTTAGCAGCAA	59.872	20
211	651	861	TGCAACAAATGATCCCAGAA	60.049	20
157	686	842	AAAGTTTGGTGAAGTCCGCA	60.668	20
219	151	369	CATTTGCAAACCGAACCTCT	60.11	20
157	524	680	GCTGACAGAAATGGCATTGA	59.805	20
230	3179	3408	GCAAGAAATTGACATGTTGGC	60.505	21
123	29	151	TGGGAAATTCTTGTACCTCCTC	59.46	22
227	146	372	AGCGTAAACACGTCCCCATA	60.386	20
219	46	264	CCGGAATCGCATCAATACTT	59.923	20
263	143	405	TCTTCTGAAGTTGCGACCCT	59.989	20
177	22	198	CTCCTATCTCCAATCCATGC	57.139	20
227	1161	1387	AACCTTCATTTGGGCCTCTT	59.94	20
276	325	600	CACCGACGATCACTCCCTAT	59.95	20
260	779	1038	GCTGTAATTTCTTCCCCGCT	60.582	20
166	3063	3228	TCAATGTCCTCTGCTCGATG	59.942	20
252	9	260	CTTGCAACAAATGAAACGGA	59.706	20
259	1051	1309	GAGTGGGGAGAAAGGAAAGG	60.045	20
164	455	618	CCTTGACTTCACGCCTTCTC	59.989	20
152	341	492	CGGACAAAATGTACCCCAAC	60.088	20
181	61	241	TATGGTGGACCGATACATGC	59.23	20
217	1807	2023	TCGAAATTGCCCCCTGTAT	60.281	19
272	64	335	CACGTGATCTATGTGACCGC	60.144	20
278	14	291	AACCATTGCACATGAGACGA	60.12	20
219	48	266	AGGATCGAGAGCTCAAATGC	59.537	20
123	50	172	GCCATCCATTCTGAAGATCAA	60.029	21
152	204	355	TGGGACTGTTAAGTTTCCGC	60.11	20
244	23	266	AATATGAAACCCAACGTCGC	59.829	20
246	286	531	TTTTACCCGCGGAAATAACT	58.629	20
269	118	386	TGCAGACGCGTGAATTTAATA	59.365	21
206	1453	1658	CACGTAAGTTCGCAACAACC	59.245	20
201	6	206	GAGCTTCTCACGACTCTCGG	60.284	20
258	553	810	TTTTGAACCCTAAAAACTCGC	58.421	21
156	112	267	TGTGTCTTAAAGTATAAAGGC	58.463	26
206	835	1040	GTAGCTCAAGGGTTTTCGCA	60.386	20
227	29	255	AACCCCTACACCACCCCTAC	59.972	20
139	701	839	ATGCTTTGTTGGGGACACAT	60.24	20
189	469	657	TCACCTTTCCTCCCAAATGA	60.43	20
152	35	186	TAGGATTTGTGAAGGCCGAT	59.528	20
224	1027	1250	ACCAAATAGCCCCTCCACAT	60.578	20
216	3	218	AGCATCTCTCTCTTGCTCTTAT	58.525	24
215	1913	2127	CGACACTTAAATGCGTTTGC	59.373	20
241	692	932	AGAGATCGGGTTTGCTGAAA	59.813	20

263	60	322	ACATGGGAGTTACAGAGCCG	60.134	20
250	17	266	TCAGTTTCGAGTTATGAAGTTA	59.749	26
209	749	957	TCGAATTCTGTAAGGCGGTT	59.708	20
203	1078	1280	TGATGTCCCTGGAAGACCAT	60.326	20
159	40	198	CACACTCGCATACATTCAAACA	59.656	22
118	342	459	TCTTTGCTTCGGATGGAATC	60.155	20
163	203	365	AAAGCGAGTTTCAATGATGAC	59.752	22
199	20	218	ACGGAGAAAGGGGATAGAGC	59.674	20
222	1876	2097	TCCACCAGACCAAGAAGGAC	60.088	20
150	300	449	AATTGAGGGAGTGGGTGTTG	59.82	20
211	23	233	GGAAGCTAGGCGGTTTTGAT	60.582	20
205	212	416	CTTCAGCCCCTCTAGGTTTG	58.931	20
233	2185	2417	TTGTTGTATTGTAAAGCCGCA	59.269	21
234	1478	1711	AATCCGTAAGAATAATCCATG	57.192	22
159	64	222	ACGCGCGTTTTTGGATTTA	61.489	19
242	4779	5020	GGCGGATGAATAAACCTCTG	59.528	20
253	1288	1540	TCGTAGTCAAAACCCTGCCT	59.734	20
201	271	471	TACTTGGTTGAGCTTGGCG	59.996	19
214	293	506	ATGGACGCCTCAGATTGTTT	59.556	20
130	2772	2901	AACATTTAACTTCGCCCCTG	59.087	20
226	81	306	GGATGCAAACCTCCCTAAAA	59.019	20
125	283	407	GCTTGCTGATTGTGGTTCAA	59.847	20
129	212	340	TCATAGAGTTCGCTAATGATTA	59.757	27
241	98	338	AAAAATCTTGCTGCACCCAC	60.118	20
192	0	191	TGACATTCGCATTTTAAGAGTA	58.527	25
192	2168	2359	CTCCTGAAGCCACGTTCATT	60.255	20
141	120	260	CATGAAAATCATGTTCCGCA	60.466	20
143	2167	2309	GCAACCAAAACACACACACA	59.03	20
146	1444	1589	GGTTCCGCTCAATTCAGAAA	60.192	20
229	1702	1930	ACCGGGCACTAAGGGATTAT	59.688	20
178	146	323	AGCTGCAGCCAGAGAAACAT	60.164	20
278	460	737	TATGTGCGCGTTTCAATGAT	60.103	20
248	2010	2257	TGAAAATCTGACGAGCATGG	59.799	20
228	4090	4317	ATGTCGCCACAGCCATAGAT	60.514	20
196	21	216	CTGATTCGCACAAATGATCG	60.22	20
147	8	154	ACGGATTTAAGGGTTATTACCT	57.667	23
201	639	839	CTTGATTCCATGACGAGCCT	60.218	20
225	81	305	TAAACAATGAACCATGCCGA	59.93	20
174	268	441	TCCCTCAACCATCTCACCTC	60.048	20
181	210	390	CGCGAAATGAGGAGCTTAAC	59.982	20
241	5	245	GGGAAACCCACAATCATCAC	60.034	20
200	1656	1855	CGATGGTCAAGCATAACGAA	59.688	20
247	593	839	TTTCCCCCTTATTTTATCCCA	59.513	21
274	163	436	CCGTTGCTTTCTCTCTCGTT	59.615	20
272	295	566	CTCAGAAATCAAGCCGAACC	59.813	20
251	93	343	GAAACGGCCATTTACCTTCA	59.938	20
205	76	280	ATTACAGAGGAGATGGCCGA	59.653	20
280	1431	1710	TTCCCTTCCAGTTACACCGT	59.449	20
259	1854	2112	TCAAGTCCTCACACACTGATGA	59.31	22
180	608	787	CACGAGCTCTTATTTGGCCT	59.476	20
237	252	488	TTAAGGGGTTTTGCAGGATG	59.931	20
279	1637	1915	TGGACAATTCAATAGAAAACC	58.987	22
209	581	789	GCATGCGCGTAGTTATATCG	59.36	20
213	249	461	GCTTCTTTCGCTTTCTCATTG	59.238	21
208	2	209	CGGGTTTCTCCAGCTTCTTT	60.733	20
202	1187	1388	TAAGGTGGAAGGGGACGTTT	60.714	20
207	4583	4789	GGCTTTTTGCTAATTGGCTG	59.853	20
266	91	356	CCAGCTCGGTGATATATGGT	57.515	20

223	2	224	CGGGATTTAGGTGTTTTGACC	60.579	21
227	73	299	TATTTCCACTCATTTGGGGG	59.617	20
176	1081	1256	CACTGACATTTCCTCGCTCA	59.984	20
171	1118	1288	GTTGGCCACCTCCATTTCTA	59.933	20
202	175	376	TGAAATTCCGATGAGCCTTT	59.645	20
115	58	172	GATATCACCGGCACTCCATC	60.312	20
245	3674	3918	AGTCACCAAAGCTCCCACTC	59.305	20
232	295	526	ACGACAAAATAGGGGGCTTT	59.835	20
225	31	255	GAACACGAGGAACTTGGGAC	59.555	20
233	474	706	AGCAGGATCTTCCCCAAAAT	59.903	20
254	9	262	TGTGCGTGTGTTTTTGTGTG	60.245	20
210	359	568	GGTTGCTTCTTACAGGCTGG	59.875	20
164	491	654	GCATATCGGTTCGGTCTCAC	60.492	20
198	838	1035	TCATCAGTCCAGCCTTCTTG	58.957	20
128	358	485	TGATGTTTGCATTTGAAGAGG	58.759	21
140	9	148	CGTTTTGACAATATATAGGTGT	59.669	27
246	123	368	ATCAACGCCCATGATCAAAT	60.163	20
252	24	275	TTTCTCAGCCAAGCTCACCT	60.134	20
250	472	721	TTGTTCCCCTTTATCTCCTCA	58.632	21
178	287	464	TCTAAAACCCTCGCCTCTCA	59.948	20
154	1808	1961	GGATCCGTGATCAAAATGCT	59.9	20
267	505	771	TCAGATTTTCGTAATCCCCTTT	58.994	22
138	359	496	CTGTGTCGTCGATCCCTTCT	60.261	20
268	87	354	CACTGTCAAAAGACCACCGA	59.72	20
255	2703	2957	AGGCTTGCAAGAAGCTGAAG	59.898	20
280	477	756	CAGCGCCACGTATCCTAGTAA	60.291	21
183	269	451	TCATTTCGGGTTATTTTCGG	59.767	20
210	120	329	ACAGGTCCCTGAAACAAACG	60.005	20
148	74	221	TCCTTTCAGAGGCAGAAACC	59.405	20
234	109	342	AAAGGGATAAAGCCGTCGAT	59.93	20
102	4	105	CCTGCCATTTCTCTCGTGTT	60.255	20
228	5	232	ACAAAATGGCCAAGAGAGTTT	57.853	21
222	310	531	AGGGCAAGAGAAAGGTTGGT	60.11	20
201	577	777	CAGAACCCGAAGTGAAGAGG	59.837	20
209	25	233	TCCACAGCAGAGTCTCCTCA	59.685	20
260	2249	2508	ACAGAAAACTTTCATGCCGC	60.257	20
222	1962	2183	TTGACAGATGACCCCACAAA	59.935	20
159	2620	2778	CTCTGTGGGTATTCCTGGTGA	59.974	21
221	343	563	CTTTCTCTCCCGTGGACGTA	60.246	20
182	773	954	AGCAAGGTGATGCGAGACTT	60.02	20
225	1265	1489	CGGGTATACTTGGAGAAACAC	59.017	22
206	754	959	GGGAGATGTGGTGCTCATTC	60.484	20
253	18	270	GGACGGTTAAATTTTGTCCC	58.277	20
231	523	753	GTTGTGTGTTGATTGGGGTG	59.701	20
156	91	246	ATCGTCAATCGTCTGAGCCT	59.834	20
124	314	437	CATGGGCCTTGCATGTATAA	59.401	20
198	4	201	TCTCGTTGCTATTCTTGCCA	59.566	20
106	37	142	GAAAGGATGAAAATCATTGGC	58.497	21
147	159	305	TAAAACCATGCACGTAGGCA	60.133	20
173	387	559	TGAATACCGTCAGGTTGCAG	59.716	20
162	98	259	AATTAGCGTGTATGCTGGGG	59.982	20
274	48	321	ACGGAGGAAAAGAAGGAACG	60.601	20
205	460	664	AAAAATGGCACCTTTGACCA	60.344	20
140	587	726	GAACGAGGGCCTTCTTCATT	60.578	20
231	1631	1861	GGTAAATCAATGTGAAATGAT	59.956	24
209	2085	2293	TCTATGGACCCTTGCAGGAA	60.594	20
280	332	611	ATATTCATGCTCTCGGCGAC	60.207	20
246	605	850	CTTGTGACCCTCACCACCTT	60.002	20

189	264	452	CAGAAACCAAAGCCAAGTCA	58.897	20
219	44	262	ACCCAAAGATTTATAGGTTTTA	58.862	27
121	99	219	CACCCACAAATCAACCACAG	59.848	20
176	18	193	CCAATTTGAATGGTTATCACCT	60.457	23
278	42	319	GATAATATGGCCGAGAGTTTG	59.962	22
181	204	384	GCCACACATGTCACAAATGA	58.924	20
150	8	157	CGGATTTAAGGGTTATTACCTC	58.81	24
171	335	505	GGAGTGGAGAGCTCGAGAGA	59.817	20
227	52	278	AACAGAAAAATCACGCAGGG	60.11	20
242	239	480	CTTCAAGCGGTCTTGATTCC	59.813	20
117	250	366	ACACACTTAGGGGGTGGTTG	59.739	20
179	1891	2069	ATCGTCGTCGTCTTCTTCGT	59.874	20
215	452	666	TCAATTAATGTTGTCATTATTCC	59.207	27
173	412	584	AGACTTGCCAACGGTCAATC	60.119	20
270	71	340	GACTCATGCTCGGCATACAA	59.83	20
139	7	145	TCAAGGCCGATAAGATGGAT	59.486	20
202	206	407	TAACGATGGACTAGGGGCTG	60.088	20
229	57	285	AAATATGCAGCAGACGCGAT	60.772	20
242	158	399	TCGGAAAGGAAAACCGTAAA	59.559	20
232	44	275	ATCGGCTGAATAGCCGTATG	60.081	20
157	230	386	TTACCTCGTCGTCCAACTCA	59.288	20
274	147	420	CAGCTCCACTACTTCCTCCA	58.03	20
237	264	500	GGGAGAAAGGGCTGAGGTAT	59.536	20
207	18	224	CGTAAAAATGGTTATTATTGGA	59.898	25
248	28	275	AGAATGTTGCCACGAACTCA	59.293	20
228	360	587	AACCCCCTCCTTCGAACTAC	59.438	20
132	1262	1393	ATGCGCGGGTGTAAAGTTAG	60.152	20
198	15	212	TTCCTGTTCTCCGATCGTTT	59.67	20
242	390	631	CCTTCGGATCTGGGTATTTG	59.382	20
145	903	1047	TGGACCAACATTTGTACGGA	59.816	20
207	736	942	ATCAAGCAACGAAGATGGGA	60.603	20
105	33	137	ACATCACACCACAAATGACTC	58.983	23
237	3879	4115	CGGCGTAACTACCATTCACC	60.386	20
129	126	254	TGTGGTTTGCTAGACATCGC	59.871	20
278	23	300	GGACCTGAAAAAGGACTTTGG	59.963	21
237	2420	2656	AGGGACGAGGAAGAAGAAGG	59.811	20
218	39	256	CATTCAGAAATGGCGATGAC	59.079	20
228	499	726	TAAAAGCCGATCGAGTTCGT	59.845	20
212	9	220	CTCCACCCTCTCACTTCCAC	59.682	20
261	33	293	CTCTACCACTGCACCACGAG	59.487	20
274	65	338	ATTTGCGGAAACAATCCAGA	60.448	20
184	320	503	CGATTCGACTGGATTCGTTA	58.721	20
202	49	250	CAACCCGAGCAAGAACAACT	60.291	20
232	1098	1329	TTGGAGTTGGAGATGAAGGC	60.195	20
195	36	230	GCTAGCGGATTTCTCTGGCT	60.997	20
273	20	292	ATCGGTTATTACCGGATCGC	61.031	20
279	737	1015	GGTGATCAAGCGTTCGAATTA	60.089	21
270	96	365	TCCAATTTCAGTTAAACACACC	59.411	23
238	26	263	TCACACTCACTCTCTCTAGCCG	59.809	22
104	104	207	GAGGGAGATATGTCGGCAAG	59.653	20
166	33	198	GCATCCAATACCAATATCTCAC	59.848	23
205	320	524	TTCCACATTGATTCCTGGGT	60.173	20
221	584	804	GTGCTTCTTGAAGCTGGGAG	60.134	20
170	373	542	CCCCCAATGATCTAGCCTCT	60.422	20
272	474	745	TTCCTTTCCCAAAAGGACAA	59.518	20
278	0	277	GCTTTTGGATAAGAATGCGG	59.682	20
116	335	450	TTTTTCCTAACCGGACCACA	60.336	20
196	202	397	TCCCCATTGTTCTACCCAAA	60.162	20

143	3	145	TGATTTGTGTGAGGAATTGTT	60.393	23
212	146	357	TTTTTGGGTTGAAAATAGCG	57.833	20
234	680	913	ATCCAACCATTGCAGAATCC	59.756	20
170	4	173	GCACACATTTTTCTCCCCAT	59.797	20
176	28	203	TTACTTTTCCGGCAACATCC	59.938	20
101	304	404	CCTAGCCAAGTTTCACGAGC	60.015	20
267	37	303	ATACCGGGATCGAATCTTCC	60.117	20
280	40	319	GAAAAGAAAAAGAAGGCACT	59.539	22
135	272	406	CCATCATGGGGTTTTCTTACA	59.671	21
221	46	266	CAAATCAACGCGAATTCAAC	59.161	20
206	375	580	TCTTCTTCAAACACCCCCAG	60.081	20
128	206	333	GAATTTGGATGGTGATTGTGG	60.044	21
238	351	588	CAAGAGGAGCCCAAGATGTC	59.803	20
259	684	942	TGCCCCTGTATGCTTTTCTT	59.708	20
164	223	386	GTACCGAAGGGATGGAATCA	59.75	20
119	0	118	CAAAAGCACAAAGTCCACCC	60.529	20
209	780	988	CATCTTTAGGTTGATCCGGC	59.528	20
237	414	650	GATGCTTTTCCCCTTCTTCC	60.017	20
184	1163	1346	CTCCCTTTACCTCCCCAAAG	59.927	20
240	211	450	ATATGGTTTGACGCCTTTGC	59.967	20
235	131	365	GAAGGAGGAGAAGTTTGGGG	60.045	20
122	11	132	CCAATACTCTTTCCCAACCC	58.359	20
156	40	195	AACAGCCAGCTTTTGACCAT	59.74	20
142	35	176	CACGGGACGTTACAAGTTCA	59.609	20
279	702	980	TGAAAGCACAACTGCAGACC	60.032	20
196	12	207	CACTTTCTCTCTTCCGACCG	59.982	20
173	73	245	ATATTGTGCGTCCCCATCTC	59.78	20
150	1203	1352	GCGTGCGAATTTAATGATGA	59.668	20
256	512	767	AGCCGCATTTTAATCGAGAA	59.816	20
237	2	238	AAAAACGGATCGGATACGGA	61.542	20
133	14	146	TGCTTTTCTAAATGGAGAGTT	59.78	23
219	8	226	ACCATATTTAAGGGTAATCAC	57.552	24
193	24	216	AAGGTCTCTTCGACGAGCTG	59.745	20
160	1463	1622	GGCGGGATATACTAATGTCCA	60.062	22
185	5	189	ACTTTTAAGGATCAAGGATAT	57.122	24
192	222	413	CTCGAGTGTAAACACGTCCC	58.215	20
189	194	382	TCCGGATACCTACTACTGCGA	59.738	21
173	231	403	TGGTATACAACTTTGATTCCC	60.007	24
269	725	993	ATGCACACCGAGATGTGGTA	59.992	20
268	334	601	AACTGATGGGTTTTCAACGG	59.83	20
220	377	596	ATCAGTATGTCACGGCCTCA	59.116	20
266	251	516	AGCCTTTAATCAGCAATATAA	58.508	26
251	240	490	TTCACTCGCATAAAAGTCTCG	58.187	21
218	325	542	CCCTTGCATGCTGTGGATA	60.637	19
139	98	236	GTTGGTTTTCACCGGAGTTG	60.388	20
168	1279	1446	CGATGTTTGTTGGCTGTCTG	60.301	20
255	1028	1282	TTGGAACCAACTAATTGCCA	59.013	20
179	69	247	ACGTTCATACCTTTGTGGCA	59.05	20
243	123	365	TTCATTTCATCGATTTTTCCTC	58.175	22
180	79	258	TCAATTTCTTGGCTCAGGGT	59.67	20
280	5907	6186	ATTGGTCAACCCCATCTCAA	60.173	20
235	2858	3092	TGAGTTGCACATGTGTGAGG	59.265	20
124	607	730	GCCATCGATCTTGTTGGAAT	59.9	20
162	12	173	AGAATCACGGCCATTTTCAG	60.074	20
257	932	1188	TCTTGTTGGCATGAGCTTGT	59.445	20
215	406	620	CAAATCCCACAGCCATGAAT	60.723	20
260	267	526	CGCATTCATTAGCTACACCCT	59.261	21
169	200	368	AAATAAATGAATGTTGTGTTT	58.463	26

201	467	667	AAACCCACCTGCTGCATAAT	59.457	20
201	42	242	AACATATCGTCGTCTCCCGA	60.483	20
246	993	1238	GTCTCAAATCGTTTCTATCGTG	60.15	23
197	19	215	TGTGCAAGGTTGAACCAAGA	60.278	20
198	706	903	GAAGAGGAGGAAAGAAAACG	59.473	21
130	1309	1438	AATTGCGTTAGGGATTTGATT	57.647	21
206	433	638	AGACTTGCCAACGGTCAATC	60.119	20
226	12	237	ATGGAACCACTTGTTGACCG	60.812	20
256	20	275	CGAAGAACAATTACAATGTTT	60.478	26
236	22	257	TGCACCTGATCATGAACCTA	57.608	20
146	1334	1479	CCACAGCCTCATTCCTCATT	60.073	20
231	1015	1245	GTTTTTAGAAGGATACTCACT	57.781	27
198	236	433	AATATTCCCCGGTATGCCA	59.987	19
273	319	591	CAAAGAAAACGGTGGTGGAT	59.83	20
266	1140	1405	AAAATCTCCCACCAATGCAC	59.797	20
234	1253	1486	GCACATTTAATTCCAGGTCGT	58.965	21
244	133	376	ACGAGCTCTGAAAATTCTCCC	59.841	21
118	86	203	TTGAAGGCAGGCAACCTTAC	60.249	20
151	51	201	CAGCCTCCATTTTGTTACCG	60.493	20
279	3737	4015	AAAGAGAAAACGAGGGGTGC	60.61	20
251	574	824	GGCATAATAATGGCAGTCCC	59.258	20
194	657	850	AGTTTGGAGCACACGAGCTT	60.058	20
227	64	290	TATTCAACTCCATCTCCCCG	59.887	20
257	2123	2379	TTCAACGGTCCCACAAATTA	58.866	20
276	19	294	CATCAGATCTGCGCTGAAAA	60.096	20
200	249	448	TCACTGGCAGCGAATATGAA	60.366	20
167	64	230	CCCGATAGAGCATGTCGAGT	60.24	20
241	5852	6092	GCAATAAAGAGGCTGGTGCT	59.481	20
205	551	755	AGCCCTCATTCCTCCCTTTA	60.032	20
273	9	281	GGCAATATGCTGACAGACGA	59.83	20
266	0	265	GGAGTCTGGAAAAGAGAGAG	59.463	24
267	349	615	ATGGCATTCTTTCTCCTCCC	60.41	20
170	98	267	AACGACATCATGACGCAACA	61.163	20
230	16	245	AAGGGTTATCACCTGATTTTCT	57.73	23
156	30	185	TCTAAATTGCGAGAATATGAG	58.988	26
250	532	781	TGCTTCAAGGTAGGTTTATTAG	60.047	24
177	123	299	TTACTGGAGGCGATAGGTGG	60.088	20
227	554	780	TGGCTGCTCCTCATCCTTAT	59.797	20
137	3948	4084	ACTCGCGAAGTTCCTTCAGA	60.134	20
256	27	282	GCCACCATTGAGAACTCCAC	60.52	20
241	3085	3325	CACCACATAATGGACGTTGG	59.691	20
251	1236	1486	ACGAGCTTTTATCGAACGGA	59.845	20
159	3047	3205	GCTATGGTGGCCAATGTCTT	59.962	20
241	1053	1293	AACTCCCCTTTCCTTTGCAT	59.94	20
251	504	754	TTGAAAACTAGAGATGGCCGA	59.831	21
260	887	1146	TGACTTTCATGTAGCGTGGC	59.871	20
217	8166	8382	ACTTTCACTTTCCCACGCAC	60.156	20
233	43	275	TGCCACTTATTTCAGGAGGT	57.268	20
272	3249	3520	TTAGCACCTGATTACTCCCGA	59.716	21
230	30	259	CGTGGACGTAGATCCTTGTG	59.161	20
222	923	1144	GCCCAGTATGTTACGGTGGT	59.74	20
179	0	178	GGGGAGAATTGAATTGCAGTA	59.033	21
231	2329	2559	ATGCAAATACGAATATCATTAT	58.103	26
106	175	280	TCAATCCAAAAAGACACATGC	59.615	22
113	238	350	TTTACATTGTATCTTGTCTTGCC	59.457	24
240	627	866	ATTACCTTGATCGACGACGC	60.103	20
120	1926	2045	CCTCCTCTCAGCCCTAGCTT	60.11	20
257	124	380	TAAATGGGCGGGAAAATAGG	60.963	20

242	1161	1402	AATTTCAGCACCCCCAAATC	61.053	20
121	287	407	ACCCTTGATTGTGTCGATCC	59.786	20
145	4778	4922	TGTAAACTGGTCGCCTCGTA	59.342	20
122	397	518	TAGTTGGGACAAAAATGCCC	59.801	20
194	108	301	AAGCTGTCCCTTGCAAAAAT	58.836	20
184	130	313	CATGTCAATATCATCACGAGTT	60.183	25
150	500	649	TTTTGGAGGGAAAACCACTG	59.942	20
169	65	233	GGGCTGTGATGGGTTGTTAG	60.375	20
112	1749	1860	CTCACTCTCGTCGCTTACCC	60.012	20
274	890	1163	GCTGAGCATATTTTTCACCCA	60.089	21
247	13	259	TGCATTGTTCGACGATGTAAC	59.605	21
174	9	182	TTAACACCAAACCATCTAATTA	57.486	27
149	123	271	GGTTACCGTCGTGGTTATGG	60.11	20
112	2	113	TGGCAGAAAGATTTTAGATATA	59.31	26
264	1121	1384	TAAGGCCTGGTCCTAAGCAA	59.839	20
228	20	247	CCGCTGCTATCTTTTATGGC	59.838	20
184	1787	1970	CAAAAATCAAAGGCCCACAT	59.801	20
215	837	1051	GGCAAGTTGAAGGAACAAGG	59.711	20
227	51	277	TTCCTCTCGTGTTTCATCCC	60.05	20
266	21	286	GGACAAAAGAAAAACCACGC	59.592	20
133	204	336	CCGAAAATCAAAGGCCTACA	60.067	20
268	5	272	GGCACAGAGAGTACATAGTTT	59.309	25
179	954	1132	TCATGCACAAGGTGGAATGT	59.967	20
169	204	372	AAAGGTGAGGGAGAGTGGGT	59.968	20
261	521	781	GAGTTTGTTGCAAATATCAGGT	59.957	25
261	635	895	ATTACGTCGATCCAACGGTC	59.82	20
106	777	882	ACAGTGGTGGCCGAAAATTA	60.365	20
216	74	289	CCCCAATCTCCGTTCTTCTT	60.434	20
234	506	739	TTGCTTGGGATTTTATTTTGA	57.337	21
264	8	271	ATTTGTATGGGTCATTGGACG	59.56	21
262	66	327	AAAGTTGAAGGATTTGGGGG	60.159	20
193	204	396	AGGAGCAAATTGAGGCTGTC	59.434	20
208	41	248	TCGGGACCTCTTTGTATCGT	59.55	20
260	226	485	GCGCATTTTCTGCTGTTAGA	59.21	20
130	19	148	AGTTCGATGTTGTAAGGGAGG	59.998	22
181	162	342	TCCACCGCTAATGAATGACA	60.073	20
104	92	195	AGAGAGGGAGACAAAAGGCA	59.014	20
206	147	352	AAATGCATGCCGGGATATAA	60.137	20
248	36	283	CAGCCTCTCTGCCTTTTGTC	60.134	20
245	271	515	TCGGCTATATTAGCGATCCG	60.172	20
194	0	193	ATGAAGTTAGGAAATAAAGAG	57.239	26
270	123	392	TGTCACAAAGAGAGGGGGAG	60.229	20
242	778	1019	CTATTCCAACTTCGGGACCA	59.926	20
154	42	195	TTCAGAAATTGCCTTGGTTG	58.745	20
255	2724	2978	GGGAACCATCATGGAAATTG	59.991	20
132	70	201	TCGGAGCATGATTTAAGTGG	58.721	20
147	86	232	CCAATGCCAATCATCCTCTT	59.894	20
256	51	306	AAGGAAAAACATGAGTTTAGG	59.774	23
205	108	312	AATGCTGTTGCATTTCGATG	59.694	20
277	967	1243	CCAGATCCTTGTGGTTGGAC	60.363	20
117	101	217	GACCTTGCTCGCTGCTATCT	59.746	20
187	343	529	ATGGTCCCCTCTTCTTTGCT	60.074	20
114	170	283	CAACGATTTTGGTTTGTTCCT	58.983	21
196	5223	5418	ATTCTCCACCACCCCACATA	60.05	20
160	322	481	GAATGTTCCCCAATCCTCAA	59.727	20
242	523	764	AATTTGACCATTTGCCCAAC	59.668	20
207	93	299	CGTTGCCGGATAATTCAAAC	60.323	20
182	63	244	TTGCAGTAAATATCGGTTTTCG	59.173	22

273	197	469	GAGCTGATTTGTGATGTTTGGA	60.118	22
243	2630	2872	AGCCCTTCGAACAACAAAAA	59.724	20
216	19	234	TCCACTGTTTTGTGCCATTT	59.024	20
104	865	968	GTGGAAAAGGAGCAAATGGA	60.051	20
269	709	977	GATGGAATTGGGTGTTGGAT	59.464	20
268	355	622	TTGGCATTCAAATCAACCAC	59.375	20
267	40	306	ACAAGATCGAACGGAACGAG	60.255	20
120	19	138	AAAATTCGAAAATTCCCCAAA	59.659	21
238	66	303	GCAGTGGCCAATGAAATTAAA	59.957	21
226	270	495	ACTCAATCTGATGCACACTCAA	58.371	22
139	218	356	TTTTAATCTTGGCCGCTGAT	59.682	20
193	51	243	TAATTTTCGTCGGGATGGTT	59.273	20
220	0	219	TCTTTCTCGACGTTTCCTGC	60.517	20
269	914	1182	TCAAATTTTGCGTAGCATCTC	58.057	21
237	30	266	TCATGAATCTGACTTCGATTAT	59.533	25
112	865	976	CAATTGGTGCAAGAAGACGA	59.84	20
239	110	348	CTTGGGCTAAAATCCCAACA	59.931	20
280	357	636	AAATACCAGGCAAAAATGCG	59.964	20
149	1833	1981	CAAAAACCGGTGAAAAATCG	60.327	20
261	170	430	GTTGGGGTTGGCAATAAAAA	59.677	20
215	748	962	TCTTGGTAAATGTTTGGGCAG	59.982	21
171	1245	1415	TTACGCTAGTCCGTGGGTTT	59.632	20
179	62	240	CTTCCGGTCTTTTTCCCTTT	59.566	20
249	2	250	CTCTCTCCCTCTCCCACACA	60.388	20
188	1304	1491	ATAGAGCCCCACGTTCACAG	60.134	20
221	168	388	AGGGTGCCAAGATTAACACG	59.993	20
183	60	242	TCTTGATATTCGAACGGCCT	59.668	20
157	293	449	AAGCACACACACGCTCAGAC	60.104	20
277	1444	1720	AGCATTTGATTAATCCCCCA	59.23	20
189	275	463	CAAATTCAACAACAGCACGG	60.149	20
247	275	521	AGCAATGACTGTCCTGAGCC	60.418	20
270	943	1212	GAGAGGAGACGCCATTTTTG	59.813	20
272	646	917	CTGATTGTAAATGAATTGAGTC	59.569	25
219	387	605	CACCTCTACATGGTTCCGGT	59.844	20
143	58	200	GGTGCTTTGACTTATGTAAAGT	57.994	25
229	125	353	TGGAGATATGGTAGCGGTCC	59.917	20
108	15	122	TGTTTTCTGTTCTGGCGTCC	61.216	20
253	14	266	CGCGAGTTCATAACTCTCTCTC	58.37	22
268	34	301	TCAGCATACAGCAGTTTCATTT	57.599	22
207	896	1102	GAATAATGGGGGTGATGTGC	60.021	20
277	299	575	TCAAAGACATCCTGCCAACA	60.24	20
209	22	230	ATTCGGAGCGAGGCTAAGTT	60.36	20
268	1	268	GCTCAATTTCCCAACTCGTC	59.676	20
251	63	313	GCTTCCATTTCACTTGAATGTT	58.239	22
206	6209	6414	ATTGGGCCTATCAATGCAAG	59.923	20
225	655	879	AAGTGGTATAAACGGGCGTG	59.883	20
247	171	417	GCGTTTGAGAGGAATCATGG	60.603	20
157	0	156	GAATTAGCATACTGGCTCATTT	57.238	25
248	94	341	CGTTGAAGAGATTACGCAACA	58.978	21
138	4	141	AAAACGAATTTGGTGTTGGAA	59.348	21
275	548	822	CGGCCATCAGATATGGAGAT	59.877	20
153	3440	3592	GGTTCCGACATTTCAACCAC	60.218	20
107	8	114	ACAAACTAATCAAGTTCCGCA	57.439	21
241	117	357	CTTTTCACACGAGGTCACGA	59.873	20
221	450	670	ATTTTGGCACAGGATGATGC	60.874	20
222	925	1146	CGCGATTTTAAACCCTAAAGA	58.45	21
212	21	232	GAAATTTCATTATTTCGTCGTTA	57.054	25
235	105	339	ACCAAAGAAAAGTGCATTACA	59.169	24

263	745	1007	TGGGAAAATTGAAGAACATTT	58.963	22
257	1002	1258	TCCACCTTCTTCCACCACTC	60.088	20
217	68	284	CCTTTGATTTCTTGGTTCCG	59.541	20
258	866	1123	CTCATTTGATCAACAGGCGA	59.799	20
151	641	791	GTAATGAAATGGGCAGTGGG	60.192	20
277	269	545	CGACTTTTTCAAGCTGGGAG	59.986	20
127	671	797	TCCCGCGTCATAAAAAGAAG	60.202	20
267	1520	1786	CCTGAATTTCTTGGCCTGTC	59.67	20
232	40	271	AGGAAGAAGCGAGAAGGGAG	60.088	20
123	73	195	TATGCTCCTTTTGGTTTGGG	59.931	20
240	1571	1810	GGGCGCTTGTAGACTTTTCA	60.386	20
246	1939	2184	CAACACATTGCCACACCAA	59.987	19
217	111	327	TGCGTTGACGTACACAGCTT	60.517	20
237	312	548	AAATATGTCTCCTCCGGCCT	59.925	20
118	1856	1973	ATGATGTCAAGCCATCTCCC	59.893	20
206	230	435	CAGCTGTCGAATCTGCTCTG	59.88	20
259	1031	1289	CAAGCTCAACGAAAAAGCAA	59.226	20
275	117	391	GGGACATATTGCATTTGGTTG	60.067	21
275	3166	3440	AACGCGATATGGATGAAACC	59.791	20
182	8	189	GATATGAAGTGTCACAATATA	57.063	27
204	13	216	GCGAAGAAACATTCAGGGAA	60.192	20
264	57	320	CCGAGCTGGTGGACAAATA	59.658	19
247	47	293	ATCCATATGGCAACCCTCAG	59.773	20
206	2038	2243	TTTCTGGGTTACACCCCAAC	59.688	20
130	368	497	TGAAGGGTTGAAAAGATGTGG	59.956	21
184	10	193	GCGAAGCACCGAGACTACTG	61.136	20
260	94	353	CCTTCACGAGTGGTGACAAA	59.72	20
112	2403	2514	TCATTTCGGATGGAAGGAAC	59.871	20
125	0	124	GGCAAATCACATAGATATCAG	59.117	23
195	4491	4685	AACTGACGGGTGATCAAAGG	59.966	20
133	99	231	TTATGAGTTTGCTCCTGGGG	60.066	20
234	0	233	GGGACTCGACCACCTAACAG	59.574	20
181	740	920	AAAAAGCCTCAAACCATCAA	57.338	20
266	108	373	AACTTATGGCGTAGACGGAA	57.395	20
184	83	266	GTTCTCTGCCCAACTGCTCT	59.604	20
186	462	647	TGCGTTCGAGTTCAGAGTTG	60.175	20
148	1493	1640	TGCATAATTGTAGATAATGGA	60.114	24
269	162	430	GGCAGAGAAAGTTGTGCCTT	59.478	20
150	789	938	CGGATCGACACGATAAGGAT	59.917	20
105	494	598	GAAGCGGGATGAAGAATTGA	60.155	20
233	43	275	AAATATCGGCCGTCAGATTG	59.923	20
219	98	316	GTACGTCCCAGTCATCCACC	60.246	20
253	239	491	ACAGCGGTTGGATTTATTGC	59.967	20
225	20	244	TTTCTCTCTTGGTTGGTGAAGA	58.955	22
217	467	683	TGAAGCGCAAGTATTTTTCG	59.098	20
251	231	481	TATGGTGATCGGGTTTGACA	59.774	20
138	43	180	CAAAACTTCACGAAGAAAACA	59.34	23
101	5	105	AGAAACTTGACGTGTGCGTG	59.946	20
203	192	394	ATGCTTAAAAGAAAGCGGCA	59.985	20
175	2759	2933	CGGTGGATGTCTTGGTCTTT	59.966	20
162	69	230	GTGCTTCAACCGACCGTTAC	60.559	20
255	23	277	AGAGTTATTCAGCCCAGCCC	60.599	20
204	42	245	TCCAGTATACAATTCCAACAG	59.433	24
268	588	855	TAGTTTGTTTCCCGCCAAAA	60.46	20
134	1	134	ATGCGATTAGCAGACCAAGA	58.477	20
103	5	107	CCCATTATCAAAACCCACCA	60.418	20
278	11	288	AGGGGATTGTAACAGGGGAT	59.513	20
240	8	247	TGTTTTGTAATTTCCCATGTTT	58.816	23

274	44	317	GTGGTATCACATCACAACTTTT	58.93	24
240	1094	1333	CCGCTTTCTCATTTCTTCCA	60.323	20
235	469	703	TCCCTTAGATGTCTTCATCCCA	60.817	22
240	431	670	AAAAATGGTCCACATGTTGTA	58.335	23
152	109	260	CAAAGTGGAGAAGGCATGAA	58.847	20
272	86	357	ATGCTGCCCCTAAAACTTCC	60.451	20
279	445	723	ATGTGCTATCCTAACCAAAAG	57.49	22
275	24	298	GAAAAATCAAAGGCCCACAA	59.916	20
197	84	280	ATGAATTTTCTGCGAATGGG	59.901	20
240	61	300	GGGTGAATTTTTGGGGTCTT	60.032	20
190	2	191	ATTGCCCATGAATGTCACCT	60.203	20
266	370	635	CAATCGGCACACAAAAGCTA	59.872	20
130	0	129	CACAGAAGGAAAAGAGCGAG	59.743	21
269	41	309	AAACTAGGCATGGAATCCGA	59.528	20
210	0	209	CCACAAAGTTCCAATCTTTTA	59.215	23
245	2	246	TTACGGCATTAGAGATAATGA	57.643	26
161	135	295	TCTAACAGAATAGAGCTTGGG	57.663	22
220	398	617	ATGCGATTCCACGTCAAAAT	60.339	20
211	14	224	GGCCAATTCCGAACTTTCTC	60.94	20
224	5	228	TTTGAGCAGTTCCAATCTCTTG	59.494	22
146	596	741	TCTCGTACACGTGTCCAGTTTT	59.702	22
274	799	1072	AGGGTGGTATTTCGTGTCGT	59.333	20
279	41	319	GGGTCATCATGGGATCAAGT	59.593	20
232	90	321	CTTAAGCCGAAAATTCCACG	59.715	20
186	655	840	TGGTGATTGAAATGATTAGCA	59.002	23
189	906	1094	GATCGCATGTTCGAATTTCA	59.628	20
139	1047	1185	TCACAGGAGCTCAGGGACTT	59.986	20
221	14	234	TTTCATCTCACATGGCAAGC	59.805	20
246	397	642	CAATTCCTCCCTTGGAGACA	60.042	20
255	1025	1279	GGGTGCTGGTAAAGACTTGG	59.592	20
230	315	544	ACCTGTAACACCCACACACG	59.358	20
145	5421	5565	TGTTGCTTGTTTCTTGCACC	59.888	20
168	3	170	CGCTCGGATGCCATATAAAA	60.923	20
274	1977	2250	CAGAGACCGAAACCGGATAG	59.688	20
275	2458	2732	TAGGGGCCTGCTAAAATTCA	59.677	20
263	86	348	CGCTACATTTACGGATTGTGA	58.713	21
160	219	378	GCGAGAACCACAAAGCTCTC	60.142	20
279	402	680	CAATTGTTGCAAACAACCAAA	59.495	21
261	246	506	CGGTTGTTCCATCTCTAATCCT	59.482	22
274	40	313	GGCGTTTTAATCTCCCCACT	60.32	20
168	591	758	GTGTGTCGCTTTGATCCTCA	59.837	20
205	12	216	CCACATTTAAGGGTTATCACC	59.654	23
236	34	269	GCATGATCAATGTTGTAATAG	60.102	24
260	185	444	GCTAGAGCCCTTGATTTCCA	59.41	20
142	1983	2124	GAAATTAAGAATGTGGAGTGC	58.311	23
122	96	217	CCAAAGGTGAAAATCGCACT	60.11	20
278	65	342	TGAATTCAATTTATTTATTGTC	59.996	27
173	85	257	TTAATGCAACCGCATGTTTC	59.567	20
258	0	257	TTTTGCAGGATGGAACTCAT	58.145	20
274	828	1101	ATAACCCGGTCAACAAGCTG	59.993	20
275	1771	2045	CACGTGGAAGGACTGAAAGA	58.852	20
137	1059	1195	AATTGAGGGGCTTGAATGAA	59.505	20
103	19	121	TCCGGAGTAAGTTCGAGGAT	58.741	20
194	50	243	GTTTGAGGCGGTACAAAGGA	60.11	20
186	185	370	CAAAGGATGAAAACGAGGGA	60.044	20
271	0	270	TTGGGTTTGTGTTGCTTCAA	60.127	20
280	1492	1771	GCCGTAGAGCCCTGTATGAT	59.178	20
256	363	618	TCCTTTAGAGTCGTTGCACAA	59.92	22

178	3239	3416	GAAAGATCTGGTCACGACAGC	59.866	21
137	287	423	AGAGGGGGTATGATGGGAAC	60.015	20
280	105	384	TGATTTGGCAGTTTGAGAGGT	59.726	21
196	702	897	AACGTAAATGAGAAACATGCA	57.397	22
240	2194	2433	ATTTCGAGCCAGACACTGCT	60.02	20
239	523	761	TTCCCTACAAAACGAGACCAA	59.595	21
150	72	221	TTACGTAAAAACCCTTTCGCC	60.342	21
201	11	211	CTTTCCATGATCAGAACGGA	58.643	20
219	103	321	AATATGGAGATTTGCGCGAT	59.534	20
273	1011	1283	TGGGCAAATCAAATGTTCCT	60.309	20
101	3204	3304	GCAGAAGCGGGAACTAACTG	60.015	20
129	0	128	GGTGACAGGCAGCTGAATC	59.361	19
108	1250	1357	TTTGAACGAGGCGGATTTAG	60.202	20
258	448	705	TTTGACGGGGTAAAATAAAAC	59.66	23
244	48	291	AAAAACATCGCTCTCTCCCC	60.578	20
177	78	254	TGGAACAGTTTGACACAACCA	60.033	21
228	111	338	TCGTAGTCCCCTTCAGATCG	60.21	20
228	539	766	ATGCTTGAAGCTATGGGTGC	60.243	20
252	382	633	GCCCTACTTATGCCCCAAAT	60.171	20
162	3243	3404	ATCCCTCTACCGCCTTAGGA	60.053	20
147	4252	4398	CAAATTTCACCAAGAACGCA	59.706	20
204	3329	3532	CATGCATGTGGAGGAAAGAA	59.648	20
197	691	887	TTTCTGGACTAAATTGCCCG	60.067	20
164	522	685	GGGATAAATCATAGCCACGC	59.397	20
161	481	641	CTTATTTCAAAACGACCCCG	59.447	20
154	2504	2657	TTAACCATTTCGCTGTGCAA	60.251	20
142	132	273	CTCACACACCCATATGTCCC	58.643	20
110	489	598	AAATTGATTTCCCTCCACCC	59.996	20
119	896	1014	AACACATATGGGGACACGCT	60.263	20
135	3807	3941	CATGCGACGTATTGAGAAGC	59.449	20
277	1439	1715	ATGTTCTCTCAGGCCACCAC	60.12	20
239	136	374	CCCTCAGTAAAAGCCAATCG	59.702	20
139	1137	1275	AAATGTTGGCTTCGTATCGC	60.103	20
265	17	281	CAAGTCAACAAGCAAGCCAA	60.027	20
265	2433	2697	CCATCTCGAAAAGATGGGAA	60.006	20
141	356	496	AAGTGGCTAAAGATCGATGTG	58.861	22
255	504	758	ATTTCGAAGATCAACGGACG	60.074	20
186	30	215	TACAAGTGCAGCGGAAATGA	60.401	20
179	167	345	GGTTATGGTTCTTGATGGGG	59.101	20
173	70	242	GCGGTGGTGGAGAGAAAATA	60.074	20
278	687	964	TGCATCGGGGCAATATTTA	59.867	19
131	570	700	CACACGCGCATATCAGTTTC	60.288	20
179	86	264	AACGATAAGGTGGCGATGAG	60.096	20
261	43	303	TGCTCTCACAGTCACCCTCA	60.614	20
260	87	346	CCTCCACAAATGGTGACAAA	59.389	20
260	579	838	ACGACGACATTAGACCACCC	59.851	20
165	80	244	TGGTTGTCACATCTTCATGC	58.019	20
140	1804	1943	GTCAATGTGGGTGCTGTGTC	60.013	20
217	1327	1543	GTGCATGGTCTTCGAAGTAGG	59.749	21
207	108	314	TCGCATGCAACGATAGTAGG	59.856	20
179	92	270	TCAACGTCTTCAACGCAAAG	60.027	20
189	466	654	CACTTCACCGCCAAAACTCT	60.291	20
265	150	414	GTGATACATAGTGTTATTCTTT	60.197	26
209	26	234	GGATCTATTACTAACCGCCCC	58.856	21
271	583	853	TATCAGGCTGCCTACTCGGT	59.859	20
184	630	813	GCAGGACAACTACCATACGGA	60.008	21
277	1370	1646	CGGAATATCAACTCGGAAGC	59.668	20
238	1564	1801	AGATTGAGGCGTGTTTAGGC	59.34	20

218	2310	2527	AGAGACCAAAATCCCAGGCT	60.074	20
177	417	593	AAGCAAACCCATGTTCTTCAG	59.228	21
263	4427	4689	TGTTAAGCATCCCCATCTCC	59.894	20
227	22	248	AATCTCGCATCCCAATTCTG	60.036	20
160	331	490	AGCAATGAACAACACGCAAC	59.77	20
255	3	257	AAATGCGCCTATCACTTTAATT	58.77	23
213	585	797	CCCAAACTTGGTTGCTCTTC	59.711	20
134	2022	2155	GCTATGAATGGCATCGAAGA	58.823	20
267	174	440	AACTTTTGTACTCAGCCCTGC	58.525	21
201	2273	2473	TGGTTCCCAAAATAACCGTC	59.662	20
212	8	219	CTGACATTCACAGGCATTGT	57.067	20
239	100	338	GCCCCTTTGAGCCTAAGGTA	60.573	20
240	43	282	TCCTCAGAAACTTCAACGCTT	59.111	21
216	257	472	CCGGAGCTAGGCTTTTGAGT	60.884	20
127	0	126	GTCGTTTACTCTTTCCGGCT	58.462	20
213	556	768	TGAAATGGATCACATGCAAA	58.464	20
252	75	326	TGACGAAAATTGCTTTGATCC	60.067	21
240	954	1193	ACCCAAAACCTCCCATATCC	59.881	20
206	19	224	AGATTGGGCTATTCGAGCCT	60.194	20
243	45	287	GTGGATGACGGTTGTGTTCA	60.426	20
217	1469	1685	GCAGTTTTGTGTGTCCATGTG	60.064	21
231	68	298	GGGGGCCTAAGTTAGATTGG	59.793	20
273	0	272	CCTTTCGAATTTTTCCTCTTTTG	60.423	23
279	1320	1598	GATCCTTCCTAGGATAACCGA	58.603	22
254	0	253	GCGTGTGTGTAACCGTGTGT	60.556	20
134	834	967	TCGAGGAGCTGTCATCCAAT	60.769	20
111	783	893	ACTACGTCGATCCAACGGTC	59.997	20
176	179	354	CAAGATCCGGCTCGGTATAA	60.053	20
200	1399	1598	ACACAATCCATCTTCAACCCA	60.225	21
181	4638	4818	CCCAAATGATTGTACGGGTC	60.051	20
280	124	403	TTAAAGTGCGGCCAAACG	60.775	18
165	650	814	ATCCCCGGAGATTCTTTCAG	60.401	20
203	606	808	AAGTTGGGCCTCTCGATCAT	60.99	20
258	33	290	ACGAAACACGGAAAAAGCAT	59.615	20
271	434	704	AATGATGATGCCAATCCAGC	60.843	20
231	79	309	TGGCCGAGAGGATTTACAAG	60.206	20
193	149	341	CGCAGCAAAGTAGCATACGA	60.177	20
175	19	193	TTTAGTGTTTTGACATGATTAC	57.557	25
245	252	496	ATACATGCGTGTGGGAGTTG	59.445	20
103	37	139	ATGAACTAATCAAGTTCCGCA	57.379	21
188	3269	3456	GTGCAGGGGATTGGTTAGAA	59.933	20
234	80	313	AAATTTCCCGATAGGCTTGAA	59.922	21
112	36	147	TGGCCCTGCTCATTTTTATT	59.547	20
279	737	1015	CGTGAAGTCCATCTCCCACT	60.112	20
152	278	429	ATTAATAAAATTTGGAATGATA	57.111	27
240	29	268	AAACTACCCTTGATCGCACG	60.132	20
247	277	523	AACTTGGGGGTAACGAGTGA	59.449	20
129	3	131	TGAAGTTAGGAATTAAGGAGG	57.525	24
268	5193	5460	CTTCCTCACGAATAAACCAAG	60.129	22
119	757	875	CGCATGGAAATATACAGAAC	59.985	22
189	34	222	TTTGACTATGTCTGCGTGCC	59.871	20
235	1247	1481	CAAAGCCACTCTAAGCGTATC	59.558	22
161	1963	2123	TCGAGTTGTACCGACACTGC	59.905	20
245	696	940	TGAAAACTGCAGCACGAGAT	59.596	20
224	369	592	TTTCACAAGTGCAAGCACAA	59.044	20
239	171	409	ACTCGTCTCAAGAAGGTGCTT	59.569	22
231	642	872	AGCGCTGAATGTCATTGGAT	60.634	20
273	352	624	ATCCAACGGATGTTGTTGGT	60.096	20

192	1186	1377	TTGATGGCTGTGAATTGGAG	59.648	20
185	17	201	CCCTAGCTTTGCCCTCTTTC	60.332	20
165	1300	1464	AAGTAAGCGAGATTTTCTACA	59.362	26
184	9	192	TGATATCTTTGAAGAACAATT	57.905	27
239	4924	5162	CCTCCAATTGCTTTCTCCAA	60.184	20
256	1038	1293	GGAACAAAAACGGCAAAGTT	59.111	20
266	2	267	TGATGATGAGATTTTAGTCCA	59.502	24
163	2868	3030	CCTTCTCCGTCTGCAAACTC	59.989	20
249	65	313	GTTGCACAGCCCTAATGCTA	58.945	20
207	586	792	TAGATCTGGGCAATGTGTGG	59.522	20
277	28	304	GAGCTGGTTTGAGGGAGATG	59.803	20
105	18	122	ACCAATTTACTAATTCTTGATG	59.206	27
241	1349	1589	ATCTCATATTGCCACACCCG	60.744	20
172	51	222	AATTTTTGTAAGGGGGTGGG	59.918	20
280	43	322	CGCATCCGACTCCTCAATTA	61.129	20
229	1225	1453	TGATGTACCCGAAAGGTTGA	58.973	20
183	84	266	GGGGACAGATTGTGGTTCAT	59.636	20
176	84	259	AGGGATCCCAAGGCACTACT	59.957	20
101	129	229	TGCATGCTGATGATTGTGTG	60.282	20
234	70	303	ATGATCGCCACAAACATCAA	59.931	20
196	506	701	CCATCAACCTCACCACCTG	59.938	19
208	22	229	AGTGGTGGTGGAGAAAACTG	59.607	21
220	8	227	CCTCAACACCAAAGCTTGAA	58.897	20
165	223	387	GGGGTAAGACCCACCTCATT	60.052	20
280	33	312	AGCAGCCCACAATTCAACAT	60.526	20
143	787	929	ACTCGGCAAAACTGAAATCG	60.249	20
191	1006	1196	GGACGCTGACCATCACTGTA	59.707	20
208	119	326	TCAACATTTTTCCCAGAATCG	59.924	21
178	598	775	ATCATCAGTAGCGCCACCTT	59.723	20
270	481	750	TCAAATTCGAAATTCGGACC	59.878	20
135	64	198	AAAATCAAAGGCCCACAATG	59.801	20
219	299	517	TACGTTCTTCCCCGTTTTTG	59.968	20
143	121	263	TGGTTGGAGTTGTCAGTTCCT	59.607	21
214	471	684	CGAAACCCCTTTCTCTCTCC	60.183	20
195	105	299	TTTCCCTCTCCTTCTCCCTC	59.749	20
182	63	244	GGGGTGTATTAAAATAGGAGC	57.616	23
180	2622	2801	CCATGGTGGGCTAAGTTCAG	60.508	20
200	420	619	TCTCTCCTCTGCACCAACCT	59.986	20
151	551	701	GGCATGAAATATCATCCGAGA	59.877	21
126	30	155	CCAAAATAGATGGCATTCAAG	59.078	22
240	43	282	TGGAAGTTCTCTCCTCTCGC	59.679	20
181	301	481	TCGTGGGCGTAAATCATGT	59.94	19
226	37	262	GGTTATGACTTGATCATGACC	59.231	23
185	70	254	CGAACTAAAGAAATAGGGGC	60.095	21
173	127	299	TGGCGTATGCTGAGAGATGA	60.526	20
150	341	490	TCTCTTTCGTCCTTTTTCCC	58.359	20
130	65	194	TTCCCGAGTAAGATGGATGG	59.887	20
119	222	340	TTAACCCTAGCCCCCTCTTC	59.549	20
278	15	292	GAACACACGAAGATTGGGAG	60.104	21
164	548	711	CAAATACGACGGAAAATCGG	60.315	20
153	31	183	TGAAATCTTACTACTCCAAAA	58.36	27
106	256	361	TCTTTCGGCTGACTTTTTCTTT	59.539	22
271	133	403	AAGATCTACGTCCACGGGAG	59.162	20
277	281	557	TGACTGCCCAAGAAATCACA	60.24	20
190	861	1050	TTCCACCACGAACATTCATC	59.348	20
256	1554	1809	TTCAAGAAAACAGAAAGCCAC	59.898	22
177	10	186	CGGATTTAAGGGTTATTACCTC	58.81	24
276	43	318	CGCATTTCCATACATTTTTACG	59.407	22

273	452	724	TTTGCCGACCTTATCTCCAC	60.074	20
268	427	694	ATGGCTTCAGCAGACAATGA	59.399	20
164	74	237	AACGAGATCGAAGGGAGACA	59.803	20
222	393	614	ATCACGATGCGTCACAAGTT	59.169	20
228	3301	3528	TGTTTGGTAGCCCACACAAT	58.9	20
182	120	301	GCGTCGTCATTTTCAGATCC	60.613	20
231	1310	1540	TCAGATGAGTTGAATGGAACA	59.726	23
272	587	858	CACTCGCATAAGTATGCATGA	60.164	23
133	468	600	CACTCACACACACGCACTTG	59.976	20
156	26	181	GCTTGAGCTCGGAGTTCTTC	59.313	20
249	207	455	TTTCAAATTGCATCCTAGCAA	59.732	22
272	119	390	GGAGAGTGGAGGCCATTTCT	60.596	20
175	449	623	CCTGCCCTAATTCTGGAAAA	59.155	20
280	135	414	TGCGTCAAAAGCTCTTCAAA	59.729	20
174	62	235	TCCAGATTTGTTCCTACGCA	59.272	20
249	62	310	TCCCCTCAAGATTTCTCCAA	59.6	20
277	532	808	AGAAATTGAGCTGGGCTACG	59.476	20
104	4	107	GGGAGAAGAGAGAGTTAGGG	60.246	23
174	134	307	TGGAGCTTTGATCCTTGCTT	59.955	20
153	0	152	AACCACCTTTACAAATGAGCT	57.599	24
209	30	238	TCACTTCATTACGAAAAACAC	59.544	23
250	2231	2480	GTGTGTCATCTAGTCCGGTGG	60.438	21
256	2251	2506	TCCATTTCCTCCACCGTTAG	59.926	20
137	1263	1399	CGGTAATTCACCGACCAAAC	60.227	20
187	110	296	AAGTCATCCGCTATCTCGAA	57.515	20
206	79	284	TTTTCATTCTTGACCCCTTCTC	59.571	22
130	14	143	AAGCTGCATGCATTTCAGAG	59.178	20
275	44	318	GCGCCGCCTATCACTTTAAT	61.434	20
265	681	945	GCGACGAACGGAAAAAGTAA	60.244	20
245	28	272	CCACATTTTTCCCGATTGTT	59.662	20
191	1248	1438	AATGAGCAAAACGGTCCTTG	60.11	20
210	24	233	AACAAAAAGGGATGAGCGAC	59.174	20
147	91	237	TGTTTCCCATTTTCACCACA	59.792	20
253	25	277	AGATAATGCCACCCAAACCC	60.94	20
246	45	290	TCTGCAAATGTCACACGTCA	59.868	20
182	1074	1255	CCAAGAGGAGTTGAAGTCGC	59.989	20
139	387	525	TTCCACAGACGACACACACA	59.737	20
203	137	339	ACGTGGTCTCTCCCCTTTTT	59.972	20
252	1199	1450	CTGCTACCAACTGCAAAGCA	60.195	20
185	90	274	CATTCAAGGGGCATTTTTGT	59.801	20
149	353	501	AGTAAACGGCCAAAGTGCTC	59.383	20
119	7	125	CCCCCGAAATCTTACTTTGC	60.792	20
176	1434	1609	CATCAAGTTTCCCAAGGCAT	59.933	20
237	1	237	TGGTTGGTGGAAGAAATCAA	58.947	20
248	608	855	TTAAATACGACCGGGCTCAC	59.96	20
201	1919	2119	AAGATGATCTCCCACATGCC	59.893	20
144	61	204	AGGGGTTATCACCTGAATGC	58.864	20
231	8	238	TGTTATCCTTTGTGAGCCCC	59.933	20
235	764	998	TCCATGTTCGTCATCACCAT	59.769	20
249	22	270	CTGACATTTGACCTGAGCGA	59.984	20
104	48	151	TTGGAAAATAACATGCATAGA	57.857	24
241	244	484	TCTGGTTCCGGTTCCAATAG	59.926	20
182	426	607	TAACTCCAGCCACTCTTCCC	59.284	20
146	465	610	CACTAGCAGGTCGACACGAA	60.049	20
207	406	612	TTCATCTCAAATTTCATTGTGG	59.442	23
183	2598	2780	TCGTATAGCTTTCCCCCACA	60.46	20
203	285	487	CGAATGAAATTATTTGTTTTCC	59.656	24
168	127	294	CCCAATCCTTGGACATTTTG	60.162	20

166	454	619	CCAAGTTGGTGAAGTAGGCAG	59.782	21
210	507	716	TAAAAACACAGCCTCCCTGC	60.249	20
203	134	336	CGTCGTTTCGTGTTCTTTCA	59.881	20
234	207	440	CATGGTTGGGTGTTTTTATCA	58.254	21
267	26	292	GTTGATCCAAGGGTGTATAAT	59.493	23
210	372	581	CGCTCAGGTTTGAATCTGTTT	59.369	21
250	1109	1358	CATGGTTGCAAAGGTGATTG	59.964	20
200	2012	2211	TCCCACAGTCATCACTTCCA	60.088	20
219	4938	5156	TGGACCGCGTTTATGGTATT	60.209	20
130	468	597	GAATGTCATGAGTTGAGGCG	59.245	20
188	462	649	AAACTCCCGCTCAAATAGCA	59.845	20
180	1587	1766	TCTGTTTGCGAAATTTGTTGA	59.335	21
280	105	384	GTTTCGGACTAAACTGGCGG	61.895	20
235	847	1081	AGATTGGGCTATTCGAGCCT	60.194	20
244	221	464	ACTTTTGCGTCCTTTGTCGT	59.78	20
106	24	129	ATGAGTTATCACCGGATCGC	59.923	20
264	54	317	TGCTACGGTTTCTTCTTCCG	60.378	20
160	2970	3129	ACGATCGCCCACTTATTGAG	60.096	20
234	20	253	AGCTTGTAGAACGAGCCGAG	59.78	20
124	2844	2967	TTGGCTCAAAGCATGAACAA	60.379	20
171	195	365	AATTGCTGGCAAATCGTAGC	60.238	20
163	302	464	TGAAGCAATCAAAAACGGTG	59.706	20
113	615	727	ATTGTGACCGTGAACCCAGT	60.284	20
215	11	225	TGATTGTAATTCTCTGCACCAG	60.028	24
116	19	134	AAAAACTGTAGTGGGTTAAAA	57.487	25
270	46	315	TGTGACGAGCTTATGAAACTAT	59.767	25
221	1	221	TATTAACCCTTCATTGTTTTTAA	57.085	26
216	18	233	ACAAATGAGCATGAGGGAGG	60.073	20
202	31	232	GTTATGCGTTTTGACGGGAT	59.829	20
280	5	284	TTGATTCCTCCCCACAATTC	59.727	20
255	451	705	GAATTGAGGATGTGGGATCG	60.281	20
260	3987	4246	ACAGAAGCAAGATTCGACCAA	59.867	21
241	96	336	TAATTGATAAGCGGCCCAAA	60.405	20
206	994	1199	CTTGGGATGGGGGAGTATTT	60.011	20
186	397	582	CCCAGTATCCCAAACTCGAA	59.926	20
246	970	1215	TGCTTTTCCATGGTGACTGA	60.24	20
264	1949	2212	TGAGAACCAAACACAAATGTC	59.928	23
278	805	1082	AAAGCCAGATTCATTTTGCC	59.162	20
205	252	456	ATTGGCAAATGCAGGTTGTT	60.374	20
270	166	435	AACGCACCAATTTCCTTCAA	60.481	20
280	215	494	TTTTGACATGATCACACCCCT	60.225	21
261	18	278	CCGACTGGGCCTATCCTATC	60.807	20
278	49	326	AGCCTTCTAGCTTCTCTTGCTTT	59.514	23
279	524	802	ATGCGTGCATAATTGCCTCT	60.636	20
148	120	267	TGTTTAAATGCACACCCCTTT	59.37	21
227	1758	1984	ATCGAACCGTTTTTCTGTCG	60.11	20
269	0	268	GCCTTCTAGCATCTCTTGCTC	58.451	21
142	14	155	CACTCAATTCATTTCACCTCCA	59.971	22
169	97	265	TCTCTCCACCAAATGTCCAA	59.059	20
237	60	296	GCGGCACACGAGGTATAAA	59.703	19
238	251	488	TTTGTGGTATCAGAGCCACG	59.716	20
132	6	137	TCTTTTGCTATGTCCTCACTCG	59.517	22
121	34	154	AGGGAGGCAAAAAGAGGTTG	60.601	20
219	44	262	TGGGATATAGCGAGTTTGGTG	59.967	21
120	91	210	GCTCAGCATACACGAAGGGT	60.285	20
105	1639	1743	TGCGTGTGAGTGTGTGTCAG	60.593	20
193	1293	1485	TTCATCGAAAAATGAGCCCT	59.645	20
278	1344	1621	TGGGATGAAAATAGGGGAAA	60.13	21

139	14	152	GAGGTTTTGACGGGATTTAGG	59.822	21
272	1	272	GGGGGATCAAATCTAGTCTTTT	57.666	22
279	222	500	CCACAAATCAATCACAGCCTT	59.985	21
180	2551	2730	GCATAGTGCTCCAAAAAGGC	59.851	20
199	50	248	TTTCTCGCCATCTCTCCCTA	59.91	20
147	45	191	TCTAGCATCTCTTGCTCTCTCG	59.125	22
179	418	596	CGTCTTCGTTCTCCGTCTTC	59.989	20
240	16	255	TTTCTCACTATAAGGTGGTGTT	59.509	25
189	1267	1455	GTCGTATTTGACGGCGAGAT	60.103	20
239	233	471	ATTGAATCTACGTCCACGGG	59.813	20
198	414	611	GCCAGCTTTTTCTTCTCCAA	59.569	20
126	82	207	CCCTTTACCTCACTGGTGGA	59.959	20
200	334	533	TCACCCCCATCTTCTCTCAC	60.048	20
271	1002	1272	CAGGTTCTCATCGCTCTGTG	59.571	20
260	808	1067	CATGGTGATAGAGCCGGATT	59.917	20
200	9	208	CTTCTCGTGTCCGACTCCTC	59.986	20
244	15	258	GGGCGAAGAGAAATGTGAAA	60.192	20
183	542	724	AAAATATGGGGTTTTCCCAA	58.15	20
262	4675	4936	ATTTCCAGCCTTGGCTTCTT	60.208	20
118	171	288	CTGAACCCAAGACCTCAAGC	59.844	20
164	1271	1434	TGTTGAAATCTTGAACGGGTC	59.963	21
280	84	363	AAAAACGCGAATTTTTAGGG	58.308	20
228	6	233	GCGTGCACCTGATTACACAC	60.192	20
241	960	1200	GCACTGAGCAGAAAAGGGAA	60.517	20
154	23	176	ATCGGTTATTACCGGATCGC	61.031	20
270	67	336	CACATTCAGTGGGAGCAGAA	59.831	20
245	127	371	TCCCCTAATTCCCTCATTCA	59.315	20
238	558	795	GGTGAAACTTGAACAACCCC	59.284	20
106	959	1064	ATCTGGAACAAGGTGGTGGA	60.363	20
185	329	513	GAGACGAGGGACAGAGCAAG	60.135	20
272	1480	1751	GCTCCCCTTGTGACACTGTT	60.159	20
259	304	562	TCCATCAGACAGTTTCTTGCAT	59.74	22
266	92	357	CTTTATGTTTTTCCCTGCGG	59.581	20
266	429	694	GGATCTTCATCCAATTCAGCA	60.029	21
250	240	489	TGGAATAGGGTTTTCAGGGTT	59.69	21
280	130	409	CAAAGCGATAGGCAAAAGGA	60.335	20
192	1226	1417	CTTAGGTTGAACGATTCGGG	59.564	20
208	4	211	CCCTTGAGAGTTTCACCACC	59.549	20
207	502	708	TTAATTTCCCGGTGGACTCA	60.301	20
108	279	386	TTTTGCTCGAGGGTTTTGTT	59.724	20
253	876	1128	ATGCAACCCTCCCTTTCTCT	60.074	20
224	0	223	GACCTACAGACCGATCATGAA	59.056	22
279	4	282	TGCTCACATCTCTTTTTCTCTTT	59.952	25
278	40	317	ATGCCTTATAAGCTCGAGAAA	58.666	23
152	488	639	TGAGCCCAATTTAGTCAGCC	60.214	20
137	1309	1445	CATCGCATTGACACATAATCG	59.968	21
250	1200	1449	TAGCCGTTTATGACCGTTGA	59.182	20
227	1431	1657	TTTTGGGATGGACCAAGTTT	59.264	20
251	1904	2154	CGATTCTCCTTGTTTCTCCG	59.807	20
164	2303	2466	CGATGCTTTAAAAGATGTCAA	60.017	23
266	66	331	GAAAGAAATAGAGCTGCTGG	57.913	22
280	112	391	TCGTCCTGGTTGTTCCAAA	60.072	19
275	1009	1283	CGACTTGGCTCCATGTTGTTA	61.064	21
104	2147	2250	TGGTTTGTCTGCATCCAGTG	60.722	20
169	58	226	GAATTCGGATTCGAGTCATAT	57.681	24
280	504	783	GTCCACCCCCTTTGAAACTT	60.204	20
120	11	130	GAAGCTTCAATGGAGGTGATT	60.081	22
278	687	964	TCGGAATTGGATTATGTTGCT	59.424	21

179	63	241	ACCCTCGAATGCTATGACCA	60.483	20
217	204	420	ATTTGGGTCAAACCCCTTTT	59.549	20
159	409	567	ACACATCTTGCAACCCACAG	59.597	20
275	19	293	CCAATTTGAATGGTTATCACCT	60.457	23
275	693	967	GAGGCTTAAAGCTGTGCTGG	60.154	20
255	11	265	TAAATGTGGCGAATGCTGAG	59.833	20
236	3	238	TCCATCATCATAGGCGTCAC	59.482	20
195	259	453	CTCCATCATCCTCTCTCCCA	60.152	20
268	1528	1795	GCGAAGTATTTCGTCGTGAT	57.848	20
201	193	393	TTGATGCTACCCACTTGCTCT	59.89	21
201	78	278	AGCGTATGGGTAGAGCGAGA	60	20
227	1029	1255	GAAGAAGCCGACAATTTGCT	59.457	20
177	572	748	CCCCATCTCGGATCTCTACA	60.027	20
187	1210	1396	AATTTTTGTAAGGGGGTGGG	59.918	20
247	862	1108	CGACTCCATTTGGGTTTTGT	59.83	20
199	324	522	CAGATCTTGGCAACTCCCTC	59.803	20
268	2805	3072	CGAAGAATCCGAATGGAGAA	60.148	20
270	547	816	TGGACCGGTTAGATCGGATA	60.288	20
258	712	969	CATCCCCACCGTGGTATTTA	60.439	20
243	1470	1712	ACCGTTTGTGAAAAGAACGC	60.154	20
274	200	473	TCATTTTTCTTGTAGCGTATTAC	58.583	26
204	218	421	CAGTCGTTCATCCCCTTTGT	59.966	20
242	8	249	AGCCACTGTGACAACACATAT	57.601	22
182	69	250	GACTGTAATGCATGGCTGGA	59.679	20
260	2294	2553	TTTGGAGGGGGTTGAAAAAT	60.514	20
183	28	210	TGATGCTGAAATCGTGGAAA	60.197	20
225	500	724	ATCTCGTTGAGGATGCTTGC	60.37	20
232	2201	2432	CCCTCACTGGCTCACACTCT	60.458	20
152	41	192	TGAAAAGCGGTTGTGTGAAC	59.74	20
263	218	480	TTTACGAAAATGCCACCACC	60.732	20
127	80	206	AGCATCTCTCCATCACTCTCA	57.528	21
271	4	274	TTCGAACCTGGTTTTCGTTC	60.088	20
157	9	165	AATACCTTGATGTGGTGGTGC	59.732	21
206	1331	1536	AAAACTCCCAATTTCCACCA	59.264	20
121	760	880	TCCCCTAGTCTAAGCCGAAAA	60.203	21
276	96	371	TGGTGGAGAGAGACCATGAA	59.18	20
116	4325	4440	TTCGCTTTTGCTTTTGCTTT	60.13	20
238	87	324	AAACTCTGGCTGCTGGTGAT	59.874	20
240	873	1112	TCACCTTTTCCCTCTTCCCT	60.045	20
151	672	822	ACTCCCATCCGAGGTCCTAA	60.842	20
165	2263	2427	TTTGGTGACTGAAAGGTCCC	59.943	20
145	1902	2046	GCAGCAACAATGATGGAGTG	60.272	20
213	27	239	AGCAAAGAAGGAATGCAACC	59.316	20
279	98	376	TCGAAGAGAGAACGGTTCAAA	59.978	21
276	78	353	CCCCGGAGCTTCATAACTAA	59.178	20
167	1336	1502	CAGATCTGATGGCCCAGATT	60.034	20
254	1737	1990	CGTGTTCCTAATCCCCATGT	59.67	20
108	524	631	TTTTACGGGCAACGTACTCC	59.996	20
221	57	277	AGCTATAAGATTGACTAGATCA	57.118	26
277	255	531	CTCGCGTCAGACTCCTCACT	60.757	20
113	487	599	ACTGATGGGGTTCAGGAAGA	59.505	20
192	923	1114	AGCCGTTGATCATTACCTCG	60.096	20
182	191	372	GCATTAGCAACTGCCCTTTC	59.851	20
126	35	160	ACACGAGAGGTTTGGGAGAA	59.697	20
160	1281	1440	TACGGTGAAAATGGATCTTGG	59.809	21
123	217	339	GCTCACCTGGATGATAGCCT	59.268	20
166	278	443	AACGGCGCGACAGTTATAGA	60.792	20
157	430	586	TGCATGAGCACTAATGAGCC	59.979	20

241	680	920	GGAAAAATGGTGATGTGGCT	59.797	20
266	1209	1474	AAGTGCCGTAGCCACAAAAA	60.669	20
192	278	469	CACCGAATGCTGTGACTTGT	59.751	20
141	186	326	AACCGTGATGGTTGGGATTA	60.051	20
162	671	832	CGGGATCTTCCTCAACTCTG	59.797	20
185	229	413	TGATGCGTTTTGGCATAAGA	60.215	20
251	1325	1575	ATGGGATAGTACCGGAACGC	61.091	20
165	385	549	CGCACACACGAACTAACACA	59.373	20
276	54	329	CTTTTGGATCGACCCATCTT	58.981	20
187	504	690	TGGCACACAGGTGAATGAGT	60.162	20
169	673	841	AATCATCCAATTTGCTTGCC	59.907	20
185	74	258	CCACGTAAAATTCCGGTGTC	60.227	20
255	6044	6298	TGGAGATCATTTCAGGCACA	60.201	20
268	452	719	CCATTTTGGTATTTGCCCTG	60.181	20
236	487	722	AACCAACTAAGGGGGTCAAA	58.41	20
182	216	397	CTAGCCCTCGTGATCAGTCC	59.827	20
224	67	290	TCATTTCACCCATGAGCTTT	58.145	20
240	1019	1258	TCCAACTCTTCACACTCCCC	60.088	20
156	59	214	TCATACACGATGGGATCGAA	59.883	20
225	2706	2930	AACGTCAAGTATTCCGCCAC	60	20
228	235	462	TCCGCGAGAGAATTAAGGAA	59.916	20
238	1428	1665	TGACATGGAAGGAAAAAGGG	59.903	20
217	34	250	TCTCCAAATTTGAGGGTTATC	58.556	22
236	16	251	ACAAATGGCCAAGAGAGTTA	60.048	23
160	100	259	GCATCAGAGCCGAGGTTAGA	60.504	20
275	17	291	CGGTTATTACCGGATCGCT	59.93	19
266	44	309	TACAAATGGCCAAGGGAGTT	59.429	20
143	1236	1378	GGGGAAGCGGTTATTTTTGT	60.184	20
220	230	449	CAGAAATGACATCACCACGC	60.12	20
189	2	190	TCAAACAACTAGATTAGTCCA	57.952	27
192	3373	3564	ACAGCAGGTTTTTGGTGGAA	60.529	20
146	3182	3327	GGGATGTTGTCTTCGACTGAA	60.104	21
232	48	279	TTACAATGGCAAGAGAGTTGC	59.044	22
242	400	641	ATTCGTATACTGTTCGCCGC	60.124	20
210	1348	1557	CACTCCGCTCTCATTCCTTC	59.95	20
252	57	308	TCTCTTCAATAAGGTAACAAC	58.381	25
238	563	800	GGGTGTGGAAGCAAAGAAAA	60.088	20
131	782	912	ATTCAACATGATGGTGCCAA	59.781	20
154	67	220	CAAAATTAAAAGTGTTCCATC	58.829	23
279	4276	4554	ATGGCTGCTTAAATTGTGGC	60.103	20
161	828	988	ATGGCCACAAATGGTTCCTA	60.192	20
251	82	332	ATGATAGCATTCAAGGGGCA	60.435	20
248	281	528	AATGATCGTTGGAAAGCCAG	60.074	20
209	1231	1439	CGAGATTTGACACGCAAGATT	60.264	21
234	661	894	GCGACCCATTCTTGATTTTC	59.51	20
263	2013	2275	CCAGTATTTGAGAGATGGGCA	60.081	21
266	38	303	GGTGTGGCTAAATTTGTTCG	58.147	20
239	92	330	CCCTATTCCCGTCAACACAC	60.232	20
273	102	374	GGGACGGAGGGAGTAGTTTC	59.935	20
246	158	403	GCGGAAATACTCTCGAAACG	59.845	20
208	80	287	ATTTCCTCGCATCTCACCAC	60.081	20
245	213	457	CCGTTAAATTACATGATTTTCC	59.56	24
242	1734	1975	AACCACGTTTTGGCTAGTTCA	59.663	21
256	830	1085	AAAAATGAAAATGGCCACCA	60.167	20
222	18	239	GTTCCTCGTGTTCCTCCTCA	60.238	20
199	78	276	GTGCGTGTGTATGCTGAGGT	59.783	20
234	104	337	GACAAGATCGTGCCAACAAA	59.697	20
183	1328	1510	ATGAGGGCTTTGTGAACGAC	60.119	20

211	309	519	ATGGCAAAAGGCATCAAAAG	60.074	20
208	1227	1434	CTTCACGCGCTCAATAAACA	60.014	20
125	0	124	TGGTAAGCAGATTGGTTTTAAT	58.41	25
139	1	139	TCAGATTTGTTATGTGTTTTGA	57.312	24
239	678	916	GCCCAGATATGGCTCGTTTA	60.06	20
260	59	318	CAACTTGGAACCCGATTCTC	59.526	20
193	1297	1489	TTGGTCTCCATCTTCCGTCT	59.655	20
195	386	580	CCATCTGAAAAATGCAACCA	59.518	20
139	281	419	AGGCCGTGTTCGTATTGTGT	60.44	20
280	373	652	ACTCATGTCACGGCACACAT	60.038	20
252	98	349	GCACACATAGAAAAGCTCCTC	60.27	22
276	19	294	GATTCGCACAAATGAACACG	60.119	20
222	3	224	TTGTCGATCAGCGGTTACAG	59.864	20
184	465	648	TCTTACCCTGCGAAAAATGC	60.209	20
258	140	397	TCGTGTTGGCGCTATTACAT	59.21	20
268	29	296	CCACTATTGATCCTGACGCC	60.483	20
244	193	436	TTGTTCGTATTTGGAAGTCGTG	60.032	22
235	9	243	TTCTCTATCTCTCTTGGTTGGT	59.411	24
197	11	207	TCCACCGCTTTAAATTGCTT	59.72	20
167	694	860	GCATGTCACGTGAGGAAGAA	59.837	20
245	2657	2901	AATGCAGTTCGGTTGGAGAT	59.556	20
269	118	386	TACTTGGTTGAGCTTGGCG	59.996	19
205	203	407	TCACGGAATTACTAAGCCCC	59.043	20
103	5	107	TCTTCCGATCTCAGTTTTTCA	57.533	21
249	538	786	AACAAGCTGGGTTTCTGCAC	60.299	20
221	409	629	GCCTGCAAGAAAGCAATCTC	60.103	20
261	16	276	TCATACTCACTCTCACTAGCCC	60.956	23
232	23	254	TGAAGGTTGGAGGAATGGAG	60.042	20
235	207	441	GATCTTTTCACTCGAGCCCA	60.34	20
209	3	211	TTGCATTGCAGCAGTAGAGG	60.157	20
128	724	851	CCAGCCATAATTCTGCATCA	59.646	20
140	1067	1206	ATGACTCCTGCAACTTGCCT	59.874	20
187	1618	1804	CCATTTCACCTTGCCAAAAA	60.836	20
264	108	371	TACAGTGAGCCTGCTGCCTA	59.764	20
201	444	644	ACTATGTGGTTGCGGTGCTT	60.581	20
279	3278	3556	TCAGGCCCATATTTCGATGT	60.296	20
255	235	489	CCTAATTTTCGCCTCCCACT	60.443	20
241	46	286	GCCAAAATCCCAACAAAAAG	59.429	20
190	2460	2649	CCTGCCTACGCAAATACCAG	60.648	20
278	897	1174	GCGTGTCGTGTCAGAAATTG	60.31	20
262	1058	1319	TCCCTTGCTAGATGGCAGTT	59.836	20
199	108	306	CGGCCATCAATATACACCAA	59.257	20
196	16	211	TCGGTTACCCTATAGCATTCGT	59.884	22
266	4212	4477	GGACCTGATCTAACCACGGA	59.927	20
255	2	256	CTACGAGCCACGGCTACAC	59.48	19
214	250	463	GCCGTTAAGCTGCTCTCAAG	60.292	20
247	974	1220	ATGGTAGCATAGCCCGTGTC	59.985	20
236	6	241	GAAGAAACTTGACGTGTGCG	59.49	20
244	1913	2156	TTGTAGCTTGCTAAATTAATGA	57.062	24
193	3	195	CAAAGGCCCACAATGGTTAT	59.685	20
194	11	204	GTGTTTGGTCTCCCCTCCTT	60.349	20
216	47	262	TTCGATCAAGGTGAGCTACG	59.024	20
186	119	304	GGCATTTGTATACCCGTTGG	60.074	20
232	41	272	ATGGCGATTACGTACCCTGA	60.352	20
251	739	989	ACAAAACAGTATACAACGGG	59.447	22
214	355	568	TGCTATCGGCTAACGGTTTT	59.742	20
272	140	411	CACAATCGATCAATAAAGCTG	59.748	22
264	65	328	AGGCTTAGAGGGTGTTTTGACA	60.165	22

203	1109	1311	CACCACGGCTAGTTTCACAA	59.758	20
237	0	236	GGAAGAATTGGAAACTCGTGA	59.16	21
157	120	276	GTCCACGGGAGAGAATGAGA	60.199	20
254	100	353	CCTTCCAATGGACTTCCTCA	60.042	20
204	74	277	GACAACAGAAAAACCACGCA	59.74	20
138	53	190	CATGCATGATCGACATTGTAA	59.448	22
237	73	309	ATTGCTTCCCCTCTTCCATT	59.903	20
237	1618	1854	TCTTCCCAGCTAGCATGACTT	59.091	21
176	53	228	GTTGATGCCCTTCGTCAACT	60.119	20
216	3	218	AACGCTTTCTGCTTCTGCAT	60.162	20
143	871	1013	TCACAAGCCTTGCATTTGTC	59.847	20
127	20	146	GGAAATAAGAAGGTGTTATGA	60.434	25
256	76	331	TCGCAGAAAATCAACTTCTCA	59.996	22
223	2952	3174	TCACCTTACACAGTGCCTGC	59.905	20
280	9	288	GAGAAAATCAGGTGATAACCC	57.73	23
234	25	258	TGCGAATCAATTAGTGTGAGA	58.439	22
225	105	329	TGGTGTTCTTGGGGTTTTGT	60.246	20
273	363	635	TCAGTACTACCCACGGGCTC	60.134	20
234	0	233	TTGGGAGTGAACATACATACA	60.064	26
238	2776	3013	ACAGCAAGCATCCAGAAAGC	60.547	20
113	167	279	ACAGAATATGCGTGATCGCC	61.034	20
269	7	275	CAGAATATGCGTGATCGCCT	61.161	20
138	18	155	GGATTTTTACCACGGCTGAA	59.938	20
199	113	311	GTTGACGGATAACCCAAACG	60.227	20
245	1835	2079	CCCTATTGTGAGAGGGGACA	59.92	20
139	219	357	TGCGCCCTTTAAAACTAAGG	59.381	20
222	211	432	AACTTTGTCCAAACAAATGAA	59.828	24
187	529	715	ATCGAATGAGTGGATTTGGG	59.75	20
263	582	844	TCCATTCCGAAAATCAAAGG	59.872	20
148	525	672	TGCGTTTACATTCAAGCAGTG	59.926	21
209	600	808	CACATCTCCTCCCACTCCTC	59.638	20
137	89	225	GTGTGTGTGCATGAGTGTCG	59.772	20
207	15	221	TGATTTTTAATGCCTTTCAGC	57.104	21
266	34	299	CCTCGAATGCTATGACCGAA	61.129	20
279	561	839	CCGTGCACCTCCTCCTAAT	60.081	19
209	4	212	TCTCTCTTTTGGTTGGTGAAGA	58.955	22
240	184	423	TGCAGCTGAAATCAATGAAAA	59.434	21
248	641	888	GTAGTTTTGGGGCAAATGGA	59.801	20
196	659	854	CTTGATTCATCGAACGCAAA	59.809	20
104	1722	1825	CATATGCGATGTTTTGCATTTT	59.867	22
243	0	242	CCAAAGTTTATTTAACACGGA	59.842	25
203	634	836	TGTTTCAATGCCACATAGGC	59.548	20
185	38	222	TTGCTAAGCTCCAGCAACG	60.287	19
108	38	145	CAATCTGGACGATACTCAATC	59.592	22
113	2757	2869	ATCTGTTTCTTCTGCGGCTC	59.579	20
186	355	540	GGGAATTACGGGATGTGAGA	59.75	20
245	4141	4385	GGTTGGTTTGAGTTCCTCCA	59.943	20
146	3	148	TGTCCATACACACCAAATAAA	59.707	25
269	123	391	TTGGGGAAATAATGTCGATCT	58.381	21
252	4215	4466	TGCATAAAGCTCATCTTGCAC	59.08	21
193	110	302	CGGTGAAGATTGGAGGAGAG	59.797	20
252	209	460	CTTTGGAAAATTCGAGAGCG	59.953	20
136	1434	1569	CTGAACTGCAACGGCATAAA	59.872	20
266	1	266	CCTTTGGTCTCGGTTGAAAT	59.028	20
195	49	243	CATGAAAGACTCTATAGACAA	57.458	27
198	118	315	AGGGTGTGTGAGAGACCGAG	60.306	20
199	198	396	TGGCTTGTATGTTCTGATCACC	60	22
218	51	268	TTGTTCGAAAGCCACAAATG	59.706	20

260	0	259	GCTAGGGCGATTGTATTGATG	59.583	21
165	263	427	GCGTTGTGGTTAGGAGAAGG	59.734	20
158	6	163	TACCGTTGGTTAATCCTGCC	59.823	20
244	125	368	TTTCGAAAACATGCAATGGA	60.051	20
207	657	863	ACCCCTCACAAGAACCAAGA	59.549	20
160	31	190	AATGAATTGGTGGAGGGGTT	60.422	20
183	127	309	AAAACGTTGGAAAAACACGG	59.876	20
124	753	876	AGCAAATGCCAATAAGGTGG	59.96	20
161	40	200	CGTGGTGCAGAGTCGTAGAG	59.641	20
208	24	231	CACTCTGCTAGGGTTGGGAG	59.861	20
170	109	278	GCTACCAAGCATCCACTTCC	59.7	20
263	113	375	TTCGAATTTTATTATTGATTGA	59.121	25
271	286	556	AACATGGCAATTTTAAGATCG	59.864	23
211	29	239	TTGCATGAACAACGTGGAAT	59.972	20
246	228	473	TGTCACCTTGAAAGAATTACA	59.959	25
155	2	156	TGAGGTCCCTTGTTTTCTAACC	59.499	22
174	524	697	AATTAGCAGCTTATACGTGTG	58.594	25
244	1913	2156	TCCTTCTAATCGATTCTTCCAC	60.082	23
217	9710	9926	TGAAGAAGACGTGGTCGAGA	59.545	20
265	2506	2770	CACACCTCCTCCGACATCTT	60.112	20
159	0	158	AAGCGACACGGGTTATTTTT	58.629	20
179	84	262	GGGACTCGGATAAAAAGGGA	60.258	20
264	2781	3044	GCTGAGGCTTCTTCCATGTC	59.957	20
148	6	153	CACACTCACTCACAAACACAC	59.744	23
215	1026	1240	TTGAACGTACCCTCGATTCC	59.933	20
151	92	242	CTCCCTAGACTCCGTAATTGG	59.61	22
244	294	537	CCCACATTGGAAAATGAGAAA	59.787	21
109	195	303	AGCAAAAGGCAAAAGCAGAA	60.131	20
148	1147	1294	ATCATGTAGTCGCGTGCTGT	59.349	20
207	55	261	TGAACAATTGAACACCGGAA	59.941	20
174	973	1146	TGCTGTCCCTCTAGCAGGTT	60.012	20
146	1	146	TGCGTTTTGACAATATATAGGT	60.083	26
181	202	382	AGCGAGAGGAAAGGGAAGAG	60.088	20
247	160	406	TGGAAGATGAGTTGCAGCAG	60.136	20
201	1060	1260	ATTATGTGCAAGCTCATCCG	58.749	20
225	73	297	CGGGTGACATTGCCTAATTT	59.823	20
195	243	437	TCACGTGTCATTGTAACCGC	60.584	20
218	2319	2536	AATTGATTGCTGCTGCTGTG	60.019	20
170	428	597	TCGTCAATTCATGGCTTCTG	59.799	20
143	4044	4186	CGGAGAATTGATGTTCCCAT	59.75	20
244	179	422	TGCAGCTAATTTTCTGCTGG	59.206	20
190	5	194	TCTCGCCTTTCTCTTTCTAACC	59.155	22
107	225	331	TCTCAACCAATGATGAGCCA	60.201	20
225	214	438	TTTACGGATCGAAAATTCTCCT	59.123	22
132	209	340	CCACGAGATGGGGACATTTA	60.713	20
179	303	481	GCTTCGATCCGTTCAATCTC	59.78	20
242	1186	1427	GAAATGCATCTCATTCGGGT	59.9	20
205	1231	1435	AACCGATTAAAAACCGGACC	60.055	20
137	344	480	CGCAACACGAGTAGCAAAGA	60.195	20
234	736	969	CGCTGAGGGATCTGGTATGT	60.096	20
240	1676	1915	GCTGGATTTTTGGCATTCAT	59.907	20
235	1077	1311	TTTTTCGGTTCGGTTCAAAG	60.081	20
215	118	332	GTTTCACTTTGGTACCCGGA	59.83	20
140	408	547	AAGTCGGCCAAGAAGAGAAA	59.052	20
118	48	165	CTAAGCGATGCCTAAGGCTG	60.131	20
185	64	248	TCTCACTCTCACTAGCCGCA	59.88	20
185	15	199	GGAAAATATCAAGTCAACACA	58.257	25
261	596	856	TGTGATTAGCATCACAGCCC	59.679	20

199	42	240	AAACAAACAATCAACGCTAA	59.976	24
257	276	532	TATGGATGCCCCAGATTGTT	60.155	20
225	22	246	TGATTTTGGACGTTCTGCAC	59.697	20
166	104	269	GTGGAAGTAGGTGGTGGTGG	60.275	20
189	96	284	TGACGTTTTCCGAAGTACGA	59.317	20
262	87	348	AATAGCGCAAACGGATTAGA	58.906	21
273	31	303	TCAAATGCACAAATTCAATGG	59.41	21
254	446	699	TCGGTGTGCAGTGGTTTAAG	59.758	20
204	628	831	TTACATTTCGATTAGGTGTGA	58.612	24
249	567	815	AAATCGTGAGCAGCAGGTTT	59.882	20
258	739	996	TGCCTTGCTCTGTACAAGATTT	59.044	22
245	32	276	CACAATAAGGGTTGGTATCAT	59.556	24
280	791	1070	GGATAAAGTACGATGATTGAC	58.013	23
168	1163	1330	TGATCTTCTTGCCACCACTG	59.831	20
166	494	659	CAGTGTCCATCCATCCAAGA	59.473	20
280	34	313	ATAGGTGTGGCCCAGTTTGA	60.375	20
162	42	203	AGGACACGTTGGACCTGAAA	60.545	20
124	21	144	AACATGGGTTATCACTTGAAT	59.308	24
264	31	294	AGTAGACGCGACTTTGGTGG	60.312	20
219	360	578	TGAAACTAAAAATGCCAAGC	58.482	21
124	47	170	GGTTCTGAAACCGGGATAGG	60.683	20
208	411	618	TTGAAGAAGTCAAATGGGGC	60.051	20
186	1012	1197	ATTTGACCTTTTACCTTGCCC	59.363	21
207	125	331	GACTCAGGGTTCTTCACGGT	59.153	20
239	68	306	AGTCCTTCGGAGGAGCAATA	58.886	20
227	64	290	GAGAGGGCTTCTTCTGGGAT	59.778	20
219	26	244	TAGAAGGCATTGAGAGTCGC	58.201	20
251	590	840	CATCTGAAATAGATCATTTAC	57.409	27
228	288	515	AGACTCCAAGCCCTGTTGTG	60.298	20
280	123	402	TGTTACATTATGTGGCCCGA	59.809	20
231	656	886	AATATTCGATCCGGAAGGGT	59.627	20
275	646	920	CCAGCATTTGTTTGACATGA	58.099	20
122	7	128	ACCTTTGGATATGGTGATTTG	59.945	22
245	246	490	CAAACCCGAGCTTCCATAAA	60.067	20
279	1615	1893	TCCTTTCACTAACCCGATGC	60.074	20
277	452	728	AACCTCTATCCCGTGCAATG	59.955	20
107	4	110	CATTTGCCTTGTCACAGCAT	59.722	20
149	2	150	TTCCATAAAAAGTTAGGCAAG	57.727	24
245	127	371	ACAACATTCATCGTTCCCCT	59.263	20
198	742	939	TGTTGTTTCCACACCCATGT	59.701	20
237	651	887	GGCTGGCTCCAGTAGTTGTT	59.357	20
184	221	404	ATCTGTGTGTTGAGAGATCAG	59.859	25
177	66	242	CAAAAACAGAGTGAGGGGGA	60.081	20
122	194	315	TGTCCTTTTGGATCCAGTCC	59.903	20
251	5	255	TTGCTGCCCTATTTTCTTTGA	59.84	21
261	261	521	AAGCAATCAAAAGCTCCAGG	59.452	20
196	805	1000	CGCTCATTTTCTCACACCAA	59.84	20
182	1596	1777	CCATGTCCCCTTTCTACCAA	59.784	20
245	303	547	AACACTTCGCGCAGACAAAT	60.837	20
192	39	230	AACTCACATCAGATTCCCCAA	59.396	21
242	56	297	TCGAGCTTGGTTCGAGACTT	60.134	20
274	836	1109	TCAGCGGCTTAACATGTTTCT	59.897	21
250	686	935	AAGCCAACCGCAAAATCTAA	59.72	20
267	1	267	CGGCTGGATTTCATCCCTAT	61.165	20
183	917	1099	GCCCTGTTCGTTCATGTCTT	60.119	20
278	3	280	TCCAATGGATGAGGATGGTT	60.135	20
261	117	377	CCCCCATATGCTATGCTTTG	60.302	20
255	199	453	AAGGCTTTTGAGGGATGGAG	60.569	20

117	331	447	GGCGAGTCTCGTCCTTGTAG	60.012	20
103	1211	1313	GTTCCTTGCTGCTGTCCATT	60.263	20
138	0	137	CCATGTTTGTAATTATTGTAGG	58.388	25
248	68	315	ATCACTAGAATGCGCCCCTA	59.691	20
255	489	743	CATGTGAGACCCATTCTCCC	60.326	20
138	164	301	ATTCTGATCGACCAGTGGGT	59.384	20
205	274	478	CATCGATTGACCCCTCATCT	59.886	20
278	4	281	GCTGGGAATTGCTGATATTGA	60.052	21
224	28	251	CCTCCCTTAGGGTTCCTCAC	59.928	20
178	303	480	AGCCGGTCAAGTAGAGGGAT	60.096	20
278	81	358	CGAGCAAGGAATAGACCGAG	59.971	20
182	62	243	AATTTAATTCCGTGCAACGC	59.971	20
272	14	285	ATGTTTCCTCTTGGGTGGGT	60.607	20
258	386	643	CGACCCTGAGAGATTCCTTG	59.797	20
229	635	863	GGGCGGTGTAAGAGATTGAA	60.074	20
170	26	195	TCACCATGAAGAAACCCACA	59.935	20
208	1413	1620	AACTGAGGATCTTGGGTGGA	59.505	20
223	2444	2666	TAGAGAAGCCGGATGCAGAT	59.939	20
219	801	1019	ACCTGGGAGCATGTTTCTTG	60.111	20
243	551	793	TTCGGTTTTTACTCCCACTATG	58.188	22
267	86	352	TCTTATATCCCCGCCACTGT	59.41	20
130	1846	1975	AAAATCCGATCTCCGAAACA	59.505	20
115	6	120	TCAAGCTTAATTAGAAGAAAA	58.427	27
251	257	507	AGAAAGCCTACCTCGCTTCC	59.983	20
204	137	340	CCGAAATACTCCCACCCTTT	60.18	20
279	1814	2092	CTCAAATCTCTGCCCTCTGC	60.096	20
224	90	313	TGCTGTGGTATGCTTTGATTG	59.744	21
148	11	158	TTCCCGTATACAAATTCCAACA	59.231	22
193	277	469	GGATAATCAGAATCCCCGGT	59.981	20
239	384	622	GTCGTTGTTGAATGTCGGTG	60.008	20
184	761	944	GGCTCCCCATTTCTCTCTCT	59.778	20
124	134	257	ATTTTCTGTCGAATGGTCCG	59.933	20
110	41	150	GCTGCATGAACACCAAGAAA	59.847	20
104	753	856	AATAATAATTCCCTCCTCTCGA	57.781	24
271	74	344	AAATCCCCGTTCCATCATAA	59.091	20
150	52	201	TTTGATATACATGGTATTTAATT	57.034	27
207	5	211	CCCTAGCTTTGCCCTCTTTC	60.332	20
196	9	204	TCGATTTGGATTCGAATTTGT	59.402	21
259	771	1029	GGCGGTGCTTAACTATGGAG	59.73	20
242	544	785	TGGTGACGATTATAAAATCAAA	57.729	24
276	137	412	TCGACCTCGAATTCTCATCA	59.322	20
274	492	765	GAGGCTGACGGATTTCCAC	60.616	19
276	22	297	CGGACTGAGCTGAGCTAAAAT	58.756	21
277	112	388	CCAGCTCCATCATCTCTTCC	59.761	20
270	125	394	TGGCATTAAAATCCACCATTG	60.554	21
245	21	265	CCCACGTGCACTTCTTTTGTA	61.092	21
117	224	340	TGAACACAGCTCGAAAGCAT	59.596	20
268	251	518	TCGAGCTTGCTCAAAAGTCA	59.864	20
210	65	274	GATGAACACCCGAACCACTT	59.827	20
224	57	280	GGCAACGGTATACCACTCGT	59.882	20
125	72	196	TGACATCTTCGAGTGCTCGTT	60.991	21
132	2076	2207	CTCCCTCTTTCCCTCTCCAA	60.695	20
277	379	655	AGAGCAAAGAGTGGGGTGAA	59.844	20
266	12	277	GATCTCCACCATTTACGGGA	59.75	20
158	135	292	TGCTAATCTACGAATTTGGGA	57.416	21
192	81	272	TAAGGGCGGTATCACCTGAA	60.46	20
276	6	281	TCCACACAGAGACACTGGAA	57.683	20
267	64	330	TGGCAATCGAGATATAATTGG	57.62	21

278	4	281	TTCTTTATTCACAATGAACTCA	57.6	26
239	782	1020	AAGAGTGTTGTGGCCGAAAT	59.598	20
182	1119	1300	GCTAGGGGTCTGCAAATCAA	60.214	20
193	3395	3587	TGAATCCGTTTCACTCGTCA	60.24	20
207	1234	1440	TGCAGACAATCCCACATGAT	59.925	20
246	1891	2136	AAAGAAGTCAAGGGCTTTTGT	58.5	22
175	803	977	AATCACGTTGAGGATTCGGA	60.461	20
127	79	205	GCACTCACACACACGAAAGA	59.937	21
249	697	945	CTATCATCCACGCATTGAACA	59.557	21
139	521	659	TCTTTACCCTTGGTTGGTGG	59.824	20
192	5021	5212	AACAAAAATGATGGTGAAGT	59.666	23
226	118	343	AATTGAACCTTGGGCTAAAGT	57.063	22
224	418	641	CCGTGATGTAATAGGACGTGG	60.256	21
253	607	859	TCGATTGACAAACTCACATGG	59.556	21
182	976	1157	CAAACATTTGAGGAAGGCGT	60.11	20
213	41	253	CAAGCTTGGCGTTATGAATG	59.325	20
250	175	424	ACCCCTTGTTTGCCTTTCTT	59.976	20
279	469	747	GCATCGTCTCAACCCTTGAT	60.081	20
184	1071	1254	AAGGTGGAATTTCGGGCTAT	59.799	20
272	4528	4799	GTCCACGCAATACCATCCTT	59.82	20
248	110	357	ATTTTGCCCACGAATTAGCA	60.456	20
141	324	464	ACCCATCTCCTAACACGCAT	59.434	20
227	14	240	GGTCTGTTTTCCATGGCCTA	59.933	20
250	82	331	ACGTGTCGCAATCAGAATGT	59.169	20
250	113	362	CACAACACACACGGACATCA	60.044	20
105	11	115	ACACGAGTGAAGAAAGGGAG	58.929	21
147	299	445	CGTGTCGTTATCGTGTTCGT	59.64	20
186	84	269	GCATCTCTCCCTTGCTCTCTT	60.11	21
230	355	584	TTTTGAAGACATGGTTGGACA	59.01	21
280	46	325	TGAAACGGAGGGAGTACACA	59.135	20
250	100	349	TGCTGACCTAACCCCAAACT	59.592	20
143	25	167	TGGTTATGCCTTCTTCTTCCA	59.693	21
168	231	398	ATGCGTTCCCAATAGCATTC	59.929	20
233	107	339	CTGCAAAAGCATCACCAGAA	59.988	20
206	663	868	ATCAATTTTTGAGTTATGATGT	57.321	26
220	28	247	GTGGACGCTCCAGATTGTTT	60.119	20
212	25	236	GAGGGATTTTGGGACGATTT	60.131	20
140	2	141	TTGTGTGGTTGTGATTTAGTTA	59.328	26
248	78	325	AGACTAAAGGCCAAGAGGGC	59.848	20
168	612	779	ATGACAGTTGGGTTTCTGGG	59.82	20
269	108	376	ACGTCTCTTCATGCACCAAT	58.158	20
278	23	300	CAACATACAGGCACGAAAAT	59.097	21
269	10	278	GGAACCCATCCACCCTATTT	59.881	20
227	4360	4586	ATTTTGGCGCGAAACATAAG	60.095	20
259	18	276	GTCACACACACTCACGGCTT	59.789	20
131	241	371	ACACCGTGGACGTAGATCGT	60.453	20
224	232	455	ATGGTCCCCTCAACACAAGA	60.363	20
279	13	291	CCTAGCCTTTGCCCTCTTTT	59.85	20
199	91	289	CTCAAACATTCATCAATATAC	59.74	26
277	4	280	TGGAAGCACGTGACAGCTAA	60.596	20
167	262	428	CAGAGAAAAGTGAGCTCGGG	60.126	20
280	1935	2214	CAGGTGGAGTTTCATCCACA	59.52	20
250	944	1193	TCCTCCCTTACTTGCCTTGA	59.807	20
222	782	1003	ATGCAAACAATGCTGCAAAG	59.879	20
170	280	449	AACCGCTCTGATGCTCTTGT	60.02	20
233	222	454	AAACCCATCACCCACGTTTA	60.088	20
271	652	922	GCGAGCAAATGAATAAGAGT	59.501	22
268	81	348	ATGTGACCCACCTTACGAGG	59.844	20

228	60	287	ATTTCCCAACAGTGCCAAAC	59.836	20
270	879	1148	TCATCCCATGCGTGTATGTT	59.805	20
135	3	137	GGCTTTATGATCCATTCTCAAA	58.2	22
276	411	686	GTGTTCCTCAAGCCGAAATC	59.676	20
168	896	1063	CCAAACCAATTCAAAAGGGA	59.772	20
256	131	386	TTCGATCCCAGATGTTGAAA	59.049	20
156	227	382	CAAAGGCCCACAATGGTTAT	59.685	20
211	508	718	TCCCTAATTCCAATTCCCCT	59.6	20
164	2	165	TGCGTTTTGACAATATTTAGTG	59.109	25
200	23	222	TATCGGTTATTACCGGATCGC	61.005	21
274	131	404	CCACATAAAGGATTCCCGTG	60.184	20
187	114	300	TCAAAAACAGAGGAGAAGGGA	60.214	22
280	1280	1559	AAATAGGAGGCTTGATCGGC	60.551	20
146	53	198	GGCCAAGTCTGGCCTATTTA	59.182	20
156	83	238	CACGGTTAGGCTCGAGAGAG	60.149	20
274	118	391	TCGTGAAGAAAATCGAACCA	59.247	20
247	38	284	GATCGATTTCAGCATCATTGG	60.429	21
201	17	217	ACCAATGGTGGTATGGTGTG	58.984	20
275	127	401	CTTCGCACGAGTGTTGAAAG	59.634	20
184	122	305	TAATGGTGTTGCTGGGTTGA	59.964	20
232	333	564	TGGCAGAACAAAACTCATGC	59.847	20
213	77	289	GATATGAGGCCAAACTGGGA	59.894	20
280	7706	7985	CCATGCCACCTTCTATTGGT	59.813	20
196	2394	2589	GGTGGTATGGTGTGGAGGAC	60.096	20
195	584	778	GCGAAAATTCCACCATAGTCA	59.952	21
172	950	1121	ACAACAAATTAGCTGAATGGC	59.652	22
226	264	489	AGAGGGAGATCGACGTGAGA	59.945	20
164	0	163	TGGGGCCTACGAGAAATATG	59.916	20
268	150	417	GTCACCTCACACACCACTCG	60.207	20
207	98	304	CAGCTATCGAAACAATGCCC	60.606	20
188	462	649	GTCGTCGAGAGAAGCTCACC	60.143	20
214	16	229	TCTTATAGCATCAACCGCCA	59.281	20
269	102	370	TGCAATCCAGTCGCATTTAG	59.833	20
240	27	266	GGGGTTATCATGGGATCAAG	59.055	20
203	1153	1355	ACCAACTGCCCCTCTATTCC	60.328	20
273	369	641	ACACACATGGATGGAGAGACA	58.955	21
277	2015	2291	GAATCGTAACATGTAACACAC	59.332	26
253	469	721	ACCGTGCAATCCAATTTAGC	59.967	20
272	72	343	GGCGGCATTCTATGAGGTAA	60.06	20
264	21	284	GAAAAGCTTGGCCATTCAAC	59.691	20
143	13	155	TGATTGTAAAACATGTATGGGA	59.898	25
178	33	210	TCGTGATCATTCTTGCCTTG	59.799	20
190	19	208	TCACCAAGGATAGCCACCAT	60.34	20
267	1	267	AATAAGTTCACTTTATGCGAAA	58.116	26
213	189	401	AACCCCCAACCAACTCCTAC	60.088	20
126	42	167	ATCCGCCATTGACCTCATAC	59.78	20
201	396	596	CGTGTCTGGTGTTTCAATGG	60.001	20
263	984	1246	AGCCCACAAAGTTGCATTCT	59.74	20
153	9	161	CGGGATTTAGGTGTTTTGACA	59.847	21
233	381	613	AATGCTCTCACCAACTCGCT	60.02	20
254	21	274	TGCTTCATTGGTGGTAACGA	60.111	20
249	235	483	ACAACCATGTCGAGGGTTTC	59.827	20
257	1262	1518	ACGGTTGAAACGTGGGTATG	60.668	20
133	129	261	CTGAAATGAAATCATGCCCC	60.274	20
214	456	669	CTATTGAAACAACCCCGGAC	59.288	20
259	6	264	ATTCACAATGGCAAGGAACC	59.797	20
110	506	615	TCGCATGCTTTGGTGATTAG	59.833	20
120	448	567	TGGATGCACCAGATTGTTTC	59.502	20

274	1	274	CTGCTCCTTCTCACTCTTCCA	59.73	21
229	38	266	GCGGTTATCACCGGATCG	62.397	18
254	1087	1340	AGTTGGGAATTGGGATAGGG	60.011	20
131	28	158	CCTAAAACTTCAAACTGTGGG	59.901	22
104	63	166	CACTTGGACCTGAAAAAGGA	57.77	20
259	1668	1926	CTCATTTTCTCCGCATCACA	59.799	20
234	0	233	GCACTTAGGAGAGAGATTGTT	59.424	23
279	53	331	GCTCGAGGCATGTAAGAAGC	60.125	20
280	1005	1284	CAACATGTGCAGGTTGAGGT	59.597	20
175	131	305	CGTTGCCGGATAATTCAAAC	60.323	20
114	487	600	CTTTCCGAACATCCCAACAA	60.863	20
139	883	1021	CCGAAAGTAGCGAACAAACC	59.747	20
230	232	461	GAAGCAGGCCTACTCTCCTG	59.187	20
160	180	339	ATTCATTCTCCAACCATCGG	59.75	20
249	128	376	GTGGTATAGCGGTTGGCATC	60.361	20
123	172	294	CCATCATTTCCCTCACCTCA	60.86	20
207	373	579	TTCCATCAATCCACTCCACC	60.725	20
144	2234	2377	GCGTACACCCATTTTGAAGG	60.365	20
159	78	236	GGGTGAGTAACGGTGCAAGT	60.035	20
205	103	307	TGAATTTGGGACTCAACGAAG	60.096	21
226	19	244	GTGTGGAAAAGGGAGTGCAT	59.973	20
278	1311	1588	GAGAGGCTCGCCATTGATAG	59.939	20
206	429	634	ATGCGACAGAGTGTGTGAGG	59.897	20
232	213	444	TGTTTTGGGCCTAAATGGAC	59.801	20
245	24	268	ATTGGAGAGGAAAAATGGGG	60.124	20
205	51	255	GCGTTGACGCTATTGAAATG	59.329	20
158	69	226	ATGCCTCAAATCACAAACCC	59.797	20
134	119	252	AGAAACGTCGGTGACCAATC	59.973	20
188	14	201	GGATTTAGCGGTTATTACCTG	57.387	22
110	18	127	CTCTCGAGCCTAACTGTGGC	60.156	20
198	39	236	TCCAATTTTGGGAAATACTAT	57.592	23
191	28	218	AGGAGAGTTGTAGAGTCAAGT	58.31	27
220	4327	4546	AAGAGCATCAAACATCATTTC	58.188	22
152	11	162	TTCCCGTATACAAATTCCAAC	59.231	22
262	467	728	GAACCACCAAAGCAATACCA	59.35	21
211	249	459	CGGTACAGATTGCACACGAC	60.183	20
142	8	149	TTCACTTAGCTCTTGATTTTCA	60.182	26
203	105	307	CCTTAGAGCTCGGTTGCAGT	59.639	20
207	412	618	GAAACCCGACCGAATACTCA	59.933	20
269	40	308	CAAGGAAGGAACCTCCATTTT	59.447	21
199	76	274	TTTCGATATGGCTCGGTAGG	60.053	20
190	97	286	TAACATGTAGTCATGCGGGC	59.572	20
273	45	317	AGGGGGAGGGCTATACTCAA	59.919	20
182	514	695	CAATTCTCCATGCACACCAG	60.112	20
228	16	243	AGCCCTAGAATCTGCCCTCT	59.443	20
204	546	749	GCCAGTCCAATGGTCGTACT	59.997	20
260	1432	1691	GCTTGCTCGTTATCGATGGT	60.243	20
237	60	296	GTGAATGAGGTGTGGGTGTG	59.846	20
238	68	305	ATTCCCAACTGATTGGCTTG	59.933	20
168	76	243	TGAGCAAGGGACAAATGTGA	60.24	20
170	525	694	ATTGAAACCATGCCCATTTC	59.628	20
150	7	156	ACCAAATTTAAGGGTTATCAC	59.579	24
236	222	457	TATCCCATGATCGAGTTCGG	60.822	20
111	87	197	TATGAAGCATAACCATGCCG	59.543	20
110	362	471	GTTCTTTGGGAAACAACGGA	59.948	20
139	12	150	TTGAGCTGTTATGCGTTTTGA	59.5	21
250	443	692	TTAGAGTTGGCATCGGGAAA	60.576	20
255	2067	2321	GCCAAGGGAAAGCTTTTATCA	60.552	21

127	144	270	GACAACCTTCGGCTTGAAAA	60.227	20
166	13	178	GCAGGAAAATGAAAAGTGGG	59.546	20
278	585	862	TTCTTCTCCTTGTCGTGCCT	59.989	20
194	314	507	CGGTGGGTGTTTGATGAAG	59.944	19
213	1213	1425	GGGTGGGTCACTCACTCATT	59.817	20
262	58	319	TCTGAAATTTTGACGGCTCC	60.192	20
222	94	315	GCATCTACTCTGGCTCTCATTG	59.927	23
258	2646	2903	AATGGACCGGACGTGAACTA	60.375	20
136	98	233	AACATGTTGATCTAAATAACG	57.516	24
249	867	1115	CGTATTGCAGTGAAATTTTAG	59.352	23
199	1696	1894	CAGACATGTGTACCACCCCA	60.285	20
260	583	842	ACCGACCACCCTCTTTTTCT	59.972	20
195	70	264	CACCTGATCGCGACCCTAT	61.041	19
125	1726	1850	TAGGTTGACGATGGGTTCCT	59.405	20
153	91	243	TTACCACAATTTCCCTTGTTTT	57.605	22
254	287	540	TTTCAGTTGGCAGTGCAGAG	60.175	20
115	43	157	TTTGCCCTTATTTAGCACGG	60.089	20
239	399	637	GCCCAAAATTATCCATCAACA	59.652	21
207	206	412	CCTGCCCAGATCTCTCTGAT	59.359	20
269	146	414	TGTAACCGTGATTGGGAGGT	60.232	20
259	33	291	TTGCGGGGTTGTTAAAGAAT	59.451	20
155	909	1063	CTTGTAAGGCCAGGCACATT	60.132	20
259	78	336	TCGAATTTCTAGCGTGATGG	58.869	20
255	51	305	GCTTAATGCGTAGCTGGGAT	59.347	20
142	0	141	CAAACGTGAGTGGGAGATGTA	60.03	22
217	549	765	AAACGCGAAGTTTGGTGAAT	59.615	20
269	2187	2455	TATCATCTGTCGAAGCTCGC	59.131	20
253	227	479	CCAAAATTTACAACGTGATCA	60.488	24
274	571	844	AATGTGCTTATCCACCGACA	59.002	20
251	33	283	AAAACTACGATCTGCCACCG	60.132	20
257	97	353	TCAAGTTCAATTGCGGCTTA	59.443	20
279	626	904	CGCCGCAGTATAGCAAAAAT	60.246	20
209	443	651	TGTTTGCTGCCGATACTTTC	58.92	20
145	183	327	TAAAAAGATGAGCCCACCCA	60.439	20
272	153	424	AGGATGGATGAAAAGGCTCA	59.629	20
181	543	723	CACCAAATTTTATCATTTTTAA	57.837	27
117	9	125	TTGGAGCTTCAAAACTTAGGC	58.64	21
280	1057	1336	TCACTTCACCATTCCACCATT	60.225	21
164	447	610	TTCGGAGGTTTTGGACAATC	59.91	20
120	20	139	GCGACAATTCTGCGTGTTAT	58.801	20
268	2655	2922	TGAGCATAATCTTGGGGCTC	60.177	20
231	38	268	GCGGTTATCACCGGATCG	62.397	18
222	13	234	TTCGGAGCATGATTTAAGTGG	60.081	21
177	43	219	ATCGGAGTTGATTTGATGCC	59.9	20
265	212	476	ATCAGCGACGAGTCCAAGAC	60.418	20
265	388	652	GCATGAAGATGACGAGATGC	59.358	20
171	100	270	GATGAGGGAGGAAGAAAGGC	60.154	20
182	789	970	TGGTGTCAGCTCATCCAAGA	60.402	20
212	3333	3544	CCAGGGCAAAACAGAAATCA	61.001	20
129	1480	1608	TACGGGTTCGAGGCTTAATG	60.089	20
245	630	874	GCCACCTCACTCTTGCTACC	59.874	20
269	4161	4429	ATGGATATTGTGGCTGGTGG	60.603	20
277	35	311	AACCGCTCGAATCCGTACT	59.708	19
257	32	288	TGCGTGTGTATGCTGAGGTT	60.333	20
267	70	336	CAAAAACCCTAGCTCTTGCC	58.973	20
214	136	349	AGGATTGTGGAGGATGGTGT	59.232	20
276	1098	1373	ACAATTTTCAATCACAAGTTAT	58.938	27
141	101	241	AATTATTTCGGGCTAACGGG	60.161	20

100	143	242	AGTGATGGAACCAACCTTGC	59.973	20
203	32	234	TCCCTTGCTTTCTAACCCCT	60.068	20
241	40	280	TTCCTTTGTCATTCCAACCA	58.947	20
160	45	204	ATAAGTTTGTGCCTCCCGTG	59.993	20
256	623	878	GTGAATATGTGGGCTGGGAA	60.723	20
212	2416	2627	TCCTAAGCTTTTCCTGCTGC	59.73	20
265	348	612	CTCTTTGGTGGTGTTGCCTT	60.149	20
156	16	171	GCTTGATTGATCGAAGTGTTG	60.257	22
111	2365	2475	CTCGAATCAATCTCACCCAA	58.643	20
233	79	311	CTATTGAAACAACCCCGGAC	59.288	20
274	309	582	GCAGTTACCTATCCCCACGA	59.955	20
244	24	267	AAGCTGTCGATGATGGTGGT	60.542	20
280	27	306	ACACATTTTTCTTTTGGGCG	59.975	20
230	20	249	TTCTTCGGTCCGACCTTGTA	60.626	20
224	252	475	GTTTGCTGGAACCCATGAAT	59.797	20
159	15	173	CCTCACCTCTCCATTCTCTCA	59.39	21
272	6	277	TTGAAGAACGATTACAAAGTT	59.101	26
175	91	265	CACAGAACATAATTCCGCAAA	60	22
279	56	334	GGGGTGGACTATTTCTTGCT	58.121	20
221	289	509	TTCCATCCAAATTAGCCAGG	59.894	20
148	214	361	CGTACCTGGCTGTAGGATGC	60.678	20
214	1420	1633	ACAATCTCGGGATGCAGTG	59.647	19
230	1071	1300	CAACTTCCTGGTCCAATGGT	59.82	20
111	37	147	ACAAACTAATCAAGTTCCGCA	57.439	21
120	10	129	ACGGTGGGCCGAGTATATTA	59.32	20
218	356	573	AGTGAAGGTGACGAAATGGG	59.966	20
275	144	418	TGCTCTAGGTAAACCCACGG	60.125	20
254	1310	1563	TTTTTCCCATTCCTGCAAAC	59.916	20
184	67	250	GGTTGAGAAACGAAGGCGTA	60.249	20
211	1041	1251	AATGAGCTTCGTGTCTGCCT	60.02	20
245	269	513	TTCAAATGGAATTCATATAGC	58.513	23
141	145	285	CTCCCCATCAGATCATCTCC	59.415	20
237	205	441	ACGAGACTGTCGGTCAACAA	59.31	20
131	130	260	TGGGTTTTTACTGGATCACCA	60.213	21
233	25	257	GAAGAACACGAGGGATTTGG	59.526	20
239	737	975	GTTTCAAATCGGACAAACCG	60.344	20
235	1094	1328	TTCATCAATTTTCAGGCCAAC	59.93	21
163	1613	1775	ACCAATAACCTGCCCCTCTT	59.827	20
157	1812	1968	TGGTGAGAGAAAATGGAGGG	60.042	20
131	1256	1386	TCCGCCGAAAAGACAAATAA	60.56	20
178	390	567	TCCAACTCCATCACCATCAT	58.721	20
218	227	444	TTGCAAAGTCAGACGTCATTG	59.896	21
190	264	453	CCTCAGTTAGGATTCACTGAT	60.155	27
205	112	316	TGACACCTAGCCCATAACCC	59.813	20
180	66	245	TCATTTGATCACAAACCCCC	60.56	20
242	83	324	TGCAGAAAACAGAGCTGGAA	59.716	20
219	567	785	GCCATGATTTCAGCTGACTG	59.399	20
164	226	389	TCCAAGCATGATACCCCAAT	60.155	20
174	347	520	CCGGATTCAAGCTGTGAGAA	61.316	20
102	482	583	GGATGTTGAGATCAGAACCAC	59.973	22
233	1792	2024	TGTTGGAGCACTGTTTGGAG	59.873	20
173	68	240	TGAGAAGGAAATTAATGTGTT	60.157	27
268	48	315	TGTCATGTAATAGCCGTGCAA	60.148	21
184	1919	2102	GCACTCTGCATTTCCCTTCT	59.434	20
250	91	340	GCTTGAAGGATGAAGGTTGG	59.67	20
266	143	408	TGCCTCTCATACTGCGAGTT	58.625	20
280	209	488	TAACCCAAAAATCAAACGGG	59.671	20
266	6	271	TGGCATTTTCCCACGTTAAT	60.188	20

121	65	185	CATTTGGTGAGGAGGGAGAA	60.042	20
146	629	774	CATGTTTTTGCGCAATTTCT	58.819	20
255	127	381	TTCTCAGCATATGGGAAGGG	60.029	20
117	295	411	GAGAGTGGAGAGAGAGAGGG	59.175	22
197	8	204	GCCCTTTATTTGGTTGATCTAA	60.095	24
146	394	539	TGTGCGAGTCGGTAATTCTG	59.864	20
224	75	298	TAGCATGCAAAAGGAACACG	59.872	20
222	1571	1792	AATTGGTATGCAAACGTGGA	58.895	20
122	574	695	TTTGACGGCACAATTCTGTT	59.174	20
270	377	646	GCCGCTCTGAAGACATCAAC	60.956	20
272	42	313	CCTCACCCATTCACACACAC	59.846	20
272	84	355	GAAAGCCTACATCCACTGGG	59.55	20
219	0	218	TCCAATGGATGAGGATGGTT	60.135	20
154	873	1026	GTTGCAAGAGAGAGAAGGGG	59.014	20
262	9	270	AAGAAATGCATGCACCTGATT	59.614	22
240	273	512	AGTCTTCGGGCTGAGTTGAA	59.989	20
271	16	286	CAAAAATCTAACGGCCCAGA	60.067	20
246	128	373	ATTGTGTGACGGGAAAAACC	59.694	20
162	6	167	CGCTCTATCTTCTTTCTCTTCA	60.159	24
227	8	234	AAATAGCAAATGTTTAGCATG	59.621	24
174	2416	2589	TTTTTGGGAACTTGTCCTGG	59.942	20
280	38	317	GCATTTTCAATGACCCGAAC	60.318	20
256	8	263	CGTGACCTTTTGGTCTCAGG	60.68	20
164	105	268	TTCTCTTCCTGGGCCTTTTT	60.18	20
147	0	146	GACATTTGGACCTGAAAAAGG	60.332	22
151	4533	4683	ATTGCAGTGCCATCACCAT	59.941	19
200	118	317	TTTAAAGCAGGCGGAACATT	59.72	20
266	357	622	AGAAATGCAAAAAGCATGAC	59.219	21
278	116	393	GATATACCGGAAGGGGGAGA	60.11	20
263	8	270	CACTACTAGGGTTTGGGAGGG	59.866	21
251	209	459	TGTCACCCAAGTCTCATGCT	59.261	20
196	218	413	GCACTGGGAGGTTATCGTTG	60.517	20
252	189	440	CCGATTGTGAGCATGAAAAC	59.127	20
274	85	358	TCTGCACACTCCTCCAACTG	60.022	20
244	1166	1409	GCCCCATCTCCATCTATTCA	59.854	20
149	364	512	GAGGGGAAATCTATCGCTGA	59.224	20
154	233	386	CCTTTGTCATCTTGGGCAGT	60.111	20
249	21	269	CAATCTAACGAAATCTGCGGT	59.238	21
221	364	584	GTTTTTGGTTGTCGTGGGTT	59.734	20
252	74	325	ACTATTATGGCCGACCGTTG	59.845	20
169	53	221	GGATATCCGAAACATCCGATT	59.998	21
252	49	300	CTGCACCATCTTTCCCGTAT	59.955	20
184	115	298	AAACCCTTCTGCCCCTTCTA	60.068	20
175	133	307	AAGATGGAACGACCCTGTGA	60.51	20
206	26	231	TTCAACAACCACCACCATTG	60.255	20
149	347	495	TCCAACACATCCCTACAACTTT	59.791	23
266	3210	3475	GGCTGATGTTGTTGTTGGTG	60.008	20
134	996	1129	CCAAAAATATGGCCGTGAAC	60.188	20
258	24	281	AGGGGGAGGATGAAGAACAC	60.314	20
205	113	317	TGGCTGAGGATGAATGAACA	60.201	20
217	2103	2319	TGCATGCATTTATTTGACAGC	59.722	21
128	1207	1334	TTTTGGAGATTCTGGGTTCG	60.044	20
125	1044	1168	TTAAGGTGGTGTTTGCATGG	59.439	20
205	1572	1776	GGGCGAATAAGAATGCGTAA	60.061	20
122	27	148	TAAAAACAGGGGCAAAGGTG	59.968	20
210	9	218	AACTCGAATTGCAACGAAAA	58.413	20
187	1850	2036	TGGGAGGATCTTCAGATTGG	60.003	20
127	65	191	ACAAACCCAAACCCAAAACA	60.103	20

114	4	117	TGCGTTTTGACGATATATAGT	60.194	26
179	2197	2375	AAACCTTCTGGCTGAACCAA	59.711	20
150	376	525	CGAAATAAGCCGCCAAAATA	60.055	20
224	251	474	TTGTGCTGAAAATCTCCTCAG	59.993	22
276	2912	3187	CAGCAAGTCAATTGGGGAAT	59.933	20
248	7	254	TCATGGATGCCATGTGAAGT	59.925	20
137	39	175	CGGTTATCACCGGATCGC	62.397	18
219	394	612	TTGCACTCTGTGGAGCAATC	59.992	20
236	0	235	TTTGATTCCTTTTGTCCCCT	58.477	20
270	808	1077	TGCATTACAGCTTGTTGCAGT	59.55	21
183	468	650	GCAATTGATTGAAATGCCCT	59.907	20
190	156	345	AGAGGCGGCCTTTTTATTCT	59.355	20
179	31	209	CTTTCAGGTCCAAGTGTCCTC	58.78	21
183	359	541	ATGCTGAAAGCACGTGACAG	60.056	20
246	139	384	GTGGGCTATGGCTCAAGTGT	60.142	20
231	31	261	CGTCCACGACCTCCACTATT	59.989	20
190	4815	5004	CAAGAAACCATGGAGAATGG	59.918	21
209	354	562	CCATGAATCTTTCACATTTTTC	58.976	23
279	15	293	CTCTCTCTCTTTTTGGTTGGTG	59.908	23
138	2114	2251	TTTCCCAAATTATGCTCACTCA	59.586	22
216	1241	1456	TCTCGCCGCTTTAGACATTT	59.982	20
253	18	270	CTCTCTCGAGCCTAACCGTG	60.149	20
257	270	526	GGTGCATAGAAATTGCTGCC	60.615	20
235	118	352	AGCTGCTGGACGAAGAAAAA	60.132	20
224	148	371	ATTCACTTCGGCAAAATTGG	59.938	20
201	941	1141	GACGTGTAAACCATCACCCC	60.096	20
198	3	200	CATTTCACTCCACATTCCCC	60.173	20
208	343	550	TTCAAAATTTGGCACTTAGCA	58.482	21
279	1229	1507	TTCCTCGCAATCACTTTCTTT	58.962	21
278	1213	1490	CTCCAAATATTCCCTTCCCC	59.6	20
233	14	246	GAGGGTTATCATGGGATCAAG	58.32	21
144	344	487	GCGTTCGTCATTCCAAATGT	60.905	20
192	337	528	TCTTCCCTCCCTCATTTCCT	60.008	20
216	137	352	AAACGCGAAGTTTGGTGAAT	59.615	20
269	2411	2679	TCATGCAAACAAACATGGTG	58.966	20
193	1137	1329	TGATCGGCCTTGTATCACAC	59.527	20
101	235	335	ATACCACCCGATCATTTGAA	57.735	20
103	264	366	GGCTAATGGGATGAAAGGCT	60.419	20
111	918	1028	TCCTCCGTTAAAGACTGTTCA	57.47	21
246	61	306	CCCAACTTTTTCTTCAAAATCA	58.274	22
172	5	176	GGAAATAAGGAGGTGTTATGA	57.235	25
111	1411	1521	TTGGCACCAAAATCATCTCA	60.049	20
191	205	395	CCGAGCTGAAAATCCACAAT	60.074	20
273	77	349	GCACGCAAATAATGGTTTCTT	59.137	21
176	240	415	GGATAAATGTGGCGAATGCT	59.929	20
188	842	1029	ACGGTACAATCCCCATAGCA	60.214	20
265	31	295	CACGTTAGACCTTGAAGGGG	59.587	20
132	1152	1283	GCAAACAAGGGGAGATTTGT	59.031	20
277	370	646	TGCATGCACCTGATTACAAA	58.703	20
134	7	140	TGAAGTTAGGAAATAAGGAG	60.026	24
131	1478	1608	CTCTGCTTTGTTGGCTTCCT	59.615	20
115	1	115	CTCTGGATATTGCTCGTCGG	60.755	20
203	519	721	ATAAGTGCCAGGCTGGATGA	60.624	20
153	303	455	CTCCGCTAGTGAAACGATCC	59.836	20
280	55	334	TTTATTTTGGCGTTTCGTGC	60.969	20
107	963	1069	CCACCGAGGAACATACAAGG	60.366	20
258	552	809	AATGCCAATCACAGCATTCA	60.08	20
271	465	735	TGGTCATTTCTGTTTATTTCGA	58.967	24

257	359	615	ACTGTCCTTGAGCTCGCAGT	60.205	20
131	845	975	ACCAGACCCACACGTTTCTC	60.009	20
250	980	1229	TGCCACCTCATATGCCACTA	60.096	20
213	6	218	CCCGGTCTGATGAGTTGAGT	60.112	20
266	74	339	GGATGATAAAGGCCAAACAA	60.312	22
145	22	166	GATGGGTTATCACCGGATCG	62.397	20
229	76	304	CACCCACAAATCAACCACAG	59.848	20
193	851	1043	GCATTCCCCATACACACAAA	59.251	20
188	103	290	TAAATGCACACCCCTTTCAA	59.013	20
252	19	270	ATGAACACCCCTAGTGACCG	59.844	20
162	106	267	ATTCTTGATGGAACGGGGAT	60.526	20
153	27	179	CGTTGGCCATGTTGGTAGAT	60.776	20
186	1080	1265	TTGCCTACATCATCCCACAA	59.924	20
228	829	1056	TGGTTGCACCATAACACACC	60.287	20
222	67	288	GTGGTATGGTGTGGAGGACC	60.096	20
140	695	834	CACCCCCAGATGAGCTAAAG	59.688	20
147	2	148	CTCGCTCACCGAGATAGGTT	59.454	20
207	612	818	CTCACCGCCTTAATATGCGT	60.117	20
197	21	217	CAAATCAAGCGACCATTATGA	58.639	21
202	13	214	ACCACCACATTACTGCCACA	59.88	20
270	1270	1539	ACATCGTGTGGAAATTGCAG	59.572	20
210	831	1040	CCCAATCCTTGGACATTTTG	60.162	20
220	225	444	CGTAGAGAATGTTGCCACGA	59.864	20
228	111	338	AAGCCTGTGTTAGGGCATTG	60.132	20
192	38	229	TTCATCTGGTTCCCTTTGGA	60.43	20
189	1066	1254	AACAACCTCATTTGGTGCGT	60.419	20
231	120	350	TCAGGCAAATCAGGCAATTT	60.585	20
162	395	556	CACGACGGTTAAATCACAGG	59.047	20
164	43	206	GTGTGATGTTGGAGTTGGGA	59.367	20
277	1645	1921	TGATGGTTTATGCTCGTAAGG	58.653	22
201	470	670	CCTTGTTGCACTGTGGTGTT	59.641	20
155	14	168	TCCACTTGAAACTATCAGTCC	59.069	24
248	4	251	CGGCACGAATCCAGTTTTT	61.016	19
280	99	378	ACCCTATTCCACCCCTTCAT	59.513	20
258	115	372	TCTTATAGCATCAACCGCCA	59.281	20
280	171	450	CCCATCATCTCAATCCAACTA	59.988	25
266	443	708	AAATGAGTGGCTGGATTTCG	60.074	20
220	506	725	GGAGAGAGGAAGGGAGATGG	60.149	20
142	636	777	CCGTGAATTCATGCCTGTCT	61.067	20
273	133	405	CATCCCCAAAATACCCTCAA	59.617	20
234	62	295	GCTCAAGGCTCAGAGGACAG	60.284	20
268	104	371	TGAGCATTATTAGCACCCCA	59.136	20
199	267	465	AATCGATTCAACTCATGGGG	59.75	20
170	456	625	GAAGAAGGTGATGTCATGGG	59.918	21
257	398	654	TGCGTGCATGTATATGCTGA	59.85	20
265	285	549	CCATAACCGTCGCATAACTC	58.12	20
248	17	264	GGAGGAGAGAGAGTGTTGGG	58.819	20
131	606	736	TGCTATGGATAAATGTGGCG	59.543	20
260	222	481	TGCATCGAAATCTTTGCATT	59.261	20
101	9	109	GGGGTGACAACTATCAACCA	59.703	21
254	3	256	CGGCCATTCTCTTTTCCTTT	60.553	20
233	28	260	TGGATGCAAAGGTGAACTTG	59.691	20
279	65	343	GCTCCACCATCTCTTCCACT	59.258	20
107	2489	2595	TTTACAAACCTGCCACCCAC	60.786	20
595	595	595	595	595	595
243	49	291	CTTACCCAATCTTGGTGAACA	57.593	21
131	611	741	TGGGTGACTCAGAAATGACG	59.676	20
280	34	313	CGGAGGGAATACAATGCTTTT	60.318	21

169	64	232	TTTGTTTGGTTTGGTAGCCC	59.839	20
110	495	604	CATAGGAATATTAGCGGTGGC	58.62	21
226	307	532	GGGCACTTTGGCTACTTTTG	59.747	20
118	27	144	CTGCGCAGATCTAATGGTCC	60.765	20
257	602	858	TTTTTACTCCCAGCCCTTGA	59.679	20
133	797	929	TAGCAATTTGATTCCGTGCT	58.388	20
266	264	529	CACAAAAATTTGTATGCGGC	59.077	20
224	1058	1281	TTCCGGCTGAAAGACGTTAT	59.708	20
108	15	122	GAAGAACAATTACAATGTTTA	58.084	27
251	1697	1947	ATAGATCGGATTGGCCCTCT	59.888	20
277	150	426	ACGCAAATACGACTGGCTTT	59.775	20
257	1861	2117	GCAAGTGGGAGGATGAGAGA	60.349	20
276	1255	1530	GCATTGATCACAAGCAATCG	60.228	20
229	100	328	TGCTTCGATTCTCAATGTTCC	60.207	21
279	101	379	GCTTCGATTCTCAGTGTTCC	57.448	20
215	416	630	CGAGAAACTTTCAAGGACGC	59.993	20
247	297	543	AACGATGAACTAGGGGCTGA	59.694	20
239	1034	1272	CGTCCCAAGTTTGTTTGCTT	60.147	20
252	408	659	AAAAGCGCAGAAATCCAAAA	59.832	20
265	20	284	AAGGGTTATCACCTGATTTTCT	57.73	23
178	301	478	TTCAATACTTCCAGCCACCA	59.123	20
186	21	206	TTCGGCCAAATTAAAAGAAAA	59.952	22
198	343	540	TTAAGGCATCCCATCCTACG	59.916	20
277	321	597	GTGAGGGGATGTTGGAGTGT	59.817	20
209	145	353	GGCATTCGTTGTTAGCCACT	60.14	20
219	666	884	GAATACAGGCCGGCTAACAA	60.096	20
224	3526	3749	CTATTGCACTGCGGTCATGT	59.746	20
247	8	254	AACATGCAGGGCTGAGTACA	59.318	20
147	13	159	AAAATTTTCCTCACTGCACG	57.878	20
267	92	358	TTTTGTGCTTCTTGCTGGTG	60.027	20
119	0	118	CAGTTATCACCGGATCGC	57.543	18
184	281	464	CTTGTTTCCCCTTCCCATCT	60.298	20
147	10	156	TGGCCCATGTACACTGCTTA	60.134	20
224	675	898	CGACGACAGGAAAAGAAGGA	60.366	20
279	974	1252	TTCCACTCAAAAGGGTCCTC	59.112	20
265	240	504	CCCATGATTCCATGATCTCC	60.096	20
197	31	227	ACCAAGAGACGTTTTTGTTGA	60.062	23
183	380	562	TTGCAGCACTTTCAACATCAC	59.903	21
144	415	558	GAAGCACATGCAAGGATTGA	59.805	20
178	1	178	ATCTCTCTCGTTCTTCCTCTCT	57.481	23
280	49	328	GGATCGTACCTTTTGCTTGC	59.713	20
130	109	238	ACAGAAAAGCCTGTTGGCAG	60.431	20
141	104	244	CCCAAAAATCTAACGGCCTA	59.075	20
254	661	914	GGTTCCGCCATTACCATCTA	59.784	20
217	143	359	ACATCATTCAAGGGGCATTT	59.249	20
251	711	961	GCATATCGCTCGATCAAAAA	58.867	20
269	2	270	GGTTTCTGAATTTGATCCGC	59.51	20
248	1566	1813	ATGGGAAAAGGACCGAAGAG	60.434	20
256	49	304	GTTATCACCGGATCGCAAC	58.941	19
173	902	1074	GGTGGTAAGCAACGGACATT	59.859	20
273	130	402	CCGTTGCACAAGTCACAGAG	60.5	20
280	989	1268	GATAGGCCACCGGTTTGAA	60.848	19
229	240	468	TTCCCATCGAAAAATTAATGC	58.927	21
115	159	273	ATGTGAGAGACCCAGGTTCG	60.112	20
246	765	1010	TTTCAAATACGGTAGACTTCC	59.886	23
243	157	399	GTGATTCACACGAGAGTGCA	59.482	21
180	140	319	AGGGGGTTATCACTGGATCA	59.213	20
223	516	738	TCCCTTCATTTTCGTTTTATTTT	58.2	23

183	359	541	AATTACCCCACCGAAAGGAA	60.534	20
151	82	232	CATTACCCACACACACACTTC	59.385	22
141	116	256	GAAGTTAGCACGTCAAGGGA	58.994	21
117	35	151	GTTCCATGTTACCCGTGGAC	60.096	20
236	311	546	AGATACAGCTCTTGTGGGCG	60.419	20
229	298	526	CATGTATTTTTCCTATGGACCG	60.082	23
259	47	305	ATCCGATGACTGGATGCTCT	59.642	20
106	120	225	TTTTCTTGATAAGCTCGAAGC	59.275	22
255	67	321	ATCATCATCACACGCTGCTT	59.276	20
126	188	313	TACATCGCGTTCAGTATCGG	59.712	20
215	75	289	GCTCTTTTGGGAGACAATGC	59.82	20
248	1264	1511	GTCACACAAGCAATTCGTCG	60.31	20
252	15	266	TTTCTCTTGGTGGAAAACTCTT	57.152	22
258	141	398	TGATGATGATGCCATTTTCC	59.284	20
266	8	273	TGGAGTTGAGATAATTTGCTG	59.225	22
201	4	204	TGCGTTTTGACAATATATAGGT	60.083	26
279	11	289	GCACAAGCAGGGGAAAAA	59.774	18
139	936	1074	CTCTACGTTCCTCAGGCTGC	60.156	20
275	489	763	GTTAAGCAAAGGTGCAAGGG	59.747	20
275	61	335	TCTCGTTAACGTCCCATTTACA	59.514	22
205	11	215	CATAAACTAAGGTGGAGATTG	58.21	27
103	14	116	GACTTGTTATGTTTCCATGAGC	59.148	23
212	167	378	GGATCTTATAGCATCAACCGC	58.686	21
263	434	696	CCCCCTACATCTGACCCATA	59.623	20
263	55	317	GCGAGTCGCTGATTTCATAA	59.019	20
278	496	773	GGAATAAAACCGTTTCACCGT	60.102	21
124	8	131	CTCTCACACTTTGCACACTGA	59.134	22
199	448	646	TGTATGGCCACTTAGGCAAA	59.182	20
140	395	534	GTTCATCGTGAACTCGCGTA	59.871	20
222	544	765	AGCGTGCCATGTGTTATCAG	59.746	20
202	0	201	AATCTTGTGGATGTTAGTGGTT	57.35	25
146	6839	6984	AATCTGAAGAGCTCCACGCT	59.191	20
217	1	217	TCGTTCGTCCTCTTCCTGTT	59.844	20
115	278	392	CATGATCCACGGTCTTTACG	58.999	20
173	588	760	ACACACACAACCACCACCAG	60.383	20
100	509	608	GGATGCGCACGAAATTAATAC	59.473	21
247	17	263	GACGATTTGCAAGCCTATGG	60.606	20
279	320	598	GGGGATACACACCTACCGTC	59.141	20
147	4574	4720	TCCAAAATGGAAATGGGAAA	60.103	20
270	38	307	CTGCCGTTTTTGTTTTGTCA	59.746	20
138	664	801	AAGTTCGTCGAAGATGGTGG	60.111	20
211	31	241	AGTTATGATGGCAGGATGGG	59.773	20
261	674	934	ACCAGACCTGGACCTACCAA	59.425	20
263	40	302	CGACAATCATCTAGTCCTCTA	59.934	24
144	748	891	GGCATGCATGTATCCGTATG	59.799	20
208	22	229	ACGACTGTCGATCCACACAA	60.162	20
173	586	758	CTCCATCCAAAGTTGCTGAA	58.847	20
257	67	323	GCTTCTCTTGCTCTCTCATTG	57.031	21
162	292	453	CTTGATTCCATGACGAGCCT	60.218	20
203	157	359	GAGAAATAAGAAACAATCTG	58.212	23
136	30	165	TGGTTGTGTGAACCAACTCTG	59.626	21
266	254	519	GAGTCCATGACTCTCAATGCC	59.676	21
237	96	332	CATCTTTCTTCTTCGACGCC	59.955	20
233	4300	4532	TGGATCAAACGTCGTCTCAC	59.682	20
271	314	584	TCTCCGAATTTCAAGAGGGA	59.744	20
278	11	288	TTTCGTCCATTGTAAGCAGTTC	59.271	22
261	79	339	TCTCAGCATATGGGAAGGGT	59.508	20
176	4	179	GCATATGTGCGTTTTATTCTTT	57.929	23

250	268	517	CATGGCACAGAAATCTTAAAT	59.133	23
205	606	810	AAAAAGAGCCATCGACAAAA	58.865	21
276	130	405	AAAAGCAATTAATGCGTTCAC	59.666	22
248	106	353	CATTGCTACTGAATATTGTTCT	59.566	27
169	244	412	GGGGAGAACACCGATCCTAT	60.154	20
217	1277	1493	TTGGGGCTGCTTTACTGTTT	59.747	20
276	53	328	CTCCCATTTGTGTTTTCTTCG	59.595	21
272	56	327	AAACCCTGCTTTGTGCAATC	60.118	20
271	333	603	CAATTTTGTACCCGCCAAGT	59.861	20
214	52	265	AAGAGGAAAATCCATCGGCT	60.039	20
142	504	645	CAGCAGGTAAAGCCTCCAAA	60.378	20
223	69	291	TTGTTGAATTGGTCCTGCAA	60.088	20
230	34	263	CAAATCTTTTTCACCGCCTC	59.685	20
170	428	597	CACACTTCCATCACCCAACA	60.416	20
255	12	266	TGCATCACTACCTCCTTGTTG	58.787	21
258	31	288	TTGGTTGGATTGGATTTTGG	60.535	20
218	701	918	CCAAATCGGACTAATGCTGA	58.721	20
217	120	336	ACTCGATAACGGATGCTCGT	59.723	20
256	766	1021	ATCCCAGCCACACATTTCTT	59.41	20
173	109	281	CGAGTCCAGGCTACATCACA	59.855	20
200	1133	1332	ATACCTTCCTGTCCCCTTCG	60.319	20
190	96	285	GGTGTTGGTGAGGCTGTTCT	60.159	20
211	57	267	GCGTGACAACAACAATTTCG	60.157	20
177	377	553	TCAGTGAGTTTCAAGCCGTG	60.025	20
207	1324	1530	CACACGCACACCTCTTCAAT	59.751	20
188	49	236	GAGGATTCGACATTGGGAGA	60.011	20
185	111	295	TACACAGCCCGTGTTCATTC	59.572	20
278	534	811	TTCCTCAGATTTCTGCACACT	57.528	21
167	72	238	CCGATTGACAAATCTCCGTT	59.933	20
241	673	913	TAGGATCTTTTCACGCGGTT	59.708	20
265	3	267	TGAAAGATGGGTGTGTTCTTG	60.529	22
144	84	227	CGTACGGCTAAGGGTAGGGT	60.385	20
191	391	581	GGCATGAGATTCTGTTGGGT	59.934	20
274	83	356	GTAGTTGGCTGCATTTGTGG	59.199	20
237	2051	2287	GTATGCTGGCGGAATTTTTG	60.456	20
246	770	1015	ATCGGATGCGAAATTGGAC	60.828	19
182	127	308	GAAAGGAGAGAGCGAGAGGA	59.848	21
203	3435	3637	GGTTTAACTGGCCCCAACTT	60.221	20
195	248	442	GTGAAGCGCTGATCTTGTGA	60.144	20
278	236	513	TAACGAGAGTGGTTGAGGCA	59.44	20
272	488	759	CGGATTGACGACAAGGACAT	60.924	20
223	2	224	TGCCTTCTTCCACTCTTGGT	59.844	20
240	54	293	TCCCAATCGTTTCAAAATTCA	60.288	21
259	35	293	ACGTAGACCTGGCATCTTGTG	60.186	21
230	251	480	TTGAAATGTAACACAAAAGGA	57.925	24
278	36	313	CGGATGGTGAATTTGTGATTT	59.677	21
266	82	347	AACGAGAGAACTTTCGACGC	59.621	20
157	86	242	AAGAGCTTCTGCGTCTTTCG	59.898	20
150	12	161	CTGATGGAGGGTAGGGATGA	59.879	20
202	887	1088	TGCCAACACCTTCTTCCTCT	59.844	20
188	672	859	CATGCTCCTATTTTAATACACC	59.997	24
238	527	764	AATCGAGCTTACACCCCAAA	59.569	20
168	40	207	GGGGAAAAAGGGTGAAGAAG	59.912	20
116	2010	2125	TAGCAAAAATGTCCCCTGCT	59.708	20
218	217	434	CACCAAATTTCATCATTTTTAA	58.865	26
247	188	434	GTGTAGGGAGTGGGATGTGC	60.395	20
186	352	537	CCATAACATGATTTTGCCCC	60.016	20
243	305	547	GTGGAAGCCGAAGCATGTAT	60.103	20

258	24	281	GGCAAACACAGGATCGATTT	59.939	20
146	895	1040	TTCACCAAGGACTGAGGCTT	59.844	20
158	350	507	GTACCCCCAACGAGTAACGA	59.853	20
195	767	961	CATCAGACTCCGCAATTTCA	59.799	20
165	3538	3702	GTTCAAATCTAACGGCCCAG	59.569	20
240	3	242	AAGGGCCGAGATTTGTTAGA	58.787	20
175	1789	1963	CGTCACTGTTGCTCCGACTA	60.049	20
217	961	1177	TGCGTCTTTCCTTGATGTTG	59.84	20
280	756	1035	CGAAATTGAAATCGGACCATA	59.781	21
106	1	106	GATGGCGGAGAGTTTTATCG	59.668	20
268	37	304	CAACCGCATAGTTAGGAGGC	59.73	20
149	507	655	CAGCAATTGGTTTTGAGGGT	59.971	20
259	209	467	GGTGTGTTGGCATTGCTAGA	59.722	20
237	1067	1303	ACTTCCTGAGTTTGTGGCGA	60.833	20
242	152	393	ATGGCAGGGGGCTTATTTAT	59.664	20
259	22	280	GGATATGCTCAGTCCGGGTA	59.917	20
254	66	319	AGAAACACGTTTTGCTTTTGA	57.616	21
128	61	188	CACAATGCGTGTATTGACAGT	60.096	22
207	421	627	GGCATGAATTCTTGGATTGC	60.423	20
251	482	732	CGGCCTAACATATTCCCACA	60.712	20
198	138	335	TGAATTAACAGCGAGCATGG	59.833	20
141	1856	1996	CAGTTCAAAATGGTTTCCCG	60.336	20
126	81	206	AGTAAGAAAGCCCACCTGCC	60.63	20
265	26	290	AGACGCGAGATTTACGTGGT	59.763	20
280	2387	2666	CAGTCGCATACTTCCCATCA	59.673	20
199	405	603	TATCCCCCATCCATGTTGTT	59.871	20
249	18	266	TAACACCTTCATCGAGCGAG	59.024	20
150	342	491	TTGCTGCTCTCTTTTTGGCT	60.27	20
258	113	370	GTCCCTTTTTACCCCTCAAA	58.02	20
264	10	273	GGAAATAAGGAGGTGTTATGA	57.235	25
166	45	210	GCAGTAACCCTCTCATCGGA	60.218	20
140	250	389	GGAACCAGCTCCGATTAACA	60.074	20
190	77	266	TTTGGAAAAATCCTAGCCACA	59.573	21
257	93	349	GACCGAATGTAATGAACCCG	60.192	20
276	154	429	GGCACAATTCGTACAGGGAT	59.82	20
245	284	528	CACGGCTTCAAATTGTTCCT	60.11	20
237	1259	1495	GGCAGCTAGGGTTGAAAGAA	59.452	20
172	65	236	TACACGCACATCAACCCACT	60.032	20
205	673	877	TTCATTTGCCTGACCTACCC	59.933	20
196	2113	2308	GAATTGCCATGTCCATGTGT	59.223	20
176	1968	2143	TGGGGCCAATTTACTCTCTG	60.066	20
100	337	436	TTCCGTAGGGAGCAAAGTGA	60.766	20
235	281	515	GATTTTGAGTTCATGGGCGT	59.939	20
280	135	414	GAACTATCTACAGGCCAGGGG	59.969	21
263	35	297	TTGTATGGACGACACGCACT	60.183	20
238	329	566	GGGGTACGTGCCATAAAAACT	60.122	21
108	902	1009	CGCATGATAGCATTCTCCAG	59.4	20
273	108	380	GCATCTCTCTCGCTCTCATTG	60.256	21
207	349	555	TCCCATTCAAAATCTTTCCA	57.983	20
249	159	407	AGTTAGTCGGAGCCTTCGTG	59.496	20
275	257	531	CTCATGTAACCGATCCCCAT	59.629	20
138	3632	3769	CTGAATGACCTGCCTCCATT	60.073	20
188	103	290	GCTCTCTTTGTAATCTCCCCC	59.184	21
161	246	406	TCCCTCTTCATCCTCCCTCT	60.149	20
185	322	506	CTGGGTTTCCTTCCTCTTCC	60.045	20
177	5573	5749	CACAAAACCCTCACACCCTT	59.861	20
278	752	1029	CCCAGCACTGCTTCTAGGAT	59.454	20
174	132	305	CAAGGGCTTGAGTAGCTTGG	60.008	20

274	64	337	AACGCGTCACACGTAATTCA	60.18	20
165	1618	1782	GTGCCATAGCCACCTGATCT	60.104	20
169	163	331	CTCTGTCTAGTGGCGAAGCC	60.156	20
131	29	159	GCGTGAGTTACGAAAGAGTG	59.928	21
254	3	256	CCTTGACCAATCGATTTCTTG	59.555	21
270	308	577	CACTCGCTACGAGCCACAG	60.773	19
216	0	215	CCATCACCGCATTTTCTTCT	60.074	20
257	37	293	TCACCCACAAACTTTTCAACTT	58.65	22
132	344	475	CCTGATCAACCTCACCCTTC	59.505	20
278	5001	5278	GGTAGCTTCGACAAGCCATT	59.34	20
138	2	139	AAAATAATCCCAAAACCAATG	57.444	22
243	24	266	ACGCACAACAAAATACAAAA	57.454	22
231	18	248	GCATCATTTTGGCCTTTGAT	59.907	20
233	219	451	GGTCTACCTCTGCATTTCCG	59.694	20
226	673	898	CCCATTTCCATGCTTCAACT	59.933	20
123	51	173	GCGGGTAAATATCAATTTCGA	59.837	22
200	1251	1450	AATTGTGGCCTCACCTTCAG	60.111	20
250	45	294	TGTGGGTTAGCACTTGATCG	59.716	20
276	1082	1357	GTTCAAACTACATTTGGGGGA	58.798	21
263	289	551	TCGATTCGAATTTTCATACACA	58.161	22
275	57	331	TGGTATGACAATTGCAAGCAT	59.055	21
226	194	419	CAGCCAACTCGATCTCATCA	59.942	20
153	534	686	TGCTTTGTGCATTCTTCCCT	60.776	20
137	24	160	TGCTTCTCCAAATCCATCTTC	59.259	21
233	413	645	AAGTGTGCCCAACACCTTTC	60.012	20
114	380	493	GCCAAATGCCTACAAATTGC	60.465	20
110	17	126	ACACTCACTCTCACTAGCCGC	59.685	21
230	21	250	CAATACCGTGACATGCCTTG	59.988	20
228	1581	1808	ATGGCTGTTGATGTGGACAA	59.967	20
225	3463	3687	GCCAGAGCTTCTATGGTTGC	59.985	20
217	121	337	TCGAACTCCAATAGCAGCAA	59.566	20
172	370	541	CCTTTGATCCATCACGGAAT	59.75	20
278	291	568	TGGGAAAGAAAGGGTGTTAC	60.207	21
108	104	211	TGGACAAGACAAGGCTAGGG	60.246	20
161	5216	5376	ATGGCACACCATACCAGGAT	60.081	20
278	920	1197	GCCCTTTTCATTGCTGTCAT	60.081	20
138	30	167	ACGGTGACGAATGGTTCTCT	59.579	20
176	432	607	TACGCGCGGAACATACATAA	60.117	20
228	376	603	AAGGTCCAAACAACGAACCA	60.388	20
107	293	399	CCCACACTCTCCTCATTTTCA	60.096	21
218	129	346	GAATGGTGGTGTTTGTTCCC	60.073	20
280	1298	1577	TCAACCCACTGCAGTACCAA	60.152	20
169	239	407	ACGTGGACAAGTCTCGCCTA	60.854	20
264	147	410	TAGTGGTGACAAGTGTGGGG	59.435	20
155	62	216	CACCCACATTACATTAAACCGA	59.625	22
280	212	491	GTGCCACATCAGCTTCTTCA	59.992	20
274	6	279	TCTCGCTGCCATATTCTTGA	59.523	20
113	655	767	GGACAGCAGCCATTAAAAAGA	59.352	21
212	54	265	CCTATTCCCTCGATTCAGCA	60.17	20
247	3	249	CCTTGACCAATCGATTTCTTG	59.555	21
166	426	591	ATCCACGAGGATGATGAAGC	60.042	20
257	919	1175	TTTCATTTGATTAGAAGTTCTG	57.172	24
266	305	570	TTCAGCAAACTGAAGAACAAG	59.534	22
189	644	832	TAGCCAACTCGCTTAGCCTC	59.752	20
245	32	276	CTGGTAATGGCCGGACTAAA	59.953	20
182	48	229	TTGGCAATGAGATACCGATG	59.499	20
267	825	1091	TGCGAAGTAGACGTGGATGT	59.318	20
173	256	428	CACTTGGAAACTCCACACGA	59.72	20

248	577	824	CTCTCCTTCTGCGCACTTTT	59.757	20
258	964	1221	GCGTAACATTATGAAGGCGAC	59.627	21
280	21	300	AAAAAGCGCTCGTACATTTTAT	59.724	23
182	161	342	CATAGACAAGCCCCTCTCCA	60.21	20
275	485	759	TATGAATTCCGTGTTGGGGT	60.051	20
223	469	691	TCTTTTTGACATTTGGGTTCA	58.107	21
229	329	557	TGTGGGTTGTTCTGATCTGG	59.52	20
280	576	855	CGCATGGTGACATCAGTACAC	60.048	21
241	245	485	TGCGTTAATGTACACAACTTCC	60.455	23
259	228	486	GTGGGCTTGGAGCATGTACT	60.142	20
280	48	327	GCCATGATCTCCTGATTCAAA	60.029	21
268	1201	1468	ACCGAAAATCACGTTTGCAG	61.06	20
105	46	150	AGTGTTACGATAGAATCACGC	58.289	22
219	139	357	TCTTGCCTCCACCATCTTCT	59.803	20
118	35	152	TGACGCTTAGAGGGTGTTTTG	60.29	21
264	0	263	TTTTGACAATATATAGGTGTTTT	58.82	27
163	242	404	GTTCAACCAAACGGAAATGG	60.206	20
257	66	322	CGCGGTGTTTTAACTTGCTT	60.298	20
144	516	659	CTCGATTAAATGGGACCGAA	59.894	20
258	508	765	ACCTCACGACGACTCCAAAA	60.69	20
123	288	410	TCTCGTGTTCTTCCTCCCTC	59.38	20
200	278	477	GGAATTGTGTGGGTCGATCT	59.786	20
272	901	1172	TGCGCGTTTTTAGGGTTAAT	59.624	20
260	84	343	TTTGAGTTGGGAGAGGGATG	60.042	20
259	508	766	TTCAGTGGCTACAAATCCCC	59.933	20
280	704	983	TCCCTGTGGGATTAGGATTG	59.744	20
225	456	680	TGACGGTTGGATTTTGTCCT	60.353	20
207	141	347	AGGCTTGAGTTTCCTCACGA	59.989	20
218	14	231	TGCTATCGTCCTGATTGGTG	59.673	20
157	284	440	TAAAGACATATCGCGACCCC	59.923	20
171	3367	3537	TGTCACATCTCGATCTTCGC	59.95	20
195	1356	1550	AACAGTCTGCAGGCCAAAAC	60.299	20
135	527	661	GATCAGTTACCCGAACTGCC	59.556	20
217	71	287	AAACGCGTCATGGATAAACC	59.829	20
143	17	159	ATGGGAAGAGGGGTATGAGG	60.147	20
256	376	631	GGGACGATTCTGAAAGGTGA	60.05	20
197	34	230	GGGACGAAAATAACCCTCGT	60.187	20
122	86	207	CAATTTGCAGCCCTCATTTT	60.074	20
261	721	981	TCAAAGTCCAAACTGCCTCC	60.232	20
169	360	528	TTGAAGCACCAACCTGTTCA	60.278	20
154	2	155	ATCTCCTCCTCCACCGTGA	60.627	19
124	2	125	ATCTCCTCCTCCACCGTGA	60.627	19
229	3014	3242	CGAGTTGCCAATCATTTCCT	60.074	20
224	359	582	AAAAGTAACACGTGCCGTCC	60.037	20
214	1172	1385	ATATCATGGACACGGGAAGC	59.78	20
279	548	826	TCGATCTTGCTCTACGTCTGG	60.544	21
139	21	159	TCTCGCTCTACACTTTCGGTC	59.63	21
260	359	618	CGAATCCAGGTAAGGCTTGA	60.206	20
199	1002	1200	ATATTCGCTGCATCAACGC	59.814	19
137	597	733	CGGCGGCTCTATAAAATTGA	60.185	20
233	1195	1427	TTAGGTCATGGATCGACACG	59.522	20
262	6193	6454	TTCCAGGGCTACTGGAGGTA	59.688	20
142	323	464	TGACTTGGGGTCCATCTCTC	60.048	20
242	2352	2593	TTCCATGCATCAAGGAAAAA	59.087	20
186	385	570	TTGCATTTTCCTGTTTTGAGA	58.4	21
164	651	814	ACTCAGGTGGTTCAAATCGG	59.966	20
254	1480	1733	AGCATTGCTGTGCTGATGAT	59.43	20
159	293	451	ATCACCCAAAGCCATTTCAC	59.797	20

157	156	312	AGTTTGAAGAAGACCGCACG	60.431	20
214	98	311	GATGTGTGCCCAAAAGGAGT	59.973	20
242	4	245	AGTGCTCGAATATCTCCCCC	60.431	20
239	1659	1897	ATTGATGTCCGAATGCAACA	59.931	20
133	340	472	CACACCTTCAGAAATGCAATG	60.037	22
251	81	331	CCTAGCTTTGCCCTCCTTCT	59.976	20
213	113	325	CTCCATTGCATCACCATCAA	60.481	20
179	568	746	TCGCAGAGCGAAAAGTATCA	59.712	20
114	2	115	TGTAATCTCTCTCGAAGTTATA	57.16	27
111	369	479	AGATTTACGTGGTTCGGTCG	59.993	20
200	197	396	TAGAGCCACAGCGGCATAGT	60.955	20
135	543	677	AACTCATTAAATGTGCCGCC	59.967	20
166	2364	2529	GAAGATCAAAGGCCCACATC	59.488	20
188	767	954	TGCCCACAAACACTCAAGAA	60.278	20
117	435	551	TGACATTTACGCAGTTTGTCG	59.784	21
135	4579	4713	GAGCTTGGTTGGGAAAATCA	60.051	20
131	869	999	GGCTCCCACAATGAACAACT	59.973	20
264	39	302	CGAAGACACGATGTTGAACG	60.301	20
275	159	433	CCCAGAATTGTAAAGCGCA	59.818	19
191	48	238	GCACCGAAACAGAGCTGATA	59.028	20
135	26	160	GAGAATGAGGGAGGGAGGAG	60.149	20
243	61	303	CTCGGAGACCCATTTCTCTG	59.797	20
117	325	441	GGTGGCCAACAGTTTTGATT	59.836	20
240	1414	1653	GGGAAGGGAAGAAGGAGAGA	59.749	20
167	679	845	TTCTAATTTGGTTACGCCGC	60.095	20
257	1424	1680	GAGGCTTTTCGCTTTCCTTT	59.966	20
238	37	274	TTTTATCCCATGTTTGTGCAT	57.885	21
280	3169	3448	CAGCGAATGTAACCGGATCT	60.096	20
159	1713	1871	GTTAGGTGACCCACCTTCCA	59.82	20
189	381	569	TCTTTCGAGTCAGGGCATCT	59.95	20
251	655	905	TTCTCCTCCCTCCTTCAACA	59.773	20
244	5	248	TGCGTTTTGATGATATATAGGT	60.054	26
124	517	640	TCACTGATGACTGACGTGGG	60.748	20
271	72	342	CGAGGAAGTTTTCACGAGAAT	61.133	22
278	912	1189	ACATTAGTGCATCGTCTGCG	59.895	20
217	861	1077	GCGGAACTCCTGAATTTGAA	60.192	20
280	94	373	TTTTTGCACCATTGGTATTGT	57.94	21
126	475	600	TGACGAATGATACCATTTAAG	59.507	23
170	270	439	GAACTAAAAACGATGAAATTT	60.149	25
223	93	315	ACATTCAAGGGGCATTTTTG	59.801	20
224	965	1188	CAGAGTATTCCCGGTGTGGT	59.844	20
199	1883	2081	TTTCACGAATATACATGTTCCA	58.485	24
108	838	945	TGCCCTAACGCCTTATCTTG	60.223	20
230	2300	2529	TGTGGCCTAACTTCTGGTGA	59.288	20
261	0	260	GAGAGGAGTGAGATTGAGCGA	59.694	21
213	2508	2720	ACCCTACCCATTTACCCGTT	59.46	20
123	937	1059	TTCTTCCCCACTGCTCATCT	59.803	20
146	20	165	TGCTCCATTTTCACAACTGAAC	60.154	22
274	100	373	GTGGGTTTGGAGAAGAGCAG	59.844	20
139	8	146	TGAGCCGTCAGTGCATTAAA	60.401	20
249	51	299	AGTCACAGATGCGTGACACC	59.744	20
181	259	439	ATGCATACATGACTCGAGCG	59.854	20
249	513	761	CGGGCCGTGTACTTTACAAT	59.883	20
144	8	151	CGCGTTACGAATCCAAGTTT	60.131	20
247	103	349	TTTTTAGGGTTTAAAATCGCGT	59.118	22
276	406	681	ATGATGGACAAGGCATCCTC	59.893	20
179	0	178	GGCCCACAATGGTTATTAGTT	57.874	21
251	12	262	GAGAGAGGGGCGAGAGGTAG	60.489	20

211	57	267	TTGTGACGGTGACTAGAGCC	58.882	20
280	16	295	TTACCATATTTAAGGGTTATCA	58.789	26
209	193	401	GACCGCGAAGTATCTGCTGT	60.428	20
280	62	341	CGTTTCCCATGTTGCTTGTA	59.585	20
267	925	1191	ATCACCATTGGATTCTCCCA	60.135	20
278	417	694	TTGGTTGTTTGAGATTGTGGTT	59.378	22
253	150	402	TTGCCTTTCTTTCCCCTCTT	60.18	20
157	362	518	AACTGTGAACGGCGCTAATC	60.278	20
279	11	289	TTTCTCACATAACTTAGCTGTT	58.762	26
276	135	410	TTATGATGGGAATGGTGGGT	59.871	20
249	56	304	TCTGGCTAATTTGGCAGCTT	59.982	20
247	1250	1496	AACCGGTTAAAACCCAGACC	60.089	20
255	424	678	GGTTATCACCGGATCACGAC	60.203	20
207	1930	2136	AAGAAACCCACAAAAAGCCC	60.332	20
256	63	318	GTGTGTGCATGCATTTGTTG	59.595	20
251	938	1188	AAGAATTGATGCCAACCCAC	59.797	20
260	149	408	GAAGCATGAAGCAGCAATGA	60.104	20
194	227	420	GCATGATCAATGTTGTAGAGG	59.457	22
156	700	855	AAGTCAACCAATGCAGATGCT	59.755	21
165	675	839	CCAGCACCTTCTCTCCACTC	59.986	20
278	1494	1771	CAGCTGACGAACACTCCCTT	60.444	20
276	108	383	ATACCCAGGGGCATATGTGT	59.009	20
232	282	513	AGACAGCGATGGTGAAGAGG	60.408	20
172	1002	1173	GGTTCCCTCTTCTCTAACGC	58.001	20
227	69	295	AACTCGAGATCGGTCCACCT	61.052	20
253	60	312	ACCCAAAGGTCTCATTTCCA	59.381	20
275	5585	5859	TTGTCAAAAGCACCAGCAAT	59.322	20
206	948	1153	AACGGTCGCAGAAAAAGCTA	60.018	20
276	340	615	TCCACAGACAACCTCACCAA	60.129	20
210	28	237	AACACGAGGAACTTTGGACG	60.149	20
218	17	234	TCTAGAGCCACTCCCTCCAA	59.943	20
270	119	388	GATAAGCCAGGGTATGGCAA	59.923	20
167	262	428	CCGGGCCATTACAATAAATG	60.033	20
243	27	269	CGGTAAGTCGTTAATGGAGGA	59.098	21
137	106	242	AGGTACGATGCTGCTGTGAA	59.47	20
203	2706	2908	ACGGGAATGGTGTGTTGATT	60.096	20
213	1785	1997	AAATGTGGCAACACCAATCA	59.823	20
246	1169	1414	GGGGATAAGAATCAGGGGAG	59.722	20
191	722	912	TAGCGATGAAGACGACGATG	59.972	20
159	1422	1580	CGCTTCTGCAAGAGATGACA	60.287	20
238	31	268	TTCGATTTGGGGTGTAACAA	58.866	20
260	2535	2794	TTCCGGCGAGGATATATGAG	60.016	20
233	15	247	CAAAAAGGGAAGAGCGACAC	59.853	20
171	106	276	GGATCCGACGTCCAATATACA	59.659	21
234	346	579	CGCGATCTCAACCAGAAAAC	60.776	20
179	356	534	AAAAATGATGCCAATCCAGC	59.907	20
149	19	167	TGATTCTTTTGTTTGGTTTGCT	58.787	22
260	1229	1488	GGTGTTTTTGGATTGGTTGG	60.066	20
145	1018	1162	ACCGCAATAATCCATACCTCA	59.31	21
273	268	540	GGTGATTCGAGATGATCCGT	59.893	20
269	1040	1308	AAACTCACCATTTGCCAACC	59.836	20
175	668	842	TGACGTGGTGTTGTGGTTTT	59.897	20
108	42	149	GTGAATCACACTCCCCCATC	60.184	20
227	1541	1767	TTACCTCATCAGAGCTGCCC	60.362	20
274	319	592	CGAACTGGGAAAGGAGAAAA	59.284	20
269	346	614	GACACTCTTCTTCACCCCCA	60.088	20
231	83	313	CCGAACCACGTAAATCTGTG	59.047	20
125	699	823	AGCTGCTGCCCAAAAACTTA	60.018	20

101	42	142	TGACCCCCTTTGTCAACTTT	59.425	20
197	163	359	AGGATTGTTGACTGCCAGGT	59.579	20
169	1789	1957	GCTTCTCGTTCCCTGTTGAA	60.375	20
203	4779	4981	TGAAATGCACCACTCGTTTG	60.699	20
241	134	374	CTGAATGCTTACCGATGCG	60.373	19
137	303	439	TCACCCTTTCTTTGATGGGT	59.381	20
170	328	497	GTCATGAATCGGTGCATTTG	59.931	20
190	705	894	CGAGAACTCGGGATGAGAGA	60.488	20
268	352	619	TCCTTTTCCATTATCCATGTTTT	59.96	24
212	1073	1284	GGTGCATAGGTTAAAGGGCA	59.96	20
280	381	660	GCATACCAACCAGATCTACGC	59.611	21
183	550	732	TCCTTGGATCTTGATGGCTT	59.629	20
240	2170	2409	GAAGGCTTTGATTCATCTCTCT	59.496	23
190	607	796	CTTCCGCCCATTCTACAAAA	60.067	20
227	246	472	TGGAATTCGCAATATCCAAA	58.958	20
134	576	709	GGGATCGATTTTTCAAGGGT	60.131	20
258	1151	1408	TGGCTTCATTTTGCAGTCAC	59.847	20
155	674	828	GGCGGACATCAAAGGAATTA	59.901	20
198	360	557	ATCACGGACCCCACATACAT	59.934	20
264	56	319	TGCAATGGACTGCCTCTGTA	60.413	20
271	56	326	GGAATGTTATTGTTCGTGCG	59.041	20
267	146	412	AGCTGTAGGTCGGATGAGGA	59.827	20
181	360	540	TGAGCAAGCGCATTGTTTAT	59.472	20
269	343	611	CTTCCCAACACCACCCTAAA	59.824	20
235	1404	1638	TCCTTTCTGCATTTGGGTTC	60.051	20
171	524	694	AACAGGGCTGGTGTGTGTTT	60.466	20
242	66	307	AACGGGATGCTTTCAAAATG	59.938	20
268	1274	1541	TTCCATAAACAGGGAAGATGT	58.949	22
144	813	956	TTGGAACTTGCTTCGGAAAG	60.357	20
209	31	239	CTTGGGAACCTAGGAGAGCC	60.204	20
220	580	799	ATTTGGGGTGATGGGTTTTT	60.278	20
198	408	605	GACCGAAATGCAACGATAAA	59.47	21
233	15	247	TTGGCATGTAAATCAGCCAC	59.548	20
249	307	555	CGAAGTAGCTCGAGCCGTAG	60.305	20
167	15	181	CCAAAATTGAACAGCCGATT	59.938	20
250	150	399	CCCTCAATCTCGAAAATGGAT	60.272	21
211	346	556	GGGGAAAAGGGTGATGTTTT	60.032	20
135	55	189	AGCGCGTCACACTTTTATCC	60.278	20
162	337	498	GGGGACAACGCCATTTATAG	59.297	20
203	2430	2632	TGAGGATATTCCAGTGTGTGA	59.485	23
213	567	779	TTCAACGTCGGACAAGACAA	60.278	20
274	1172	1445	AGCAGACAGGGGAATCTTAG	59.721	21
208	93	300	CCTCTAGCATCTCTTGCTCTCT	59.048	23
166	63	228	CCGATAGAAGCCCACATGTAA	59.967	21
197	544	740	TTGCCCAAATATGCAGTGAG	59.688	20
110	971	1080	TTTAAGTCGTTGTCGTTGCG	59.911	20
225	2837	3061	CAAGATGATGAAGGTCAAAC	60.11	22
130	18	147	GAGAAGGGTTATCACTTGAAT	59.113	25
221	215	435	ATAGGCACCCCTGGAAAAAG	60.312	20
245	69	313	GGTGAACCGCGTAAATCTGT	60	20
126	227	352	GCATTATCCGGTCGATTGTC	60.304	20
275	122	396	TCGTTTCAGAGCTGGGTAGG	60.388	20
258	19	276	AACCGATTGCTTTTTGATCG	60.074	20
279	744	1022	CAAAGTCTTGCGATGGATTG	59.272	20
182	73	254	TTCACCCATTGTTTGCGATA	59.93	20
209	76	284	TTTTCCGATTGACAAATCCC	59.739	20
262	1244	1505	TGCCACACGTATACCACGTC	60.459	20
237	54	290	TGTGCACGAGAATACATCCAG	59.731	21

201	428	628	GAGACATGGACGGGAAGAGA	60.199	20
264	146	409	ACATCACCGGCATATTCACC	60.613	20
214	1832	2045	GACAATTGCTCGCAAAGGAT	60.221	20
166	1275	1440	TTCTCATTTGCAACCGATGT	59.127	20
106	1297	1402	CTCAGATCCTCGGAAAACCA	60.187	20
252	316	567	ATGACCCACCAAACATGACA	59.656	20
164	0	163	TCTCTCTTGGTTGGTGAAGAA	58.955	22
223	277	499	CGAATGTTTCTCCTTTCTTGG	58.82	21
273	1028	1300	TGGTACTTGCAATGTTGGGA	59.964	20
113	248	360	CAAAATTTGGCATCAAATTCA	59.82	22
268	121	388	GGATGGGAGTCAATCCAGAA	59.862	20
127	259	385	ATGTCTTGCCGGAACTGTCT	59.727	20
178	4	181	ACATCTAGCTCTGTTGAATCTT	57.773	25
221	110	330	TGGAGATGTGAAACATGCCTT	60.511	21
156	13	168	TCGGTTTGGCCAATATTTCT	59.411	20
142	390	531	GATATTTGATTTTGCGGGGA	59.735	20
251	1254	1504	GCTTTGGTGACTGAATGATGC	60.661	21
230	75	304	GTGGTATGGTATGGGGACCA	60.317	20
192	357	548	TCACGTCAACTTATTCCCCC	59.79	20
262	150	411	AGAGAGGAAATTAGGAGGGG	59.913	21
220	2032	2251	TCAAACAAAACCCTACACCCA	60.248	21
186	1086	1271	TTCGATCTACTGGGCCACAT	60.483	20
246	513	758	GGAGTCATCGGTCTCTGCAT	60.231	20
152	328	479	AGGCAAAATTAAAAATGCCAC	58.188	21
127	928	1054	GCTTCGTTTTATTTGGCAGG	59.72	20
259	113	371	TGCCTACCAAACACTAGGGG	59.986	20
171	779	949	CCGTACCGGAATTTAACGAA	59.826	20
197	2302	2498	GCCATGTCTAGCATTGGGAT	59.923	20
251	1080	1330	CTGCCATAACCCGAAAAAGA	60.067	20
190	165	354	TGCCGTGTTATTGTGAGTCC	59.572	20
132	2089	2220	TTTGCCCATCTTCAAACTCC	60.051	20
206	2596	2801	TGCTTTCGGCCTTACAATCT	59.845	20
186	2496	2681	TGGAATCGCGATGAGATTTA	59.212	20
214	304	517	AACCCGATCCTTGAGGAAAC	60.306	20
254	20	273	AACAAGTGTCGGCACAAACA	60.199	20
120	383	502	GAGAACCAAATGTGCAGGCT	60.263	20
279	381	659	GGTCGACTTACGCCATGAAT	59.962	20
276	91	366	AGCCTCTATCCCCATGTCCT	59.919	20
200	2700	2899	TTGATCGAAAGGGAATCGAC	60.014	20
274	681	954	TCTCTTCTCCCCCTCTCCTC	59.883	20
239	544	782	TTCAGGAGGCCTATGAGACG	60.353	20
197	70	266	CACGTGACATAAAATGCATCG	60.006	21
223	49	271	TGAAACCAGGGGAAAAAGG	59.888	19
249	165	413	CGGCACAAAATTTTCCACTT	59.975	20
169	764	932	TTGCTGCGGTACTTTCATTTT	59.772	21
252	203	454	ATTTTGACCGAAATACCCCC	59.888	20
260	78	337	TTCACAGTTTTCATTTGATCAC	58.986	23
260	61	320	GGCTATAGAGCCGTTGAATGT	58.366	21
134	117	250	TGATACGGGACCCTCATCTT	59.361	20
124	439	562	TACAAACCACCTTAACTTCCG	60.395	22
223	933	1155	CAGCGGTATGTTCGGATTTT	59.96	20
274	81	354	CGAGCCACAATACTTCGGAC	60.657	20
141	20	160	CGGATTTAGCGGTTATTACCT	61.448	23
132	444	575	AAGAAGATGCCGAAGGATGA	59.773	20
146	14	159	GGGAGTGCTCTCACCTGAAT	59.258	20
276	2091	2366	AGGAGACGAAAGCTTCCCAT	60.212	20
221	153	373	GGGTTCTCGTGATAAGCTCG	59.836	20
279	21	299	AGAGGGTTATCATGGATCAA	58.32	21

276	190	465	AGGGATTTATGACCGTTTGC	58.906	20
146	80	225	GGTTGTGGCTCTGGTTCTGT	60.159	20
219	8	226	GGAGCTGTGTGATGTTGGAG	59.261	20
272	2325	2596	CAGATCGCGAGAAATTGAGA	59.101	20
269	156	424	CATGTTAAGCCTTGGGATGAA	59.946	21
127	43	169	CGTTGATTTGAGGCAGGTTC	60.636	20
122	1119	1240	GGGTGTAAGAAGGTTTGGCA	59.971	20
113	374	486	TTTACTCCGAAAGGGACGAA	59.679	20
228	2	229	GCTTCAAGTTTCCTCCTTTTG	58.111	21
123	2295	2417	GTTGGAGAGTTGACGGTGGT	60.009	20
214	295	508	CGCCTCCGGACTTTAACTCT	60.753	20
186	96	281	GCACCCCTACATTCATCGTT	59.82	20
243	315	557	AGTCCCCGGTCCGTAAAATA	60.553	20
133	299	431	AACTCCATGCAAATCACACG	59.572	20
186	249	434	TACTTTGCGGGTAGGGTAGG	59.108	20
196	141	336	CGCTTCGAGTTGTTTTCACA	60.027	20
252	216	467	GGAAATGGGAATGGGTTCTT	59.996	20
218	2391	2608	TGCTTAAGTGCTATGCAAATC	58.307	23
278	1371	1648	TCTCCACTCCCTGAGTATCCC	60.462	21
261	456	716	CCATCCCAATTATACGGTCC	58.974	20
211	240	450	GTGGACGCTCCAGATTGTTT	60.119	20
234	430	663	ATCAAGGAGGGGAAATGGAT	59.588	20
159	993	1151	GATAAGCACGCCACAAAACC	60.511	20
270	25	294	CCCTTTCTCCTCTCCCACTC	60.186	20
179	1997	2175	CCACAGCATGGACTTTGTTG	60.152	20
261	2000	2260	CAAAGCAACCCTTAAGAGCG	60.011	20
151	102	252	GTTTTGAGATGGGTGGTTGG	60.21	20
159	5	163	ATTGCCCCAGGAATCTTGTT	60.693	20
280	266	545	TAGCCGGGTCGTGACATAA	60.08	19
200	95	294	GGGAAGAAAACGCAACACAT	59.978	20
273	288	560	CCACATGCTATGCCTCAAAC	59.152	20
244	484	727	TTATCTACAAAACGAGACCAA	57.613	25
109	1390	1498	TCTATCCGCCAGTGCTCTTT	59.978	20
182	799	980	TGGCATTACAAACTTCAAACC	60.389	22
207	2649	2855	ACCAACACTGCATCAGTCCC	60.999	20
232	78	309	TTGAGCTCTGATGCCACAAT	59.399	20
277	148	424	GAAGACTTCGCATCTCGGAA	60.483	20
142	4	145	GAGTTGGTCATTCTCAAGATG	58.646	22
279	161	439	GCCAGAGATTTCCGCTAACC	61.091	20
241	97	337	CCTTCCTGAATGCTGCTTCT	59.574	20
102	18	119	CACCAGCCATCCAAAGGTAT	59.813	20
180	1823	2002	GGCCCATGTGTTAAATCAAGA	59.815	21
103	329	431	TTAAATGACCTTGGGATGCG	60.827	20
248	233	480	AGCGCCTAGCGATTTCTACA	60.138	20
244	3669	3912	AGCCGCACATTGATCTTACC	60.103	20
278	546	823	TGTTTTGGTCTCACCGGAAT	60.353	20
204	702	905	AATAAGATACGGGCAGCGAA	59.704	20
235	112	346	CTTCCCCTGTTCTTGCATGT	60.111	20
269	493	761	CGCGGAGCATTGTTCATAC	60.235	19
229	75	303	TTTCACCCCCAAGTCTCCTA	59.521	20
139	9	147	TTTTGTCTATATCGCTCAGTCA	57.221	24
248	92	339	TTGGCGAAAAAATGTTGACAG	59.706	20
234	98	331	TTTGTAAGTCCGGCCATCTC	60.074	20
174	989	1162	CATCTAGGGGAGCAAATGGA	60.029	20
211	914	1124	TCTGCAATGAACGAAAATGC	59.816	20
259	259	517	GAATGAGGGTTGTGGGACTG	60.363	20
138	27	164	GGGCTAACGGGCTACACAA	61.036	19
276	2356	2631	GAGCTGGAAAAGAGAGGGAA	59.948	21

119	275	393	TCCAAAGGTGGCCAAAATAC	59.801	20
181	250	430	TAAGGGCGGTATCACCTGAA	60.46	20
258	867	1124	ATTTGGGCATAAAAACGTGC	59.838	20
157	15	171	TCATCAACAGCGAAGCAAGT	59.596	20
267	228	494	ACAATTGGCAGCACCAGAAT	60.526	20
210	970	1179	GGTGGACTGTAGTGGGCAGT	60.033	20
270	0	269	GTAAAACAGCGCCCGTACAT	60.025	20
141	442	582	TGTTGGCCTATGGTGCAGTA	60.134	20
184	249	432	ATGATACGCAAGCGGAAGAC	60.243	20
277	7	283	AGGGACCACTAGACATTCGCT	60.146	21
201	702	902	AACCTGGTTCTCGTTCCAAA	59.569	20
266	1179	1444	CAAACGTATGGAGTTGTGCG	60.172	20
189	766	954	GGATGAGAGATTTGGGTTCG	59.483	20
141	4	144	TTAGTTAGCATGGGGGAAGG	59.04	20
125	275	399	GACCGCTCAAATCACTCACTC	59.866	21
252	9	260	ACCCCACATTTGTGGCATA	59.639	19
165	253	417	AGATCTCAACGCATCAACCG	61.208	20
237	117	353	TAAATACTTGCTGCCCGAGG	60.223	20
231	50	280	CCAACGAAACCACTGACAAA	59.585	20
243	513	755	TTCGATTCGCAACAATTGAG	59.809	20
234	1485	1718	AGCACCCTTATTGTGGCTTG	60.132	20
147	31	177	GATGGGTTATTATTGGAACGA	59.242	23
280	1780	2059	TTGTACGTCCAATATGTAAATT	57.296	27
125	2896	3020	TGCATATACATACGCGCACA	59.736	20
280	24	303	CGGACTCCTTCTTCCTTCCT	59.811	20
264	8	271	CAATGGTTGTGGGGGAGTTA	60.605	20
230	983	1212	AGTTGGGGATGAATCCAGGT	60.575	20
190	145	334	ACCTAAGGGGGTGTTTGCAT	60.61	20
139	35	173	TACCAGGGTCAACAATGACG	59.415	20
139	35	173	TACCAGGGTCAACAATGACG	59.415	20
181	1712	1892	CTAATGCTTATGCTGCTGCG	59.77	20
144	322	465	CCTATTTGCCTTCCCTCCAT	60.278	20
252	439	690	CTCCACATGGAATCCCCTTA	59.744	20
177	1155	1331	TTTTTGCGATGGAACATGAA	60.051	20
236	101	336	ACCCGAATTGACATGCCTAC	59.82	20
181	86	266	TCGACGACTTGTTGGAAATG	59.691	20
174	633	806	TATTCTTTTACGCATGCCCC	59.928	20
114	15	128	TCATCTATAGGGAAGTTATCA	59.464	26
145	34	178	CAACGGATTTGGTTTGTTCC	60.206	20
202	149	350	TGGGATTACACATTTCGCCT	60.331	20
115	131	245	TGGTCATCCCTTTCTGACCT	59.505	20
229	803	1031	TTTGAATTGATATTCAGTGAAC	60.276	25
213	1346	1558	TCATCCTTCACCTGACCCAT	60.326	20
164	157	320	TGGGGTGTCATGATAAGTGG	59.215	20
139	8	146	CGGATTTAAGGGTTATTACCT	59.9	25
200	58	257	CGATGAGCATAGAGAGTGCG	59.722	20
232	171	402	AAATTACACCTTTGTCATTTTT	57.864	25
162	741	902	TCGTTAAAGGGAATGCACAA	59.157	20
279	474	752	GAGTGGGGGTTTTGAGTTTG	59.425	20
264	591	854	GCAATCCGATATCAACCAGC	60.444	20
235	4230	4464	AACTTGGTTCCACGCAAAAC	60.015	20
231	286	516	TTGAAGCATGACCTGCAAAT	59.276	20
238	863	1100	CTTCAACTCGACCTTTTCCG	59.846	20
154	72	225	GGGATAAGATTGGTGGTGATG	59.115	21
265	301	565	AATGCCTGCTTGCCTTAAAA	59.853	20
256	177	432	TTTTTCTCCCAAAATTGCC	57.656	19
243	273	515	TGTGGCGTATGTTAGAGGCA	60.28	20
272	211	482	CAATCCCAGCCATTCATTTT	59.762	20

163	18	180	AGCTGGGCACTTGAAACCTA	59.875	20
177	117	293	TCTTTCCAGTTGTGTCCTGG	58.695	20
254	94	347	GGCATACCGCAAATCAACTT	59.967	20
113	578	690	CTTCCTCCCACCTTCGTCTT	60.619	20
258	492	749	GGAGATATCGGTTGTCGGAA	59.894	20
277	801	1077	GGATGTGCAATTGTCTTTGC	59.131	20
253	37	289	TTTACATCTTCCCGCCATTC	59.901	20
276	219	494	ACCATTTCCCTATCTATACCAA	59.104	25
162	292	453	AAAAGGAGAGGAAGGTTGGC	59.691	20
199	482	680	GAGCGAGTTGGAACTTGGAA	60.375	20
280	1120	1399	CACGTTCGCTATCCAAGTCA	59.864	20
248	519	766	ATAACATCAACCGCCAGCAT	60.361	20
269	688	956	AATTCCCAAGATAATCTCAAT	58.532	23
191	1510	1700	CCCGTAGAACTTTCCCTGGT	60.353	20
162	199	360	TTGTGAAATGAATGCACCAAA	59.961	21
109	305	413	TGCAACAAGATGGTGCTCTC	59.992	20
115	4	118	GGCCGAGATTTGTTAGAGGTT	59.607	21
274	48	321	TGAAGTTCGGAAATAAGGAGG	58.315	21
257	198	454	TCTTATCCATTTCGCCATCC	59.862	20
269	140	408	TTGGAGGGCTGTTTCTTCAT	59.67	20
165	161	325	AGGTGGGAAATCATCCCTTC	60.133	20
235	93	327	GACCAAGTTGCTCTTCTCGG	59.989	20
108	301	408	TCTCTGATTTCTCACGCCCT	59.95	20
272	11	282	TAAATGAGCCGTCAGTGCAT	59.301	20
264	1832	2095	CACTACATAAATTTGGCAAAG	58.849	25
105	86	190	AATTTTGAATGAACACGGCA	59.016	20
174	660	833	CTTCCCCAAGAGCTCACATC	59.803	20
134	39	172	CTTGCCCCTTCACTCTCATC	59.803	20
253	92	344	TGACGTGGGTGTTGGAATAA	59.816	20
204	425	628	TGCGTGGTTTTTCTGTTGTC	59.74	20
269	135	403	AAACAGCGCCCATAATCTTG	60.096	20
246	389	634	CTTACAACCGCAAGCCATCT	60.27	20
166	216	381	TGTTCGAAAATGGTGGTTGA	59.941	20
161	1542	1702	TGATTTCATCCGAATGTCCA	59.859	20
203	741	943	TGTGGGTTCACTGGATACGA	59.96	20
201	315	515	GGACAAATTTGGAATTTTAGG	58.775	22
269	51	319	ATCGATCCACGTTCGAAAAC	59.939	20
232	580	811	ACAACGCAATTGTTTCCCTT	59.476	20
220	31	250	TCCAAACTGTATGGTCCGGT	60.232	20
273	1638	1910	CCCATAGAACCATTCCCCTT	60.011	20
249	281	529	CTTTCTTGCGAGAACCCTTG	59.986	20
216	156	371	GACCAAATCAATCCCATAGCA	59.776	21
199	1690	1888	GGCAGCAGTATTCATGGGAT	59.923	20
227	44	270	GGATTCAGCATTGTAAGGGG	59.387	20
222	232	453	CCCACCCAAAAGTTGTGAAG	60.38	20
258	23	280	TGGGAAAAGTTATGAGTCTAG	59.317	26
273	56	328	CGCTATGAGTCACGGCTACA	60.035	20
280	107	386	CCATAACCGTCGCATAACTC	58.12	20
163	1462	1624	AATTACAAGCCGCAGTGGAC	60.14	20
124	10	133	TTTTGCTAGAGGATTTTGTTAA	57.359	26
164	698	861	CGAAAGTTTTGGAATTTGAAG	59.978	22
117	51	167	GCACCATCTTCTCAACACCA	59.682	20
204	66	269	GAAAAGGCACTCGAATTTCC	58.765	20
222	3385	3606	TAGATTGCTGTTGGCCATTG	59.688	20
111	1209	1319	GAATGATGACACCCAAACCC	60.034	20
262	806	1067	AGAGCAGGAAGAGCCGTGTA	60.156	20
200	32	231	CCACACTTTTAAATATTTTAGC	60.573	26
107	62	168	GCTAGAGCTCACTTCACGAGC	59.54	21

191	1559	1749	TTATTCCCCAAGCAGGAATG	59.894	20
134	226	359	GATACGCGTCACACATGCTC	60.304	20
215	1067	1281	GGGGTGTTCAAAAATATCCG	59.135	20
149	156	304	AGATGCCAATCTTCCATTGT	57.043	20
278	921	1198	CTCGATGCAAATCGTGCTTA	59.976	20
230	470	699	ACTTGAAAATGCGATGAGCA	59.425	20
122	391	512	GGTGATCGATGGCATTTCTT	59.9	20
245	2331	2575	CCCTTGGTCCTTGAGCATTA	60.066	20
113	23	135	TTCTACTGGAACTGACGCCC	60.255	20
214	13	226	CACCCAAAAAGGAGTTATTAT	59.696	25
209	1535	1743	AGGAGAGAAGAGCGGACCTC	60.096	20
241	1757	1997	TTTTGCTTTGTTTTTGCTGG	58.979	20
190	34	223	AAAATCAGCGAGGCAGAAAA	59.96	20
150	729	878	GGTTGTTTAAATGCCCCCTT	60.055	20
202	1398	1599	TCTGTGTGGGTGTGTGTGAA	59.568	20
150	3187	3336	CACCAGAATGACACTCGACG	60.309	20
120	1438	1557	TGTTTGCAAGTTGATCGGAG	59.84	20
174	10	183	TCTCTCCCTTTCCACACTCG	60.377	20
108	390	497	GAAAGCCGTCGATGTAGCTT	59.481	20
191	437	627	CGATGTAGCTTCGCCCATAC	60.626	20
228	45	272	CCATCAAAAATGTTTTCCCC	59.111	20
238	9	246	TCTCAATGCCTTCTACCCAA	58.298	20
274	68	341	TGGCCCACCCATTTTTACTA	60.181	20
108	56	163	TGATTGCACCATAATGCACC	60.352	20
178	93	270	ACCAGTTATCCATCCATTCCA	59.115	21
257	624	880	TCAGATCCACTAGACATTTGA	58.475	23
134	114	247	CTGCGCAGATCTAATGGTCA	59.972	20
228	32	259	TCCCTCCAATCAATTTTCCA	60.244	20
250	161	410	TTTCAGCGACATGTTTTTCG	59.849	20
188	989	1176	CGAAACAAGTGGCTGCATAA	59.872	20
100	706	805	TTATGGGCCAATTATGCTCC	59.757	20
179	3	181	GGAGAGTTCGCGAAATAACAT	58.341	21
278	1010	1287	CTGGACTGCCTTCATCTTCC	59.803	20
213	150	362	TTTGGATAGGTGTGGGGAAA	60.162	20
265	4583	4847	TCAATGCAATAACAGCAAAAA	57.022	21
280	117	396	CTTGCTGGCAACAAAAACAA	59.888	20
163	1144	1306	GGGACGATTCTGAAAGGTGA	60.05	20
151	150	300	AACAAAGCTCTCTTCTGGCG	59.757	20
148	1312	1459	TGACCATTGAGAAAGGGAGG	60.042	20
157	77	233	GCTGGCCATTTATTGGTGTC	60.339	20
184	835	1018	TTAAGGGTGTTGAGGATGCAC	59.985	21
226	82	307	GACCCTTCACCCCCATAACT	60.052	20
254	2352	2605	TTAAAAGTGGGCTGGCTTTC	59.338	20
269	219	487	GAGAATTTTAATTCGTTCATCT	59.576	25
106	1381	1486	TGGTGGTATGGTGTGGAGAA	59.806	20
258	137	394	GTAGGGGTGTACATGGTCCG	60.111	20
280	55	334	TGCCGTGGTTCGATATACCT	60.352	20
189	1053	1241	AAAACAAATGCGTGGGCTTA	60.488	20
206	538	743	CCTCCCCAAGATATCATCCA	59.703	20
204	811	1014	ACCCGTGCTTCAATATCCTG	59.955	20
165	12	176	CTAATGAGTTTCCAGCGCAA	59.062	20
247	6	252	TTGTGCTCAATGGCAGAACT	59.445	20
126	750	875	GCCCCACTTCTTCGTTAAAA	59.202	20
251	4378	4628	TGTTCAACTAAATAATGCAGC	58.075	22
140	161	300	TTTTGCCCTCGAATGCTATC	60.175	20
237	44	280	CATGCATGATCAATGTTGTAA	60.258	23
216	18	233	GGGGTTATTAGTGGAGTAAGC	58.117	22
185	892	1076	AGGTGGTTTCTTGCCTGAAG	59.328	20

274	19	292	AACGATCGGGAGGAAGAAGA	61.095	20
219	212	430	GGCCACTTTGTTGTGCTGTA	59.764	20
128	1345	1472	GACCGAGATCGAACCCTTTT	60.443	20
271	338	608	GCAGGATCGCCATAAGGATA	60.023	20
275	14	288	TTTAGTGTTTTGACATGATTAC	57.557	25
198	100	297	CTCGGAGGCTCCAACATCTA	60.353	20
267	169	435	TGCATGATCGATATTGTAAAG	59.468	23
258	365	622	TGTCAAATCCGACGTCAAAA	60.088	20
240	41	280	CTATGGTGGTATGGTGTGGG	58.569	20
127	127	253	TCCACATAGGAAAACCCCAA	60.162	20
183	163	345	TTTCGGGTTGCTTTTTGACT	59.724	20
178	4	181	CACGTGGCATCGTAAGGAA	60.671	19
250	1378	1627	AGACGAGGAGATGTTGGTCG	60.261	20
207	338	544	TGCCACCATATCCATAAAACA	58.758	21
106	21	126	ATCGGTTATTACCGGATCGC	61.031	20
166	1088	1253	GGCGAGGACTGAAATTGGTA	60.074	20
153	785	937	TTTTGCCCCTTCTTTCCTTT	60.048	20
129	21	149	ATCGGTTATTACCGGATCGC	61.031	20
176	906	1081	CGTATCCATGGTTGAGGTCC	60.195	20
223	61	283	AAACTCAATTCCCATGTCCG	59.79	20
268	476	743	GGGAAGGGTATTTTGGGAAA	59.992	20
226	29	254	AACCACGGCTCTGATACCAA	60.517	20
249	170	418	TTCTGATAAGCCAGGGGATG	60.029	20
235	86	320	AAAGCAAAAAGAGGCGATTGA	59.96	20
277	572	848	GAGATCACTTGCGGAGAAGC	60.104	20
263	455	717	AAACTGTAATTCAGGCACCTA	59.61	23
248	105	352	TCCGATTCATTTTTCGATGA	59.04	20
229	1332	1560	TCAACCTCACAATTTGCTCG	59.84	20
227	124	350	TCGAAAATTCCGCCACTATC	60.038	20
280	679	958	GAAGAAAGACCACCCTGCAC	59.703	20
168	18	185	TGTGGCAGATCTGAAAAACG	59.84	20
251	91	341	GGCATTTTGCTACGTGGTTC	60.511	20
152	2232	2383	GCTTGCACACAGCAGTTGTC	60.672	20
268	551	818	TGATCATGCTCAACATGCAA	59.789	20
102	276	377	GACAAAAAAGTTTGAGGCCGT	59.218	20
280	364	643	AAAAATCACGAGACAACGAA	59.091	23
234	2798	3031	ATCAGCCATGTTTGATCAGC	58.674	20
135	161	295	TTTATTTCATCCCTTGTCATGC	59.857	23
222	62	283	CTGTTTTCTCAAGGCTCCCA	60.366	20
269	1279	1547	GAAAGGCAAAGATGGGTTCA	60.051	20
111	66	176	CTCTCTCTCAATTGCCACCC	59.803	20
167	5	171	TGGTGTTTATGCTACTTTGAAC	59.238	23
197	641	837	GGAACACGTACCTTCTGATTC	59.921	23
215	133	347	GATTCTTCGGCTCTTGTGCT	59.579	20
275	164	438	TCTTGCGCATTGATTTTGTC	59.816	20
140	39	178	ACGTTGGACCTGAAAGAGGA	59.697	20
230	739	968	TGCCTGAAAATGAACACCGT	61.475	20
175	80	254	TTGTGAATTTGCATCGTGGT	59.972	20
173	23	195	CTTTTCCGGTCAAAACCAAA	59.947	20
152	402	553	TCGAAAATTTAAAGGCCCAA	59.538	20
218	41	258	GGCTCCATGACCGATAAAAA	59.901	20
233	103	335	GGCAACGACTATCGATCCAC	60.492	20
238	217	454	ACCCCTCTTCTCTCTACCCG	59.694	20
244	98	341	TGCAACCGAAGTTTCATTTC	58.747	20
234	180	413	CTCACCGTCGATCAAATCCT	60.073	20
158	6	163	CATGCAAGACCCGAAGAACT	60.255	20
280	681	960	CACACATTTCCTTCCTACCAA	57.593	21
165	312	476	TGTCGGTACCTTCGGAACTC	60.111	20

254	65	318	TATGCGATCTGCACGTGATT	60.251	20
251	116	366	CTGTGGCTTGCAAAGAGTGA	60.175	20
275	2329	2603	TGTATTCATGTGTCAGCGCA	59.859	20
172	6288	6459	GTGCACTCCTGGAGGTCAAT	60.12	20
178	1316	1493	ACACCCAATAGCTTGCTTGC	60.278	20
211	142	352	CCCTCGAATGCACTCAAACT	60.255	20
228	70	297	ACAATTCGGGGAAGGAGAGT	59.935	20
234	168	401	TTAATAAATTGTCGCGAACGG	59.975	21
262	50	311	AAATACTCAGTAAACCAGATG	57.497	26
258	41	298	GGGGAGTATCACTTGAATGCA	60.753	22
158	1	158	CTAACCTTGGGCTCTGATGC	59.836	20
259	22	280	TCCACACTCAATACAATATGA	58.945	24
253	90	342	TTTTCGCCTCCGACTAAAAA	59.826	20
187	0	186	GCATCAACGGCGTGTATTATT	59.873	21
240	1832	2071	GCATGCAATAGGTTGTGCAG	60.288	20
211	128	338	AGCATATGCAAGCTCAAATTC	59.881	22
227	127	353	GATGAGTTCCTGAACCAGCAG	59.859	21
246	0	245	CGCACAGAATGGTTGAATTT	58.625	20
108	640	747	TCCACTCACCTAAACCCGAC	59.966	20
167	3631	3797	TAACGGGCAGCCTAAGTACG	60.277	20
242	700	941	AATTTCCCGCATCACACTTC	59.939	20
279	148	426	ACGTTCACGTTCTGCGATTT	60.699	20
117	148	264	CACTTTTGGGACCCCTTTTT	60.193	20
250	80	329	GCAGGTGTGAATGGAGGAAT	59.934	20
278	107	384	TGTTGCATACGATGTGTAGCA	59.822	22
158	2338	2495	TATGGGCCAACTAAAGCGAC	60.096	20
232	24	255	GGCGTGACATAGTGGATTGT	58.444	20
198	168	365	TGCCCTATTGCTACCCCTAA	59.564	20
243	524	766	GGGCTTATTCCGTCATTTCA	59.901	20
249	163	411	AAAAATTCGATCTTGGGGTGT	59.696	21
164	361	524	TCTCGAGGTGCTGTAAGGGT	59.867	20
273	102	374	GCTAGTGTGTTTGCTTGCAAC	59.63	22
219	477	695	TTTATTTCTTTCCCGCCTCC	60.381	20
181	502	682	AAAAATGAACTTTATCGGATC	58.637	26
237	50	286	AGGACCCTGCTGACGAAGTA	59.867	20
247	406	652	GTGTGCGTCTGAGTTCGTGT	59.948	20
169	103	271	GCCCATGTTTTGTCTGGATT	59.797	20
269	25	293	CCCAACTGAAAACTTCCCCT	60.332	20
111	204	314	CAATCAATCCATCGTCTCCC	60.281	20
131	55	185	GCACGTGACATCTAACGGAA	59.722	20
130	156	285	GTCACTAACCCCACCACACC	60.135	20
123	1	123	TCCGTCAAGGAGATCTTGAAA	59.799	21
272	320	591	GGGTGGCTTGATTTTGTTCA	60.874	20
216	25	240	CGGATCGCGACCCTATACAT	62.112	20
262	243	504	CCTGCCCTTTTTGACAGTTG	60.659	20
250	377	626	TGGTAAGTGATAGGTAATGTC	59.603	26
211	389	599	CCTATCTTTGCCATACCCGA	59.916	20
246	47	292	CCTTACAACCAAACATGCCC	60.227	20
179	124	302	TGCATTCACACAAGGCATCT	60.272	20
251	836	1086	TGCCTACATCATTTACCCCAA	60.195	21
230	903	1132	GCCAAATCCTAGCCACACAT	59.962	20
274	1343	1616	TTTGGTGACATGACCACGAC	60.426	20
208	232	439	CTCACGTTTTTAGCCCAAGC	59.883	20
136	866	1001	TTCTTTTATGTGGGGGTGACA	60.213	21
280	461	740	TCTCCTTTGCGTGGACAAGT	60.833	20
209	1923	2131	TGGGGTGTGTGTTCTTGAAA	59.976	20
221	1782	2002	AGCAAAGAAATGCAGAAGGC	59.597	20
171	684	854	TGGTTCTCACTAAAACGCGA	59.464	20

122	1048	1169	TCGTTCTTTCTTGCTTCCGT	59.993	20
248	585	832	GCATTTTGGGTTTATGTTTGGT	59.99	22
276	125	400	CTCCATCGAGTCAAGCTCAA	59.112	20
144	597	740	TGGAAGGGGAAATGAGAAAA	59.476	20
246	11	256	ACATCCACTGGCCAAGAATC	59.934	20
230	3	232	TCACGAAAAACCAAAAACCC	59.817	20
221	19	239	GGCCAGTAACACAAAGGCAT	60	20
158	867	1024	TACCCGTCTCCATCTTCTGG	60.065	20
162	27	188	TGAGAGATCAGTGAGCACGA	59.299	21
221	19	239	AAGTAACCACCAATAACCGC	60.122	21
233	660	892	ATGTTGATCTTATGAGTGTGA	59.039	26
256	1649	1904	TGTTCGAAAATGGTGGTTGA	59.941	20
116	63	178	CTGATAACAATGGGCGATCA	59.499	20
220	296	515	ATTGGGAGGCATATCACGAG	59.917	20
166	161	326	TGGGAATTTTGTGGAGAAGC	60.051	20
262	1190	1451	AACAGTGTCAATTTTGCAAAT	59.549	23
210	455	664	CAACAATCGAACCAAAGCAA	59.706	20
280	57	336	GCCCTCAACTTTGTACGTGAA	60.161	21
224	152	375	AAGATTGATTCGGAGGCTTG	59.269	20
118	1962	2079	CCTTCGGAACTGCGATTTTA	60.202	20
163	184	346	AGACGACAATCTTCGGCTTG	60.397	20
230	172	401	TGCATCAGATTCAGGGAAAA	59.2	20
251	2053	2303	AATCACGGCAGTTCCAATATG	59.837	21
209	557	765	AGAGGATTTTGCTGCTGTGG	60.397	20
267	1746	2012	TGGCTGATGTGAAATCTGGA	60.201	20
104	26	129	TCACCACGTTCTACGCTCAA	60.449	20
100	12	111	TCTCACAGGATTTAGCTGTTCT	60.424	24
111	277	387	CCTCTCATGTTTTCCCCAAA	59.903	20
245	181	425	TTCCTTTCTTCATTTTCGCC	59.273	20
269	1580	1848	CTCCCAAAATCTCAATCCCA	59.864	20
233	407	639	CCCGTGACATGGAAACTCTT	59.966	20
277	220	496	AGTAGCAGCTGTGGATTCCC	59.313	20
263	1670	1932	AGCCATTTTTGTTTTGCTGC	60.251	20
190	286	475	AAGAAAAACAGGGGAAAGGG	59.433	20
268	36	303	GGGGGAGGAATGGTAGAGAG	59.89	20
194	292	485	CTATTGTCGGACACTGGGATT	58.923	21
268	439	706	TCAAATCATAAGACAATCGCC	57.71	21
264	4236	4499	TCGAGAACTTGCTTGGTGACT	60.043	21
230	603	832	CACTCGGATTTTTGATCGGT	59.933	20
134	742	875	GCAAACATATGGTGGCATTT	58.362	20
220	588	807	TCAACAATTGGAGACAACGC	59.697	20
271	1897	2167	CTCCCCCAAATTCTCTCCTC	60.008	20
261	6	266	CCAACACAAAAACAGGGAAA	58.5	20
175	60	234	CCTTGTGGGGTACAAGTGCT	60.028	20
279	698	976	AACTTCAAGCACTGGAATGAG	59.295	23
250	66	315	CTTCCCCAGAAATCGAACAA	60.044	20
124	250	373	GAACTGACGTCCTCCTGTGC	60.873	20
249	379	627	ATGAACAAGGGCAACTCGAA	60.636	20
217	251	467	GACTCTTCGCTAGGTGGGGT	60.649	20
218	408	625	TTTTGGAGCATCTCCCATTT	59.505	20
232	103	334	AATTCATGGCTGTTCCAAGC	60.081	20
270	1678	1947	CCTTCCCAACAGAGGAAAGA	59.255	20
262	76	337	TTACCCTAAGGGCATCCACA	60.323	20
230	854	1083	GGCCACTAAAACAGGGATCA	59.933	20
174	279	452	TATCCCGTGCTCCAATCTCT	59.653	20
274	2717	2990	CCTTTGCATAGAGTGCGACA	60.011	20
152	1883	2034	ACACTTGTCGAAGGAGACGC	60.453	20
209	1377	1585	TATGCTGTGATTTTGGCTCG	59.833	20

181	173	353	AAAAATGAACATGGCCGAAG	59.938	20
276	322	597	TCGTCACCCTTATCCTACCG	59.948	20
183	7	189	ATTGCTTGGAACTTAGCCCA	59.708	20
135	17	151	TGTACGTTACGATGGCATGA	58.575	20
255	17	271	TGGTAGCTTGAATACACGTAT	57.44	23
172	445	616	TTGATATCAGAGCCACTGCG	59.972	20
267	681	947	GGTCGGTAAGACGACTTGGA	60.111	20
229	2767	2995	TTTCTTTCGACCCATCAACA	59.097	20
242	2	243	TGACGATATATAGTGTTTTGA	57.754	26
181	15	195	AAATAAGGAGGTGTTATGAAG	59.323	24
189	14	202	TCAAGGTAAATGGGTCTAGCA	60.01	23
277	742	1018	TTTGGGTAATTGGTGAACCTT	58.34	21
103	6147	6249	AATCGGGTCCTCATCATCCT	60.682	20
258	130	387	AAACAACCCAAGAAAAATAC	59.307	22
129	1788	1916	AGGGGACTAGGGTTGAAGGA	59.928	20
203	336	538	TAGAATCCGGCGAGTGAAAT	59.668	20
271	23	293	CCTAGAAAGAGAAGAAACAG	59.255	24
268	842	1109	TGGTTTTCTCACCATCAGCA	60.24	20
234	8	241	CCGAATTTGCTAGGTTGGTC	59.569	20
275	319	593	CATGGACGCTCCAGATTGTT	61.067	20
245	521	765	TTTCCCTCCAAAAATATGGG	58.735	20
270	390	659	CGTGATAAGAACACTCATGTC	60.045	23
224	1064	1287	CCCCCACCACATTCTTGATA	60.572	20
260	298	557	TCGAATCGAGTTCGGGTAAT	59.528	20
180	1600	1779	CGAAAATAGGTCGAACCGAA	60.067	20
111	430	540	ATCCTAAACGGCTCGGAAAA	60.92	20
208	83	290	AACCATTGAGCAAAAACAATG	57.677	21
230	780	1009	TTTTGCCTTTGCTGTTCCTT	59.861	20
220	73	292	GGGAGGACAGTCCGTAGACA	60.112	20
274	1632	1905	ACTGTGGGCAATACCAGCTT	59.621	20
239	465	703	TGACTTGCAGCCACTCTGAC	60.187	20
197	490	686	TCCAACTCCCTCCATTCTTG	60.042	20
207	466	672	TGTTCGTGGCTTTGTTGAAA	60.271	20
237	15	251	AGGGAGTGCTCCCACATTAG	59.162	20
217	291	507	TCTTTTTCCACATTTGAAGTTC	57.12	23
239	447	685	TCGCAGCGAAACGTGAAC	62.18	18
228	656	883	CCATCAACAAATGCAATGGA	60.321	20
265	889	1153	ATCAGAGCGCAGAGGATTTT	59.034	20
122	19	140	ATGGGAAGAGGGGGTATGAG	60.147	20
236	352	587	CCAAACAAACCGGCATACTT	59.861	20
266	265	530	GCACACGTATTAGGACCTCCC	60.758	21
209	117	325	CACCCTGTGACAGATACAGCA	60.058	22
151	531	681	GCGCATGCACCTAATTACAC	59.214	20
205	131	335	CAACAATCAGCAGTGGCAAT	59.722	20
273	2185	2457	ATGATCAGCGCAGTCCAGTA	59.425	20
240	271	510	TTGTAGAGCACTGCCAGATCA	59.606	21
254	1032	1285	CAGGAAAAATGCGTGTGTTG	60.149	20
109	270	378	GGTTAACCCATGTACGCAAA	58.413	20
226	139	364	TGGTTGAACCCTTACGTTGC	60.924	20
174	95	268	GCCTTGCAAGCCAGTTTATT	59.365	20
260	754	1013	TCAAGCCCTAATTCCAAAACC	60.299	21
215	28	242	TACCTCTGAGGGGAAGACGA	59.797	20
213	164	376	TCAACTTCTGTTCCGACACG	59.873	20
260	1445	1704	GTCGGGAAAGAGACATCCAA	60.05	20
145	2656	2800	AGCAGCCGAAAAAGGGTATT	60.095	20
198	3089	3286	AGGCTTAAACCAGGACCGAT	59.962	20
259	809	1067	GCAACAGTTGTGGTTGATGG	60.008	20
274	972	1245	TTCGAAGCTTTGCTACTGGC	60.658	20

238	24	261	CAAGATAACCCTTCGATTTAG	58.703	23
213	637	849	AACTGGCCCAATAACCTTCC	60.187	20
242	1694	1935	CGTAAGGCCTACTCGAGCC	59.985	19
249	327	575	TTGGTGGCGGTAGGTAACTC	59.993	20
263	32	294	CAGTGTACGACATTGTTTGCG	60.224	21
258	55	312	TAGCCTTTGCCCCTTTTCTC	60.683	20
242	741	982	GGGAAGTTTTCCCACACTTG	59.425	20
159	261	419	TGAAATTCACTTGATCCGCA	60.197	20
253	104	356	TTCGAAATATCGGGGCATTA	60.242	20
197	35	231	TTTCCTTGGACCAAAATAGCC	60.299	21
265	1391	1655	GGATTACGGCAGCGATTTTA	60.061	20
267	163	429	TCAAAGCGATGGAACATAAC	59.172	21
164	26	189	GAGGACCGATTGGAGAAGTG	59.655	20
267	184	450	ATCATGAATGCTGATGTGGG	59.327	20
261	22	282	CCCCTCGAAGTTTCGTAGAAT	59.601	21
214	21	234	AGGGGGTTATCACTGGATCG	61.095	20
241	1275	1515	ACCTTCAATTTTATAACCGAA	58.155	24
247	217	463	TTGGACAAAAATACCCTTTCT	59.865	23
204	780	983	ACCTCTTTCCAATCTGGCCT	60.074	20
198	65	262	GAGGGGATTGCCTAAAATTGA	60.266	21
276	2368	2643	AGCGAACCAGAACCGAACTA	59.875	20
275	526	800	AAACTTCGAAAGCGAAATGC	59.479	20
128	1381	1508	TTTTCTCTGGATCACACCCC	59.903	20
123	833	955	ATTAAGGAATTGGAGGCGTG	59.043	20
225	183	407	TGCAAAAGTTTTTGTTGGGT	58.174	20
242	71	312	CCACCTTACTCACGCCTCTC	59.867	20
106	280	385	ATCCAAGCGTTTGCTGTTTC	60.257	20
214	410	623	CTCTCCATTCTCTCGCTGCT	59.851	20
217	125	341	CCTCCTTTAACCAAAAATCCG	59.825	21
242	79	320	GATTGAACTCCGAAAAGGCA	60.192	20
204	291	494	GTGGCGGTCAACAGAAAACT	60.156	20
245	2694	2938	TCAGGAACCTGCAATTAGGC	60.214	20
259	126	384	TTGGGAGGAGGAGATTGTTG	60.042	20
230	594	823	TGGACTGCTGTTCAGAGACG	60.178	20
225	4954	5178	TGTGCCCACTTAAAAATTTGG	59.855	21
215	959	1173	CTGCAGATCTAAGGGCCAAG	59.971	20
162	1227	1388	TAACGACAATGCTTCATGCC	59.694	20
113	292	404	ATTTGGGTTTTAGGCTTGGG	60.177	20
242	2201	2442	TGCAAGTTCAGACAAACCCA	60.278	20
174	4368	4541	GGTTCAACCTCCCAGATTCA	59.903	20
273	41	313	TGATTTCCTCACCTTGTTTGTG	60.008	22
269	160	428	ATCCAGAAATCCCCCAACTC	60.133	20
160	270	429	GCATCACCTCAACCCTTGAT	59.934	20
270	526	795	AAGTTGCACAATCCTAATGAT	57.046	24
143	1416	1558	CTTGATGGCTGACTCACAGC	59.577	20
150	697	846	TGCCAATTGAATGGAGTCAG	59.648	20
188	1444	1631	AATTGTGGGGAAATGATCCA	59.991	20
134	4	137	CGTGGTTCGATCGTAAATGA	59.542	20
274	257	530	CCCGAAATAAGCTGCGTAGA	60.356	20
114	45	158	ATAACCATACCCACACCCCC	60.558	20
255	4357	4611	GCTGCTGTAGTCGGAAGTTGA	60.586	21
202	413	614	GGAGTCCTACGCTGATCTCG	59.973	20
211	256	466	TTGACCATAATGCCCCTATCA	60.16	21
278	177	454	ATCTCATGCCTTAGAGGGGG	60.422	20
232	3220	3451	CAAACCTAACTGAAATAGGA	59.802	25
148	416	563	GGAAATTGATGGATTTGGGA	59.558	20
189	1800	1988	TTCAAACTTGCCAATCCAAA	59.133	20
270	89	358	AAGGATGTGTTATGAAGGGAT	57.577	24

163	713	875	CAGTCCACCCGAATTGGATA	60.713	20
215	46	260	ATGTGTCGGCCTGAATATGG	60.744	20
249	408	656	ATAGTTCCGTCGTCGTTGGT	59.478	20
168	150	317	TGGTGGGTTGAATGCTATGA	59.924	20
132	1028	1159	TCACAAGCTTGAAAGCAACAA	59.641	21
156	4	159	ACGCACTCTCAAGCACACAC	60.104	20
240	8	247	AAAATCAAAGGCCCACATTG	59.801	20
172	453	624	CTCCACACCAGCTGTGTCAT	59.738	20
160	32	191	CCTTTGCCCCTTTTCTCTCT	59.821	20
116	89	204	TGTATGGGGAGGGTTATCCA	60.006	20
210	95	304	TGATTTAACTTGCATTCTTTTTC	59.518	26
215	338	552	AGGATGAATCGAGGGAGGTC	60.421	20
155	6	160	CTAGCTCCTTCCCCTTCACC	60.204	20
213	627	839	ACAAAGTGGTGAGCATTCCC	59.973	20
280	389	668	CCTGAGACCAAAAGGTCACG	60.68	20
181	2977	3157	CCCAAGATTTCCCATAAGCA	59.894	20
162	3	164	TTGACGATATATAGTGTTTTGA	58.972	27
186	1	186	GATTTTAGGATTTCAGCTCACT	57.228	23
276	62	337	TAATTCACGCACCTCGGTC	59.664	19
235	1081	1315	ATGGAAAACCACGAGTGGAG	59.966	20
138	100	237	AGGCCAGTAAACTCCCCATT	59.827	20
206	79	284	TTGGAAATCAAGTAGAACTGA	57.228	24
276	1164	1439	TACAGCCAAACGCCAAAGA	60.386	19
276	4152	4427	CGGCGAAATAGTTGGACATC	60.469	20
114	1167	1280	AAAATTTGTTTCCCACCAAATA	58.744	23
152	144	295	CTGACGTCTTGTGGGAGTGA	59.864	20
237	1111	1347	ATCGAGTATTGCTTCGCTTCA	59.996	21
279	135	413	TCACTCCTGCACATTTCCTG	59.831	20
248	1574	1821	GGATTTGACTGGTTGGGAGA	59.903	20
224	122	345	TGGTGTGCTTGGATTTTTGA	60.088	20
159	2069	2227	ATGCTTTCCAGCCAAGAGAA	59.955	20
233	419	651	TGAAGTCGTCACCCTCAACA	60.285	20
177	2	178	CAAAGGCCCACAATGGTTAT	59.685	20
152	50	201	AACGAATCTTTTCGTGGAGC	59.316	20
150	115	264	TATTTGTCCGGTTCACCCAT	60.051	20
242	101	342	AATTACACATACACGTGGGCT	57.046	21
278	1	278	GGCTAGGCTGGATAAGTTTCA	59.415	22
179	58	236	GCCATAATTCCTTTCAAATTGC	59.822	22
277	10	286	CCATGCATCCATATGAGAGAG	60.059	22
247	101	347	AACATTGTTCTCCCCCACAA	60.21	20
258	240	497	CAAAGAGGAAATTCGAACGC	59.823	20
228	86	313	TTAACAGAGGGGTGGACTGG	59.959	20
133	65	197	GTACTCTCATGCGCTCAGCA	60.319	20
279	40	318	GGAGAATGCTTTTGACGGAG	59.813	20
249	2281	2529	CAAGAAACACCACCAGCAAA	59.734	20
196	157	352	GCAAGGCAATATCCTTGTGAG	59.722	21
278	87	364	TCACGGGTTCGAGTTTCAA	60.224	19
278	132	409	CTAATGGCGAAGTGGATCGT	60.096	20
129	42	170	ATTTTACCGGCATGGTGTTT	59.205	20
269	585	853	GCAACGGAAACAACCTCTTT	59.218	20
210	91	300	TCCATCTCCACGTACGACTG	59.701	20
103	388	490	GGATCGCATATCCCAAGATG	60.26	20
117	2	118	TTTGTCGATTCAGTTTCCCC	59.91	20
229	211	439	TGAATTCGGTCAAGCATCTG	59.799	20
182	711	892	TGGTGTTGGGAAGAATCACA	59.935	20
268	0	267	GGGTAAATACATGGGCTGGA	59.645	20
246	2243	2488	AGAAATTCAAACCCGGAACC	60.166	20
154	721	874	TTCTTCAGTCCCTACCGTCG	60.246	20

122	342	463	ATCATTTTACTTTTGGGGCG	58.943	20
270	95	364	TTGAAGGGGTCTCTTGGATG	60.042	20
146	4	149	TGCGTTTTGACGATATATAGTG	59.092	25
280	129	408	GGAAGATTCAAACCCCATCA	59.727	20
109	402	510	GGATCGCATATCCCAAGATG	60.26	20
124	158	281	TTCCATGTGCATGCAGAAAT	60.08	20
255	1821	2075	GACATGGGCACCTTATTGGT	59.676	20
266	823	1088	TCATGTCGCCGATCATAAAA	60.035	20
165	17	181	AAATAAGGAGGTGTTATGAAG	59.323	24
272	3	274	ATGAATGGCCCATATTGGTT	58.977	20
257	440	696	TTTACGATTTCGATAGCCCG	60.054	20
184	165	348	GCCCAGTCATTTTGTCCCTA	59.933	20
249	475	723	AAAGAGTAGCACGACCCGAA	59.875	20
111	15	125	TGAGATAAGGGGGTGTTTGC	59.933	20
120	1588	1707	TGGTCTACTTCTATGGCGGG	60.088	20
175	310	484	ACCGTGAACACCCCTAGGTA	59.328	20
260	265	524	TGACATCCCTTTGATTCCCT	59.336	20
184	321	504	GGCTACCCCTCTCGCTCTAC	60.37	20
158	86	243	TGAAAAAGATTGCTGATGTCG	58.906	21
100	1	100	CAATTACAATGTTTTTCCAATC	60.64	24
194	266	459	CGCATCAAGTTCCCTCATCT	60.218	20
239	1332	1570	TCCCGTATACCTCCAATTTACA	59.632	23
216	323	538	AGAGTGGACTGGGTTGTTGG	60.002	20
140	1127	1266	GTTGTCTGGGCCACAAAGAT	59.973	20
133	43	175	CAACTATCTCCAGCCCCATC	59.508	20
280	511	790	TCTGCGTTTCAGTCTCTCCC	60.533	20
114	36	149	AAAGAAACTTGGGACGGAGG	60.467	20
237	22	258	AATTCTTCCTCCGGAACACC	60.306	20
154	595	748	CAATTTCTTCACGGGGTTGT	59.83	20
134	147	280	GTTCCGTTTTCCTTGTTTCG	59.587	20
191	47	237	CTAGGAGGTTCTCGCATTGG	59.83	20
207	94	300	ACTTCAAAATCTAACCGGCCT	59.146	21
192	532	723	GCGAGAGCTATGTGGAGACC	59.981	20
147	227	373	AGGGAGCTGGCACTAGATCA	59.973	20
207	1159	1365	TGCAGTCGTCCAAAACGATA	60.257	20
274	1303	1576	GGGTTGGATCAACCACATTT	59.508	20
236	1142	1377	ACACAAGCACACACATGCAA	59.785	20
155	487	641	ATGCACGTAGGCATGTTCAA	60.142	20
126	27	152	CCAACTCAGTGTGTGAGTGGT	60.111	22
248	80	327	GGATCGAATGAACAAACACG	58.976	20
212	3929	4140	TGTTCTGCTTGTCCTGCTTG	60.175	20
149	3	151	GGTTATTAGTTATTACGGATTT	58.826	27
140	95	234	GATCTGCACCCTCCATGAAT	59.893	20
251	15	265	CAATAAATTGGGGTCGGCTA	59.789	20
220	11	230	GACTAGAGTTGGTTTCTTAAAT	57.439	27
164	478	641	AAGAAAATGGGCAGAAACGA	59.685	20
190	20	209	TCATATATAAACGCCGGGGA	60.13	20
225	1882	2106	CGAAAACATTTACATACGATG	60.593	23
205	149	353	TTTTAGGGTTAAAAATAGCGCA	58.109	22
239	2089	2327	CCAGACGACTGCAAAAACAA	59.881	20
275	271	545	CTAGGTGTCGGATTTGGGAG	59.545	20
181	81	261	ATTGTTGCTTTGCCATCTCC	60.081	20
153	344	496	AGAAACAAACGGAATGTCGG	59.971	20
205	1376	1580	GGCTTCTAAGCTGCCGATAA	59.592	20
280	91	370	CTTGTGGAATGAAAGGGTGG	60.345	20
263	799	1061	GGAGGTGAAGATTGGGTGAA	59.903	20
130	550	679	TCCTTCCTTGCTCCTTTTCC	60.683	20
271	166	436	AATAGCGCTTTTTGCCTGAT	58.992	20

191	772	962	ACCGCTTACATTCCGATTTG	59.96	20
213	1084	1296	ACTGTTTCCACCGCTTGACT	59.769	20
199	304	502	TTCAGCACTCCATCAGCAAG	60.136	20
180	7	186	TGGCCAAAACATCAACTCAA	60.088	20
232	123	354	GGTCTTTTGATCCCCACAGA	59.903	20
204	8	211	GGTGACGATGGTGATTGATG	59.769	20
271	0	270	AGTAGTTCCGCCCGTGTCTA	59.757	20
258	88	345	GGCATTTTGGGAAAGACAAA	59.916	20
225	1918	2142	CGTATAGGGATCGGTGACAAA	59.831	21
248	169	416	GATGCAGCTTGGTCTCCTTC	59.957	20
236	176	411	AAAATGGTCCCCTCATGGA	60.119	19
256	830	1085	TTTGTCCAAATAATTCATCACC	59.221	23
268	2531	2798	CTTCCAACTCTTCGCCATCT	59.43	20
214	1221	1434	GGGACTGCACAATATGCCTC	60.492	20
272	146	417	TTGCTGCCACTACCTGTGAA	60.449	20
206	51	256	ACTGCTTGTGGACAGTGCAT	59.341	20
127	1820	1946	TCATGGTCGAAGAAGCTTGA	59.522	20
246	1641	1886	TATACAAATGGGCGCATCAA	59.92	20
211	621	831	ACATTCTCGGCTTCTTCCTG	59.43	20
206	507	712	TCCTCCTTTTCACAACTGGC	60.232	20
201	99	299	TCAAGTTGGTTACGGGAATTG	59.847	21
203	961	1163	AAATTCAATGACAATTGGAGG	58.418	22
188	1350	1537	TGGCATTAAATATTAGCCCCC	60.018	21
268	3	270	GCCAATAATTTTTAGCAAGCA	58.513	22
111	404	514	AATGACTGCTGGAACAAGGG	60.111	20
236	646	881	CATGATCCCGTGAGATACCA	59.322	20
167	304	470	CCGCTCAACAGCGTACAATA	59.895	20
255	789	1043	GTCAATTTGCCGCTTGATCT	60.221	20
266	43	308	CGAATATGCAATCACCAAAGA	58.639	21
107	36	142	CACGAGATTTACGTGGTTCG	59.195	20
273	65	337	AAAACTGCATGCACCTGATT	58.229	20
223	24	246	CACATTCACTTCCTCCCTGA	58.641	20
232	784	1015	CATGCATTTGTTGTCGTTTTCT	60.039	22
132	191	322	ACACACACCGTGGACGTAGA	60.072	20
141	45	185	CACACATTCTCACGCATTCC	60.12	20
262	681	942	AAGTGCACAGAAAAATGACTT	58.487	23
136	805	940	GTTCAGGTTGGTAGCTCGGA	60.255	20
118	1888	2005	CTGCCAACTGAATGAAAGCA	59.988	20
167	2083	2249	AACAAACACGGAGATTTCAAC	59.517	22
156	673	828	GCGCATCTGTAATGTCCAGC	61.758	20
252	1596	1847	ATTTGGGTGTAGAGAGGGGG	60.183	20
267	52	318	ACGTGCACTTCCACTCACAC	59.789	20
178	101	278	TTGTTGAAGGGTGGTTGTGA	59.976	20
178	473	650	GTTGCTTAGGGTCTGTTGGC	59.74	20
163	325	487	TTGCTTAGGGTCTGTTTGGC	60.249	20
241	391	631	GAGACGGGGCTCACTAAAAA	59.312	20
104	72	175	TACCCCGCTACCACCAATAG	59.839	20
224	1285	1508	CCTTGATTTCAACTGTCTCCG	59.72	21
154	2593	2746	TTAAAACCGACACCCACTCC	59.83	20
270	51	320	TTTTTAGTTTCGATAGTTTTCAT	58.852	27
185	182	366	ACAAGCGATGTGTGGTGAAA	60.16	20
142	2669	2810	AGATGCAACATAGGGGAAGC	59.154	20
224	247	470	AAGCACATCACCGGCTACTC	60.285	20
280	138	417	ACAATATGGTGTTGGGTATTA	57.156	26
136	83	218	TCAGTTTTTGAGTTATGACGTT	58.418	24
173	117	289	GAAATATGCATTTGTCGTCAC	59.347	22
164	2	165	ACAATTCAAAAATGAGTGAAC	58.528	23
279	32	310	TCTCTACACATAGAGACCAAT	58.467	26

249	159	407	GACACGGACGGGAAGAGATA	60.073	20
272	87	358	CCCATCGTTGAAATGGTTTT	59.662	20
236	165	400	GCGACAATAACTGTCTGCGA	60.019	20
264	1561	1824	GCCTCCATAACGAGCTCATAG	58.965	21
277	21	297	GGGGTGCATGTTAGCCTCTA	60.096	20
190	5	194	AGCACAACGGCTATCTGGTT	59.763	20
261	82	342	ACATATTCCACTCCGCAAGC	60.103	20
195	129	323	CTACTTGCGTGCTGGAACTG	59.658	20
181	258	438	GGCCATTCAAATTTCAAATCA	59.765	21
262	1166	1427	TGTCTATTCCTCCGATGGCT	59.653	20
246	21	266	AGGATCGAAAGGGTGAGTGA	59.655	20
263	248	510	CGAACACGATCCGACATTAC	59.002	20
135	178	312	CGGTGGAAATGGCTGAGTAT	59.955	20
225	667	891	GAGCTGCGACATTTTCAACA	59.995	20
254	588	841	GAAATTCAAGCATTTTCCGC	59.666	20
233	157	389	GTACTGAACCACCGTCCACC	60.284	20
159	3705	3863	CCATAGTCCAAGATGTGGTGC	60.39	21
273	2	274	TGGATGGATGGATTAGCAGAG	60.044	21
197	273	469	ATTCTTTCTCATCACCCCCG	61.211	20
155	171	325	ATGGGAAGAGGGGGTATGAG	60.147	20
168	167	334	TTTTAAAAGGATTTATGGCATG	58.122	24
146	25	170	GGAAGAATGGACCCTAATTCA	59.311	22
276	470	745	CGCTTTCACCAGAATCTTCC	59.813	20
184	56	239	ACAGACGGCCCAATGATAGA	60.483	20
185	192	376	CGCCAATTAATCATAGCCGT	59.95	20
194	998	1191	CAGTAGGCCATGTGTTCGAG	59.314	20
160	14	173	AAGGGTTATCACCTGATTTTCT	57.73	23
209	182	390	GGAGGGTTAGATGGTGGACA	59.779	20
173	0	172	GAAGTGTTATGCGTTTTGACAA	58.249	23
195	156	350	GTCGGCAGAAAAGCAAGAGA	60.657	20
231	397	627	AAAGGGGGAAACAACTGAGAA	59.963	21
246	91	336	AGTGTGTGTTTGTGCGTGTG	59.234	20
279	185	463	ATTTTTCCTTGTTGGGGTGG	60.938	20
126	326	451	TCCGACCGGTTTTTAAATCA	60.294	20
274	780	1053	CGTTTGATTTTTCACTAGAACC	58.358	23
268	2	269	CAACACAAAACCCTACAGCA	57.251	20
259	1315	1573	CCAAATTTCACGTAGACCCAA	59.847	21
172	288	459	TGCAGGGTATGCATGTTTGT	59.995	20
251	3827	4077	CTCCCTATCCAACTGCGAAA	60.206	20
277	1289	1565	TCAGCCTTTTATCGACTCCG	60.344	20
189	177	365	CAACGATCAAATTCGCTTCA	59.809	20
180	795	974	TCGCCTTTACTCCATTCCAA	60.576	20
218	1106	1323	CGTGGAAGGGAGAGATTGAA	60.187	20
234	1211	1444	AAGGCCCTTGGATTTGAGAT	59.903	20
278	2552	2829	TCCGTCAATATTAGGGATTTAT	60.272	24
219	49	267	CGCCCCAAGATTTGATAATG	60.281	20
190	108	297	CAACTCTGCGTCTCCTTTCC	59.989	20
253	846	1098	ACCAATGCACATTTCCTGCT	60.526	20
258	1918	2175	GATTTCCAGGCATGAGGTGT	59.934	20
233	79	311	TGCTTTCGGGAAAAGCATAA	60.691	20
232	105	336	AAGCTCAAAGCTCCACAAGC	59.763	20
248	205	452	TCCCACCTCCATCTCATCTC	60.008	20
265	40	304	GACCAATCCCAGATCCCTAA	58.787	20
279	165	443	TTTGGGAATTGGGTTTTGAA	60.138	20
280	609	888	TGTCGTAGCATTTTTGTATGTTT	59.109	25
218	104	321	TGACGCCTAGAATCATCGAA	59.375	20
239	1329	1567	ATGTCGTATTTGCATTGGCA	59.96	20
257	677	933	CAGTATGTCCGCCTTTAGCG	60.782	20

184	298	481	GATTTCAATGGACAGGCACC	60.326	20
143	265	407	AGCCGTTTGTCCGATTTATG	59.96	20
193	3854	4046	CCAGGAAAAAGAAGATTGCA	58.823	21
113	531	643	AATTCCCTTAATTGGAAGCCA	59.795	21
241	714	954	AGTTTGATGCAAGGCATGTG	59.722	20
153	5	157	TTTGGGGATTTTAGAGAGTATT	59.802	25
255	266	520	ACCCCCTTTCTCTCCCTACA	59.928	20
167	203	369	GGCCCACTTCTTGGTAAACA	59.971	20
252	95	346	TCGACTTTAACCGTGGGTTC	59.971	20
224	556	779	CGAGATTACCCCTGTATGCTG	59.601	21
162	291	452	GGGTTGACATGGCTTCGTAT	59.82	20
268	92	359	TCCCATTTCTGTGTTCTTCGT	59.583	21
269	183	451	GCCTCCTCCTCCCTCTCTT	59.898	19
220	39	258	TTTTTACCCCATTTTGCCCT	60.519	20
242	99	340	TGAGTACAAGCGGGTGACAA	60.301	20
280	44	323	AATTGAGAGTAGCCGACCCC	60.464	20
202	57	258	GTACAGCTGAAATCTCCCGC	59.843	20
167	39	205	TGGCTGGAGAGTACAAAACTT	59.812	23
202	943	1144	GCATGTATGCATATCCCTGG	58.823	20
223	1175	1397	CACTTTTCCAACAACATGCG	60.149	20
277	123	399	TCAGGGACTCATTTCCCAAC	59.903	20
272	1222	1493	AGCAATCAGCTCCTGCAAAT	59.985	20
273	408	680	CAATCGGCAGAAGTTTGCTA	59.062	20
257	1236	1492	GTACTCGATCCCGAATGAGC	59.658	20
187	2771	2957	CACGGGAGACATTGCCATA	60.487	19
245	57	301	CGGACGAATTAATCACAGCA	59.688	20
254	407	660	ATATGGGTTGTCGATCTCGC	59.923	20
192	1448	1639	TATGAATTTTGGCCCTTGGA	60.26	20
279	705	983	AACTTTTTGGTTGGCAAGGA	59.587	20
200	87	286	AAATTGGCAAAAATGGTGGA	60.167	20
265	145	409	TGTTTCCCCAATCCACATTT	60.029	20
251	677	927	GACGACCTTGTCATCCAACA	59.525	20
183	68	250	AGCATCTCTTGCTCTCTCATTG	58.842	22
179	40	218	GGAGATGCACTTCACCCAAT	59.934	20
256	88	343	AGAGGCATTTTGTTTGGAGC	59.316	20
243	169	411	CAAAACCCGTTACATATCTTT	59.667	23
240	1499	1738	GAAGAAGTGGTGGCGGATTA	60.074	20
249	361	609	ACATTCGGAATTCATTTGGG	59.622	20
278	618	895	GAAGAAAAGGCAAGAAGTAC	59.433	22
138	134	271	TTGGTGCTCCACTATATTGCC	59.974	21
253	22	274	TGATAGATGCCACTAACCCTT	59.111	22
109	950	1058	TGAGAATCCTGGGCTTTGTC	60.195	20
242	56	297	GTAACCGTCATGTTCCGGTC	60.24	20
280	1087	1366	TATGAGATGTGGGGGAGAGG	59.879	20
214	2487	2700	TTCCCTCCCAATTCTGTTTTT	59.801	21
171	2003	2173	TCAACGGTGAGTTATGGCAA	60.111	20
102	261	362	TGTTAGAAACAAACGCGGCT	60.802	20
234	1489	1722	CAGTAAATTTTGTTGCCGGG	60.348	20
197	133	329	TCGCCCACAATTTGATACCT	60.331	20
134	442	575	ACAACGTGATACGCTGCAAG	59.935	20
226	363	588	CGTTGCATTCGTCTTTCTCA	59.988	20
257	11	267	TTACCATATTTAAGGGTTATCA	58.789	26
190	288	477	CTAAACCTTATCCCCCACCG	60.545	20
274	13	286	CAAAATTTGGAACCTGTCTTC	59.108	22
207	1075	1281	CTGCCTTCTCCACCATCTTC	59.803	20
120	286	405	TTATATTCTCCCGAACCGACA	59.42	21
236	238	473	TTCGTGATCTTTGTTGCGTC	59.847	20
147	88	234	GACACCTCCAACTTGCCAAT	59.973	20

198	11	208	TTCGAAACTGCATGAAAATCA	59.291	21
274	2	275	ACACGTGTAAGGGTTGAAGAA	58.304	22
278	3147	3424	TATCATTCCGCGCTATGTCC	60.962	20
248	1192	1439	TGAACTGGCTACTGGCTGTC	59.037	20
225	144	368	GAGAAAATGGCAATCGGAAA	60.016	20
233	25	257	TTTATGCGTCGTGGATCAAG	59.688	20
264	148	411	GGTTACGGGCTGGTATTTTG	59.338	20
258	1291	1548	GGACAGATCAGAAGCAAGGC	59.957	20
234	1228	1461	AGAGCCACAAATTTTTCTTCAT	57.073	22
238	21	258	TGTGTGGTTCTATGTTGTGAGA	59.958	24
186	579	764	CAGCAGGTTTCTGTTCCGTT	60.291	20
183	3077	3259	TGCAGATCAATAAAATGGCG	59.662	20
195	768	962	AAAACGATGGATGACCCCTA	59.244	20
169	21	189	ACACTCTGCTAGGGTTGGGA	59.721	20
256	88	343	CCACTGGACCAAGTGACCTA	58.565	20
174	482	655	AATGTCAATCCCTCAGCAGC	60.226	20
248	297	544	CTCTCGCTGCGATCCTTTAT	59.574	20
238	416	653	TCGCTGCACCTTCAAGTAAC	59.076	20
266	6	271	CACGAACTGCATCAAAGGAG	59.44	20
272	469	740	AAAGGCAGAATCCACATGGT	59.41	20
121	343	463	TTCTTATACCAAAACCTCCACT	59.832	25
255	1157	1411	TCTACCACCGGGAGATCTGT	59.53	20
200	258	457	TTGCAAGCCTGTGGTAGGTA	59.342	20
238	156	393	CCTCCACTTCGACAAGAAGC	59.989	20
150	2176	2325	AGAGGAAACCACCACCGTTA	59.449	20
190	1360	1549	TGTGGCATATTGATGATGGTG	60.213	21
184	270	453	TTGTTTGCGCTCAACAATG	59.42	19
163	470	632	TTCCCCCAGAGAAGTTGTTG	60.081	20
260	32	291	CGCCCCAAAGTGCTTTAATA	60.089	20
178	1342	1519	GGTGACAAGCATTCCTCCAC	60.52	20
263	618	880	AAGGCCTTCCTTGGTAGTGG	60.488	20
237	496	732	TTTGACACATAGCCCGATGA	60.073	20
255	449	703	AAGCTGAAAAGTCGAGAAAAT	58.643	23
159	514	672	TCGATGAAATAGGGTCGAGG	60.029	20
178	81	258	GGAGATTGGGAGGAATGGAG	60.791	20
178	155	332	GAGGAGAGCGAGCAAGAAAA	59.836	20
196	142	337	ATGGACCCACGAGATTTGTT	59.263	20
193	445	637	TTTTTGAGGGAACAATTTGAGA	59.971	23
261	103	363	GCATGTGTGAGATGGAATTGT	59.866	22
193	403	595	TTCAATCAGCCAATGGACAA	60.049	20
216	385	600	AAATCGGACGTCGAAGAGTG	60.255	20
246	134	379	ACTTCGACTCTCGTTGGCAG	60.589	20
145	59	203	CACCGGATCGCTACCCTAT	59.925	19
143	855	997	TGCATTAGTCTTTGGCATTCA	59.315	21
206	437	642	AAGGGAGGCTCTGCATCATA	59.797	20
230	352	581	GCTGAGCATTTTCTTCACCC	59.82	20
188	28	215	GCCCACAACTCTGGTTTCTC	59.703	20
262	96	357	TGAACTTATGGGAAGGAGAAC	59.46	22
228	1301	1528	CATAGCGAGGAAGTCCCAAG	59.83	20
255	144	398	CGAATATCAGCCACCCTTTC	59.528	20
160	114	273	ATCATTACTGACCGCGAACC	59.962	20
203	195	397	GACCCGGTCCAATACGAAG	60.324	19
120	2081	2200	AAAAAGGGATGAAAAGGGGA	59.75	20
142	143	284	CGCGTGCTGTAATCTGTACC	59.371	20
227	243	469	GCTTCCAGGGACAGATATGC	59.658	20
275	72	346	AGCACACAGGTGAAGACGATT	59.784	21
206	2176	2381	ACTCCCTCCGTCCCATAAAC	60.19	20
181	899	1079	GCATTTTCTCCATGTGGGAT	59.756	20

220	158	377	CATGTCCACAGCCACAAGTC	60.162	20
205	3750	3954	GGTGATAAGCCTTGCCCTTT	60.451	20
123	280	402	AGCCTTGATCTGCACTCTCC	59.56	20
154	607	760	TGGGGCGCGTATTTAGATTA	60.424	20
221	58	278	CATTAATCACCAATTCGCCC	60.153	20
279	478	756	TATGCATGGCATGAGTGTGA	59.656	20
255	722	976	CCGGAGTGTGAAGACGAACT	60.298	20
279	735	1013	GAATCTGACACGTCGGGAAC	60.52	20
131	1406	1536	TCAGCAATGAGTTGCTCCAT	59.399	20
199	314	512	CTGTGGTTGTCGTCTCTTGC	59.467	20
219	38	256	ATGTTCGGATTTTGAAACGG	59.801	20
228	2891	3118	CAGCCCAACTCAACATCAAA	59.691	20
118	0	117	GCGTTTTGACAATATTTAGTGT	60.205	26
256	357	612	CCGTATCTCCTCACGCACTT	60.277	20
200	1243	1442	TTGTGGCCTGTGTGAGAGAG	60.022	20
265	17	281	AAGAGTGTGTGTGTGGGTGTG	59.527	21
190	106	295	CTACGTGAGGCGGTGATTTT	60.132	20
125	27	151	TCACAATACAACTGCCGAGC	59.871	20
229	200	428	TGGATTTTCCCAAATTCAATC	58.726	21
125	1044	1168	GTTTTGTTTTCGTTCCCTCG	59.587	20
278	1256	1533	TGCAATGTGCAGACTTAGCTT	60.082	22
201	181	381	AGGTGGCAACATAATCAGCC	59.962	20
258	2942	3199	TTATACCTGCGGGGTTGTGT	60.249	20
267	1561	1827	TTTGGTTGGTCAAGTGGGTT	60.246	20
191	86	276	TCACATTCACACCTAACGCAA	60.165	21
279	10	288	TGAGACCTCTCAGTCCCAGG	60.388	20
260	74	333	TAAAGGCCGCATCCTATCAC	60.06	20
114	17	130	CGGTTATCACCGGATCGC	62.397	18
243	145	387	CCAAGAATCAGTTAAGCCCG	59.702	20
184	2549	2732	AACCACACGGCGAGATAGAG	60.277	20
249	1345	1593	AAGCTGAGGAAGCCACTCAC	59.604	20
132	454	585	CGAGTCGGCAGACCTAAGAC	60.012	20
210	595	804	ACGTGTTTTCATACGGCCAG	60.944	20
271	569	839	GGAGGCATGGAAGAGAATGA	60.158	20
134	265	398	AGTAGAAGCATTTCGTCGGG	59.336	20
153	1282	1434	TTGACATGGTGTAGTCATCAA	59.906	23
201	420	620	GTGATTGGCTGGAAGAGCA	59.934	19
255	2016	2270	CTGACGGAACACGTCAGATT	58.725	20
211	519	729	CATACTTCCACCGCCTTCAT	59.955	20
187	348	534	CACTCACGCACACCACTACC	60.227	20
234	900	1133	TTCAGGGAATCTTCGAATAAA	59.14	23
206	311	516	TGAGGCTTGTGGTTCAGGTT	60.69	20
274	308	581	ATCGCGGAAGGTTTAGCATA	59.704	20
186	517	702	TGCAAGCGGTTCAGACAATA	60.401	20
244	451	694	AAAGAGCTCTCGACGCAAAA	60.27	20
269	184	452	CCCGGTAAACAGAATTGACC	59.288	20
166	15	180	ATGTATGGCCCAGATTGGTT	59.129	20
194	23	216	CCGGTCCAAATCCAATAAGA	59.756	20
272	182	453	TGTTGGGATGAAATGTGAGG	59.343	20
227	192	418	GGATATGAAGTGGGAGCCAA	59.894	20
189	436	624	GCAATTGCAGGCTTATTCCA	61.105	20
267	39	305	TCAAACCCTGTCATTCACCA	59.935	20
234	1	234	CCCAATTTGCCCTTATATGC	59.282	20
135	331	465	GGGTGAAAATCGAATGACGA	60.843	20
270	627	896	TGCTGCAAGCTTAAGAAACAA	60.183	22
233	36	268	TCTTTTTCGAACCGAACCAC	60.088	20
200	7	206	GGGACTGCTGGATAATCCCT	60.293	20
230	84	313	ACTAAACTAGACCGGGCCGT	60.019	20

217	957	1173	TGATTCTGGGTTTCCAGTCC	59.903	20
212	2224	2435	AACACCAACATGCTGACGAA	60.16	20
209	47	255	AACCTCTCGTGCTCCAACAT	59.727	20
221	247	467	AATCGTCCCAAATTCCCTTT	59.644	20
277	522	798	AACTAACGGTCTGGTTCCGA	59.592	20
174	550	723	TCAAAATTGGCACGATACGA	60.073	20
277	227	503	TCACAACCAAAATCTTGCTCA	60.154	22
275	1069	1343	AATCACCATTCAACGCAACC	60.765	20
275	951	1225	ATGCTGCTGTTTTCCATTCC	60.081	20
198	8	205	AATCATTGCTTGAGCTTGAAAT	58.025	22
265	332	596	TTCAATCCAAACTCTATTTTAT	59.778	25
110	39	148	TGAGACCTGTCACCGTTTTG	59.72	20
125	39	163	TTTTAGTTATCACAGGATCACC	57.201	23
131	3909	4039	ACTTGGCCCACAAGAACAAG	60.149	20
275	154	428	ACGGGCACTGTTTTACCATT	59.359	20
102	961	1062	TTTCAATCGTGACACCAAGG	59.541	20
234	105	338	CACCGATGTTGAGGCCTACT	60.134	20
268	175	442	CATGGACGAAAATAGCCTCC	59.528	20
275	174	448	GGGGTGTTTGTTTGCTGTTT	59.875	20
209	2039	2247	CCATGCGCGGTCTAAATAAT	59.95	20
195	11	205	TTGACAATATTTAGTGTTTTGA	58.99	27
139	60	198	GGACCTCTGGACAATCCCTT	60.314	20
274	21	294	CAGTGTACAACCCCGGAATC	60.232	20
280	27	306	CTACAACATCATGCAAATCAAT	57.395	25
166	1432	1597	TCCACAATCACTTGTGCCTC	59.682	20
144	257	400	CAAGAACGAGAGGGTCAAGG	59.837	20
245	2	246	CAGCTCCAAGACATTCCACA	59.831	20
235	252	486	CAAATGTGGCGTATGCTGAG	60.28	20
212	285	496	GCATTCCTTTCCCATCTTCA	60.014	20
149	205	353	AGGTCATGGGGTATGTTTGC	59.676	20
188	172	359	TTCGGAGCATGAATTAAGTGG	60.081	21
122	11	132	AATTGGCATATGTCCCCAAG	59.645	20
239	273	511	TTCGACTCGTTTGAAATCGG	61.137	20
199	1388	1586	ATCCAACGGATGAAAAGCTG	60.074	20
217	473	689	TTGCAAAAGAAATTGCTTAGCT	59.604	23
169	821	989	TTTGTGCCTCTGATCCCAAT	60.461	20
150	74	223	TTGCAGCACTCTGGACTCTC	59.288	20
222	2636	2857	TGAATGGACTGTGTTCTTGGA	59.124	21
261	8	268	ATGGATGGAGTCAAAGCCAA	60.461	20
259	889	1147	CGAAAATTCGGATCGGCTA	61.051	19
278	53	330	GGTTAGGAATGCATTAAATAC	58.456	24
267	1364	1630	GATACCATACGTAACGCCCAA	59.734	21
236	105	340	TGCATTCATCAATTTTTGGAGT	59.456	22
118	157	274	TGGAGCATGGAGAAAACTGC	61.329	20
251	154	404	AGCCTCCCTCTCTTGCTCTC	60.238	20
240	80	319	CGAAGAGCACACACTTTTGG	59.485	20
175	350	524	TCTCGAGCTCAAATCCCAAG	60.474	20
190	138	327	AGTTTTCCGCATGAATGGAG	60.074	20
236	962	1197	CACCATATTTCACAGCAGCG	60.28	20
268	543	810	TCTCCATTTCTGTTTCCCCA	60.43	20
268	130	397	GAGAGTGGGTCGTAGCCTGA	60.408	20
184	2825	3008	GTCGTCAAAGAACTCGGAGG	59.844	20
239	405	643	AAAGGAGATTCCAGCGATCA	59.773	20
266	431	696	AGATCGACGGTCCGAAATTA	59.528	20
234	256	489	GGCCATAGCAGAATTTGGAC	59.533	20
187	425	611	CCGAAAATCTAAAGCCCACA	60.067	20
222	2847	3068	GTTCGATGGACCTCGATCAT	59.893	20
212	1142	1353	TCACCCCAATTTTGGATTCT	59.22	20

122	44	165	GGAAATAAGGAGGTGTTATGA	60.02	25
233	1624	1856	TCTCGAATGAATCCAAACCC	59.871	20
182	4	185	AATAGGCCGGTCTTTTAGCC	59.593	20
166	51	216	GCATTGTAAGGGGGACAGAG	59.55	20
109	15	123	GCTTGCACCAATAAAATTTGG	59.485	21
248	5477	5724	GCAATCCGTACTTGCCATTT	59.967	20
218	266	483	GCCATCCATTCCGAATATCA	60.638	20
160	675	834	GTCACACAAGCTTGACTCGG	59.467	20
156	414	569	CGTAAATTGTTGCAACCGAG	59.226	20
169	523	691	GAAGAAAGCGCGGTAGTCAG	60.154	20
280	36	315	TAGAGCCCTTCAATGGACAAT	58.659	21
182	34	215	AACGGTACGTTCGGATTTTG	59.861	20
187	608	794	GCCCAACTTATTTGGATATTTG	59.268	23
210	195	404	CAGTTAAGAGCGTTGGAGGG	59.869	20
110	448	557	CACTTCTCGGAACGAACAAAA	60.269	21
279	86	364	GTTTTACGTGGTTTCGGAGC	59.615	20
238	390	627	CTTGGCTATGTTGGGATTGG	60.323	20
114	1005	1118	CAAATGCCACGAGATTTACG	59.182	20
122	451	572	ACTATTCACATATCGCCGCC	59.951	20
270	147	416	TGGTCTGATCTGTCCTACCCTT	59.994	22
172	304	475	ACCTTCCTTTCCGTTCCTGT	59.972	20
138	282	419	GCCGATTGTTTTCCTTGATT	59.022	20
198	336	533	TCCTAGCCACACATGTCAGAA	59.303	21
159	1622	1780	ATTTCTGCTCACTGCCTCGT	60.02	20
271	2836	3106	CCAAATTAAGGTCATATTGCA	58.927	23
172	916	1087	GCGAAGTCAAACCACCAGAT	60.119	20
274	828	1101	CTTCGCCCTTGGATGAAATA	60.031	20
190	505	694	TTACCTGGCTGGCGTAGTTT	59.769	20
194	371	564	TCGGGGATTAAACCTCCTCT	59.897	20
280	178	457	TTCAAATCCCACAAACGTCA	59.941	20
215	81	295	CGCCCCAGATTGTTTCTTAT	59.043	20
227	2438	2664	TGGTCCGAGTTCTCCATTCT	59.655	20
219	65	283	AAAATATGGGGTTTTCCCAAA	59.428	21
280	114	393	AAACACCGCCGCTTTTTAC	60.124	19
254	11	264	CGAACTAAAGAAATAGGGAC	59.311	22
236	3106	3341	ACCTGATAGGCCAACTGTGC	60.142	20
113	380	492	TGTGTTCATGGGGAATTCAA	59.75	20
196	178	373	GTTTCTTTGCCACGTAACGC	60.678	20
222	171	392	TCGACAAAGAAATCATCGGAC	60.066	21
148	24	171	GGGTTATCACCTGATTTTCTCC	58.826	22
204	186	389	AGCAAATATGATATGCCTGCA	59.613	22
279	162	440	CAAGGGTAATCCCAAACCTT	57.904	20
100	126	225	AACCACAAAAAGGATAAGTG	59.282	22
140	329	468	CGAAGCTTTGATGGTGTGAA	59.84	20
251	5672	5922	GTTGCTCTTGCTCCAACACA	60.032	20
192	1043	1234	CGTTTTCAGACAAGCCCATT	60.11	20
179	525	703	GCTGGCAGCTTCAACAGATA	59.178	20
185	0	184	GGTTTTGATGGTTGTGATTTGT	58.72	22
194	0	193	AACCTTGGAGTCCCTTCTCC	59.534	20
272	761	1032	CCTGGACCCCCGATTTATAG	60.514	20
248	444	691	TATTAACGGTCCGGTTCCTG	59.817	20
153	760	912	ACGTCAGATATGGCTGTTGG	58.597	20
246	922	1167	GGGAGCTTTACACTCCCCTC	60.074	20
279	69	347	GCGCGTTTAGAAAAGGGAAG	61.198	20
160	9	168	TTTATCGTGGTGCATGTTTTT	58.084	21
204	3502	3705	ACCTTGTCCATGAACTCCCA	60.363	20
231	354	584	TGTCTGCATCTCTAAACCAAA	57.573	22
211	288	498	CGAACTTTTTACAGCACGCA	60.052	20

208	177	384	CCTGGAGAAGGTCAATTTGC	59.67	20
244	163	406	GGCAAATGGTTCACATGGTT	60.624	20
195	138	332	ACCTCGGCACATTTACCAAA	60.365	20
246	457	702	CAGTTTTGCTATCGTTTATCTTC	59.392	24
277	93	369	CGGTTCCAACGACTGAAATC	60.495	20
268	144	411	TCGGTAATTTAGTCCAGCCCT	59.973	21
161	1295	1455	AAACAGGGGTACAAGGGTGA	59.304	20
217	1978	2194	TTTAACAATGCTGCACTCCC	58.773	20
201	11	211	TGGTTTTGAAAGTGTGATCTGC	60.008	22
201	260	460	AACGGGAGAATCGTGTCATC	59.934	20
189	30	218	TTGATTCTGGATTATCCTGCG	60.045	21
269	272	540	TCCTCAAGATTGTGCAACCA	60.24	20
271	3256	3526	GGCCATCTATCCCTATCCGT	60.138	20
153	270	422	GACAACCATGTTGGGGTTTC	60.073	20
266	3207	3472	TCCTCCTTTCCTCTGCATTG	60.331	20
263	64	326	TCGCGGGTTTGAAAATAACT	59.586	20
213	918	1130	CGGTGTAAAGGAGGGGTGTA	59.846	20
267	13	279	TCACTTCTTCCCAAGGCACT	59.844	20
203	142	344	TGAATCAATTTAACATCATGCA	58.44	24
152	39	190	TGCAACACACGCACATACAT	59.621	20
274	938	1211	ATTCCTTGCACTGGGAAAAA	59.546	20
232	163	394	ACATCAACCGTTCACCACAA	59.855	20
151	251	401	ATGTAGAGGGAGTTGGGGGT	59.676	20
272	112	383	TTATTGAGCGCCATTGATGA	60.179	20
189	25	213	ACTTTTAAGGATCAAGGATATT	57.122	24
271	62	332	TTGGTCTAAATTGCCCCGTA	60.315	20
211	171	381	GGGGAAAAATAACAGGGGAG	59.639	20
271	606	876	ATCCACGCTGCAGAGAAACT	60.02	20
173	440	612	GCCAAGTGGCACCACTCTAT	60.142	20
264	6672	6935	CCATGAATGGAAAATGGAGG	60.126	20
102	825	926	AAAGTCACGCTTGAACCATAA	60.05	23
206	1119	1324	CCAGACTGTGGCCTCTCCTA	60.399	20
195	88	282	CGAACCATGAACACCCCTTA	60.745	20
185	1340	1524	AATTGCCATTACCATTCCCA	60.016	20
257	621	877	GATTTTTGGAGGGTTCTTGCT	59.585	21
202	7	208	CAGGAGACGCTCATTCATCA	59.942	20
235	150	384	CACATCCACTCTGAAGTTTGAA	57.856	22
197	1510	1706	GACCAGGATTAGCCCAACTG	59.55	20
278	1498	1775	CCTTCATAAGGCCCACTTCA	60.066	20
275	489	763	CTTGCTAGATGGCCGAAAAT	59.32	20
228	5760	5987	TTTTCGGGAATCTTTCATGC	60.016	20
265	167	431	GGAACAAAAAGGTCCCAGGT	60.204	20
205	53	257	AATGAGGGTTGTTGTGGGAC	59.679	20
210	1449	1658	AAATGAACGTAGCAAAGGGG	59.087	20
125	11	135	CTCTCTATCTTTTTGGTTGGTGA	60.045	25
256	20	275	TCCATGCTCAGAAGTGTTCG	59.984	20
183	254	436	ACTCTGCATCCACCTTGCTT	59.874	20
256	1129	1384	CAGATTAGGAGATTTGGGCG	59.662	20
277	36	312	TGATCACCCAAAATAACGGC	60.701	20
221	139	359	TTGTGTCCCTGAAAGAGGTGT	59.607	21
274	84	357	CACCCCCAAAAGAACAAAAA	59.811	20
272	1138	1409	CCGAGAAGAGGAAGTGTTGC	59.989	20
255	1192	1446	CGAGATTACGAGAAGGAGGC	59.031	20
225	266	490	TGACACGTGGCGTAATCTTC	59.722	20
249	97	345	AGAAGACACTTGGGCCTGAA	59.844	20
280	2295	2574	ATTATGGGTGGGGTCATGTG	60.317	20
239	155	393	AAAGGCTGCATGAGAGAGGA	60.096	20
280	106	385	CCCCGGTGTAAAGAAATTGA	59.795	20

209	830	1038	CATCAGACCCATCTTTGTGC	59.09	20
180	308	487	TCCAGCCCATTCTTATTTGG	59.894	20
269	1008	1276	GACGTTGAAAGGAGAGCGAC	59.997	20
127	290	416	TATCCAGCAGCAACATCTCG	59.972	20
128	87	214	AAGGAGGTGTTATGAAGGGAC	57.273	21
219	561	779	TCTCCCACGCACTTTCTCTT	59.989	20
264	782	1045	TGCAACCCTTTTCTCTCACC	60.232	20
165	2062	2226	TTTCTCCCTCATCCCTCCTT	60.008	20
182	43	224	CAGAGCGCACTCGAAGAGTA	59.49	20
279	681	959	CGCAGTAATAGCATGCCAAA	59.864	20
178	205	382	TTCTCCTTTCTTCCGACTGC	59.55	20
238	266	503	AAATATGGCTGTTAGCCCCC	60.171	20
263	1806	2068	ACCGTGGCATCGAAGATTAG	60.096	20
175	169	343	ACCAATGCGAGGTAGGTGAA	60.517	20
268	8	275	TTTTAAGTTATCGGTGATGACA	58.612	24
215	4116	4330	GGTCATGGACGATAGCTGGT	59.957	20
201	109	309	CGTGAAGATTTGGGTTCCAT	59.79	20
170	0	169	TGCGTTTTGATGATATATATGT	58.859	26
277	173	449	GTATCGCTGCAAAAAGCACA	60.021	20
236	656	891	ATTGAGCGGGTATGGTTTTG	59.823	20
165	36	200	TTTGTGAATGAAATGGTTGCT	58.134	21
207	189	395	ACCCTCCCACACATCAAATG	60.634	20
242	204	445	TTTCCTACGACAACCCTTCG	60.103	20
153	345	497	ACTCCTCGGGACGGTTTACT	59.994	20
114	2498	2611	AGGAAGGATGGATCTTGCAG	59.239	20
236	895	1130	AGCTCCGACTTTGTTGTGGT	59.769	20
173	357	529	TGCGACACCGATTAATACCA	59.953	20
110	57	166	TGGGTTTTGTAATTTGACCCA	60.074	21
243	164	406	CAAAATAACCCCGAATGCTG	60.315	20
114	697	810	AGGAACGATTCACCGGCTAT	60.846	20
276	201	476	CATAAACCCTCACTCCGAGC	59.694	20
172	506	677	GGCCAACTGAAGTTGATCGT	60.119	20
266	170	435	AAAATGCCCTTGTATGCTGC	60.103	20
240	1535	1774	AATAATGTTGGGTGAGGCCA	60.192	20
218	273	490	TTTGGGGGAGGAGAAAGAAA	60.9	20
142	298	439	ATAAAAATGACACTCGGCGG	59.96	20
278	211	488	GCAACCAATTTTCTCTCTGC	57.544	20
274	194	467	GCAATAGCATTCCAGTAACGG	59.622	21
276	345	620	TGCGCTTGAATAAGAGAATCA	58.664	21
226	2921	3146	TCTTTTGCGCTTTCGAGAAT	60.096	20
203	189	391	AATGCCTTTTGTTTGCATCC	59.945	20
235	624	858	GTCCTGCCCTCTCATAGCTG	59.973	20
270	2458	2727	TTCTAGTCCACCCGACCAAG	60.103	20
153	38	190	ACGTCCACAGTGGTTTGAGA	59.152	20
245	423	667	GTCGATACGGCATGACACAC	59.999	20
186	3253	3438	AAATCTGGTGGCGATCAAAG	60.074	20
218	447	664	TCGGTCGTGGGATTTTTATC	59.762	20
280	83	362	CGGGTCGAGAGAGGAGAAA	60.472	19
135	22	156	TATGGGTTATCACCGGATCG	60.544	20
168	1001	1168	CCGATCAAATGAATTTTTGC	58.082	20
264	802	1065	AAATCAATGGCATCCCACAT	60.021	20
174	766	939	ATGGTGCGTGAAGGAGATATG	59.97	21
126	1	126	CTCTATAGCAAGATCTCACGCA	58.464	23
240	41	280	AGGTGAAGAGAGGGAGAGGG	59.801	20
165	45	209	ATCATCCAACACCCATCCAT	59.869	20
152	65	216	TGATTCACTCACATGCACTGG	60.739	21
214	334	547	GCGTGGAATTCACCTCAAAT	59.939	20
263	214	476	TCCGGATTCGAATACTCACC	59.894	20

183	391	573	GGATTGATGGAACGGTGATT	59.611	20
198	751	948	GCCCAAGATGTTAAGCTTGC	59.851	20
153	1	153	CGTAATGTTTTGGTGGGAAGA	59.847	21
256	30	285	ACACAACTTAGGTGTTCTCATT	57.432	24
223	334	556	ATCTGCCTGAGAGGGAATCA	59.761	20
280	648	927	CAAGCAGGAGTGACTAGGGC	60.012	20
245	274	518	TGATTGCACCTGAATAAGCC	58.723	20
278	908	1185	TGGATTATAGATGCACGAGGA	59.569	22
279	41	319	TGACAAACTTAGGGACCGCT	59.734	20
234	719	952	GAAATTTGTCGACCACACCA	59.394	20
252	651	902	CATGGACGAAAATAGCCTCA	58.721	20
249	166	414	TCATGACTGCTTTGGTTCATGT	60.559	22
271	3658	3928	CCCCCAAGATATTGCAACTG	60.323	20
236	497	732	CATTCCTGGTGGCCATAGAT	59.773	20
109	371	479	AGGCAATCTAGGCGACAATC	59.297	20
238	138	375	TCGTGTTCTTCACTCATTCCA	59.278	21
224	2620	2843	AAAAAGTGAGGAGCGGTGAA	59.853	20
137	734	870	GATCCGTTCCTACACATGCC	60.348	20
238	107	344	CCTCCAGTGCCCACTCTAAA	60.246	20
268	10	277	TTAGGCAAGCAGTGGTGAAA	59.464	20
232	2480	2711	CCCTCCGCACCTATTATCAA	59.916	20
181	40	220	TAAGGCAAGCAGTAAACGCC	60.397	20
205	2009	2213	AACCTGCGACATGATGATTG	59.527	20
251	415	665	GTTGGCATTCAAATCAACCA	59.375	20
117	144	260	TGCAGATTCATTGCCATTGT	60.08	20
279	1856	2134	TCACAATGGCAACTCAAAGC	59.847	20
101	3461	3561	CTTGTGGGACTCTCTCTCCC	58.819	20
279	380	658	CCATTTTAACTTTCTGATTGTG	57.817	24
106	542	647	AGTTTCCCTCAACCACGTGTA	59.506	21
241	1492	1732	GATTCCTCATTAAAGCACAAC	58.766	22
246	418	663	AGGCCAACTCAAAAGGGAGA	61.123	20
243	3503	3745	TCCATCCCCTGAAATAGCTG	60.029	20
275	428	702	TTTAGGCTCTGACGGTCCAC	60.255	20
270	186	455	AATTTCAACGTTGCTGCGTA	59.373	20
104	169	272	TACCGTGATTTCCTTCCACC	59.79	20
148	817	964	ATTCTATCTCCTCTCCGCCC	59.634	20
277	113	389	ATCAACAACACCATCACCCC	60.497	20
259	137	395	GACAGCATACGCGCTCATTA	60.006	20
247	12	258	GTTCGAACTGTTGCATGTGG	60.16	20
252	71	322	ACAAAAATGCCCTCGTATGC	59.967	20
188	618	805	GGTGTGCTCGAATTTTTGGT	59.978	20
195	1581	1775	ATTCTCCCAATCTGACAGCC	59.094	20
175	446	620	TGTTCTCTACTATATGTCATGT	58.033	27
250	285	534	AGAAGAAAACGGCTGAGCAA	60.132	20
235	458	692	AAAGAGCTTCCTCCCACACA	59.844	20
277	196	472	TTCAGTCGATTTTTGGGACA	59.097	20
112	65	176	GGACTTGATTCCATGATAACC	59.537	22
260	91	350	AGTGCATGCAAGGAAAATGA	59.276	20
214	151	364	AAAACCCCATATCTGTGGCA	60.192	20
246	366	611	ACCGTTGAGACTACCGGTTC	59.065	20
268	354	621	CAGTCGGGCAAGTCTCCTAC	59.867	20
277	1993	2269	AGGCACATCGTTGACGTAAG	58.802	20
223	343	565	GCATGTGGTCCCTAACTCAAC	59.468	21
256	1244	1499	ACGTGTGCGTGTATCCATGA	61.035	20
277	382	658	CATCCCAGTTATGTCAAGCG	59.148	20
245	1782	2026	CAGTCCTTGGATTTTGACGC	60.636	20
244	22	265	TTGGTTATCGCTTGAATGAGA	59.229	22
110	2831	2940	CTCTCCAGCTCCTGCTGACT	59.883	20

119	2311	2429	AGTTTTCCTGGAAGGGATGG	60.298	20
280	842	1121	GTCCTTGTTTTCGGATGTTCA	59.963	21
275	1521	1795	GCATTGAGAAAACTGGTGCTT	59.373	21
145	757	901	AATGGCCGACACTGCTTTAC	60.14	20
271	50	320	TTGTAAAAACTTCCTATACATA	59.5	27
270	41	310	GTCCCGGGAATGAAGAAGTT	60.306	20
257	190	446	AGCGACACGGGTTATTTTTG	59.996	20
257	1408	1664	TCCCCCTTCTCATTTCCCTA	60.757	20
256	2314	2569	ACAAATATCAGTAAAAATGCG	57.188	23
167	193	359	AGACAACCCACAAATCCGAC	59.827	20
236	734	969	ACTAACAGTCCGGTTCACGG	60.028	20
254	33	286	CACAAGGAACTTGGGACGAT	59.966	20
200	4	203	CCCAATTCTCCATCATTATTAT	59.864	26
186	16	201	CCACTCCATCACCATCACTG	59.954	20
275	504	778	TCGAGCCTTAACATGAACCA	59.272	20
205	468	672	TTGAGATTTGGACGGGAGAG	60.187	20
187	357	543	CCCCTACTTCCTCGTTCTCC	60.067	20
276	1246	1521	TGCAAGATTTCAAAATCGCAT	60.572	22
210	964	1173	TGAGGCAAGAAAAGGTTTGTG	60.269	21
147	252	398	GAAAAAGTCGGCCAAGAAGA	59.429	20
156	7	162	TCACATACTCATGCAAGCACA	58.878	21
166	321	486	GTCCATCGTGAAAAACCTTCA	59.963	21
212	561	772	GAAGCATGCGAGACATTTCA	59.955	20
255	2977	3231	ACGCAATCGATCTTCCATTC	60.043	20
105	28	132	GCGATCAGAAATGCTAGGGT	59.297	20
212	160	371	GTAATCTGTACCGTCCGCGT	60.022	20
228	1184	1411	ACCACTTGACATTTTTGCCC	59.836	20
253	296	548	CCTCAACACCACCACCTTTT	59.861	20
218	271	488	CCCTAATTGTTTCGGGCTTC	60.792	20
199	22	220	TCATTCCAACTTTGTAATCAAG	57.875	24
187	21	207	GTGATGATAATAGGCGGCGT	59.951	20
252	14	265	CCCAAGACCCCAATTTGATT	60.91	20
279	2504	2782	GCAGTGCAACGCATAACAGT	59.942	20
259	110	368	GTGAATTGGCGTGAGTGTGT	59.603	20
246	2687	2932	TGCCTATGATTCTCCGATGA	59.179	20
192	502	693	AAATCAGGGACCCAACAACA	60.21	20
183	604	786	TGTCATGGCAACAAACCCTA	59.964	20
280	551	830	TACCGTACCCTTCGCACC	59.522	18
221	0	220	CTCCCTTGAGCAAAGTGGAC	59.844	20
261	1671	1931	GCTGAAGGCAACTTGAGGAG	60.134	20
277	210	486	CCATTCACACGTGCTTATCA	58.129	20
279	326	604	GAGGGAGGGGAGAGAGATTG	60.149	20
213	1327	1539	TCTGCCATAGCAGCTTACCA	59.59	20
183	4	186	TTGATTGAACTACATTACAAC	57.557	27
181	116	296	TTGGATTCCCAAGCTTTTTG	60.046	20
187	4666	4852	TTTGTTGGCAGACATTTGGA	60.088	20
122	62	183	GTCTTCCGGAGTACGAGCTG	60.012	20
145	885	1029	AATCCTCGTAGCTCCCGTTT	60.096	20
190	20	209	TTCGAATGCGGTTTATCACC	60.837	20
234	198	431	CCGAATACTTTCTTTTGTAGGC	58.131	23
256	731	986	CAATGCAGAGATGGACGAAA	59.799	20
205	11	215	TTAATGTTGCGTGGGCTTTT	60.488	20
248	1459	1706	GTTGATCATCCTGGAGTAAGA	59.027	24
213	121	333	AAATCAGTCTCCATCCGTGC	60.081	20
268	613	880	ACCCTTGGTCGAATTCCATA	59.244	20
273	75	347	GATGAACACGCGCAAAACT	59.862	19
163	2162	2324	GATGATGATCGGTGGAGGTC	60.297	20
182	127	308	TCCCAATCACCATTCAAGTG	59.343	20

210	11	220	CCAGGATCGAATGGAGGATA	59.848	20
181	9	189	ATTTTCGTTGGAGGAGGGTT	59.805	20
244	256	499	AGAAAGGGAGGGTAACGAGG	59.571	20
211	147	357	GGTAGAATAAGCGACGGCAG	59.867	20
269	3473	3741	AATTCAGCAAGAATGATAAAT	57.507	23
186	93	278	CCAAAAATTAAAGGCCCACA	59.805	20
191	3146	3336	AATTCATTCTTCCATTTGCACT	57.747	22
168	339	506	GTGGATTCACATGCCTGAAA	59.502	20
205	344	548	TCGCGCGAATATTGTTACAT	59.197	20
275	883	1157	ATGGGTGTGGTGCTTTGAAT	60.24	20
209	302	510	CAAATTGATCCAACGACACG	59.964	20
245	432	676	ACCCTAAGGACTTCGTGCCT	60.132	20
164	254	417	TCTTGGACTCGGGTCTTTTG	60.224	20
236	1310	1545	CCATCAAGTTTGCACGGTTA	59.585	20
268	153	420	AGGCTTCTCAAAATGCATGG	60.214	20
275	385	659	ACCTAATCATGTTTTGGGCG	59.823	20
199	525	723	CACCCACCCTTCCCTTTATT	60.046	20
112	1905	2016	GCCAGGGAAATGTTATGGAA	59.762	20
230	1013	1242	GAGGATTTTTGGTGGTTTGG	59.264	20
140	12	151	TTGGGAAGATCTCTCCGTCA	60.737	20
203	2417	2619	TTCATTCATCGAAGCACACA	58.782	20
220	477	696	TCAACCCCCACGTTATCTCT	59.405	20
175	140	314	GTTTTCTGCCGAAGCAAGAG	60.132	20
230	1562	1791	GTGGAAGTGTTTTGTGGGGT	59.721	20
117	621	737	TTTTGCCGCCTTTGATTACT	59.72	20
217	50	266	AGCTGACGTGAAACCGAAAC	60.299	20
186	615	800	ACGAAATTAGGGAGGGGAGA	59.897	20
261	184	444	TCACTCTGCATAGCATTAGCA	57.3	21
261	49	309	TATGGGTTATCACCGGATCG	60.544	20
234	485	718	CTCACGACAAGAACGTGGAG	59.461	20
252	197	448	TCGAGCACTTTTTCTTTTGTAG	58.382	23
163	704	866	CATGTGGATTCTATTCCGGC	60.296	20
166	2	167	GAATGACACACGCACACACA	60.218	20
135	1196	1330	AGCCATCAAAACCAACGAAA	60.481	20
267	1901	2167	CACTCTTCCTTCTGCGGTGT	60.444	20
252	385	636	CCAAAATCAACGTCCCAGAT	59.79	20
239	489	727	CCGACAACTATGTTCCCTGC	60.517	20
242	142	383	TTGGTGCAAGGTATGTTTGC	59.59	20
168	38	205	TGTATGCTGTAAATGAAACTG	59.381	24
272	1048	1319	TTCAGATATAACGGAGGAATC	59.816	23
227	476	702	GAAGGGTGAGGCTAGGGAAG	60.204	20
263	4399	4661	GGCCTTAGTCCATGTCCTTG	59.55	20
151	1671	1821	TGACCAACTCCATGTTTCCA	59.935	20
171	682	852	CAATCAATTATGCTAACAATT	59.87	26
218	268	485	GTTTCTGCATTTTGGGAAGC	59.691	20
268	200	467	GATTCAGTAGCACAACCACCC	59.468	21
139	839	977	TGCTATTTTCAGCCCAAACC	60.074	20
217	412	628	GTTGCTATTGCGGGCTTTAC	59.748	20
128	170	297	GGAATATGGGATATGAGGGG	59.822	21
210	341	550	CGGTAATTTGAAGTCAAGGGA	59.994	22
271	10	280	GCGGATGCTCTTAGTTACGC	60.01	20
238	681	918	TACCTCCCCAATCAATCCAG	59.744	20
277	113	389	GTGTCCATTTCCCCCTTTCT	60.169	20
136	10	145	AATGAACGGGCTCATTTTTC	59.022	20
124	6	129	AAAGATGGCCAAAACTGTGC	60.118	20
240	774	1013	GAAGGCAAAGAGAGCGAAGA	59.836	20
121	1	121	TGCGTTTTGACGATATATAGT	59.092	25
248	25	272	TACATCTGACCCCAAGACCC	59.779	20

152	268	419	TTGCATTGACACAATCAAGTG	58.172	21
148	0	147	AAGGGCCGAGATTTGTTAGAG	59.733	21
251	365	615	TATGACTTCGGCATTACCGC	60.991	20
214	133	346	CACGTGTCAAAAATCTGTTCA	57.234	21
102	13	114	TCAACTGGATATCAAACGCAA	59.172	21
144	2123	2266	TGCACTTCAGTTTTGGTGGA	60.278	20
277	95	371	GTTTGAATACAATGCTTCATCC	59.002	23
164	312	475	TGATGTGGCTGAAATCCAAC	59.502	20
170	7	176	CTTGAACATGGCCATCACAC	59.967	20
109	260	368	ATTAATGGGCATTCGAGCAA	60.424	20
124	170	293	ATTATTTGCATTGCTTGCCC	59.935	20
110	955	1064	ATGTGTTGTGATGGGGGATT	59.91	20
183	2717	2899	ATGGATTGCAGAAAGATGGC	60.043	20
116	1135	1250	GAATTCTCCCAAACTGACGG	59.526	20
279	368	646	GTGTTATGCCTATCCCTATCAA	57.816	25
175	3890	4064	TTTCTCCTTGAGCCTCTTCAA	59.181	21
204	691	894	CGGGCTAAGAACCTTTCTCC	60.2	20
225	615	839	TCCGGAGAAAATGAAGAAGA	58.89	21
193	277	469	TCTTGGGAACTCGAGAGGAA	59.92	20
211	197	407	TGTCTCCAAAACAATGGGTG	59.389	20
196	398	593	GTCGGACGATTAATCACGCT	60.103	20
229	48	276	TTTGATCCCTAGAGTGGCCT	58.741	20
202	0	201	TTACGTCGATCCAACGGTCT	60.517	20
107	18	124	TGAGTGCTAGACTATTGTAAA	57.09	25
275	73	347	TTTATTCCCCACCCTTCACA	60.162	20
222	381	602	ATGATGGCGTCATGTTTTCA	59.931	20
211	685	895	CATTGATTTCATTGCATAATCT	59.005	24
278	1231	1508	AATCCACGAAACGGTTTGAA	60.344	20
254	1108	1361	AAACAGCCCATGTGAGAACC	59.973	20
208	180	387	AAACCAATTGGCAACGAGAG	60.11	20
229	206	434	TTCCGAATTTGGCTCTTTTC	59.273	20
172	97	268	ATCTGCTCCTCTCCTAGCCC	59.942	20
253	490	742	ATTGAGGATTTCTTCCCCCA	60.632	20
155	366	520	TTGAATCCATGACGAGCCTT	60.603	20
264	3	266	TCGGTCTCTGGGACCTTTAG	59.28	20
276	14872	15147	TTGGGCGATTTGAAGCTAAA	60.691	20
204	176	379	AGGCAATGGTTTGGTTTCAG	59.971	20
279	226	504	CTTGAGGCCCACACAAGAAG	60.822	20
267	20	286	TATGCACGTGACTTGCTTCC	59.871	20
189	1589	1777	TCCCGGAAATAGTTCCAAAAT	59.666	21
176	13	188	GTTGCATAAACCCTAGGCCA	59.96	20
256	281	536	AGGTCAGTTCCAACCCACAG	60.002	20
257	1151	1407	GGTTTCAAGTGGCAAACGAT	59.978	20
179	1459	1637	CCCTAACCCTAAAGTAAGGAC	59.788	23
251	1528	1778	TCAATGCACCAGAGTAAGTTG	60.168	22
230	141	370	GATGAAGATCCTGGACGGTG	60.475	20
247	140	386	TAACTGCTGGGCTGGTAAGG	60.262	20
257	213	469	TGATCCGAGCTTGGAATAGC	60.318	20
179	1166	1344	GAGGTCTCCCTCCCTTTCTC	59.226	20
161	260	420	CATGGAATTGAAACTTTCGGA	59.924	21
245	178	422	TCGAACACCAAACCAATTCA	59.941	20
274	63	336	TGATGGCAACCAAGAACTCA	60.24	20
177	1341	1517	AATTGCATTTGGATGCATGA	59.898	20
186	742	927	GGCTTTTCTGGAATATAAAGCC	59.297	22
209	1469	1677	AAATTCGACAGCCACAGACC	60.119	20
267	283	549	GGACATGGGATTGGAGAAGA	59.862	20
276	211	486	TCGAAAACCGGTTAAAGACC	59.064	20
276	465	740	TTGAGAAACGAATGCACATGA	60.25	21

182	60	241	GGGCCAAAAGAACAACAAAA	59.953	20
271	2325	2595	TTGTTGTACCATTGTGGAAAG	58.054	22
262	196	457	GCGGCTTCCTACGTCATAAA	60.23	20
179	1004	1182	ATCTCACCACAAACATGGCA	59.967	20
112	339	450	AGAGAGAAAATTGCATCGGG	59.269	20
276	866	1141	TCGCATTAAATTCGGAACAG	58.769	20
190	307	496	AAGATCAGCATTCGGTTTGG	60.074	20
233	1211	1443	CCCATTTATGGGGTAATATAA	58.9	24
252	1284	1535	CCGATTCAGATACTCCCCAA	59.887	20
226	263	488	CGTGCGCAAAAATTATGAAA	59.715	20
198	87	284	ACAAAACAGGGGACAAGGGT	60.64	20
108	72	179	AGTGATGGTGGGTGGAAGAA	60.363	20
199	8	206	CAATTGGATTAGTGACATGGC	58.976	22
244	131	374	ACACCAAAGGAAAATTGAATG	60.089	22
130	318	447	TCCCTCCTCATTTCCAACAT	59.336	20
270	134	403	TTCAAGGTTTTGGTGTTGGG	60.756	20
208	24	231	TCATTGTTTGAAGAGTGGGAA	59.587	22
238	950	1187	TTTTCTTGGCCCAACCTTTA	59.559	20
271	1266	1536	CCAACCTGTATCGCTCTTTC	57.422	20
185	621	805	CGACTCAAAATGGGTCACCT	59.966	20
148	1201	1348	TGCAAAGATGACAGAAACAA	59.912	23
161	985	1145	ATGCGATATGCTTTGTTGGG	60.857	20
257	1022	1278	AAACCCTCTCAAGAACTCCAA	59.255	22
143	349	491	CAGATCTGGCGATATCAATGG	60.442	21
122	7	128	GGCTGGCGGTTTTAAATAAT	58.151	20
274	14	287	TTCGGGTCTCAACACATTCA	60.088	20
154	918	1071	AAAAGGGGGAAACTCGCTAA	60.068	20
273	356	628	TCGAAGTCCCACTTCAGCTT	59.989	20
101	672	772	AAATGTGACCGGATTCATCG	60.723	20
179	5229	5407	CCTCACAGGGTCATTCCATC	60.326	20
271	54	324	TGTTGTGTATAAGGAAGTTTTT	57.546	24
169	78	246	TTTTGAAACCTAAGTGGCCTG	59.254	21
196	1591	1786	GAGGTTGATGTTGTCGGGTT	59.827	20
136	163	298	TCGATCAAAGTTATGAATTGG	59.851	24
265	4044	4308	AGACCACCGCTACTTCTCCA	59.867	20
109	132	240	AGCATCTCTTGCTCTCTCGTT	58.444	21
157	15	171	TATGGATCTTTGGCAGGTCG	60.992	20
277	351	627	GGTGCCACGTGTCATACTCA	60.604	20
177	281	457	AAATCCTTGCACCTCCTCCT	60.074	20
246	1032	1277	GGATTGGACCTATAATATTGA	59.848	24
157	1029	1185	CTTGCAGAATCATAAAGTGCA	60.186	24
196	110	305	GGAGAACGCCATTGTTGATT	59.939	20
244	153	396	TCATGGCGGATTTACAACTG	59.542	20
270	1051	1320	CCGGGGTCTGATACTTTCAA	59.926	20
142	3780	3921	CAAATACGGCCCATAAAGGA	59.789	20
217	382	598	CCACGTTACGCTCAATTTCA	59.729	20
264	168	431	AGCGAAATTGATCTCTGCGT	59.985	20
271	992	1262	GCCTATGTGTCTGGGAAACC	59.41	20
268	850	1117	CAAAGGCCCACAGTGGTTAT	59.853	20
170	44	213	GATGATTGCACCATAACGCA	60.498	20
280	580	859	TTATTGGCAGCGACCAAGTT	60.637	20
226	162	387	CAAGAGGAATTGAACCCAGG	59.521	20
165	602	766	GGCAGGAATGAGACACCAAT	59.934	20
269	1024	1292	GTGGACAAACAAGCCTCACTC	59.76	21
233	156	388	CTCGTAGAAGGGCAGTGGAG	60.005	20
215	14	228	CCTGGGTCTGTGAGAGAGGA	60.388	20
253	94	346	GTGAATTCAATTGTGTTTTGGG	59.225	22
184	0	183	ATCCAAGGGTCAATAATGGTT	57.278	21

210	75	284	TGGAGGAGTTCTTCCAGGAG	59.375	20
209	1061	1269	CCCATTTTTGACGGCTCTAA	60.067	20
220	499	718	TAATCTACCCCCAGCATCCA	60.288	20
273	584	856	GGAGAGATTGTAACGACCCA	57.58	20
124	19	142	AATGTAGGGTGGGTGACTATT	57.914	23
161	503	663	TGCTTCCCTCAATGGTTTTC	60.051	20
250	2573	2822	CGCTCTCTGATGGTCTCACA	60.138	20
134	376	509	TTGAAGATCCCGGACAGTTC	60.05	20
248	335	582	CGCACATCGTAGAAAATGGA	59.688	20
251	1437	1687	TTTGGATCACTAGGGCTTGG	60.066	20
168	35	202	TGGAAAGGTGAGAAGAATCA	59.711	22
175	10	184	CCCTAGCTCTTTCCCCTTTG	60.193	20
114	66	179	AGCGGTTATTACCGGATCG	59.93	19
209	824	1032	CGCTACTCTTCGAGTGCGTT	60.73	20
243	660	902	ACACCGGTTCCAAGTGATCT	59.43	20
232	259	490	GGAAGGGGAGTTAGCGTATG	58.671	20
250	67	316	GAAAAGCTGCCACATCACAA	59.847	20
218	257	474	AGGAAAGAGCAAGCAACGTC	59.621	20
273	411	683	AGCCTTTAAGACACGCCAAA	59.883	20
245	86	330	CGCGTGGGTGATATGCTAGT	61.071	20
263	995	1257	GTCACACTTGCTGCTGCCTA	60.207	20
261	5409	5669	ATTTGTTCTGGGAAGGGTCC	60.169	20
208	127	334	CATTAAAGCCTCACCCCTCA	60.066	20
125	28	152	ACACCCAAAATCCTTTGCAC	59.836	20
146	385	530	CAAGAATTCCAAGCTTGCCT	59.452	20
280	1202	1481	GCTACATCACTTCCCCACAA	58.57	20
148	270	417	CGAAGAAAACACCCGGACTA	60.103	20
218	1954	2171	AAGGGAGCTCCTCAGCCTAC	59.979	20
194	2371	2564	TTACCCTCATATGCCCACAA	58.843	20
251	993	1243	CACCGCCTCATCTCTGATTT	60.218	20
233	1890	2122	CGGGAGGAAGACGAAGAGTA	59.425	20
215	36	250	TTGGGATTAAGGCTTTGGTG	59.931	20
172	10	181	CAATTCCTCCCTTAGACACAA	59.64	23
238	146	383	GCATCTCTTGCTCTCTCGTTG	60.292	21
239	102	340	TTTTGACACGTAGCGACACC	59.764	20
279	2	280	TGTGCGTTTTTGGCATAGTG	60.698	20
185	773	957	AGAGTGATTGTAGGCGGTCG	60.277	20
242	79	320	GTTTTGACCTAATCGCACCC	59.434	20
254	185	438	AAGCTTTAAACGCAGAAGCG	59.801	20
200	917	1116	CGACGTCGTTCTTGATTCTTC	59.867	21
216	776	991	TACCGTTTCAAGGTGCAATG	59.585	20
166	1439	1604	GAATTTGCGCTACAAAAACGA	60.252	21
148	232	379	TTAGTAGTTAGCATGGAAGGG	59.194	23
183	285	467	TCGAATTGATGTTTGATCCAT	57.872	21
122	1115	1236	CAAAATATCGCATTGCCTCA	59.662	20
240	2466	2705	ATTTGGTACATGGATGGGGA	59.871	20
189	484	672	TTGAGCCCTGCCAAAATATC	60.038	20
266	125	390	CGAATTTTAGTGGGACATCCA	59.809	21
111	754	864	TCATGAGAGCGGTGATTTTG	59.799	20
204	294	497	GCTATCACGCGAATGGGTAT	59.951	20
266	384	649	AGTCCTAGCCCCACATCTCA	59.679	20
274	179	452	TAATGCGGGCATAAGACCAT	60.31	20
168	954	1121	TTATGTTAACGGGGTTGGGA	60.046	20
238	2180	2417	GCTGTTAAGGTTCGGGTTCA	60.11	20
183	135	317	AGTCTCCCCATTTGATGCAC	59.934	20
155	70	224	ACTCGATGAGTAGCGGATGC	60.393	20
197	117	313	CCCCTTTCAAGTAGCTGCAC	59.875	20
166	565	730	GCAACCAATACCATGCCTCT	59.962	20

157	338	494	CTGTGCGCTTTTGTCAGTGT	60.096	20
129	1999	2127	ATTTTGATGCCGGGAATGTA	60.153	20
232	974	1205	CACGCTGATATCGCACAACT	59.895	20
228	471	698	ATCCCAGAATGCCTACACCA	60.34	20
210	74	283	TTAAATGCACAGCACAGCTC	57.662	20
250	691	940	TCAACTTATATTTCAGCGACGA	59.236	24
160	128	287	TCAACAACAGCAGAAATCGG	59.84	20
182	662	843	AACGACACTCATCCGCTCTT	59.874	20
255	759	1013	TTCTTTCACGGGTTTGAAGC	60.227	20
221	3	223	TTCATATATCACGTTAAGACAT	58.031	26
245	2	246	TAACCCTTGTTAGCCCGTTG	59.99	20
277	69	345	ATCAGCCAAATGCAGAGATG	58.826	20
279	123	401	CTATAAGGTTGCACCCACGC	60.523	20
162	4	165	TCAATTTCTCTAACCTGTAAAA	58.065	25
167	326	492	CAACTTGCCCTCTCTCTTCG	60.126	20
227	231	457	AATACACCCCAAAGTGGAACC	59.969	21
150	12	161	CCAAATGTTAGGGTTATCACAC	59.654	23
216	1068	1283	CCTTCATCCCCTGTCTTGAA	60.042	20
146	2395	2540	ATGGTTGCCTGCGAGTCTAT	59.723	20
273	102	374	AAAATGCATCATACGGCATAC	60.233	22
252	703	954	TGATCCTTTTTATGATAACCCA	57.592	23
268	10	277	TTTAGATCAAGTGTGTTGTAAA	58.765	27
255	159	413	TTGAAATATACTTTTCATTTCAC	57.253	25
277	68	344	ATTCGAAGCCCAAATCATGT	59.391	20
222	169	390	GGGTGGGTTATAATGGGATTG	60.137	21
270	170	439	CACGGGAGGTGAAAATTGAG	60.486	20
238	1241	1478	TGGGCACTTTGCCTATTCTT	59.708	20
197	454	650	TCCAACCGCTATTTGAATCC	59.901	20
103	8	110	TTTAGTGTTTTGACATGATTACT	57.557	25
174	141	314	TGCTGCTTTAGGTCTTTGCC	60.523	20
245	5450	5694	CACGAACACATGAGGGAATG	59.96	20
131	1006	1136	TGAATGCAGCTTTGGTTTCTT	59.875	21
280	470	749	ACAGAGGGGAGAGAGAAGGG	59.801	20
275	1149	1423	AAGAAAAGGGGGAAAGGTGA	59.912	20
265	462	726	CTTATTGAATTTTCGCCCCA	59.901	20
115	0	114	TCCCCTTTTACTTTATTCTTTCA	57.604	24
161	218	378	TAACGATGGACTAGGGGCTG	60.088	20
177	184	360	TCAAGGGGTATTTTTGTCCG	59.795	20
229	215	443	TGTGACTGTCGATGAAGTAAA	60.095	24
108	9	116	CGAACGATGACATGCTCCTA	59.823	20
107	197	303	ACTTGCAAAAGACTCCAGGC	59.478	20
213	101	313	ATTCACACCATTTGCCATCC	60.591	20
121	512	632	AATCCCCGCCTATCTAAGGA	59.888	20
267	69	335	TGGATACATGGGTGGATAATA	58.461	23
128	429	556	GCGAGGAAATTAAAGCAGCA	60.476	20
273	2134	2406	CCTGTGCTTGTTGTGTCGAT	59.751	20
138	498	635	TCAACTATTGCCCCTTGGAC	59.933	20
145	374	518	CAAGACCACGAGCCGTTAAT	60.132	20
195	11	205	CAAAACTCTCATACAGCCAAA	57.14	22
225	486	710	TGTAATCTGGGATAACGGGG	59.64	20
160	3004	3163	GTAAGCATCGCCCTCCATAA	60.06	20
232	635	866	TCGGAGAAAGAATTAGCCCA	59.778	20
271	395	665	TGTCTAGGCATCAAGGAGCA	59.547	20
100	185	284	AGGGGTTCGAGTGGAAAATC	60.306	20
201	570	770	AGAATTGGAACCCCAAAACC	60.032	20
207	619	825	GTCAGCCCCAAATCACAAAC	60.362	20
279	214	492	CCCCTCGTATGCAGTCATTT	59.955	20
179	296	474	TCAGACGAAACATCCCTTCA	59.215	20

142	197	338	TCAAAAGCAACCTTCCAACC	60.088	20
267	210	476	TCGGCCAGAGAGAAGAAAAG	59.688	20
234	520	753	CCCTCACCCTTTACGGTTTT	60.214	20
190	99	288	GAGCGTGAGAGATAGCCGAG	60.263	20
267	61	327	TTCACCTACCAATTCCAGCAT	59.443	21
278	63	340	ACACGCGATACCATTCAGTTT	59.513	21
242	4	245	TTAGCTGCTGGGATTTTGCT	59.982	20
151	1291	1441	TGTTCGTCGCTGGAACTATG	59.864	20
166	394	559	TGTTTGCTGTCATCGCTAGG	60.011	20
278	559	836	ATTGGGTTGGGTATTGATGC	59.51	20
218	649	866	TTGGATAAATGGGAGGCTTG	59.894	20
194	554	747	TTCACCCGTGACTTTGACTG	59.72	20
169	659	827	GGTCAACCTACAGCACCGAT	59.997	20
249	122	370	TCATGGGGAATGGAAAAAGA	60.244	20
278	611	888	GCCTCCTACCCCACTTCACT	60.511	20
172	995	1166	ATCTCTGTCGCCATCGAATC	60.189	20
234	410	643	ACGCGCGTTTTTAGAGTTTA	57.824	20
221	97	317	TTATTTTGGGCACCCACCTA	60.181	20
206	1271	1476	TTCCGAAACTTCCAATCAAGT	58.682	21
223	1276	1498	GGTCCCTAAACCCAAATCGT	60.053	20
243	230	472	CATTTGGAGGTGCACACAAC	60.008	20
199	971	1169	GGAAACCTTATGCGATTGGA	59.901	20
235	2961	3195	TGCTTGAGAGTGGGAGGAGT	59.986	20
222	71	292	CGAATACGTACGGGTGTGC	60.003	19
213	576	788	TAGATTTTCATTGCCGCCTC	60.175	20
279	182	460	GGCCAAATCCTAGCCACATA	59.923	20
196	301	496	TAAAATGATCAACCGCCTGC	60.971	20
253	484	736	ACTCGTCCTCGTTTCTTTGC	59.478	20
258	1550	1807	CTGAATCCGCCCATGATAGT	59.917	20
211	595	805	CGCCAAGCACTCACAAACTA	60.05	20
224	12	235	AAGGGGGTTATTAGTGGATCA	57.425	21
188	1396	1583	GCTGGTATTTTGGCCTTCAT	59.046	20
247	2581	2827	TCAGAGAAGAAGAAAGAGAG	59.088	24
241	45	285	CATCTCTTCTCCACCAACCG	60.646	20
259	1898	2156	CACCAGGCGCAGAGTATTTT	60.27	20
141	339	479	CTCAATGTAGCTTCGCCCAT	60.235	20
120	409	528	CCATCTTCAACCCGTCACTT	59.966	20
134	974	1107	TGTTGTGTACGCGAGAAACC	59.764	20
107	13	119	ACCCCCTTCTACTTTGGTCA	58.498	20
176	3756	3931	AACGAGAAAAGACTGCTGCC	59.621	20
131	38	168	ATCGGTTATTACCGGATCGC	61.031	20
277	896	1172	CAGGTGCGCCTTATCTCTCT	59.598	20
195	216	410	TGCATGATTTCTTCAATCTTCG	60.209	22
256	774	1029	GGGAAAGCCTCAAGTCCAAT	60.443	20
243	642	884	TTGTTTTGTTCGACAACGACTC	60.19	22
144	3	146	TTTTTGTCTCACTAGTGTCGTTT	59.786	25
135	47	181	AGTTTTAGCGTGTCAGGCGT	59.943	20
158	41	198	AGAGGACACGTTGGACCTGA	60.713	20
226	500	725	CATATCACGATATCCACATTTA	60.127	25
176	821	996	TGCAGAGAGGCAGTTCATTG	60.136	20
280	1213	1492	CCGTACGGCTTGAATGTAGG	60.514	20
185	927	1111	TTGCGAACTAGTTGTCGTCG	60.05	20
203	170	372	TCCCACTGCCCAAACTTATT	59.429	20
263	446	708	AGAGCATGAGAATCGGATGG	60.181	20
196	1558	1753	CGATAAAAATGGCACCCAGT	59.823	20
280	50	329	CGCTGCTTTCGTGTTTAGTTAC	59.142	22
239	701	939	GGGGGAGAGTTGGAGATCAT	60.278	20
183	379	561	CAGCGGCTTACTAGCTTCGT	59.813	20

177	125	301	CCCCCAAATCATTCAGCATA	60.66	20
259	413	671	GCCCAAGTGGGATATTGTTG	60.192	20
161	4	164	ATCACATAAATAATGGTTTCTT	57.797	27
177	456	632	TGCGTCAGAAGGTGTCCTAA	59.44	20
243	83	325	CCCCCGTGCATTAATAAAATC	60.385	21
265	210	474	GGAGGAGAGGCTCTTGGTTT	59.817	20
199	852	1050	TGGGCTTCATTTCTGTCAAA	59.247	20
153	808	960	ATTTGGAAACTTGAACCCCC	60.032	20
233	899	1131	CAAAATCCACCAACCAAACA	59.268	20
204	16	219	CCAAAACCCATTTCATGTCA	59.222	20
248	225	472	GGCCACTGCGTTTGTTAGAG	60.827	20
229	205	433	ACTTTTCCTCCCCCATCATC	60.133	20
191	2618	2808	TCTTACTTTCCGCCATTGCT	59.845	20
159	1180	1338	CCTCTGCAGCCTAAAACCAC	59.875	20
174	180	353	ACCTCCACACCCAATCTTCA	60.363	20
235	164	398	GCAAGAAAGCAGTGCACCTA	59.224	20
278	59	336	TTGGCGTAGATTCCACTTGA	59.272	20
115	2872	2986	CACTCATTTGAGGATGGATTG	59.933	22
152	86	237	GGTGCTTTCTGGTTCATCGT	60.119	20
235	321	555	AATGTGGCATGGGTCAAGAT	60.203	20
268	1062	1329	TCATTTTTCAATCCCAGCCT	59.505	20
102	9	110	ACGTCCTCTAGGTGTCGTCC	59.179	20
263	782	1044	GATTCGTTGCAGAAATCCGT	60.081	20
219	2784	3002	TGCAAGGACAAGCTCAGAAA	59.716	20
230	39	268	TGATTTCGCTGATTTTGGTG	59.664	20
274	571	844	CTTTCCCATGGAGTTCAGGA	60.042	20
103	0	102	GCTTAATTGTAAACCGTTGTC	57.369	23
156	356	511	GCACTCAGTTAAGGGTCCGA	60.255	20
241	310	550	ATAAGCCGTTTATGCGTCGT	59.636	20
176	22	197	TGAATCCTTCCTTGCTAGTCA	58.462	22
256	377	632	CAATGTATCCAAACATGATGA	60.124	23
202	241	442	ATCAGGCAAAAACGTGCATT	60.511	20
264	348	611	AATATCAACCACCAAAGCGG	59.823	20
148	1194	1341	TCAGCAGCCATCATTTGTTT	59.276	20
266	1191	1456	CCACTCACATGGGAATTGTT	58.258	20
147	1054	1200	ATCGGAGCATGACGAAGAAC	60.226	20
218	3589	3806	TTTTGAATTGGCAAACATGC	59.543	20
204	325	528	GGCATGTCCGAGTTCTTAGC	59.843	20
228	959	1186	TTCCATACGACATTGCAAGC	59.694	20
249	704	952	CCAGAACCCAGCTTCTTCAG	59.982	20
218	0	217	TCAACGTACCTATTTTGTTCCT	57.56	25
242	85	326	ACACACACAAGATTTGGGAG	59.876	21
122	41	162	CTTCAGGAGATCGGGGACTT	60.586	20
228	183	410	CGGATAATGCTCGAATCCAT	59.885	20
251	144	394	ATCCTGTCCATCACCCCATA	60.011	20
262	201	462	CAGCATACGCGAAGGGTATT	60.117	20
168	8	175	TCAATAAAATGCTTCCAATCG	57.792	21
147	1059	1205	ATCCAAGGAGCACACCTGAG	60.261	20
225	816	1040	GTGTTCACGGTGTTTCTCCC	60.408	20
215	12	226	TCACCAATTTGAATGGTTATC	57.873	22
260	276	535	ATTTGGCCCTATAAAATGCG	58.96	20
146	64	209	CCTCGCAGTCATTCCAGACT	60.408	20
150	23	172	GGAGGGGGTATAATTTGAATA	59.165	23
114	1	114	TTTGAAATTGGATATTTTCAGG	60.18	25
221	118	338	AAGGCAACGCAATCAAAACT	59.752	20
222	12	233	CTCCTGAGCCTTATCCCTCC	60.169	20
162	422	583	TCTCTCTTCTCCTCCCTCCC	59.883	20
268	515	782	TGACCTCTACGAGGCATACCA	60.663	21

183	56	238	ATAGGGATTTCGGATTTCGG	60.109	20
161	1854	2014	TTCCACGGAGAGCGTCATAC	61.208	20
232	284	515	GAAACTGAGCTCCATAGCCG	59.978	20
251	138	388	AAGTGAAGCCCTTTCTTCCC	59.691	20
146	2862	3007	TTGCGTTGTGGATACAGCAT	60.142	20
188	13	200	CGGATGAATTTCACTTCACG	59.123	20
169	798	966	CATTCTCTCAAATCGTGGCA	59.799	20
141	297	437	ACACAGATCACAAATGGCGA	60.12	20
199	3	201	CCGTCAGTTTCAAGACATTCC	59.583	21
235	154	388	AATCCCCCAAACCAATTTCT	59.51	20
143	201	343	GCAGGGCTGAGTACACGAAT	60.285	20
134	1954	2087	GAAGGGAAGAGGAAGATGCC	60.154	20
237	327	563	CGGTTCAACTTCCCATGTTT	59.83	20
174	324	497	TGACATTGAATCCCCTCATT	57.775	20
248	1543	1790	GCTTGCTTGCTGAGGTAAGG	60.154	20
190	2014	2203	GGTAGCACCATCAGCAGACA	59.862	20
262	208	469	TTAATGGCGCCGCTAATGTA	61.44	20
112	520	631	AAGTGGTTCACCCCTACACG	59.884	20
226	665	890	ACCACATAAGCGTCATCTCAA	59.637	22
122	4	125	GGGCTGCAGGAATTCAATAA	60.038	20
278	973	1250	TTTTGCCATCATAAACTCTATT	59.557	24
261	73	333	CCATTTCAGCCAAGCTGTTT	60.249	20
280	1114	1393	TCGGAAGGTTTATCCTCAGTG	59.181	21
211	369	579	CATTGCCGAACACCTTTCTT	60.11	20
256	669	924	TGACTCCACCCACCCATTAT	60.05	20
244	1	244	CCTCTCCTCTCTCTCTACTCTC	59.156	26
251	311	561	GGGTGGGTCTCCCTTACATT	60.052	20
227	2295	2521	ATACCCTCCGGTACACGAAA	59.312	20
201	283	483	AGTGGAACCAGAGTGGCCTA	59.721	20
190	1446	1635	TCGCAACTTCACCTTTACCC	60.11	20
197	635	831	AATGTGGAACCAAACGATCA	58.824	20
239	90	328	TTGGAATAGGTCCTTGGCTG	60.066	20
189	21	209	TTTAGTGTTTTGACATGATTAC	57.557	25
205	96	300	GGGTTACCAAATTAGTTCGTC	59.773	22
175	121	295	TTGTTGTTTTCAACCCCTCC	59.807	20
138	19	156	CACCCAAACAATGCACAATC	59.823	20
255	3115	3369	GGATCATCTTCCCTCTCCCT	59.449	20
262	1440	1701	TCATTCCGGGCAGTAAGTTC	60.074	20
250	1914	2163	AAGGAGGTGTTATGAAGGGA	58.028	22
271	169	439	TCCCAAACTGATGGAAGGTT	59.381	20
176	4	179	TGCAAAAGTTATGGTAACAAG	57.203	25
198	815	1012	TTTACCAAAACGCCCCAATA	60.178	20
218	5	222	TGGTGAATGATTGACGATGAA	59.916	21
140	10	149	TCGAAAATCAATGGTCCACA	59.9	20
176	20	195	TCTCTCTTGGTTGGTGAAGGA	59.829	21
265	456	720	CGTGGTTGGTGTGAGATTTG	60.001	20
212	1611	1822	TACGATTCACCAATTCGCAC	59.548	20
266	1246	1511	CAGCGACAATTTGCAAGAGA	60.134	20
190	525	714	CAAAGGTAGTCGGCAGAACC	59.734	20
185	1042	1226	ATCACTGCATTTCGTCCTCC	60.081	20
252	102	353	TGCCTTTATTTTAGCCTCCC	58.337	20
236	2106	2341	CCTCACATCGCCAAAAACTT	60.11	20
191	3	193	CCTCATTTTCAACACCCCAC	60.21	20
278	90	367	CTACGAGCCACGGTTACAGG	60.7	20
234	814	1047	AAACCGGGCCTACAAGATTT	59.835	20
223	371	593	TTTCTCCCTCTCTCCCTTCC	59.749	20
160	469	628	GAGGAACAGAGCTTCAACGG	59.989	20
232	694	925	AAACAATTGGGATGAGCAGG	59.933	20

243	910	1152	AATGGTGGCCGAAAATTAGA	59.411	20
213	53	265	CTAACCCTAGGTGGTGCCAA	59.986	20
280	31	310	CCCAGGCATAGAAAGAAAAGA	60.889	23
248	1943	2190	CGTCGGTGTATGACCTGTTG	60.025	20
227	390	616	CAGATTCCCGTTCCATCCTA	59.887	20
242	1049	1290	GTTGTGGTCTTTTCAGCGTG	59.339	20
264	202	465	AACACTATCACCCCACCCAC	59.555	20
187	206	392	CTAAACCCAGGTGGCAGTGT	60.028	20
139	489	627	AAGGAGTGGGATCTGGGAGT	59.929	20
271	62	332	TCGGATCGGATATCCAAAAA	60.225	20
243	529	771	TCCCAACATTAGGGGGAAAT	60.37	20
227	138	364	GGCATTGGAGGAAAGACAGA	60.195	20
177	404	580	GTTGGAAAAAGCCAATCGAG	59.685	20
203	665	867	TTTTTGGAAATTTTCGCACG	60.94	20
263	26	288	CGAAGCCAAACCTAGGAAGG	61.096	20
242	474	715	TCCATCCACCTCTGCTTTTC	60.195	20
274	242	515	TCGTACAAATTGCCACAAATG	59.476	21
201	637	837	GGAACCTGAGAATGGGGAAT	60.133	20
188	1123	1310	CATGTGGATCATACAACAGGG	58.709	21
236	124	359	TCTACCAAGATCCTGCCTGC	60.362	20
276	1051	1326	CGACTATTGTTTGTCATCGCA	59.744	21
233	70	302	GGGCTAGATTTGTTGCCTTG	59.708	20
242	611	852	AGGCTACTTGGCCCCTATGT	59.983	20
176	10	185	CCGCTCCTCCTTTTCTTTTT	59.829	20
194	15	208	AAGGAGGTGTTATGAAGGGAT	58.028	22
162	221	382	GCAAGGTAGTAAGCATGGCTG	59.919	21
245	488	732	TTTGGGGGTGCATATTTCTC	59.762	20
254	379	632	GTGGATCTGGGCTGCATTAT	59.923	20
163	825	987	TCAACCACACCTCCAACTCA	60.129	20
279	173	451	TGCAGTTGAGATAAGGGAGGA	59.822	21
104	87	190	TGAACATGCTCATATTTTAATA	58.521	26
196	71	266	AGCATCTCCAATGCCAGGTA	60.624	20
207	902	1108	TTTCGCATTCTTATTCCGATG	60.047	21
184	629	812	GGGTTATTTAGAGGGGCCTG	59.793	20
264	739	1002	AGGCCCACCAATTACAACAC	59.717	20
113	1050	1162	CGCATGCACATGCATTATTT	60.505	20
140	16	155	CCCAAGAATGGGTTATTATTTG	59.973	24
190	41	230	AGACCGCAATAGCCACTGTC	60.285	20
166	605	770	CATGATCTGATGAGGCAGGA	59.743	20
238	125	362	TTAATCGGGCTCTGAGCAGT	59.978	20
174	1518	1691	AGAGCTTCTCCAACGCAGTC	59.751	20
132	1557	1688	GCTAGAAGCAGCCGTGACAT	60.569	20
278	188	465	ATTGAATCTACGTCCACGGG	59.813	20
188	534	721	ACCCTTAGTATGCTGTCCGAAA	60.021	22
141	66	206	TCATGAGCCTTCTTCAGCAA	59.673	20
100	887	986	GATGGAGGAGGACAAAAGGG	60.822	20
168	422	589	GTTTCCGCCGGAGAAATAAT	60.28	20
268	57	324	TCCTTACAACCTCACCTCCG	60.103	20
166	77	242	TGTCCATGCAACCTACGATT	59.002	20
278	118	395	GCAGACAACTGACAATGCAAA	59.903	21
276	2487	2762	GTGGAAAGAAGCTAACCCCC	59.94	20
141	220	360	ACTCCTCTCGATGCCCTTCT	60.358	20
232	696	927	GCAGCAAGCTCTTTTCAATG	58.799	20
131	213	343	TTGTTAGAGGTTTTGACGGGA	59.595	21
107	23	129	TTCGAAAAATGAATGGCCC	60.771	19
207	477	683	TTGACAAGCCAATTCGAACA	60.234	20
206	1667	1872	CCTCCACGAATGGTTTTGAT	59.79	20
114	1165	1278	CACGGTCATGAATAAAATCGT	57.5	21

272	501	772	CCAACTGACCAAGCATCCTC	60.656	20
254	139	392	ACATGAAAGCGGTGGAGATT	59.556	20
128	1022	1149	AGACAAACAAAGCCAGGTGC	60.299	20
164	621	784	CATGCCCATCGTAACATGAA	60.343	20
174	570	743	CTACATGCTGAGATCGAGCG	59.722	20
277	390	666	AAATAAAGGCTGCATGGCAC	60.103	20
112	438	549	TAAAGATGGAGGGTGAGGCA	60.594	20
232	3382	3613	TCAAGCCCAAAGATGTCTCA	59.369	20
204	355	558	AATTCCGTCCCAAAGGAAAA	60.644	20
184	388	571	ATGCCCTTTTCTCGAACATC	59.129	20
124	560	683	TCGTGGCTGGTTAAGCTTCT	60.015	20
149	695	843	AGGCCAAGGTATTTGTGTGG	59.853	20
144	2	145	ATGAAGTTAGGAAATAAGAAG	57.239	26
251	144	394	CCTTGAAGATCAAGACATCTA	59.685	25
262	582	843	AGGGCAATTGATCTTGCCTA	59.668	20
144	2838	2981	GAGAAGGTGGACAGAGGCTG	59.986	20
142	248	389	TGAGACCGGAAATGGATGTA	58.923	20
260	385	644	TGGTGGAGGCTCGGTTATTA	60.46	20
188	394	581	GGCCATTAAAGCTTCACCAA	60.074	20
238	168	405	ATCATCAACCTCCTGCTGCT	59.834	20
173	167	339	AAAACTCCAAATCCCCCAAC	60.032	20
262	1644	1905	GAAAATGACCAACCATTCGG	60.17	20
208	251	458	TCAGTGATAGAAATTGAGGGG	59.952	23
273	376	648	GAACACAAGACCCCATGTCC	60.223	20
248	17	264	AGAGGGTTATCATGGGATCAA	59.307	22
239	186	424	AGACAAGGACACACCACACG	59.623	20
276	555	830	GGTGCACCCTCACTTTTGTT	60.012	20
196	721	916	TAGGGTTCGAATCCCCACTC	61.211	20
239	2434	2672	TTTCCAGCAAAACATTGACG	59.706	20
229	198	426	ACACCCAAGCCCACACTTAC	59.891	20
262	69	330	TCCCATTTTGGGATGAATTT	59.067	20
262	1588	1849	CATCAGGGCAGAGATTCGTT	60.218	20
126	322	447	TGATCTCAAAAGATCAACGGT	59.994	23
102	6954	7055	TCTACCTAAAGCACGCCAAAA	59.897	21
222	416	637	GACGATGGTTGGAAACAAATG	60.22	21
235	155	389	ATTCATGAACCACAAAGGGG	59.647	20
173	6944	7116	GATGCTGCTCAATCCGAAAT	60.185	20
213	184	396	ACAAGTATTGGGGCAGCAAG	60.132	20
110	833	942	CACGGACGAAATGTGAGAAA	59.691	20
253	936	1188	CCACATAATGTTGCGCATGT	60.41	20
256	565	820	CCTGCTCAAACACATCAGGA	59.831	20
162	303	464	GTGGCTTCATGCAAATTCAA	59.67	20
258	780	1037	CACGTTAAATCCCTTGCACA	59.585	20
254	250	503	TTTGTGGTATCAGAGCCACG	59.716	20
242	249	490	TGCAACAACAGAAGGATCAGA	59.43	21
246	129	374	CGTGCAGTTGGGTAAAGGAT	59.993	20
243	1835	2077	AATGCAAAGGATTTGATCCG	59.901	20
181	3095	3275	GCCTTCCTTCTTCCTGTTCC	60.19	20
121	205	325	GGACGCACCAGATTGTTTCT	60.119	20
132	1155	1286	TGTAAGGTGCTCCACCATGA	60.112	20
245	82	326	CTCTTCATTTGCTTCTGGGG	59.807	20
155	346	500	TCCATTCCCCATCTTATTGG	59.576	20
265	92	356	CGAACTACAAATGGCACTTCA	60.166	22
100	16	115	TTTTCTCAACCGAGCTCACC	60.375	20
218	3484	3701	AAAAACAGCCACCAACCAGT	59.496	20
239	26	264	TGATGTGATTAATTCCCACCAT	60.306	23
186	3273	3458	AAGCGTCGTGGGCTTGTAT	60.672	19
266	1296	1561	TTTTGAGCAATAAATCCAGGG	59.065	21

225	151	375	TCCGAGGGAGAGAAAGAGTG	59.525	20
270	158	427	CGCCACTCCAAACTTCAAAT	60.11	20
247	198	444	AATGATTGTCACAGTTGGGCT	59.468	21
197	325	521	CTGCTGTGCGTCGATTTCTT	61.513	20
197	314	510	CTGCTGTGCGTCGATTTCTT	61.513	20
266	396	661	CAGCAAATCACCTCATCCCT	60.073	20
185	2	186	AGCTTTAGTAGGGTGCAAGCC	59.926	21
128	118	245	AGCAGGTTAGCAGGATAAGG	59.755	21
134	1391	1524	TTGCAGGAGAACTAATCTTCA	59.453	24
269	2377	2645	TCTGGTTTCCAAACAAAGCC	60.088	20
173	512	684	CTGGCTGGGCTTTGAAATTA	60.202	20
208	1217	1424	TTTTAGATCCAATGCCCCAC	59.762	20
131	227	357	TGATGTTTTCTAGAGGGAAAC	60.05	25
245	749	993	TCCTTTCCATTGGAGGAAAC	58.956	20
238	885	1122	ATTGTTCGACGTCACAGCTAA	58.446	21
186	29	214	CCGAATCCCGATAACTAAACA	58.953	21
276	231	506	TGCTGCCTTAATCCACACTG	59.864	20
205	415	619	GCTTCAATCCGTCACTCCTC	59.81	20
272	493	764	ATGCACACCCCGAGATACAT	60.226	20
274	221	494	GGCGGAGGAGTCTTCTAACA	59.43	20
187	36	222	GGTTATCACCTGATTTTCTCCC	59.734	23
264	1021	1284	ATGGCCTTATTTGGCCTACC	60.171	20
215	1688	1902	GGACAATGGAAGGCATTCTG	60.461	20
277	202	478	GGCCGATATTTGCTCACATT	59.929	20
267	49	315	GCACCTCTATGGTTGGGAGA	60.073	20
233	72	304	CGTGTTTTTGGTGAAAGCCT	60.147	20
272	2434	2705	ATTTTGTCGCCAATTGTTTG	58.532	20
256	20	275	GATAGTGCGTGTGTGCAAGC	60.491	20
280	710	989	GCAGCCACGATGATATGACA	60.663	20
151	677	827	TCAATCGCACCGTCACTAAA	60.257	20
198	924	1121	CATTTCGGTGTGAATTCGGT	60.755	20
255	115	369	TTCTACCACCACCCATCTCG	60.913	20
240	96	335	ACGCGCGCTTTTAGAGTTT	60.166	19
219	13	231	TTCATTTTTAAATCCTATATCA	57.503	26
222	232	453	GTCCCAACCAGGCTGAATAA	59.933	20
114	251	364	CAGATTCCAAAAACGGGAAA	59.91	20
108	3	110	CAGATTTGTTATGCGTTTTGAC	60.048	23
198	221	418	CGCATGGGAATATAATGGAG	59.765	21
261	626	886	TCCTCCACTACCCAAAACAA	58.049	20
274	260	533	TTCGAATGTCATTTCACCCC	60.702	20
154	4635	4788	GTCTCTTCAGCATCCTTCGC	60.104	20
194	347	540	CAACAAAAATGGCACTCTTTC	60.145	22
163	2271	2433	CTCAGGAGCAATTGGGTGAT	60.073	20
178	787	964	TGGATGATTTTGTGGTGTGG	60.216	20
213	161	373	AGGGCTGTCTCTCACTCCTG	59.579	20
171	368	538	CGCACACAAAACACACACAC	59.669	20
111	1147	1257	ACTGCACTCAACCACAACCA	60.203	20
116	562	677	ACACCCCTACCCTCTGTTCC	60.23	20
207	840	1046	GGCCTTTCCATTTTCCTCTC	60.017	20
254	20	273	GGGTGTTTTGACAATATCGC	57.943	20
247	1146	1392	CCCTTTGGTATGAGAAGCCA	60.066	20
217	303	519	GCTCTTCTCCCCCAACTACC	60.074	20
279	580	858	ATGGCCGAGATTGTATGAGC	60.066	20
241	88	328	GCAAGGATTGTAGCAAAGGG	59.708	20
241	1020	1260	TAGCAATCAAGTCCCTTCGG	60.206	20
236	354	589	CATTGCTTTCCGACTGTTCA	59.84	20
136	380	515	TCCTTCCTTGCTCCTTTTCC	60.683	20
120	128	247	TCACCTTATGGACTCAGACGA	59.734	22

165	943	1107	AACCGAAAAAGAAACCTTTCA	59.913	23
182	179	360	GGTTTGCGTTAGATATGCCC	59.438	20
267	452	718	GTCGAGGTGATCTCAACGGT	60.12	20
163	354	516	TTACCGTGGTTTCTACCCCA	60.22	20
241	174	414	TAATGAATAGGGGCGAGTGC	60.06	20
261	177	437	AAACTGAGTGATGCCAGCCT	59.874	20
237	393	629	AAGGCGACATGTTTCAATCC	59.939	20
236	139	374	GCAGCACGAGCTCTGTCATA	60.319	20
221	1306	1526	CGTGGAGCAAAAACATCAAA	59.706	20
222	185	406	GTTGTTGGCCCACTTTCAAC	60.397	20
243	292	534	AGCCAGATCCAAAATCATGC	60.043	20
185	648	832	TCTGACCCGAATATGTCCATT	59.259	21
237	401	637	TTCATCTGTCTCCTACTCCAAG	59.899	23
153	14	166	TTTCTCAACCGAGCTCACCT	59.989	20
241	497	737	CCATCCTGCACCATCATACA	60.353	20
192	1218	1409	AAATTGCACCTCGTCGACTC	60.263	20
231	394	624	CAATGCCTCGTGCAATTATG	60.096	20
230	848	1077	TTTGGATCCATAACATGAAAA	57.065	22
223	841	1063	GCCAACTTTCTTCATCCGTC	59.676	20
205	1627	1831	TCACCTTCAGGGGACAAAAC	59.943	20
217	23	239	ATGGGTTATTACCGGATCGC	60.903	20
208	259	466	TGTTGCGATTTTCATTTTCC	58.601	20
209	1388	1596	TTCGTCAGTGGATCTTGCTG	59.984	20
240	26	265	AATGAATGGAAACGAGGTGC	59.939	20
135	919	1053	GAACCACAACCCTTCTCCCT	60.349	20
156	29	184	CAGAAATTGCCTTGGTTGTTC	59.601	21
231	643	873	GCCAACGATATGATCGCTCT	60.207	20
215	126	340	CGCCAAAAACACAAACAAGA	59.746	20
227	21	247	GGAGTGAGACGGAGGGAGTA	59.254	20
152	169	320	ATGTTTTCAATCTTGGCCGT	59.434	20
249	162	410	GCACCGGATTGTTTCTCATT	59.939	20
268	1783	2050	ATTTATCGATCAACCATTTCTT	57.324	24
191	14	204	CCAATTTGAATGGTTATCACCT	60.457	23
229	172	400	GGGCTCGAAGTTTCTTGATG	59.813	20
223	764	986	GAGGCGAGAACCAACTTGAG	59.989	20
210	881	1090	TGTGTTTATCATGGGCCAAA	59.786	20
195	584	778	TTTGATTTGCATGCGTACTTG	59.756	21
150	511	660	ACAAGGGAAACGTTTTGGTG	59.869	20
177	161	337	TACCCAGAAACCCCAAACAA	60.198	20
257	497	753	GGTCTGGATCGGATCACCTA	59.886	20
247	0	246	TTCATTCACTCAGCACCGTC	59.837	20
235	347	581	ATCCGCTGCATACAGTCACA	60.296	20
243	603	845	TGGATTTCCGCAAATTTCTT	59.525	20
181	21	201	CACATGAATGGATGTGATTTG	58.201	22
262	23	284	CCATTTGCAATGGACAAAAA	59.396	20
280	357	636	CAGAGAGAAAGTTCAACAGG	59.551	23
233	174	406	GTTATCAGCAAATCTGGCCG	60.606	20
211	214	424	GTGGGCAAAACCATCCTTTA	59.801	20
279	139	417	CCCCCGAACTGATGACAATA	60.713	20
266	1100	1365	TAGGTTATGGGCTGCCTCAC	60.096	20
259	488	746	TCGTACGATCTTCCCACTCC	60.073	20
164	191	354	CCCCAAATTGATGGTTTCAT	59.481	20
126	113	238	CCTTCCCTTGACGACTTACG	59.728	20
271	178	448	TTCCACTTCTTGTTGTGATTGC	60.154	22
277	524	800	TTCTCTCACTAGTCAGCCCCA	59.997	21
255	856	1110	GCTTATGAGGGTGAGTTGGC	59.7	20
155	934	1088	CGAAAATTAGAGATGGCCGA	60.167	20
273	727	999	GCCTTCTCTCAAATAAGGGTG	58.783	22

207	240	446	TCCACGTTTCCATCTTCCTC	60.05	20
250	181	430	AGTCCGAGGATAACCCTTCC	59.397	20
272	51	322	GCAGAAAGACATTGATAACCA	59.891	23
252	200	451	AATCGAGACACCGACGAACT	59.727	20
191	123	313	CCCCTCCTCTCGAACTCTTT	59.811	20
131	16	146	TTTAGTGTTTTGACATGATTACT	57.557	25
207	287	493	AAACTGGACTGGGTATCAACA	58.486	22
280	127	406	TTTTGGCAATTCCCTTCATC	59.878	20
254	45	298	CAACAACACATGCTTCGACA	59.298	20
254	151	404	ACGTGCCAAGACTCAAAACA	59.339	20
134	996	1129	ACTGAGCCCTTCTTATTCATGT	58.358	23
145	2043	2187	CTCCTAGCTTTGCTGAGCGT	59.92	20
195	243	437	CGGCCAAACCAATAAATACG	60.198	20
120	455	574	TCTCTCTCACCTCCGCACTT	60.135	20
215	1451	1665	TCAAACTTCACCGCATCATC	59.654	20
267	1445	1711	GCACATCAACACTCGCAAAT	59.728	20
171	3307	3477	CCGTGACAGGTCAAAACCTT	60.005	20
209	719	927	TCAGCTGAAGGAGGAGGAAG	59.673	20
128	3519	3646	AACCCTCTTCACCTCCCACT	59.968	20
226	25	250	TCATGCAATCACTATTAAGACT	60.036	25
232	233	464	ACCCATCTATCGCTGTCGTC	60.104	20
219	340	558	CCAAGGCCGTACCTACTCAA	60.125	20
237	622	858	TGCAGCGAAGAAAGAAAATG	59.182	20
224	735	958	GGTCTTGCCGGATTCATCTA	60.036	20
212	2992	3203	TGCATTAACCCCGCTTAGAA	60.58	20
213	340	552	CCCACTCATCTTCAACCTCAA	60.096	21
217	558	774	GGCGTTCTTGCTATTGTTTG	58.439	20
121	2757	2877	GGGTTTCTTCCCTCGATTGT	60.306	20
224	118	341	GCGTGAGTCGGTGAGTGTAT	58.755	20
182	113	294	CTCTCGTTTGATGCAGCAGT	59.191	20
270	654	923	TTCCAGCACGATCACCACTA	60.263	20
107	1358	1464	TCTCATCATCTGCCCAAAAA	59.2	20
255	531	785	TCCATTTAATATGTCGATGACC	59.202	23
235	51	285	GCCTAACCTTGGGCTTTGAT	60.451	20
265	351	615	TAGCTGATAAGGCCGAGGAC	59.434	20
277	195	471	CTAAGGCTGATGGGGTTCAG	59.688	20
139	78	216	CCTTATCCAACGCTCCGTTA	60.089	20
262	4780	5041	TTGAGATTCCGTGAGGACTG	58.8	20
229	631	859	AAAACTTGACCCGATCATTG	57.517	20
208	524	731	CAGCAAAATCCTTCACCTCA	58.847	20
280	139	418	CCAAAAAGGAAAAATAATCCT	59.984	26
176	414	589	GCAACTTGCATTATGGATTTTA	58.985	24
246	44	289	TGCAATTGGTGTTTTGGTTG	60.393	20
159	558	716	CTGGGACAAAACGGGAAATA	59.795	20
273	3	275	CCCGTATACACACCACGGAT	60.517	20
266	80	345	CGGCATGTTCCTCAACTACA	59.716	20
240	512	751	TAGACGAAGGTCGAAATGGG	60.066	20
273	65	337	AAAGCATTAACAGCACGCCT	59.911	20
255	91	345	CTTCAAACTCCCGCTGAATC	59.813	20
268	2403	2670	TGAGTAAAAGCACGATTTTGGA	59.758	22
129	364	492	CGTAATTTCGTCCAGCCATT	59.96	20
160	242	401	TGCAAGCACACTCAGACACA	60.235	20
223	498	720	GAGGCAAAGCAAGGCATAAG	59.982	20
239	3346	3584	TCTAAACCCAGGTGGCAATC	59.933	20
229	138	366	ACCAGACCGGACCGTTAATA	59.312	20
214	1564	1777	ACTTACCGTCATTTCCGTCG	59.993	20
279	1318	1596	CACTAAATTGGTGATGGATGA	57.487	22
179	311	489	GGCCTAGGTTTCGAGGTAGG	60.089	20

202	799	1000	TTTTCCCATGAAGCCAAAAC	59.916	20
225	548	772	CATGCAGCTAAAGTGGCAAA	60.014	20
196	253	448	AAATATCGGCCGTCAGATTG	59.923	20
155	800	954	ACAGCCATCAAAGTGGTGGT	60.431	20
218	566	783	AGGCCACTGGTTCTCGTATG	60.134	20
202	496	697	GCCTTCCATTCCAAAAATCA	59.878	20
251	2090	2340	AGTGGGGAGTGAGGGAAAGT	59.968	20
135	2	136	TGAAGTTAGGAAATAAGGAG	58.743	25
269	95	363	TTCGTATTTGTCTAGCGCCC	60.23	20
189	886	1074	CTTGAAATTCGCAACAGCAA	59.992	20
210	157	366	TTGGCTTTGAACACCATCAA	60.088	20
275	102	376	CGCCTCTGCTCTCTGTTTCT	59.891	20
198	1158	1355	ACCGTATCACCGGAAACGTA	60.249	20
140	24	163	ATGAAGTTAGGAAATAAGGA	57.086	24
192	517	708	TGTGCCCCCATGATGTTAAT	60.983	20
264	787	1050	CCCGGCTTGAACTAATTCCT	60.443	20
181	459	639	TCACTCACGAAAAGACACGC	60.032	20
201	1283	1483	ACCGTAGTTCCGAATGGTTG	59.853	20
136	168	303	TCCATCCATCACCATCTTCA	59.85	20
185	299	483	TCTTCCCTCTCTCCCCATTT	60.008	20
262	856	1117	TTTGGTTGCGAAACTCAAGAT	59.738	21
221	104	324	CTGTGTGATGTGGAGTTGGG	59.997	20
239	3552	3790	ACAGGAATTCGCTTTCTCCA	59.813	20
202	248	449	TCACCCGGACCTCTTCTTAG	59.28	20
171	1216	1386	CCCTCCCTTCTTGGTTTCTC	60.045	20
201	170	370	CGAAATTGAGCTTTTTGGGA	60.181	20
251	240	490	AAAGCAATACCACCCCAACA	60.227	20
268	228	495	TATATGGGCCGTTAGATCGC	59.913	20
155	1001	1155	AAGCATTTCATTGGGCAGAG	60.214	20
276	378	653	AGCGTGCCTATTGCACATTT	60.667	20
252	1879	2130	AACGCCGTCTGGATTTTATG	59.96	20
279	602	880	AAACCCTGTCGTATCTCATATT	59.685	27
238	268	505	ATTTCGCATTACAACGAGGG	59.96	20
259	110	368	GGAAAAATCTCCAGACGCAG	59.813	20
250	38	287	ATCACATTAAATTTGGCGCAG	59.978	21
173	676	848	ATTAGCAAATTTCGGGACGA	59.547	20
155	431	585	ACAACAATCAGCACACGGAT	59.014	20
142	645	786	TCATGATTTGGCTTTAGGGC	60.038	20
274	106	379	TTGACGAGGGAGGATTAGGA	59.623	20
244	153	396	TACCAAGGGGCTTTCCCTAT	59.793	20
259	21	279	CGCCTCACTTCGTCTTCTTC	60.134	20
139	47	185	AAAAGGGTGTGTGGATTGAA	57.894	20
147	371	517	TAGGGTCCCACCACCTAACA	60.224	20
171	195	365	TGCTCCGTTTTCGATTCTCT	59.955	20
142	19	160	ATCGGTTATTACCGGATCGC	61.031	20
235	813	1047	AAAGTGCAGCCCACCATTAC	60	20
196	29	224	TCAGATGTTTGGTCGGAAAA	59.097	20
223	213	435	GTGGGTTTCATCAAGATTGGA	59.782	21
254	966	1219	GTGGTAGGCCGAGTTCAAAT	59.056	20
206	88	293	AGTTGGGTTGGAGCATTGAG	60.111	20
245	843	1087	TCAAGAAAGAATGTGGAGCA	58.488	21
231	2586	2816	GCACATAGCGTCTTCGTCAA	60.019	20
170	11	180	TTCCTTTCTTGCTTGTTTCTTTC	59.088	23
181	629	809	CCCCAGCAAGCAGTCTATCT	59.454	20
159	409	567	TTTCCACCATGATATCGACAC	58.285	21
255	7	261	GGCAACGGAATACCATTTGT	59.691	20
269	5680	5948	ATTTCCAATTTCACGAGGGA	59.363	20
121	68	188	CAGGTTAGCACGATAAGGGC	59.73	20

280	263	542	GAAGGTTGGAAAGCGTTCTG	59.853	20
236	1169	1404	TGCATGCAAAATTGAGCTTC	59.96	20
252	6	257	TGAAGTTAGGAAATAAGGAG	57.525	24
190	491	680	TTAGGACCCATAATCTGCCG	59.916	20
247	1685	1931	GTGGTTTAGGTGAACCCCTG	59.304	20
210	238	447	GGTTCAAAACCATGATTCCA	58.243	20
123	4054	4176	GCGCCAGATGACCAGATTTA	61.141	20
118	102	219	TTCTTTCCTTGTTTCGGCAT	59.685	20
206	164	369	AAAGCAAGCAAAACGAGTCA	60.046	21
263	92	354	CGTAGGAACTTACACAAAGTT	59.917	25
133	23	155	AGGGCATTGTTGTACATTGG	58.352	20
106	17	122	TCAAATTTGTTATTGATACCGA	58.024	24
174	547	720	CTTCCACATCTCTCCGTCGT	60.261	20
199	181	379	AAGTTCCTGCCCCTTCTTGT	60.11	20
280	725	1004	TGTGGATGATGAGGTCGAGA	60.205	20
261	393	653	GGAGACCTCTACGAGACCCC	60.073	20
264	46	309	ATCTCTGGCTACGCCACTGT	59.898	20
209	1691	1899	GTGGAAGCTTCGATGGAGAA	60.34	20
198	61	258	ATCACGCGGAAATAAATCCA	60.289	20
214	709	922	GCACCTTTCCTGAGACCAAT	59.141	20
238	320	557	GTTGCTTTGCAGACCCTCTC	59.997	20
159	26	184	CGGAGATCCAATCTCGTTTC	59.629	20
117	16	132	CATCCCTATCAACTCTTTCGAT	59.973	23
276	256	531	TCAAATGCACTTCATAAGCCC	60.089	21
157	179	335	TTGAACACACAGTTCATGCC	58.081	20
215	119	333	ATTCTAGGTCCGCCTCCTGT	60.096	20
143	600	742	TCGAAGCAAAGTCCTCATCC	60.34	20
234	336	569	AAATGATGTCAATCCAGCCG	60.864	20
215	484	698	ACAACCACGTGACAACATCC	59.288	20
236	990	1225	TGGGTTTTACACATTGGCAT	58.747	20
206	3307	3512	CAACATCTGTGAAATTGCGG	60.111	20
178	33	210	AGATCATTTCCAAAAACAATG	59.272	24
273	190	462	CGACCTTATAACATTTATTTTT	57.518	27
243	369	611	AAATCATGAGCGTCCGTCTT	59.7	20
111	581	691	GACACCCTTTCCATCGTGAG	60.51	20
131	85	215	CTTTTTGCCCTCGTATGCTC	59.845	20
268	756	1023	ACCAAGAGGTTCAGTGTCGG	60.151	20
193	1201	1393	AAGCAGAATGCAAGCAAGGT	60.022	20
279	115	393	TTGTGACCAATGAAAAGAGCA	59.307	21
235	550	784	TGTGAATCGTGTCCTTCTGG	59.676	20
108	17	124	TCAAATTTGTTATTGATACCGA	58.024	24
215	129	343	CAGACCATTCGAAAACAGCA	59.84	20
272	89	360	GATGTCTTTTGATCAGTTGGTG	59.091	23
179	2224	2402	AACCGAGAGCATAACCTGAC	59.749	21
276	1119	1394	TCTGCATTATCGCATCAGGA	60.329	20
223	15	237	TTTAGTGTTTTGACATGATTAC	57.557	25
202	421	622	GCTGCTGCATCATACGAAAC	59.454	20
236	418	653	AACTTCATTATTTGGGGGTGC	60.068	21
272	1845	2116	ACCTCCTCAACAGAGGATATA	59.53	24
129	508	636	CTCTTTGACTCCCCAAATCG	59.665	20
274	480	753	GTCGGACGAAACCATGAAAC	60.362	20
242	607	848	ATAGCCCTAACTCTTGCCCC	59.576	20
270	467	736	TGTACTCTGTGCAGTGCGAA	59.191	20
124	466	589	TCCACATCACATGACCTTCTG	59.535	21
177	460	636	TCTCATCTGCTTGTCGTTGC	60.144	20
105	451	555	AGGGGGCAGACATTAGCATA	59.551	20
129	332	460	GCGGAACTCAAAATGAAAGC	59.829	20
187	1417	1603	AGGAACCAGACCCACTTTTG	59.037	20

191	5	195	TGCACTCGAAGAATAGCGAC	59.178	20
224	3	226	TGAAGTTAGGAAATAAGGAGG	58.743	25
155	688	842	CATTTTAGCTTTGGGAGCCA	60.202	20
251	224	474	AGGATTAGGTGGACATTTGGG	60.06	21
194	27	220	CCATTGATTTCCAAGATCCG	60.266	20
242	1	242	ATCGGGTACCGAAGGGATAG	60.166	20
248	869	1116	TGATTCACCTCCCATGATCC	60.692	20
207	252	458	ATGGGTTCGAGTCTCAATGG	59.927	20
203	335	537	TTTCCCGAAATCCGAATAAA	59.367	20
259	1279	1537	AACACAACTCGGAACAACGA	59.187	20
273	244	516	AGAGACAAACAAGCATGGGTT	58.709	21
227	118	344	GCTTCTCCATGGCTTTTTGA	60.331	20
261	591	851	CATTCATATGAGGATGGCCC	60.118	20
147	395	541	CGGTACGGTAACGGTAAGGA	59.876	20
184	1	184	TCTTCACCACCTGAAGAGGG	60.229	20
220	7	226	TTGCTTGATCCAACGGTCTA	59.272	20
201	19	219	CCAATTTGAATGGTTATCACCT	60.457	23
153	485	637	CAGAGGAGCCTCAAGATTGC	60.096	20
217	546	762	TCAGAGTGCTCAAAACCAAGA	60.03	22
212	1136	1347	CGAAACCCTCTCTAATTTGATT	60.785	24
219	1128	1346	GGGTTATTATTTGATCACCTCC	59.813	23
161	624	784	ATAAAACGTGGAGCGAGCAT	59.736	20
245	1462	1706	TGCGAGTCATGCTCGATTAG	60.119	20
256	245	500	TAATTTGCATGAGACGCCAA	60.215	20
258	462	719	AAATATCGTCCCGGTGATTG	59.645	20
246	345	590	TGAAGAAGATTCTCATCCCACA	59.954	23
153	420	572	GCTACAGGAAGTCAACGGCT	59.501	20
204	707	910	CCACTCGATTTTGCTGGTTT	60.11	20
247	1431	1677	TAAAAGTTGATGATCCCCGC	59.901	20
215	988	1202	TCGACAGAATTAGCATATTTCC	59.788	24
106	90	195	TGTGAGGGACACAATTCTTGA	59.124	21
213	3553	3765	AAATTCCAATGGTGGCCTCT	60.693	20
231	955	1185	CGGCTAAATTGCCTACATCC	59.569	20
193	1	193	AGAGCAGGGAGATAAGAGAG	59.318	24
113	2187	2299	TTGCATGCCTGAGAGAGAGA	59.812	20
214	361	574	GGAGTTTCCGGTGTTGAAGA	60.088	20
254	1273	1526	CTCCACAATTTCGATCTCTCC	58.729	21
157	837	993	GGTAAACATGCACAGGTATAG	59.854	24
229	3423	3651	ACGAGCTTCTGCTGCATTTT	60.162	20
272	201	472	CAACCATTGATTCCCGAGAT	59.75	20
260	2253	2512	CTTGTCACCAACCAAACCAA	59.435	20
269	206	474	TCACGCGAATGAGTGTTACAA	60.309	21
280	1013	1292	GGTCCCAGAAGCAAATATGA	57.61	20
244	845	1088	CAAAGCAGAAATGGGAGAGC	59.955	20
208	783	990	AGTCTGACCACCACCACACA	60.045	20
258	83	340	TCCTTGACCGCGTAAAGATT	59.708	20
173	174	346	TGTTCATGCATTCACCATACG	60.395	21
220	2854	3073	AACTGCATTTCCAAAGCACC	60.118	20
156	1299	1454	TCGCTACCACGAACTAACCC	60.132	20
254	2510	2763	AAACTCCACATGGGCAAAAC	59.836	20
175	2715	2889	ACGGATCCGATCAAGTTCAA	60.461	20
245	186	430	AGACTTGCTTGCAAGAACATA	59.101	23
273	2297	2569	CCACTTCAAGCAGTGCAGTC	59.622	20
185	335	519	GAATCTCAGCCACAAAATTCG	59.699	21
204	25	228	GGGTTATCATGGGATCCATTC	60.225	21
190	251	440	AAGAAGCAATGGTCGCAAGT	59.882	20
258	198	455	AACTGGTTTGGTGGTTTGGA	60.246	20
218	10	227	AAAGTGGAGGAAGCATTGGA	59.67	20

239	2685	2923	AACCTTTTTGCTTTATTAGAAA	59.585	26
201	577	777	TTTCGGTTTGTCTCATCCCT	59.526	20
237	0	236	GGCGTGACACCATGTAAAAGT	59.912	21
244	639	882	TTTTTGGTGGCGGTAGGTAG	59.99	20
252	514	765	TTGTTGTTTTCATCCCCTCC	59.767	20
216	474	689	CATTGATGGACCTGCTCTCA	59.787	20
256	1984	2239	AAAATTTCTACTATACCCTTGC	57.252	26
268	66	333	TTTGCATCGAGACCAGTTTG	59.84	20
147	213	359	TCACAAGATTGTATGGTCCTTG	59.485	23
213	952	1164	TTATACACCCCGCATCCATT	60.038	20
226	50	275	TTCCCTCTCCAGCAATGTTC	60.195	20
263	2253	2515	AAGTTAGGCCTGCCATTGTG	60.132	20
182	12	193	TCCAAATGAAATGAAAACCG	58.454	20
231	123	353	CATTTTCATGGCAACCACAC	59.823	20
272	1035	1306	ACATGACTCGAGCCTGTCCT	59.866	20
276	878	1153	CCTACGAAGAAATACTGCGCT	59.939	22
197	990	1186	TGGCTGTGTGACGTTTTACC	59.615	20
208	495	702	ACCTCCATCTCTGCTCCTCA	59.945	20
115	15	129	CATGCATGAGCAAGAGACAGA	60.152	21
234	123	356	TTCCATTTCGTGATTCCTCC	59.871	20
135	14	148	CAACCATTATTATTCCAATCGA	58.736	24
219	498	716	TGCATTCGCAAAGAAGAAAA	59.562	20
261	2460	2720	GGTCTCCTGCAATGTGCTTT	60.263	20
264	2854	3117	AACTATGGAAAGTTGCCCCC	60.187	20
104	122	225	TTTATGCGGCATTCATGTGT	59.96	20
266	179	444	CTGCATTTTCTGCTGGTTCA	59.988	20
241	836	1076	CGAAAACAAAAGGTACGGATC	61.205	22
194	76	269	TGATTCGGTTAATCCAAGGG	59.756	20
143	2842	2984	AGCCTTGACTTGATTGGCTG	60.397	20
230	646	875	TGGGGTGTTATGACTAGAATGT	57.562	23
268	4388	4655	GGGCCATCTTGAAAAATTGA	59.878	20
259	365	623	CCACCCTCGCATAAGACTGT	60.134	20
276	101	376	TACAATCGGGGAATCACACA	59.774	20
103	6	108	GTAGATGCGTGTGGTCGATG	60.144	20
147	974	1120	TTTCCCTATGAAAACCGTGC	59.938	20
136	66	201	AAGCTGTCGGAAGTGGAGAC	59.455	20
271	33	303	ACAAAGCCACCGTCAGAGTC	60.307	20
214	1647	1860	CTGCTTTGTCCAGCATTTCA	59.988	20
159	401	559	AAATGCAATTGTGCATGCCT	61.432	20
257	133	389	GATTCCGGTTTCAAATCCAA	59.739	20
258	1620	1877	TCATTATCATCCGCCTTCAA	59.065	20
127	911	1037	ATGGACCAATGCACCAAAAT	60.059	20
181	59	239	TGGAACTCACAAAAGCATGG	59.691	20
215	26	240	TACGAAGCTGGAGGAAGTGG	60.388	20
145	1559	1703	CATGTTTGCCTGTTTTGTGG	60.004	20
197	270	466	TGCATCGATGATCTTGAAGG	59.756	20
231	14	244	TGTTTGAGCGACGTATCTCCT	59.89	21
234	1925	2158	AGGAAAATGTGATAGCAGCGT	58.874	21
132	282	413	TCATATCATTGTTTCCGCGA	60.035	20
250	383	632	TCCGGATCTGATTCGATTG	59.544	19
127	371	497	TCCACAGAGATTTCCCACATC	59.918	21
263	8	270	GGTGACGATGGTGATTGATG	59.769	20
224	226	449	CCAGAACATAAACACCGCAA	59.585	20
250	250	499	CTGGTACGTGCGACGTATTG	60.195	20
277	422	698	TTTGACTTGGTGAGTGCAAGA	59.475	21
275	726	1000	ATTGTTGGATTTGACGGCAT	60.199	20
238	251	488	TGATGATGATGGATTTAGCGA	59.079	21
150	777	926	TGGATTTGTTTCCGCAAAAT	60.302	20

150	821	970	TTCTAATTTGGTTACGCCGC	60.095	20
133	274	406	GCTGGTCGGTTAATTCCTCA	60.074	20
216	17	232	TCCGAAAATCAAAGACCCAC	59.91	20
173	922	1094	GGAAGACTCATTGCCCAAAA	60.051	20
238	502	739	GCATCTCTCCCATCTTCTGC	59.917	20
135	390	524	AGTGTTTTGATCGAGTCGCC	60.263	20
278	5	282	TTATGATATTTCCATAAGTCAC	57.297	26
234	157	390	GTCATGGTGTTGGCACTGTC	60.013	20
237	459	695	CCACAAATCATCCATGCAAC	59.781	20
277	59	335	GGCAAGCGTCTTTGTTTGTT	60.292	20
165	53	217	TGATGTGGCTTCTTTAGGGC	60.214	20
132	1531	1662	AATGGGGAACTTTCTCTGGG	60.298	20
253	423	675	TAGGTAACCGGTTCGACCTC	59.052	20
217	140	356	TAGTACGAAAATGCCCCTCG	60.089	20
240	507	746	AGGTGGGCCTAAAGTTTGGT	59.864	20
212	1569	1780	TTCCCAGAAAACCTCACCAG	60.081	20
230	935	1164	CCCCTCAATCATCCTCCTTT	60.264	20
252	151	402	GGCCTGAGTTGGCTTGTTT	60.248	19
233	877	1109	ATACTAGTGCCTTGCCCGAG	59.359	20
124	118	241	TTCTAAAGGGGAAACGACAAA	58.727	21
148	1565	1712	TTTGCGATAGTACACGTGGC	59.759	20
172	1066	1237	CAATTCCTGTGGGCTACTCC	59.55	20
239	230	468	AGGAATGCTACCCATTTCCC	60.152	20
251	983	1233	TCCCATTCCCAATCTTACCA	60.126	20
230	570	799	AAACCACGAAATCAAGCAGG	60.11	20
212	172	383	TCCCATCAACCCTCAGTTTC	59.903	20
268	119	386	CTGGCCACCCTCTATATTGC	59.551	20
162	2699	2860	GGGAGATGGGTTGAAACAGA	59.903	20
225	1547	1771	ATCGAACCATTCCTGCTTTG	60.074	20
217	578	794	TTCACTTACTTAAAGTCAACTC	59.189	25
231	566	796	TTGATCGAATGCTTAATTGCTT	58.896	22
225	156	380	AAAAGAGAAGCCCTCCAAGC	59.962	20
153	1348	1500	CGGCAAAGAGTTATTCGGAG	59.839	20
141	335	475	GAAGACGGATCGTTGATTGG	60.461	20
269	3788	4056	TTACGAAAATGCTTCCTTCCA	59.707	21
269	70	338	TCAATGAATTGAATAATCCCAA	58.357	23
210	48	257	TCACCGAAAAGATATGAAAAT	59.851	24
154	21	174	TGCCAATACAAAACCAACCA	59.826	20
256	0	255	GCGTTTTGACGATATATAGTGT	60.194	26
221	3952	4172	GACTTCTTTTCGAACGTCGC	60	20
276	2751	3026	GCAATCGGTGACCTTTTCTT	59.174	20
225	2622	2846	GGTGGTTATCAGTTGGCAGG	60.375	20
280	210	489	TTAAAGCCAAGTCCAGGTCG	60.241	20
273	1154	1426	ATGCTGCATTTTGTGTGAGG	59.722	20
237	1130	1366	TCAATCCCACCACCAAGTCT	60.363	20
144	77	220	CTCGGGTATATCAGCTCGGA	60.192	20
250	5285	5534	GAGCAGGATTCTGTGGAACC	59.661	20
184	786	969	GGCAGCTCACAAATCTCTCC	59.957	20
216	350	565	TCCCCAGCACAGTTATTTCC	59.933	20
169	85	253	AAAAAGTGGCATTTTGCCC	59.93	19
115	27	141	AGGAAATAAGGGGGTGTTATG	58.756	22
218	546	763	GGACCAACTATGGCACAACC	60.24	20
280	1610	1889	CTTTTCATCTCCAACCCAAAA	59.05	21
214	39	252	TTCTCGCTCTCTCTTCGCA	60.104	19
237	1001	1237	GTTATGCAGCAAAAATCCGA	58.771	20
275	1919	2193	CGCATTTACGAGATGACACG	60.28	20
280	4899	5178	CCATTCCTGAGACCAAAAGG	59.521	20
202	1558	1759	GGAATGATTTCCCTGAGCAA	60.014	20

223	51	273	TGTCCATTGGCAGTTAGCAG	59.864	20
268	213	480	CCAATAGTTCTTCGGTCCCA	59.926	20
239	674	912	GCACTCGTTTCTTTCTTCGC	60.14	20
133	246	378	TTCCCCTTTTCATTACACCATC	60.055	22
183	740	922	TCCGTGGACCTCATTTTCTC	60.05	20
177	185	361	CGTGTTTGGATTTGGGTAAAA	59.723	21
232	73	304	ACCCTGGCCAGTCAGTTCTA	59.721	20
209	788	996	CGGTGTCCTATTCCGATTTC	59.387	20
142	795	936	AGATCTTCCGATCGGTTCGT	60.99	20
159	445	603	GAATGAAAGGGTGCGCAATA	60.971	20
169	698	866	TCTCTTATTCTCCCTCTCGCC	59.933	21
226	72	297	TGACCTTGGGACCCTTGATA	60.309	20
142	1037	1178	TCGACTTCAGATGGTGTCAAA	59.278	21
278	1014	1291	TGTAATAAATCTTTAAAATGG	57.036	26
167	606	772	CTCAGAATCCACTCCTGCAA	58.957	20
278	169	446	GGTGTGGTACTTGGGACAGG	60.275	20
219	248	466	TTTTAGCCACTTTCTTGCCC	59.338	20
201	73	273	TATGGGTTATCACCGAATCGC	61.919	21
257	1533	1789	AACCGACCTTACATAGCGGA	59.592	20
275	143	417	ATTTGAGAAATGGCCCATGA	60.274	20
235	76	310	GGCAATGGAAAAATCACTGG	60.309	20
195	284	478	GAGGAGTGAGAAACCCGACA	60.238	20
142	8	149	GCACTTTTCTCAACCTCGCT	59.621	20
248	223	470	GTAGGAACCGTGCAGCACTA	58.952	20
261	442	702	AACCGCGTCTCTTAGTTTTATG	59.362	23
100	941	1040	TTGCACGAATGGTTTGACAT	59.972	20
270	943	1212	TCATTTTGATTACTTTTACTATT	57.299	27
275	660	934	TGGTGTTTTCTCCACAATCG	59.541	20
237	605	841	AAGTTGCAGCGAAAACATGG	61.196	20
156	43	198	TTGGTTCACACAACCACTCC	59.415	20
256	1190	1445	GCAATCCTTTCACTGCCAAT	60.081	20
175	131	305	GAAGTTTGGGAGCGACGATA	60.214	20
203	1838	2040	TGGCAACTATCCCTAACGGT	59.452	20
220	189	408	TCAAAACGGTCAAACGATGA	60.088	20
108	1461	1568	CTAGCAACGATGATAGGGCA	58.895	20
205	447	651	AAGCAGGAAGTCATGCCACT	59.874	20
216	837	1052	GCAACAATTCACAAGAGCCA	59.847	20
230	12	241	TTCGAGTTTTGATGGGAACA	59.097	20
221	3482	3702	AGAGGACTGGTCCGAGGAAT	60.073	20
251	70	320	AAGTAGGTCCTCTTTTCGACCT	58.892	23
137	60	196	TGAAGGTAGGAAATAAGGAG	59.461	24
248	272	519	GCATTATCCGGTCGATTGTC	60.304	20
126	279	404	AAATCGAATCGTGAACACCC	59.797	20
177	113	289	AGACCCTAGCTCTTGCCCTC	59.979	20
145	41	185	CAATGAACAACCGGCCTAAT	59.823	20
105	1	105	TGCGTTTTGATGATATATAGGT	57.703	24
198	1438	1635	ATGTTGCATGAGTGAGCTGC	60.024	20
265	132	396	ATGACTGGCCCATATTGGAT	59.083	20
100	176	275	TGCTGTGGTTGATTGACTGG	60.722	20
227	14	240	GGAATTGTGATTAGTGACGGC	59.448	21
269	850	1118	AGTTACTCGTGGAGGTGCCA	60.711	20
104	176	279	TCGAATTTCTGATGTTGGGAC	59.925	21
163	1186	1348	ATCATGTTCCTGCATGTTGC	59.533	20
273	906	1178	ACCACTCATCAAAGGAGGGC	61.429	20
245	411	655	CGGCAGAAGGAGAGAAGAAG	59.304	20
121	1036	1156	GTTAACTGGTATAGCGGCGG	59.63	20
180	2919	3098	AATTTGACCATTGGACCTGC	59.797	20
263	1277	1539	ATTTGCGAAACCCTAAACCC	60.184	20

176	531	706	TCGAGGAGTTTACACGGAAGA	59.861	21
146	284	429	GGTTCAAAAATCGGACTGGA	59.91	20
250	600	849	GCGATCTATTTTGGCTTTTCA	59.336	21
154	212	365	CTTGGAAACCTTTTACCCCA	58.922	20
276	403	678	AGTGATAAAAATGGCACCCG	59.823	20
257	1135	1391	ATTCAGCTTGACGAGGTTGC	60.406	20
177	184	360	TTGCGGGTTTCTCACGTTAT	60.502	20
215	214	428	AACATGGTTGGAGTGGGAAC	59.679	20
261	1	261	GCTACATATTTTGATGCATACG	59.363	24
245	590	834	TCACCAAATTGAGGGGTGAT	60.173	20
187	496	682	TAGCCCTAACCCTTGACTGC	59.336	20
125	355	479	CAACTCCCAAATCCTCCAAA	59.903	20
260	186	445	ACAAATTGGTTTTGGCGTTC	59.845	20
279	1181	1459	ATGAATCCACACAAGTGGGC	60.79	20
240	2085	2324	CAAAATTGGAACGACTTGCAT	59.989	21
218	15	232	AGTTAGCATGGGAAGGGGAG	60.455	20
111	22	132	ACAAACAACAATTCAGCAAAT	59.374	24
156	1532	1687	CTCCTTCTGTTGATCCCCAA	60.042	20
216	758	973	GGAGAAGGGAGCCGAAGTAG	60.34	20
135	32	166	CGTTTCTCATCTGATTACCGC	59.722	21
100	21	120	GAGGGTTATCATGGGATCAAG	58.32	21
224	95	318	ATATATGGGTTATCGCCGGA	59.127	20
120	275	394	TCTCCTTTGTTTTTCGTGGC	60.227	20
214	47	260	TTCGAAATCTAACGATCCGC	60.175	20
146	446	591	GGATCGAGTCCATGCCATTA	60.833	20
125	162	286	TACGTGTATGATGGAGGCCA	59.948	20
243	243	485	AATGAACCACCACTGCATCA	59.967	20
191	1238	1428	CAAGTACAAATTGCCACCCC	60.227	20
166	239	404	AACCAAACCAAACCAAGCAA	60.378	20
169	68	236	GGGGACCATCTCAAATGTTTT	60.046	21
206	8	213	GCAAAGTGCCACCAACACT	59.742	19
158	2914	3071	TGGTTAGGATTTCTCTTTGCC	58.315	21
230	2662	2891	AAAATGGCTGCAACGAAGAG	60.386	20
225	489	713	GAGCATTCGGGGTGCTATAA	60.06	20
262	334	595	TCTCCTCCCTTCGTCTCTCA	60.064	20
203	4045	4247	CCATTCATGCATCCAATCTG	59.883	20
144	2011	2154	GATGGCTTGGTACGCTTTTC	59.713	20
177	416	592	TTCATGGATTCAAAAGGGGA	60.244	20
145	179	323	TTTGATCCTTGCTTTGCCTT	59.823	20
278	19	296	TTCAGTTGGCCGAATGATTT	60.448	20
126	2853	2978	CAGCACAACGTTCCATTGAT	59.572	20
189	186	374	CGATCTAACGGCCCAGATT	60.044	19
169	498	666	CAACGGTTTATCTGCGGAAT	59.96	20
172	828	999	CCGGACATGCTAACGAGACT	60.277	20
264	1017	1280	TTTGCACTAGATCACTCCCCT	58.803	21
244	3169	3412	AGGGGAGGATAACTGAGCGT	60.096	20
278	133	410	TGATTGCAAAGAACCTCCAA	59.247	20
216	368	583	TGCAGTCTTACAGCCCAACA	60.449	20
273	836	1108	CAACCAAAATGATGGCGATA	59.377	20
196	10	205	TGTGTGTGTTGGTGGTGAAA	59.425	20
217	469	685	CGTGCCATGTTTCCATGATA	60.343	20
137	77	213	GCAAGTAATGCGGAGCTAGG	60.003	20
219	355	573	GCGAGCTCACCACTTCTTTC	60.142	20
182	200	381	AGTGTTGAGCAAAAGGGCAG	60.431	20
204	4269	4472	TGAGGCTCTTTGCCTTCTTC	59.694	20
276	521	796	TATTACAAGTTGTCGCCCCC	59.823	20
141	465	605	ATGATGCCAAGTCTTCGGTT	59.556	20
205	3306	3510	CAGCGGCAGCGATAAACTAT	60.384	20

233	61	293	CATCCCTTAATCCCCATCCT	59.974	20
204	619	822	AAAGTGATTGTGAAACCGGAA	59.462	21
277	947	1223	TGTTTTTCCACAACTCAACCC	59.861	21
209	1375	1583	TGTCAGCTACCTAACAGCTGG	60.074	22
223	1948	2170	TTTCCCCATGCATCATCTTT	60.274	20
280	2109	2388	CCTTATGCGTTCCAAAATGG	60.315	20
249	257	505	CCACTCCCTTTTGGCAGTTA	60.103	20
278	582	859	ACCGGAATGAAAATCGGATA	59.23	20
116	397	512	TCTTTGTTTTCAACGCCTCC	60.227	20
264	18	281	GGAAAAAGAAACCCACATGC	59.41	20
132	77	208	GCAAGTAATGCGGAGCTAGG	60.003	20
236	491	726	GGACCAGAAATCCCAGTTGA	59.903	20
193	129	321	TTGTGAAAAGTGGTTGCGAG	59.881	20
106	539	644	GACACGCATAAAGGGACCAC	60.384	20
259	248	506	TGATGATTGCCCCCAGTTAT	60.155	20
248	164	411	AGACGGGGTCGGATTATACC	60.039	20
275	102	376	TAAATACCAAGCTCCGCCTG	60.223	20
237	494	730	TGATTGGCTGTATAGGCGTG	59.712	20
162	2438	2599	TTCTTTGGTGACCTGTTGGA	59.109	20
173	680	852	GCCCACCACCTGATAACAAA	60.755	20
229	161	389	TGCATTTTTAATTTATTTTCCTG	57.15	24
280	92	371	AGGTGCAAAGGATGAAATGC	60.081	20
240	3691	3930	AGTTCCATGGCAGTGAAAATG	59.985	21
101	4	104	AGGTTTTGACCATATTTACTGT	60.393	27
235	206	440	TCATAATGGTCTCCATCGCA	60.033	20
198	623	820	GGATTCATGAGATCGACGGT	59.893	20
228	60	287	AATTTACTAATTTATCCACCTC	58.189	27
279	1242	1520	ACAAAACAAAATGTTGGCCC	59.708	20
268	2556	2823	CAGTTTTATGCATCGTGCCA	60.665	20
160	2103	2262	TTTTTACACGAGGCGAAACC	60.11	20
236	120	355	GAACGTCCAGTGCCAAAGTT	60.156	20
126	27	152	GGTTATCACCGGATCGCTAC	59.415	20
274	1637	1910	AAGTGGCACCAGTCGTAGGT	59.646	20
250	387	636	AAAATCAAAGGCCCACAATG	59.801	20
276	221	496	GCACCAATATTAGGCCATCG	60.31	20
264	6588	6851	TAAATTGTTGGCAGCGTTTG	59.742	20
144	31	174	AATCTCGAAAATGGATGACCC	60.145	21
136	1292	1427	ATGGCATCCCACAAGTATCC	59.635	20
169	9	177	GCGAAATTCGTTGGTTTGAC	60.49	20
180	900	1079	TGGATTGATGTGGGTGTGAG	60.378	20
223	280	502	GTTTTTGGATGGAAAACCACT	57.943	21
265	39	303	GAGTTATCATTGGAGTAAGCC	60.212	23
267	1377	1643	ACTTTTCCGGCCTCTCATTT	60.074	20
270	965	1234	TCGCAAATTAGTGGCTTGCT	60.905	20
209	560	768	ATTTGGGTCTCTTCGACACG	60.111	20
231	198	428	CAAAGCCAGCACATGCATAC	60.288	20
118	250	367	CAGGCATTCAGCAAAATCAA	59.809	20
218	89	306	TTGAAGACCGCCTCGATAAT	59.668	20
177	530	706	TTCATATTCACTTGAAGACTTG	58.494	26
216	1169	1384	TCTCACCTTCGGTCAAAACC	60.088	20
214	1	214	CCGGGGTATGCTATAAACGA	59.81	20
115	262	376	TCGTGAAACACTTCAACCCA	60.128	20
280	142	421	TGGACCATGTTTTAACTGTATG	58.935	23
155	297	451	TTAACTCAAAGCACGAGGGG	60.241	20
217	474	690	ATTTCTGATGGTCAGGCCAA	60.461	20
259	706	964	TTTCTCTTGGCAATGATCCA	59.2	20
269	1	269	AAATAGTTCGGGTTTTCGGC	60.312	20
239	1026	1264	ACGGCAACGTTTTACGTCTT	59.677	20

226	694	919	GAAATGGAGGTTGGGTGGTA	59.647	20
260	335	594	CTCCACTTCACCGGCTTTTA	60.241	20
252	350	601	AATACCCTTGTATGCTGCGG	59.982	20
201	518	718	TTCAAGAGCCTAGGAAGAGG	59.963	21
191	573	763	CCCACTTTCACCATTCCACT	59.82	20
198	457	654	AACTGCACCACAAAGAACCA	59.187	20
223	701	923	TGTGATCCGTTGAGGAATGA	60.048	20
127	475	601	TCTACCCCTCAGAATCCTCGT	60.081	21
222	13	234	TTTGGGTAAAATTGCTGGGT	59.315	20
246	1407	1652	GAAAGTTGCAGCCCAGTGA	59.976	19
206	934	1139	AGTAATTGGCACCATACCCG	59.708	20
274	251	524	CTGTCCGTCACGTTGAACC	60.146	19
197	513	709	TTCAAATTGCGGATGGATTT	60.268	20
153	3	155	GAAAATCAAAGGCCCACAAA	59.916	20
193	2397	2589	TGCACTTGTTTTCCCAATATCA	60.356	22
267	195	461	TCGGCGAAGGAAAACAATTA	60.56	20
176	224	399	TGACACGATCGTTAATTAAAT	59.06	23
172	146	317	CAATTCGACGACCAAATCCT	59.933	20
268	2663	2930	ACAGGGCAGCACCTATTGAC	60.142	20
275	488	762	AAAATGCCGAACTTCCAAGA	59.685	20
263	197	459	TCAGATCGCTATCGTGTTCG	59.972	20
171	545	715	CTATGCAGCCTCCAGCTTCT	59.74	20
262	1133	1394	AAGAATAAATATGAACGAAA	59.536	26
131	841	971	TTCGTGGTGTAATGGCAAAA	59.969	20
230	313	542	GTATCCCAGGCCGAATTTTT	60.15	20
277	490	766	CTTTCTGTTTGAGAGGAAAAA	57.731	23
204	2124	2327	GCCATCACCAACCTCTATGG	60.34	20
249	538	786	GGCATTGTCAGACGACGTAAT	60.015	21
274	1652	1925	ATATATTGTGCAGGCAGGGC	59.951	20
264	282	545	GCAGTGCACTTGGACTTGTG	60.51	20
162	960	1121	ACCTGGCAAGATTCATCGAC	60.081	20
112	30	141	TATGATGGGAAGGGTGGGTA	60.006	20
208	2942	3149	ATTTTCATCGGAAATGCTGC	60.045	20
136	782	917	TACGCAGCATCCTATTCACG	59.856	20
134	1896	2029	ATTTTCAACGGTGGGAACTG	59.83	20
150	89	238	AATGACTCAATCTGCAAGCGT	59.896	21
259	415	673	GGTCAAATCGTGGTCCATTC	60.181	20
267	2093	2359	CGAAACCAGAACCAACAAGC	60.668	20
186	402	587	TACCCCCACCCACTACTCTG	59.837	20
267	1856	2122	GAAAGCAATGATGACGACGA	59.805	20
280	29	308	TCCGCCTTAATCCATCAAAC	59.901	20
184	629	812	GATAGTCCATGCCCCATGAT	59.592	20
102	628	729	ATGATTCCTTTATGGCGTCTG	59.057	21
172	1185	1356	TCTCGCCAACGTACCTCTCT	60.012	20
224	1193	1416	AGGGAGGAGAGAGAAGGCAA	60.468	20
243	10	252	TTCATAACATTTCTATCGGTAT	59.71	26
140	41	180	TTTGCACCTGAGGAGGTGTT	60.69	20
170	744	913	ATTGCGGTAAAGACCACGAC	60	20
261	1005	1265	GGAATGCCTCCACAACATTT	59.797	20
231	2181	2411	TCTCACATATTCCCATTGCG	59.499	20
129	184	312	AAGCACTTGCTACGAGCCAC	60.602	20
246	929	1174	TCCGGTCTATTCTCACCTCAA	59.679	21
145	501	645	TTTGCTACTTTGTCCCGGAT	59.569	20
211	2432	2642	ACACGATGATGATGAAGGCA	60.08	20
174	240	413	CTCCCAACCCACAATACCAC	60.088	20
206	204	409	ATGAGAGGACTGCGAGGAAG	59.555	20
165	443	607	GACGAAGAAAAGGATGTCCG	59.67	20
263	1937	2199	GAAAGCAGTGACGAAGGGTC	59.851	20

240	409	648	ATCGTGTAAAAGCACGGTGA	59.199	20
266	494	759	TTTTGTAGGTGTGAGGCCAA	59.17	20
218	1074	1291	CTGGAAAAGACAGCCATCGT	60.255	20
248	2151	2398	AAGCTAGTGTGCTGGCTGCT	60.364	20
127	71	197	GGCATCATATATGCGGTTGG	61.077	20
253	14	266	TCGTGTTAAAGCACGGTATCA	59.24	21
184	743	926	TAATGGACGTCATGACCGAA	59.924	20
191	429	619	TACCAATGGACCACAAGCAA	59.964	20
122	258	379	CCCTTCAATCCCAAGGTTTT	60.159	20
277	720	996	GCTGTTTTCCATTTGATCTGC	59.705	21
206	83	288	AGCGCAAGAGCATAAGCATT	60.145	20
250	601	850	AAGGTGGCTTCACACACAAA	59.187	20
223	267	489	ATTCAATGGCAATCTCCTGG	59.894	20
100	1120	1219	ATTGATGCCTGAAGAATGGG	59.894	20
124	17	140	AATTGAATGGCAAGGATTGG	59.762	20
265	30	294	AAGGCAATATGCTGACGGAC	60.103	20
217	2940	3156	CCAAGGGCATTACACTCGAT	59.955	20
173	265	437	CCCCGACAATCATCACTCTT	59.927	20
114	863	976	CAACCCCTCTCCTTCTGTCA	60.229	20
266	1480	1745	GCTAATCCAAACGATCCCG	60.42	19
177	1708	1884	TTTCCCGTGAAGCACTAGTTT	58.893	21
241	32	272	ATCAATGCATTTTCCAAGGC	59.907	20
238	1017	1254	CATGGAATCTTTCCCAGCAC	60.461	20
249	741	989	CGCACTCTGCAACACTGAA	59.742	19
277	216	492	TACCCGCCATTGTTTCTCTC	60.074	20
246	1692	1937	CCCAATAGTTCAGCACCATCA	60.899	21
280	963	1242	TTGTCAATCGAATTAAACCGT	57.181	21
164	285	448	TGATACTTTTGAATCGGGGC	59.901	20
207	2758	2964	AAAGGGGAGAGCAGGAAAAT	59.171	20
250	178	427	TTTGTTCAATCGCTTTGCTG	59.992	20
221	566	786	TCAAAAGCTTTGATGGAGCA	59.542	20
172	1	172	CATTGGAGGGAGAAAGGGA	59.988	19
278	85	362	GCATGGAGCCAAAAGAAAAA	60.188	20
202	2806	3007	ATTGAATCTCCCACTTCCGA	59.483	20
183	2230	2412	TGCTCTTGCACTTGAGCCTA	59.888	20
270	536	805	CCGGCTATCTCACTCCAGAC	59.827	20
266	589	854	GATCCCGTATTCTCACCCCT	60.154	20
210	2625	2834	CAGTCACAAAAGGGGGAAAA	59.942	20
265	1992	2256	AATCCCTCCGGTTCAAAATC	60.131	20
232	255	486	TCAGTCCCATCAGCCAGATT	60.622	20
193	919	1111	AAAATGCGCTTTCTGCAAAT	59.859	20
225	235	459	TCAATTTGATAATTTGAAGCTC	60.214	27
149	508	656	CGTAACGTCAGCTTCTTCCC	59.875	20
178	79	256	TCTGAAACCACACCTCCACA	60.129	20
221	20	240	CTATGGTGGTATGGTGTGGG	58.569	20
232	621	852	TATGAGGGGAATGCACCACT	60.34	20
222	1158	1379	GCTCAAGTTTCCGAGCTGAC	60.142	20
265	5366	5630	AATCCAAGATGGTGTCCCAG	59.779	20
208	237	444	GCCGTTCTTCCCTTCTCTCT	59.957	20
231	248	478	TTCCAATCCAGTTTTCTGGG	59.903	20
277	147	423	CAGGAGCAACCATTTTGTGA	59.691	20
198	823	1020	ACTTCACCCATTTCCACCAA	60.21	20
193	2750	2942	CCTGAGCGGATAAATCCAGA	60.17	20
276	20	295	AAGGAGGTGTTATGAAGGGAT	58.028	22
250	930	1179	CATCATGTAGGAAAATGTTTAC	57.372	25
224	2786	3009	GTGGACGTCCCAGATTGTTT	59.827	20
171	60	230	TCAAACTCATTGTTGTTTCACA	59.575	24
237	314	550	CACCTAACCCCTCTCTTGGC	61.008	20

278	866	1143	CTCTTCGGTGATCAAGCGTT	60.397	20
102	7842	7943	AAACCCCTCCATCAACAAGA	59.381	20
272	651	922	GCTGAAGCAATCGAGAAGGT	59.579	20
148	686	833	TACAGCGTGGACGGTACAGA	60.324	20
180	21	200	ATTAGTGGGGGATGATGTGG	59.483	20
187	26	212	AGGCCTAATTGCCGTCCTAT	59.951	20
111	2162	2272	TCCGAGCTTCACATCCTCTT	59.95	20
229	589	817	AAACACAAAAATTAGCATACA	57.517	24
254	299	552	CAACAAAAATCCTAGTCCATCC	60.223	23
258	654	911	CCTTCCCACATTCCACATCT	59.779	20
154	1600	1753	GGGCCTACACTATCTCTGCG	59.859	20
222	515	736	ATGTTGCCACCTCAGCTTCT	59.874	20
118	1980	2097	TCATGACTCACGAGATGGGA	60.205	20
144	11	154	CCCAAGCATTAAAGCCCATA	59.922	20
166	425	590	GCTCCAAACTTGATCCGAGA	60.34	20
256	23	278	CCTTATCCCGTTATGATTCGTT	59.251	22
208	103	310	TCAGACCAAATCAGAAGGCA	59.369	20
242	1619	1860	TGAGGGATGATGCATACGAA	60.033	20
225	937	1161	ATCACAAAATTCACACCCCG	60.615	20
181	825	1005	GGGCTAAAATGGTGTTGGAA	59.801	20
224	1380	1603	TCCTTCCTTCAGATTGGCAT	59.629	20
223	1547	1769	ACTCGACTTCATCCGTTTGG	60.111	20
125	251	375	TCAAGCTAACCAGCCAACCT	59.875	20
216	197	412	CATCATTTCACCTCCTATCGC	59.542	21
229	5360	5588	CCGTGGAAGACAAGGGATAA	59.926	20
184	1072	1255	AAAACGCAAACACATACGCA	60.177	20
271	1048	1318	ATGTCGTGTAGGGAAGGCTG	60.134	20
265	2696	2960	ACGAACATTGTCACCGTCAA	60.008	20
276	962	1237	CTGGTTTGTTACCCCTTCCA	59.824	20
277	662	938	TGATGGGTGAAACCATCTCA	59.893	20
150	810	959	AAGCAAGAGCAAAACCCAAA	59.861	20
245	743	987	AAAGCTGTGGTCGGCATAAG	60.27	20
149	38	186	TTCGAACGCAATGCAATAAA	60.211	20
113	2969	3081	CGAGTTCAGCTCGTTTTTCA	59.195	20
134	41	174	AGCAAAATTGGTCTCTATGTGT	59.656	26
254	1010	1263	TCTAAAAACCGACACCCCAC	59.83	20
173	445	617	GAGAAATCAATCTCAGCCGC	59.923	20
256	149	404	CCGGTTATCCAATCCATTTC	59.091	20
169	675	843	TCCTCCTAAAATAACGGCCA	59.542	20
100	634	733	TGTCGTGGGTGTAGTGATGG	60.44	20
279	521	799	GTGGCATCGTGAGGAGTGT	59.682	19
205	143	347	AAAGTCCTACATGCCGGTTG	59.993	20
167	2049	2215	CCCCACTTCCTCTGTTTCAC	59.549	20
223	2437	2659	TTTATGGAGTGGCACTGTGG	59.566	20
241	634	874	ATGAGTTATCACCGGATCGC	59.923	20
221	502	722	GCGAGAATTAGCTGCCACTC	60.125	20
181	272	452	CCGGCTCCGATCTATACAAA	60.053	20
188	425	612	AAAACCTCCAATCCCTCCAC	60.169	20
182	623	804	GTTGATAGATGGGCATTGGC	60.304	20
110	279	388	AAACGTTGCCTCAATTTTCG	60.11	20
254	20	273	GGAACCACCGAGTACCAAGT	58.917	20
262	446	707	ACGGTGGGAGAAATGAATGA	60.317	20
101	24	124	GGTTATCACCGGATCGCTAC	59.415	20
212	587	798	CAACTCAGCAAGTCCTGCAA	60.175	20
211	445	655	TGAAATTCATGTGGGTCAGC	59.502	20
188	2632	2819	CTTGATTCGGATCGCTTTTC	59.784	20
247	440	686	ATCGTTGAAGATATTCCGCA	58.187	20
119	166	284	ATCTGGTATCGGAGCCAGG	60.042	19

247	559	805	AATTACATTGGGCCATCCTG	59.645	20
214	162	375	ATATTCGGATCAGGAATGCG	59.885	20
163	242	404	TTCCAAATGCAACTGGTGAA	60.088	20
261	306	566	ACGTCGCAAGCACATAACAA	60.324	20
198	383	580	TTCTCGGGATTTAACGTCCA	60.439	20
203	137	339	AGCTTAAAAGGCCGGTCAAT	60.095	20
268	123	390	CCCAGATAATTTTATATGTGGT	57.101	24
209	403	611	GTGATTGGTGGTTTTGTGGA	59.241	20
248	805	1052	GGCTTCTTCTCTACCCAATCG	60.214	21
209	338	546	CTCTCCAAAAACAGTCCCTCT	59.365	22
253	250	502	TGAACATATCGTCCCCTTCC	59.75	20
161	778	938	ATGAATTGCCACTCGACCTC	60.081	20
277	2455	2731	CGTTCATTGCATGTGGTTACA	60.43	21
179	835	1013	CCCATCTCGAACATTCCTGT	59.927	20
149	247	395	CATGCAGGTTTTGTCCAATG	59.964	20
258	577	834	GCCGCAATATACATGGCTTT	59.956	20
213	2361	2573	GTTCTTTTTGCATTAGCCTTTG	59.795	23
276	360	635	GACTAGCAAATTTCGGGATGA	59.172	21
168	3	170	GGAGTTTTGACCTAATTAAGA	58.571	24
258	1464	1721	TTCTCATGTGACTGAGGGCA	60.402	20
232	837	1068	AAGAAATTTATGCCCCCTCAA	59.795	21
279	575	853	TGTTGCCTTGCAAATTATTTCT	58.808	22
274	199	472	CTGCAAAGAAGAGTGGAGGC	60.134	20
238	8	245	TTTCGTGTTTCTTTTGATTTTTC	60.019	24
227	309	535	ACTCAATGGACACATGCCAA	59.967	20
195	276	470	TTTTACTTCCCCTCGTGCAT	59.569	20
176	733	908	ACCCTTTTTGACTTTGCGTG	60.147	20
240	902	1141	GGCCTGGGCCTACATAAGTT	60.34	20
275	712	986	ACCAACATCACACTCGACCA	60.005	20
188	328	515	GGCTTTTGGAGCTGTAGTCG	60.015	20
269	24	292	GTGGTTATTAGGGGATGGTGA	58.634	21
223	1489	1711	TTTCAAACGAGATCTCAGGG	57.865	20
192	270	461	AAAGGCCCACGATGGTTATT	60.562	20
114	1264	1377	GGAATTCAATTGTTTATTTGTT	59.706	25
237	1729	1965	TGTGTCGTGTTCGTGTCAAA	59.751	20
229	1278	1506	CTGGACGACGATACAAACGA	59.716	20
206	493	698	GGCAACCCACTTGTGAAACT	60.012	20
278	103	380	TTGATATTCTCACCATCCTACT	57.774	24
255	1456	1710	TGGGACCCTAATACACCATCA	60.059	21
210	286	495	CCAAAATTGGCGGATAACTG	60.315	20
246	16	261	CAGAGCGCACTCGAAAAGTA	59.366	20
240	473	712	AAATATCGGCCGTCAGATTG	59.923	20
204	24	227	GGCCTCTTGACAAAAAGCTG	59.993	20
159	524	682	AACCGGTATCGTATCACGGA	60.214	20
205	43	247	AGCCATCCATTCCGAAATTA	59.369	20
279	681	959	CATGGTGTGTGAGAGAGGGA	59.659	20
232	487	718	CTCAGCTGGTATCTGCGGTT	60.419	20
188	675	862	AATCACCAAACGTCACACGA	60.008	20
134	2110	2243	CAGAAAGAGCCCATAGCCAC	59.836	20
212	297	508	CAGCATGTTGCCATTAGGAA	59.688	20
269	16	284	AAGGAGGTGTTATGAAGGGAT	58.028	22
269	2812	3080	TCTTCTTCTGCCCCACCTAC	59.284	20
163	595	757	ACCGACCAACATCACCTCTC	59.969	20
251	452	702	ATGGGGTTCTTCTCCTTTCC	59.373	20
128	306	433	AGGTGGCTTCTTTAGGGCTC	59.848	20
264	141	404	TCAGCATGTTCCATGTTCAA	58.62	20
144	49	192	CCCAAAATCGATCCCTAGAA	58.971	20
272	573	844	TTGGCCTCACGATAGCTCTAC	59.49	21

237	550	786	GTGCCTGAACCACCAACTTT	60.012	20
222	261	482	CACCGCTTATCATCAACGAA	59.688	20
125	393	517	CACCACCTGCAATATCCACA	60.39	20
110	1637	1746	ACACAACGAATTCCTACGGG	59.853	20
266	42	307	TTCAAACCTTTGCCACTTCC	60.088	20
272	2639	2910	TCAACGAGGAAATCGCTTCT	59.955	20
274	3391	3664	AACCAACTCGTCAGACAGCA	59.467	20
158	877	1034	CGCCCGTATGTTTCTCTCTC	59.836	20
132	77	208	ACTCGAGCAAACTTGGCAAT	59.882	20
125	1000	1124	AAGGGATGGTATCATTTGATC	60.041	22
252	3617	3868	GGTTGTCCGAGGCAAAAATA	59.938	20
213	221	433	GAAAAGAGAGAGTGCATGCG	59.636	21
129	8	136	TGTGTGAGTGTGTGTCTCGTG	59.352	21
276	137	412	GTTTGAAGGAAAACTCGTCCC	59.969	21
167	276	442	GTGCCTGCTCCACTTTCTTC	59.997	20
245	664	908	CTGTGCAAGTTTCGTAGGCA	60.05	20
168	913	1080	AAATGCAAGTTCCGAGTTCAA	59.738	21
238	1700	1937	TCTCAGCTCGATAAGTGGCA	59.697	20
277	144	420	ATATCCTTTGAACCGGCACC	61.072	20
136	269	404	TCGATCTGGGCTCTCTTGTT	59.95	20
223	190	412	CGAGTGCTGTTGACGAAGAA	60.175	20
209	3583	3791	TTGGAAGAGGAAAGTGGGTG	60.081	20
222	564	785	CCACCATGATTTCGATACACA	59.262	21
254	511	764	CAATCATTCACAGCCCTTCA	59.648	20
107	7	113	GGTCCATAAGTGTTTTGAGTT	58.561	25
187	915	1101	TGGTCTTGGTCACGATTCTC	58.643	20
216	293	508	GATTTGGTGTGCTCAGTGGA	59.682	20
259	467	725	ACCAAGCATGTGCAATTGTG	60.584	20
140	35	174	ATTCAATGCGCGAGTTCTCT	59.985	20
133	807	939	ATAAGGATCAACCGCCTGC	60.051	19
178	1209	1386	CAGATGAAATCAAGCTGGCA	59.948	20
193	247	439	AGCATCAGACCAATGTGCAA	60.272	20
270	1063	1332	TGGTGCAGATGTCCTGGTTA	60.112	20
166	1261	1426	CTACGCAGGGGCGTATGTAT	60.003	20
170	2995	3164	GTGATCGCTGGTTCTTTCGT	60.263	20
278	3149	3426	AGGTTGCGTCAGATTGGAAG	60.255	20
241	429	669	GGCTTGGTCGGAGTTCTTC	59.794	19
221	611	831	AATGATGTTAATCCAGCGGC	59.929	20
204	599	802	CCACTCCATCACCATAACCA	59.215	20
165	2618	2782	CATGCGTAAAGGCACAGTTG	60.316	20
256	36	291	TGCGAGTATCAAAACCGAGC	61.304	20
205	193	397	CAAGTATTCTCTCCCCAGCC	58.741	20
272	77	348	AAATGGTTCCCTCATGGACA	60.173	20
228	1379	1606	TTCCACCTCAAAAACAAATGG	59.825	21
275	682	956	GACAAATCACGCGAGGAAAT	60.081	20
187	3820	4006	TTGGATATTGTTGGGCGAAT	60.153	20
231	3419	3649	TTTAATGGGATCATCACGCA	59.891	20
135	972	1106	ATGGTGGTGTTTGCCTGTCT	60.431	20
273	263	535	TTTCCGGTACTTTCTTCCCA	59.541	20
160	269	428	CGCAGATCCCAGATTTGTTC	60.603	20
255	981	1235	AATGTTGCTTGAAGGTGATCA	59.891	23
262	539	800	ATATCAGGCCAAAAACGTGC	59.967	20
178	39	216	GTTCAATGAGGTGTCTGCCC	60.52	20
232	1785	2016	CCCGAACTCCGAGTACAAAA	60.103	20
124	19	142	TGCTGATCTATTTACATGCTTT	60.158	25
144	423	566	GAATGAAACCCTAGGGGGAA	60.124	20
250	591	840	TCTGTCTGAAGTTCCTGGGG	60.229	20
278	1361	1638	CATTGCCCTAAACATCCCAC	60.192	20

252	291	542	AAAATAATGGTTTGAGCAAATT	59	24
200	1010	1209	ATTGTTGTCCATACATTTTGGA	58.612	24
198	2209	2406	ACCCAACTGGGTAAACCCTT	59.593	20
158	526	683	GGGATGGATTGATGAAGATGA	59.7	21
274	578	851	AAAATCCTTTCCACAACCCC	60.032	20
238	652	889	GAGATGTGGGTGGTTTGCTT	59.973	20
104	10	113	AGGGGTCCAAAAGCAGAAGT	60.11	20
122	199	320	ATCGCAATCAACCATCCATT	60.163	20
239	253	491	TTCTGCACAGATTTGATGGTCT	59.74	22
165	977	1141	ACCGGGCAAGAAGAAAACTT	60.11	20
257	515	771	TTTGCCGTTCTTCATGAGC	59.94	19
278	931	1208	GCTTCGATGTTGATGCTTGA	59.955	20
160	1227	1386	TTTGCCATGTGTATCGTTGAG	59.6	21
257	9	265	TCACCCAAAAATGGGTTATTAT	59.753	24
216	735	950	TAGCCCATACACACAAGGCA	60.134	20
113	2265	2377	ATTGATGCCCTGGTTACAGC	59.962	20
254	1699	1952	ATGCCAGAACTTACCGACCT	58.672	20
252	781	1032	CCAAATTTTGATCAATTTCCA	57.478	21
272	905	1176	TCCCTCTGTGTGTGATTTCC	58.482	20
205	1082	1286	ACGAGGGGTTTCTCTCGTTT	60.11	20
274	403	676	ATCTTGCATCGGCAAGAGAC	60.37	20
254	18	271	AAAATCGATATTGAATTAAAG	59.114	26
149	1685	1833	TTCACAAAGGGCTTTTCAGAC	59.345	21
135	85	219	GGGTGGGGACATGCATAATA	60.414	20
275	6	280	TCAACATCATCATCAACATAC	59.565	23
173	752	924	AGCACTGCAACGCAACATAC	59.942	20
211	879	1089	GCCTGCGAAAATCACAAGAT	60.221	20
137	16	152	TAAGGGCGGTATCACCTGAA	60.46	20
245	2489	2733	TGAACCGAAAATTGGGTAGG	59.795	20
277	616	892	GAGCAAAGACAAAATGCCAA	58.895	20
280	514	793	ATTGAGGAAGGGGTTTTTGG	60.159	20
243	428	670	TGTTTTCGTTCTGAGAGGGG	60.224	20
158	432	589	CTCGGCAAAAGTAGTGGACA	58.923	20
224	51	274	CCGAAGCCCAAAAACAAATA	59.937	20
253	511	763	CATCAGCAGAGGCCAGATTT	60.362	20
183	139	321	GTTTCACAGGAGGCGGTTTA	60.11	20
245	1153	1397	TATCAGATTCAAAGACGGCG	58.869	20
257	2359	2615	CTGAAACCTGGCATTCACAA	59.691	20
210	48	257	CCAGCCGTATTCTTTTCCAA	60.067	20
213	276	488	ATCGAACAATTCCTTCCACG	59.933	20
248	1596	1843	CGCGAGATTCGATGGTAGAG	60.894	20
265	107	371	ACTTCGATCACTTCGTTCCC	59.141	20
205	479	683	TATATGTTGCAGGCCGAGAA	59.281	20
127	1986	2112	CCCACACACAATGCAAGAAT	59.42	20
132	1097	1228	ACCCCTTTTACCCTTTCCCT	60.048	20
275	694	968	AAAATTTAGGGAACACGCCC	60.184	20
232	431	662	TTTCAGACATTTCGATCCCAG	60.059	21
110	1606	1715	GCAATGAGAAGAGGGACACC	59.661	20
248	1469	1716	CAAGCCCAAATCAAGGAAAA	60.046	20
147	23	169	CTCTCCTCTTTCTCCCTCTCC	58.627	21
172	522	693	TAACAATGCAGTGGCTGACC	59.722	20
238	645	882	CCCGAAAAATTACTCCCACA	59.795	20
273	535	807	CAATTCCCAAACCATATCCA	58.133	20
227	445	671	TCCTGTGAACCTTTCAGATTAG	59.776	23
223	4	226	CCTGCATGTGCAAATTGAAA	60.644	20
244	1838	2081	GTTAATCCGACGGCTGAGAA	60.214	20
111	613	723	TGTTGCGTCTTGTATTGGAGTT	59.677	22
267	226	492	CAAAACATTTATTTATGCACA	58.489	26

239	3240	3478	CCAATGATGGGTAACGGAAT	59.505	20
218	817	1034	GTTTATGTTGCGAAATCGGC	60.465	20
227	950	1176	TTCGCACAAATACAAATCGC	59.708	20
228	288	515	ACATGCAATGAAAATGCCAA	59.937	20
277	344	620	ATTCTATGGTGCCCCCTCTC	60.293	20
278	1326	1603	CGAAAATTTTGCATATCGGTC	59.446	21
254	206	459	GAATGATGCATGCTCTCACC	59.201	20
206	309	514	GAAGGTGACGTGTTGCAGAA	59.88	20
211	123	333	GCCTTTGGTGTGATTTTCCT	59.031	20
183	655	837	ATGCCACCTAATTCTCTCGC	59.297	20
124	234	357	TCCTTGGAGCACCGACTAAT	59.694	20
267	203	469	GAATGAGGGTTTTTGTGGGA	59.767	20
265	1554	1818	TTTCTGTGGACATTCAGGCA	60.24	20
245	203	447	TCCCTGACCACCATCAATTT	60.173	20
238	700	937	TGAGTGGATATATTGGGAAGG	60.034	22
234	1235	1468	CTATCCAGACCACCCCTGAA	59.92	20
276	2072	2347	TTTGAATTGGGGGATCTACG	59.756	20
127	279	405	AAGCGATGCTCCAACTTGAT	59.843	20
255	1115	1369	GTTGATGCAGATGGTGGCTT	61.078	20
192	586	777	CCAAGCATACGGTTATTGGG	60.202	20
161	732	892	TCTCTCCCTTCTTCTGCTTCA	59.294	21
148	116	263	GCGTGTTTGTGCAAATTAAGG	60.534	21
246	530	775	CAAGATGGCATCATCCATTG	59.883	20
175	569	743	ATTTGGCCTTGTCTGTCGTT	59.598	20
129	582	710	GCGAATTGTTCTTGTCCGTC	60.646	20
213	11	223	TCACCAATTTGAATGGTTATCA	57.873	22
210	2476	2685	TCGGGTAAATTTGAGGTGGA	60.301	20
213	415	627	TATGCTCGCTGGATTACGTG	59.856	20
231	273	503	CTTGCAGTTTCCTCACCTCC	59.844	20
166	282	447	TCGCTCTTGATGCAAGTTGT	59.596	20
227	2301	2527	TGGAATTGGGATTGATGGAT	59.952	20
141	30	170	GCACAACCACTCCACAAAGA	59.726	20
213	794	1006	TTTGATAATGGTTTTGTACACA	58.037	26
104	0	103	GATCTAAGGGCCGAGATTTGT	59.568	21
257	1312	1568	CTGTCGGTGCATTTGATGAT	59.527	20
268	389	656	GGTGGCAGTGGTGTCTCTTT	60.159	20
254	477	730	TGCCTTGCCTCTTTCTCTGT	60.134	20
212	150	361	TGCATACATGAATGGCTATGA	57.617	21
113	35	147	GGCAGTCGTTTTGAGACGTT	60.299	20
233	175	407	GCGGGAATCAACTTTATCGT	59.046	20
226	1125	1350	TTTGTGTCGATCACCTGCAT	60.12	20
145	1727	1871	TTCCTGAGTTGGTGAAAACG	58.746	20
158	2365	2522	AGGAGAGGTCGAAGGGGTAA	60.067	20
232	368	599	TTGCTATTGAGAGGAAGCGA	58.747	20
270	781	1050	GATGCTCGGTTACGCTTTTC	59.851	20
197	2886	3082	TGCTGCTGCTGTAAACGAAC	60.203	20
247	9	255	AGACAATGTTATCGATGGCG	58.6	20
202	680	881	AATCCCCTCTCACCTTTGCT	60.074	20
259	1522	1780	TCAAAAATCAGGCCAAATCA	59.087	20
166	1237	1402	TTTCTGCATGATTTGGATGATT	59.415	22
150	285	434	TAAAATGAGCAGAGGCCGTT	59.845	20
191	1994	2184	TGAGCTGGTTGATTCATTTTG	58.759	21
191	48	238	GTGGGCGCAAGTAAAGAGAG	60.015	20
222	2165	2386	TTGAACTTGTTTCAAATCCATG	59.483	23
125	944	1068	TTTGCTCTCTCACACATGCC	59.992	20
189	350	538	GGAAATAATCGAACGGCAGA	60.038	20
261	805	1065	ATCACCCCCTCTCCAAGAAT	59.755	20
253	8	260	CGAACTTCCATCCTGCTTGT	60.255	20

182	1294	1475	CTGCTCTCATCTCACCACCA	59.98	20
147	47	193	AATTGCCTTGTGTTTCTGGG	59.971	20
266	2487	2752	TGCTGTGGAATACCTGGGTTA	60.372	21
203	694	896	GGGCGTGATCTCTCAGTTTT	59.288	20
269	36	304	GAGATATACGCGGTGGTGGT	59.843	20
202	6	207	TGATTCTATTCTGTGCTTCGGA	59.845	22
189	1255	1443	CCGATGGAAAATGGAAATTG	60.124	20
241	43	283	TGCCAAGTGCTCAAATGACT	59.445	20
244	318	561	CCTAGTGGGCCAAACCCTAT	60.2	20
226	1340	1565	GTTGTTCCCAAGGATTGTGG	60.21	20
174	1320	1493	ATCAGCTCTCGAGCCAGTGT	60.167	20
256	746	1001	GGTTGATCGTAATGGGATGG	60.014	20
218	1487	1704	CTCCTTCCGTTTGTTGAGGA	60.224	20
269	310	578	TATTGGGATTGTGCCCAAAG	60.692	20
242	1466	1707	AATTGTTCAACCTCTCCGCT	58.792	20
249	1237	1485	CATGTGGTTGAATTTCGTTCA	59.43	21
113	4750	4862	ACACGCAAAAGCAAGACACA	60.494	20
247	316	562	AAACACGTTCGTGAGTCGAA	59.339	20
203	228	430	GTTTTTCCTTTCCGTCCGAT	60.299	20
151	267	417	CACATATAATCAGGGGCGGA	60.681	20
189	531	719	TAGACGGGCGAGAAAGAGAG	59.711	20
221	811	1031	TGCTCTCCGAAGATTCATCA	59.476	20
127	2516	2642	AAAAACCAGCACCAATCCAG	59.971	20
259	208	466	TTTTTCTCGACACATAGAGTCC	60.162	24
207	853	1059	CCGATCATCATCCAAGTTCA	59.451	20
125	2376	2500	GCTCCACTTCTTCTTGCTGC	60.285	20
266	253	518	AATAATGGCGGGTACGTTGA	60.209	20
204	3815	4018	AGCTTCGAGCCAAAGTCTTG	59.757	20
218	167	384	GCGTCTCACCTAACCTCACC	59.727	20
260	295	554	CTTGATTCCCCAGAGCTTGA	60.331	20
190	3	192	TTCCATGTAATAAAAAGTTTCC	58.876	24
216	203	418	GGTCCAGATCATGGGTCACT	59.774	20
130	1	130	TCCGATGGTTGTAGTGGAGTT	59.463	21
226	15	240	CGTTTTCAGCACTCCCAAGT	60.291	20
198	177	374	CTGATAAGCCAGGGTATGGC	59.551	20
166	128	293	GGACCAGCTCCAAATTCAAA	60.051	20
169	356	524	ACTCAGAATTTGGCCGACTG	60.255	20
236	4442	4677	ATGGCATGACTCTTGAGCCT	59.834	20
164	2249	2412	TTCTGATATGGAAATGCCCC	59.722	20
247	1454	1700	TATTACATCAGCCCGTGGGT	60.214	20
169	31	199	CCAAAAACATCAAACCACCC	60.066	20
247	823	1069	TTCGACGAGGCTTATGGACT	59.836	20
275	218	492	TCGAGTTCAGACTCCAAAAAC	59.891	22
274	159	432	ACCCTTGCATGCACATCATA	59.955	20
220	46	265	AAAACACAGAAAGTTGCAGGC	59.415	21
215	211	425	CCAGCTGACAATCCCCATAC	60.34	20
280	1723	2002	TCCAAACTCCAACCTCCATAA	59.415	21
188	1112	1299	GCATGATCAAAGAGGCCATT	60.043	20
242	824	1065	TCCTTGGCATACATTCTCTCTC	58.411	22
141	463	603	TCTACTTTAGCCGCCAAGGA	59.975	20
255	796	1050	CCACCTCTACCCATAGCAGC	59.717	20
276	991	1266	AATGGGGGTATGTAACGACG	59.569	20
232	15	246	CACAGCTGTCAATCAACAAGA	58.975	22
223	208	430	CTGTCTCAGTCACCGTCGAA	60.022	20
246	224	469	TTACACTGCAGTACGTCGCC	59.935	20
274	1338	1611	GACTTCTGGTGGACGACGAT	60.12	20
118	491	608	CCTTACTCTCTTCGCCGTTG	60.008	20
169	333	501	TGCAAGAAGGTTGCTCCTCT	60.134	20

237	0	236	CCACCCTCCATTGCTCATAA	60.853	20
256	2061	2316	TTTGCCTTTGATCGACACTG	59.84	20
163	692	854	GGGATTTTCTCACAGCTTGG	59.67	20
278	1834	2111	ACGCGTGTGACATGTTCCTA	60.183	20
237	466	702	TATTGGCCTGGCCTAGTCTG	60.227	20
272	402	673	TTGGCCTTGTCCTCGTATAAA	59.595	21
269	1922	2190	TCGATTGTATTTAAGCACGCA	59.365	21
275	47	321	TGTTTTGTCACTGCACTACGA	59.047	22
250	1070	1319	ACCCCTTTGTCGATTCTCCT	59.935	20
188	241	428	CCCATAAACCACACTAAAGAT	59.654	23
259	704	962	CAAGGCAAGACTTGTGGTCA	59.873	20
272	337	608	TCCCGTGAGGTAAACATCCT	59.405	20
174	144	317	CAATACCTTAACCCCCGACA	59.679	20
184	1682	1865	CCTTCGGACAGCTCTTGAAC	59.989	20
167	359	525	AGTGATCACACCTGCCCATT	60.395	20
275	337	611	AACATGGAATGAGTTAAGGG	57.608	22
268	185	452	GGTGTGCCTTGTCCAATTTT	59.836	20
238	409	646	AAGAGGGCCAGGAACAAAAT	59.94	20
280	1542	1821	TTTGAATGGATGAAATCTGCC	59.893	21
243	691	933	TCAAACCATTATACCTACCGC	59.385	22
270	897	1166	GCTTATCTTTTCGGGCTGTG	59.845	20
110	568	677	CTACGTAGCTCGGTTCTCCG	60.03	20
170	145	314	AGAGTGGTCCTGCCCTTTTT	60.11	20
232	135	366	GAGTGGAGGATTCGGTGAAA	60.05	20
238	2992	3229	GCAGATCCCAGTCTCTCTGC	60.104	20
255	6639	6893	TGAGGCCAATTCCTCAGTGT	60.656	20
279	85	363	ACTACCACCAGCACCTCCAC	60.033	20
271	59	329	AACAAACGAAAGGGACCACA	60.388	20
215	728	942	TCAGCAGCCATTGAGACATC	59.95	20
170	655	824	ACAAAACAAAACAGGGGCAA	60.378	20
121	1	121	CGAACCACGTTAAATCTCTGT	59.671	22
232	890	1121	AGCTCATGGATTTCTGGTGG	60.073	20
196	57	252	TAATCGTGTTGCATTGCCTC	59.694	20
152	280	431	TCGTGAGAGAGAGGCAGGTT	60.135	20
195	582	776	TTTGGCGATATGCAATCAAA	60.037	20
157	1642	1798	TTAGGGCAGACACTGCATGA	60.413	20
160	778	937	TGCTGAGACAGTGGAAGGTG	60.022	20
168	1423	1590	GCGTGGTTGTGAGCGTATAA	59.759	20
251	8	258	CCGATTGACAAATCCTCGTT	59.933	20
143	2631	2773	CATGGCAGTTTCACATTTGC	60.119	20
202	309	510	TTTACAAGATCAATGGTCCCA	59.315	22
159	11	169	TTAACATCAACGGCTGCAAA	60.251	20
198	1432	1629	GTCGACGTCTACAAAACGCA	59.911	20
252	589	840	AGGAGGACGAGTGTGGTGAC	60.161	20
153	1635	1787	CATTTTTAATTGCAAAATTAAT	58.536	25
257	1064	1320	ATAAAAATGGCACCCGACTG	59.823	20
101	18	118	AAGGGTTATCACCTGATTTTCT	57.73	23
268	2748	3015	AAACGAAGCCACCTTTCAGA	59.853	20
214	522	735	CCCAAAATCAACGTCCAGAT	59.79	20
188	3625	3812	GCCTTGCCTTTTACGTCTTG	59.883	20
170	616	785	CAGCCAGAGCATCAGATTCA	60.096	20
239	3636	3874	CCACTGAATCGCACAAAAGA	59.84	20
278	172	449	TCTGCGTTACTTGCTTTCCA	59.609	20
266	496	761	TGAATATTGATTGGTCCATGC	58.296	21
196	1547	1742	GTGCGAGATTCAACAACACG	60.31	20
216	3546	3761	ATGTGCACAGCGAGGTATTG	59.746	20
157	831	987	GGCCAGAAACTGCTCAAAAA	60.365	20
279	2063	2341	CCCCTATGAAGCCCAGAAAA	61.291	20

179	13	191	TTCCGGAAACTCACAAATCA	59.097	20
125	586	710	AAGTGTGCAAATGGGTCTCC	59.973	20
250	865	1114	GATTTGTTCACCCTGGACGA	60.903	20
137	40	176	GATTCTCACGCCATTCTCAAA	60.207	21
246	493	738	GCGTGGCATATTTCTGATGAT	59.944	21
212	561	772	TCTGGACAAGAAGCCATTGA	59.369	20
108	1410	1517	GTTTGTTGCATTCACGTTCG	60.157	20
255	454	708	TTTTCATTATTTATTGCAAGTTT	59.837	26
248	718	965	GTCGGCAATTTCTTGATGCT	60.221	20
255	382	636	TGTTGAACGTCTCCAACTCC	58.697	20
264	1166	1429	AGAAAAGGGGAGTTGAGGGA	60.045	20
149	565	713	GCAGAAACTTGCGGAGTCTT	59.621	20
170	950	1119	CCGTGGTGATTCTTTGGACT	59.966	20
227	508	734	AGTTAACCTTGCAAGCTGCC	59.522	20
240	565	804	TCTTGCTCCTAATCGTCGGT	59.836	20
219	732	950	GCCATGAACTATATTGATTTTC	59.28	24
267	6061	6327	TGCCTCAAAATATCTGCTCCA	60.727	21
213	195	407	ATTGGTTTGGCAAAAGCCTC	61.339	20
272	1771	2042	CCTTTCTCAAATGAAGAGAAA	58.971	24
177	770	946	GTGCAGAGATTTGTGGCAGA	59.992	20
259	352	610	TTTTCAGTGGTGTTTGTTGTTT	57.248	22
223	1059	1281	TATAAAAATGCAGCCAGGGG	59.922	20
230	3322	3551	CGAAAGCACAAACATCATGC	60.265	20
225	1292	1516	AAAAACGCGGAAATCACATC	59.945	20
110	1079	1188	GTCGTCGTTTCCACCTCTGT	60.159	20
233	376	608	GCGGCTCTGCAACTTTTAGT	59.66	20
267	1205	1471	GATCAGGTTAGCCTTGTCCG	59.694	20
260	966	1225	GCCATTCTCCTTCAAAACCA	60.051	20
254	341	594	GCCCAAGATACTCCATCCAA	59.894	20
240	3097	3336	AGGCATTGGTTTGTTGGAAG	59.971	20
249	17	265	AAGGAGGTGTTATGAAGGGAT	58.028	22
229	3256	3484	CGCTTGTTCCTTGGTAGGAG	59.869	20
274	70	343	GGTTGATGTCATCGTCATGG	59.769	20
262	17	278	ACGGCACAGATTACAGCACA	60.333	20
114	3225	3338	AATGCAAAATGGGCACTTCT	59.574	20
137	882	1018	TGAAAGGTAGGGTTTTCGCA	60.608	20
240	513	752	AAAATCGTCGTGCGTAGAGG	60.27	20
269	6259	6527	TGAAGTTGACGAAGAAGATGA	59.906	23
189	541	729	GGTTGAACTGTTGTCCTGTCTG	59.664	22
275	453	727	AATCTCCGGCTGAAACTGTC	59.288	20
144	338	481	TGAATCATCGATGTGATGGG	60.291	20
238	2766	3003	TCTGAAACTCTCAACAGATTC	59.743	23
196	14	209	ACACTTAAGGGGGTTATTAGT	59.26	24
161	25	185	TGGGAACACTCTTCAGGACA	59.23	20
197	965	1161	TTTCCGGATTTTTCATTGGA	60.239	20
252	0	251	CAGATTTGTTATGTGTTTTGAC	57.29	25
213	1	213	TGGTGGCTGAAATGCTTGTA	60.257	20
240	367	606	TTCTGCCCTTAAGGCTGTTG	60.378	20
256	3985	4240	ACCGAAAGAAGCATTGGCT	59.828	19
176	476	651	GAGTCATCAAGAAGGCCAGC	59.957	20
136	33	168	CCAGGATGGTGATACATTTGG	60.059	21
183	1130	1312	GCTAGATGGCCGAAAATGAT	59.142	20
157	134	290	AGCCTGTACGACTCCGACAC	60.329	20
270	145	414	ATTTGAGGGGGAAAGGAGAG	59.508	20
204	856	1059	GGCATAGGTTTGGGTTTCAA	59.801	20
195	196	390	GAGGATCTGTGGGGTGGTAA	59.779	20
156	216	371	GGAATTCCAGCAACCTCTTG	59.67	20
204	3424	3627	TTCGAGGCGTTTTCTAGGTG	60.378	20

266	200	465	GTGTCAAATTCGCAACGAAG	59.322	20
236	1316	1551	TTTGATGGGATGGTATGTTTAT	58.618	23
273	296	568	TTAACCAACATCCCATCTCCA	60.177	21
121	9	129	AAAAATCAAAGGCCCACAAT	58.418	20
139	763	901	CATGTGCCATCAAAAGAGGA	59.648	20
204	21	224	CACGAATGAAACAAGTTGGG	59.021	20
181	566	746	TGATTTCAGTTGGTAGCAGGA	59.747	22
205	1327	1531	ACATGGCGTGCTACAATCAA	60.142	20
207	347	553	TCTTCTTCCCAGTTTCCCCT	60.045	20
255	333	587	GGGTTATCATTTGAACGCGA	60.837	20
139	53	191	CCCAAGCAAAAGACGACACT	60.291	20
280	572	851	GCTTTGGAAGTGAGGACCAA	60.232	20
200	397	596	ATTTCGTGAATTGGCTACGG	59.96	20
256	454	709	TCTTTTGCAGCCCTCCTTTA	59.953	20
137	747	883	TCGAAAAATGTATGGGGTCG	60.692	20
278	1633	1910	AGGGACTTAACAAGCCATCG	59.195	20
146	12	157	TTTCTCATACAAAAAGACATTT	58.494	26
225	281	505	TTTGATGCTCACAAGCAACC	59.847	20
156	3088	3243	ACCTTAGCAACGAAGGAGCA	60.015	20
235	1562	1796	TACGGTTTTCACCTCGGGTA	60.357	20
217	610	826	TTGACTGTCATTTTACCTCTTTA	58.392	26
165	4275	4439	TAGCTTGCTCACCAACCCAC	61.236	20
257	402	658	CGGTTCTGACCACTAAACGAC	59.648	21
141	57	197	TTTGGATCTGTTTGTCGAGTTG	60.147	22
126	2260	2385	GATAATCACCGGAAAAGCGA	60.038	20
149	1508	1656	GTGACCCTTTGTGGGAAGAG	59.549	20
157	14	170	GAAATAAGGAGGTGTTATGAA	59.323	24
265	514	778	TTGAGCGAAAGGGAAAGGTA	59.817	20
252	110	361	AATCCGAAAATCTGCAGTGG	60.074	20
178	668	845	GGAGCTCATGAACGAACCTC	59.81	20
276	838	1113	GGGCATAAGCTGTCAGGTCT	59.313	20
277	192	468	GCCCAAACTATTTCCAATCC	58.368	20
217	269	485	TAGCCCTCTATCGGGCAAGT	61.099	20
151	54	204	GGTAGTAGAGCCACGAGCCA	60.419	20
204	2328	2531	TTCACCTTCTTTCCCCTTCC	60.414	20
243	644	886	GGATCGCCAATACGTGAGTT	59.962	20
199	3751	3949	TAGCGCTGCAGAATTCAAGA	59.856	20
251	692	942	GTAAATCACGAGACCGCCAG	60.657	20
262	249	510	AGAAATCCAGCAACCAATCG	60.074	20
219	1096	1314	TGGGTTTCTCACCCTTCACT	59.549	20
267	234	500	CGTGCAAAATAGCACCAAGA	59.872	20
248	108	355	AATGATGTTAATCCAGCGCC	59.929	20
258	633	890	CATGCGTTGTCTGCCTTG	59.978	18
273	221	493	TAATGGCCCTGAATCTTTCG	60.031	20
188	1089	1276	ACGCCTCAAGCACTGATCTT	60.02	20
278	689	966	GTGGGTGCTTTTCTTGCTCT	59.478	20
181	939	1119	CTGCCCTATTTCCTTGTCCA	60.066	20
244	747	990	GTCCAACGATCTTGTGGTCA	59.525	20
176	632	807	CAGAGCGCACTCGAAGAGTA	59.49	20
209	609	817	TTCCCCCTTTTATGGTCAAA	59.246	20
189	2355	2543	TTTATGCAGCCATCAGACCA	60.22	20
139	1910	2048	TTCAAAAATGCCACTGCTTG	59.849	20
241	181	421	TTGAGGAAGGATTTGAGGCT	58.861	20
237	24	260	CGGTTATCACCGGATCGC	62.397	18
146	3720	3865	CAGCATCTTTGCCTCAACAA	59.988	20
267	963	1229	TCAACAACGGTAAGTTGCTCTT	58.951	22
187	1313	1499	CCCAGCACTTTCCTGTCATT	60.111	20
203	3419	3621	TCAAGAATCCCTTTAGCCGA	59.778	20

274	58	331	CCCCATTACCATCTTTCTCG	59.382	20
113	234	346	AGGGAGTTGCTAGGGTGTGA	59.721	20
118	920	1037	GCAAAAGCGTTTCTCACCTT	59.499	20
262	920	1181	CTTCCCCTTCGCTCCTACTC	60.34	20
150	142	291	TCAAAAACCGAAAACCGAAC	59.953	20
223	692	914	ATTCTATTGTAGCGGCCCAA	59.569	20
220	1072	1291	GCATCGTAAGGAGCGTTGAT	60.243	20
265	319	583	ATCAGCACCCAACCAAAGAG	60.111	20
198	263	460	CATGTTTGCAGTGGATGGAC	59.967	20
174	1262	1435	TTGTTAGGGTTTTTGTCGGG	59.833	20
229	280	508	TGGAAATGAAGCGAGTTTCC	60.192	20
177	26	202	TAAGAGTTGTCCGGAGTCGG	60.246	20
258	345	602	CTTGTTGAGAGGTGGCTGTG	59.461	20
238	238	475	TCAACGCCTCTAAAATGTTCC	59.215	21
228	652	879	AATTTGCGTAGTGCAGAGGG	60.27	20
277	2224	2500	TTTTGGTATCAGGGTTTCAGC	59.077	21
258	534	791	TCCACCACTGTCAGAAAGCA	60.44	20
178	204	381	AACCAGCTGACCATGTGAAA	59.139	20
218	0	217	AATTTCTTGCTCCAAACCTTTA	57.172	22
231	961	1191	AATCAAAGAGCAATGAGCCG	60.352	20
191	54	244	CAACAAATGCCAACGCTATT	58.701	20
265	314	578	TTGATGTGAGATGGGCTTGA	60.201	20
219	12	230	CCTACCTAAGGAGGGAGGGA	59.526	20
240	557	796	CCCCTACGCACTCGTTTTT	60.118	19
233	392	624	CCTGCTGTTGATTTGATGGA	59.648	20
231	245	475	GGCGAAATGTTTTGCACTTT	60.117	20
128	145	272	GAAAAATTCGTAAGTGGCCG	59.586	20
213	90	302	TAACTCAAGGCCCATTCCAA	60.439	20
223	586	808	TTTCGGTTTGACCTTCTTCG	60.22	20
189	377	565	ACCAAACCCATTCTTGTCCA	60.21	20
167	682	848	TTGATGGATTTTTCAAGCCC	59.878	20
142	804	945	TTTCTTCAAATTTGGGGTGG	59.772	20
222	295	516	AGTGCAAGCAAAAAGACGAA	60.046	21
249	1306	1554	GAGGGAGCTGCAACAAGAAA	60.517	20
100	560	659	ATGGCCACAAATGGTTCCTA	60.192	20
235	0	234	TGTGACCTCAATTGCAAAAC	57.15	20
276	505	780	AGATGGAAAACCGTTCAAAA	58.592	21
246	1044	1289	TATCAAAGTTTGCGTTGGCA	60.251	20
257	279	535	TGAGCTGCAGCATTTCTCAC	60.296	20
119	194	312	GGTCAGTTTCTTGCTTGCAG	58.65	20
128	1333	1460	CGTGCATTACTCGGTTACTTG	58.384	21
237	2967	3203	GGAACCAATCTGGTGCATTC	60.326	20
213	118	330	TCAGATCACCACCGGACATA	59.918	20
136	1562	1697	CGCACACACCATCTGTGAAT	60.604	20
250	73	322	GGGATTCAAACCCAAACTCA	59.767	20
209	269	477	TGAGGCAGCCAATTACATGA	60.22	20
252	2063	2314	GTGAATGGAAATGGAATCCG	60.133	20
228	560	787	ACTTCAAGGATTTGAGCCGA	59.813	20
261	32	292	GCTTCTTCTTGCTGTGAGTGG	60.186	21
263	312	574	TCCATCCCTTTCAACCATTC	59.727	20
272	1277	1548	GCCACTCAAAATTGCTCCAC	60.646	20
238	396	633	TATTGTCACATGGTCCGCAT	59.805	20
266	1684	1949	TGTGCCTTGATTCATTGAAAA	59.147	21
193	670	862	TCAAGATTTTGTGTGGCTGC	59.847	20
140	344	483	CACCCCTGAAACTCCATCAT	59.779	20
229	556	784	TGGAGTGCTGGTGAAAGAAA	59.415	20
260	85	344	AACGCGCATTTTAGGGTTTA	59.624	20
274	17	290	TGTCGGTGGACTGATTTGTG	60.57	20

265	39	303	CGTGAGAAGCGTTGATATGGT	60.147	21
189	407	595	ATGGTCAGGTTCACGACAAA	58.984	20
238	293	530	TCTGCGTCCATTTCACTCAA	60.39	20
277	1515	1791	AGACATGGAATTAGGGCTCAG	58.28	21
211	803	1013	CACCAAATGTATGTGCATGAG	59.469	22
234	143	376	GGGATGGGGGTAAGTAATGC	60.399	20
235	325	559	GTTCAACCGCCAGATTTTCT	59.174	20
153	75	227	AATCAGCTGCCAAACCAAGA	60.776	20
128	602	729	AAAGGTCCCTCACCAGTCAA	59.549	20
129	898	1026	GCTGCTCCTGTCTCTTTGCT	59.898	20
188	671	858	GGTGCTGCAACTGAACTGAA	60.032	20
203	273	475	CCCCCTTCTCTGACAGTTCA	60.229	20
232	519	750	TGGCTATAGGACATCGAGGG	60.051	20
226	324	549	TTTGCATGGAATAAGAATTTTG	59.858	24
166	328	493	TTAACCGCCAAACTCAAACC	59.975	20
173	1502	1674	AGGGCTATTGTCATTTCGACC	60.334	21
174	3913	4086	CCTCTGGCTGTTCTGGATTT	59.284	20
240	579	818	GCCATTGTTGTCTCTGTCCA	59.682	20
261	52	312	CATGAATTTTTGGGAAGCTGA	60.06	21
194	3677	3870	TGCTGGAACATCGAAGAAGA	59.522	20
274	940	1213	TTCAGAGAATGCTGGGTTTG	58.847	20
135	1299	1433	GCCCCCACATTCAATACAGT	59.676	20
254	321	574	GCGTCACACGTGATTCAAAA	60.709	20
195	28	222	TGTACGTGCGTACGTGTGTG	60.293	20
189	926	1114	TCCTGTTTGATGAAATGCCA	60.049	20
201	14	214	GTCTGAGCGAGAGTGTGTGC	59.771	20
248	326	573	AAATGAGATTGGTTCGAGCTT	59.268	22
275	1065	1339	ACAAAGGTTGGAATGGCTTG	59.971	20
187	656	842	CGGGTTAGACTTTGATTCGG	59.564	20
138	308	445	TCAGAAATCCATCCCACGTT	60.317	20
199	1603	1801	TGAAAGAAACCCATGTGCAA	60.088	20
226	2858	3083	CGCCTTTGCATCTCCTGTAT	60.235	20
218	21	238	ACATTAAAATGTGTATGCACC	58.505	24
102	1848	1949	TGTGCATTTCAACTTGGGAA	60.088	20
238	993	1230	AAGGGGGAAAAGAAAAGGGT	60.156	20
210	380	589	ATATATGGCGGTGGAGATGTG	59.682	21
194	12	205	CATTGTGGGCCTTTGATTTT	59.801	20
202	1549	1750	GCGGAGGCAACTATAAACGA	60.23	20
215	446	660	GCGGCCAGTTCAATACAAAT	59.967	20
212	537	748	AGAGAGAAAAAGCTTCGGGG	59.955	20
108	688	795	AAAAACATCAACTGGGACCG	59.83	20
272	2071	2342	TACCTTAGTGCCACCGATCC	59.955	20
220	0	219	AGACCGGACCGTTAGGTAAT	57.55	20
129	837	965	ACCTCCCTCCTCCTCAGTGT	60.112	20
237	327	563	AAATGAAAGGGAATGAAACTT	59.026	23
276	120	395	TTCACACCAGTCACCTCTGC	59.872	20
126	213	338	CAGTGTTTGCTCTGCCAATC	59.445	20
270	1181	1450	TCTACGGATTTAACCCCCAA	59.269	20
188	4330	4517	TCGAAAGTCCAATTTCCACC	59.91	20
228	412	639	AAGAGGTGAGGGCTGTGATG	60.261	20
206	394	599	GTGCTCCCCTCATCTTTTGA	60.195	20
251	109	359	CTTTGATTCCCCACCTTCAA	59.903	20
227	772	998	CGATACAAACTTTCCAAGGCA	60.117	21
262	564	825	CCAATAGCTTTCGGCAAATC	59.682	20
276	683	958	CCGATGGAATGCAGAAAAAC	60.448	20
157	16	172	CGCTTGTGGTGAAGAAGAGA	59.161	20
202	2452	2653	TGTAGCGTTATGTTGGCAGC	59.902	20
164	482	645	GGGATTGGACCCTCATTTTT	59.996	20

180	746	925	AAACTCGGTTTGGGCTTTTT	59.98	20
169	831	999	CGCTTGTCCTGAGTTGTGAA	60.025	20
216	1980	2195	AGTTGCCGATTGGTAAGCAC	60.14	20
264	491	754	CTGGATCGCGACCCTAGATA	60.192	20
252	1645	1896	CCATTTTGGCATTTCATTCC	60.132	20
238	74	311	ATGTCAGTCTGCCAAAGGCT	59.874	20
275	604	878	TGGTCTCAGGAATGGTCCTC	60.048	20
275	241	515	TTCGTAAAACATGAACTTCTTT	59.592	24
236	1062	1297	TATTGTTTGTTTTTCCGCCC	59.81	20
217	236	452	GCTATCGAGGCTTTTCCCAT	60.551	20
137	60	196	TCCACCTTGAAGCTCTCGAT	59.95	20
265	601	865	ACCTCGTTCCACATCCTTCA	60.51	20
172	697	868	TCCACAGACAGATTTCCCAA	59.059	20
149	1099	1247	ATTTACGCGTCAACTGGGAA	60.502	20
141	7502	7642	CATCATCTTCGCTCCTCTCC	59.91	20
220	747	966	TTAGCAAGAAACCCCCATTG	59.931	20
234	257	490	ACCACAATGTAAGGAGCACAA	59.54	22
216	377	592	TTCGCCTTGCATTGACATAA	60.215	20
278	721	998	TTCAAGAAGGGAGAAGGGGT	60.045	20
192	1281	1472	TAGTGACCCATTTTCGACCG	60.883	20
270	997	1266	AAATTGCCTGCACCTCCAAT	61.759	20
268	224	491	GAGAAATGGAGCAGCCTACG	59.978	20
182	870	1051	TGGCGTTGTTATCGTTTGAT	59.041	20
254	1091	1344	CCAAATTTCCAATACAAGGCA	59.818	21
242	600	841	TCGACATATTTTCTTCCGCC	60.038	20
248	0	247	GCGGGGTTGTTAAAGAAGAGT	59.645	21
229	416	644	AATTCAACCTTGGATGCTACA	57.23	21
227	392	618	CCGGTTTGCACCAATTCTAT	59.823	20
204	226	429	TGGGTCAATTCCAATTCAAAA	60.153	21
181	438	618	TTGTTGCCATGCTGTGAGAT	60.272	20
253	1045	1297	ATTGCATGCCACAATTTCAA	59.937	20
103	1055	1157	TGATATTCATTGCCTTTGCG	59.662	20
245	205	449	TTCCAATTATCCATGTTTGCAT	59.193	22
273	688	960	GCATATTGGCAAGAAATAACA	60.012	23
153	722	874	CCCCCACAGACATATTGACTC	59.274	21
182	267	448	AAATCTAATGCAAACATGGGA	57.121	21
148	1677	1824	CGCTTCAAACAAAAGCAGAA	59.226	20
194	700	893	CAGCAGTTGGGTTCTTCTCC	59.844	20
217	344	560	ATCTTGTTCCGTGCATTTCC	59.939	20
247	1427	1673	AACCCAAACCTTAATGCCCT	59.704	20
193	333	525	CGATTTACGAGCATCCCATT	59.923	20
191	47	237	CACCCTTTAATGTCACCATCG	60.234	21
174	710	883	TCCCCTTTCTTCTCAACTCG	59.401	20
255	819	1073	GGAGCTGATTATACGCTGGC	59.835	20
262	10	271	GGCCTCCAACGTTTTCAATA	59.938	20
239	317	555	CGTCGTTGGTGCTATACCCT	60.015	20
280	3629	3908	GGAACGCAGAGGATCAATTC	59.635	20
268	163	430	ATCTGGGCTACCGATTTGTG	59.955	20
165	166	330	TCTCCTCGCTTCGGATACAT	59.797	20
153	402	554	GTGGCACCAAGAATCCCTAA	59.933	20
270	79	348	AATTTGTTGCTTGTGGGGAG	59.971	20
239	1330	1568	ACTCCATCCCTGCTCTCTCA	59.945	20
183	1715	1897	TTGATGGGTGGAATGTAAAGG	59.671	21
145	59	203	ATTAACGCACACACGTGACA	58.628	20
193	341	533	GTGTGGCCTACCAAACACG	60.016	19
153	963	1115	TTAAAATGAATGAAGGGCGG	59.901	20
275	1346	1620	GGTTCTCATTTGAACGCACC	60.504	20
179	616	794	CTGGGCTGCTAAGAAAGGAA	59.587	20

264	118	381	TTGCTGATGCCATTGAAAGA	60.343	20
240	119	358	CCGAATTCCGACCTAACAAA	59.931	20
206	1253	1458	AGCGACAGTGAATGAGGGAT	59.685	20
277	2106	2382	ATCAATCGGCAAATTCAGGA	60.414	20
215	1477	1691	TCGGAAAAAGATTCCCATTG	59.872	20
249	1031	1279	GGGGCTGAAAAATCAAAGGT	60.299	20
254	302	555	CATGGCAGTATTGGCATCAC	59.955	20
236	2665	2900	GCATAATGACCCGCTAAAGG	59.569	20
138	74	211	TTGGTGCTGACTTCCAACAA	60.278	20
203	246	448	TAATAGCGGCCGATCTGAAG	60.323	20
272	723	994	ACGTCCTACTCGCCCACTT	59.736	19
178	3669	3846	GCAGGTTTCCATATGTCGCT	60.103	20
268	2420	2687	GTGAAAAGTGGCCAACATGA	59.547	20
227	358	584	TGTATCCACCCACTGTCCCT	60.238	20
247	669	915	ACGCCCCAGATTGTTTCTTA	59.569	20
237	14	250	TTGCCTTGCTTTCTCTCTCC	59.694	20
179	225	403	CGTTCGGGATCATAAAAACG	60.315	20
226	10	235	CATGTCCATTGATCTGAAACAA	58.476	22
197	97	293	GAATCCCCTGGCAACTTACA	59.933	20
271	716	986	GAACGGTGTTGCCATTATCC	60.199	20
124	393	516	GTTGTGATGGGGGATTTGAT	59.464	20
214	682	895	GCATGACCAATGCAGTACCA	60.549	20
142	959	1100	TTGTTGGAATACGTGGGAAAG	59.847	21
249	985	1233	TCTGGACAAAATTCATCAGGG	59.918	21
139	26	164	GATGGGTTATCACCGGATCG	62.397	20
184	2018	2201	TGGGATAGGGAAAAGCAAGA	59.64	20
263	816	1078	TCTGCCCATAAATTGTGTATGA	58.044	22
124	0	123	TTTTCTTTTGGGCAGCAACT	59.861	20
109	400	508	CCCTCCGGACTATTCTCTCC	60.03	20
259	1655	1913	AAGAGCACAGTATTCCCCCA	59.55	20
183	75	257	TGCACCTGTGGAGGTGTTAT	59.01	20
256	7	262	TGGAATCCAAAGCTATTAGAC	59.977	23
120	418	537	AAAGCCGACACCATCAGTTC	60.119	20
261	20	280	TTCCTCCCTCTGCTAGATGC	59.532	20
184	959	1142	CACAAATCGCCATTCAAAAA	59.538	20
215	718	932	CAAAAACACACCCAAACCCT	59.728	20
159	290	448	TGAGAATGGAACTTGCCTCC	60.195	20
140	518	657	CGAATTCTTGATCATCGCCT	60.177	20
226	353	578	AAAACTAGAAACCCGTGGCA	59.609	20
177	966	1142	TGACATGTGGTCCCAATACG	60.24	20
101	7	107	AGGAAATAAGGAGGTGTTATG	60.131	25
202	674	875	TTCGATACCGTACCAACGTG	59.464	20
279	335	613	AAATTGACACACGCATGCAC	60.594	20
262	394	655	AGCACATGTTCAAACACGCA	61.339	20
252	609	860	AAAATGCCCTTGTATGCTGC	60.103	20
194	274	467	TGTCACTCCCCAACTCATCC	60.934	20
266	4275	4540	CAACTTATGCAGGGATCGTG	59.148	20
277	911	1187	AAAGAAAGGGATGTGAGCCA	59.67	20
181	159	339	GCCACAAATGTCACAAATCAA	59.435	21
155	1421	1575	CTCGTTGACCCAACCGTTAT	59.853	20
273	590	862	AAAAGGCAGTCTACCCCACC	60.361	20
269	133	401	TGTGCAATTTGTAAGAAACAC	60.564	23
266	241	506	GAAGGAGGCGTGGAACACTA	60.255	20
139	659	797	ACGTAGCACGTCTGCACTTG	60.12	20
268	204	471	TCCTGCATTTTGCATTTCTTC	60.203	21
261	712	972	ACAACTCGCGAGCGTAAATC	60.416	20
239	6316	6554	TGTTAACGATGGGAGCATTG	59.542	20
280	14	293	CGGATTTAAGGGTTATTACCT	59.9	25

267	47	313	GGTTGAGAACAAGGGGTTGA	59.943	20
199	1501	1699	GAATCATACCGCTTCTCGCT	59.439	20
184	2519	2702	GATTTGGGTTGTTTGATGGG	60.029	20
255	131	385	TCTACACCATCCACCTGCAC	59.551	20
264	599	862	CGGGAAAAAGTCTCACAGTTG	59.76	21
266	410	675	GCAACTGGCGTGATTATTGA	59.694	20
216	7	222	TATGCCCGGATTTTTGTTTT	59.3	20
162	941	1102	TAAACTTGAGCTCGTTTGCC	58.174	20
166	122	287	CAGTGAGGATTCCCAGCATT	60.073	20
245	431	675	TGATCATAATTTTCGCGCTT	58.396	20
133	996	1128	AACAATAGGACCTTCAGGCAA	59.653	22
274	344	617	TCCGTCATATAAATGCCACAA	58.901	21
194	27	220	CGTTGGTCAAGGATAGCAAA	58.771	20
158	19	176	ACACTCACGCCTTCCAAACT	59.769	20
174	350	523	GCGTCCATTTTCACCAAATC	60.318	20
172	146	317	GGCGCAGTCTACGAGGTAAC	59.904	20
177	1022	1198	GATGACATCAGCACACGGAC	60.13	20
204	590	793	ATGGCCACAAATGGTTCCTA	60.192	20
252	356	607	TCGAGCAGATTGGAAGAGGT	59.95	20
268	1359	1626	TGGGAGAGCTACCATAATTGC	59.196	21
222	297	518	TGGGGAAGAACACATAAATTA	59.66	24
120	854	973	AATGCTTGGTGGTTCGAGAT	59.556	20
258	297	554	CTGGTTTCAGGTGGTGGTTC	60.399	20
204	94	297	TCTCTACAAAACGAGACCAAT	59.732	25
130	1672	1801	TCTCTCCCTCTCCAACTCCA	59.913	20
243	938	1180	CACGGTGCTAATGCAGTTGT	59.788	20
241	329	569	TCAAATGACTTGGGCATGAA	60.049	20
275	752	1026	TTCATCCAAAAGCAAAGGAAA	59.685	21
270	936	1205	GTGTGTTTAAGCCCTTCCCA	59.971	20
215	151	365	CGAAGATTTATGCGGGGTTA	59.922	20
266	994	1259	TTGTGGATAAACAAAATTGAT	58.773	23
238	4969	5206	CCCGGAATGAATTAGTTTGG	59.269	20
278	2089	2366	ATTTCGAGAAGCAGCGGTAG	59.615	20
233	915	1147	ACGTCCAAAATACCTTTTATTC	60.01	24
165	1125	1289	GTGAACCCAGAAACAGCACA	59.726	20
240	1543	1782	TCCCCCTCACTCATCCTCTA	59.606	20
255	1505	1759	GCCATGGATGCGATAAAAGT	59.929	20
244	122	365	ATCTAGGGGCCGAGATTTGT	59.925	20
143	9415	9557	CGATTGTTGCGTGCATAAAC	60.14	20
149	443	591	AACCCAAGCCATGGAGTAGA	59.55	20
245	984	1228	TGAAGTCTAAAGGGAGACGG	60.606	21
220	54	273	CGACTTAAGCAAATTGCAAGC	60.034	21
193	280	472	AGTTGGCACCGTATCACTCC	59.997	20
278	1158	1435	GCAAGTTCTTGCAATTGGG	59.262	19
280	2676	2955	AAGCAAACATTGTTCCAGGG	59.971	20
206	1250	1455	AGGTACCCCACATGAGAATCA	59.274	21
219	369	587	GGCTCAATTATTTAGGCCCAT	59.33	21
273	1797	2069	AATTGGACCGGACCATTAGT	58.24	20
111	20	130	AGGGGGTTATCATGGGATCA	61.3	20
241	109	349	GTTCTCTTCTTCTGCCACCG	59.989	20
158	1625	1782	GTGCCGTAAGTGTGCTGAGA	60.056	20
198	2289	2486	GGAGGAGTTGATCGTCGGT	60.064	19
109	971	1079	CCCTTGGTATCAAAAGGGGT	60.046	20
280	315	594	CATTTTGCCCCTGTATGCTC	60.469	20
231	745	975	TCCCACCACCTCTAATTCCA	60.309	20
269	378	646	TGCATGCTAAGTGGGGAAAT	60.469	20
166	529	694	GAAGAAATCCCTGCCTTTCC	60.017	20
236	563	798	ACACAAGGATTGTTTTCCCG	59.83	20

194	727	920	ACCTATTGCTTAAGACGACAT	59.706	23
108	434	541	CTCCATTGGTGGAACGAGAT	59.927	20
171	893	1063	TCAATATAATGGGCCCAAGC	59.757	20
191	215	405	TGCAATTTATATGCTTTTGCAC	57.955	22
265	152	416	CATAACAAGTGGCGAAAGGG	60.493	20
250	1941	2190	CCCGCAAAATTGCATTATCT	59.928	20
244	66	309	GGAGTCGGCCATGTAGCTTA	60.235	20
265	449	713	GCACAATCGATTTACGTGGTT	59.881	21
240	527	766	AAATTGTTTCGCAAGGCAAA	60.599	20
116	403	518	CCCTTTGTTTGTGTGAGCCT	60.149	20
181	1927	2107	TGAGTGCTGGAAGATTCACG	59.984	20
148	1480	1627	GAATTCGGGGTGTTTTGAGA	59.91	20
189	119	307	TGCGTTGTTTTACCATTGGA	59.969	20
221	123	343	CTCGTCCAGGACAAATCCAT	59.927	20
174	2603	2776	CATTGCCGCAAGATCAAGTA	59.833	20
260	471	730	CTGCATGTCTACGTCCCCTT	60.134	20
278	101	378	TCCCAACCCCATTTACAAAA	60.024	20
220	29	248	GTGGGTTTACCTAGAGCGCA	60.27	20
268	438	705	GGTAGGAATGAAGTATGTGGA	58.904	23
279	693	971	CGCCCTTTTAGTTAAAACCTTG	59.246	22
264	206	469	ACAATGGGTTCATTTGCCAT	60.059	20
244	8	251	ACCCCGTTTCGTTTCCTAAC	60.221	20
264	3120	3383	TCCTCCAGCGAGTCGTAGTT	60.012	20
195	677	871	TGTGAGTTGCCACTCTCCAC	59.872	20
267	645	911	GCAGCCATGAATTTCACCAG	61.588	20
270	3198	3467	TCTTGATGGAAAGGCAAGGT	59.67	20
213	1717	1929	ATCACACACACCACCTCCCT	60.291	20
224	389	612	CCTCACAGGCAAATATGCAA	59.688	20
240	908	1147	CCGCCAGCTCAATTTTATTC	59.682	20
278	829	1106	TTGAGCAATGTGGAGCTTGT	59.445	20
180	233	412	GTTAGGCTTCCCATCCCACT	60.328	20
230	2655	2884	TTTTCGCTCTGATATCCCCA	60.544	20
146	1378	1523	TATTCCCGGTATGTAGCCCA	60.167	20
249	1706	1954	CACACAATCAAGCCCACACT	59.597	20
236	1133	1368	CTCCACAAAGCTCTTGGAAAT	58.449	21
138	143	280	TAGTATTGGAGGTTGGGGGC	61.061	20
150	1357	1506	TGTGGCCAATTCTTGTTGTC	59.547	20
277	211	487	TCGTTCCTACTTTGTGGTGGA	60.535	21
273	1112	1384	TATCGGGAGTGAGAGGGAAA	59.623	20
167	1660	1826	TGTTAGATTTGGGGTTTCGG	59.795	20
206	20	225	CCCGATTACCCTACCCATTT	59.903	20
177	543	719	GGTCGTGATTGTATGCGAGA	59.679	20
241	40	280	CCTAGCCACACACGGAATCT	60.134	20
280	1192	1471	TGCCAATTTAAGTTCGAATGA	60.017	23
183	476	658	AACCGGTTTGACCGATTTTC	61.08	20
246	426	671	CTGCACCGGATAATACAGCA	59.712	20
242	316	557	CCACAAGATCAGCTTTTCCC	59.67	20
102	8	109	AAGTTTATATCAATAGTTTTGT	58.261	27
172	901	1072	TAGGACTGGAGGAGAGCGAG	59.697	20
231	437	667	AGGAGTTTGAGAGGGGCAAG	60.756	20
265	2330	2594	TTTCATTGCTGCTGCAGTTT	59.614	20
265	888	1152	GTTCACCACCAGCCTTGATAA	59.985	21
223	567	789	AGGAAAACATCAGGCAATGG	59.933	20
276	1841	2116	GGTTGAGGCGGATAAAGTCA	60.074	20
274	3152	3425	GTTCGTACCGAACAACACCC	60.277	20
122	998	1119	CAAAGCTCAGCCGACCTAGT	59.639	20
109	1	109	CTGCAAGAAAAACAAGCCCT	59.494	20
101	729	829	TTTGATTTGTTGTCGCTGGA	60.234	20

196	233	428	CGACTGAAAATTTTGGCTAAT	57.958	22
144	2156	2299	ACTCCCCACTGTGTGCTTTT	59.622	20
245	60	304	CACGAGCTGTTAATCACCACA	59.773	21
234	193	426	TGGGATTTGGATGGTTATGA	58.618	20
272	456	727	TTAATCAGATGAGGGCAGGG	60.029	20
266	314	579	ATGGACCACACCTATCATAAC	60.366	23
234	1419	1652	AAGAACTCTGTGGGCGTCAG	60.444	20
262	2002	2263	TGTTGGATTGGACATTGGGT	61.025	20
186	368	553	TCCTGTATGTAGTGACACGAA	60.102	25
138	723	860	TTTGGTTTTTGGTTTGCTCC	59.953	20
205	9	213	CCAATTTGAATGGTTATCACCT	60.457	23
252	1565	1816	TCTTCCTGGGCTTTGTTCAC	60.232	20
254	1053	1306	TGAGAGTTTCTGCGTTGGTG	60.025	20
158	113	270	CCCATGTGTTGGCTTTTTGT	60.786	20
226	2365	2590	CATCTTGATGTCCCCATTGA	59.296	20
265	76	340	GGCACTTTTCCTTCCAAACA	60.088	20
230	598	827	TCATCAGCAAACTTCCCACA	60.24	20
259	454	712	TGGATTTAGCCGATTCCAAG	60.031	20
273	302	574	ATGATTGGTGATAGCTCGGC	60.066	20
178	54	231	GCACTCTCCAGCAATGTTGA	59.992	20
112	430	541	GGTGAAGAAAGTGGGCTTCA	60.232	20
261	1190	1450	GCAGTGGAACGAGGAAGAAC	59.851	20
127	148	274	CGCATTTCATCTGCTTTTCA	59.953	20
232	67	298	TTTTATTGGGGGTGCAACAT	60.053	20
225	1059	1283	TTCGCAGACAATGTTCCAAG	59.84	20
245	547	791	TCACCGAATATTCCCAACTCA	60.316	21
265	766	1030	TACTTTGAGGCCGTCATTCC	60.074	20
204	604	807	GATAGCTCTGAGGCTGGTGC	60.127	20
212	484	695	CCACTTCTCCCATTTGCATT	59.933	20
263	0	262	CCGTAGCTGTTATTGATGGAA	57.795	21
227	135	361	AGGAGCGCACCAGAATTTAG	59.476	20
223	429	651	CCGAATATCCCCCAACTAAA	58.759	20
192	495	686	TCGAAAAAGGAGTCTGCGTC	60.517	20
235	3408	3642	AGCTGCTTGCCGTAATTCAT	59.873	20
237	1195	1431	GAGTGCTAGAACCCCATCCA	60.073	20
152	1018	1169	CGTCGTCTGTTTCATCATCG	60.263	20
234	1756	1989	ATTTGTGGGAGATGGAGGTG	59.779	20
188	438	625	ATCGATTAGGTCGCACAAGG	60.096	20
227	1301	1527	TGCCTGCATCAAAGTACACC	59.722	20
130	1084	1213	ACAATGGCTTTAAAGGGGGT	59.704	20
262	14	275	AACTGGACCTCTGATCTGCAA	59.859	21
190	1980	2169	CATTTTCGTCCGTCACACAA	60.552	20
222	444	665	AAAAATGGTTGATTAGATTAC	59.68	24
175	457	631	TCTCACGAGGATTTTCGATGT	59.685	21
236	887	1122	AAAAAGGGCCTATATCCAATA	59.2	24
189	3157	3345	TGCGAATTTGGAATTATCTGC	60.054	21
276	35	310	GGGGTTATCATGGGATCAAGT	59.895	21
125	108	232	AACGCAGATCTGATGGCAC	59.81	19
249	4531	4779	TACTCTGCCTGACGGGATTT	59.694	20
227	393	619	ACAATGCAGTAGCTGGTTGG	58.802	20
236	965	1200	TGGTGATTTTTGATTATAGGAA	60.496	27
267	2	268	GGAACAAAGACACCATTGATA	59.311	24
266	19	284	TTTGATAACGTCAAATCCAACA	59.394	23
264	1130	1393	ATCATTCCAATCATTCCCCA	59.952	20
182	624	805	GACCCATTTCTCATCATTGG	57.775	20
276	1178	1453	GCCCTCGAATGTTGTGAGTT	60.119	20
131	98	228	TCCCAACTCACAATCCATGA	59.893	20
215	46	260	TTCTGCATGCATTTATTGGG	59.52	20

101	1173	1273	TTGCGGGGTTGTTAAGAAAT	59.451	20
207	1393	1599	AGAGAGAAGTGGAGAGGGGG	59.801	20
106	976	1081	GGATCCACGTCCACTATGCT	59.957	20
249	2822	3070	CTCGTTAGCAAGCAATGCAC	59.638	20
260	248	507	TTGAAAGAAGAGGGCTCCAC	59.405	20
215	2987	3201	TTTCCTGCAGCTGAAGAGGT	60.134	20
265	626	890	GTGAGGATATGGCGAAAGGA	60.036	20
169	711	879	CAATGTCAGAGTGGTGGTGG	59.997	20
266	1237	1502	TCTTCTCGCATACCAAAGGT	57.422	20
241	405	645	GCGTGGGGAATAATGAGAGA	60.036	20
206	1067	1272	CTTCTTTCCCCAAACTTCCC	59.912	20
253	1456	1708	AAATGGATGCTGATAAATGGA	57.059	21
233	1215	1447	TGCATCTAAGTTTGCACCGA	60.401	20
248	1127	1374	GAACGTGCGTAGAACGTGTG	60.37	20
226	262	487	TTTCCCCTCCCTCATTTACC	60.124	20
259	705	963	CCATTCCGTCGTTGTAGGAA	60.883	20
211	1611	1821	CGAAGAAGCCCTGAAATTGA	60.323	20
197	4229	4425	TGCAACGTGAGTAGTGACTCG	60.104	21
265	1097	1361	ACCCTCTTCAACATGCAAGG	60.111	20
152	1867	2018	CCAGACCCAAAGCAAATCAG	60.626	20
248	413	660	GGGAAAAAGCGTTATCGTTG	59.586	20
166	893	1058	GTGCCAGAGATCGGAGAAAG	59.95	20
139	1578	1716	CACCACAAAGCAATTGGAAA	59.561	20
235	1177	1411	TGGGTGCCATTTCTATCACA	59.924	20
153	424	576	ATAAGGGCTTAATGAGGGGC	59.424	20
268	461	728	TGATCTGGAAGTAAGGAATCC	59.657	25
145	2243	2387	GCAAAGACCATTCTTGAGGC	59.82	20
274	619	892	TCAATGGGGCTCTTGAGTTC	60.195	20
252	377	628	GATGAGAGAGAGAGCGGTGG	60.096	20
209	462	670	AAGTTCCCCAGCTCAAGACC	60.628	20
137	434	570	AAGTTGCATGCCATTTACCA	59.041	20
183	1559	1741	AATGCCCTCCTATTATGCCC	60.137	20
280	713	992	ATGGGTTATCACCGGATCG	60.554	19
223	292	514	TACCAAAATTGCGTGCAAAG	59.742	20
186	394	579	GGATTTTGGATTGGTCGAGA	59.871	20
263	146	408	CAATGTTGGTGACGTCTTGC	60.16	20
262	2506	2767	TTCACAGCTGGCATAACCAA	60.257	20
234	59	292	TCACGGATTCACCAACTGAA	60.088	20
232	2227	2458	TTGCAAACTTAATTGGTGCG	59.742	20
279	1060	1338	CGTGATCCGGATAGAGTGATG	60.489	21
268	1020	1287	GCCACCATTGTTGGTTCCTA	60.755	20
134	861	994	TTCCTGATTGAGGGTGGAAG	60.042	20
248	43	290	AGAATTTCAAGGTAATGGGGA	57.54	21
230	36	265	AAAATGCACGTCTCTCGGAC	60.263	20
153	953	1105	CTCAAACTTACCACCCGAACA	60.016	21
130	2774	2903	TTGCACTTAAGAGGAGTTTTGA	58.249	23
232	1054	1285	GCATTGCAAGCTTCGATACA	59.983	20
225	876	1100	TGGAAGGCCTCGTCGTATAG	60.227	20
109	89	197	TTCCATCGCGAAGCTAATG	59.922	19
263	400	662	GTTAAAGCCAAAAGTCGGGC	60.958	20
169	3501	3669	CAGCAGCAAGCAATAACGAG	59.776	20
259	1114	1372	CCAGGAGACGAATGCTTTTT	59.312	20
177	904	1080	TTTGCACTTCCTGGAGAACC	60.232	20
252	473	724	ATTTTGTCGCAGTTGATCCC	59.939	20
280	2706	2985	CACACATGGAAAAGATCTCCA	59.971	22
185	1148	1332	TGGACAGGGATATAAGCCGA	60.427	20
195	2544	2738	GAAACAAGCATGATCACGGA	59.654	20
197	410	606	AACACATTTCTTCAACATTCAT	58.541	24

280	47	326	TCAACGGTTCACATCGGTT	59.951	19
233	649	881	TGGAGAACTCATTCTTACTGCC	59.517	22
144	895	1038	CACACGCACTCACAACACAC	59.818	20
138	1096	1233	GGCCAGATTTCGTCCCTATT	60.286	20
181	42	222	TGTTTGCACGTGAATAAGCC	59.735	20
217	21	237	GGTTCAACCATTTTGTTGGG	60.066	20
218	836	1053	CGCCGACCAATCATGTAGA	60.637	19
225	3168	3392	TTGTGGATGCCCTAACCAAT	60.192	20
261	1384	1644	CACCCAAAGAAGAAAGCACC	59.711	20
234	405	638	CCCATGAAATATGCCTTACTCT	59.871	23
243	2451	2693	TGAAAGAATTTGGGGGATCA	60.244	20
233	869	1101	ATCTTTGGGCTGGAAACTCA	59.67	20
249	4136	4384	ACCCTCCACCCTTTCTCTGT	59.968	20
187	610	796	CATGTCGTGTCGTGTCAGAA	59.265	20
153	4444	4596	TTTTCCTGCCTTGTCAGACC	60.232	20
105	10	114	TTGTGTGATCGAACCACGTT	60.008	20
253	1284	1536	GTGTCCTTCCTCGGACAAAA	60.088	20
235	2204	2438	TTGTTTTCCGAGGATCATGC	60.983	20
184	1251	1434	AAGGGTCATGATCGTTCTGG	59.927	20
267	19	285	TAGGGCTATGGGTGGTAGGA	59.406	20
198	580	777	TTCAAGCAATAAAGCCCGTC	60.209	20
194	385	578	GGTGACAGTGATGGTGATGG	59.801	20
152	0	151	AGCCGTGAGATTTACTTTTAAC	57.02	24
186	0	185	GCGTTTTGACAATATATAAGTG	59.394	27
269	973	1241	CCAAACCAAAACTCATCAACC	59.322	21
251	372	622	TCAATCCCATTCACCCTTTC	59.727	20
278	946	1223	GAGGATAACTGGCCAACCAA	59.933	20
188	1908	2095	CAACTCCCCCGTAGTTTTCA	59.964	20
267	2317	2583	TTGGTGTTTGCTGGGATTTT	60.344	20
212	1157	1368	GTCGAGCTGAACGAAAGAGG	60.134	20
110	491	600	CGTAATCCTTCAATGGCAGC	60.606	20
243	391	633	ACCCAAAACAAAATGCATGA	58.869	20
218	423	640	TATGGCAAAAACACCAACGA	59.969	20
238	357	594	AACTCTGATCGGTGGGAGAA	59.655	20
224	558	781	AGGAGATGGAGGGTTCAAGG	60.447	20
161	206	366	GCATTCTCAGCATACACGGA	59.83	20
148	1004	1151	TGTGATATGGTGTTGGGAGG	59.215	20
251	502	752	AAACCAGAGAAATCCCCCAC	60.169	20
253	1393	1645	CTCAATGCGTAGGCTTCTCC	59.978	20
230	941	1170	AAACCGCACTTTAGCTCGAA	60.018	20
204	397	600	ATTCCCTTGTATGCTGCGTT	59.597	20
165	736	900	CACGTCTCGTTTTATCGCAA	59.872	20
181	2457	2637	GATTCTAGCATCGTGAGGGC	59.803	20
235	748	982	ATTCCAACAATCTCAGCATCA	58.159	21
271	737	1007	AAGTATTGATCGACGTGGGA	58.019	20
145	127	271	CCGCAAATAGGATCGAAAAA	60.033	20
220	1402	1621	TCAAACTGCCTCCCTTGTTC	60.232	20
250	719	968	TCCCTAATCATCTCCCCTCC	60.228	20
265	523	787	CCTAGAGCACACTCGAAGGG	60.005	20
272	2691	2962	TCCTCCTTCCATAGCAGCAA	60.874	20
250	3334	3583	TGATCAAAATCCACACCTCG	59.496	20
278	513	790	CAGAGTTTGTTTCGCAACCC	60.668	20
250	7	256	ACTGGTGGAAACTGGATTGC	59.973	20
170	500	669	CCACCTCTCTGCTCCACTTC	59.986	20
277	181	457	GAACCCAAACCTCAAGCTCA	60.232	20
254	209	462	AGGAAGCGAGGTAGGCTTTC	59.983	20
266	86	351	CCAGATTCTCTTGGTGGAGG	59.649	20
266	26	291	CCTTTCTCCATGGGCATCT	60.019	19

226	1215	1440	TCGACTGCTGTGTGGTTAGC	60.056	20
201	1867	2067	GGACAAAACGACCAAAAGGA	59.948	20
191	1114	1304	TGTTTCTCTCACCTCCTCCC	59.228	20
243	248	490	AGGGCCCAACAATTTCTTCT	59.94	20
219	201	419	GCATATGCATGGTTCTCACG	60.104	20
259	462	720	TTGGTCCACCATTCTTTTACTG	58.994	22
197	19	215	TTGAAATTAGATTAAAGAAAA	57.335	27
280	2419	2698	AAAGGCAGTCAGGTCTAAGG	59.899	21
176	93	268	CGAGTTAGGAAATAAGGAGG	60.478	23
232	393	624	GCAGCTCAAAAAGACAGTCC	60.565	21
241	264	504	CACTTTTTGTGAAACCCCTCA	59.994	21
176	1043	1218	GGGGATTCCTGCAATTTTCT	60.265	20
241	261	501	ATTCAAACCGCTAGTGTGGC	60.14	20
222	374	595	AATCCCATCAGAACCACCTG	59.779	20
267	1025	1291	ATTTCGTGTGAAGCCTTGCT	59.882	20
202	14	215	CCTAAGTCTTCCGTGTGCGT	60.312	20
217	516	732	AAATTATTCAACTTGGATCAC	57.303	25
263	368	630	ACTTGTCAATGCCGGTAAGC	60.14	20
265	764	1028	TCACAACGGGGTCAAATGTA	59.816	20
244	834	1077	ATCAGGCTCGAGTCCATGTC	60.231	20
254	415	668	TCGGCATGAGATGAGATGAG	59.9	20
159	227	385	AACAGAGCAAGACGAGGCAT	60.02	20
251	1287	1537	TCTGGTTGGAGTCTGCTTGA	59.545	20
213	17	229	GCCAATCACTAACCAACACG	59.05	20
195	1452	1646	ACTCCGCCCTCGTGTTTTAT	60.875	20
170	346	515	CGTAGGCAGCATCCTTCATT	60.235	20
168	2422	2589	CATTGCCATTGCAGAAGCTA	59.976	20
250	498	747	TCCTTAAGGTGTCAGAGGCG	60.388	20
178	2347	2524	TGATGCATTTTCCCAGTTCTT	59.56	21
256	2239	2494	ACCAACCAGCTTAGCGAAAA	59.883	20
228	1461	1688	CCCTCGTTGACCTTGCTAAA	60.241	20
259	1687	1945	AAAAAGTCCCCAGCCAATCT	59.94	20
273	259	531	TCCCACTAACCTTGTCTCCC	58.989	20
254	761	1014	GGTGTGCTCGGATCTTGATT	60.081	20
193	527	719	AAGATTCTCTCTTGTAGGTTGT	59.72	25
114	717	830	CACGGCAAAGCAAGTAATCA	59.872	20
205	1150	1354	CGAGAACTTCAGCCCCATAG	59.83	20
221	101	321	CACCCCCTGGCTTCTTTTAT	60.312	20
186	5863	6048	AGTCGCCTCCATTTTCTCCT	60.212	20
164	1343	1506	AATCGTGAAATCAAACCAGA	57.201	21
153	484	636	TGCCACTACTTTTCTTGCCC	60.249	20
146	2022	2167	TGTTGTCCGCTGTCAAGAAA	60.427	20
263	67	329	AATCGAATTGTTCCTGCTCG	60.214	20
247	42	288	CACTGGATCTGCCGATGTTA	59.673	20
146	248	393	CTTTTGCTTCAGACCCCCTT	60.601	20
204	666	869	AGTCACGTCTATTCATCATTG	58.654	24
176	1014	1189	AGGACTGATGATCCGGTGAC	59.928	20
117	60	176	TTTAAGATGTGCATGCATTTG	59.217	22
217	3701	3917	CGCAAACGATGGCAATAAT	59.534	19
204	639	842	ATTTTGCACCGCCATATCAT	60.182	20
188	50	237	GAACGCGAAGTAGCATGGTT	60.278	20
198	98	295	ACGACGCAAAAATGGAAAAC	59.982	20
147	516	662	ATGCCACCACTTCCCTGATA	60.34	20
280	2155	2434	GGAGCAAACATGCTGCATAC	59.306	20
138	224	361	TTCTAACGGCCCAGATTTTG	60.067	20
214	115	328	CAAAAATCTAACGGGCCAAA	59.937	20
190	332	521	CGCTTCATTATCAACCACACC	60.38	21
277	539	815	TGCTCTCAATTAAATACACCC	59.912	23

234	416	649	CGCTGCAACTGTTGGACTT	60.04	19
228	498	725	TTCGAAGATCAACGGATGGT	60.461	20
278	1086	1363	GCCATTATGGTGCATTGTTG	59.816	20
202	1313	1514	CCACTCTCTTGCGCTTTTTC	60.132	20
176	2338	2513	CAAGATGATGAGGGCCAAAT	59.894	20
108	625	732	GGAGACCAATTCTTGGCTGA	60.195	20
110	2594	2703	CAATAAATTGGGGTCGGCTA	59.789	20
195	26	220	TGGTTATTACTGGAACGCGA	59.182	20
193	301	493	CGGCCTATCGTCTTCCTACC	60.968	20
257	5800	6056	TCGATCATAGATGTGGTTCCAT	59.273	22
247	521	767	TGCAACCACCACTGGAGATA	60.112	20
145	501	645	GCAAAAGTGCCTACTTCACCA	60.298	21
262	597	858	TGAAACCAACTATCTCGGTGC	60.125	21
131	984	1114	CTGACCTGGTGTCCCATCTC	60.527	20
253	481	733	GGCAATCTATCCCATACAAGG	58.406	21
136	155	290	TCTTCTCTCAGGTGGGGGAT	60.991	20
203	471	673	CAACCAATTCAACTTTCATTAT	59.788	24
216	1125	1340	ATCCGGATCATTGACATTTG	58.215	20
213	883	1095	ATCTGTCTCCTGCCCATGAC	60.08	20
250	759	1008	ACAGTGGCTAAAATGCACCG	61.08	20
199	2295	2493	GGCTTTGTTGCTGGAGTATTG	59.761	21
256	508	763	AACCTGCATCACAAAAGCAA	59.322	20
274	20	293	TGACTGTGGATTTCCAATCAT	57.849	21
263	464	726	TGTTGGTTTGTGAGGTCAGC	59.726	20
182	1156	1337	AGTGTTTCATCTCCGCCATC	60.081	20
210	4965	5174	TTGGTTGTTCATCTGCGGTA	60.111	20
275	1749	2023	GCATGCAAAGTTGCAAACAA	60.827	20
241	743	983	TCAGACAGCCATCATGTTACG	59.731	21
270	447	716	GATGAAGGCACAGAGCATCA	59.95	20
232	77	308	GGTAGAGGAGCTGATGTGGC	59.834	20
273	569	841	CATATGGTGTCAGGTTTGGG	58.695	20
226	548	773	CATCAGTTGTAGCTGGGGGT	59.989	20
194	394	587	TCATGTACGTGATGCAACCA	59.543	20
175	260	434	AGACCAAACCTCAAGCATGG	60.111	20
218	1133	1350	GGCCACTCAGTTACAAAGGTG	59.648	21
163	1546	1708	TCACCTTTCCAACAGCTCAA	59.415	20
212	708	919	GTGGTGGAACTGATTGGGAG	60.363	20
194	510	703	AAAGTGCCTTGTGTGTCACG	59.794	20
217	408	624	TCCCTTCTTACATATGGCCC	58.857	20
200	459	658	CGTCTGAGTACCCCGTCTTC	59.721	20
268	2579	2846	GTGTGCGAGTGGTTTTTACG	59.245	20
262	356	617	GCTGTGCAAAACAATGTCGT	59.77	20
231	961	1191	TGGAGTTTTCAACGCAGACA	60.427	20
263	1639	1901	ACTGCTCCTCTCATGGTCAAT	58.758	21
264	193	456	AAAATCCAATTCGAATCCCC	59.963	20
236	2261	2496	TTCCTCTTGTCAATAATGGGG	58.89	21
257	56	312	CAGGGGATCTCAAGCCTGTA	60.21	20
147	519	665	AGATCAGATTCCCAAACCCC	60.133	20
140	306	445	CAGCTGAACCAACCATCCTT	60.111	20
225	176	400	CCACCATGATTTCGACACAC	59.812	20
261	157	417	GCGAGCAGACCAGAAGTCAG	61.3	20
193	473	665	CGCTCACCACAAAGAGAAGA	59.161	20
264	724	987	TCGTGAGAAATTAATGGAACA	59.885	24
273	1259	1531	TGGAAAAAGGGAGGAATCAA	59.476	20
204	540	743	CATGCACATCCCTCTTTCAG	59.241	20
172	2499	2670	GCCAGTTCTTTTTCATGGGA	60.051	20
252	788	1039	CAAACACGCATCACCACCTA	60.574	20
204	1354	1557	TTCCAATTTGAACTACCGGC	59.938	20

278	62	339	CATGAACTCCATGAAGCATGA	59.664	21
223	1210	1432	GATCACTTGTCCGAGGCACT	60.269	20
254	2122	2375	AGTGAACCATGGGTCCGTTA	60.232	20
278	1136	1413	GGCGGGAGCATATTTCTGTA	60.06	20
270	2248	2517	GAAATTAATGCCGTCGCATC	60.432	20
280	41	320	AAACCGAAAAACCGAAAACC	60.197	20
167	1074	1240	AGAGCAACACATGCCAACAT	59.169	20
175	0	174	TCATTTGTTAGAGGTTTTGACC	58.663	23
240	482	721	TACATCGGCTCAAACTCCAA	59.272	20
135	173	307	GCTACTGCTGTCATAGCCCC	59.866	20
280	2	281	TTGATGATATATAGGTGTTTTG	57.297	26
254	203	456	GTTTGTTATTGGGGTATGGGA	59.823	22
254	6125	6378	GTCACCTGTCACCAGAGCAA	59.872	20
124	512	635	TGGATCGTTGCATCATCATT	59.89	20
249	2464	2712	TACATGCGTTCACGAAGAGG	59.864	20
280	2284	2563	CGGACAAACACGACAACATC	60.008	20
279	373	651	CCATGAGAAAATGCACTGCT	58.877	20
149	109	257	GTACTGCTCCATCTTCAACCG	59.749	21
274	23	296	CAAGAGTAGAGAAAATCCTC	58.901	23
249	130	378	TGATTCGCTTCGCTTTCTTT	60.096	20
164	2192	2355	CAACTGACCAACAACAGCCA	60.757	20
153	138	290	TTTCTCTCTCCTCTCGCTGC	59.973	20
273	171	443	ATCTCGGCCTAGCTGGATTT	60.194	20
225	167	391	TAGACCCAGGCTTCGAGGTA	59.83	20
213	558	770	CCACCTAGCACTTCAAGGGA	60.246	20
143	1885	2027	AGCAACCATGCAATTAAGGG	59.96	20
135	1599	1733	AACGAAGAAACGCTGCAAAT	59.889	20
248	1909	2156	GATGCCCTCCACATCAGATT	59.893	20
239	584	822	GCCTGCTACATAGGGTTTTCC	59.979	21
269	1121	1389	GAGAATCTGCAATGTGAAGG	59.835	21
189	114	302	ATCTTGACCGCTGATTTTGG	60.074	20
245	9246	9490	TTCGAGGGGATTAATGATGG	59.717	20
221	1721	1941	ATTGGCAATTTTTGAAACGC	59.95	20
279	914	1192	GAAGAAACACCGAAGCAACC	59.717	20
219	2492	2710	TTCCATCCCTCTCCAATGAG	60.003	20
259	409	667	AGCAATGAGCAACATTCAGC	59.031	20
170	2	171	TTTTAATTCACGCACAATTACA	58.984	25
242	315	556	GTGTTGAATGTTGTGCCTCG	60.16	20
254	103	356	ACAACACGCAAACATGAGGA	60.16	20
216	2570	2785	CACTGCGCTTCAGTCTGGTA	60.199	20
199	723	921	AGGTTGCACCTCTGTTTTCG	60.291	20
154	167	320	TCCAACTACGTGGGTGGTTT	60.269	20
195	253	447	AGCATCTTCCATCTGGCATT	59.658	20
279	417	695	CACAGGGAGAAGACGAACTC	58.533	21
212	62	273	TGTGTGTTGGTCTGAGAGGC	59.872	20
191	839	1029	AGGTTTTTCAAGGAGTGCCC	60.476	20
100	1283	1382	AGAGGACAGGAATGTTTCTGG	60.11	22
205	553	757	TAAAGAATGCCCACTCCCAG	60.066	20
257	468	724	CAGAAGGCACCGAACTTACC	59.734	20
185	5055	5239	ATGCAACGTGAAGAAGAGGG	60.255	20
206	1198	1403	TGAAAAGGCCATTCGAGACT	59.813	20
127	2319	2445	GAAGCATTGTTGGAGGGAGA	60.195	20
244	1292	1535	GCTTCACCAACCTTTTGAGC	59.859	20
217	8	224	CGGCTTGGATTATTTCCTATTT	60.169	23
207	9	215	TTAGTTAGTACCGATTTCAGG	57.499	24
142	0	141	CCGAAAATACAGGCGCATA	59.671	19
188	824	1011	AAGGTTTCCTTAACTCTGCGA	59.433	22
149	41	189	CAAAAACAACTTCAATATGGA	58.211	25

240	1733	1972	TGGCTTCTGCACTTTCCTTT	59.993	20
279	13	291	CCAATTTTCTCTTCGGGCTA	59.292	20
115	57	171	TGATTGTACGAAAAACCCCG	60.722	20
187	502	688	ATTGGTTTGTTTTGGGCAAG	59.839	20
240	754	993	CTCTCATTTTCGCCCGATAC	59.668	20
235	1148	1382	GTCTGATAGGATTGGCTCGG	59.653	20
244	531	774	GGCAGAGATTTCATCTCCCA	60.158	20
228	1651	1878	TCTAGCCGGTGTAGCCATCT	59.859	20
265	1510	1774	ACTGTGGATGGAGTTCGGTC	59.969	20
126	1464	1589	AATTGAGAGGCTCCAACGAC	59.288	20
231	218	448	CCATGCACGTAAGCATGTTC	60.142	20
216	2153	2368	TGCGTGATTTTGGCGTATTA	60.096	20
240	8300	8539	GAGCTCTCTTTTCCTCCTCCA	60.081	21
207	800	1006	CCCAACAAACCCTTTCTCAA	59.942	20
231	1635	1865	CATGGCATGCAAAGAAGAGA	59.948	20
277	1113	1389	AGATGCATAGGTGTCTGCCC	60.104	20
229	2664	2892	CTTCCATTCCATTCCACACC	60.173	20
272	838	1109	CCTGGAAGAGCTTGAAAACAA	59.48	21
128	297	424	ATCCGACCTAATGAAAGCGA	59.668	20
234	260	493	CGGAGAGAGATGCAAGGACT	59.555	20
245	3851	4095	GGAAGTGGCAAAACAGATTGA	60.103	21
223	319	541	GGATGATTTGGAGAATGGGA	59.685	20
256	716	971	TCATGTTTTCTCACTTGGGATG	59.971	22
252	127	378	AGCCACTGAACCAAGTGACC	60.159	20
222	477	698	CGAATGAGATTTGCGTGTTG	60.257	20
261	579	839	TGGCCTCTAATCAGTTCGCT	59.978	20
230	3371	3600	TCCAAAAAGAGGATCCCAGA	59.6	20
221	507	727	CGGAAAAGCTTAGCTCAGGA	59.724	20
119	1576	1694	TGAAATTCAAAAGCTGGGATG	60.06	21
188	891	1078	GAGATTTAGTGCGCGAAAGG	59.982	20
267	2793	3059	GGAAAAGGCATATTGTGGGT	58.765	20
220	186	405	GGGAAGATGTGATGAGGGAG	59.46	20
117	1142	1258	GCACCACCCTACCCTTCTTT	60.361	20
216	2694	2909	GTGTGTTGGGTCTTCCAGGT	59.859	20
279	181	459	TTGTCAACCAACACCTGCAT	60.008	20
203	1006	1208	AATGTGCCCAGAGAAGTTCG	60.255	20
260	224	483	TTTCTCGCATTGGTCAATCA	60.197	20
272	52	323	GGTGCTGTGTGATGATGGAG	60.121	20
180	316	495	GCTCGCTTTCATTTCACACA	59.995	20
239	1116	1354	GCCCCATTTATACCCTTTCG	60.508	20
181	988	1168	TGAGACGGAGGAGAAGAGGA	60.064	20
271	1055	1325	GACTGAGGGGAATCCATGAG	59.46	20
137	1446	1582	TGTTAAACGGACTGGCCAAC	60.924	20
142	783	924	TCGTGTAGAATCGCCTTCCT	59.836	20
203	1944	2146	TTTGGGTTGGAGATGGTTTT	59.264	20
225	490	714	CAAACGAAAAATTATCAACTG	59.853	26
256	4870	5125	ACCAAGTTGAGGGCATTGAA	60.495	20
164	2258	2421	CCTGACCGGATCTCTCACTC	59.792	20
248	3216	3463	CTCTGTCCACTCTTCTCGCC	60.135	20
279	1209	1487	AGGGGACTTTTTAACCAACCA	59.728	21
100	6	105	TGTGAGTGTGTGTGCAATGA	58.12	20
265	456	720	ATTCAGGTAATCCGCCATTG	59.784	20
274	572	845	AATCGAACTGGAGGAGGCTT	60.212	20
226	245	470	CTCAGTTGCACTGGTTTCCA	59.873	20
201	2038	2238	ACAGGATAACGGATGCCTTG	59.955	20
172	1881	2052	CAACTCACATACGGATGACCC	60.248	21
271	1314	1584	CGCGTGTCATTCTAGACCAG	59.465	20
133	545	677	CTCCCCTCTTTCTCGCTACA	59.569	20

227	5715	5941	GTCATCGAGCCTAATCGAGC	59.946	20
130	0	129	GCGATTTTAACAAAAACGGG	59.472	20
248	1090	1337	CATTTTCCCAAACCCACAAC	60.066	20
186	322	507	GCAATCCAAGGGAGATGAAA	60.014	20
262	559	820	TTCAAAAGCTTGCTTCCCAT	59.823	20
255	364	618	ACTGTCCCCACGGTCTAATG	59.844	20
275	552	826	CGCATTTGTCTCTCACCTCA	59.984	20
259	441	699	AGACTGCACCTGCGGTAACT	59.937	20
213	1661	1873	CCTGGTGTCCACTGTGTTTG	60.039	20
228	408	635	GGGTTTGGATGAAGGAGGTT	60.169	20
198	995	1192	CCACCTGAGGGAGTTGATGT	59.962	20
105	1909	2013	CAAGGTCTGACGAAGTCGC	59.561	19
112	1869	1980	CAGCCCTTGGCTCTTTTAGA	59.587	20
275	654	928	AGAGGAAACGATCAAGCAGC	59.579	20
266	2708	2973	CATCGATTGAACCAAACACC	58.824	20
170	224	393	TTGAAAAATAAGTGCTGGGGA	59.573	21
265	35	299	CCAACGTCAAAGTTGCTAGG	58.431	20
201	902	1102	TTGTCTATGCCGGTTTTTGA	59.157	20
261	481	741	AATTTCGGTTACATGGCAGC	59.967	20
241	2	242	TTGTTAGAGGTCTTGACGGGA	59.72	21
274	257	530	TTTGGGGAGGAGAAAAGAGA	58.833	20
189	16	204	ACTTATCCAACTCAATTTATAT	58.178	27
250	1045	1294	ATGCGATGTGTGGTCGAATA	59.955	20
229	36	264	GGGTTATCACCTGATTACTAC	58.824	25
273	1021	1293	TGTCGTGCGATGTATGATGT	58.517	20
176	600	775	GGGAGGAAGATGCAACTCAG	59.803	20
217	2152	2368	AAAGGCCACGTGTTAATTGC	60.003	20
207	863	1069	TTTCCTTTATGATCCCCTGC	58.974	20
245	211	455	GGAAACGATCGTAATACGCC	59.438	20
129	580	708	TGAGACGATGTGCGATAGGA	60.376	20
163	560	722	TACTAGGTTGTTGTGGCGGA	59.195	20
249	2282	2530	TCATATATGTTCCTGGCGGC	60.827	20
256	1973	2228	TCGGGAGTCAGAAATCGAAG	60.331	20
206	186	391	AATTCACATGGGACTTGCGT	60.384	20
141	70	210	ATGTGGCTTGCTTGCTTCTT	60.022	20
150	274	423	TCAACCCCATCTTCAACCTC	59.903	20
227	560	786	TTGATTTTTAATGGGGCAAAA	59.313	21
200	1835	2034	ACCTTGCTTGTGGTCCTTGT	59.622	20
277	1149	1425	GGACTCTGCAGCATGTTCAA	59.992	20
264	565	828	CATTAGGTGTTGGGGCTCAT	59.813	20
150	1033	1182	ATTTGTGTTGGCTTCAGGGA	60.495	20
222	1529	1750	GCGATCATTCTCGTGAAGAAA	60.346	21
265	248	512	AATGCTTGTACCCGTAGCGT	59.66	20
241	1064	1304	AAGCAGCGGTGAGAGCTAAG	59.92	20
132	1184	1315	CATAATTGCCTAGCTGGCGT	60.251	20
265	391	655	TTCCCACCATGACTTCAACA	59.935	20
196	242	437	CCCCCAAATCTACAAAAGGG	60.525	20
261	577	837	CGAGCAATCTGTAAGGTGAA	59.517	22
279	901	1179	TCTGCGGGATTTAGAGGATG	60.17	20
245	1396	1640	GCCTTTGAATTGCTCCACAT	60.081	20
245	92	336	GTCAACATCACCTTCACCCA	59.367	20
241	1198	1438	GTGTGGTCTGCAAAGTGTGG	60.203	20
115	318	432	GCTGAACTGTTTTCCGAACC	59.717	20
271	1174	1444	CAATTCAAAATTGAGCCCGT	59.938	20
279	2083	2361	GGCCAACATGATTAGCATCC	60.304	20
225	1492	1716	TTGTCAGCGCGTTTAATGAG	60.014	20
167	545	711	TTGGTGGTTTTGCAGATGAA	60.088	20
261	5577	5837	GGACACCACGTAAGCATTCA	59.572	20

155	568	722	GAGACATCAGCTGAGGGGAG	59.945	20
271	508	778	ATTCATGGTGGTGGTTGGAT	59.91	20
232	19	250	CTCGCTCGGAAAAGCAATAC	59.982	20
206	2149	2354	GATTGTTGGGTTTTCCGATG	60.17	20
196	1248	1443	TCTTTGGGATTCCTCTCGAA	59.744	20
264	635	898	GCCTTGTACAAAACCTCGGA	60.11	20
118	1232	1349	CCTTCGAGACTCCATCGTTT	59.284	20
245	499	743	TTTGAACTCCGTAGCAACCA	59.317	20
213	532	744	GGATCTGCTAAGATCGCTCG	60.081	20
199	883	1081	GTCCTCACCTGCATCGTCTT	60.269	20
217	642	858	CTGCTCTCCAGAAGCAAACC	60.134	20
215	1394	1608	CGGAGGCTGAGGCATTATAG	59.823	20
160	613	772	CGCAGGATTGTACGGTTGTA	59.609	20
234	0	233	TGAAGTTAGGAAATAAGGAG	57.525	24
117	1277	1393	TGTTGGCATGGTTGATGAGT	59.967	20
134	642	775	GGATTCGAGTTTTTGAAACCA	59.054	21
125	73	197	TGTTGGTTGAAAGATGAGGG	58.541	20
273	452	724	TCGATTAACTTGACAAGGTTT	60.037	24
215	3524	3738	AGGCGTGTTTTGTTTGGAAG	60.147	20
128	71	198	TATGAGAGACGAGCTCACGC	59.297	20
181	238	418	TTTGGTTATCATTTTGTCACAG	58.935	25
247	784	1030	GCCCACCATACCACAATACC	59.939	20
167	60	226	CTTGAGAAGGCATGGTAGCC	59.836	20
206	18	223	AGCAACAGCGGAAGAAGAAG	59.757	20
121	2267	2387	ACGCCTTTCCAAACTTTCAA	59.724	20
213	42	254	AATTTGTTCAAAATCCGCGA	60.436	20
261	518	778	AACTTTGGAATCGACATTGCT	60.007	22
220	1613	1832	GTCGAGCAACAGCAGGTGTA	60.056	20
106	4	109	GTTTACCCATAGCGCACTCG	60.658	20
144	626	769	TTCTCCTCACAATGCTTCCA	59.369	20
163	66	228	GAGATGGCTTTGTGATGGGT	59.934	20
198	697	894	TCCCAAGAATGAAGCCACTC	60.195	20
208	687	894	CCTTGTTGAATGCGAATGTG	60.111	20
275	675	949	TGATGCCCCGTTAAACATCT	60.331	20
145	1015	1159	GGATCCTGAGCCATCAATTC	59.445	20
137	502	638	CCGGTACATTCGGTAGATGG	60.206	20
267	635	901	TTGAGCATTGATACAGTGGAG	58.379	22
179	1566	1744	TCTCGATTCAACTCATCGGA	59.322	20
126	4974	5099	CTCATTTCGGAAGGAGCAAC	59.813	20
278	2351	2628	TGTTAATGAAATTTACGCACA	58.225	23
234	1621	1854	AGGTGTAACCGTGGATCAGG	59.844	20
209	102	310	GGGCTGTACTTCAGAGGCTG	60.012	20
191	1852	2042	ACGCTCAGTGAGGTTCAGGT	59.907	20
250	2842	3091	TGTTCCCACAAAAACAGGGT	60.246	20
142	123	264	CGATTTTAACCTCCCGTTGA	59.931	20
251	390	640	CGGGGAGTAGATGAATCGAA	60.029	20
225	298	522	GTGTGCGAATTTGGAAAAGG	60.481	20
275	427	701	GGGGGAAAGATTGCAAATTC	60.623	20
128	3913	4040	CATCTTCACCGGCTTCTCTC	59.95	20
247	1362	1608	ATAAAAATGGTGCTCGGTGG	59.823	20
190	2139	2328	GGAAGTTTCACCGGAAGATG	59.526	20
167	599	765	GTGGCTTGTGTTTCCTTGGT	60.012	20
100	3093	3192	CATTATGGACACATGACCCG	59.648	20
261	136	396	TTGATTCTCGCCATGTACAAA	59.172	21
203	555	757	CTGAGTAAGCCGGTGCATTT	60.27	20
175	48	222	GGCGTGCATGTTTTATCTGA	59.694	20
175	310	484	GCCAGATTTCATCTTCTGCC	59.78	20
239	446	684	GATTTTGGCAATTCAACGGT	59.807	20

245	4462	4706	ATTCAATCGGATGCAAGAGG	60.036	20
248	369	616	CGTCCCTTAGATTGGTGAGG	59.545	20
163	672	834	TGAGAGCGAGCAAGGGTTAT	59.978	20
263	607	869	TGATTAAAAACTGAACCGGAC	59.492	22
181	1361	1541	GGTGAAGGGAGCAATAAGCA	60.214	20
120	885	1004	CACCGCCTCGTATCTTCATT	60.096	20
158	608	765	GGGCTTGGTCAGAAAATTGA	60.051	20
213	2405	2617	GTCGTGTTCGTGTCGTCCTA	59.751	20
263	625	887	TGATTTTATCGTGATTCATGCC	59.801	22
179	3217	3395	GGATCCCGGTCATATACGTG	60.036	20
114	640	753	GTTCCTCCTCAGCTCCTCCT	59.952	20
279	1127	1405	TTGGATGCGTTGATTGAAAG	59.664	20
174	323	496	TTTCACCCAAATCACGAACA	59.941	20
278	1136	1413	AACCCTGATCACCAAACGAG	59.966	20
221	2692	2912	TTCGGTTGGTGAAGTTGTTG	59.585	20
259	612	870	ACACGGATCGGAAATCCATA	60.155	20
150	601	750	TCCAACGGAAATCCTTATACT	59.851	23
180	776	955	AACCCACTTCCACAGAATGC	59.973	20
124	630	753	TGCACATGCAAAGCTAAAGG	60.014	20
245	1203	1447	TTCAAGCGCCTCTCTGTCTT	60.277	20
216	301	516	GACCCAAAATCGCACAATCT	59.939	20
177	1056	1232	GCTGGGATATTTTGCCATGT	59.791	20
248	583	830	GAATGTGTTTTCCGGGTAGC	59.434	20
270	452	721	TGCCACTCACCTTAACCAAA	59.17	20
214	651	864	GTGTTGGTGCTTGATGGCTA	59.722	20
212	627	838	AGGTTGCCATTTGATGGAGA	60.461	20
275	221	495	CGAATCCAGGTAAGGCTTGA	60.206	20
108	656	763	GGCAGCAAGTTAAACAAGGC	59.889	20
156	4818	4973	TCTCTCTTTCCCCCTCCTTT	59.252	20
272	12	283	TCTCTCCCCACTTTCCTTCA	59.773	20
166	1147	1312	GCCATTGCACTTATGCTCCT	60.243	20
235	401	635	ATGGACTTGCTGAAACACCC	59.973	20
280	844	1123	CGTTTTCCACCTTCAAGACAT	59.087	21
241	192	432	TGCATGGCAGGTATGAGAAA	60.22	20
178	1459	1636	CATGGGATAGTCGGTGGAAT	59.629	20
185	2345	2529	GGAGGAACTCCATCTCCCTC	60.012	20
226	3138	3363	CGAATGCAGTTGCTTGAATG	60.401	20
123	104	226	ATGGAGATCCGTGCTTCACT	59.685	20
181	693	873	GGTGAAAGGCCATGTGAACT	59.973	20
186	1100	1285	TGTCCCTGGTTACACACCAA	59.848	20
176	1360	1535	TTTCGACCAATGAGAAAGGC	60.192	20
234	88	321	TGGTCTGCCTAATTTACTGCA	59.779	22
161	1546	1706	TCAGAGACTGTTCAAGGGCA	59.545	20
190	630	819	TTGTCTTGACGCTGACAACC	59.88	20
264	3985	4248	GCTTTGAGTTGTTCTTGGGC	59.859	20
117	1198	1314	TCTGTCACATCCAGACGAGG	59.82	20
228	923	1150	TTCCTGCTTTTCATCGCTCT	60.096	20
226	1670	1895	GCACAGAAGGCTTGGAGATT	59.434	20
255	2280	2534	TGGTGCTTTCGAGGTAATACG	60.138	21
212	4626	4837	TGGGACTACTGACCCTCACC	59.962	20
148	272	419	TTTTAAGTCGTGTTGCGTGC	59.918	20
219	1003	1221	GCAGACATAGCAGGGGAATC	59.658	20
261	255	515	AGGAAAATCCCAAACCGAAT	59.644	20
220	77	296	AGGCGTAACGGCTCAAATTA	59.742	20
205	1115	1319	GGGCTGTTGTAAAACCCTTG	59.471	20
204	9	212	AAAGCAATCAGTCAAAGGGG	59.17	20
240	657	896	AGAGAGCAAGCAACAATCCA	60.008	21
235	1406	1640	GCCATCGATTGTGCTGATCT	61.192	20

253	1169	1421	CTATATAGGTCCCCCGTCCC	59.51	20
269	1787	2055	CCTGCGTGGTTTTTCTTTTG	60.639	20
176	4995	5170	AGTCCTCCGCCTCTAGCTCT	59.745	20
279	482	760	GGTTGAGATTTTGGAGGAACA	59.017	21
268	2951	3218	ACCAGGAGTGGTGAGAGGAA	59.682	20
199	685	883	CCACTGGACCTCGATGGTAG	60.523	20
241	4375	4615	GTATGACAAGCAGCAGTGCC	59.476	20
266	7	272	CGGATTTAAGGGTTATTACCT	59.9	25
221	1453	1673	TTTGGCTTGAACAGCACTTG	60.027	20
172	627	798	TGGAGCCGAGAAGAGAAGAG	59.82	20
251	48	298	GCGGATTATAATGGGTCGAT	58.741	20
246	1398	1643	GAATGTGGGCGATCTTGACT	60.081	20
268	630	897	GCATATAAACCCGGAAACGA	59.795	20
196	670	865	TTTTACCACTTTCCATCCAAAA	58.518	22
216	1680	1895	AGCACAAATTTTCAATTCACG	59.932	23
252	2107	2358	ATGATGGTGTTGCATGCTTT	59.005	20
250	405	654	CCATTTAATTTCCAAAGGGTT	57.078	21
258	476	733	GCTTACGTGTTTCAGGGCTC	59.882	20
195	61	255	CCTTGCATATGATGGTTAGCA	58.664	21
233	1321	1553	GCGCAAGAGCTTTTTCTGAG	60.407	20
233	739	971	CACATTCTTTAAGCCATGGGA	59.946	21
189	705	893	ATCCACGTTAGAACCCCCTT	59.691	20
274	1154	1427	TCCGATCTCTGTTTCGATTTG	60.199	21
228	1396	1623	TGCAAATGGTACTAGGGACGA	60.508	21
172	90	261	ACGGTTTCCCGCCTAGTTAT	59.856	20
132	1906	2037	AAGGCCGGTATGTTCCTGTA	59.452	20
278	758	1035	TAAAGCCCATTTGAACCCAA	60.294	20
193	1177	1369	TAGCAACGCATCTTTGGAGA	59.566	20
130	638	767	CCTCAATTTCTGCAGCCTTC	59.955	20
232	1126	1357	TGGATGGGTTACTGGATCAAT	59.115	21
226	116	341	ATATTTTATGGGACGGGGGA	60.219	20
270	4672	4941	GTGCGTTTTCGTCCAGAAAT	60.118	20
243	1890	2132	TTCGATGAATGTGCTGCAA	59.931	19
274	1334	1607	TTAGAGGTGTCCAACAGGGG	59.959	20
228	1528	1755	CCACGCGCTCCTTAACTTAC	59.904	20
243	740	982	TTGATGGCATCGATGAGGTA	60.033	20
275	1419	1693	GCACGGCCAAGATAATAACG	60.476	20
237	1698	1934	CACCCACATTTCACACGAAG	60.001	20
203	616	818	TGTTGAATGTAGGTCGGGGT	60.232	20
182	1078	1259	ATTCATCACCACCTCACCCT	59.232	20
213	38	250	TTCGTCCTCTCCCTTTCCTT	60.183	20
184	286	469	TCACGATTTACCGCAGTCAT	59.152	20
241	3176	3416	TGTTCACGTCATGGTCGTTT	60.008	20
228	100	327	TTGGCAGAGTGGACTTCTCA	59.545	20
214	4492	4705	GCCTGGTCCAAATAGCACTT	59.198	20
278	373	650	GAGGCGCAATTGGCTATTTA	60.192	20
275	1176	1450	AGGAAGAAATTAAAAACCCC	60.051	22
166	92	257	GATTCTGGGATGGGAATGAA	59.685	20
277	629	905	AATCCTCAAAGCAATAACGC	57.014	20
278	697	974	TTGATGTTTCATAATTTGGGCA	60.185	22
194	663	856	TCAGGCTTACAGCCATCCTC	60.362	20
162	371	532	TCATCCATTCCCAGTTCTCC	59.862	20
231	1880	2110	CTCGCAGTAGGTAAAAGGCG	60.032	20
235	1717	1951	CACAAAAGGATGGGAATTGG	60.162	20
199	678	876	ACATTTTCAACGGCACGATT	60.374	20
125	2002	2126	CGCACAGATCGCTTCATAGA	60.119	20
259	2192	2450	CTGCACCCTGCAAAAGTACA	59.904	20
102	727	828	TCGATCATTTGACAAGTGGG	59.496	20

280	1705	1984	AGGTGGGATTGTTTGCTTTG	59.971	20
102	2	103	TGCTAATCTTCGATGTATCAAC	58.287	23
257	219	475	ACTGTCCAGCCTTGCATTGT	60.721	20
220	0	219	TGACAGATGCACTGATCCAA	58.728	20
262	1343	1604	TGCATGTGTGCATGTTTGTT	59.595	20
185	2047	2231	TGCATTTGAATCCTTGAAAAAC	59.101	22
207	1628	1834	AAACGTCAAATTCTGGTTTATC	57.752	23
273	1076	1348	CCGCAGCCTGAGTTGATTTA	61.292	20
160	1886	2045	TGTGATGGAACGAGGATTTG	59.496	20
191	3149	3339	TCACTTCTCCGAAGGCATCT	59.95	20
249	1278	1526	CGCATGAACCATGAAATCAG	60.073	20
229	876	1104	CTGCTGCAAATGCTTCTCAA	60.28	20
238	750	987	AATATGGGGTTTTGCCATCA	60.016	20
248	140	387	TTCTGCCCATTCTTCCACTC	60.195	20
163	510	672	AGCCCCAATTTGTAAGGACC	60.187	20
234	378	611	TGTTGGTCTCTATAGTGTTTTTA	59.05	27
228	1090	1317	ACACCGAAATCGGAGTTAGC	59.198	20
228	210	437	GCATAGGGAGATTTGCGGTA	60.06	20
151	54	204	AATTCGGTGTATTTAGCCCCTT	60.095	22
170	650	819	CAAAGACGAATTGGCTCCAC	60.636	20
280	4358	4637	TTTAAACCGGAACGTGAACC	59.839	20
236	892	1127	TTGGGGAAGAGGAGTGAGAA	59.773	20
182	5219	5400	GATTGGAAAAGGGTGGGTTT	60.032	20
280	276	555	CCCACAATCAACTTGCACAT	59.42	20
101	0	100	AGAGATCACTGATTATCTTTTC	57.297	27
200	2002	2201	TTTCAGCTGTAAGCAGGGCT	60.154	20
185	2089	2273	CCATATCCTCCGAAAAGCAG	59.662	20
230	1277	1506	TCGAATTGACATCTTCGTGC	59.805	20
260	1542	1801	TTGTGCCAAACCACTCTTGA	60.278	20
139	1976	2114	TTCTCATGCCCCTTCAAATC	60.014	20
186	60	245	ACATGGTGGTGGGTTCAGAT	60.096	20
278	618	895	TCGATTGAATTTTCGCCCTA	60.528	20
158	1857	2014	CAATGAGACCATGTTGGTGC	59.967	20
266	2098	2363	AACATTGGCTGGATTTCAGG	59.933	20
116	5083	5198	TGTGTCCGGTGGTCATCTTA	59.96	20
265	2106	2370	CCTTCCACCGCTACTCTCAC	59.867	20
209	753	961	TCCCCAGTCAATTTCACACA	59.935	20
243	416	658	CAGCGTTTTTGAGTCCATCA	59.84	20
212	708	919	CGGTGGTGGAAAAGATGACT	59.966	20
178	372	549	TGCATTGAAATTGACAGGGA	60.049	20
235	42	276	TTTCCTAGAAATGCTCTCTTTCT	60.033	25
266	255	520	CAGATCAGAAGCCACTCCCT	59.405	20
252	67	318	TGTACCTGCTTGATTTTGTTGG	60.032	22
130	767	896	CGACTTGCGCTAGAATCGTT	60.543	20
228	1848	2075	CCCATGATTTTCTTTCCTCG	59.5	20
272	320	591	ACTTGAAAATTCGACGAGCA	58.502	20
209	1811	2019	ATTCCTTGTCCACTGCTTGC	60.263	20
133	279	411	TCCACCGACGCTTTAATCTC	60.214	20
221	4885	5105	ACATCCTACGCATTAAACCCA	59.352	21
210	4060	4269	GCCCCTGGTTTTGGTCTATT	60.187	20
220	293	512	TACAGGCTTTGCATCTGCTG	60.157	20
208	11	218	AAGTTTTAATCGCTTCCGCA	59.853	20
204	1860	2063	ACCTGAGGGAGTTGATGTGG	59.962	20
277	1458	1734	TTGACAGCAAGCCAGATTGT	59.445	20
171	517	687	AAACCACAGCAATCGACCAT	60.384	20
260	753	1012	CCTGCAGATGACTGGCTACA	60.008	20
264	2750	3013	TCATTTCAAGCAAAATCGCA	60.334	20
207	761	967	TTGGCAATTTATGGTCACCT	57.944	20

232	760	991	AGCTCAGGCTTACATGGGTG	60.277	20
201	5506	5706	GGTTACCGCCTGTCTGCTAT	59.222	20
230	67	296	CTTATGGTGGTATGGTGTAGA	57.59	23
171	106	276	GCGGGTCAAGTTGAGGAATA	60.074	20
184	363	546	TTCCCAGAATTTGCCTTCAA	60.555	20
278	3081	3358	TGATTTTTGGAACCGTAGGC	59.938	20
194	1308	1501	TGGTGGTGAATAGGGGACAT	60.05	20
274	1153	1426	TGAGTTGGCTTTTTGGAGAAG	59.48	21
277	174	450	TGGAGTTCTTCCACCAAACC	59.943	20
214	700	913	CGAAACGAGAATAACCGGAA	60.067	20
213	1044	1256	GGTGGAAAACATGCACACAG	60.008	20
261	6834	7094	GGAACCACAACCCATCACAT	60.497	20
257	28	284	TAACGATGGACTAGGGGCTG	60.088	20
259	10352	10610	CGTTGTCTCCAACTCGGATT	60.111	20
274	143	416	CCAAGTCCCTTCGTTTTCAA	60.081	20
280	835	1114	TTGCTTTGGTCATACAAACATT	57.253	22
249	770	1018	TCAAGTTGTAGCCCTTTGGG	60.103	20
206	1654	1859	CACGAGCACACAATTCCAAG	60.301	20
225	124	348	AGAGTTAGGCGGAGGGTCAT	60.096	20
277	2885	3161	AAGGTCCACACTTCCAGCAT	59.579	20
246	560	805	GGGACGTGGTTAGCAGATGT	59.997	20
247	2209	2455	GGCCTTGGATGATATTTTGC	59.374	20
161	2786	2946	AGGCACAATGGAGCAGAAAG	60.397	20
193	581	773	GGTCGGGTTTTCAGCCTTAT	60.32	20
103	862	964	AGTCAGTGCTCACCGGATCT	59.866	20
189	1149	1337	TCCATTTATCGGAGTTACGGTT	59.737	22
211	1709	1919	CACTGTTTGCCACAGGAATG	60.152	20
246	100	345	ATCGGGAATTTAGTTTGGGC	60.15	20
218	3990	4207	AATAAGCCTCCACACCCCTC	60.328	20
161	39	199	ATCGATTGAACCAAACACCC	59.653	20
280	292	571	GCCATGTGGAGGTTGATTTT	59.797	20
273	443	715	AAGATTCGATTCCCGACTGA	59.629	20
274	8	281	TTTACTCCGCCACGGTTAAG	60.124	20
229	3484	3712	ACAGGTGAAATGTCCAAGCC	59.973	20
268	781	1048	GAAAATGTCGTGAATGCCAA	59.523	20
279	1042	1320	TGTGTTGATGCAAGTTTGGAC	59.606	21
254	2570	2823	TTGATTACGATTTACGCCGA	59.169	20
134	46	179	AAGCCTCCCAAGTCTCCAAT	60.074	20
171	2	172	AGCCCCGAAAAAGTAATGGT	59.835	20
212	2235	2446	TTACCCCTGCCATTAAACCA	60.181	20
261	105	365	ATTGGGGTGGAGAGAAGTGA	59.505	20
164	2334	2497	GGTGTTGGACTTGGGTCATC	60.223	20
173	8	180	TCAGTCTGCACAGCTGACAA	59.293	20
186	742	927	ACGATGGCTTTGCTGTTCTT	59.882	20
213	1635	1847	AAGGGCGTGCCTAATGGTAT	60.711	20
246	209	454	TGAAGCCCATGTTGAATCTG	59.648	20
232	1874	2105	TGTTTTGATGCCTCCTTGAA	59.247	20
159	34	192	GGGGTTATCATGGGATCAAG	59.055	20
270	44	313	GGCCAGGAGATGAGTCAGAA	60.349	20
154	100	253	CCAAGATCAATGGTTCCTAAG	59.879	23
254	47	300	ATGAGGGAGAGGGAGAATGG	60.412	20
217	4301	4517	AGATGAGCCGAGGAGCAATA	59.939	20
226	1627	1852	AGCAAGGTCCAATTCCGATA	59.528	20
221	432	652	GGCTGCAAACATTTGAGGAT	60.081	20
242	223	464	TCGTCGTTTCCAACATGAAG	59.691	20
170	859	1028	GTTCCGATACGTCTGAAGGC	59.7	20
266	30	295	GGTAGGAACTGCATGACCAAA	59.985	21
133	0	132	GGATAATCCAGAATCAACACA	60.082	24

135	2677	2811	TCTGGTTTATTCACGCAGGA	59.272	20
253	1744	1996	TTCAACATTCAGCCGATCAA	60.197	20
197	5382	5578	CTTTCTTCCACGCCTTTCAA	60.357	20
255	1761	2015	GGACAAAGCAGATAGGGGGT	60.328	20
171	857	1027	AGTGGGAAATGGTGAGCAAG	60.111	20
274	1267	1540	TCTGAATCCGACACGTTTGA	60.24	20
227	68	294	TTTTGAGTTGTGATGTTTGCATT	59.549	23
275	2369	2643	AGCTAGAGCCAAGGACATGAA	59.091	21
280	3478	3757	TTATGAGATCTCGCCATGACA	59.241	21
131	2367	2497	ATCGCCCCTCAAAACTTACC	60.32	20
255	897	1151	AGCTAAATATGAGTTTCCTCTT	58.944	25
258	621	878	AAAACGATGGTTTCTGGCAC	59.978	20
121	159	279	GCCATCTATCTTGTTCGTGACA	60.14	22
242	2211	2452	GCGTATTAATGCCCACATGA	59.405	20
278	761	1038	TCGAGGGGTTTAGTTGCATT	59.569	20
172	2751	2922	AGCTTTTTCCGATGATCCCT	60.039	20
174	8	181	TCCAGTCTTCTGCCAATCAA	59.369	20
254	538	791	CGGCAAGTTCGAATTCATTT	60.074	20
260	2500	2759	TTGCACTGAAGAGCCAAAAA	59.585	20
280	1537	1816	GGAATCGGCTTAATCGACCT	60.419	20
272	185	456	GGTCAGAATCACGGCAGTTT	60.119	20
277	1961	2237	GTTTGATGACGTGGTTCGTG	60.008	20
241	3041	3281	TGCCAACCTAACCTGGAAAA	60.472	20
278	1041	1318	GTTACCAGCAACCATGTGGA	59.42	20
236	2000	2235	CGGTTTCCTGTTTTCCTCTG	59.705	20
260	224	483	CTCCAGTGTCTTGCCAACAA	59.873	20
214	1688	1901	AGTCGTTCAGATACACCGGC	60.142	20
252	726	977	CGTTGGTAATGCAACCAAAA	59.462	20
272	369	640	GGATTGCAGACTCTTGGGAA	60.195	20
251	1331	1581	CCACTGCATCACAACCATTC	59.967	20
260	746	1005	CCAAGGTCGTACTAGCCAGC	59.898	20
224	720	943	ATGTGGGGTTGAGATCTTCG	59.927	20
173	840	1012	TGATGGCCCATGATTAAAGA	58.917	20
265	95	359	AGCTATTCCCCAAACCAACC	60.187	20
193	21	213	AAATATGTGCTCTCATTTGATT	58.709	27
274	1963	2236	TGGTGGTAATGGACTTGTGTG	59.324	21
117	579	695	TTCTGGGCTTCTGAGTCATGT	59.859	21
280	3182	3461	TGGCGAAGAACTTCAATGACT	59.867	21
252	1729	1980	TTACAATTACGAACGCGTGG	59.625	20
211	1767	1977	CATTCAGTTCATCATTTTCATG	59.329	23
226	208	433	TTGACCGTCCAACAATTCAA	59.941	20
279	541	819	TGAAACTGAAGCTTGCATGG	59.988	20
271	1341	1611	ACCACGACCAATTCTTACAGC	59.115	21
271	269	539	ATTCTCTCCAGCCCCTTCAT	60.037	20
234	340	573	AACCGGTTTATGGATGAGGA	59.244	20
271	241	511	TAATATCCAAAACGCGCACA	60.096	20
178	1364	1541	TCATCATGTGATGCAGACCA	59.61	20
210	2135	2344	TGCCTGTATGAAAAAGCATCA	59.315	21
170	382	551	TGAATGGAACACACACACCA	59.376	20
243	1978	2220	TTTGAGCCCATTTCACATTTT	59.442	21
206	806	1011	GTGGTGGAAGTTGTCACCCT	59.859	20
199	7	205	GGCATTCGAAAAGCTCATTTA	59.336	21
277	3774	4050	TCCTCTGGTTTCTGTTTGCC	60.232	20
193	8	200	GGCTAATTGTTGGCCTTTGA	60.074	20
154	2003	2156	GATTTAGGGAGCGTGGGTTT	60.32	20
274	366	639	TTGCAAAACAAAGCACGATT	59.349	20
182	508	689	GCCGTGAAGAGAATCTCCAG	59.95	20
134	372	505	AAACAAGTCATCCATGTCCCT	59.735	22

268	1100	1367	ATGCCTCATCATTTCTTGCC	60.043	20
230	1882	2111	TTACCTGCGTGTTTTACAACTG	57.971	22
226	254	479	CAACAAGCCCTAGGACTCCA	60.246	20
161	37	197	GGCCATTGGGCTTATCCTA	59.87	19
238	1043	1280	GTCGTCAGTAAACCCGAATGA	59.985	21
133	291	423	ACCATGCACGTCAATGTTTT	58.903	20
223	3	225	GCTTGAGTGTGGCACATTTAG	59.313	22
249	2623	2871	AGCCAAAACATCCATCAAGG	59.933	20
274	897	1170	TGTCCTGAGAGGCAGGAAAT	59.803	20
278	785	1062	GATGGAATCGTTTGTCCACTT	58.9	21
254	2934	3187	CTTTGCTGTTCGTGGTTCAA	59.881	20
241	946	1186	CCATAGAAAACGGCCAGAAA	60.067	20
235	2014	2248	GAAATTTTTAGCCATGGTCCC	59.672	21
276	785	1060	CTACAGCGGGTTCTTCTTCG	60.008	20
207	185	391	CACTGAATTTGCCTGAAAAAT	59.625	22
119	265	383	GACCACTAATCCAACCCCCT	60.052	20
278	783	1060	ATGGGATGAAATTGATGGGA	59.952	20
203	1774	1976	TCGCAAAAGTGATCTTCGTG	59.988	20
149	666	814	ATGCGTGGGCGATATTATGT	60.203	20
138	4172	4309	TCAACACCCATCAAGATGCT	59.09	20
268	118	385	ATCCCGTTCTACCTCAGCCT	60.096	20
230	909	1138	GACCCAAACGGAGCATCTAA	60.074	20
213	1088	1300	TGTCCAGAAGCAGTGAAGCA	60.745	20
251	4990	5240	TTTTCCACAGAAATGTTGGCT	59.601	21
224	4172	4395	GAGTGCTCGCTCTAACGCTT	59.927	20
135	1913	2047	TTAAATTGCAGGGCCTGTTT	59.586	20
265	2354	2618	CTGTCACGGTCAGCACTTGT	59.94	20
233	979	1211	ATCGGGGGAATAATAAGGGA	59.468	20
271	3176	3446	GTGGGTTTAGGGATTAGCTGC	59.979	21
222	2265	2486	GTTTTCGCACTGAAAAAGGG	59.724	20
278	2369	2646	CGAAGGGAACAACCTATCCA	59.926	20
141	982	1122	CAAACACCCATTCAAACCCT	59.688	20
254	907	1160	TCCTTGAATCAGCCACACAA	60.24	20
235	2211	2445	TGTGGATTCGTGTCGGATTA	59.924	20
236	1720	1955	GAACCTCCTCGTTAGCTCCC	60.212	20
102	1501	1602	CTCTGCTTCCCATATTTCGC	59.807	20
253	170	422	TTCTTTTATGGGCCATGAGG	59.894	20
165	2179	2343	GGGGTATTCTCCAAGCCCTA	60.278	20
252	870	1121	TTCGGTCAGATTATGTGGGG	60.713	20
231	1380	1610	TGCTTCATGAACCGACAAAA	60.234	20
187	1868	2054	GGAACTGAGCTTTGAGGGTG	59.844	20
211	1093	1303	TGACCACAGTGTGCTTTTCC	59.726	20
229	522	750	CACAGGAAAAGGAAACGGAA	60.081	20
170	258	427	GGAATCCAGTCTGCTGATCC	59.617	20
232	3812	4043	TGTCAAGTAACCATTCAGGGC	59.985	21
178	1217	1394	ACCACCTGCCCAACTATCTG	59.989	20
238	61	298	CAACAAGGTACTCGAAGAACA	59.337	23
274	1657	1930	GCCTGGTTCCAAATTTTCCT	60.299	20
251	131	381	TCTGCTTAACCCCTCATTGC	60.214	20
165	484	648	ACAATCGGAGTGCCATTTTC	59.939	20
273	1252	1524	CAACCAAGCCTTTGCAATCT	60.249	20
274	731	1004	CTCAGCCCTGAGTGGTTTTT	59.328	20
137	360	496	GAGAGGGGTGTTTGGTGCTA	60.111	20
213	577	789	TAGACAGTTGCACCCAGCC	59.846	19
108	8589	8696	TTGGCTTTAATCAGGGCATC	60.038	20
236	872	1107	AGTCGGGAGAAATCTCGTTG	59.284	20
127	430	556	GAGGAGTAGAAGTCGGCGTG	60.012	20
215	3239	3453	ATGACGCCATGGGTGTATCT	60.226	20

280	219	498	GCAAGAGAAATGCAGTGGAA	59.002	20
105	6	110	GAGGTGTTATGAAGGGATTAC	59.255	23
162	1837	1998	GAGGTAAATGTGGAAGCCCA	59.933	20
278	1881	2158	GCCATGATGCCTGTGAAGTA	59.679	20
207	397	603	AGGAATTTAGACGATTGATCC	59.463	22
179	1264	1442	TTCCACCAGATACGGAGACC	59.927	20
145	12	156	CGGATTTATTGGTTATTACCTG	58.742	25
220	519	738	CGACACATACGAATTGCCAC	59.995	20
128	3453	3580	CAGATACCCTGGTGGTCCAT	59.655	20
245	104	348	TGAAATTTGGCTTGCATTTG	59.679	20
235	915	1149	GCAATGTCAGTGTGAAATGTC	60.428	22
237	846	1082	ATGCAAAAATTGGTCCAACG	60.732	20
228	2488	2715	AAAGAAGGGGGATTGTTGCT	59.94	20
208	587	794	AGGTCTTTCGAACCCCCTTA	59.934	20
210	205	414	ATTTGGCCACCATTTACCAA	60.053	20
259	143	401	CGAGAAGGGAACATGGAAAA	60.044	20
213	742	954	TCCCTTTTTCTCAAGGGAGG	60.54	20
202	68	269	TTGGTGAAGGAGATTCCTCG	60.187	20
211	1174	1384	TGTTCATGGCTATCATTTGCT	58.254	21
276	938	1213	GCGGTGAACTCCACACATTA	59.572	20
177	129	305	CTTTCCTTGGGGACTGTGAA	60.081	20
149	1036	1184	CTAAACTCCGCCAACTGCTC	60.015	20
247	46	292	TGAAACCCTTTTTGGACCAC	59.807	20
241	715	955	AAAAGCCAAGAATACCACCG	59.087	20
207	2194	2400	GGGTATCACCAATCTGCAAAA	59.815	21
259	1500	1758	TATATCAGCATGCGTCGTGG	60.654	20
207	1057	1263	CTCTGTTGCTTGGTGCAAGA	60.175	20
203	13	215	ATTACGTCGATCCAACGGTC	59.82	20
228	1405	1632	CTCGGTCGTATCCAAGTGCT	60.277	20
198	1950	2147	CTTTTCCATTTCCGATCCAA	59.872	20
271	3055	3325	ATGCACGTAGGCATGTTCAA	60.142	20
268	2380	2647	AGATGTGCATTCAGAGGGTG	58.671	20
237	367	603	CATCGTTAATGTTGATTTTTATT	58.943	25
187	1903	2089	AGCCCTCCACGATAACATTG	59.955	20
231	638	868	CATTTCCACCAATTGCCATA	59.232	20
149	456	604	AGCAGCCATTTCGGACTAAG	59.476	20
238	1418	1655	TTTGGAAATAGGGTTGGTGG	59.657	20
252	16	267	CACGTATGGATAAGGCTAAAG	59.845	25
263	390	652	GTCGGGTTCGTATCATTTGG	60.192	20
250	2118	2367	TGTGCCTCCTCCTTTGTCTC	60.386	20
178	547	724	ATGCCAAAGCAAAGGCATAA	60.588	20
257	1039	1295	TCGATTCTTGTCATCCATGC	59.61	20
132	1123	1254	GCCTAGCCGGTCAGTTACAC	59.763	20
239	1477	1715	TTTCTGATGGGGTTGAGGAG	60.042	20
227	3734	3960	TTGTGGAGCGAAGAAATACG	58.917	20
218	538	755	TCAGAAACCACTCCCTCACC	60.088	20
270	1548	1817	GGGCAGCAACACCTTAAAAA	60.11	20
203	1828	2030	CACATTTCCATTTCCATTGGT	59.537	21
245	322	566	CACGCTTGCTAGACAACGAC	59.664	20
166	380	545	AGGATTTTAGCGATTTGGGG	60.272	20
254	3628	3881	TCTCCGGAAAATGGACTGTT	59.526	20
278	2627	2904	GATTTCTTGATGGCGGTAGG	59.528	20
264	1131	1394	GGGTACACCCAATTAACCCA	59.406	20
223	2376	2598	TTTGCTGAGCATGTCATGTG	59.409	20
220	5549	5768	CAAGCTGAGCAAAGAAGCCT	59.898	20
214	340	553	AGCTACAGAGCCGATCAAGC	59.746	20
232	4541	4772	ATCTCTGCGTCCATCCTGAG	60.372	20
277	141	417	TTAGTCCATCCAGGTCACCC	59.779	20

251	1971	2221	AAAGGCCTCGATAAATCCGT	59.93	20
237	1012	1248	TTCCGAAACAAACCCAACTC	59.948	20
276	1330	1605	ATCCCATTCAGGCTTGAGGT	60.853	20
137	9	145	TTTAATCGGGATCCGGGC	62.966	18
276	2198	2473	GAGCACTTGTAGGAGGAGGG	58.891	20
172	2929	3100	AGCCTCCTCAAATGCAGAAA	59.955	20
240	457	696	TGGTTGGTTGCTGTCACTGT	60.203	20
271	1460	1730	CATTGGTGTTCGGAATAGGG	60.184	20
154	40	193	TCCGACCGGTTTTTAAATCA	60.294	20
278	362	639	TCAACTAGTGCTGCGAATGC	60.165	20
245	3652	3896	AAACTTAGTGCCCCAGTCCC	60.361	20
280	646	925	AAGCAGCCTCACACAAGTCA	59.622	20
184	108	291	CCAACGCATCCATATCATCA	60.307	20
208	2349	2556	AGGAATCTGTTGCGTCGTCT	59.874	20
171	139	309	AAGTGCACTCGCTACGACCT	60.081	20
182	16	197	CACCACATTTAGTGGTTATCAT	59.605	25
204	2215	2418	CGAACGTAGGATTGGCAGAT	60.096	20
270	1041	1310	ATTGGTCTCTCAAGCACGGT	59.727	20
161	550	710	AATGAAACGGAATCCAGTCG	59.933	20
280	67	346	TCGCTTCGCTTTTTGCTATT	60.116	20
271	403	673	TGCACTTGCAAATTTAAGCTG	59.155	21
248	1183	1430	CAGAGAGAAAATCGGTGGGA	60.187	20
182	3	184	CGACTCCATGTTCCGACAC	60.105	19
168	2273	2440	TGTTGGAGACCCTTCTTTGC	60.232	20
257	21	277	CCAGACTTTTGGTCTCAATATA	59.335	25
250	1154	1403	GCAATTTGCGCTCTTGTTCT	60.531	20
243	755	997	AAGTACCAACCGGTTCCCTT	59.729	20
168	983	1150	TACTGCGTGATTACCAACGG	59.609	20
266	1833	2098	TTTTTGGCATCAGCAACAGA	60.379	20
106	5542	5647	ATATGATTCGCTGCAAACCC	59.929	20
227	2375	2601	GGATCTTCGAGGAGTGGTGA	60.199	20
180	1199	1378	GAAGAAAAATGGGGGCTCTC	60.017	20
179	1159	1337	TGTCGGAGTTTTGTGAGCTG	60.025	20
277	3576	3852	CACCATCTTCTTCACTGCCA	59.831	20
195	1756	1950	CCTTCAAGGCCTCAAACTCA	60.366	20
260	441	700	ATATGATGCTGGACAAGTCGG	59.97	21
151	2936	3086	TAGCTACCCAAGCCAATGCT	59.867	20
277	9341	9617	TCTTTGATTTGGCTGCTTTG	59.037	20
259	1353	1611	TGGATCTGGATCTGGGATTG	60.828	20
127	4109	4235	TGTTGGTGTGATGGTTTTGG	60.255	20
262	627	888	AAGCAACAAATGGCAGCTTT	59.889	20
219	3461	3679	GGAGAAAGCAAAGAGCGAAA	59.708	20
103	1734	1836	TTGCAGCAAATGGATCTGTC	59.805	20
139	2194	2332	GGATCCTGCAAAACCAAGAA	60.051	20
146	2633	2778	CCGGAAGGTTGAAAATGTTG	60.336	20
226	1127	1352	CGAAAACTAGATGCCGAACC	59.708	20
131	844	974	CGATGTTTCTCGTCTCACCA	59.831	20
199	2234	2432	TGCTTTGCCTAGGCCTATTAAG	59.904	22
277	289	565	AGGGGTGTAACATTCCATGC	59.676	20
268	2584	2851	TTTCTTGCTTCCAGTTTCCG	60.357	20
224	1222	1445	CGAAGCACACGATATTTCCA	59.688	20
168	2824	2991	TCTGCTTGTCAAAGTCGCAC	60.183	20
230	1278	1507	GCAAGAATACCAGCCCACAT	59.962	20
199	1355	1553	TGAAAGCCTGTTCAGCTCAG	59.314	20
254	2236	2489	ATTGCTGAATGTTGATGGCA	60.08	20
260	940	1199	TGTGCATGCTCATCTCTGTG	59.547	20
218	3969	4186	GACAAAACAAGGGCAAGCAT	60.118	20
168	73	240	CGTTAGAGGTTTTGACGGGA	60.103	20

213	3292	3504	TGGTGAATATAGAAGGGCGG	59.916	20
164	4116	4279	AAGCGCCAAATGTAAAATCG	60.095	20
234	73	306	CACACGCTGGAACTGCTTTA	60.05	20
108	1833	1940	ACTCCTCACAATTTCCCCCT	59.795	20
264	3302	3565	GGGGCATCGTCTCAATAGTT	59.009	20
139	2780	2918	ATAAAGTAGTAGGCCCGCCC	59.485	20
205	3636	3840	ACAAGAAACGGTGAGAACCC	59.04	20
226	1310	1535	CTGATGCAGATGCAGACAGT	57.466	20
194	5444	5637	CAGCAAGAACTGATGGAGCA	60.136	20
266	534	799	AAATGAAGTTGGGCAGTTCG	60.11	20
274	2215	2488	TCCCTATAAACACATTTCCCCT	59.962	23
268	3873	4140	TCGACGTTTAACAGCCGTAG	58.989	20
213	3409	3621	TCGTGTTCTCAGGATGTTGC	59.837	20
210	24	233	CGGTGTGTATGTGCAATGTG	59.457	20
270	2627	2896	GGTTCGAGTTTCGATGAGGA	60.195	20
277	2476	2752	TACCAAGGATAAAGCGCAGC	60.364	20
218	3167	3384	CCAAGAAATCAAGGATCGGA	60.006	20
223	4635	4857	CTTTGATGCCAAGGAACCTG	60.626	20
269	1256	1524	AACGTGCTATTGTGTCGTCG	59.788	20
209	1324	1532	GATGCATGACTTTTGGGGTT	59.797	20
258	713	970	TGTTTGTGGTTGAGTACGCC	59.615	20
194	3140	3333	GTTGAAACCCCGGTATCCTT	60.053	20
252	2107	2358	TGTTCTTCAAATGGGATGTCAA	60.344	22
221	1348	1568	CCCAAATCAATCAACTTTCCA	59.787	21
271	3888	4158	ACTTGAGCTGGACGGACATT	59.727	20
226	2534	2759	AGGCGTTGGAAAAATGATTG	59.938	20
238	523	760	GTTTTGCTTCCACTGCTTGA	59.05	20
165	1644	1808	GCATGTTCCCAAACCCTAAC	59.292	20
258	1375	1632	ATGGAGACTTATGGAGGGGG	60.147	20
276	2520	2795	CAAAAAGCGAGATATACGCGA	60.361	21
234	4974	5207	AACCTGTATTGGGACATCGC	59.82	20
193	3252	3444	TCCTCCAATCTTTCCACCTG	60.042	20
192	2037	2228	TGCTCTTATTCATGGTCCCC	59.894	20
207	1635	1841	TGAATTTGCATCTAAGGAGGA	58.467	22
197	2791	2987	ATCTCTGCCATTGTCTTGGC	60.226	20
274	397	670	GTGTGGATGTCCATCACTGC	59.97	20
217	3222	3438	AAATCTGCATGCACCTGTTC	58.726	20
226	777	1002	TGTTCAAACTTTTGTGGGCA	60.127	20
260	2926	3185	TCACCACAGAAGAGGGAGAA	58.349	20
276	20	295	GGGCCTCATCAAAACTTGTC	59.532	20
230	1185	1414	AGCAAACACCACAACACCAC	59.493	20
231	177	407	ATATATTGTGAGCCCTGGCG	59.945	20
206	69	274	GCTTCAAGAGGGAACTGGTG	59.844	20
240	801	1040	TCTTCAATTTGCCTGTGGAA	59.247	20
209	1162	1370	CAGAGTTTTCGCCTCTCAAGAT	60.019	22
100	103	202	AACACGCACTCTTTCACACG	59.946	20
230	701	930	TAATTGGGAACGGTGGTGTT	60.088	20
225	1772	1996	GAATAAACGGCGGTAATGGA	59.795	20
236	142	377	CGTCATCGTATTGGCTTCCT	60.096	20
163	2636	2798	TTTTGGACCTCCCTTCCTCT	60.045	20
251	4262	4512	TCTCCTCCGTGGACGTAGAT	59.679	20
271	18	288	GCTCTGATGCCAAACTGTTG	59.445	20
248	1296	1543	GTGGCAAATGAGGAGATGGT	59.934	20
262	2627	2888	GGCCACTTGATTCACAATGA	59.502	20
236	1285	1520	TGTCTGAGTTGTTCATTTCAGA	60.089	25
242	1377	1618	CAGTTTTTGAGTTATGATGCTTT	59.727	25
138	2	139	CTCTCTCTCTAACACACAAACA	59.707	27
251	740	990	GACTCGATTGGGACATCAGG	60.475	20

203	3902	4104	CATTTTGCTTTGCAGGAACA	59.849	20
181	2064	2244	GACTACCGATCGGGCTACAA	60.096	20
240	2584	2823	AAGCTGATGCCATATCCTCG	60.199	20
126	4089	4214	CAGGTCGCTGGATTCAAAGT	60.255	20
168	5815	5982	TCGATCCAAAAGGTCAACAA	59.097	20
179	6076	6254	TCTCCTTGAAGGGAGGATCA	59.731	20
200	38	237	GGGTTCCCGCGTAATAAAAA	60.999	20
228	561	788	GAGGAGTGGTTGAGAGGTGG	59.682	20
200	1092	1291	GTGGGTATGAGGGGAACACA	60.634	20
205	2224	2428	AATGATTCCTCCAAAGGCAA	59.505	20
232	1961	2192	TGACCAAATTAGCAGCCTCC	60.214	20
129	20	148	AAGGGGTTATCATGGGATCA	59.055	20
181	6950	7130	ACTTGCGTAGCATCATCCAA	59.301	20
260	2230	2489	ATCATCTCGTTCTGAACCGC	60.226	20
199	1930	2128	ATTGCCAACCCATAAGCAAA	60.323	20
198	1798	1995	TCGTCACGTGCGATTTTAAC	59.735	20
242	1233	1474	CCCAGTTCGTCGAGAAAGTC	59.844	20
176	479	654	AAATCAGACCATCTGGGAACT	57.567	21
256	785	1040	TGGGATCGAATAAATGGAGC	59.862	20
257	2734	2990	CTGCATTTGGTGGTACTGGA	59.566	20
237	967	1203	AAGAACGAAGATTCCAGCCA	59.813	20
202	712	913	GCAATAAAAAGACCTTGCATT	60.019	23
241	1206	1446	TCTCTTCCACAATCACGCTG	59.984	20
266	1741	2006	CCAGGAAGACTCATTCGATCC	60.974	21
278	8	285	TCACACCCACATCCATCAGT	59.801	20
149	1767	1915	ACCTATTGAAAGCCTCCCGT	59.962	20
277	596	872	TGACGGCTTTCTCAACACCT	60.833	20
266	2532	2797	GAGTTTGGATGCTTTGGAGC	59.82	20
197	330	526	GGGGCTGCTTTCTCTTCTCT	60.096	20
271	2972	3242	TACTGCAAATTCCGCCTCTT	59.845	20
242	5322	5563	TTGCACTTTACCATTGTATGGG	59.758	22
267	715	981	TATGCATCGCTCAGATTTCG	59.937	20
188	643	830	GGTACTGGTGGAACTGCCAT	59.851	20
250	9045	9294	AATGTTTCCTGCCACTCAAA	58.201	20
229	7846	8074	TCGAACCATACAAGCAGTGG	59.716	20
280	911	1190	GGAAACAAACTATCCCATTTG	59.722	22
219	408	626	TGTGGAAACCATCAGCTCAA	60.24	20
246	2563	2808	AAATAGGGACATCACGTGGC	59.82	20
161	2081	2241	CAAGAACCGAAAATCCCAAA	59.91	20
239	1403	1641	TGCTGACATTTGAGTGACAGT	59.946	22
222	260	481	GTTGAATCGATTGTACCGCC	60.339	20
197	641	837	TTGGCCACATGCTCAATTAC	59.548	20
204	7	210	TGAAGTTAGGAAATAAGGAGG	57.525	24
255	7392	7646	GATCCTTCCTCTCGTTATGGC	60.053	21
280	2078	2357	TCGCGTAAACAACACGATCTA	59.382	21
266	292	557	TTATCGGCTGTACTCTCTCGC	59.629	21
217	1979	2195	TCCTACAACTCCGGTTCCTG	60.103	20
255	2209	2463	AAGATTTTTGTCCAGTCGGG	59.028	20
176	231	406	CAGATCCCTTTCATCCCCTT	60.264	20
100	274	373	TGGGTGTCATGTTTATGGGA	59.623	20
211	4456	4666	GATTAAAGCACCTTTCGCGT	59.365	20
206	2264	2469	TCATAGGTTCGAGGCTCGTT	59.836	20
219	88	306	CTGGTCCATTCAAACCTGCT	60.111	20
145	4685	4829	CCGCATCTTCTAACGAGAGG	59.971	20
185	3260	3444	GTCGCCGTCTCTCACAAATA	58.877	20
255	1308	1562	CTCTCTCCCTCCCTCAATCC	60.149	20
154	5112	5265	CTCGAGGAAGTAATCGCAGG	59.971	20
126	38	163	TTTTCGAGTTATGAAGTTAGCA	58.926	24

276	230	505	CCCTCCCTTAAAATCGGAAA	60.245	20
278	154	431	GCCAAGTTCACTAACCTTTTTC	59.724	24
162	1026	1187	AACCAACATGCACAACCAAA	59.864	20
270	2900	3169	GGGTTCCTGCGTCATAAAAA	59.938	20
205	0	204	GGAGAGAGAGTGTTGGGTAG	59.009	23
276	2253	2528	AAGTCTGGGACTCAGCCAAA	59.844	20
135	20	154	CGCCGGTGCCTATCATATTT	62.045	20
219	6770	6988	AGGTGCAACCAGGATGAAAG	60.111	20
255	3140	3394	CAGCAAATACTCTGCACCGA	60.011	20
280	1156	1435	TATTCCGAGTTTCATTCGGG	59.894	20
227	2364	2590	TTGGAAATTGAAGCTGTTGC	58.895	20
223	34	256	CAGATGCTCGAACAAGTCCA	59.984	20
280	1697	1976	GTTTATGTAGCGAAACCGGC	59.614	20
245	1642	1886	GGCGACAGTGAAAGTTGACA	59.88	20
274	2238	2511	TCAGTCGAAACATCATGGGA	60.048	20
106	3701	3806	TTCAGGTGCGAATTCCTTTT	59.685	20
238	162	399	TTTTCCTAGAGAGGGAGGGG	59.64	20
256	2089	2344	TCACTGTTTATCCCCCTTGC	59.933	20
262	558	819	GGAGAAAGTTGATTTGTTGGG	60.332	22
204	1597	1800	TGTTTGTTGCCTTCTGATGC	59.847	20
240	854	1093	GGCCAACCCATTTGACTTTA	59.801	20
243	58	300	GGGTGGTATGGTGGAAGAAA	59.647	20
215	594	808	ATTTCTCCCGACATTCACCA	60.317	20
122	271	392	CCCTTTGAGAATAATGACATTC	59.724	23
131	289	419	TTCCCAGTGATGCACAAAAA	60.088	20
237	33	269	TTTCTGGCTCTGCCACTGTA	59.591	20
275	646	920	TTGAAATATGGCATGTGGGA	59.745	20
240	276	515	AAAGCCTTCAAAAACCATGC	59.205	20
246	618	863	GGTGTTGATTCCAGCAGCTT	60.263	20
275	196	470	CCCAAGACCCCAATTTGATT	60.91	20
247	55	301	TTTCGTTGCCAGGGTAAATG	60.856	20
249	184	432	TCCGTTACCCTCGACTTTGA	60.626	20
190	51	240	AGTTGCAGCAGCATTCCTCT	60.164	20
269	1819	2087	CTGATCAAAACTGCTTCGGA	58.999	20
239	460	698	ATCGGTGGATCTTGAACTGG	59.927	20
140	74	213	AGGATCGAGTAAGCGGAAATC	59.701	21
161	1333	1493	GTGTTCACCGGTCCACTTTC	60.408	20
256	785	1040	GCATCAAACGCACACAGAAC	60.319	20
257	4999	5255	ATGCAGGGTTCTGATGGTGT	60.395	20
154	627	780	GCTCATGTCAACGTTTTCTGG	60.684	21
269	1137	1405	TCTGATCCCATGTTTTCTGC	58.645	20
221	306	526	TCCCTATAACCGATACACCG	57.459	20
168	9	176	TGGGTTTGAATTGGGCTTTA	60.294	20
182	448	629	GGCTTTGGAAGTTATGGTCG	59.569	20
273	303	575	ATGCTATCGGGTGGAGATTG	59.917	20
227	69	295	ATCACCGGCAGCAGATTAAG	60.235	20
182	78	259	TAAAGTGGCGGAGCTAGGG	60.35	19
175	3499	3673	TGGAAAGGCGTAATTCTTGC	60.209	20
146	84	229	CCACAGCATTGACATTAGGGT	59.867	21
115	1511	1625	ACTGAAATCCCATTCGCATC	59.9	20
242	8	249	ATGTAGCCGACCCCAATTTA	59.297	20
251	478	728	CGTTTTATCTGCGGATTTCA	58.769	20
261	2353	2613	AGTTCGAAACCTGGACCATC	58.992	20
170	4	173	CCCAAGACCCCAATTTGATT	60.91	20
203	1495	1697	TGGACCCATGGATGTACTCA	59.762	20
195	22	216	TCAATATCTTACAATATCACA	58.479	26
263	156	418	TGTTCGGACTGAACTGGTGA	60.285	20
102	91	192	CGAGGCTGAATTTATGGCAC	60.606	20

165	4317	4481	CCTCATCAACCTCAGCAACA	59.831	20
126	59	184	GGATGATGGATTCGAGTGGA	60.839	20
187	1851	2037	AATCGCCTTCGATTGTTTTG	60.074	20
217	17	233	GAAGCTTCTCACGATTCTTGGT	59.892	22
112	161	272	CCAATATTTTTGGTCTCACGG	59.325	21
119	1547	1665	TTGTTCGAGTGTTGTCCCAC	59.571	20
159	407	565	AGCAATGCGAGGATGAAGAT	59.803	20
196	12	207	CTACCTCGCCTCGCTATTTG	59.996	20
254	1080	1333	TTTATTAGAATGCCGGGGAA	59.389	20
267	78	344	GAAAAAGATGGTAAAAACCTT	59.776	24
160	7	166	CAGCCAAACATTGAGCAGTT	58.926	20
157	872	1028	CCTCATTGCTCTGCCATGTA	59.823	20
251	268	518	CAGAGCGCACTCGAATAACA	60.157	20
262	192	453	TTCGAACCTTCTGCAAAATATA	58.036	23
271	30	300	AAGAACATTTATGGCAAACAA	58.601	23
173	462	634	TTCTACCACTGCCGGAAAAC	60.11	20
176	5789	5964	GCCTTTTTGAAGAGAGGCAA	59.569	20
242	1547	1788	CCTCGTTTCTAGCCCACAAC	59.734	20
277	191	467	AAATAATCAGGCTTCGTGCG	60.23	20
257	10	266	CCTGAAACGAGTGATGCTCC	60.801	20
204	1876	2079	CCGAACCGGAAAAGTCACTA	60.103	20
212	695	906	GGAGCAACTCCAAAAGCAGT	59.478	20
104	1341	1444	TTGGCTATCGGTTACTTGGG	59.953	20
265	12031	12295	CCTTCTTGCAACCAACGTACA	61.092	21
262	2360	2621	ATCGAACCGTGAACACCCTA	60.375	20
280	121	400	AGGGGGAGAGTTCTCTTGGA	60.186	20
269	21	289	ACAAAAATCCAACAAACCCG	59.702	20
228	641	868	TTTGATGTGACCGTATTGCTTC	60.003	22
273	1353	1625	CTATTCATCTGGCCGACCC	60.432	19
263	500	762	TGTACTGTGTTGGCTTCATGTT	59.593	23
220	14	233	TGGTTTTAATTGTGGGCTCTC	59.077	21
252	30	281	GTTTTTCACGGTTGGAAAGG	59.448	20
197	5	201	CAATCACCAATCAACACTTGA	58.528	22
268	397	664	TGAAAACCAAGGTGATGTCAA	59.01	21
172	14	185	CCAATTTATTGGGATTAAGGC	57.539	21
238	414	651	CAGCAAAACAACTTCATGTAC	60.214	23
279	684	962	CAGGCACTCCAAAATCAGGT	60.111	20
140	13	152	CGCCGTTAGCAAAGGAATTA	60.218	20
189	8	196	TTTGGTTCATGTAGCCGACC	60.894	20
166	3	168	TACAAATCAAGCACGCAAGC	60.021	20
260	57	316	TGAATTGGGTTTGACAATCG	59.371	20
243	90	332	GTGGATCAGCAGTGGCTTTT	60.263	20
253	1138	1390	TAGCTTGGCCCTCGATAGTC	59.434	20
250	708	957	TCTCCAACTCCTGCACCTTT	59.844	20
206	753	958	CACAAGTTATCACACCCCCA	59.262	20
277	298	574	TTTACGTTGTACGAATCCTATC	57.585	25
273	10	282	ACATCGCATACGTGTATGTTTA	57.646	24
221	965	1185	TGTCAACGACGAGATGGAAA	60.24	20
129	2029	2157	ACGTGGGACCTTTCAGTCAC	60.009	20
226	185	410	AATGCTGGAAATTCGATTGG	59.901	20
204	2002	2205	CCACAATTGGCACTAGCCTT	60.132	20
188	149	336	TCGGGTCAACCTTTGAACAC	60.934	20
100	17	116	TGTGGGTTTATGTGATGCCA	60.79	20
168	95	262	TTAAAAATCGGACCGGAGAC	59.019	20
231	166	396	TCGTGCAATAAAACTCGTGC	59.879	20
191	364	554	ATGTTGAGTCCGAGTCCCAG	60.112	20
186	84	269	TGAAGGACCCGTCATACAACT	59.463	21
215	552	766	CATGGGGCGCTTTAAAAATA	59.927	20

178	51	228	TACGGCCGGGTAAATTACAT	59.212	20
166	2901	3066	CGCAACAAACATTCGATTTG	60.111	20
211	275	485	AGGTGCGCTACAGTTGGAAT	59.763	20
151	35	185	ATTCATGTAGCCGATCCCAA	60.296	20
129	638	766	TGGCAACTCAAAAATGCTCA	60.379	20
242	34	275	AATACCGATACCCACTCCCC	59.903	20
241	1456	1696	CCACCAGCAGAACAAGAACA	59.873	20
222	568	789	GCGACGGGTACATTCCTCTA	60.096	20
121	253	373	CCCAGTTTTGGTCGTACTGG	60.401	20
273	301	573	ACCGTCCACGTCAGTATTCC	59.851	20
264	446	709	CTTGCTTCCTCGCTTGTCTC	60.277	20
257	179	435	CCTTGTTGAAAGAGCCTCCA	60.366	20
262	389	650	CGCACACTTCTGTCCCGTAT	61.116	20
204	1754	1957	TGTGCTTAGCTGTTGGGATG	59.864	20
244	202	445	ACCCTACATAGCGGGGAAAG	60.332	20
102	219	320	GAGGGGGAAAAGAGAGGATG	60.008	20
276	486	761	AGATGGGCGTCCACTTGTAG	60.134	20
164	240	403	TCGACCCAAATAGAAGACCG	60.066	20
125	414	538	CAAGACCCCAAATGATTGGT	59.647	20
148	1475	1622	TGCATCCCAGCCTCTTATCT	59.797	20
277	235	511	CCCCATCTTCCACAAGGTTA	59.784	20
200	567	766	TGGAGGAATAAAGGCTGGTG	60.066	20
274	2	275	CTTCTGGATGCGGTGAGTTT	60.255	20
183	25	207	TTTAACATCCAAGTTATTCACG	59.782	24
107	73	179	TCGATTTTGGGCCTACTGAT	59.528	20
248	1540	1787	ATACATTGCTTGGGAATCCG	59.784	20
131	251	381	ATCAAACACGCCAATCATCA	59.931	20
160	156	315	ACGCAACCATTTCATTGTGA	59.972	20
115	373	487	AATGCGTAACCCTTGTTTGC	60.003	20
173	2014	2186	GAGGTAGAAAGAGTGGCCGA	59.43	20
258	6	263	TTTGTGTCGATCAACTTGTGTG	59.658	22
242	90	331	TGGACGTCAACATGAACGAT	59.967	20
177	1239	1415	CGAAATGGAGATCCAAATCCT	60.272	21
192	317	508	GCCAATCTCCTCTCATCAGC	59.917	20
223	86	308	CCGGATATCCAGTTTCATCC	59.2	20
162	819	980	TGTTCTTCTTCAACCCCACA	59.109	20
201	534	734	CGCCGAAGTCATTAGGTCTC	59.836	20
266	36	301	TGATCCATGGGATGATGATG	60.096	20
193	1252	1444	TGGTGGAATTGCGGTATTTT	60.188	20
231	1609	1839	TAAGGTTGGCTGTAATGCCC	59.96	20
265	71	335	CCCAAAACCCCAATTTGATT	60.754	20
205	60	264	CCACCACTTATTCTTTTGATTT	61.027	24
168	32	199	TTTCGAATGTTGCTGCTCAA	60.523	20
232	963	1194	AAAGAAGAGGGAAAAGCCCA	60.18	20
195	4	198	CCCAAGACCCCAATTTGATT	60.91	20
250	59	308	TTTCATGGGTACACATTTGAG	59.867	22
271	86	356	GGGAAGGGGACAACATTTCT	60.169	20
254	290	543	CTTTGGCCGGATCTCTTTCT	60.703	20
217	71	287	TGATCACACACGAGTCCATTT	58.999	21
144	400	543	CGTTGGTGAAGAACAACTTTG	60.182	22
250	583	832	CCAAAGGGAATCAAATCTGG	59.359	20
186	382	567	CACGTGGCATGTTGATTTCT	59.572	20
223	3	225	TTTGGTTCATTTAGCCGACC	59.938	20
255	205	459	AGAAAGCCCACCTTTTTGCT	60.242	20
196	0	195	AGGAGGATGACGACGATGAT	59.491	20
255	67	321	CCACCAATGACAGCAATCAG	60.112	20
278	28	305	CCACCATCGTCGTCTCATC	60.063	19
154	246	399	TGGATTTCCACTCCACGTTT	60.353	20

162	44	205	TCTACTTAGAGCAGGGCCGA	60.11	20
223	424	646	TAACCTTGGCTGGCTCCTAA	59.839	20
222	2748	2969	GATGGTGAAAAGAGGCGAAG	59.813	20
268	652	919	AAAACCTTGGTGAACAGGCT	58.695	20
241	0	240	TGTAGCCGACCCCAATTTAT	59.297	20
238	845	1082	GCTTTGGAAGAGGTGTGGAG	59.844	20
226	514	739	CCGTCAAGCTCTATGCTTCC	59.978	20
274	4319	4592	CAAACCTAAGACCGGGATGA	59.926	20
188	7	194	TTGGCTCGAATTACAAAAACC	59.111	21
278	698	975	TGCACTGCTTATCAGATTCAAC	59.057	23
245	293	537	AAAGTTGAAATGCTTGCATGG	60.124	21
109	396	504	TGCCTCAGACTCTTCCACCT	59.986	20
203	259	461	GCTCCTCCACCTCTGTTCTG	59.986	20
262	1735	1996	GTTGTGTGCCATCATCAAGC	60.128	20
209	10	218	GAGCAAGAAGAAAGGACGA	59.55	20
147	141	287	TTCTCATCTCCAGTCTCCATGA	59.803	22
193	3484	3676	CCATGGAAGAACAGGGAGTT	58.989	20
200	455	654	GATTCTGGTCGCTCCACAGT	60.269	20
244	154	397	CACCCCTATTCTTTTTGCCC	60.664	20
204	155	358	GAAGATTTTTGCCACCCAAC	59.41	20
242	54	295	TTCCATGACCCTCGACTTTG	61.034	20
250	705	954	TTGCTGTCTCTGGCTCTTTC	58.315	20
184	12	195	TTGCCCACTCCACCACTT	60.088	18
199	959	1157	AATGCAGGTTGGAAAAGGTG	59.971	20
279	2429	2707	CCCTTTTCCAACTCACAACA	58.594	20
104	14	117	TCACATGTTGTCAAATAGATTC	57.753	25
162	869	1030	CAATCGGTCATGAGTTCGAG	59.241	20
197	1811	2007	ATGCCCCAACTATTGGTGTT	59.174	20
179	0	178	TGTAGCCGACCCCAATTTAT	59.297	20
274	330	603	CTCGGATTCTATTAGTGATTCA	58.084	25
108	318	425	TCAAAATCATCACTCTCCACTC	59.726	23
259	1916	2174	TGGCTCATTACACAAAAACG	57.291	20
255	1521	1775	CCTTGCAGAAAAAGGCTTAGG	60.362	21
272	186	457	TGGCAAGATTTGTTTTGACAG	58.808	21
169	23	191	ATTCAAGGCCAACAATCCAG	59.933	20
272	1230	1501	TCACACATGGAGAACGAAGC	59.837	20
203	53	255	TTGTGATGGAGTAGAGGGGC	60.073	20
106	2216	2321	TTTTAGCCTCAGGCCTGTTT	58.973	20
210	0	209	ATGTAGCCGACCCCAATTT	59.259	19
240	158	397	TGGTTTTCCGATGTTCGATT	60.309	20
254	288	541	CGTACATCCCCAAAGTCCTG	60.366	20
187	2794	2980	TCAGCAGCAACTGATCCAAC	59.992	20
189	57	245	AACAAGGTAAAGTCTGGCCG	59.238	20
183	6	188	CCCAAGACCCCAATTTGATT	60.91	20
230	2917	3146	GACCCCAATTTGATTGGAAAT	59.881	21
268	768	1035	TGTATGATTTGCTCGCAACG	60.807	20
278	66	343	AACGGCTGGCATTTGTTAGA	60.637	20
141	390	530	CATATGCAAACATGCGAAGC	60.245	20
239	1484	1722	ACGGGGCATAAAATTGATTG	59.66	20
179	2266	2444	GATGCATGAAACTTTGTAAAAC	60.27	24
215	155	369	GATACCACGTCAAGCAACCC	60.384	20
221	304	524	AGGATAAAAGAGGCAGGGGA	60.032	20
266	746	1011	TGTAGCACGAGTGATGAGGC	60.016	20
182	104	285	GCTTTGATGAGCCATAACCC	59.533	20
208	13	220	CACTTTGACGCTGCTTGAAT	59.076	20
213	115	327	CGGAGGTGATCTCAAATGGT	59.927	20
101	59	159	CAAACCATGAATAAGCAATCC	59.832	22
157	22	178	TTTGCTTACGGAAACAGCAA	59.486	20

251	325	575	TTCCCCCTCCTCTCATCTTT	60.008	20
183	1482	1664	CAGTTTCGGTTTTGGTGGAC	60.388	20
131	1701	1831	CTGCTGGTGATGCTCAAAGA	60.136	20
263	107	369	CCCAATTTTCCGCATTTTT	59.759	19
260	32	291	ATGTCCTTGAAGATGCTGGC	60.226	20
257	14	270	ACTCACTGCGGTGGAAAATC	60.119	20
204	1473	1676	CATCTCGGGATTCAGTGGTT	59.927	20
269	63	331	TATTCTCGCTTCTTCGCCAC	60.49	20
128	73	200	ACGTCGCGACTCCTCTCTAA	60.156	20
275	2107	2381	AAAGGACGGTCTCGGTATCC	60.328	20
221	929	1149	TGATGGCATGTGTTCTGTTG	59.085	20
160	17	176	TGGGCAGCCAAATATTGAGT	60.469	20
226	725	950	TCGACTTTGTTTGGTTCGGT	60.529	20
102	2942	3043	CGAGGATCCTTCACAACCAT	59.927	20
250	8745	8994	TTTGTCTTTCCCTTTGATGCT	58.823	21
112	0	111	ATGTAGCCGACCCCAATTTAT	59.585	21
182	1650	1831	TTTCGGAGTCACAGAAGGCT	59.989	20
153	421	573	GTTGTGCATGGGTTCAAAAA	59.42	20
111	360	470	TCCATATAGCCGACCTCACA	59.101	20
150	489	638	TCTGCAACCCTAATGGGTGT	60.375	20
110	8	117	GCATTCGTATAAAGAAAATCG	60.449	23
266	153	418	ATCTCGTCGGGTATGAGTGC	60.104	20
148	227	374	TGTGATGTAGAGAAATGAAGG	59.317	25
175	309	483	ATAGACGAATGGGCGAGATG	60.059	20
198	0	197	ATTCGAAGGTGTTGATCCCA	60.317	20
218	783	1000	GCACAAAATGTTGCTGCTCA	61	20
222	43	264	ATTTCCGAAACCAAACACCA	60.206	20
269	16	284	GGTGAGTTTGAAGCATTGCAT	60.138	22
106	2543	2648	GGCCCAAAGATCTCAAACAA	60.051	20
242	1160	1401	ATTGTCTGCAAACCCGAAAG	60.11	20
201	271	471	TTCCTATCTATTCCGCGTGC	60.196	20
201	523	723	TCAAATATACGAAAAACGGTG	59.792	24
107	10	116	TGGAAATCCAATTAATACAGT	60.572	25
234	123	356	AAGGAGCATCCTTGGTTGAA	59.67	20
103	4	106	ACCCTTGAGCTTGCATCTGT	59.874	20
176	32	207	GTTGGCTTCGGTGCAGTC	60.412	18
188	437	624	TGGAACCATTGCAGTCAAGA	60.24	20
223	11	233	TGTAGCCGACCCCAATTTAT	59.297	20
224	406	629	TGTGTACGTAGTTGAGCATGT	58.837	23
278	541	818	AATGTCACGAGTTGCAGCAG	60.056	20
210	1272	1481	GGTGCAGGCTAAAAATGTTG	58.294	20
202	5	206	TGTAGCCGACCCCAATTTAT	59.297	20
260	293	552	TCGATGGTTGATCTTGATTGTT	59.434	22
149	470	618	GATTAGCAAATTTCGGGACG	59.547	20
173	32	204	TGATGGATCGAATATTCTCAC	59.923	22
191	1941	2131	ACACGATAGCCATAGCCGAC	60.125	20
232	5608	5839	ACTCTCATGCTCCTCCTCCA	59.945	20
270	300	569	GAAGTGGTGGCAGTCCATTC	60.52	20
147	101	247	AGCAGCCCCTCTTTTGAAAT	60.208	20
163	338	500	GAATCTGATTTAAACATGGTG	59.735	23
245	20	264	TTCTTGTGAGACTGTTGTTCTG	59.429	23
186	4	189	CCCAAGACCCCAATTTGATT	60.91	20
270	4	273	CCCAAGACCCCAATTTGAT	59.59	19
280	4	283	CCCAAGACCCCAATTTGATT	60.91	20
115	471	585	GATGGATGAAAACCCACACC	60.034	20
178	2	179	CCCAAGACCCCAATTTGATT	60.91	20
119	230	348	ATGTAGCCGACCCCAATTTA	59.297	20
100	23	122	ATGATCGGATTTTGTTGGAGA	60.194	22

135	3072	3206	TGAATTAAACTGGCACCCATC	59.815	21
269	1036	1304	GAGGCTCAATGGGGAGATTA	59.08	20
178	37	214	TGCATAGAGGAAATTGCATAG	59.371	22
187	703	889	CCTATAATTGAAGCCGCCAA	60.054	20
163	3405	3567	GGTGGAGGAGATCGAGAGTG	59.792	20
156	31	186	TTGCAAAAGTGATGTGACCG	60.699	20
189	19	207	GGGCAGCCAAATATAGAGCA	60.196	20
229	7	235	CCCAAGACCCCAATTTGATT	60.91	20
251	1527	1777	CTCAACTTTCCAACTGATGGC	59.726	21
217	27	243	AGCTGTGTCTCCAAACTCCC	59.305	20
220	1607	1826	AGCTGAAGGAGAGGAGGAGG	60.088	20
247	3	249	CAACGGTTTACAAGTGTTGTT	58.187	22
279	26	304	GCTTAAAGGTGGAGGATAGT	59.155	22
112	264	375	CGTTTTTGTCAATGCGTCTG	60.293	20
154	7	160	CCCAAGACCCCAATTTGATT	60.91	20
239	73	311	TGTCTTGGATGGATCACCTG	59.473	20
170	3	172	TGGGGTCTACAACAAACTGAA	58.119	21
246	35	280	TCAACATATCATAAAGATAAA	57.289	27
176	33	208	CGAGCTGCATCGAGCTTT	60.399	18
168	7	174	CCCAAGACCCCAATTTGATT	60.91	20
110	7	116	CCATCAAAAAGCATGCAAAG	59.301	20
111	6	116	AATTAAGTTCTACGAATTCATT	58.046	27
142	1936	2077	GCGGTGATTTCCTGAGTGTT	60.119	20
101	313	413	TTTGGCTCCAGCGACTTATT	59.845	20
198	69	266	TGCAACACAATCATTATGGCT	59.055	21
265	303	567	TTGATGAGCCATAACCCTCC	59.894	20
227	161	387	TCCCAAAAAGGCAGAAACAG	60.22	20
179	772	950	ACGAAATTTGGAAGTGCCTG	60.11	20
208	1409	1616	TGATTTTGGATTTTAGGCGG	59.901	20
226	24	249	AATGAATAAGTTTGCATTTAA	58	26
268	358	625	GCTCGTGTCCAAATCAAACA	59.697	20
126	5633	5758	GCAATGAACACTTAGCAGCG	59.638	20
104	20	123	GTCAGGTTTGACTTTCATTCTC	60.158	23
278	502	779	GACCGAAATTAACGTGGAGG	59.429	20
257	2	258	TCACAAACCGCTGTTGTTTC	59.74	20
109	16	124	CAAAATAGCCCGAGGTTGAA	60.067	20
204	168	371	TGTGTTGTTTGATGTCTTTGTG	59.133	23
270	6	275	TTTCTTTTTCCTCAACAATTTC	59.647	23
168	913	1080	CAGGTGAGGGTTCTTGAGGA	60.229	20
255	467	721	GTTTTCTTGCCCTTTCCCTT	59.571	20
111	6	116	AATATGCGGGAAGAAAGCGT	60.949	20
275	1498	1772	TCATGGCTGAGAGGAAAAGG	60.331	20
229	951	1179	TGAGATGGAACTTGACGGTG	59.676	20
252	278	529	AAGTTGTCGACGTGGAGGAG	60.298	20
141	1051	1191	CCTATGAAAAATCCAGCCCA	59.894	20
222	1624	1845	GATCGTACACGATGGCGAC	60.096	19
274	4	277	GTTTTGTGTGTGTTTGCAACG	60.103	21
273	695	967	CTGGACTTGGCGAGATCATT	60.218	20
264	3193	3456	CGATTGTGGTGACGAAGATG	60.112	20
223	353	575	TCGTTGTGAATTTGGGGAAG	60.863	20
250	18	267	CGGTGCGGAGCTATTATCAC	60.626	20
103	18	120	TTGGCATAACAAGCTAGGACA	58.789	22
123	0	122	ATGTAGCCGACCCCAATTTA	59.297	20
149	2053	2201	CGGTGGTTTAATGGAGTTGC	60.365	20
179	707	885	TTCGATCGAGTTCGGTTCTT	59.813	20
266	2144	2409	AACGAACGAAGCTGAGCAAT	60.022	20
191	4	194	CCCAAGACCCCAATTTGATT	60.91	20
279	5	283	ATGTAGCCGACCCCAATTTA	59.297	20

159	717	875	ATGCAAAATTCGGCAGATTC	60.045	20
244	34	277	AAATTTACTCGCTGGTCTATCT	57.335	25
133	2	134	ACCTGAGGTTCAGGGTCCAT	60.77	20
243	292	534	GATGAGATTCCCGAGGTTGA	60.011	20
101	22	122	GAAATGCAAAGACCAAGAACA	57.864	21
217	518	734	TGTCAACCATAATATATGCATC	60.127	25
211	6	216	CCCAAGACCCCAATTTGATT	60.91	20
253	771	1023	TACATCTGACGCCCCAAGAC	61.067	20
221	29	249	GCGAACACAGTTTTTCAGCC	60.817	20
264	25	288	CTCTTGAAATTTTCTTATTGTTC	58.722	25
241	1527	1767	TTGTGTCAGACTTGTTCGGC	59.88	20
202	651	852	CCCCCAAACTTATTGACAAA	57.462	20
279	445	723	TCAGCGAATTGTTGCAGAAG	60.134	20
277	4966	5242	TTGCATTTTTCATAGCCCAA	59.146	20
255	726	980	CCTCCTCAACCAGAGTCTCC	58.819	20
275	1790	2064	GTATTCCACCACGCTCCTTAT	58.085	21
137	7	143	CCCAAGACCCCAATTTGATT	60.91	20
166	752	917	AGTGAATAGCTGCTGGTGGG	60.277	20
246	710	955	CAACTGCCGATCAAACTGTG	60.301	20
216	6	221	GATGGATGGATCAGAACCGA	60.839	20
212	2642	2853	CAATTCGTGTCATGGTCGAG	60.112	20
260	110	369	CTTGCGGTCTTGAACATGAA	59.84	20
233	494	726	GGCAGATTCCCTTGATTTTG	59.505	20
184	13	196	CAGAATGATTGAAGCAAACAT	60.124	23
254	467	720	TGGGACGATAAGGGATAGTGT	58.398	21
225	29	253	ATGAGATTTTTGGTGTCAGTG	58.958	22
240	127	366	ACCCGGTTTGATCTGTGAAC	59.827	20
260	42	301	CCGGTTAATGACCCATTTGT	59.546	20
218	1409	1626	AATTGGAATTCAACATCAATG	58.671	22
274	2146	2419	TCGAGATGTGAAGATTGAGGC	60.355	21
256	17	272	CGGCTACTTTCTCCCTTCCT	59.842	20
197	985	1181	TACGCAAAGGCACTTCTCAA	59.609	20
138	18	155	GAAGTACCTGCCTACTCGTCT	59.957	23
138	205	342	GAGGGAGGCACTAAGAAATG	60.082	21
184	135	318	CCACCAACGTCTCTTGGTCT	60.151	20
128	1836	1963	CGCAATTCATCACAACTGCT	59.871	20
208	2658	2865	CCCAGAAGCAGAAGAGGTTG	59.982	20
113	368	480	CGAGATTGGGAAATTGGAGA	60.006	20
256	7	262	ATGTAGCCGACCCCAATTTA	59.297	20
107	174	280	CAGCCGAGAACATCATCAAA	59.799	20
261	88	348	GGTGGATTAGTTGTCGTTTTGA	60.263	23
118	2	119	TGTATATTCCTGAAGACGATG	60.346	23
280	869	1148	GCATGCATAATGTGACACCC	59.812	20
195	38	232	TGATGATTGAGTAAAAACGAC	57.385	23
223	3810	4032	GCACACTTGATGTGACGGTT	59.603	20
224	9	232	CCGTATCAAGCCACCAAGTA	58.649	20
207	231	437	ATCTTGACGTCGAGGAAGGA	59.803	20
151	9	159	CAAGACCCCAATTTGATTGA	58.395	20
271	628	898	TCTTTGCGATGAGCTCCTTT	60.096	20
169	196	364	AGAAACGTTGCTGTCAAGGC	60.44	20
245	12	256	TTATAAACTGTTACTCCTGGGT	58.698	24
205	2001	2205	TGCCACCGATTTGAACATT	59.916	19
204	286	489	GACGCTTGGTTGGATAGCTT	59.34	20
226	3311	3536	CCGCCTCCGTAAATAAACAA	59.958	20
215	75	289	GATTCGCTACCGTGTGGAGT	60.142	20
266	25	290	CGGACAGAAGGATGGCTTTA	60.206	20
143	37	179	ATTGTTTTATTGTGTCTTTGTCA	59.258	27
247	16	262	CATAAACCACTTCGAACGGC	60.502	20

100	4	103	ATGTAGCCGACCCCAATTTA	59.297	20
171	410	580	ACAGCTCTTCAAACTGGGCA	60.975	20
233	519	751	GCCACAACTTAGAATCGCATC	59.728	21
278	263	540	TGATGTTAAGAAACATTAAAA	58.601	26
254	161	414	AGCCAAAAGATACTAAACTTC	57.727	24
105	4757	4861	ATGAATGCCATCATCCCAAT	59.982	20
130	82	211	GATGATGATGCCACTCTTGG	59.04	20
221	828	1048	TGATGAGCGGGAAGAAGATT	59.773	20
201	124	324	AAGGATGAGCGAAATGAGGA	59.773	20
161	7991	8151	GGAACCTATAACGGCGATCA	59.923	20
183	1	183	TTCTTCGCTACACGGACCAT	60.657	20
138	640	777	TAGGGCTAGCAGCTCCAGAA	60.249	20
113	45	157	GGGCCGATCCTATCACTACA	59.917	20
276	3	278	TCCCGAGACTGAGATGGATT	59.612	20
270	366	635	TTCTGGTGGAGTTCATTGAGA	58.272	21
280	32	311	CTCTTTCTCTCTGTGCTGATCG	59.377	22
213	4527	4739	GGAGAGCTTCGACTTCTCCA	59.679	20
215	8	222	CCCAAGACCCCAATTTGATT	60.91	20
280	1354	1633	AACTACCCTCGCCCTCTCTC	59.84	20
175	10	184	ATGTAGCCGACCCCAATTTA	59.297	20
230	7	236	TCCCTTTAAGATAAAAATGAA	59.214	27
109	11	119	CAAAATAGCCCGAGGTTGAA	60.067	20
174	1217	1390	ACAGATCCCAACCGGATTTT	60.558	20
223	18	240	CCAACTCATTTTGCCCACTAA	59.982	21
188	572	759	GATTAGCAAATTTCGGGACG	59.547	20
105	287	391	GCGCCAAAAAATTGGTAAAAC	59.477	20
229	13	241	AAAATCAGACCAAAACTTTTC	57.078	23
275	922	1196	AGCTAGTGAGGGTGGTTTGG	59.208	20
256	497	752	CTGACCTCGTGTAACTGGCA	59.897	20
125	920	1044	TTCCATGGGTACAGAGGAGC	60.073	20
154	203	356	GAAGATGAAAAGACAAGCGG	57.546	20
142	26	167	TGAAGAATTATGCATCAGGCA	60.588	22
270	1136	1405	AGCAGCTACAACGGTAAGGC	59.545	20
175	1149	1323	GTTTCTAAGGCCTGAAGGGG	60.068	20
237	964	1200	TGAAGAGGAGGAGGAGGTGA	59.913	20
270	2501	2770	TCCGTTTGGTGTAATTGCTG	59.585	20
137	285	421	TCCCAAGCATGGAATCAAAT	60.274	20
120	132	251	ATCCACCACTTCTCCTTCCC	60.314	20
185	1339	1523	ATGGGATCTATTTGATGAGGG	59.627	22
107	520	626	GGTCTTGCTCTTTGTGAGCC	59.997	20
227	294	520	CGCATCTTTTGGGATGATTT	59.901	20
169	3195	3363	CCTATTTGGCATCAACCTCC	59.387	20
206	692	897	CTTGATCGGGTCCGACTTTA	60.066	20
270	2593	2862	CGGTTTCGTTTTAGACCCCT	60.345	20
211	177	387	AATTAAATAACCTCGCCGGA	58.583	20
180	1780	1959	GGCTCGCCAAGGTAGATAAA	59.32	20
208	469	676	GAAATGAAGCCAAACCCTCA	60.051	20
272	891	1162	CGCACACTTGGAGTTGAAAA	59.881	20
207	3	209	TTGTGGAGAAAGGAATGGGA	60.43	20
274	43	316	CCATGTAAGAAAAGTGGAAG	59.865	22
210	47	256	GCAAAATTAAAAATGCCCCC	60.484	20
161	282	442	GGAGGTGGTGGATTTGGATA	59.605	20
280	694	973	CTCATTGAACTTGGCAAGCA	59.988	20
260	551	810	CATGAGGCTGCTGAACTCAC	59.577	20
233	3	235	TGTAGCCGACCCCAATTTAT	59.297	20
173	403	575	TCTCGGGGTTCGAGTTCATA	60.594	20
117	736	852	TTGCTGCCACACTCTCTCTG	60.333	20
113	992	1104	AACATCATCCCCATCACCAT	59.869	20

244	34	277	TGGTTGAGCTAAAATCTTTGA	59.453	24
273	2808	3080	TGGTGGTTTTTGGATGATGA	59.75	20
255	344	598	TGCTAAACGATGAGCTTGGAT	59.859	21
264	349	612	CGTCGTCGCTACATGAAGAA	60.011	20
228	1205	1432	TAGATCGGTGGAGTTGGGTT	59.405	20
199	8	206	CCCAAGACCCCAATTTGAT	59.59	19
241	1953	2193	ACAAATGCGAAACCGATCTT	59.574	20
187	1105	1291	ACGTGGAGCCTATTTGGATG	59.955	20
165	57	221	TAAAAAGGCGCTCAAAAACC	59.363	20
248	282	529	GTATGAAGGCCAAAGAAGCG	59.845	20
149	249	397	AAATGGAGTCGAAGCAGCAT	59.843	20
213	1	213	GGCGTCTCAAACGTATCTCC	59.7	20
255	1194	1448	TTTGAAGCAAAAGTTTGGGC	60.223	20
272	820	1091	GTGTGGCTGTTCATTCTTGG	59.139	20
116	2	117	ATGTAGCCGACCCCAATTTAT	59.585	21
266	191	456	GTGGTAGAGGCGGTTATGGA	59.955	20
275	634	908	TTTCAATCATATAGAATCTGCT	58.155	26
100	388	487	TATGAGAAGAGCAAACCCACA	59.747	22
165	6	170	TCAACGTGATTTGTCATTTGTG	59.488	22
186	132	317	GGCACAGAAGGGGATAGGTT	60.328	20
224	207	430	AGTGTGCGCTCTGATGACTG	60.211	20
115	2190	2304	TTTTGGGGGTTGAAATGGTA	60.024	20
143	349	491	TGAAACTCCCCACAATCTCC	59.903	20
141	836	976	ACACACGCATACACACACGA	59.649	20
177	2190	2366	GTGTGAAACCTCCTTCATGG	57.971	20
274	375	648	TTGCCTCTAATTTTGGCTCC	59.297	20
275	6	280	TCTGGTCAACATCAATCTGAG	60.263	22
271	410	680	CGTTGGCCAGTCGGTTAAT	60.899	19
223	307	529	TCTAAATTGCAAAAGCGCAA	59.602	20
218	151	368	AACCATTCATCCATAGCGGA	60.296	20
157	1	157	GTCCAGCCTTTACCTCTTTTTG	59.304	22
156	2	157	CCCAAGACCCCAATTTGATT	60.91	20
237	279	515	AATGACTGGGGTAAGCTGGA	59.55	20
186	164	349	TCTATCACAACCCAAGGCG	59.658	19
214	0	213	TGTAGCCGACCCCAATTTAT	59.297	20
171	666	836	GTTTTTCTGGCAGCCACTGT	60.299	20
259	272	530	TAGCAGGGCATGAACAAACA	60.257	20
165	1523	1687	AATGGCATTTTAACTTTGATCA	58.109	24
246	1	246	ATGTAGCCGACCCCAATTTA	59.297	20
151	86	236	TAATTCGCTGAAGCAGCAAC	59.21	20
223	566	788	AGCATGAAACTTGGAATGGAA	59.56	21
212	3222	3433	TTGACGCGCATTTTTAGAGA	59.585	20
222	3872	4093	ATAAAATGGGAGCGGAGAGG	60.411	20
229	45	273	GGCATGAAACGGAATAGCAT	59.929	20
214	486	699	GAAGAGGACCAGCACCAGAA	60.386	20
168	37	204	TGTGAAATTCTCTGGGAGCA	59.369	20
280	1930	2209	CTTGTTGTCGCGTTTAATGA	57.446	20
200	502	701	TGCATGAAATCAAACTCCCA	60.049	20
100	21	120	CCAACTGAATTGCAAAACTGA	58.808	21
139	105	243	ATAATTGTTCTTCGTGGCCC	58.906	20
267	405	671	TTAAGACGGAAATCCACACG	58.623	20
254	10	263	GACAGGGGTCTCGCAAGATA	60.218	20
103	356	458	GATCATCAAAGCCCCTCAAC	59.488	20
247	157	403	TGTTTGTTGTGTGTCTCCCA	58.508	20
245	15	259	ACTCGGTCTTGCACAGTGG	59.881	19
256	0	255	AGTCCGTGTTCCGATGAGT	58.067	19
259	53	311	TCGGCCACAGAGACATTGTA	60.263	20
240	285	524	GCAACCTGAAAATTGAACATT	59.496	22

179	58	236	CAGGTCAACTGAAATCTGAAA	59.799	24
181	768	948	TCCCCTTTCTTGACCATCAG	60.042	20
247	488	734	GGATTTGTTCACGATGCCTT	59.939	20
237	31	267	ATTGGTGCAAAATGTGTTGA	57.442	20
215	13	227	ACTACAGTCCGTGTTCCGATG	60.043	21
167	237	403	TCTTGGTGAGTGAGAAATGAG	58.969	23
225	526	750	CCTTGATCATTCCCGAAAAA	59.872	20
152	610	761	GTCTTGAATGCCACCCACTC	60.52	20
243	490	732	TTCCAATGCAACCCATACAA	59.786	20
224	2613	2836	TCTTGAAATTCCATGTTTGTGC	59.982	22
280	1559	1838	ACCTTGGGCTCCACCTCTAC	60.511	20
279	2160	2438	TTGGAGAATTGAAAAGGCGT	59.685	20
250	1232	1481	CGAGTGGCTGCTACCTGAAT	60.419	20
254	228	481	TTGATGAGCCATAACCCTCC	59.894	20
128	522	649	TGGATTCCCACAATTCCATT	59.991	20
245	982	1226	TGGTTTGACCATCATTGCTC	59.502	20
220	352	571	TGGATGGGTGCACATAATTG	60.197	20
275	52	326	GTTGGGCAACTTGAAGATTAA	59.549	23
176	45	220	CCCCCAAACTTATTGACAAA	57.462	20
202	71	272	GTTCGGGAGAGAAAATGCAG	59.813	20
270	885	1154	CATGCAGCAGCCAAGACTTA	60.157	20
236	121	356	TTTCATTCAGCAGTTCAGGC	59.002	20
162	967	1128	TGTAACCATGGGCCAAAAAT	60.053	20
199	20	218	GAATTGGTAGGGTTTTCTGTC	59.871	22
177	678	854	CACGTTGGTTTTTGCTTTGA	59.746	20
280	1550	1829	AGTACGACCAGGGAAAAGCC	60.496	20
166	182	347	CGTACGGAAATCTGATAGGAA	58.274	22
272	2	273	CCAAATTTGTAAATGCAAACA	59.711	24
280	2149	2428	CCAATGGGTGAAAGAATATG	59.145	21
165	8	172	ATGTAGCCGACCCCAATTTA	59.297	20
159	66	224	TGCCAAATAATTCCGTCTCAC	59.952	21
267	1282	1548	ACCTCTGAAAGCTCGGTTCA	59.989	20
174	6948	7121	CCCTGTTGAGCATACACCCT	59.989	20
142	50	191	TCAGTTCCGTCTAGGCTTCAA	60.001	21
204	31	234	ATCAGAGCCAGCGTTTGAGT	60.02	20
251	934	1184	AGGTCATGTGTTCGAGTTTCA	59.639	22
257	415	671	GATGCAAGGTGCATGTGTCT	59.714	20
144	212	355	GGGAGTCTTGAATCTTGGCA	60.195	20
132	560	691	CGGAGATTCGCAAGTTCAGT	60.397	20
267	46	312	CTCAAGGTGGTGAAAATCCG	60.486	20
127	177	303	TGGACCGAGTCATCTCTGTG	59.82	20
245	1475	1719	GCAACGGAAACAACCTCTTT	59.218	20
120	107	226	CTGGCCTGATCTACAGCCTC	59.973	20
186	27	212	CTCTGCTCAGCCCCTTCAG	61.242	19
249	217	465	GCTGTAGCTGACCCCAATTT	59.198	20
231	8305	8535	GATGCGTTTGAAGGGAAAAA	60.053	20
273	992	1264	CAGCATGCAATTTCAAGAGC	59.572	20
258	453	710	ATAAGGATTCCGGGTTTTCG	60.143	20
267	17	283	GGTTATTTATTAAAGTTGGAG	59.924	26
232	7	238	AAAATTGCGTCTCCTATGGC	59.186	20
192	2507	2698	ACCTATGCATGTTGCCGTC	59.542	19
205	718	922	ACAACGGTCATCTGCTTTGA	59.293	20
273	1131	1403	TTGATGCAAGGGCAATAGGT	60.469	20
271	65	335	TGCAATGGACTAATTTGATTG	59.832	22
217	168	384	CCCAACCCTAACCCGTTTAT	59.939	20
246	4	249	TCGCATCTGGGATAATGAAAC	59.915	21
274	111	384	CAATTTGATTGGGAATATATT	60.467	24
250	959	1208	GATGTAATCGAGCACCCACA	59.527	20

259	446	704	AGGCATGTATTTATTATTGGA	59.038	25
260	5784	6043	TACGCGCATCTAATGCAAAC	59.87	20
254	166	419	GGTTCTCGCTCTAATCCTTCAA	59.856	22
134	55	188	GCATTATGTAAGCTCAAATAG	58.177	24
250	15	264	CTCAAGATGCGAAGCAAACA	60.134	20
256	2322	2577	AAGTCACGAAGACGGCAAGT	59.914	20
113	8	120	TCGCTTTGATTATTAAATCTTC	58.199	25
246	484	729	TCTAAAAATGGCACCGAAGG	60.067	20
100	164	263	CCAAGACCCCATTTTGATTG	60.162	20
208	8	215	CACCGGTTGGACCGTCTT	61.968	18
110	0	109	CCTGATGGAGGTGATGATGA	59.425	20
205	72	276	TGTGTTGGTTGCAGGTTCAT	60.008	20
151	627	777	CAGTTGACACTTGGGGGACT	60.002	20
275	1218	1492	CGCAGCAGATATTGTTCCAA	59.833	20
243	61	303	CAGAGGATGAAATTCCCGAG	59.623	20
216	2051	2266	TGTGGAACCAACACGATTTT	58.874	20
234	27	260	TGGTGTGATAAAGGGGCTTC	59.933	20
166	645	810	GGATCTTACGGAGTTGAGCG	59.836	20
102	27	128	AAGTTGGTGCCCAGAACAAA	60.529	20
225	417	641	GAAGGCCCCAAGCTATTCTC	60.173	20
189	410	598	GTTTGGAGGTCAGGTGTTCG	60.545	20
264	98	361	CCTTGTGCAAATTAATCCCG	60.315	20
244	678	921	TAGGGAAAAGTCATCACGGC	60.074	20
156	80	235	TGTTCTTGAATATCGGCGAA	59.257	20
271	4	274	TGTAGCCGACCCCAATTTAT	59.297	20
123	1961	2083	ACATCCATCATCATCAGCCA	59.882	20
220	37	256	TCATTTTCTTCCACTTCGCC	60.192	20
236	1310	1545	ATTATTGAATGGGCCCAAAA	59.124	20
169	24	192	ATGGCTATCCTCAGCTGCTC	59.561	20
224	6006	6229	TATATGTGGCCTTCTTCCCG	59.916	20
229	511	739	CGACCTCGGCTACTTTGTGT	60.312	20
269	244	512	AGCAACACCAACAGCAACAG	59.946	20
177	608	784	TAGCTCTGTTGCAGCCGATA	59.735	20
160	43	202	TAAAGCCAATTTTGGTGGGT	59.315	20
239	2499	2737	TCCAATCACTTACCAAATGCA	59.867	22
175	16	190	AATTACCTTGCCGGAAATTG	58.943	20
122	2255	2376	CTTTCCCCAGCATCAACATT	59.933	20
272	802	1073	AGAACTCGAGCTTGACCCAC	59.455	20
148	13	160	TCAGAAGGGGTTATGTCCTCA	59.536	21
230	19	248	CAAGTTCTTTCAAATTGGTGG	59.9	23
221	1218	1438	ACACATGGCTCAGACGACAC	59.744	20
171	85	255	CCAACCCTCCTCCTTTATCC	59.761	20
170	272	441	ATCATGCCACCAAGGAGAGT	59.535	20
240	1793	2032	CAACCTCTGCCGTGAAATCT	60.255	20
241	41	281	TGACCCTAGTGGTAACACGG	58.496	20
275	3	277	CAGCCATGAATGAGAGTGGG	61.63	20
196	95	290	TACTGCTCTCGCTGCTTCTG	59.64	20
193	29	221	AATAAAACCTGCCGGAATCG	61.155	20
173	1423	1595	GTGGAGATCGGAAAATTGGA	59.871	20
152	4602	4753	ATAGGGCTGTGGATTGGATG	59.773	20
160	392	551	GGGGGCCAAACAAATATACA	59.525	20
271	1404	1674	TGTACTTGTTCGTGTTGCCC	59.615	20
176	170	345	CTGAAAGGTCCCAGGTTCAA	60.081	20
200	3354	3553	CCCTTTTGCTGTGGCATTAT	59.96	20
239	587	825	GCATATGCAAATGAAAAAGG	59.446	21
101	321	421	TATGGTAGCTGGCTCGACCT	59.859	20
250	68	317	CGCCAACTTCCTCTGATTTC	59.813	20
249	58	306	GTTATGCCCGAATTTTCCCT	60.15	20

162	317	478	ATTACCTGGAAATCGGTGGG	60.929	20
158	16	173	CCTTCGCTTCATCCTTGCTA	60.481	20
133	90	222	GAAATACATGCAGGGCTGAG	58.326	20
112	656	767	AAGAACCTGTTGCCCGTAGA	59.734	20
190	186	375	TCCTCTTGGGTTGTTTCACC	59.943	20
209	59	267	AGAAAAAGAAGAGGGAGCGG	59.955	20
181	144	324	CTTGCCAATGCTCCACACTA	59.864	20
173	5	177	ATCATCATCATGTCCACCGA	59.724	20
159	453	611	ACAGTTTCTGGATCCCATCG	59.927	20
128	549	676	GCTTTGCAACACACATTTGG	60.157	20
215	607	821	ATAAATCGAACCTCCCCACC	60.017	20
116	583	698	GCTCACAATGCAACCTGAAA	59.847	20
229	437	665	AGTCAGAAAAGCCCACCTCA	59.844	20
161	128	288	TAAGGCCGTATTAACCGTCG	59.979	20
196	4	199	AGGCTACATCCAATGCTGGT	59.579	20
270	880	1149	CCGATATTTTGGCCTTCGTA	59.922	20
201	1308	1508	CCATTGAGACTCGAACCCAT	59.927	20
233	576	808	CGATTTTGCCCAAGAATACC	59.411	20
224	3716	3939	TCTCAATCACGGTGCTCAAC	59.837	20
160	7194	7353	CACATTCAACTGGATGGCTG	60.112	20
236	65	300	GCGCTGTACCAGGTTTGAAT	60.14	20
238	674	911	TATTGTGGCACTCTCCCCTC	60.073	20
269	873	1141	GGACCAGTCGCTGGAAGTAG	59.867	20
202	324	525	GAAGTCTCACCTCAGCCACC	59.841	20
259	75	333	CGTGTTCGTGTGCATATCCT	59.596	20
260	2	261	ATGAGTCGGTTTGTTGAGGC	60.119	20
232	97	328	ATCTGCCCTAATTTTTGCCC	60.28	20
215	211	425	CAAATTCCCGTTCCATCAAA	60.671	20
157	35	191	CCTCGACGCTGAATGATCTA	58.976	20
227	567	793	ACATGCAAATCCATTACCCA	58.697	20
246	201	446	AACGTGGAGGACAGTGGTCT	59.604	20
275	41	315	CCCAATTTCCCAACACTCAC	60.21	20
210	1	210	CAGAAGATTCATATTGATTTTG	58.292	25
249	729	977	GGCGGTGTATTATGTCGGTT	59.713	20
267	341	607	TGATCTCTCCCGTGAAAACAT	59.541	21
258	808	1065	TTTTCTTGGCAAGTTCACCC	60.088	20
186	208	393	CGTTTTTGCTTTCTTGCTCA	59.226	20
134	56	189	TTTCCAACAATAACCCCGTG	60.587	20
199	1	199	AGCTCGCTGGATCCCTAGAA	61.383	20
245	12	256	TTGAAAACCGATTTCCCTT	57.113	19
104	252	355	GCTGACCTGTTTCCAAGCAT	60.263	20
244	1051	1294	GGTTCCAATTATATCCTTATGC	58.413	24
276	121	396	TGTGATTTGGATGATGTGTAAC	59.881	23
159	3161	3319	TTTTTGAATGGCCGTTTACC	59.81	20
194	11	204	CAAGATTGGCTTCGTGTGAA	59.84	20
224	467	690	TTCGGCTTTTGTTACATGCTT	59.772	21
125	1	125	AACATGCCCAACATTCAGC	59.517	19
267	909	1175	CTTCCAAAATAGGGGGTTCC	59.639	20
271	3	273	TTTTTGAATTAAATGGTGAGAA	60.107	26
272	170	441	TTTTGGGTTTATGTGTTTATCAC	60.038	24
267	537	803	ACCCTTGGCCATTACTTGTG	59.853	20
133	70	202	GATGATTACCTCAAGGCTTGGT	59.487	22
236	1048	1283	GCCAACTTTGCTTGCATTTT	60.251	20
277	153	429	GTTTAAATGTATCCGCCGTGA	59.846	21
242	43	284	ATTTGAAGATCCGGAAATTTGT	58.866	22
159	7	165	GGATCGTAAAGCCTGGTGAA	60.074	20
170	160	329	CACGGCTCGTAATGTGGATA	59.566	20
100	4	103	ACAGTGGAGGAGCTCGCA	60.736	18

264	300	563	CTCGAACACGAGACCTCCAG	60.997	20
250	67	316	GGACCAGACTCCAACTTTTCC	59.965	21
222	462	683	TATAGCCGACCCCACGTAGT	59.476	20
226	122	347	GGGCATCAAAACCTCCAGTA	59.933	20
180	1	180	TCATAGTACGCCACCCGTTT	60.386	20
188	21	208	TTCCTCAATTTTGGGACCAG	59.903	20
221	170	390	GATGTACGCACTTGGTGGTG	60.032	20
256	96	351	CGTGACAATATCAAAGCCCA	59.542	20
162	354	515	TCAAATTGTCGCCACAAGAA	60.234	20
140	1280	1419	GTATGAACCGTGAACCGGAC	60.24	20
218	298	515	AGGCCAACTGACATCTGGAA	60.656	20
207	3225	3431	TCGGAGGCGATTTACATAGG	60.053	20
170	3861	4030	TATGTGACGGCAACCAGAAA	60.111	20
148	26	173	TTCATGTGTGCTTATTGTTTTCA	58.277	23
191	0	190	CGAGTAAGCGGAAATCAACA	58.917	20
204	189	392	CTCTCCAACAAAATTTCGGG	59.541	20
268	538	805	GTCACCACGCTCCCTAAGTG	60.711	20
216	1135	1350	GGATTGGATCGCATGTTTTT	59.768	20
180	1250	1429	CCAGCGAGTCTTCTGAGCTT	59.891	20
158	558	715	TTGTTCGCGATTTGCATTTA	60.211	20
139	17	155	CCCTGCTCAGTAGATTCCTTTG	60.254	22
176	2475	2650	CGTCAGACTAAAGCCCCTCA	60.388	20
275	822	1096	GCTGTTGAGAATAGCGAGCG	61.207	20
273	433	705	GCCAAACTGATCAACAAGCA	59.847	20
199	199	397	CCTGAAACGAGTGATGCTCC	60.801	20
278	1235	1512	GTGTCTACGGCTGCCTCTTC	60.02	20
137	294	430	CTGCAGCATTGAACCTAGCA	60.157	20
127	731	857	CACCTGAATGTCTCCCAACC	60.363	20
279	503	781	ATTAACCTGCTCGCGTGATT	59.736	20
199	1109	1307	TGTCTACATTCCCTTTCGGC	60.074	20
198	21	218	AGGAGGTATACTTTGCTGCAG	60.546	23
253	19	271	TTCAGCAAAGAGTAGTTTCCCA	59.017	22
120	11	130	GTTCGGAGTTGGGTAGTTGC	59.598	20
252	2374	2625	ACCGACAAAAGCTAGGATCG	59.336	20
235	1422	1656	CGGTAATATGGTTGGATGGG	59.894	20
251	252	502	TCCTTCCATGCAAACTCAAA	59.247	20
129	135	263	GGTGCTCTACATTCGGAAGC	59.843	20
277	1579	1855	TCTGTCAAGGCTTCTCCACC	60.386	20
245	298	542	GAAGCTGAGCAACGAGAAGG	60.277	20
249	1097	1345	AAGGTAGGTCTGCCCCTGTT	59.994	20
254	52	305	TCTCGTCTCTCCCTATTCCCT	59.29	21
133	374	506	ACCAATCACACCGTTGAACA	59.855	20
136	93	228	CCTCGCCTCTTACATCTGCT	59.598	20
270	1270	1539	CGAAACATGTCAGGCAAAGA	59.84	20
269	548	816	CGAAAATGATCAGTGCAACG	60.257	20
230	2367	2596	GAGCAGGTTGAGGAGAATGC	59.957	20
270	187	456	TGGGTCTAAAGATGTTGCCTC	59.184	21
217	14	230	GTGACACAAACCAAAGGTGC	59.037	20
233	2326	2558	TGCACAAAAGAGAACCGTCA	60.427	20
189	35	223	ATTTTGAACGGTAACAGCCG	59.996	20
232	1617	1848	TTGAAACTCCCAACCCATGT	60.21	20
265	57	321	ACGTTCAGGCCAAAAACAAT	59.476	20
184	2201	2384	AGCATTGGCTTCAGCTGTTT	60.022	20
125	110	234	GCCTGGTGCTAGTACATCCG	60.678	20
272	465	736	GGTGATGGGGTATTTTGGTG	59.91	20
166	412	577	ACTCCCCCGTAAATTCCGTA	60.553	20
175	33	207	TAATTTGCAGCTCGGTTTCG	61.251	20
165	773	937	CGGGAACAATAAATGCCAAG	60.315	20

120	10	129	CAAAACCGTGTAGTTTGGGC	60.399	20
277	309	585	ACTCCGTGTTCACCTTCTGC	60.307	20
193	27	219	TGGAGTAATTGCATTACATTCG	60.374	24
177	51	227	TGAACATTAAAGAATATCTACT	57.829	27
201	43	243	GAATATTATGGCACCATGGGTA	58.585	22
162	2282	2443	TGTAGCCGACCCCATTTTAT	59.297	20
268	19	286	GCAGCTTCAAAGTTTGGACA	59.05	20
201	792	992	ACCGATTTCTCCCCTGAGAC	60.456	20
259	1097	1355	TTGACGTATCATTTGGTGAGC	58.639	21
264	842	1105	GCTTGATGGTTGTTGCCACT	61.107	20
182	1	182	AATTGGGGTGTTGGAACTTG	59.688	20
157	232	388	GAAAAAGGGAATAGGGCCAG	59.903	20
279	16	294	GCAATCATGCATCACCACAT	60.371	20
149	763	911	AGGCGTGTGTTTGCCTTAGT	59.803	20
173	297	469	TCTTGGTCTCCAAAGTCCGT	59.697	20
127	39	165	TTTGAAGATCCGGAAATTTGT	58.544	21
238	58	295	TGAGGGTAGTTTACGCAGCC	60.27	20
275	95	369	GAGATTGAGCCCGAAAATTG	59.645	20
141	271	411	GAACCCTTCTTCGTTGGTCA	60.088	20
143	89	231	GTGGCAGAAGGTGGCTATTG	60.657	20
224	7	230	TTCTTTCGATGCTCCTCTCG	60.615	20
256	162	417	GACTCCTGATGAACCCCACA	60.934	20
277	11	287	AGAGGCGTTTGGGAGAGTTT	60.247	20
185	9	193	CTTTGCCCTCTCTCCATCTG	59.943	20
241	15	255	TTTGGTTCATGTAGCCGACC	60.894	20
171	55	225	GTGCAGAAGCATTATTCATCG	58.401	21
159	146	304	GATGATGCTGGGAACCAATC	60.289	20
154	73	226	TCTGCAGCCATCTGTTCTTG	60.136	20
164	269	432	GGTTTTCCAAATGCTCCAAA	59.916	20
138	197	334	CGATCCATAGGGCTCAGAGT	59.263	20
205	200	404	TGAATCGTTCAATTCTGCCA	60.197	20
197	1	197	AAGAAGATCCGGACGAGGAT	60.037	20
159	288	446	TTTTGACGACGAAGCGATAA	59.443	20
260	7	266	TCAGAAGGGGTTATGTCCTCA	59.536	21
174	160	333	GATCCCCTGCAAGTGTGACT	60.12	20
224	771	994	GCATCTAAGGAACATGGATAC	57.787	23
236	25	260	CCGGAAGAAAGAGTGGGTTT	60.467	20
101	10	110	CAATATAAGAACATTTATGGCA	59.649	27
268	16	283	TGTGATTCGTTGTGTTTTGC	58.158	20
227	574	800	TCCCAAACTTGAATCCTTCG	60.044	20
212	618	829	CCCAAATTCTTGCAACACAA	59.561	20
276	226	501	TAACTGTGATCACGAAATGCG	59.744	21
212	28	239	TGCAGCAACTTCCTCTCCTT	60.134	20
178	381	558	GGTTCTCCCTACTCCCCCTC	61.195	20
162	82	243	TGCCCACACTGCTCAACTAA	60.449	20
172	24	195	CATCATCAACGTTCTTGGGTT	59.845	21
194	6	199	TGTAGCCGACCCCAATTTAT	59.297	20
243	634	876	AATCCGTACCAAATCCCTCC	60.017	20
100	71	170	ACGGTTAGAGTGACCGTTGG	60.028	20
150	33	182	TTGGCAATTTCTTGGAGGAG	60.184	20
113	72	184	TTAACGTCAAATGCGAATGG	59.562	20
146	10	155	CCGAAGTGCTAGACCCAAAG	59.869	20
190	189	378	CCCCAAACTTATTGACAAACG	59.366	21
172	84	255	GCAGTACTTGAACCTTCGCC	59.882	20
231	67	297	CTAAAACTTGAAAACGCCGC	59.89	20
231	106	336	TATTCCAGCAGATAGCCCGT	59.691	20
109	259	367	TTTTTCACGTTTTCTTGCCC	60.089	20
232	187	418	GGGGAACACTCGAAAATCCT	60.306	20

266	1593	1858	TGTGGACCATCAATCTCAATTA	57.944	22
154	76	229	ACCCAGAACACCAGTTCACA	58.992	20
214	3401	3614	GCAAAAGACAATGAAGGGGA	60.051	20
233	15	247	TTTGTGGAGCGATGTTTGAC	59.697	20
195	466	660	ACCGGCTACTAATTCGCTGA	59.867	20
279	308	586	GGGTGAAGTGACCAGCTCAT	60.12	20
244	48	291	TCTTCGTTCTCTCACCACCG	61.39	20
226	36	261	CAAACCCACAAAGGACCAAG	60.38	20
126	779	904	GCCGCGCCTAAATAGTTTT	59.358	19
268	649	916	ACATTCCCAAGGCTGAGATG	60.073	20
107	230	336	CTAATTCGCTGAAGCAGCAAC	60.166	21
280	236	515	TGCAGAAACCATGTATTTACTT	59.95	25
130	483	612	TTTGCCAGCCTTTCTTGACT	59.993	20
159	20	178	CTGGGCAGCCAAACATAGAG	60.786	20
236	504	739	CATGAAAGCATTTAACCGCC	60.456	20
234	1404	1637	AGTGTTGCATGGTTCCGATT	60.384	20
172	770	941	CTCCCCAGGGAAAAAGGTTA	60.284	20
239	397	635	GATCGAGCGATTTGTACGGA	61.141	20
133	41	173	CAGAGAGGCACTATACAGTTC	60.321	23
242	17	258	TTTTAATTCCCCATATTACCAA	58.654	24
159	405	563	AATGGGACAACTCATCCTCG	59.927	20
173	9	181	GATAGCCGTTGGTGGTTGAT	59.82	20
264	477	740	CGTCTCTTTTCCGTCGACTC	59.989	20
165	44	208	AGGGTCCCTTTCTCCATTGT	59.795	20
119	305	423	GGAACCCCTTCAGGATTCTC	59.874	20
151	4066	4216	CGTTGGACAATCTGTAGCCA	59.716	20
227	57	283	GAAATGCGGCTTCCATTTAG	59.682	20
221	20	240	ATTACCTTCACTCGCCGGA	60.609	19
196	92	287	CCAGATCTGCCAACGTTTTT	60.11	20
238	243	480	CTTTTCTTTTCCTTTTATGCTCG	58.685	23
243	2269	2511	TATAAGGCAATTTGCGAGGC	60.192	20
128	63	190	TATCCTTCATCAGTTCCGCC	60.036	20
153	336	488	TTTGGGTCCTCCACAAGAAC	59.943	20
164	58	221	GTCTTCGGAAGCGATCTCAA	60.483	20
228	67	294	GTCATACCAGAGGAGCAGGC	59.834	20
187	1780	1966	ATCGTTTGTTGCATCACGTC	59.577	20
271	356	626	GCGACAATTGCTCAAAACG	60.395	19
250	2472	2721	TGACCCACATAGTGGGAAAGA	60.36	21
136	48	183	GATGCAGATGAGGACGTGAA	59.794	20
133	399	531	CTTCTTCGCTACGGCTACGA	60.669	20
243	427	669	AAAGGTTGAGAACCATGATGA	57.096	21
236	862	1097	ATGCCGTGATTGAAACACAA	59.972	20
144	334	477	AGCTTCCATGCTTTCGGTAA	59.845	20
208	9	216	CCCTCCTCCTTCTTGCTCTT	59.95	20
117	14	130	GAATCAAGTATCTGATCTGAG	59.752	24
231	28	258	CACTGAATTGCTGCTGCTTT	59.224	20
216	17	232	GAAAACAAAAGATAGATGGA	58.863	24
250	871	1120	CTGGAGGAGCTGGAGAATTG	59.943	20
187	142	328	ACGGTTATTGGGAAATGCAA	60.188	20
209	254	462	GATTGCGACCACCCTTACAT	59.82	20
254	458	711	GCGATTAAGGCTTTGGTGTT	59.229	20
119	385	503	GGCGAAAGTGTAGATCTGGC	59.843	20
144	228	371	GAGTTATTCAGCCCAGCACG	60.796	20
246	980	1225	TTGCATTGTCGTGTCGTCTT	60.31	20
247	94	340	CCCGCAGAATATAATTCCCA	59.751	20
112	673	784	TTTCTGGAAATAGGGGGACC	60.124	20
256	8	263	TCATGTAGACGACCCCAATTT	59.302	21
222	801	1022	CGATCTCGTTGTGTTTCGTG	60.301	20

169	829	997	CCTCTTCCTCGTACTCGGTG	59.861	20
247	1141	1387	TGGCTCCACAATTCATAGCA	60.22	20
268	1236	1503	CGTAGTTTGTTGGCTCAAGG	58.431	20
148	40	187	GAACCTGTGGTAGTACGGCG	60.571	20
202	3134	3335	GGACCTTCTCACTGCTGGTT	59.305	20
242	2046	2287	ATGATTTGACCCTAGCGAAA	57.306	20
279	102	380	TCGAATCAAATCCATCAGGAA	60.399	21
235	2042	2276	GCATCAACTGCGGCTAACTT	60.416	20
229	3	231	GATGATGATGCCACTCTTGG	59.04	20
260	296	555	GGATTGGGGCGTGATAAATA	59.621	20
257	798	1054	TTTTCGCGCCTTATTTGTTT	59.732	20
219	180	398	AGCCGATTCTGAAGTTCCAA	59.813	20
105	593	697	AGTTGGAGGATATGGGAGGG	60.147	20
256	40	295	AGCACGATCATCCCTCATCT	59.642	20
273	360	632	CACCCCGTATTTTCGAATGA	60.692	20
177	3719	3895	GCATTGGCATTGCATGATAG	60.066	20
234	999	1232	AGGCTTAATGGATCGTGTCG	60.096	20
224	707	930	GATGTGGGCTTTTTCCGTTA	59.938	20
185	48	232	GCGACGACTCTCCGTCTATG	60.966	20
264	285	548	GATCATGCTGCTCCCTATCC	59.616	20
262	61	322	CTGCCCTTAGCCGTTAGATG	59.861	20
277	141	417	AAATTCAATTACCTGCCGGA	59.411	20
158	15	172	ATGACGTCGGCGGTGATT	62.522	18
260	221	480	CCAATCAACGGCTTGCTACT	60.27	20
273	1042	1314	ATCCTTTCAATGGCAATCCA	60.274	20
209	802	1010	GGTGGGAGTAGCCTCATCAT	58.969	20
169	20	188	GAGAACAAACAAAGAAGAGA	59.436	26
276	329	604	TTGTATGAGCAAGATGACGAA	59.772	23
147	583	729	TTGCACAGACATTATCGCATC	59.709	21
122	174	295	AAACCTCCACCAGAAATTAAA	58.259	23
278	112	389	GGTTTCATACAACCGTATAGG	60.141	23
257	32	288	GTCCCAAGTAAGGTCGGTTG	59.449	20
182	2	183	TTCGAGGACGAATCCTTTCC	61.46	20
203	479	681	TTCCCTACCCCAAATTTTCC	59.992	20
277	100	376	GCAAATAATTGATCGCCTTG	58.253	20
222	34	255	GCATTTCAGGATATTAAAAAC	59.378	25
129	669	797	CGTTCATGGCATATTCAGGG	61.246	20
132	84	215	ACGCTATGTACCTTGGGTCG	60.015	20
163	101	263	CAAGGATCATGTCGCAGAAA	59.799	20
114	146	259	GATTTAGACAGCCCCGACAG	59.694	20
187	276	462	CGGGGAATTATATAAGTATGT	57.343	25
201	30	230	ACGAGGGTGATGTTGGAGAG	60.112	20
260	142	401	TCAATGCTTTGCCTATGTTCA	59.315	21
235	0	234	TGTACCGGTATCATCCCCAC	60.461	20
177	69	245	TGTGGAGACAGCCACACATT	60.162	20
242	363	604	TTGGTTGACAAGACCCCCTA	60.345	20
263	416	678	GCCGGCTTATTTGAAATTGA	60.04	20
251	621	871	TCAACGAATACCTGCTACCAA	58.307	21
197	370	566	CTGTAGCCGACCCCAATTTA	59.953	20
280	25	304	CCACCATCGTCGTCTCATC	60.063	19
143	1743	1885	TTGGGGGAAGATTAGGGATT	59.6	20
206	1621	1826	GGGTTCCATTTTTGAGACCA	59.767	20
253	79	331	GATGATGATGCCACTCTTGG	59.04	20
116	45	160	TGTGGGGCAGCCAAATATAG	60.846	20
172	3	174	GCGTCCGACTCCTCAACTAT	59.313	20
192	202	393	TTTGTTGGGAAGGTCGTAGC	60.11	20
263	39	301	AGGCCTAGTTGGCTCTGGTT	60.268	20
268	160	427	CGGTTAGTTCTCCCACCTAGC	60.137	21

230	72	301	ATGGTTGCCTTTGTTTGGAG	59.971	20
238	665	902	CTGGCTCTAACGATGCCTTT	59.476	20
213	27	239	ATGCAGTCAACACTCCACCA	60.162	20
232	271	502	GATCGGAGTCACGCAGAACT	60.418	20
158	487	644	TTCGTTACCCGAGTTGAGGT	59.592	20
277	1083	1359	TGGGAATGTATTGGGTATGTTC	59.451	22
225	225	449	CAGTGTGGGTTTCGGTGTTT	60.843	20
179	1085	1263	CAGGAGGAGGGAAATTGTGA	60.042	20
170	227	396	GTTGAATCTCGGCTGCAAAT	60.221	20
191	660	850	GGAGGGATGTCAAGATCAGC	59.617	20
167	693	859	AGTATCCAGCATGAGGGGAA	59.508	20
173	618	790	AGGTCATTGGTTTTTGGTGG	59.688	20
272	90	361	CTCTATAGCCGCCTGCATTT	59.479	20
185	2423	2607	AACCCTCTTAGGGTGGCAAT	59.827	20
278	712	989	TTGGAGTTGCATAAATTGTGG	58.544	21
194	84	277	ACAATGAATAAACGGGGCTG	59.823	20
141	1056	1196	TAATATGGCAAAGGCTGCTG	58.936	20
158	6	163	TTCAGGGGTTATGGTGGAAG	59.784	20
121	6	126	GCAGCAACTTCCTCTCCTTC	59.166	20
201	106	306	TCTCCTGCCCTATCTGCATC	60.326	20
192	841	1032	CCCAAGAATATCATGTGCCC	60.155	20
181	2410	2590	CTGTCGAAAAAATGGGATGCT	60.074	20
273	20	292	GAACTAACTGCTGCAAGGAAA	59.946	23
174	269	442	TGGGACAAGCTCTTGTGTTG	59.873	20
279	50	328	CTTCTCAGCCTCAGCCTCTG	60.422	20
279	323	601	GGCTCACAGTACGTCGATCA	59.862	20
252	1189	1440	ATTTGCAGGAATTGGTGAGC	60.081	20
192	4898	5089	ACTAGCGCCCAAGTTAGCAG	59.677	20
171	34	204	AGAATCTTCCGACAAACCGA	59.67	20
124	17	140	AGTGGGTGAGGAGAGGGAGT	60.112	20
162	0	161	GGAACTTGATTATGTATCTGAT	58.072	26
213	286	498	GCCCACCTTATTGTTCGAGT	59.056	20
120	263	382	CGCGAAGGTGACTGACATAG	59.465	20
120	50	169	AGCATCATGAGGAGGAGCAT	59.792	20
216	41	256	TTCCCTTCCCTCTATTTCCG	60.382	20
153	35	187	GTCCAAGGACTTGTCGGTTC	59.555	20
179	458	636	GCTCGTTGCAAGCATATGAA	59.983	20
141	0	140	AGTTGGGAGTTGGGAGTCCT	59.968	20
269	277	545	GATCCATGTGTCCACGTGTC	59.808	20
205	102	306	CTCACTCTCTCCCTCCCTCC	60.336	20
122	1	122	GTTGGGCAGCCTCATATTGT	59.962	20
246	603	848	GGGTCCATCATTCCCTTTCT	60.133	20
264	213	476	AACAAAGGATGGATTTGCCA	60.309	20
280	192	471	GCTGGATCACTATTTGGTGG	58.019	20
274	307	580	AATCGCCAGCGAATATGCTA	60.709	20
159	202	360	TACATGCCTCCAACAATTCG	59.542	20
144	71	214	ATCCCCGGACAAGGATCTTA	60.652	20
197	3	199	TCCTTACTGAATTTGGGGTTGT	59.741	22
255	99	353	TTCGAAGGTGTTGATCCCAT	60.317	20
214	39	252	GGTTTTGGAGTTTCCGTCAT	58.886	20
198	127	324	TTCTCCTCCCTTGTGATTGG	60.042	20
258	36	293	GCGGAGGCAATAGACAGAAG	59.978	20
262	10	271	TCATCCTCGGAAGCAATCTC	60.303	20
256	836	1091	AGTACCATTTCGGCCATTTG	59.823	20
207	18	224	CGTCGACCACCATCTTAACAC	60.425	21
111	83	193	GAAAATGGAGCGGAGGTTCT	60.578	20
140	21	160	TTTTTCGTTTCTGGTTTCGC	60.223	20
224	1136	1359	AGACCTCGAGTCGGAGATGA	59.945	20

252	2365	2616	TTGCCCTTCATTATCCCATC	59.722	20
268	2464	2731	AAACGAGGGCGAACTGTAGA	59.875	20
100	8	107	ATGTAGCCGACCCCAATTTA	59.297	20
214	5032	5245	TTTCCCTCCAAAGCCAGTAA	59.679	20
277	344	620	TGTTGCAATTCGTGTTAAATCT	57.397	22
102	100	201	GCCATCCGTTCTTGAATCTC	59.635	20
208	498	705	TCACCAACATGCCCGTATAG	59.42	20
100	390	489	TCCTCTCGATCCTCGTTACAC	59.298	21
153	287	439	GGCTTGCATTTGAAAGTACAG	59.406	22
185	231	415	TATGAACGAATGCGATGCTC	59.799	20
199	0	198	ATTGCCACCATCCGAACA	60.915	18
252	1058	1309	CTTTGCTCGATCTATTCGGC	59.945	20
107	1038	1144	AGCTTCTTTCAATCGCCTCA	60.096	20
212	37	248	TTCAAAATTATACCTGCCGGA	59.442	21
172	6	177	ATAATTCCCGGCGTCATCAT	61.42	20
252	231	482	GGGATAGGATTTGGTGTCCA	59.605	20
160	674	833	TCCTATTTTCCCATTGCACC	59.762	20
217	322	538	GCAAATTGCCATCATCTTCA	59.628	20
213	3588	3800	GAGATACCATCCCGTGGAGA	59.886	20
251	654	904	TCGTGGTGCACTTGCATACT	60.333	20
270	12	281	AGCAGATATGGGAGTGGTGG	59.95	20
269	48	316	TGTTGAGTGGGTCTCTGCTG	60.022	20
131	874	1004	CGAGACTCATCCACTTGCAG	59.571	20
113	134	246	GCCTTTCCTGGGAACGTAGT	60.496	20
127	3	129	GAACAAAATAAAAATTTGGGA	59.637	24
232	401	632	GGCACTGGTAAGGTCTGAGC	59.874	20
137	23	159	TTGCTTCCGTGTTTTATCCAT	59.465	21
217	1173	1389	ATTTCTAGACTGCGGGGTCA	59.694	20
216	628	843	AAGAAGAAGCTCCTCCCACC	59.817	20
122	9	130	CGTTGGGGGTGACGTAGT	59.388	18
277	438	714	ATGTGTGTGGCCATTTTCAA	59.823	20
172	1171	1342	AACTGCCACCCCTTGAATG	60.908	19
254	79	332	GATGCAGCAACTTCCTCTCC	59.957	20
215	3082	3296	TTGTCACACCCACGCATATT	59.847	20
112	108	219	TGTCTGCACTCCAGGGTATG	59.701	20
195	160	354	CAGTTCAGCAGCGGAATTTT	60.386	20
271	225	495	TCCTTCCCCTTGAGTTGTTG	60.081	20
200	3672	3871	GCGGAATAGCATTCACGTTT	60.103	20
245	764	1008	AAACCATGCAATGAACACGA	59.972	20
269	2883	3151	GGCGACATCAAACACAACAA	60.562	20
250	1548	1797	GTCGCCAATTATTGATGCCT	59.929	20
153	767	919	CCATCACAGGCCATTAGTTG	58.999	20
157	236	392	TGGTTCCCTTCTTGTCCTTG	60.081	20
238	37	274	GCGGTTTCGATGGACATAAC	60.339	20
274	456	729	TCCATTTTTCTTCGTGCATTT	59.578	21
252	19	270	CGTTCTGCAGGAGCTTGAG	59.864	19
122	104	225	AGCACGATCATCCCACATCT	60.507	20
108	227	334	TCCCGAGACTGAGATGGACT	59.792	20
268	162	429	TCTTCAAACTTTGTTCCGCA	59.439	20
239	47	285	GGTAAGGTTGCGTACATCCG	60.386	20
117	2398	2514	CGTGTGAAAATGAAATCGCA	60.644	20
151	978	1128	ATCGAATGGTTGAGAATGCC	59.9	20
266	857	1122	ATCGAATGATCCCTGAGTGG	59.886	20
189	1195	1383	TTTGGATCACGCTAATGCAG	59.833	20
267	1297	1563	TTCCACGAACCAACCAAAAT	60.206	20
277	393	669	TCCTCGCTCCTAACTTGCAT	59.978	20
200	1724	1923	AAACCGAGTGTTTTTGCCTG	60.147	20
263	105	367	GGCACTATGCTATGGTTCGG	60.49	20

232	734	965	AAATGGAGGTGTTGAGAGCG	60.255	20
104	10	113	AGGTGCACGTGACTCCAAC	59.728	19
271	345	615	CCCCTCCCCCTCTCATATTT	61.36	20
176	809	984	GATGTGCTCTCCCACGACTT	60.269	20
168	5	172	CATTGAAGAGCTCGCTGGAT	60.504	20
219	0	218	CGAAGGACCTGTCCACTCTC	59.835	20
111	1903	2013	AAATTTGGGAAGGCCTTTGT	59.814	20
260	1796	2055	TAGTACTGCAGGCGAAGCG	60.309	19
215	79	293	TTTCTCTTGAATGGTTACGGC	59.215	21
278	70	347	CTCCTTGGGGATAGTATGCTT	59.98	22
206	24	229	GTCATCCGGGTTCAGTCAAT	59.786	20
258	1178	1435	TCCTCATGTCAGGAATGCAC	59.637	20
112	149	260	GGCTCACTTAGACAGCCTGC	60.164	20
106	344	449	ATATAGGGCATGGCAAGTGG	59.807	20
101	25	125	AGAGGTATTGGGGGATTTGAG	59.294	21
202	59	260	AAATCTCTCAATCTTGCGTCG	59.467	21
276	214	489	TAACTGAGCTGGCGGACTCT	60.156	20
267	8	274	AGTCGGATTGCAAATTGGTT	59.434	20
167	11	177	GTTTAGACGTCACGCACAGC	59.52	20
181	40	220	CTGTGTCTCCAAGCTCCCAT	60.261	20
215	1139	1353	GGCGACATATGCTCCATACA	59.529	20
118	1	118	GGCGGCTCCTCCTATGTAA	60.185	19
165	761	925	GGTCCGATTGAGGAGATGAA	60.011	20
275	372	646	GGGGTTTTCTGAAATCGTGA	59.91	20
210	582	791	CAATCTCCCACTCTTGCCTC	59.803	20
185	105	289	TGTTCTTCGTGGACCGATTT	60.495	20
280	486	765	CATTTGTATGCCTTGAGCCC	60.469	20
217	667	883	ATGTTGAGCCCAACCCAA	59.893	18
272	82	353	CGCTGCCTCTGTCAACAAT	60	19
234	601	834	CTGTATCGAACGAGCATCCA	59.823	20
141	73	213	CCAAATATTACAATAGCTCAC	57.479	25
217	49	265	GTGAGAAAGTTTGCTTCGGG	59.853	20
193	58	250	TTTTAATACCCCATTTTACCAA	58.695	24
189	24	212	CCGAAGTGCTAGACCCAAAG	59.869	20
162	212	373	GGAGTCACTCACGCTCTTGC	61.167	20
193	53	245	TCAGCATGCAATACCAAACAA	60.126	21
209	43	251	AGCTCCCTTCCTCATCATCA	59.761	20
237	69	305	TCCATACTTGGCATCGGTTT	60.331	20
156	5	160	TGTAGCCGACCCCAATTTAT	59.297	20
164	0	163	TGTTTTCTTAAGTTGTGATTTG	58.708	25
272	1056	1327	TCCACTAATTATGACGCGCT	58.414	20
221	19	239	TTGAGCTGCACTTGTTTTGTCT	60.096	22
256	775	1030	TCGATCGAAAGGTGATTGGT	60.461	20
269	614	882	TATCAGATGGGACCCACACA	59.762	20
267	1422	1688	TCTCCTTTTCCTCCACAAATTC	59.571	22
188	22	209	CCATCAAAACCATCACCTCC	60.173	20
147	126	272	TTTATTCCGTGACCCTCGAC	59.933	20
229	701	929	TGAAAGTAATGCCCATGGAA	58.965	20
117	655	771	TTTGTGGTGATTGTTGCAGG	60.552	20
100	266	365	GTTAATACCGCTGATGGCAAC	59.492	21
257	67	323	CACGTGCATTAATTATTGTTTT	59.015	24
177	3	179	TAGCAGGCCAAAGAGGAAGA	60.088	20
202	536	737	CTCCCAAGTTCAATCCATGTT	58.898	21
203	1635	1837	AGGCGACTTGCATATTCCAC	60.103	20
234	829	1062	ATGCCTTATATGCCGGACAC	59.813	20
181	64	244	CATTCTCTAAATGGTTTCCATT	60.076	24
221	1035	1255	GATCTCGATCGTGACCCAAT	59.893	20
276	104	379	TGAGACGGACTGGGGATACT	59.53	20

256	183	438	GTCCAAATAAATTGGGGTCG	59.135	20
248	124	371	TAGTGTGCGTGATCGAGGAG	60.008	20
184	65	248	CACCATTCTCTAAATGGTTTCC	60.223	23
103	282	384	AACCTCAGCCATCTCCACC	60.064	19
216	2220	2435	TTGTCGCGAATTTTTCAATG	59.679	20
182	95	276	CCAAACAAATGAAGCCCAAT	59.801	20
195	3974	4168	CCTCTCACGGTTGGAAGAAG	59.837	20
243	2574	2816	TTCGGTTTCTACTAACCCGC	59.225	20
276	905	1180	ACCCGGATTACTCCGATGAT	60.546	20
148	369	516	TTCCCTGATTGGCTTCCTAA	59.64	20
258	1817	2074	GATCGAAGTTGTGCAAACCA	59.697	20
213	12	224	TTGAAAGAGCATCGTGCAAC	59.995	20
166	0	165	GTGGCTTCTATGGGCAATGT	59.962	20
145	335	479	GGGCTGCAAATAGATGGAGA	60.177	20
109	5	113	TGTAGCCGACCCCAATTTAT	59.297	20
244	547	790	CTCTGCAAACAACCATTTCG	59.317	20
265	407	671	CGGATGAATTTTTGTTCGCT	60.074	20
228	0	227	TTGGCTGGAGCTAAAAAGATG	59.483	21
262	72	333	GGGATCACCTTGGAGTTGTC	59.359	20
215	511	725	GCTCAACACCTGGGAGGTTA	60.111	20
170	64	233	AAGGGGGAGAGTTCTCTTGG	59.671	20
233	15	247	GAGAGTCTTCCGACAAACCG	59.844	20
134	7	140	TTTATTGGGATTAAGGCTTTGG	59.375	22
277	672	948	CCCCACTCGAAATTAACCAC	59.288	20
109	0	108	CCCAAGACCCCAATTTGATT	60.91	20
180	2059	2238	GGTCCTATATTGTGGTTTCCG	58.315	21
235	246	480	AAACCTTAACGCCCTCACCT	59.998	20
156	1112	1267	ACTCCGACATGGAGAACACC	59.969	20
259	836	1094	CCCCCTTTCCTCCTTTCTTT	60.755	20
275	413	687	CCATTTTCCAAGAAAGGTTGT	58.085	21
102	572	673	TTCTTCAATCCTCCAAGAGCA	59.94	21
242	241	482	CGATGATCACGTCAAAAACCT	59.985	21
108	279	386	TCTCGGTTCCGATCTTCACT	59.803	20
219	15	233	CCTGAAACGAGTGATGCTCC	60.801	20
108	97	204	GGTGAAACTGCCCTGAAACT	59.187	20
276	276	551	AAGTTGGCGTGGTGGTAGTC	60.035	20
159	2808	2966	GTTTGCTGTTGGATGGGTTC	60.362	20
150	57	206	TCCTGAAATGAGTGATGCTCC	60.211	21
132	4116	4247	TCTCACGTGCAGAGGAAGAA	59.701	20
225	38	262	ATGGTAGTATGGTGTGGGGG	59.405	20
151	99	249	TCAGGTTTGTCCTCCAGTGA	59.23	20
261	986	1246	TTCTGATTTCGAGCTTTCCC	59.387	20
174	2300	2473	TTGGGCTTCATCTTACCACC	59.933	20
279	38	316	GACAACGGGACGGAAGATT	59.918	19
247	841	1087	CTCGCTTGTGAAGAGTGACG	59.77	20
232	11	242	GATCCCGAAGTGCTAGACCC	60.99	20
216	273	488	TCTGTGCCGCCTAAAAATGT	60.637	20
203	2139	2341	TTTGCTTTGACTTTCGGGTC	60.227	20
280	1764	2043	ATCTCCTGCAACACTCCCAC	60.12	20
237	1684	1920	TTTTTCCAGATTCCGACAGC	60.192	20
242	166	407	GTGTTGCTCGATCTTCCGAT	60.226	20
197	6	202	TGTCACCCAACTTATAAAAGA	57.119	24
271	251	521	GGATGCTCGACAGGGACTAC	59.685	20
129	323	451	TGAATTCTTAATGGATTGGGG	60.489	22
224	328	551	GCCACATGCTTTGTGTGAGT	59.758	20
265	655	919	CCCATAATTTTATTGGGGGA	58.487	20
256	100	355	TTTGTTGCTCATAGCGGGAT	60.606	20
117	3175	3291	TTATGTTGTGGCCCATTTCA	59.786	20

249	15	263	TAGCCGACCCCAATTTAATG	59.789	20
144	141	284	CAAGATGTTTGGCGATTGAA	59.664	20
247	2200	2446	GAGACTGCTGATGGCCAGTT	60.418	20
278	1429	1706	ACCACAAATTCCTCAACCCA	60.21	20
181	617	797	TAAAATTGCCCTATTGCGCT	59.717	20
144	187	330	TATCATCCTCGGAGGCAATC	59.998	20
114	18	131	CATGAAACATTTCAAAATATC	58.726	25
204	147	350	ATTGGGAAACCACCCGTATT	60.299	20
223	41	263	AACGTAAAGAGGGGTAGGGG	59.344	20
182	47	228	TGAATCAGAAAATCCCCTGC	60.014	20
192	4679	4870	ACGGTTAGAATCGCGACAAC	60.14	20
153	10	162	TCACACCTCACTAATTTCTTGT	57.077	24
212	300	511	GACAGTGGATGAAATTCCCG	60.317	20
219	87	305	TCTGAAAATTGGTGCTGCTG	59.988	20
113	11	123	ATCGGCAGCAGATGTAGGAG	60.384	20
200	374	573	TCAGAGCCACGTCAGCTTAG	59.339	20
241	5379	5619	CCATCCTCATTTGCTCGATT	60.036	20
196	2136	2331	TGCTTACTCCATCACCCTCC	60.073	20
251	414	664	TCAACAATTTACGGGCTTCC	59.938	20
168	111	278	GAGGATGATGTAGGCATGGA	59.909	21
199	273	471	ACCCCAAAACCACATCAGAC	59.679	20
172	99	270	TTGATGAGCCATAACCCTCC	59.894	20
173	1686	1858	GATTTAACGGATATGCTTGGG	60.168	22
279	656	934	ATGTAGCCGACCCCAATTTA	59.297	20
189	132	320	TGGGACAAGGTGACATAAAAT	59.724	22
169	186	354	TGGTGTCGAGCAGCCTATC	59.959	19
114	927	1040	CTCTTTCGCAGCCTCCTCTA	59.853	20
161	22	182	AGCCATGAGCAATAACAGCC	60.243	20
192	16	207	CTCAGCCGAAATCTTCAAGC	60.096	20
163	3	165	ATGTAGCCGACCCCAATTTA	59.297	20
206	963	1168	GATAAGGCCCAAACTAGCCC	59.93	20
267	2	268	CCCAAGACCCCAATTTGATT	60.91	20
243	0	242	GGGCATTACATTTACGTTGGA	59.712	21
205	512	716	CAGCCTCAGGACTCCTCATC	59.945	20
256	42	297	CCCGTATGGTATCAGAGCCA	60.874	20
170	535	704	TTATTTGGCGGGTTAATGGA	60.144	20
198	145	342	TCCCGCCCTCTACCTTTATT	59.924	20
227	734	960	TTCAAAAACCATGCCACTGA	60.088	20
218	535	752	ACTCAGGTTCAAACCCTCCC	60.349	20
236	770	1005	ACAGCTTCGGCAGATCACTT	60.02	20
173	849	1021	CCTAAGATTTTGCAATCGCC	59.682	20
214	460	673	TCCGTTTCTAATGGAGTGCC	60.074	20
166	227	392	GTTTCTGCCACGTGCATTC	60.265	19
165	186	350	CGCTTTGCTAGATTTTTGCC	59.985	20
263	4569	4831	GGATGCATTCCAGAGTTGCT	60.226	20
167	4	170	ACCGTAACCGCCAAACAC	59.42	18
278	573	850	AAGAACTGCTCCCTCAACAAA	59.795	22
186	1574	1759	TGGGAATGTAACTTGACTGCC	59.985	21
167	83	249	TCACCGGAAACAAATACATCA	58.881	21
103	15	117	TTCTTCTGTACAATTAATGTCC	59.121	27
257	253	509	GTCCGTTGGGTGTTTGACTT	59.867	20
161	278	438	GGTAGCCAGTTTCACCAATCA	59.985	21
223	796	1018	TAACAATTACGTCTGGGGGC	59.823	20
178	631	808	ATGCTGTGTTTGAGCGACTG	60.056	20
268	17	284	CCACCATCGTCGTCTCATC	60.063	19
246	550	795	TGTGATGAGATCGTGAACCTG	59.692	21
209	498	706	TCCATTTAATCCCCCTTCTTC	59.257	21
233	856	1088	CTTTCTCGGGCCTGGATATT	60.411	20

182	1674	1855	AAGTTATGTAGCCGACCCCA	59.452	20
238	838	1075	AAGTGATATTTTCGGCGGTG	59.96	20
184	2456	2639	GGGAACCCAGTGAAAATTGA	59.767	20
234	261	494	CAAGGCAGAGAAAAAGCCAG	60.125	20
162	1189	1350	TCCGCTGCTAATTTGCTTTT	59.985	20
271	980	1250	TTCAGGTTGAAGTCTTGGGC	60.232	20
181	52	232	GCGACTTGTTTTCGTCCACT	60.299	20
194	1825	2018	TGTATGGCACGAGTTCTTGA	57.836	20
246	1	246	CTCGTCCTCCGTGGATATGT	59.95	20
233	823	1055	GCGCAGTTGCCAAACTTATT	60.272	20
263	247	509	TGTTCGCAGGTTGCAATAAA	60.251	20
247	4887	5133	GGATGGAGAGGAGGAAGGTC	60.012	20
271	58	328	CGGAAGAAGCACAGACAACA	60.025	20
273	3882	4154	AAAAGAAGATACGGCCCACC	60.32	20
227	422	648	AGCCTGGATATCTTGCTCCA	59.797	20
266	1	266	ATGTAGCCGACCCCAATTTA	59.297	20
222	4	225	TGATATTTTCAATGATGGATCG	57.46	22
267	4227	4493	TCAAATGCAAATCTACCTGGG	59.946	21
206	793	998	TTCGACGCGGAAGTAAATCT	59.845	20
233	2217	2449	ATTGCCCATGCATACACATTT	60.096	21
230	1074	1303	TTTTCGGTTACCATGTCGTT	57.999	20
175	152	326	AAGGATGAGGAAGGCAAGGT	60.074	20
248	467	714	TCGAAATTCAAGCACACGAG	59.988	20
251	977	1227	GAGAAAGAATCAACTGCGGC	59.962	20
252	728	979	TCTTTTCTTTTCTTTCCCCCA	60.034	21
155	776	930	TTGGTTACTCTGGGAATGGC	59.933	20
160	1101	1260	CTCGATCTCTTGCAGAAGGG	60.088	20
262	2283	2544	CGGGTTGAGACCCTTGTAAA	59.964	20
173	2	174	GGTTCATGTAGCCGACCTCA	61.067	20
266	534	799	GAGAAATTCGACTCAGGGGG	60.959	20
210	624	833	TTATTCCCACCATCACCGTT	60.051	20
239	16	254	CGGAGAAATGGTTTCTGCAT	60.074	20
219	513	731	GAAGCCGGTAATCCCCTTAC	59.799	20
143	1461	1603	TTGCACCAAAATGGACAGAG	59.691	20
258	164	421	CCACCATCGTCGTCTCATC	60.063	19
279	470	748	AGGGCTTCCCACCTTCTTAC	59.576	20
228	65	292	AAATCGGGGTCGAAAAATCT	59.777	20
100	962	1061	CATGAAAATCCAACAAGCCA	59.518	20
239	1589	1827	CCTATGGCTTTCTCCCACAC	59.55	20
262	253	514	GCTCTTATCCATTCAACGCC	59.674	20
132	29	160	GATTTTACACCTGCAAGGGC	59.574	20
214	1006	1219	TATGACACAATGTCCCGTGG	60.24	20
255	623	877	AACCAGGAACCAAACACCAA	60.246	20
185	196	380	ATTAGCACGCTTGGATGTGA	59.301	20
143	26	168	TCAAACCTTTCTCCAATTGCT	58.823	21
256	967	1222	ATAGATCCGGAATGATCGGA	59.3	20
268	568	835	GCCTACATACCGACGTGACC	60.406	20
152	276	427	TAATTGTCGGAAATCTGCCC	59.901	20
201	5712	5912	CTGATCTACTCCGTCCCCAA	60.065	20
106	2447	2552	CGACGAAAAGAACAAAACGA	58.939	20
154	618	771	GAGGAGGAGTGTTGGAGGC	59.783	19
182	99	280	GCTGTAAATGAAACTGCTGTAT	60.212	24
235	12	246	CAGAGCGCACTCGAAGAGTA	59.49	20
187	43	229	TTGTCATATGAATCATGAAATT	58.012	25
174	835	1008	GTTCGCTGAGGCAACAACTT	60.44	20
147	468	614	AGATCTGACTGCGCGACTTT	60.164	20
186	1057	1242	CCGGGTATTACATCAAGGCA	60.712	20
144	44	187	ATGCAGCTCATGTCTGATGC	59.982	20

241	332	572	AGCAAAAGGTCGTCCTGCTA	60.015	20
189	325	513	CTTTAGGCCAAGTTGTACCCA	59.141	21
248	939	1186	AGGGGAAATTCACGAGGAAA	60.797	20
162	102	263	CCTTTATGATGGAGGCGGAT	61.165	20
237	252	488	GGCGAAGCTATAGAGATCGG	59.046	20
133	32	164	TTCCAAAGTTGGACTTATGTAA	58.31	25
232	875	1106	GAGCAACTGCCAAAACGTAA	58.967	20
117	505	621	GAGAGAGAGAATGGCTGGCA	60.645	20
277	1	277	CATTGCGTCATACGATGTATTA	58.997	24
279	31	309	CTAGCCCAGCATATTCCCAC	59.551	20
231	66	296	ATCCCAAGCCATTACCATCA	60.155	20
238	1232	1469	GATTTCTGCAGCTTTGAGCA	59.301	20
274	672	945	TTCTTCTCCCTCTGCTACGC	59.717	20
188	647	834	GCCAAAAGTGAAGCGAGAAG	60.132	20
262	477	738	AGCCACTGACAGCCACAGTA	59.493	20
108	340	447	CTCACACTCTCGCTCCCTCT	59.732	20
219	172	390	GGCAAAATTAAAAATGCCCC	60.484	20
249	7	255	GCATCTCCCAAACTCAGCTC	59.957	20
194	962	1155	AGACGTAAATGGGCGTGAAT	59.457	20
268	8	275	CCTATTACTTCCTCGACTTTAAT	58.761	25
153	639	791	GGCAATAGAGCAAGAGCCAG	60.118	20
182	65	246	TGGAGGTTCTAGGTTCGTGG	60.103	20
261	72	332	CTAGAGGGCGGCACATTTAC	59.73	20
264	36	299	TTGTTCTTCGTGGTTTCGTG	59.734	20
199	259	457	AGCCGCTACTATTCGAGTGC	59.643	20
233	384	616	AAATTTTGTAGGTAATAGCAAT	58.623	26
173	470	642	TCACCAAAAATCGAACACACA	59.996	21
208	2637	2844	CGGGGCAGATGATCATAACT	59.917	20
233	2	234	CCACATTTTCCACCTTAGCC	59.429	20
166	262	427	CTCTTCACGTGAGTCTGGCA	60.178	20
266	10	275	CACCAACAGCTTGGTCTCAA	59.873	20
238	293	530	AAGATTACGACGGCGATACG	60.117	20
250	587	836	CTCCCATCATCCTTTTTCCA	59.864	20
233	156	388	CCGAGCTTACACCAGGAGAC	59.867	20
100	232	331	ACTCTAAGGGATGAATGCACG	59.208	21
237	17	253	CATGCGCTCAGCATAAAGAA	60.118	20
273	6	278	GGATCAGCAGTGGCTTTCTC	59.957	20
107	2604	2710	TTATCGTTCATAGCCGACCC	59.923	20
232	388	619	AAACTGCCAAGTGCCAACAT	60.559	20
113	437	549	AACCGTCTCAGTTGTTCGCT	59.914	20
230	904	1133	ACAAGACCTTTTTGTTCGCTT	58.048	21
274	2085	2358	AGGTTCGAGCTACCGAAACA	59.875	20
172	273	444	ACATGTAAGGGACTCCGAGC	59.166	20
191	374	564	GAGAGGGAGAGAGAGGGGAA	59.883	20
186	1080	1265	TAATACCCCGAGTCTCCCCT	59.783	20
242	4383	4624	CGGGAACCTACAGACGCTAC	59.757	20
197	938	1134	ATGGAGGAGGAGGAAAAGGA	60.008	20
223	2527	2749	TCTCGTTCAATTCACACACG	58.246	20
175	287	461	ATTTGGGGGTTTGAGGGTTA	60.403	20
266	23	288	GGTGGCTGAAGATAGGAATGA	59.14	21
159	1272	1430	GGTTAAATCGACACGATGGG	60.192	20
187	673	859	CTGTGCGGAAGTAGCTTTGA	59.22	20
107	916	1022	GAGCCATTGATGGCATTTTT	59.907	20
253	973	1225	CAGAAAGCGCTTCGAGAACT	59.898	20
178	752	929	ATTCTCGAGGCTGAGATGGA	59.91	20
227	7	233	TGTTTGGATTTCATGAATTAGT	58.5	27
153	332	484	AACCTCAACGATGAAGGCAT	59.556	20
240	1453	1692	TGTGGGTTTACTGACCACCA	59.848	20

117	13	129	GCTCCTCCAAGAACAACTCG	59.989	20
212	216	427	CCTTTAAAGCGATTCCCCTC	60.034	20
178	433	610	ACGAGCCCTTTCAAGAGTCA	59.989	20
267	447	713	TTGACAAGGTCAATATGCGG	59.542	20
205	57	261	TCCAAATCCAATCCATCTCC	59.685	20
228	25	252	ACCAACCAAATTGGACTTGTG	59.743	21
235	2591	2825	AATTTTGAGCAAGGCCAATG	60.074	20
106	6	111	CCCAAGACCCCAATTTGAT	59.59	19
172	2095	2266	CGCCTCTTGATTAACCTCCA	60.206	20
275	241	515	TGGTCCCTTTCGAATCCAT	60.265	19
127	7	133	AGGGTTAGTTATGGAACGATG	59.398	22
230	278	507	CATGTCACAACATGGAATCTC	59.42	22
280	1731	2010	CAGGATGGTTTGAAATGAGG	57.992	20
149	195	343	TAATTTATCGATGGCGGACG	60.792	20
150	38	187	TTGATTGCTTTAAATCCGGC	60.04	20
111	89	199	GCAAGGTGATTCCTTGTTGTT	59.091	21
230	55	284	GCCAAAATCTGTATACCCCG	59.297	20
155	276	430	AGAACCTTTTTGAGCTCCGC	60.875	20
275	3873	4147	CATGCATGACTTGGTGCTCT	59.862	20
157	936	1092	ATGTAGCCCACCCCAATTTA	59.158	20
230	47	276	CGCTGAACGAGCTAGAACTTG	60.332	21
130	12	141	GGAGAGGAAGATACGATTTG	59.531	24
191	1281	1471	CCTCTCCATTCTGAATCCCA	60.003	20
199	352	550	TCGTGGTTTCGTGTCTTTCA	60.278	20
275	3319	3593	CAGGAATTGAAATGACGGGT	59.79	20
165	0	164	TGCACAAAAATGTTTTAAAATT	60.26	24
280	319	598	GCCATCTCCTTGATCGAAAA	60.155	20
273	6089	6361	GGAATCGGTTTTCGACTGAG	59.67	20
100	3	102	CAGCCATGAATGAGAGTGGG	61.63	20
277	1	277	ATGTAGCCGACCCCAATTTA	59.297	20
268	196	463	TCATTTATTTCCTTTTTATATGT	59.326	27
221	126	346	TCAAGTGTGCTTCCACCAAA	60.278	20
276	2101	2376	TAGCATTCGTGTTTCCAGCA	60.401	20
234	1	234	CCCAAGACCCCAATTTGATT	60.91	20
228	166	393	CCGATCCATTTTAGGAACGA	59.894	20
214	286	499	CGAACCTAGGAAAAGTTGCG	59.876	20
231	0	230	CTCCTCCCAAGTCAGGTTTG	59.691	20
208	574	781	TTGATAAGCCAGCCACTTGA	59.42	20
133	795	927	TGGGTAATGGCTTCAACTCC	59.933	20
173	1061	1233	TCAGACCATGCTATTGTGCC	59.679	20
103	151	253	AAACGTGAGAACGGATGGAG	60.111	20
262	39	300	TCCGACACATGAGCTATTGG	59.673	20
191	542	732	GCAGTTAATAACGAAAAACC	58.393	24
126	201	326	AAAGTCTCCTGCTCGCTCTG	59.891	20
107	8	114	ATGTTCCACCTCCCAAGGTT	60.607	20
276	304	579	GACGGGTGTGGGCTAAAAAT	61.099	20
195	230	424	CGTGTGCATGTGAAATTTTTAT	57.655	22
251	147	397	TCCAAATCGCTCAAACATTG	59.664	20
244	508	751	CCTAGACTCCGACGAAAAGC	59.077	20
278	2	279	CACTCTCCTCAATGGCGTC	59.356	19
139	2785	2923	TGAGACTCAGATGAAATGTAG	59.438	24
200	108	307	TTTATGCATTGCCGTGAAAA	60.074	20
134	3	136	ATCAGGATCGAGTAAGCGGA	59.797	20
180	720	899	ACTTGTGAGACAAAGAGAAC	57.292	24
206	475	680	ACGTCCCTCATCACTACCCA	60.386	20
117	22	138	ATTCACATTTACAACCTACATC	59.227	24
271	1784	2054	TTTCGATTTGATTTGGGTTT	57.08	20
114	351	464	TTATATGCCACTCTTCCCGC	60.06	20

266	2444	2709	CGAATGGTCGTTTACCGAAT	59.823	20
219	3138	3356	CAACGGCCTTTCTTTAGCAG	60.011	20
174	1630	1803	AGCACATTTCTCTTGGGTGC	60.263	20
167	67	233	CCCAAATGTGTAGGCCATTC	60.192	20
194	162	355	CATTGGAAAATATTACTGGGG	59.458	22
234	397	630	TAGAGTTCAAGCACCCCCAG	60.246	20
254	3155	3408	GGCGAAGAATGCACACTACA	59.871	20
103	3679	3781	CCGAAACAAAGCACAATTCA	59.706	20
268	301	568	TCTTCTATACATAGTGCTTCCG	58.446	24
224	264	487	GTTCGGTTCCGGTTTCAAAT	61.08	20
201	515	715	ACTTCCACAGGCATTGGGTA	60.375	20
127	6	132	CAAATCACCAATCAACAAAAC	59.225	22
279	5	283	CCCAAGACCCCAATTTGAT	59.59	19
191	1509	1699	AATTCCTGCAACTCCAACCA	60.495	20
274	126	399	AGGGTTGAGTTGAGGGGAAT	59.795	20
192	254	445	ACCCTCAGCAATATGCCAAT	59.415	20
231	448	678	CGACAGAGTTGCAAAGAAGTT	60.088	22
138	88	225	TGGCCGATGTATGTTGTCTT	59.002	20
181	121	301	TCACGAGTTGGCTCTTTGTG	60.025	20
147	129	275	GTCAACGCGTCTTTGAGGTT	60.299	20
150	4033	4182	GAAGGCAGAGACCGTGAAAG	59.989	20
100	8	107	CCGACTAGGACTAAGGGTCCA	60.493	21
110	1379	1488	TTTGTACCACCACCACCAAA	59.709	20
185	158	342	CAGCAACCACCAAATACTCTT	59.671	22
195	461	655	TCAGGGAAAAGGGAGCATAA	59.64	20
277	26	302	GTGTTGGGCAGCCTCATATT	59.962	20
276	364	639	CCTGTCAAGACCCAATACGA	58.569	20
220	18	237	TCCAAAATTAGTACAAGCATC	59.168	25
170	25	194	ATTTTCGCCTTCTTTTGCAG	59.474	20
232	4091	4322	TGTAAGCAGCACGCCAACTA	60.599	20
203	231	433	CTTCCACTTCTTCAGCTGGG	59.982	20
224	3575	3798	CTGCACACCTGTATGTTCGG	60.175	20
276	586	861	TTGAAATGAGTTGGAATGAGG	59.546	22
278	326	603	CACTGAGGCAGAGATGGAGA	59.074	20
259	223	481	CCATTCTCACGATTGTTGATG	58.987	21
260	489	748	TGTGACGTCTAGCTCGATCC	58.987	20
218	331	548	TTTCCACAAAGCGTCGTACA	60.293	20
145	182	326	GGTTTTCTCCATTTACGGCA	59.938	20
170	4278	4447	CCACTGATTCCAGATGGTGA	59.473	20
199	10407	10605	TAATGAAATTGGGTGGGAGC	59.762	20
270	495	764	CCGACTCCACATAGTGGAAAA	59.978	21
252	70	321	TTGGATGATTCTGGCCTCTT	59.629	20
185	479	663	AAACCTCACCACAAACGGAG	60.005	20
213	0	212	TGTTGTTGAAAAAGGCGACA	60.271	20
243	4272	4514	TAGGGCTTTTGTGTGGTTCC	59.971	20
141	329	469	TCTCGTGGTGCAGTGGTAGA	60.463	20
258	71	328	TTGTTGAGCAAGAAGGGTGTT	59.766	21
254	118	371	CCCAAATTTTCTTAAGCCCTG	59.951	21
241	11	251	TGTAGCCGACCCCAATTTTA	60.315	20
253	442	694	ATCGATCCATCCATGCATTT	60.126	20
182	1975	2156	TCTTCTGTTCTTCTCCCCCA	59.773	20
260	4	263	TGGTTCATGTAGCCTACCCC	59.813	20
248	1	248	GAATGTCAAGATGAGAGATG	59.598	24
277	682	958	CCGAACAACACTCAACTCCA	59.72	20
121	22	142	GGGTTGAGGCCACTATATCCT	59.321	21
102	338	439	TTACTCCTCGAAAACAGCCG	60.378	20
273	567	839	AACGAAGCAATACACTTTTGA	59.391	24
148	384	531	CAAGAGTGCAGGCAAGAACA	60.175	20

151	106	256	GCTCTTTCAATAAACAGAATC	57.589	23
280	1118	1397	CACAATTAAAAATGCACCGC	59.077	20
231	2618	2848	CTGGCAATTCAGCCAAAAGT	60.249	20
263	956	1218	TCAAATTCCACAAACACGGT	58.874	20
184	940	1123	ATACCGCAGATCCCTTTCCT	59.925	20
152	41	192	TGAGCAATTGAGCAGCTTGT	59.746	20
158	198	355	ACGTAGGCGGCTTTACTGTG	60.326	20
134	200	333	GACCAGAAAGGTGTTGGTGG	60.399	20
133	11	143	CCCAAGACCCCAATTTGATT	60.91	20
233	65	297	AGAGATTTTATCCGGACGGG	60.278	20
101	165	265	CATCCACGATCTTTGCCTTT	60.074	20
167	532	698	TTGTTACTAAGGGTTGCGGG	59.99	20
270	17	286	GAAGTTCATTTTGGGACGGA	59.91	20
196	689	884	CCCCCATTGCTAACAACATC	60.192	20
273	255	527	TATCCCACCCGATCACTTGT	60.195	20
101	42	142	TGCACAAATTGAAAGCACAC	58.317	20
271	435	705	TTGGTATGATGGAATGGGGT	59.871	20
105	1	105	CCCAAGACCCCAATTTGATT	60.91	20
217	246	462	CAGCTGCTGTCATCATCGTT	60.016	20
206	105	310	TATGAGGAGTTCCCCATTGC	59.894	20
146	416	561	TCGGTGAGCCTACATCTGTG	59.855	20
206	200	405	GCCGGTTAATATGCATTTGG	60.172	20
180	255	434	CAGCCTCTCATTCTCTTCGG	60.088	20
277	22	298	AAGGAGCAGCTGTCTTTTGTG	59.671	21
164	837	1000	ACATGTGCAATTGGCAAAGA	60.119	20
234	1768	2001	TCCGCCTCGAATTCTTGTAG	60.344	20
245	3029	3273	AGCATTCACGTTGCCTTGTA	59.347	20
223	82	304	AATGTCCGGGCTACATTTCA	60.331	20
210	77	286	TCGCAACTATCTGCACCATT	59.301	20
271	18	288	ATGTTGAGCCCAACCCAAC	60.774	19
224	601	824	AATCATTCGATTTGGCAAGC	60.045	20
243	78	320	GGGAGGTTTCGTCACACAGT	60.009	20
245	52	296	ACCCCTAGCGCAATGTACC	59.97	19
176	1610	1785	CAAAACTCGAAGGTTGCACA	59.881	20
280	560	839	GTGGGTTGCACCAATTAGGA	60.755	20
247	1	247	TGGAGAATGATCTTGTTTGAT	59.56	23
204	218	421	CTAGCTCTGAGATCCCGGC	60.065	19
126	0	125	CTCGAACCCATGACCTTTTG	60.486	20
198	5049	5246	ACGTCGGCATTGCTAAAATC	60.103	20
269	108	376	TTACCGAAGCCAGGGAAAG	60.191	19
128	489	616	CTGGACTCGGCATTTGAGTT	60.255	20
237	233	469	ATGGCGTCGGTATGTTATGG	60.606	20
229	196	424	TCGTCGCCCCTCTTATTCTA	59.801	20
181	0	180	GTTGCGTACATCTGACCCC	58.948	19
138	967	1104	GCGGGACCTAGAATGTTGAA	60.074	20
249	20	268	CTGCCCTTAGCCGTTAGATG	59.861	20
174	2648	2821	TCCTTCTCACTGACCTGCAC	58.968	20
163	231	393	TAATTTACGGCTCGGTTTCG	60.089	20
229	2019	2247	AAATGGCCGAAGAGATTCCT	60.039	20
257	52	308	TGTCGAATCTTGTGATGGGT	58.933	20
240	380	619	GTGCCCTGTTCTCTCACTCC	59.841	20
155	402	556	CCAAGTCCTCATCTCGTGGT	60.112	20
126	1057	1182	TTCCTTGTGAAGCACAATCC	58.697	20
134	11	144	CCCATACATTTGTGGGGATAG	59.03	21
242	687	928	TCGTGACCAACCCAAACATA	59.816	20
197	597	793	GAGACGATGTTTTGTTGCGA	59.847	20
104	11	114	GTCTACCCCGCCAGATCC	60.439	18
170	321	490	TCCTCGCCATACTCGTTTCT	59.836	20

201	202	402	CTTTGATTCTGTCCTCCGCT	59.43	20
242	262	503	TTAGGTTTTGCCCAGGATTG	59.931	20
175	230	404	CTCGGCTTCAATCTTTGTCA	58.999	20
215	89	303	AACAAAGGTGACGAGAGCGT	59.914	20
137	211	347	GGGTTATATCCCCGTCTACCC	60.623	21
165	5781	5945	TGACTTATGCGTGCATGTGG	61.713	20
146	92	237	CCCAGCGGAGAGCTATACTG	59.993	20
121	13	133	CCCCTCAACTATTCACTCCG	59.545	20
277	708	984	GGATGTCATGCCAACCATTA	59.205	20
192	124	315	GATAAGCGGCTGAAGGTGAA	60.352	20
259	84	342	CAGCCGAGAACATCATCAAA	59.799	20
274	1784	2057	ATCCTGTGGTGGCATGTTTT	60.24	20
246	789	1034	TTGAGCGCACTCGAAAAGTA	59.752	20
261	278	538	CAACTTTAGTCGTCGTCATCAT	58.781	23
153	252	404	TTTCGCAGTATGCCTCAGTG	60.011	20
254	234	487	AGCTCCTTTCAACACGCATT	59.882	20
245	536	780	ACCCCATTCCGTTGAACAT	60.042	19
168	1537	1704	CCGACAAGAACCACCACTCT	60.151	20
243	18	260	TCACATTGCGAGGCAAAATA	60.215	20
157	58	214	TGAAACATCTTGAGAGTCGGG	60.239	21
241	157	397	CACTCCATCGGATCCAAGAT	59.886	20
128	209	336	TGATGTTTAGGCTGCAGGAA	59.42	20
173	55	227	TCACAACATTTCCGTGGTGT	59.855	20
241	346	586	TCAATTGATTTTCGTAATCCTG	60.187	23
270	428	697	TTCATAACGGGTGAAGGACC	59.79	20
169	1639	1807	TGAATTGGGATCAGTCACGA	60.048	20
220	29	248	TACCATCTCGGGATGCAGTT	60.483	20
142	1273	1414	TGGGGCCTTACACCAACTAT	59.312	20
108	33	140	CTCAATTTTTCCGGCGAAT	60.024	19
279	211	489	GGACTGTGATGGGCTAGGAA	60.073	20
101	636	736	CAACCCTGCCGAAAAGACTA	60.241	20
210	3	212	GAAACCAGCGACACATTGC	60.265	19
212	22	233	CACAAATGGGGTTGACTTCC	60.21	20
246	41	286	ACCAAACGATGCAGATTTCC	59.939	20
181	1739	1919	AAGCAAAATGAAATTCTCGAC	59.614	22
182	2369	2550	GCCCTTACAAGACCATCCAC	59.41	20
246	132	377	ATGCCGGATCGAATAATCAG	59.885	20
278	232	509	CAATATCTTCCTCCCCTCCC	59.722	20
277	676	952	TGTATGCCCTGCAAAACAAA	60.111	20
229	3086	3314	TAGGCACAAATCTATCCGGG	59.916	20
231	6	236	CCAATTTATTGGGATTAAGGCA	60.037	22
237	207	443	CCTCATTTTGAACCCGAATG	60.301	20
236	2300	2535	GAGCCATCATCACTCCCAAT	59.893	20
162	1037	1198	GATCCTTGCGCAACTCTTGT	60.406	20
235	1430	1664	CGTTTCCAACACCGACCTAT	59.853	20
233	40	272	CATTGGAGATGCCCTTAGGA	60.029	20
263	3643	3905	ATTCCGAAACCTGCTGTTTG	60.11	20
165	221	385	TGCAAGATTGAGCGAGATTG	60.096	20
134	127	260	TTTCAGCCCTGCTTTTCAAT	59.823	20
270	38	307	CAATTCTCCTGAATGTCCCC	59.336	20
269	870	1138	TCTCATCCAAACCTCAACCA	59.059	20
225	287	511	TTCATGCCTGTATTTCAATCG	58.639	21
257	3245	3501	AGTGGGCCTTATCTTGCCTC	60.599	20
272	3891	4162	GCCTCTTCTTCAGCAGCATC	60.249	20
191	612	802	GAATATATCTTGCCGTTGCCA	59.942	21
262	194	455	TTCACGTTTCACGCTTCCTA	59.464	20
216	242	457	CGGACCAGCCTAGAATTTGA	60.206	20
243	305	547	GAGAATGGCGAAGAAGTGGA	60.34	20

238	12	249	CGAACCATAGTTGTTGGACG	59.047	20
265	93	357	CATGCATAATCGAACTGGAGC	60.621	21
260	77	336	CCGTGGCTTTAGAGAGGAAA	59.448	20
279	123	401	GCCACCAAAAATCACACAAA	59.42	20
256	99	354	GCCATAACTCCCACTCCAAA	59.933	20
276	292	567	CATGACAACCCTCTAGTTCGC	59.749	21
151	14	164	TGTGGAACTCATCATCTAATC	59.443	23
158	930	1087	CATCCCTGCCTCCCATTTAT	61.034	20
203	550	752	TCGTACAAAGGAACTTGGGC	60.11	20
218	59	276	ATCCCCCTACCCCAAACATA	60.258	20
171	980	1150	GGGTTTTACCGCCGTTATTT	60.076	20
279	90	368	CGCACGAGTGTTGTCGTAAG	60.507	20
160	837	996	TAGAGAAATGATCGCCGGAC	60.177	20
274	220	493	TCTGGTGGGAGATCAAAAGC	60.195	20
264	363	626	AGCAAGGCTTGGATCAATGT	59.7	20
170	1069	1238	GCTTCTGCTCCAGAAACTGC	60.285	20
186	174	359	GCGCGGGTGTAAATCTAGTG	60.658	20
109	985	1093	GAAAATGGGTGTGACTTGGC	60.362	20
235	241	475	GCGGTGGATTTAGGATTTCA	59.901	20
168	18	185	GGTTGCGTACATCTAACCCC	59.316	20
110	12	121	CAAATACAAATTCAAGGATTA	59.247	27
161	2061	2221	TTGAAGGCCGCAATCTTTTA	60.691	20
102	38	139	AATTAAACCCAAACCAAACTC	57.427	24
226	21	246	TGTAGCCGACCCCAATTTAT	59.297	20
268	4003	4270	GTTGCAAAACGACTGGGAAT	59.978	20
231	46	276	CATCGATGTCAAACCACAGC	60.12	20
269	4725	4993	TCCTCTTTCTTGGGTGATGG	60.042	20
271	117	387	GCGATTGTCGGTGAGGTAAT	59.962	20
170	1381	1550	GGCACACAATCATGGTGAAG	59.967	20
224	3476	3699	GGGAGAGAGAGGGGAGTGTC	60.198	20
201	403	603	ATCATCGCAATCTCTCGGAC	60.189	20
132	194	325	ATTGGGCCTGAGTTTTGATG	59.933	20
230	123	352	CGCGGTTATTTATGTCCGTT	59.853	20
123	941	1063	GTCTAGCATCCTTTGGCAGC	59.985	20
202	2	203	TGTAGCCGACCCCAATTTAT	59.297	20
177	19	195	GGGTTTGTTCTAGTTCATCCCA	60.221	22
251	19	269	CCGAGGCTGAGATGGACTAC	59.827	20
280	1583	1862	GGTGTTGAATGAAGGGAGGA	59.903	20
265	110	374	TGATGGGTGAGTTTTATATGAT	60.102	24
279	1262	1540	AGCTGCAGATCACAGAGCAA	59.887	20
228	232	459	CTGTGTGACTATTTCGGGCA	59.716	20
260	311	570	ATGTAGCCGACCCCAATGTA	60.214	20
256	76	331	CTCACATCAGAATCCCCAGA	58.586	20
110	577	686	TGAAACCTTCTGCCCTCAAT	59.67	20
254	84	337	AGCATGAGTACATACATTTCT	57.669	26
224	5711	5934	TGGTGTAATTTTGGAAGGGA	57.917	20
186	50	235	AAATCCCCAAAAGAACATGG	58.738	20
113	66	178	AGCCTTTTGTGAATGATGGC	60.081	20
205	2430	2634	ACTGCTTTCTCACAACGCCT	60.058	20
187	54	240	GGATTCGATGTCTGCCAACT	60.081	20
149	471	619	GGTTCATCGGGTCCTGAGTA	59.927	20
218	364	581	ACTCAATATGCCCAAGGTGG	59.813	20
243	16	258	GGCGTTTGACTCCCTACCT	59.151	19
257	860	1116	AAAATGAGGGTTGAGTGCGT	59.598	20
280	723	1002	GCAGAAAGCGTTTTAGGTCG	60.018	20
240	14	253	TTGTCCAAGTGGGAGATTGTT	59.439	21
193	342	534	TGGATGAAGGGGTTGTTGAT	60.173	20
116	89	204	TTCAAATACCTTGACCAACGA	58.134	21

196	422	617	CAAGGCATATAAGCTGGGGA	60.053	20
255	992	1246	CTTGTAGACGCTTTACGCCC	59.904	20
241	50	290	TGGAATTGGTATGTGTTGTATG	59.644	23
203	168	370	CACACCGCCTTAATTTCTCC	59.569	20
269	100	368	CCTTTATGATGGAGGCGGAT	61.165	20
268	218	485	CCATGTGATGCGTCAACTCT	59.707	20
201	2031	2231	TGCCTCATGTAATGGTGGAG	59.522	20
193	4228	4420	GGGTGGATTCAATGCTCTTG	60.461	20
220	1090	1309	GTCGGGGTAATCCGACCTAT	60.039	20
253	3716	3968	TTGACCGTACTGGTGATGTACC	59.78	22
271	691	961	CTGTTTCTTGTCTGCCACCA	59.873	20
271	61	331	CATCGAATCAAATCCATCAAG	59.901	22
152	876	1027	CCATTTTCCCATCAACATCC	59.991	20
150	140	289	TTACTATGCGGACTGGGACC	59.955	20
238	71	308	AAGGGAGCTACAACCTTTCAT	59.685	23
111	458	568	CTTTCCACCACTGGGGTTTA	59.824	20
272	27	298	GCTACGAGGCAGATAAACGG	59.867	20
228	538	765	CATAGTACCGTGGGGCAGAT	59.836	20
208	228	435	TGTGAATTCCATCGGTGTTG	60.367	20
272	586	857	CGATTCAACCACCAAATGCT	60.894	20
254	929	1182	AGCCGATGTTGTCTGAAAGC	60.406	20
113	24	136	GAATGGCATGTGGATCTGTG	59.925	20
238	223	460	TCCGCGACAAACATATGAAA	60.073	20
247	12	258	TTACAGCTTGGTTTCGGAGG	60.241	20
247	969	1215	TGCATAGGATATTTATTACACC	59.27	25
167	3962	4128	GCCCTCAAATCTGACCAAAA	60.051	20
251	480	730	TCATCATCACCACCATGTCC	60.189	20
239	772	1010	CAATTTGATTGTGCGATGGT	59.4	20
165	81	245	TTTCTCTGCAATTCCCTTGG	60.184	20
276	104	379	AATTGGCCCTCATTTCCATT	60.511	20
221	15	235	TGCTCATCAAAAAGTTCCCA	59.247	20
103	963	1065	GGGTGGGATTACCATACCCT	59.766	20
269	253	521	CGATGTACGGTGTAATGCTTG	59.122	21
241	376	616	CTTGTAATCCGCATCCTCGT	60.096	20
181	315	495	TCTACCACTGCACCACGAGA	60.463	20
206	395	600	ACAAGTATCCACCACTCGCC	59.997	20
246	2	247	CCTCCTCTATTGCTGATTTAAG	60.108	24
159	453	611	GGGCGTTTCTTTGTTGAGAG	59.853	20
223	959	1181	AATTGTGCTCCATTTCCCAG	59.933	20
245	243	487	TCATCGAATCAAATCCATCG	59.43	20
245	176	420	GGTCCACTTCCAGCTTTCAT	59.141	20
227	108	334	AGCATCATGAGGAGGAGCAT	59.792	20
210	996	1205	AGGCTTGCTCAACCAAATCA	60.776	20
151	327	477	CTGACGGTGTCGTGGAAGTA	59.745	20
206	10	215	CCCAAGACCCCAATTTGATT	60.91	20
221	417	637	TTCTCAGTGCTATTTTGTTCCG	59.402	22
103	273	375	CAGCGGAGGAGAAGAGAGAA	59.82	20
208	236	443	CTCTTTCCGCCGTCTGTATT	59.336	20
270	548	817	GGTGCATGCAAGACAACAAG	60.31	20
276	187	462	TCCATCTGTCATCTCATCCATT	59.366	22
216	308	523	ACATTCACCATCAGACGCAA	60.12	20
272	455	726	CGTTCTAAGGCGTGCGTATT	60.285	20
242	11	252	AGCTTTGGTTCATGTAGCCG	60.27	20
229	318	546	AAATTCGCAAAAACGAAAGG	59.231	20
155	241	395	ATCTGCCGACAAAATTGAGC	60.221	20
110	8	117	CGTCATCGTGACGTCTGC	59.981	18
156	337	492	CTCGTGTCACCAGGTCAAAA	59.72	20
257	27	283	CGACCCACATAGTGGGAAAA	60.745	20

277	4	280	CTCTTCCATCCAATAATTCCTG	58.528	23
231	268	498	GTGTGACTGCATAAAGGCCA	59.722	20
279	213	491	CCACCAAGAATTTGTGCCTT	59.971	20
242	1139	1380	TGTTTCCCTTTCCCTTCCTT	59.912	20
197	62	258	TTTCAAAAGATGAGCTACTAG	57.65	24
212	204	415	TGCCTTTAACCAAAAGTGCC	60.11	20
208	1321	1528	GATTCTTGCTAACATCTCTGCG	59.933	23
124	3227	3350	GCCACAATAACTTGTGAAACC	59.904	22
274	39	312	CCACGTTGGGATCTTGGTAA	60.745	20
221	483	703	CCTTTTTCTGTTTCTTGCGG	59.855	20
275	569	843	TGGGAAAAGAAAATGGGAAA	59.36	20
208	208	415	CCCAAGGATCGTATGTAGGG	59.264	20
158	224	381	GCAGGTTGAACCGAGATGTT	60.119	20
277	917	1193	GCCTAGGGTTTAGGCACCAT	60.34	20
269	803	1071	GCGATGAAGCAACCACAAAT	61.043	20
228	335	562	GTCCGTGGATATAACTCGGC	59.415	20
274	1623	1896	CCCCATATGAATCCTTTCCA	59.576	20
141	5	145	TGTAGCCGACCCCAATTTAT	59.297	20
212	2150	2361	AGCTGTTCATGCTGTTGTGG	59.905	20
262	83	344	GGAGTAGGGTTGGGAAGAGG	59.928	20
173	326	498	GGGGTCCTTGTCGTATAGCA	59.955	20
132	427	558	TGCCTTCTGAATGATGGACA	60.201	20
264	23	286	ATGTTCCAGATCCATTTGCC	59.756	20
160	52	211	TTGATGTAGATATGGAGCGAT	59.073	24
273	1450	1722	AAGGGCCAGTCTGCTTACCT	60.268	20
261	539	799	GGGTAAGATCCGACCCCTTA	60.145	20
230	986	1215	CCACCAATGACAGCAATCAG	60.112	20
257	1953	2209	GGTAGCCGAGCAGCTTCTAA	59.752	20
236	5817	6052	GGCAATCTTCAGTGGAGGAG	59.803	20
117	23	139	GAAGCTCGGAGAAGTTACGC	59.222	20
247	1517	1763	TCCTGCAGTTTTTGTGGTTG	59.734	20
184	122	305	TTTGGAGGGGTTTAGGTTCA	59.401	20
277	233	509	TCGGGCTTTGATTTCAAGAT	59.645	20
218	2192	2409	CGTTCCAGGATATGCTTCGT	60.096	20
138	1199	1336	TGGTTCGGATTGACATGAAA	59.9	20
195	32	226	TTCAGAATCATTTACTTCCAAG	57.589	25
167	56	222	TTCGAAGGTGTTGATCCCAT	60.317	20
121	244	364	AGAGGAAGAAAGGCTGTCGG	60.892	20
256	1190	1445	CGATGTTGCCACAATTTCCT	60.894	20
277	41	317	GGTGTAGATCTGGCGGGTAG	59.574	20
264	108	371	GCCGACCATTTTTAGTGACC	59.434	20
137	212	348	CAAAAAGGAACGCAAAAACA	58.839	20
234	45	278	TATCAAAACTGGATTGGCCC	59.762	20
226	250	475	GTGGATCAGCAGTGGCTTTT	60.263	20
198	1322	1519	ACATGCAAGGAGTGAAAGGC	60.263	20
252	31	282	GGGGCGTGACATTAACACTAC	59.373	21
185	43	227	GCCGGAAGAAAAGACACAAG	59.853	20
220	209	428	TCACCGGTTTATCCAAGCTC	60.074	20
253	259	511	CCCCAACCTTTTACTCCTCC	59.799	20
216	34	249	AATGTTGCGTACATCTGACCC	59.874	21
218	964	1181	TGAATAATGTGGGCAAACCA	59.786	20
193	675	867	AATGTTTCTACGCATTGGGG	59.823	20
107	3	109	GCAAAATCTCAATTGTAGTGC	58.768	22
148	277	424	ACATGTGGTGGCAGGTTACA	59.88	20
257	92	348	GGCTGAAAAGGCTGAAACTG	59.993	20
229	39	267	TACTGGGCTTCTCCGACCTA	59.83	20
127	568	694	TGTTAGATTTTCCGACGCCT	59.708	20
194	2293	2486	TGTAGCCCGTGACTGTACCA	60.175	20

269	4	272	ACCCTCACTAGTTTCGGTTAG	57.456	23
229	746	974	ACAACCAAGCAGGTCCAAAA	60.529	20
127	24	150	CGATACCCATAACGGGTGAG	60.206	20
205	4	208	GGAGGAGAGAGAGAGGGGA	59.489	20
218	385	602	TGTCAATGCATCTGCCTCTC	59.95	20
276	6	281	GAAAATGCTGGAAATGAGGA	59.148	21
275	1114	1388	ACGGCTAAAATCAGGAGCTG	59.476	20
173	730	902	TAAATCCTTCGAGGTCACCG	60.066	20
133	17	149	GAATCAGTGCTTGCCGATCT	60.37	20
255	80	334	CTGTGGAAGCATCAAAGCAG	59.591	20
119	9	127	GCGTTATCGTGACGTCGG	61.269	18
186	2615	2800	CTTTTTGTTTTGGAGTGGGG	59.443	20
134	2465	2598	TAGCAACTGCACCAGGATGA	60.413	20
123	59	181	CCGGATCCACTACAAGTTCC	59.405	20
163	1113	1275	TGCATCTGAATACACGAGGTT	58.242	21
261	895	1155	TGCTCATTGTCAGTTTCCCA	60.24	20
125	1831	1955	TCATCAATTGCAGCCAAAAG	59.809	20
172	312	483	CTCAATAGCACATGGCCAAA	59.688	20
217	483	699	TAGCCGACCCCAACTTATTG	59.953	20
203	372	574	GTTGGCCCTCTCTGTGAAAC	59.703	20
276	1030	1305	TGCACATTTTCCATTGAAGG	59.518	20
205	106	310	CCAAGGCAGAGAAATATGAT	60.445	23
216	327	542	ATTGGCATTTTGTAGGCTCA	58.241	20
181	11	191	AGCTTTGGTTCATACAGCCG	60.27	20
260	1428	1687	CACCCGGAACTCGAAAAAT	59.918	19
228	2917	3144	AGAAACAAAAGCAAACCGCT	59.02	20
155	575	729	CTGCACATTCTTGCCTGTGT	59.905	20
204	7	210	ATGTAGCCGACCCCAATTTA	59.297	20
262	17	278	GACCCCAATTTGATTGGAAA	59.599	20
188	269	456	GAATCGATCCGACGACTCAT	60.042	20
175	138	312	GTTGGTTCAGGGTTAGCAGC	59.74	20
278	15	292	TTGTATTGTCTTGATTGCAGGA	59.639	23
209	10	218	GGTACGTTACTGTAAAACCCT	58.153	24
271	4	274	CAGAGCGCACTCGAAGAGTA	59.49	20
245	4049	4293	CAGAGGCACAGATTAGCAGC	58.777	20
161	592	752	TACTGCTGATTCAAGTGGCG	60.011	20
274	8	281	AGCTAACCATTTACTTGCACA	59.566	25
120	234	353	AAAGCATTCACGTAACGGGT	59.499	20
271	2481	2751	AACACTATCCCACAAATCACC	59.218	22
174	17	190	TCGATGTATTGTTTGGATAATA	60.024	26
206	248	453	ATTCGGATTGCATCCAAGAA	60.414	20
113	1760	1872	TTTTCCCACTCTCATCCACC	59.903	20
228	30	257	TGCATTCAACATCATTACAAA	59.952	25
244	5	248	GGACTTTGGTGTGAGAAAATT	58.602	22
136	3	138	GAATTTCACCAATCGGGAGT	58.838	20
260	44	303	TGAGATTCCCGCATCCTATC	59.998	20
278	1731	2008	AGGTGGGATCTGAATGCTGT	59.535	20
197	718	914	TGAAGATTCGTGCGATGTGT	60.272	20
201	417	617	AGATTTTGGATTCGTGGCTG	60.074	20
279	3	281	CCTCAAGACCCCAATTTGATT	60.173	21
228	993	1220	ATGAACCGGGTCCCAAAT	59.987	18
154	714	867	AAGCAGAAGAGAAGGTGGGA	59.014	20
241	15	255	AACGAGAGAGAGAATGAGTG	59.93	23
229	49	277	GTGGCCGATCGAGTTAGAGA	60.362	20
250	358	607	TGTTGATGGTTGAGAGGTGTC	58.553	21
278	808	1085	AGAATCACAATGCTCCTGGC	60.226	20
124	331	454	AAAAATGATGATTCCGGGTC	58.691	20
190	475	664	TCAATATGAATTGATCGCCG	59.478	20

270	363	632	TGCTCGATCCACCTCTTGTA	59.394	20
274	347	620	AAATCAAATTGTGTCGAGGC	57.668	20
183	3242	3424	GTCTAAAATTCGGCAGCGAC	59.851	20
246	1071	1316	GGGATCCACCACTGAGTCAT	59.774	20
203	189	391	TACGTTGTACTGACGCCCTG	59.781	20
153	6	158	TGAAGTTTCGAAGACTGGAAG	59.097	22
200	321	520	AACGGTTTTTCACCGTTGTC	59.875	20
100	461	560	AATATTGGCTTCCCCAAACC	60.02	20
129	8	136	TGTAGCCGACCCCAATTTAT	59.297	20
174	263	436	TGAAAACGATTTAAACGTGGG	59.855	21
206	4486	4691	TAATTCATGTAGCCGACCCC	59.784	20
253	718	970	AGTTTCTAGGTCGGCCCTGT	60.132	20
258	815	1072	TGCATACCAAGTTATTGGCG	59.585	20
126	977	1102	CAAAACGCCTCCAATTTTGT	59.975	20
175	721	895	TTTCTCATGGGTGTGGGATT	60.173	20
235	15	249	CTGCCATCTGGTACAACTGC	59.318	20
249	959	1207	ACCTATGGATGCACCGGTTA	60.214	20
155	224	378	CTCGTAAAATCCGGCAAAAA	60.068	20
271	8	278	ATGTAGCCGACCCCAATTTA	59.297	20
209	49	257	TGATCACAAACTTAGCGGACA	59.332	21
218	559	776	TGCTTATTTGGATTGGCCTC	60.038	20
236	936	1171	ATTGATCGAGACCGAACCAC	59.934	20
142	13	154	AGTTCTAGTAGCCCGGAGCC	59.87	20
214	141	354	CCTGAATTGCATTTTCGTCA	59.664	20
213	180	392	GCAGACCTAACATAGTGGGAA	59.552	23
223	40	262	ATCCTCCTCCACCCGTCTAC	60.336	20
273	235	507	GAATTCATGTCGGGTTAGCG	60.469	20
242	1217	1458	ACAGGCTGGCTCTTTCAATC	59.434	20
251	42	292	GGCTGCAGAAATGAGAGGAG	60.096	20
117	2	118	GGCCTAGACTTCACATTTTTCA	58.378	22
262	710	971	ATGCTTGCAAGGGTGTAAGA	58.379	20
242	18	259	GTACCGATATCATCCCCACC	58.937	20
220	473	692	AGGTCAGATCGAAGGTCTCG	59.405	20
257	108	364	ACTGCATCTGGATCCTCCAC	60.08	20
183	3253	3435	CAACACTGCAAAATTGGTCG	60.149	20
112	2998	3109	AAGGGAAGTGTGGGGAAGAA	60.852	20
221	728	948	ATCCCAATTTGGCAACTCAT	59.249	20
179	288	466	CCTGGAAAAGGTTGCTGAAG	59.846	20
268	323	590	TCTGGTGGAGGTTATGGGAG	59.92	20
244	458	701	TTCAGTCATTGCGTGCACTT	60.459	20
253	4	256	CAGAAATGACAAAATTCATGG	59.456	22
198	60	257	AGTCTCCCTCGCCAGAAAAT	60.212	20
276	959	1234	CAAACATTATGCACCAAGCG	60.133	20
168	192	359	CGCGCACTCAAATAGTAGCA	60.177	20
271	388	658	TGAGAGAACCTCCCCCTTTT	60.045	20
146	1360	1505	GCGGTTGAAGGTCTTATTGC	59.713	20
110	175	284	AAGCCAACAATGGAGGAGTG	60.111	20
154	7	160	ATGTAGCCGACCCCAATTTA	59.297	20
203	386	588	GCCTTCTCGAATTTGTCTGC	59.962	20
139	1	139	TGTAGCCGACCCCAATTTAT	59.297	20
210	1001	1210	CCGCAATTTGATTGGGAATA	60.641	20
280	88	367	TCACGGGTTTGGGAATTAAA	60.16	20
228	4452	4679	AGAGAAGGTCCCCAAAGCTC	59.817	20
230	949	1178	CCCAGCTCACGTTTACCCTA	60.125	20
245	57	301	TTTTATCTTCGGTGCGGAAC	60.074	20
253	31	283	GTTCATCTGTAACGGGTGGG	60.232	20
182	57	238	TCAGGTTGCCCTCCTTTTTA	59.679	20
217	24	240	GGTGGTATGGTGTGGAGGAC	60.096	20

269	35	303	TCTTCGTGTTTGTCCATTCG	59.691	20
279	815	1093	ACGCCATTTCGTGTTTAATGA	60.37	21
119	441	559	GATTTTCTCGGATTCCATGC	59.468	20
206	0	205	CACAATTTGAGGTGTATGGCA	59.454	21
252	376	627	TGCATTTGACAATCATGCAC	59.078	20
150	541	690	TATCATCCCCAAAGCAAAAA	58.082	20
209	48	256	CGTAAAGAATGGGCTGGATT	59.043	20
210	295	504	TTTGCAACGTGGTCTTCATC	59.697	20
138	939	1076	CAACTGTCCTTGGAAGAGGG	59.691	20
204	451	654	GTGTGGAAAAGGGAGTGCAT	59.973	20
215	483	697	CCACCTGCGAACCATAAAAT	59.823	20
251	292	542	TTTTGGATTGCAACCTCCTT	59.546	20
127	865	991	AATGGGTGGCCAAGTTAGTG	59.853	20
214	913	1126	GGCCTACAAACTGCCCATAA	59.96	20
277	272	548	GAAATCCAGAACGCAGGTTT	59.174	20
137	506	642	TGGAGTAAAAGATGGTGGGG	59.784	20
164	258	421	TTTTGCATGATTTTTGTGGAA	59.039	21
123	265	387	TTCTTTCGGCCATGACAAAT	60.448	20
155	892	1046	CCCCGCACATAGTCAAGAAT	59.955	20
268	2824	3091	TGTCCGGTGTCGTTTTAATG	59.439	20
251	453	703	GCTGCAATAATGGAGGGAAG	59.668	20
180	21	200	GAGAATGGAGCGGAGGTTCT	60.735	20
248	14	261	AGGGAGGGAAGAGAGGAGAA	59.367	20
152	40	191	TGACCAAGATACACCTTGCAT	58.09	21
186	2721	2906	TGGAATGATGAGGTGGGTAAA	60.177	21
218	638	855	AACCAATGGCGCATATAACC	59.688	20
251	12	262	AAATCCCCCTTTCCTAGGGT	60.014	20
117	398	514	TACTGCTCTCTGGGGCATCT	59.973	20
184	811	994	ACATTCTGGTCCGTAGGTGG	59.844	20
262	259	520	TTTTCCCCCTCATCTCATCA	60.395	20
140	8	147	TGGCCCAACCTCAATATTCT	59.387	20
196	1171	1366	GCGTGATACCAATGGATGTG	59.805	20
242	80	321	ATCGGGGTCTTGGAAGGTTA	60.683	20
106	36	141	CGGTTTTCCCTACTCTCCCT	59.571	20
176	5186	5361	TTTTAGCTTCTGGTGGGCTG	60.378	20
265	71	335	TTTGCCGATCATCCACTACA	60.073	20
253	2	254	TTCTGTCAATTTATGTGTTAACT	58.056	27
163	77	239	GCCATTGGAGTTCCAAAAAG	59.546	20
148	206	353	CTAGCCGAATTCTCCTCGAA	59.546	20
208	797	1004	GGGGGTTTTGGATGAACTTT	60.032	20
242	2286	2527	CTTCATCCACCTTCACACCA	59.52	20
123	34	156	AATAATTTACCGGCAATGGTG	58.751	21
270	123	392	GAAAACTGAGCCAACCCAAA	60.088	20
119	157	275	CCGGTAATTCAACAAAACGA	58.531	20
279	1611	1889	CCACGAATATGACGACAACG	59.988	20
261	1847	2107	AAAAAGGGTCCAAAAGTGGG	60.193	20
208	1363	1570	TGCCTTCTTTAACAGCCCAT	59.708	20
266	715	980	TTCATCAGGCGTATGTGGTC	59.527	20
235	2126	2360	TCCCACGAGGAATTTGAGTC	60.05	20
268	362	629	GAGGTTATGGTCACGGTGGT	59.703	20
253	282	534	ACAACTCGTCTTCCGTGGAT	59.579	20
120	26	145	GCCAGCCTATCTCCAGTTTG	59.836	20
213	140	352	GCATGGGGTTATTCAAGAGG	59.387	20
122	209	330	TTGGTTCGAGCCATTGTGTA	60.111	20
270	192	461	AGTTTGGGTATCCGCTCCTC	60.464	20
269	1620	1888	TAAAGCCGAATTCGTTACAACA	59.661	22
119	116	234	CCGGTAATTCAACAAAACGA	58.531	20
218	971	1188	GGACCGTCACAGTTAGTGCC	60.577	20

110	691	800	CGTTGTTAAACGCATACCACA	59.541	21
201	457	657	AAATCCAGCAGCAAATCGAC	60.221	20
153	128	280	CCGAGAGATGTCTCCCAGAA	60.34	20
245	44	288	TTTCGGGAATTCAAAGCATC	60.016	20
267	726	992	CTCCCACCCAAAAATCTCAA	59.903	20
268	80	347	TTGGGAGCAAATTTCAAGAGT	58.823	21
279	52	330	AAATTGGTGCGGATGTCTCT	59.556	20
256	437	692	CAAACCGACAGGGAAACACT	60.005	20
249	31	279	ATTCGGTTGCTTTTGTCACC	59.978	20
136	147	282	ACTGTTGTTGCTGCTGTTGC	60.104	20
154	633	786	AAACAGTTTCCCTGCAATCG	60.11	20
241	3776	4016	CAGCTTGACCACAATGCTGT	59.905	20
186	313	498	CAAGGAAGTGGCATGCTTTT	60.249	20
241	305	545	GTTTTGCTATTGTGGTGTTTCA	59.088	23
277	1729	2005	TGTGAACTTCCTCCAACAACA	59.172	21
185	1653	1837	CCACCAAAACCACCAGTACC	60.126	20
159	28	186	GAATTTGGCCAAGTCGATTC	59.51	20
268	5474	5741	CTTCGGGGCTGCATAGATAA	60.188	20
274	270	543	TGTTGAGGCATGGCTATGAA	60.22	20
230	3121	3350	ACAGTTCAGCTCCACAACCC	60.159	20
221	728	948	CATGTGCATCAAACGGAAAC	59.972	20
168	1030	1197	AGCCACCGAAACAAAAAGAA	59.724	20
183	83	265	TGAGATTCACTTGCCCCTTC	60.195	20
190	2468	2657	GAGGGCTCTTGGTTCTCTCA	59.53	20
274	3241	3514	TCTTCTTGACCAATAATAAAGA	57.423	27
137	101	237	CCAAACCAACCTCGCTCTTA	60.241	20
223	36	258	AAGAGATAGGGGAAGGAGCG	59.805	20
143	207	349	AGTTCTCCTATCCTTCGGGG	59.531	20
165	1	165	CCAGACATCGAAGAAGCTGTT	59.487	21
269	8	276	AGGAGCCACCTGATGAACAC	60.12	20
228	1554	1781	GCTTGTCCTCCACTTGAAGC	59.997	20
184	330	513	GGGAGGTTTCGTCACACAGT	60.009	20
111	1	111	TGTAGCCGACCCCAATTTAT	59.297	20
229	127	355	ACAACCAGTTGGGTTCGAGA	60.545	20
165	56	220	ACCTAAGCAATTGATAGTGCC	60.036	23
279	70	348	GTTTTCCACCAAGGTTGCAT	59.836	20
160	1627	1786	CGATCTTTTCTTCGCCATGT	60.214	20
279	187	465	TCGGTTTATACAATAACCAATT	57.809	27
252	21	272	TGACATTCCTTTCCATTGGC	60.843	20
279	90	368	AGTCACGGGTTCGAATTTCA	60.495	20
174	36	209	GCGAGTTTCTTGAGGTCGTC	59.997	20
270	351	620	CTGTTGTCGGTGGTCATGTT	59.441	20
162	247	408	TCGTGCAAGTTTTCAAGATCA	59.454	21
152	922	1073	AGGTTGCGTACATCTGACCC	59.997	20
253	3200	3452	AGGTGCTAGCAGCATGGAAT	59.866	20
173	327	499	TCACGATCCTTCTGTCCCTT	59.655	20
200	295	494	AAATCCCCTTCCCATCATTC	59.959	20
240	479	718	CGCTTCCCATTGATTTAAGG	59.542	20
254	304	557	TCAATTCAAAATCAAACCATG	59.816	22
167	514	680	CTTGAATGTTCACGGCAGAA	59.84	20
134	122	255	TTGATACTACACGGTGGCGA	60.134	20
188	310	497	TTAATGCATTTTGCCTGCAT	59.173	20
119	2149	2267	ACTTGGCACGATCCAATTTT	59.434	20
118	889	1006	CATCCCATGGCTGTTGTTCT	60.924	20
107	429	535	TCTCCTGTACTTCGTTTAGACA	59.377	25
239	245	483	ACCTATGGATGCACCGGTTA	60.214	20
209	85	293	ATGTTCATGTTGGGTGCTGA	59.967	20
189	880	1068	GGGATCCAAACCTCGACATA	59.75	20

162	768	929	GACGTCGCAGAGGAGAACAT	60.418	20
262	13	274	GTGGAGCTTATGTTGCATGG	59.152	20
182	56	237	TGCCATGATTGTTGAAGGAA	60.049	20
189	1205	1393	CCATGCATTTCAGGTTTTCC	60.309	20
160	2407	2566	CTCCAAAAGCTTGCACACAA	60.027	20
257	394	650	TGGTGATTCCTTGCAATGTG	60.517	20
261	134	394	TGACATTGTGACCTTCAGGC	59.682	20
279	10	288	ACCATGAAACTAGCCAAGCA	58.379	20
136	3215	3350	ATCTGGGATTTTCTGGCTCA	59.629	20
246	262	507	AAAATCTTTTGGGGCGTTCT	59.945	20
218	612	829	ATGTCTATCCCCTTGGGTCC	60.015	20
259	2165	2423	GAAACCGAAACCCGACAAAT	61.08	20
265	1173	1437	CTTCCCTAACCGTCCCTTGT	60.353	20
110	310	419	GCATTTGTTGTTGTGGCATC	59.979	20
271	455	725	ACAAAACACAACAACCCCGT	60.171	20
230	533	762	TGCGGATGTTGTGGGTAATA	59.809	20
250	541	790	TGTCAAGCTCTTGCATAGCAG	60.219	22
135	1587	1721	CCGCATTGGGTTGTGTAATA	59.301	20
111	1231	1341	CTGGGTCCAGACAACACAGA	59.705	20
158	958	1115	AAGCGTTGAAGCAGCAAAGT	60.197	20
103	358	460	CCAACCTCAGAATCATCTTTC	59.17	22
144	337	480	TTGATCTCAGTCAGCCATGC	59.95	20
238	17	254	TCAAAACATTTAGTTGGCACA	58.601	23
181	274	454	CTTTCTCCATCCTCAACCGA	60.187	20
246	6	251	ATATAGGCCCAAATCTGGCA	59.392	20
190	17	206	CTATCGGTACTCGGATGGGA	59.91	20
175	3093	3267	GTATAGGGGCGTTGGCTTTT	60.332	20
181	459	639	AACCCTCCCCTCTCCAAATA	59.761	20
120	54	173	ACATCATATGGCGGAGGAGA	60.448	20
221	2046	2266	ATTGGTCCAGTGCCCAGTAT	59.288	20
166	385	550	CCGTGTTCGATGACTACGTG	60.175	20
262	535	796	TCTCGCAGAGGAGGTCAAAT	59.95	20
178	421	598	TCATCAAGATTGAGATGGCG	59.756	20
184	1180	1363	TGCGGGTAAAAACCCAATAA	60.178	20
113	1972	2084	TAGACACATGCCAACTCCCA	60.112	20
233	655	887	TGATGGTGACAACAGGAAGC	59.682	20
112	1183	1294	GGGACAACGGGTTCTGATAG	59.405	20
206	142	347	CCAGCAGACACGAAACAGAA	60.025	20
280	86	365	GGTCTCAACTTCGCGATCAT	60.226	20
103	71	173	ATGGTTTGGGAATAATTGGG	58.483	20
276	715	990	GATTCGTGTCGGGTTAGCAT	59.962	20
243	65	307	GGGTGGTTTATGGCCTTTTT	60.055	20
108	0	107	CATTTGGGGGTATTACAATTTT	58.2	23
278	130	407	GCGTTTCTTAAACTGCCTGC	60.025	20
142	52	193	AGCTGCACGACATGATTGAA	60.423	20
102	289	390	GAAGGGGGAGACCGAAATTA	60.258	20
153	62	214	TGCTCTTTTCACACCACCAG	59.873	20
163	625	787	CGACCTTTTGTTGTGCTTGA	59.881	20
160	254	413	GTGGAGGGGATTTGTGTTTG	60.21	20
248	15	262	GTATTCGAGCAACCACCTCC	59.556	20
257	459	715	AAAATATGGTGTGCATAACGA	58.579	23
199	126	324	ACAGTCTTGCGCCACAAAAT	60.699	20
141	816	956	TTTGGATTGACAAGTCGGGT	60.353	20
254	1856	2109	TATCGTCGTGGTGATCTTGC	59.679	20
220	840	1059	AGGTGCAGATGTGTCTGTCG	59.897	20
206	1738	1943	TACAAGAGGCCACCGAAACT	59.734	20
222	173	394	AAAGAGGTTGTTTCCGTTGC	59.218	20
110	2958	3067	ATGATGCCACAGGAAGAAGG	60.073	20

149	504	652	TGAGATTCACTTGCCCCTTC	60.195	20
192	1423	1614	TGACCCAAGGTCCCAAGTAA	60.345	20
144	721	864	ACCTGCACCACCACCAAG	60.59	18
228	250	477	AATGATTGGGTGTCCATTGAA	60.044	21
204	3160	3363	GCCCAAACAGCAATTCAAGT	60.118	20
225	1146	1370	AAAAAGGTCCCCTTTCCAAG	59.433	20
254	99	352	GTTGCAAGGAATCATTGGCT	60.081	20
197	125	321	CCCATCTCTTGTTTTCTTCATC	60.469	23
153	300	452	TTTCGATTTCCACCTTCTCG	60.184	20
279	741	1019	AGGCTTGCGGGTCTTACTTAG	59.92	21
175	972	1146	CCTGAGCTCCTCTCGAATTG	60.088	20
248	1929	2176	GCAATGTGGCATTCATTCCT	60.874	20
151	76	226	TTTGCTGAATTTTCTTCGCA	59.562	20
275	2339	2613	CAAGCACAAAATAGCGAATC	58.971	21
244	49	292	TAGTGGGGGTCAGAACATGC	60.924	20
274	24	297	CCACAACTGGTCGGTATGGT	60.69	20
107	3	109	GCAGCAGCAACATACAAACC	59.351	20
150	2162	2311	TCTCCGCCATCAAATTCTTC	60.155	20
280	1437	1716	TTGTTGTGGAGTTTCAGGTG	57.109	20
228	189	416	TGCCTCCACAAGAATTGGAT	60.461	20
131	434	564	GCAAGACTGTCGTCCTCCTC	59.993	20
261	6	266	CCCAAGACCCCAATTTGATT	60.91	20
115	404	518	TGTTGTGCGTGCTTTTCTTC	60.035	20
150	6	155	TGTAGCCGACCCCAATTTAT	59.297	20
280	24	303	TCGAACTCCACTGTTCCATTT	59.583	21
207	1958	2164	CTCCTCAACCACGCAGTCTT	60.444	20
220	1078	1297	AATTATGGCGTTGGGTGAAC	59.691	20
242	9	250	TTCATGTAGCCAACCCCAAT	60.192	20
145	93	237	GCTACCTCTCCCTCTCTCCC	59.396	20
147	1322	1468	TTGAATGAAAAGAAGAGCTC	59.835	22
255	42	296	ACATCTGACCCACCCAAGAC	59.817	20
273	1236	1508	AACAGATGGGGTTGCAGAAG	60.111	20
229	1107	1335	CCCCACAATGTCTCGTCTTT	59.966	20
256	122	377	CCATTATCGGACGTTTCCTG	60.323	20
271	235	505	CGCCTTCTTTGCACCTACTC	60.015	20
148	859	1006	GGATTTGGCCCTGTGTGTAT	59.676	20
221	15	235	AGGAAAGGACATGGCATTGA	60.461	20
223	1000	1222	GTTTCCAACGAAGTTCCCAA	59.948	20
278	66	343	CCCCAATTTGACTGGGAATA	59.617	20
187	494	680	TAGATGGCTGGGAAAATTCG	60.031	20
247	89	335	GGGCAGTATTGTCAAACCAG	59.985	21
237	89	325	TGCATCCCGAGAGGGTAGTA	60.615	20
236	107	342	CGACCGAATAATCCTGTGGA	60.853	20
276	244	519	TCAGTGCTGTCCAAACCTCA	60.44	20
189	1091	1279	AGAAGGAAATGGGAATGGCT	59.903	20
266	126	391	AAAATGGTGGCTTTCTTCCC	60.299	20
263	2629	2891	GACAACATGGGGTTTTGGAC	60.073	20
110	66	175	TAGACAGCCACACCAGCAAC	59.905	20
173	1182	1354	TTTCCTCCAACATTGCTTCC	60.051	20
202	914	1115	CCAAGTCACCCAAGAATTGC	60.495	20
222	148	369	TTTGTTGTGGGTTACCCGAT	60.088	20
255	6	260	ATGTAGCCGACCCCAATTTA	59.297	20
244	122	365	CTTTTCACGTCGGGATTGTT	59.971	20
226	2424	2649	CGGAGAAGGAAATAGGACCC	59.897	20
160	2136	2295	ATCATGTCAAGGGCTCAAGG	60.073	20
243	148	390	GATGCTGTCACAGACAGGGA	59.827	20
268	474	741	CGAAACAAAATTGGGAGGAA	59.91	20
243	71	313	GACGTGGTTTTGCAGGCTAT	60.14	20

146	647	792	TATCCGTTCGGCTGTACCTT	59.592	20
186	113	298	GTCAATGGGAACAACCGTCT	59.827	20
176	2704	2879	CACATCATTTTCCCCACACA	60.216	20
186	270	455	ACCCCATCTCAACCAAATGA	60.173	20
265	610	874	CCAATCATACATGCAAAGTGC	59.055	21
264	1635	1898	ATTTGGGACCACTGTGGCTA	60.375	20
184	993	1176	GCTGCTCCTCATTGTCATCA	59.95	20
218	1650	1867	AAATGCCTGTCAACCTCCAC	59.973	20
112	29	140	CAATCATGTACACCCGCTTC	59.002	20
258	28	285	CAGCACCACCAGCGAGAA	62.247	18
113	161	273	TGCGGATAATACAATGGAGC	58.603	20
275	139	413	AGTGGTGGCAGTCCATTCAT	60.395	20
243	66	308	GGAAAACTTTATCATTTCCCTT	59.743	24
257	6	262	TGGCCTTTTAATAGGATGCG	60.054	20
206	4164	4369	TTGGGAATTTCTTTCCATGC	59.878	20
277	52	328	AAGGGTCGGAAGTGTGAATG	59.966	20
200	45	244	GTCCAAAAGCTTATCGGCTG	59.845	20
280	474	753	TGAAATCCCTCAAATCTTACC	59.83	23
206	100	305	CCAGTGGGTTTGTTTCTGGT	59.861	20
230	83	312	GCCCAGAATGGAATAGACGA	60.036	20
176	1316	1491	CCCATCATAGGGAAAGGGAT	59.974	20
230	4796	5025	CCGACCCCACTTAGTGAAAA	59.964	20
238	1467	1704	AATGGAGGACATGATGAGCC	59.893	20
272	2829	3100	TGGTTTATGTAGCCAACACAA	59.72	24
109	918	1026	CTCGTGATTCAGTCCTCCGT	60.261	20
211	82	292	AGGTAATTAGCGCACCCACA	60.523	20
217	1210	1426	ACAGGTGCAGGAGTAGGTGC	60.329	20
269	895	1163	TCGTCTTGATTTTGTTCTGCAT	59.752	22
234	135	368	CCCGACTTCGTCTCTACGAC	59.867	20
278	487	764	TCACAGACTCACAGTGTTGGC	59.931	21
222	2180	2401	GGCATAAGAATTGGATGATGG	59.244	21
196	871	1066	AAGGGAAAAGCCCCTATTTT	58.152	20
253	120	372	TCATTTCTAAACCGGAACGG	59.931	20
252	120	371	TCATTTCTAAACCGGAACGG	59.931	20
143	4	146	AAAACACAAACCTTTTACACC	58.964	24
220	1327	1546	TCGAAGTAGTGCCTCTTCCC	59.43	20
176	948	1123	TCATGGCTTGACAAACTCGT	59.293	20
172	1943	2114	GCTTCAACCATAGCACCCAT	59.962	20
264	13	276	TTTGGTTCATGTAGCCGACC	60.894	20
163	133	295	TTTGGTTCATGTAGCCGACC	60.894	20
249	2238	2486	GGTGACGGAGTTGGATTCTG	60.51	20
163	139	301	CGAGATTTATGAGAGCCCCA	60.17	20
277	469	745	GTTGGTGGATTTTGGGAAGT	58.741	20
153	2664	2816	TCTCGTGTAACGAACAAGCAA	59.521	21
197	127	323	CGTTGCAGAAGTTTGCTTGA	60.172	20
278	104	381	TCTTTGCCTTTGTCTGGAGC	60.517	20
235	386	620	CACCACAAGCGACAAGACTTT	60.341	21
183	457	639	CAGTTGGTGTTGAAGCGAAA	59.881	20
108	856	963	CGTAAACCGAAACCATGGAG	60.357	20
222	1101	1322	TCAGTTTATCCGTTCCTCGC	60.214	20
144	12	155	ACTGGTGGTCCCTTTTTCCT	59.834	20
193	207	399	GGATGATGATGTTCAGATGGG	60.15	21
236	450	685	CATCCTTGCCAATTTCCATT	59.762	20
254	3	256	ACCCCTTGCGGGGTAATA	60.148	18
240	1725	1964	CACGAACACCCCTGCATATC	61.329	20
261	125	385	GCTTATCTGGACAACCCCAG	59.55	20
222	812	1033	GGCAACCTCAATGTCCAAAA	60.874	20
191	334	524	TATGGAGAAAATCCCTCCCC	60.089	20

236	2089	2324	AATCCGAGGTGTGTTGCATT	60.384	20
212	558	769	TGCAATTATTGGGTTCCAAAG	59.818	21
169	949	1117	CATAATCAGCAGCAGGAGCA	60.119	20
206	1492	1697	TGCATTTTCACGTGCATTTT	60.118	20
189	26	214	TCGAAGCTGGAGATGTGACTT	60.005	21
252	267	518	GGCAACGTGATTCAGTTCAA	59.697	20
176	97	272	GCCGAGGGTGAAATAGATGA	60.036	20
215	1	215	TTCCACGTTTCCTTAAAATATG	60.01	24
269	734	1002	TTTTTGCAACGGCTACAATG	59.742	20
167	142	308	CCCGGATCAACTCACTCCTA	60.065	20
182	50	231	TTGGTACTCACAAAACCCCC	59.688	20
123	405	527	TCGCACCACTTCACTTTCAC	59.88	20
151	671	821	TCGCAATTTTCACTGATGGA	60.197	20
244	411	654	TTCTTGCAGGAGAATGCAGA	59.673	20
153	320	472	TGGAATGTCTTCCATTAAGTG	60.014	23
265	3523	3787	AACTACCGAAAATGGGGACG	61.088	20
175	491	665	TAATGGGGAAGTCCTAGGGG	60.138	20
235	355	589	GCGGACAATATGGGATCCTT	61.044	20
192	209	400	TCCACCACTGAATGCTACGA	60.263	20
171	1348	1518	TTGGGCAAGAACGCTAATTC	60.209	20
215	24	238	TTGCAAGAAAATTGTCCCGT	60.481	20
247	478	724	CACCACCGCCCTACAAGTAT	59.875	20
160	329	488	ATGATCCATACAGCCGACCT	59.39	20
243	474	716	TAATTTCCCCCAATTTTCCC	59.833	20
243	1649	1891	AACATCCCTCCACTCACTCG	60.112	20
168	704	871	GCCTAAGAAGCCCAAATTCC	60.041	20
153	3	155	TGAAGTCCGGATCAACTTACG	60.118	21
192	420	611	CAGCCATGCTTCTTATGCAA	59.976	20
136	43	178	CAGCGAAGTGACAACCTTGA	60.025	20
179	253	431	TGCAAAATCAAGTATACGTTT	59.098	23
245	116	360	CAGCTTGTGCCTTGCAACTA	60.195	20
161	885	1045	ACCCAACTGATGTGGAGGAG	59.962	20
206	1888	2093	ACTGGCGACCTAGCAAAATG	60.27	20
110	266	375	ACATTAACCACAATGGAGGC	57.39	20
142	1429	1570	CAAAACCAGAGCAAGGGAAA	60.22	20
218	791	1008	GGATGCCATTTCTTCTCCAA	60.014	20
171	497	667	ACTTCCGATTTTCTCGGATTC	59.546	21
223	165	387	TCAAAACCAGCACACACACA	59.751	20
193	733	925	GTTTCTTGGACAAAGCAGCC	59.859	20
105	0	104	GTTGCGATTTTTAAGGACGG	59.586	20
108	82	189	GAAGGGTGATGCTTTTGAGC	59.82	20
217	409	625	AATGTCGCCATAAACCAAGG	59.823	20
122	1822	1943	AGGCAAGAAAAGCTCGAATG	59.592	20
136	902	1037	TCAATACATGGCATTGGTGG	60.197	20
279	1326	1604	TCTGCAATCAATCAGCAAGC	60.104	20
251	102	352	TTCTTGTGGTTGTTGGTGTTG	59.495	21
252	311	562	TAGCACCCGTAGTTGCTGTG	59.928	20
245	2186	2430	GCCACACCTGGAGTTTCATT	59.973	20
123	5	127	CCAATTTATTGGGATTAAGGC	57.539	21
197	560	756	TCGCCCATTTTGAATTAACAC	59.824	21
226	48	273	CACGCATCTTGCCAGTACAT	59.746	20
169	738	906	TACCTCTTTTTCCACGCCAC	60.11	20
259	56	314	CCAATCATCGGCCTTTTCTA	60.031	20
274	82	355	GGGGACACATCACAGACCTT	59.817	20
263	822	1084	GAGGTGAGGTTCCATCTCCA	60.048	20
244	478	721	CACAAAAGATCGCAGCAGTC	59.596	20
209	146	354	AGTTTATGACCATCAGCCGC	60.103	20
213	3484	3696	CTTGGCCATGAACCTCATTT	59.933	20

120	1846	1965	AAAAATGTTTCTGTAGTGGTTG	58.647	25
117	569	685	TCACCGTAACTCCATGATGC	59.527	20
269	24	292	AACATGGACTGGAAGTTGCC	59.973	20
258	418	675	TTTCGCCAAATTCTTCAACA	59.277	20
162	267	428	TTTATTCCGTGACCCTCGAC	59.933	20
213	144	356	GATTGGATTTAATTCCCCCG	60.329	20
169	873	1041	GCACAGACTGAGCCATTTCA	59.992	20
168	1610	1777	CTGCAGCGCTGTATAATTGC	59.636	20
151	339	489	TTGGTCCCAAATCCCTACAA	60.162	20
195	630	824	ACCAAGTTACGTGGCGTAGAA	59.685	21
121	1226	1346	TTTGAACTCGATTTGTCCCC	59.91	20
279	2294	2572	TCCCACTCCCATTCAACTTC	59.903	20
224	579	802	AGGAAGCAAAAGGGAAAACC	59.571	20
130	423	552	ATTCCACAGACCAAAACCCA	60.21	20
275	9812	10086	GGTCATTGCCTCGGATTAAA	59.901	20
182	341	522	AATCCCCGTCCAATCATTTT	60.378	20
216	783	998	TGGGACTTGGAACTAGGGTG	59.959	20
110	9	118	TGATTCATCCTCCGTTGTGT	58.933	20
100	14	113	TGATGATGATAATGAGGTTGCT	59.974	23
232	3792	4023	CGGTGTGTTGCATCTCTCAC	60.319	20
265	261	525	GCTGAGCTGAAGGAGATCCA	60.645	20
219	93	311	TTAGAGGTGTCAAAACGGGC	60.11	20
119	377	495	TAAATTCGCAAGGGGACAAC	59.938	20
120	11	130	GGACTGGAGCAGGTGTGAAT	60.12	20
278	129	406	CAATCAACAAAACAAGCCCC	60.344	20
159	1884	2042	AATCACCCTCGAATCAGTTTG	59.042	21
207	444	650	GCATAGGAATGAATGGAGAA	59.93	22
175	6	180	TGGGTGAGAACGAGGAGAAT	59.655	20
177	219	395	ATGCATATATTCCGTTCCGC	59.785	20
244	767	1010	AAAACGGAATCTACTTAGGGG	58.99	23
248	138	385	GTGGCTTCTGATGACGAGTG	59.42	20
280	1143	1422	ACTAGAAGCATTTGGCGCTC	59.62	20
182	118	299	ATGTACACCCACTTCGGCTC	59.997	20
104	32	135	TGGATTCCTCATTTTGGTCAC	59.782	21
171	132	302	TTGAAGATGATACGTTGAACC	58.952	22
247	2472	2718	GTTAAGGCGGTGGTGATTTT	58.952	20
270	606	875	TGGCATAATGATGTTGATTTG	60.568	22
125	142	266	AACAGGGGGAGAATGGAGAT	59.755	20
273	73	345	GGGGTCGACTACATGAACCA	60.78	20
242	249	490	ATCCTCAACTCCATCGCTTG	60.218	20
205	134	338	AATCCAAATTCCGTGACCAA	60.17	20
208	134	341	CCAAATTCCGTGACCAAATC	60.17	20
185	65	249	CCATCAAGCTCAAGTGCAAA	59.988	20
107	9	115	AGCAAACCCTAATCGGCAG	60.22	19
267	513	779	TAGAAGCAGCAGCAGTTTGC	59.517	20
211	10	220	ATGTAGCCGACCCCAATTTA	59.297	20
244	50	293	TGCTCAAGAAAATGAGAGCAA	58.785	21
233	301	533	TTCCATGCACTCTTTTGTGC	59.847	20
278	228	505	GCGTAATCCCCTATTTGCCT	60.3	20
136	1313	1448	TCACCCTCAAACATTCCACA	59.935	20
225	90	314	TCGTCTGTTTTGTGCGAGTC	60.032	20
278	54	331	TGTTCAAATCTGTGAAGGCA	57.806	20
269	25	293	TCCATGAAACATAAATCTTGC	58.946	22
227	938	1164	TAGGTCACACTTGCAGTGCC	59.905	20
199	1055	1253	TGTGAAAATCTCGGTTAATCCA	59.729	23
239	616	854	GGGTCAGATGTACGCAACCT	59.997	20
159	1	159	TGGGTTCAATGCATTTACTTCT	59.891	23
114	938	1051	CAGCAATACACGAACTGGGA	59.716	20

181	2	182	TGAAATTGAAAACCTTAAAAA	58.297	25
194	2816	3009	TCCTTTTCAAGGTGCTTCATTT	60.109	22
189	307	495	GAGGACCTTCAAGGGTGTCA	60.088	20
136	927	1062	AGATTGCTGTGATGTGGGTG	59.551	20
192	820	1011	AGGCACAATATTCGACGAGG	60.096	20
148	1	148	ATTTTCCTGATGCCGATCC	59.846	19
277	262	538	CAAAAATGATCATCCAACGG	58.818	20
193	718	910	GACCGGGACTGTAATCCTCA	59.927	20
110	1206	1315	GTGTGGATGGTCTGAATGGA	59.318	20
245	175	419	GCATCAAAACATTTCAGCCA	59.67	20
274	61	334	AGGGTAGGAAGCCCAAAGTG	60.488	20
165	115	279	CCATCAGTTCCTTCTAGGGC	58.741	20
256	205	460	TTTGGTTCATGTAGCCGACC	60.894	20
193	128	320	TCATTGGCTCCTTTTTGGTC	60.051	20
125	136	260	CGTTGCTGGTGATGAAGAGA	59.984	20
265	186	450	TTCTTCAACATTCCTGGGCT	59.67	20
243	483	725	CCATCGGGTGCAATGATTA	60.291	19
249	8	256	CCCAAGACCCCAATTTGAT	59.59	19
270	642	911	TAACGGGAGAAATGGTCCAA	60.301	20
229	256	484	ATGGTATGGTGTGGAGGACC	59.511	20
171	147	317	ACGGGGCGTGCATATATTAG	59.838	20
212	258	469	ATCCTCCACAGAAATGCCAC	59.934	20
213	30	242	GGGTTTAGGGTTTCCCATGT	59.919	20
235	8	242	AGTTTCATACCCCCACCACA	60.088	20
278	295	572	GAACACATTGCTGAGAGCACA	60.048	21
114	1797	1910	TTTCTGATGTTGTTGCCGAC	59.697	20
261	99	359	CATCTCATGTCCTCGCCTCT	60.372	20
163	7	169	ATGTAGCCGACCCCAATTTA	59.297	20
127	59	185	TGTTTTTGAGAAGAAACAAGA	59.141	24
250	222	471	CCGTACTCCCCAAGAACAAC	59.449	20
279	428	706	TGATTAATAAACACTTTAATCT	58.996	26
217	88	304	TGTTGATGCTGTTTGGAGCTA	59.478	21
130	472	601	GATGTTGGAGCTGAAGAGCC	59.957	20
246	72	317	CCTCCATCAGTTCTGTCTAGGC	60.124	22
176	144	319	CGGGGCTTGCATATATCAGT	59.945	20
251	71	321	AAATGAAATCGTGCGAAAATG	59.957	21
175	985	1159	TGAGGTGTGTGATTCCATGC	60.544	20
262	6	267	CATTTTCATTTTCTTTTGTTTTTC	57.143	24
270	231	500	GGCACACTATTTTGGAGGGA	59.933	20
120	20	139	TTTTTCGAATATTCCGGTGG	59.767	20
164	298	461	AATAACATTAAACCCTAAACC	57.104	26
250	1744	1993	TTTGATTGGGAATAATTGGG	57.289	20
147	461	607	ATCCTCCATTTCCCATTTCC	59.959	20
261	1077	1337	TTAACTGGGCTGGCTAGGTG	60.262	20
262	156	417	TTGCTGTGGAACACCAGAGA	60.44	20
276	703	978	AGCCCGACTTGAAAATCAAA	59.685	20
174	1406	1579	ACCTCATTCCTCCCAATTCC	60.133	20
238	18	255	TCACTGTTGCCGATCACTTC	59.837	20
157	759	915	CATATTTTTCGTCGGAGGGA	59.894	20
201	366	566	TAAAGAGATGCTTGGTCGCC	60.352	20
279	1109	1387	GGGCCTCGTCTTTCAAAACT	60.61	20
144	290	433	AATTATCAAATTTCGGGACGA	58.437	21
219	2443	2661	CCAATCAAATCCAATCCCAC	59.991	20
252	469	720	GAGGATCTCGGGGAGCTAGA	60.832	20
172	237	408	CCCGACAGGCCACAATATAC	60.214	20
230	1455	1684	GTCGATCAAGGAACACATGC	59.093	20
163	1398	1560	TTCCCCGACTCACACTTAGC	60.255	20
264	1579	1842	CGAAAGCTGTCGGAAAGAAA	60.493	20

138	48	185	GAAGGGGTAGGAACTGGACC	59.795	20
243	3494	3736	ATGATGGACTTGCTTTTGGG	59.933	20
262	2	263	TGAATTGCTTTAATTTGTTGCT	59.278	24
221	291	511	TTGAACGCCGTTAAGTTTGA	59.344	20
169	3656	3824	CAAAGGGGCTGAGTTGAGAG	59.982	20
265	6780	7044	TCAAATTTTGGCACTGTTGC	59.712	20
262	504	765	TTCAGTTCGGTTTTCGGTTT	59.587	20
243	1440	1682	ATCCGTGCAGTAAAATGAAAA	57.327	21
275	82	356	GACGAAAGTCCTTCGGTCAA	60.232	20
137	466	602	CTCTCATCTTCACCGCCACT	60.408	20
268	2618	2885	CTCTGGTGCAACTCCATCAA	59.831	20
251	551	801	ACTCAGCGAAGTGGCAATCT	60.02	20
131	218	348	GAAGAAGGAGGAGGGGAAGA	59.749	20
201	1930	2130	AAACCACTTTTGGCGTTTGA	60.514	20
240	802	1041	TTAATGGGATGATAAGCGGC	59.892	20
213	99	311	AGCTAAGTTGATTATGGTGGG	59.528	22
105	19	123	CAGTTGCCCTTGGGATTAGA	60.066	20
180	898	1077	CCCATCCGGAAATCTCTACA	59.887	20
218	538	755	GCATCTTCCCACAAGCAAAT	60.081	20
146	24	169	TTTGCTGAATTTTCTTGGCA	59.42	20
270	1427	1696	GCAGCCACAAATGACAGAGA	59.992	20
250	182	431	AACATGAAAAATCCTCAATCC	60.069	23
104	50	153	TGGCCAAACGTTTAGTCTACTT	60.554	23
166	0	165	TGTTTCCATCTACACCTTGAGA	58.754	23
250	170	419	AATTCCAGCCCAACACCATA	60.192	20
250	94	343	CGGCATCCACATAACATGAA	60.343	20
117	44	160	TTCAATTGAGATCCATGGGG	60.66	20
213	63	275	TTGATTTTGCTTTTGCATCG	59.819	20
189	440	628	AATAAACATTGGGGGTGGGT	60.166	20
258	19	276	TTTCGTTGAATGTGACTGGC	59.697	20
235	1219	1453	GGAAAACGCATAATTCACCC	59.277	20
160	73	232	AAGGATGAGGAAGGCAAGGT	60.074	20
183	1556	1738	GCATTGCATCCTATCCCATT	59.751	20
169	243	411	TGGAAATCTCTCAGTTCGGG	60.187	20
143	3851	3993	AGGTTGCGTACATCTGACCC	59.997	20
115	284	398	AAGAGTTCGGTTGCGTTGTT	59.78	20
145	347	491	CCATTCTTAAAAGCCTCATTTC	59.632	23
252	154	405	TGTCTCCCTCACACCCTCTT	59.682	20
143	112	254	AACAGGTTCAAACCAGTGGC	60.012	20
220	1016	1235	ATCTTGAACCCCACCATCAA	60.173	20
261	102	362	TGGAAAATCGTTGTTGACCA	59.941	20
264	31	294	TGAGAAGGTTTTCTGGGGAA	59.641	20
254	272	525	GCCGCTAGCATCTATTACGG	59.859	20
194	206	399	TGAGGCAACATGCTTTTGAA	60.379	20
130	28	157	TACTCTCAAACGTAGGGGGC	59.195	20
178	2541	2718	CCTTAAAATCAGTCCCGCAA	60.067	20
277	872	1148	CGGCCCAATATTTAGGCATT	60.991	20
113	1	113	ATGTAGCCGACCCCAATTTA	59.297	20
241	269	509	AAATGCGTTAGAAACCGCTG	60.264	20
196	0	195	CCAAGAGACTGAAAGCTCCAT	59.886	22
255	91	345	GGTTTTAAATTCGTTGAAACCC	59.67	23
193	185	377	AACTTCAAATTTCAGCGGGA	59.685	20
210	451	660	ACGAGGAATCCGAATCTGAA	59.629	20
270	364	633	AAAGGCCGCATCCTTTGATA	61.795	20
139	23	161	TAATCCTTGAACTCGGTGGC	60.074	20
212	168	379	AACAAGTCGGCAAAAATTGG	59.975	20
160	306	465	GAGTAATCGTCTCCGCTTGC	59.985	20
229	89	317	CTTGCCAGGTTGCAATTATG	59.182	20

195	1320	1514	GCATTTGAAACAATGCCAAA	59.543	20
134	591	724	GCGATAGTCATGGCTGAAGG	60.765	20
278	1958	2235	TCTGTGGTTGTTGGCATAGC	59.722	20
146	400	545	ACCCTTCAGCCACTGACCTA	59.721	20
114	14	127	CCATTGCACTCCGAATAGGT	59.955	20
136	310	445	GCCAATTCTGTGGACCTCAT	59.934	20
243	13	255	GGAAAGAAGCCAGCAGAGAA	59.694	20
214	1189	1402	CTGGGTAAATCTACGGGCTG	59.587	20
138	16	153	CTCAGATGATGAATCCGCAG	59.348	20
248	186	433	ACGTGAGAAGATTGGGAGGA	59.655	20
274	1780	2053	TCTGGCCTTCTTCGTGTTCT	59.989	20
164	483	646	TTGGCCGTCTAACGGATAGT	59.592	20
279	23	301	AAAATACCCGCAAAGTCGGT	60.721	20
275	397	671	ACCCAGCCTCGATTATGTTG	59.955	20
220	212	431	GGAATCCCAATCAGAGAAA	58.578	22
270	335	604	CTTCAGCTTGGTTTTGGAGG	59.846	20
263	1428	1690	TTGAAAATGACGACGTGGAA	60.088	20
156	186	341	GCAATGTATATTGGGTCGCA	59.405	20
147	0	146	ATCTACAACAGGCGGCGG	62.174	18
278	702	979	TCTTCTCTAGCCTGGTGGGA	59.943	20
217	57	273	AAAACCGCAAATTGAACGAG	60.11	20
261	64	324	TCAAACCCATCATGAAATCC	58.187	20
178	238	415	AATGCTCAAACGCTGACTGA	59.596	20
246	75	320	CCCGATTTCAGTTGTTCCAT	59.79	20
255	1879	2133	TCACGCCTGTTTCTGTTGAA	60.427	20
237	17	253	CATCTGGGTGTGTGAGTTGTG	60.055	21
192	426	617	GTGTAATTTGGTTCACGGGG	60.088	20
161	504	664	TTCGCGACGGTTCTAATAGC	60.364	20
171	5	175	GGGTCCAACTACGGATAATGC	60.576	21
226	350	575	TTTCAAGCAACCTCGCTTTC	60.502	20
271	597	867	AAAGAGCGGTAGTAGCAGCG	59.813	20
212	437	648	CAGTGAGCTCTCCGAAAAGG	60.126	20
188	2349	2536	CAACCACTTTTCGGTGCTTT	60.147	20
266	317	582	TGATCGCCACTGAAAGAAAG	58.999	20
112	814	925	AAGGGTCCCATCCCACTTAC	60.052	20
106	12	117	CATTCAAAATAAAATGATGAT	57.394	27
108	347	454	ACTCGACCAAAAAGGTGTCG	60.149	20
240	981	1220	CCGGAGTGGTACACAGGATT	59.844	20
169	1632	1800	TAATGTCTTCAGCTTGGGGG	60.066	20
200	157	356	TTGACTCGCGTAAAAGAATAT	58.574	25
222	211	432	CGAAATTAATTAAGGAAAAGA	60.089	26
194	310	503	AATCCCCCTACTCCTCCAGA	59.89	20
182	3473	3654	GATCTCGGAACCGCTGTTTA	60.214	20
220	729	948	ACGACATGAAGCTTCTGCAA	59.596	20
230	1446	1675	TCACAATAAACCTCCAGTTCC	60.221	22
278	407	684	ATTTTGCTCACCCTGCTCAT	59.7	20
130	601	730	ATGGGGACATCAAGTTGGAA	60.173	20
244	345	588	GTCTAATGTTTCCGCCTCCA	60.074	20
137	227	363	ATTTTTATGGATTGTGCCGC	59.801	20
248	66	313	TGTTTTTGACGGGTCCCTTA	60.336	20
261	417	677	CGCAGTTGATCTTCTGTCCA	59.984	20
228	5	232	TGTAGCCGACCCCAATTTAT	59.297	20
188	1677	1864	ATTCCAAAATAATTCGGCCA	59.259	20
215	826	1040	GCCCTGCCAATCTCTATCAA	60.177	20
266	704	969	CGCATCTTCCGAGCTATCAT	60.339	20
123	34	156	TGGGCTAGTAATCTGGGTCCT	59.969	21
274	628	901	TCCTAGGAAATTGCTGTCCA	58.298	20
238	100	337	TGTTGATGCTGTTTGGAGCTA	59.478	21

274	0	273	CCTGTAAGTCGCGCCTAAAT	59.384	20
265	148	412	CTCGATGCCATCTCCTGATT	60.181	20
186	14	199	TGCTAAAAACAAATGCCAAGG	60.116	21
270	118	387	AACGTGAAGTCAATTTCAATG	57.673	23
228	527	754	GCATCATGCATGGTCTTACC	58.956	20
200	2	201	AAAAATTGGTGCGGGTGC	61.826	18
277	2	278	GGAAAATTGGGTCATATAGCT	60.057	23
267	483	749	TTGTTGCAGTAGCCATGCTC	60.019	20
268	20	287	TCATTCCCCCTACACCACTC	59.779	20
157	31	187	TGTCAACGTAAAAGGAGGGC	60.11	20
164	164	327	CCATTCATCGTCGAAGACCT	60.073	20
267	873	1139	TGTTATTTGCACAATCATTTCC	58.556	23
230	932	1161	GCTTTGCTTCTTATGCGGTT	59.501	20
126	31	156	GATCAGCAGTGGCGTTGTC	60.429	19
239	145	383	CACAAGAGAAGGGAGCTTGC	60.134	20
267	113	379	GCTTTTCAGTTGGCATTTTTG	59.75	21
226	93	318	GGTTCCTGCGTCTTCAAAAA	60.227	20
276	345	620	TTGGCAGCTAGTGCTCATTTT	60.032	21
137	4	140	CCCAAGACCCCAATTTGATT	60.91	20
149	410	558	CACCAATCAATAATGCACGC	59.96	20
174	31	204	GGATAGAATGAGGGTTTTCCC	58.768	21
136	1686	1821	CGTGCGTGTTGAATTCATGT	60.584	20
276	6	281	CGTGCCAATAATGACACAAAA	59.476	21
131	615	745	TGTGCTCTTGAAACTGGGC	59.976	19
209	1498	1706	ATGCCAAAGTCGGAATTCAA	60.448	20
121	7	127	GGATCAGCAGTGGCTTTTTC	59.82	20
242	54	295	CAGCCGGAATCTGAGAGAGA	60.634	20
135	872	1006	AGAGCCATCAAAAGCAGAGC	59.723	20
280	90	369	CGCATACGATCTTGATTATGGT	58.992	22
207	352	558	TTGGGATTAAGGCTTTGGTG	59.931	20
262	298	559	TGGTGAAAAATCAAATACTTG	59.763	24
204	300	503	TGGTGAAAAATCAAATACTTG	59.763	24
217	376	592	TGGAATAGCTTGATAAATGAT	60.207	26
256	502	757	AATCATCACAAGCCCCAAAG	59.933	20
136	31	166	TAGCCGACCCCAACTTATTG	59.953	20
166	0	165	GGGGGAGAAAAATAAAGAAA	57.789	22
267	841	1107	TCGAGAACCAATAATGATGAG	59.186	22
163	1118	1280	CGACGTCGGTTATTTTGGTT	59.861	20
257	1240	1496	TCTTCCTTGTTTCTTTCTTTGGA	59.398	23
148	106	253	TATGAACGAACAGAGGCAGC	59.028	20
188	13	200	CTCTCCTCCTTCTTCCCACC	60.186	20
257	160	416	AACCTTGGTTCATGTAGCCG	59.993	20
128	85	212	ATTGACAGCAGGGAGGTGAT	59.535	20
247	17	263	TTGGTTCATGTAGCCGACCT	60.517	20
189	816	1004	AGTACGCCTCGGTGGTAAAA	59.632	20
157	18	174	GATGTTCGTATTAAATTACCG	58.746	23
275	570	844	ATGGCAAAGGTAAATGAGCA	58.241	20
211	661	871	ACCATTTAGAATTTTTCGGGA	57.623	21
257	511	767	CCCACCTTAGATACCGTTCG	59.448	20
230	433	662	AAGTCCAGCACTCCCAATTT	58.646	20
224	102	325	CACCACGACACACAGAGAGA	59.924	21
204	1	204	CCCAAGACCCCAATTTGATT	60.91	20
146	289	434	AGGTTGATCGTGTTGAATTAT	60.122	23
233	581	813	AAGTGCCGTTACAATCACCC	59.859	20
217	123	339	GACGATGGTTGCCTTTGTTT	59.978	20
146	257	402	GGAGGAGATCTGCTTGTTGG	59.803	20
262	300	561	AATGAGAGCAGTCCTTTTCCC	59.705	21
116	828	943	TGGTTGGAGCAATGAGTTTG	59.691	20

204	271	474	TCACCACATCAAAAATGAGCA	60.104	21
206	186	391	ACCTCGACAAATTCCCATTG	59.79	20
275	2267	2541	CAAAGATGAGGGTTGGCAAT	59.933	20
210	2321	2530	ACAGGAAAACCCAGAAGTGA	60.146	22
181	1060	1240	CACCGCCATGTTCCTAGTG	60.12	19
238	283	520	AAAACCTCATAAAACTGTCAT	57.456	25
183	172	354	CTCTTGCTGCTTTTTCCACC	59.993	20
152	803	954	AATTGGGGTGCAAAACAAAG	59.839	20
267	2146	2412	AGAACCCAAGAAGCAACATG	60.048	23
165	508	672	GTAGGGTTCATGTCCGGTTG	60.232	20
255	61	315	CGTTCCAAACTTCGAAGAAAA	59.366	21
256	1882	2137	CATGCTTTTTGACAACATTGC	59.22	21
219	521	739	GATTAGGAAGGTGCGTGCAT	60.103	20
162	258	419	TCTCCAGCTATCCCGTTTTG	60.206	20
267	533	799	GCAGTGGCGTTGAACTAACA	59.911	20
274	2225	2498	CCTCACGCAAAAAGAGTCAA	59.047	20
175	730	904	TGGTTCTTTTGGCATTGTGA	60.088	20
216	366	581	AATAAAGAGGGGCAGGGGTA	59.793	20
252	454	705	CTCACGGTTGATTGATACGC	59.152	20
262	23	284	GTGACGGTTGAATATCCGGT	59.676	20
164	857	1020	AGAAGAAAGGGGGAAAGCAA	60.18	20
272	525	796	ACTTCTCCTTCCACCGCTCT	60.393	20
117	775	891	GAGAACTGACTTCGGGGTGA	60.238	20
222	89	310	CAGTAAAATGCTGCCCAGGT	60.132	20
274	1396	1669	ACTCAGATCACTCAACCCGC	60.269	20
170	6	175	GAACGTGGGAGGTGAAGAGA	60.238	20
118	497	614	TCGAGCTAGAACCTCCTCCA	60.088	20
209	1283	1491	CAATGAGGACATCCGAGGAG	60.612	20
268	3603	3870	ACAATTGTTTGTGCACCTCG	59.615	20
251	3343	3593	AAGGGGTGAGAAAGCACAAA	59.711	20
148	12	159	TGTGTGCGATTTAATCCTAACC	59.013	22
169	42	210	TCCATAAGCCATAGCTAAAAG	60.125	24
230	2103	2332	TACAATTCGTCGAGATGCCA	60.22	20
160	1069	1228	TTCATAGCACGTTTTGATGCT	58.452	21
245	1725	1969	TGCCATTGCCATTGCTACTA	60.237	20
138	15	152	TTTGGTTCATGTAGCCGACC	60.894	20
280	90	369	CCCAATAACGAATAGCAGCC	59.569	20
200	3245	3444	TCCTCCCATTCTTCACATCC	59.862	20
189	81	269	ATTCGCAAGGTCAGTTCTCG	60.397	20
257	1105	1361	TGAACTCGCTCCTTCCATCT	59.95	20
137	322	458	GAGGAAAGCATGAGTGGAGG	59.803	20
188	19	206	GTTCGAACCCTTTCACCGT	59.958	19
260	3417	3676	TCAAGCAAAATGTGTTGATTG	59.575	24
245	541	785	ATCATTTCGTTCGGGTCAAG	59.933	20
225	393	617	AAATGCTGCTGTGTCGTGAG	60.056	20
278	81	358	TCAGAGGTGCACTCGAAGTT	58.594	20
239	1433	1671	GACCAGTTCACAAAAGTCCCA	59.997	21
267	281	547	AATTACCCACCGGACACATT	59.031	20
241	320	560	CGACACACAAAAAGTCGCAT	59.764	20
231	72	302	CAACTCGGCAAGATGAACTG	59.44	20
256	78	333	CGTGCCCAATAAATCCTTTT	58.943	20
180	203	382	GTTCAGGGATTCGATTTGGA	59.871	20
226	385	610	AAAATGAACGGCCAGGATTA	59.411	20
252	114	365	GGGTTCTTGGGTGTCAGAGA	60.088	20
280	12	291	CGTGTAGGATGGGAAATTGA	58.422	20
203	260	462	TAGCCGATCTCACTTCGTGG	61.336	20
170	45	214	CATGAAGAGGACGAAGCGTT	60.397	20
114	182	295	GTTAACCGCATGTCACTTCG	59.199	20

159	436	594	TGCACTGTCGAGAATTCGAT	59.399	20
280	791	1070	GCATGGATCTTTGGGAGAAA	60.014	20
269	762	1030	TATCTCCACCACCACCATCA	59.762	20
120	94	213	TTCCGTTGGCTTATTTTTGC	60.075	20
167	9	175	TATTACGAGCCACGGCTACA	59.349	20
251	684	934	AAATTCTTCCCCAATCCCAG	60.124	20
132	704	835	TGTTATTAAATCCTGCGGTATC	59.289	23
114	200	313	GCACGTCCAGAGGAGACCTA	60.408	20
148	324	471	GATAGGCGTTCGAAGGTGAC	59.7	20
262	624	885	AGAGATCGAAACCTGTTGGC	59.288	20
187	972	1158	TTCCATGTTCTGGAGAAGCC	60.195	20
171	794	964	TTCCACCGGAAGGTCTTAAA	59.541	20
168	83	250	GAAAACCCCCACTCAACTCA	59.943	20
270	69	338	CATCGAGACATATGCAAAAAC	58.701	22
262	1058	1319	TGGAAAAGTATGGAATTATTG	59.24	25
208	49	256	ATGTCCGGTGCTGTCTTTTC	60.119	20
239	245	483	ACTCGAAAAGTAGCGGTTGC	59.522	20
238	890	1127	GAACGTCAACGCTCGTACCT	60.321	20
277	1114	1390	AACTGCTGCCAGAACCAACT	59.914	20
209	10	218	TGCATAATCAACGGTCAATCA	59.945	21
203	413	615	CAAAAATGGCATTCAAGCTG	59.301	20
196	708	903	TCTTTTCAACATGTAGCGCAGT	59.948	22
279	779	1057	CCATGCCTTAGTGCAGTTTG	59.342	20
272	372	643	GGCCCAAACCATCAACAATA	60.564	20
109	440	548	CGTTGGAGCTGTTCGAATTT	60.249	20
279	811	1089	AAATCAGCACTCCCCATGTC	59.934	20
139	1376	1514	AAATTCCCCACCATTTCCTC	59.996	20
241	126	366	CGCCTTGAGTTTGGGTAAAA	60.103	20
158	1459	1616	TGCAGATTGAATGTGGAACG	60.665	20
151	3803	3953	CCAATTTTTGGCTCCATTGT	59.801	20
100	595	694	TGTTCTGTTAAAACTTCACATC	58.848	26
265	229	493	ATCGATCCGGGACTTGAAAT	60.662	20
176	29	204	ACTTCAAATGAATCTTCAACAC	59.177	24
238	178	415	TGAAGCCCAACAGATTGATTT	59.56	21
126	11	136	GAATTCTGAATGCATGGTTCTT	58.188	22
277	81	357	AGAGAGGTAGTGGTGACGGG	59.175	20
175	632	806	GCAATGGCAATAGCAACTCA	59.839	20
209	307	515	CGACCTCACATAGTGGGACA	59.545	20
252	1158	1409	GTGCACATGTCAAGTTTGGG	60.008	20
103	846	948	CTCGCCATCTCGGATAGAAC	59.797	20
154	364	517	TTTCTGCTCTTCCTCTCGGA	60.21	20
231	242	472	GATTGCCTTGTTTACCCGTG	60.365	20
267	68	334	ATGGAATCTGGGGTTCAACA	60.173	20
202	612	813	GAGGAGTAGGGGGATTACCG	59.783	20
153	347	499	TGGGCGAAAATTCAACTAGG	60.067	20
176	6	181	CCCAAGACCCCAATTTGATT	60.91	20
257	417	673	TGAGCGAGGTGAAGAGTCAA	59.701	20
140	9	148	CCAATTTATTGGGATTAAGGC	57.539	21
247	795	1041	CACGCGGATCTGTGTCTATT	58.751	20
280	999	1278	TTGGTTCCATTCAAAACGGT	60.206	20
125	21	145	TTGCCTTTAATGCTGTGCTG	60.014	20
203	166	368	GCCCCTCTCTCTCAATTCCT	59.778	20
251	2683	2933	TCCCAAAATGAAACTTGTAAAT	59.763	24
273	58	330	GGCCTTAACACCAACAACCA	60.786	20
238	490	727	TGATTCATCGCATTTACGGA	60.035	20
191	2159	2349	CCTACACAGGTACAACCCCG	60.282	20
261	334	594	CTCCTTGGGGTATGCAGAAA	60.066	20
280	357	636	ATTGCCACGTGTAATGGGTC	60.646	20

227	311	537	ATGGAAAACAAGAAGCAGCG	60.386	20
223	0	222	TTGGTTCATGTAGCCGACCT	60.517	20
196	173	368	TCAGCTCTTGTTTCCCCAAG	60.366	20
256	1218	1473	GCACGAACCCATGACCTATT	59.82	20
217	470	686	GGAAATCGCTCCACAGACTC	59.81	20
266	4874	5139	GCATAATGCACAAAAAGGCA	59.708	20
259	1213	1471	GCCGGTGCAGGTCTCTCTAT	61.72	20
178	858	1035	ATGCATGCAAACCAGGATCT	60.492	20
190	268	457	TCTACCGGAGGAAACCATGA	60.452	20
253	510	762	CTTCCACCCTTGTTTTCCAA	59.942	20
170	258	427	ATGGTGGTAAGGTGTGGAGG	59.697	20
215	144	358	AGATCCCTCCCTCGCTACAT	60.059	20
233	4809	5041	AAAAATTGATGAACGGGTGG	59.662	20
148	398	545	CAAAACCTTCAATGGCCAAC	60.344	20
186	351	536	CACCAATCCGTAGAGAAGGC	59.694	20
256	923	1178	TTCTCTTGCAATGCTTCACG	60.134	20
177	61	237	ATTTGAGGAGAGCAGCCACA	60.945	20
210	893	1102	GGTGCGGGATAAAAATGTTG	60.188	20
268	175	442	ATATCAGCTCGCACAATCCC	60.066	20
197	5	201	ATGTAGCCGACCCCAATTTA	59.297	20
279	478	756	TTCCATTAACTCATCGTTAAAA	60.124	26
160	3	162	TTTAATCATAACTGGCCTCGC	59.225	21
269	1371	1639	ACATATTCAGAGTCGTTTGAG	58.548	24
155	282	436	CCAATATCTGATGGATTGCG	58.943	20
238	1207	1444	GAACTTTTTGTTCCTGCGATG	59.738	21
268	54	321	CGAACAAGAAACGGGGATAA	59.931	20
218	436	653	TGAAGGCTTTTCTCCTGCAA	61.021	20
106	4	109	GGGGACATCTGAGTGTGTGA	59.502	20
151	1220	1370	GCCAACCTTTGCCCTCTCTA	61.633	20
110	479	588	GCAAATTTCTCCCCCTTCTC	60.017	20
209	3	211	ATGTAGCCGACCCCAATTT	59.259	19
233	573	805	TTGGCTAGTTGCATTATTTTGG	59.173	22
225	849	1073	TGAACTATGACCGAGGAGCA	59.394	20
187	2339	2525	TGGTCGGATATGGGTTGTTT	60.051	20
225	167	391	AGCCTTTTGTTGATGATGGC	60.081	20
210	198	407	GCTGGGTCTGAAGCAGTAGC	60.164	20
254	481	734	GAGGCTTTTGGTATGTCAGTC	59.242	22
224	1271	1494	TGAGCATATTTTGTGTTGCTTG	58.89	22
214	1293	1506	TTTAGTGGGAATCACGGGAG	59.926	20
272	640	911	ATAATCGTCTCCGTCGCTGT	59.723	20
255	857	1111	AGCAGAGGATTGTTGACGCT	60.02	20
203	841	1043	CACCCAACCCGAGTATCCTA	59.807	20
145	0	144	CCCAGTTTATTGGGATTAATGT	59.443	24
221	970	1190	GTCCTTGCATTAGGCAGAGC	59.985	20
271	2385	2655	CCCAAAAGGGAGGAGTGAAT	60.298	20
163	2377	2539	GGACAATGCTGATCTCCTCC	59.617	20
197	838	1034	TGACAATTCTCAGCCCCTTC	60.195	20
228	2345	2572	TAATCCCACTGAATTTGGGC	59.762	20
109	14	122	CGAGCTCGATCATGCAACTA	60.119	20
214	523	736	TGGTGAAAAGTAAGCATGCAA	59.359	21
109	452	560	GTCATTACTCCCACCGGAAA	59.79	20
273	1860	2132	CGAATGCAACACTGGAGAAG	59.44	20
155	330	484	TGACGAGCTTCCCTCTTGTT	59.989	20
179	1840	2018	AAGATCGGACAACCCATCAA	60.317	20
213	1041	1253	TTTGCTCACCCCTAACCACT	59.592	20
209	427	635	TCTCCTCCATTTCCACCAAC	59.903	20
270	517	786	AAAACATGCATCCACGAACC	60.765	20
272	1699	1970	CCCCAAATGATCTACCAAGG	59.24	20

109	347	455	ACCCCAAACTCATGCAAAAC	59.836	20
223	1547	1769	TTACCTAGCAAGGGTTTGGG	59.084	20
239	1235	1473	AGAGAGACGGGGAAGAGGAG	59.945	20
263	671	933	GCCCATAAGCCCATCAAATA	59.757	20
251	155	405	AATGGAAAATAAGCAGGGGC	60.28	20
250	2899	3148	AGCACACTTCTCCTGCAACC	60.453	20
268	197	464	GGGAATCTTGTTTTAAGTATCC	59.762	24
248	52	299	TGTTGATGCTGATGATGACG	59.197	20
171	2969	3139	TTTTTGATGACGCAGGAACC	61.012	20
226	49	274	GGAACCTCCTCTGTTCCCTC	60.05	20
208	918	1125	AAAGGGTATGCAGCAGGATG	60.096	20
262	411	672	GAGAATTCCCGCAGATCAAA	60.155	20
129	1370	1498	GCAGCCAAGTTTGGTTTGTT	60.154	20
279	58	336	CCACCCCCTTCTTTTTCATT	60.159	20
232	415	646	GGCATCAAGACGAATCCAAT	59.9	20
160	851	1010	TATTGCATCTTGGCCCAACT	60.469	20
108	309	416	AGGGCATGCATAGGTGTAGG	59.978	20
274	4409	4682	TGAGCTCTGTTGGTCTTTGG	59.007	20
247	1088	1334	TGATTGAAAGCACCGTCTTG	59.84	20
235	131	365	TGGAAGAGTGCCCAAATACA	59.123	20
108	1843	1950	AACTCACATGGGGAACAAGG	59.82	20
247	1186	1432	CAGCTCCAATGCAGTAGCAA	60.157	20
161	1275	1435	TTTTCTCCTCCGGAAGTCATT	60.06	21
221	114	334	AGATGGATGTTCGAGTTGGG	59.927	20
235	505	739	AGGCGAATTCTAAAGTGATCA	59.302	23
274	28	301	ATTTTATGGGACGGAGGGAG	60.145	20
243	1015	1257	TCAGTTTGCACACTTTCCCA	60.278	20
270	1940	2209	CATTTTTCTTAACGGATTCTCC	59.507	23
271	149	419	TCCATCGTACCGAGGCTAAC	60.096	20
153	171	323	CCTCCGTCAGTGTTGAGACA	59.864	20
204	2658	2861	GCGTGGGAATTGTTTCAAGT	59.978	20
253	137	389	CCGTGGTCACACCACTTTTT	60.843	20
136	18	153	GGGGTCCCTGTCTTATAGCG	60.836	20
259	2227	2485	TGAAAGCAAGGAACGACTCC	60.375	20
269	1094	1362	CGTATAGTCCCGAGCAGAGG	59.853	20
230	1810	2039	TGCCTTGCGAATTGTGATTA	60.215	20
271	544	814	CATCCCCCACTTTTCGTTTA	59.795	20
252	1060	1311	TAGCCCATAAGCAACACGAA	59.325	20
245	306	550	TGGGTGCGAACAACATTATTT	60.237	21
262	29	290	TGCAGGCGATAAGCAGAAGT	61.071	20
178	3	180	CCCAAGACCCCAATTTGATT	60.91	20
229	1383	1611	AGATCCAATCCAAATGCTGC	60.043	20
256	160	415	GATTCCAACACTTGGGCTGT	59.973	20
268	10	277	CGTGTAGGATGGGAAATTGAA	59.809	21
254	253	506	ATAGGTTGTTCAAAGCCGGG	61.217	20
225	231	455	TTTGGGAGTGAATGGGAGAG	60.042	20
193	443	635	TCGCCTAGACGCAGAAAAAT	59.982	20
260	1398	1657	CCTGTGCCTGATTTGTTTCA	59.691	20
233	1031	1263	CCACTCATGGAACCCAAAAC	60.21	20
225	3223	3447	CCACCAGTTCTGATGCAAGA	59.831	20
272	1081	1352	CCAAGTTCGACGAAACCATT	59.971	20
172	225	396	GAGGAGACCGATCTGTTGGA	60.199	20
177	9	185	CCCAAGACCCCAATTTGATT	60.91	20
196	90	285	CAATCAAATTGGGGTCTTGG	60.162	20
239	89	327	AGCAGGCTCAGACCAAGAAG	59.745	20
255	7	261	TCATCGAGTCCGCACATTAG	59.823	20
204	2323	2526	TTGAACACGCTCAACAGGAG	60.025	20
143	1488	1630	GGCCATTCGAGTTATGGAGA	60.036	20

255	7	261	AATTGTTGCATCTATTTTCTAA	57.91	27
212	339	550	CAAGACCGTGACAGGCACTA	59.897	20
128	1268	1395	ATTGTCCCTCCACACCACTT	59.279	20
225	404	628	AATCGCATTTTCTCGACGAC	60.221	20
238	172	409	GCCAAGAGCCCATAGTTCAA	60.214	20
141	572	712	TTCCGATCAGAGCTTCTCGT	60.096	20
235	726	960	AAATTTGTCCTTTCTACACGC	58.811	22
249	723	971	CCATAGAGGTGTCAAAAGGG	60.719	21
148	9	156	CCCAAGACCCCAATTTGATT	60.91	20
244	8485	8728	CAGTTGGAGTTCCATCAGCA	59.831	20
191	1704	1894	CATCCCGTTATCCAATGCTC	60.296	20
242	950	1191	TAGGACCATGTGGGCAGAAT	60.34	20
191	4	194	GATCCCACTCTCCTTCTCGC	61.284	20
137	2098	2234	CCGTCATTAATCTCTTGGATC	59.043	22
140	3895	4034	TACTGCCTCCAGATCCACCT	59.679	20
228	835	1062	TCGATTTTGTTTAGGCTCGC	60.343	20
238	444	681	GAGCATGTTTCTGCGATTCA	59.955	20
103	1422	1524	ATCAAAAACCAATTGATAGCA	58.556	23
191	555	745	GAATTCTTTCCTCCATGCCA	60.014	20
151	353	503	AGCAAAAATGATCCCACACC	59.797	20
177	277	453	GAGGCGCAAAACACTTCAAC	60.817	20
223	0	222	GCAGGCCAAAGAGGAAGAGT	60.903	20
263	185	447	GCTTTGGACTCGGAGTTTGA	60.375	20
239	185	423	CGTGAACTAACAATATTGCGA	60.068	23
105	1137	1241	GAACTCGAGCATTGCAACAA	59.995	20
280	1489	1768	CAAGAAAGCGAAATGCTTCAA	60.494	21
171	83	253	GGAAGCACTCGCAAGAAAAC	60	20
203	148	350	CCCCCATACCCACATACTGA	60.452	20
251	140	390	TTTGGTTCATGTAGCCGACC	60.894	20
166	5	170	AGGAGTGGGTGTCGGTTTTT	60.776	20
277	39	315	AAAAATACGAGTGGCGATGG	59.96	20
260	125	384	TTTGGGTTTTAAATTCGTTGAA	58.567	22
261	88	348	AGAACCAGACCTGCTTGCAT	59.874	20
273	888	1160	CGACCCACATAGTGGGAAAG	60.366	20
203	0	202	TTCGACGGTTTCAAAGAAAAA	59.723	21
265	380	644	TTTTGATTGGGAATAATTGGG	59.441	22
167	835	1001	TGTTCGTCCAGAGACAGCAC	60.03	20
260	457	716	ATGTCTATCGTTTGGGCTGG	59.955	20
147	1504	1650	ATGCTCTCCAAGACGTCCAC	60.269	20
155	480	634	CAAGACAAGCTGAGCAGTCG	59.922	20
269	597	865	GCCTCATCCAAACTTGCAATA	60.089	21
218	109	326	AAAATTTAAGGGGGATTGCC	59.167	20
245	370	614	TGACATTGTTTCGGTTGCAT	59.972	20
218	346	563	TCATGGTGGGGTGAGTTTTT	60.21	20
255	386	640	GATTCTGGTTCGGTGATGCT	60.081	20
215	57	271	GCTCGTACATCGAGTGATGC	59.43	20
276	170	445	TAAAGGTGGAGCTGTGGTGG	61.084	20
279	1860	2138	ATCCTATGTGCACCACGACA	59.992	20
185	3099	3283	AATGAGAAAATGAGGCGCAC	60.221	20
126	813	938	TTATGGCCAAAGACCAACCT	59.429	20
129	628	756	CGGATTGTTTTTGGAAAGGA	59.91	20
182	287	468	TTTGGGGAGATCATTTTTGG	59.733	20
225	134	358	CCGTCTCCATTCTTCCACAA	61.034	20
276	988	1263	AAGGCCCTCTCAAAACCAAT	59.94	20
203	2688	2890	ATTGAAGGGGCCATACAGTG	59.813	20
200	12	211	CATCTGTGGCATGAGGAAAA	59.648	20
155	456	610	ACCGCAGAATTTAGGAGGCT	60.228	20
248	162	409	TCTTATTAGGGGCTTGTGCG	60.223	20

256	3602	3857	TCTCCTTTGGAGACGGTGAG	60.377	20
277	430	706	TTTTGTTGTGGCGTCTCTTG	59.881	20
200	541	740	GGAGATAGAGAGGGGCCAAC	60.037	20
123	1517	1639	TGATAAATCGTTGCTGGCTG	59.833	20
242	631	872	AGATTCCACCGTGTTGTGGT	60.284	20
216	325	540	AACGTATTCCTTCCCCCACT	59.691	20
242	5886	6127	TTCCCCACCATTTCATCATT	59.991	20
209	270	478	CCATCTCAAGGGTCTACCGA	60.065	20
234	108	341	TCTGTTACATTCTCCAAGCCAA	59.747	22
165	708	872	AATTGGTCTCCTCAATCCCC	60.133	20
255	60	314	CCCCAAGACCCCAATTTTAT	59.882	20
232	116	347	ACAACAACCTCCAAATTCCG	59.83	20
207	1576	1782	GGCACCCTCTCATGGATACT	58.969	20
277	1293	1569	GTGTTTGTGATGGGCAACTG	60.008	20
128	828	955	AAGTCGTCGTCATCATCCTCT	58.758	21
166	0	165	GAGCATGCCTAGATGTTGCTT	59.495	21
140	47	186	ATGGGTTCGAGTCTCAATGG	59.927	20
109	1959	2067	ATCCTCCTCAGATCCTTGGC	60.563	20
159	933	1091	TTGCGGTTGTTCAAGCATTA	60.251	20
197	258	454	TCCAAATGCTCCTCTACCGA	60.734	20
213	1069	1281	TCGAAACCCTTGAGTTCGTC	60.232	20
122	173	294	TGAGGTGAAAGGGTAGTCGG	60.103	20
259	647	905	CGCGACAACTCCAGTCCTA	59.992	19
241	1166	1406	CACTTACGAAATGTCAAGACG	59.813	22
215	898	1112	GGACTACCGGTCCGATTATTT	59.214	21
101	3022	3122	CCGAATGATGAGAAGTGGGT	59.927	20
161	739	899	AGGGAACTTTGTGAACCCCT	59.834	20
253	402	654	AGCTTAGGGCAACACGAGAA	60.015	20
196	411	606	CAATTCTTTTGTGCGTGAGC	59.469	20
182	361	542	TCCATAAGCCGACCTCACAT	60.483	20
263	189	451	TGGACCCAATATGTCATAACC	59.938	22
267	10	276	CGAAATTAACGTGGAGGACG	60.493	20
226	319	544	TTTGTTGAGCGACCACAATC	59.697	20
186	602	787	CATCATTTGATTGTGGTCCG	59.774	20
278	370	647	CGAAATTGACACGATCCAAA	59.518	20
175	228	402	AGGAGGTCGCCAAAGAAGTT	60.247	20
124	762	885	TTGTATCGAACGAGCATCCA	60.22	20
218	65	282	CAGAGAGGCGGTGGTAAAAA	60.241	20
212	203	414	CTCCATTTTGATGGAGACCG	60.452	20
127	14	140	TGTAGCCGACCCCAATTTAT	59.297	20
196	367	562	CGCCTCTTCTTTCTCTCCCT	60.088	20
277	2998	3274	TTCCCTCTCAAAAACATCACA	58.187	21
244	1178	1421	AGTCGTCTCCTATCCCATCG	59.116	20
278	36	313	CACACACAGACGTTCCCATT	59.441	20
221	4452	4672	CATGAATGTGTGGTTTCATCAT	59.606	23
227	431	657	TCGTAGCTCCCTTTGCATTT	59.845	20
201	310	510	AGGCGTTTCATTGTTCTGCT	59.882	20
137	501	637	CTGGTTTGGTTGAATTTCCG	60.336	20
231	435	665	TGCATGAACGCTTCTCACTC	60.144	20
187	179	365	AGGGGTAAAGTGCAAATCCC	60.187	20
140	1816	1955	GACGGAATCGTGAACAATGA	59.502	20
217	248	464	GTACCCTTGGCCAGAATCAA	59.933	20
212	1452	1663	TTCAGTTGGATGGTTGGACA	59.935	20
185	1025	1209	ATTGTCCAGCCCAATCTGAA	60.461	20
184	8	191	ATGTAGCCGACCCCAATTTA	59.297	20
195	120	314	GTCGCCTCACCTTCATCTTC	59.81	20
246	217	462	CCATTACCGATGCCTTACTTG	59.483	21
134	20	153	GACAGCGGTTGGTTCAGC	60.412	18

195	101	295	TAGGTTTGGGTTTCCACCTG	59.824	20
271	594	864	GGTGAGCGATCAAAATCCAT	59.9	20
269	751	1019	GTTCTTTTCTGATGAGGCGG	59.813	20
220	574	793	AGAGGGGTGTTGAAGGTGTG	60.002	20
246	4168	4413	TCCGGCGATTACTACAAACC	59.96	20
258	420	677	TGGCTTCAGAAGAAACACCA	59.415	20
219	1866	2084	TTTGTCAGGACGGGTAGTCC	59.966	20
142	7	148	TGTAGCCGACCCCAATTTAT	59.297	20
121	813	933	AAATCGAAGTCGAAGGAGCA	59.955	20
173	68	240	TGAGGGTCCTAGCATGATGA	59.193	20
127	1003	1129	GGTGTGCTGGAGATACCGAT	59.957	20
273	113	385	TGCTCGCTATTTGGATGCTA	59.567	20
251	1104	1354	GGTAACAACGGTGGAAATGG	60.088	20
246	997	1242	TAAAGTGAACAACCTCCGGG	59.964	20
116	2	117	TGTAGCCGACCCCAATTTAT	59.297	20
126	630	755	TCACGAGGTGCATTGTGTTT	60.16	20
279	1779	2057	TTCTGTTGCTTGGTCATGGA	60.24	20
200	412	611	GGTGGATTGCTGACAAGTGA	59.682	20
259	537	795	CGTTGCTCCTACATCATTTGG	60.508	21
112	723	834	TGTGAATAGGGGCATAGCCA	61.382	20
276	36	311	TTTCTTGAGGTCGTCTTGGG	60.224	20
237	1482	1718	TGCATGAAACATCTGCTGGT	60.272	20
119	5	123	TGTAGCCGACCCCAATTTAT	59.297	20
232	338	569	CATTTTGTTACCCGAGCGA	59.673	19
223	205	427	GGGATGAATCTGGCTGAAGA	60.158	20
171	399	569	TCAAATACATAATTAGCACGG	59.504	25
149	1413	1561	TGGATGCCTTGAAAAACCTC	60.051	20
200	397	596	GGAGGTGACCGTTTGACAGT	60.009	20
215	675	889	TGGAGCATCCAACATGAGAG	59.787	20
231	2291	2521	TGGGGTGGACTAGAGATGCT	59.679	20
233	884	1116	TGGGATTGTCATCCTCATCA	59.85	20
257	8	264	CCCAAGACCCCAATTTGAT	59.59	19
233	132	364	AAATGAAATCGTGCGAAAATG	59.957	21
162	438	599	AGGTGGTGGAGGAGGAAAAT	59.795	20
148	2	149	TGTAGCCGACCCCAATTTAT	59.297	20
230	192	421	TCGCGAGAGAGAAAAGGAAA	60.206	20
202	585	786	GCAATGCGATCCCTATGATT	59.891	20
183	1132	1314	ACGGCAAAATTCATCCAGTC	59.939	20
195	1143	1337	AGCACCTGACAAGACCAACC	60.159	20
198	570	767	GAGTTCTCCGGTGATCTTGG	59.655	20
241	173	413	CCAAAGCTTGAAGAAATGTTT	58.919	22
110	8	117	GCAGACGAATTTAGTCGGGA	60.214	20
277	1124	1400	TTTGTAGGCGTGGGCTAAAG	60.257	20
185	570	754	ATCTCAAAAGACGCGAGGAA	59.955	20
162	1461	1622	TCATTAGATTGGGAATAATTG	59.101	23
273	437	709	GGTTCTGTTGGGGACTCAGA	60.088	20
197	373	569	CCTCCTCCTCCACATTTCAA	60.042	20
192	2515	2706	AGCAACTCATTTCCAGCCAT	59.7	20
252	42	293	TCCTTTTGCGTTTTATGTGC	58.819	20
233	1009	1241	GGACTCGGGTGAGTCTCAAG	59.835	20
105	198	302	ATAGGTCACGGGTCGAGTTG	59.989	20
267	519	785	TGGGATAAAATCTCCGAAAAA	58.547	21
170	60	229	TCGGGGATAATATTGCTGGA	60.247	20
257	243	499	AAAACCGTTCCCACCCTTT	60.575	19
233	358	590	CTGCAAACAACACACTTGCC	60.347	20
248	960	1207	GAAACTCGATTGCTGCCCTA	60.352	20
264	679	942	GTCCATGTCCTCGTCCTCAT	59.928	20
274	1077	1350	CAAGCTTGGAAATGCCTGTT	60.249	20

238	1620	1857	GGCTTCTCTGAAATCCTCCC	60.154	20
235	48	282	AGCAGGCTGAGAGAATGAGC	59.857	20
261	1727	1987	TGCACAGAAGATCCTGCAAC	59.992	20
269	902	1170	TTTAAATCCAACTCACACATAT	58.233	27
219	2821	3039	ACGGTCTCGAACTCGCTTTA	60.015	20
206	155	360	CCACTTCCCAAATTTCCCTT	60.159	20
228	1427	1654	ATCCATGGGAATTGGACAAA	59.991	20
272	709	980	TTCAATCAAACGGTTCATGC	59.523	20
154	210	363	GCAAGATCATGCACCATCAA	60.641	20
199	2062	2260	TTGTACAATGCATGCCGTTC	60.532	20
272	501	772	ATTTCAACTACGACGGCCAC	60	20
177	3	179	CACTCGAAGAGTAGCGGCTG	61.263	20
246	218	463	TGTTTTTACCTGCGTATCTGTC	59.698	23
235	1337	1571	TGAAGATGAAGGTGGTCGTG	59.676	20
252	68	319	AGTTTACCTGACTGGCGTGG	60.171	20
234	409	642	GAGCACGAGGTGTTCGATTT	60.263	20
197	334	530	GTGCTTCGGTCTGGATGACT	60.269	20
105	358	462	CAGAAAGGTCGGCATCATCT	60.218	20
187	14	200	ATCTCCACTTGTTGTCTCCAA	57.211	21
254	106	359	ATTCCTCGGGTTCTTGGAGT	59.935	20
238	192	429	TGATTTAGTAAAGTTGGAGGT	59.098	24
119	430	548	TCCCTCTTTCTTTTGGGTGA	59.641	20
232	114	345	AGGTTATGGTGCGTCGAGTC	60.142	20
222	64	285	TCAAATGTTCGTCTTGCAGC	59.995	20
232	1027	1258	TAATGACGCAGACGGAATTG	59.688	20
223	1	223	GGTTCCTGCTGCAGATTCAT	60.226	20
120	38	157	AATCGTCGAATTCGGTTTCA	60.448	20
195	552	746	ACCATCGTGGCCAATAAAAA	60.188	20
148	14	161	TGTAGCCGACCCCAATTTAT	59.297	20
247	613	859	AAAGATTCAGCAATGGGTGG	59.933	20
217	5	221	ATGTAGCCGACCCCAATTTA	59.297	20
269	178	446	AATATGCAAGGGGGAGGAAT	59.627	20
221	740	960	ACGGATTCGAGTTTCAACGA	60.636	20
216	1909	2124	GAGGTCTAGCAGAGGGAGCA	59.703	20
226	510	735	TGTAGTCATCGAGCAAGCCA	60.562	20
243	80	322	TGACCAATCACCAATCAACAA	59.808	21
221	23	243	AGTGCAAATGTTGACGGGTT	60.419	20
225	430	654	GCTTAACTGGCGAACTGACC	59.882	20
176	2	177	CCCAAGACCCCAATTTGATT	60.91	20
232	5	236	CACGCCAACTTACAAACTATC	59.706	22
275	1953	2227	GTCTCAGGTTCGAATCCCAC	59.511	20
213	1812	2024	GCAGCTTCTGCCTCACTTCT	59.898	20
196	317	512	ATTGTTGAGAGCCGAAATGG	60.074	20
101	0	100	TTGGTTCATGTAGCCGACC	59.512	19
270	2100	2369	TTGAACAAGGTGAAGGCTCC	60.232	20
167	773	939	TTGCCCAGTTCTTTTGTTGA	59.293	20
159	555	713	TCTGTTTTATTTCCCCGTGC	59.938	20
260	566	825	GAACAATGCCTCGAAACGTA	58.773	20
107	418	524	TGCATTTCATCGCTTTATGC	59.809	20
252	90	341	GCCGTCTGATTGGAGGATTA	60.036	20
189	365	553	TGAAAATGAGTTGGGGGTGT	60.21	20
244	428	671	TGAGCATGATGTGTCTTGAATT	58.307	23
275	90	364	ATCTCCTCCATTTCAACCCC	60.133	20
265	1017	1281	AAATATTTTAGAAAGAACAGA	57.114	27
198	0	197	GGAACAAACCCGACGTAAAA	59.839	20
202	36	237	CCGACCTTCCAAATTGTTGT	59.83	20
269	137	405	GGTTTCATCACAAAATTCTTCC	60.21	23
167	8	174	CAGTTCCATGTCACAAACGC	60.16	20

192	150	341	CCTTCGAGACAGCCGATAAA	60.344	20
278	45	322	TCATTTCCGACAACTCGATG	59.648	20
279	123	401	ATCATTCCCTGCAATCCTCA	60.426	20
273	155	427	CCATTGTAAACCCCTGCACT	59.853	20
185	342	526	CCAGAACCATGGACACACAG	59.997	20
270	888	1157	ACTTATTGGCACGAAGTCGG	60.132	20
251	310	560	CTGCTAGACCCAGTGGTGGT	60.174	20
266	547	812	ATGTTTCTTCCGAGTGTGGG	59.966	20
188	318	505	GATGAGCAGCTCGACAATGA	60.104	20
219	1	219	GGCCACCAAGAATCTCAGAA	60.195	20
214	426	639	GGGTTGTTAAGATTTAATGATT	57.624	26
201	880	1080	AGTGTCCCTTCGCCTATGTG	60.134	20
234	38	271	TCAAAGAAAGTGAGTAGAATC	57.273	24
256	380	635	TTTGGTTCATGTAGCCGACTC	60.125	21
251	0	250	TGTGTTTCATGTTTGTTGTGAT	58.06	24
251	31	281	TGAAGTTTCGAAGACTGGAAG	59.097	22
261	320	580	CCTCGATCCTGACCCAATTA	59.887	20
113	702	814	TGAATATTGGGGTGGGAAAA	59.988	20
136	125	260	AAATCACGGGACCAAAATGA	60.17	20
126	2347	2472	CTCCAGAGCAAATCGACCTC	59.95	20
150	17	166	TGCACATGTTAGCCAGAACTT	59.813	22
278	180	457	CGATTGTATTTGTGCTGCAA	58.354	20
241	561	801	TCATTCTCTTCACCGGAAGC	60.34	20
216	160	375	AAGGTAACGGAAGGGTCTGG	60.353	20
211	0	210	TGTAGCCGACCCCAATTTAT	59.297	20
250	348	597	CCTCCATTTCCCCACAATAA	59.617	20
267	335	601	ATTTCCTGTTCTCTTCCCCG	60.434	20
183	5	187	CCCAAGACCCCAATTTGATT	60.91	20
226	493	718	ATGCTCGATTCTTGTGGGAC	60.081	20
280	1449	1728	CCCGTTCAGACCACCTTTTA	59.964	20
142	111	252	GAGTCTCCATCCCCACAGAA	60.048	20
263	5	267	CCCAAGACCCCAATTTGATT	60.91	20
237	594	830	TGGGATGAGGAAAAACATGA	58.897	20
168	575	742	TCGACGCATCAGAAGACAAC	59.992	20
261	746	1006	CATGGTCTGGCTATTCCCAT	59.773	20
246	1173	1418	TGGGATTTTATGCAGAAGGG	59.894	20
243	1197	1439	TTCTATGAAGCCCTCAGCGT	59.978	20
188	740	927	GCACTGCAGAAGGTCTCCTC	60.143	20
183	366	548	ATGGTTGCCTTTGTTTGGAG	59.971	20
140	870	1009	TCAACATTGCAAAATGGGAC	59.375	20
148	6	153	CCAATTTATTGGGATTAAGGC	57.539	21
149	940	1088	TTTACACGTGTGGGATATGGA	59.091	22
232	218	449	TATCTGCAGCGCATCATCTT	59.553	20
172	211	382	CACGTGAGGGAGGGTTTAGA	60.103	20
225	142	366	ACCTATGGATGCACCGGTTA	60.214	20
125	3659	3783	GGCAATTGACCACCGTAAAC	60.235	20
274	199	472	GCCCAATGACAAAGAGGAAA	60.051	20
240	968	1207	CGTTTAGTGGTGCGAGGAAT	60.132	20
200	200	399	ACCAGTAGTTTCCGGTGGTG	59.884	20
201	303	503	TGAGGCGTAAGCAAATTTCA	59.443	20
258	95	352	AGAGCGTCGCCTAAGTGTTG	60.592	20
212	384	595	GACTATGGCCCAAAACCGTA	59.823	20
243	334	576	AACGAGGACATCGGTCTGAG	60.261	20
107	118	224	TGATCCATATAGCCGACCCT	59.368	20
117	529	645	GGTTCATGTAGCCGACCCTA	59.955	20
131	422	552	ACCCACCACCATCTCACAAT	60.096	20
173	1322	1494	CAAATCAAAATAATTGCAAAG	58.304	24
268	119	386	TGGTTGAATTGGAAACGTGA	59.941	20

167	462	628	TGGTTTCTTGCTTGATTAGCAT	58.901	22
273	419	691	GGAAGCCGTTGAAGATTTGA	60.192	20
268	797	1064	CACGTCTCCGAAAGACAACA	59.873	20
256	467	722	CTTTGCCTTTTCTGCCTCTG	60.125	20
150	2145	2294	ATACGATCCATTTTGCCGAC	59.791	20
270	287	556	AATCCTCAGTGCCATCAACC	59.934	20
208	1864	2071	ATCTTGCTGTGTCGATCCCT	59.685	20
155	196	350	TTTCGAGGCTCGGTCAGTAT	59.836	20
246	10867	11112	CAAGTATGGTCTCGCACAACA	59.773	21
163	346	508	GCAAATAAATCGGCAGAGGT	59.186	20
270	456	725	ATGAGGTCGGACATCTCGAA	60.622	20
159	9	167	AATTTGATTGGGAATAATTGG	58.965	22
274	149	422	AAACGCCTAGCTCTCCACAA	60.015	20
259	534	792	GAGAATTGGGTAACCAGCCA	59.933	20
278	5649	5926	GGGGGAGAGGTTAGATTGGA	60.264	20
220	157	376	TTATTTGCTCCCAACGATCA	59.112	20
277	564	840	TATTTTATCTCCTCCGCCCG	61.245	20
196	1041	1236	GGGATGGGTAGAGTAACGTC	59.705	21
176	408	583	TGCAAGTTTGAGCGAGATTG	60.134	20
261	120	380	ATCTCGTGGGGGAAGACTTT	59.935	20
209	904	1112	GCATTTCCACGTTCAGAGGT	60.119	20
186	22	207	TTCAACACTATTCAACACGAC	59.715	24
197	2337	2533	CCGAATGGAATTGAAGCAAG	60.576	20
140	2409	2548	TCTCACTCAGCTCGAAAGCA	60.008	20
150	736	885	CGGCAGTTAAGGCTCAAAAG	60.011	20
271	557	827	TGAAGGCCTTAAATCACCAAA	59.573	21
179	1028	1206	TCCATATACCGACCCCACAT	59.894	20
161	799	959	TTTGTTTAGGGGCTTTGTGC	60.11	20
174	174	347	GCTTTTTCCTCTCCTTCCGT	59.827	20
151	2174	2324	TTTCCTTGTGCATTTTGCTC	58.895	20
201	28	228	CAGCCGCTACTCTTCGAGTG	61.263	20
191	188	378	TGAACGAATGGAGAAGGAGA	59.799	21
246	2005	2250	ATTATCTCGCAGCATTGCCT	59.835	20
169	19	187	GATTCAGGTGTGATCAATGAC	60.124	24
261	4347	4607	TGCAACATCTGAACGCATTT	60.265	20
256	516	771	TGTACACAGTGAGGTCATACT	57.473	25
198	154	351	GTGGTGACATCCACTACCTGC	60.447	21
152	462	613	AAATCAAAAGGGTGGTGGTG	59.688	20
270	625	894	AAATGTGCTGCTGGCTCAAT	60.807	20
202	1073	1274	AAAATTAAGATGAGATTTGTC	59.826	27
241	593	833	GAATTGCCAGAGAAGAAGCG	60.096	20
276	408	683	AAGCATCATCCTCCCAACAG	60.073	20
166	1718	1883	TCCTCCTCTCGTCTCCAGAA	60.064	20
167	69	235	GCCATATCACGGTGGAAAAG	60.331	20
170	7	176	TGTAGCCGACCCCAATTTAT	59.297	20
159	1253	1411	AGCTATAGGTGGGGATGGGT	59.674	20
259	10	268	TGGTTTACCCGATCTTGCTT	59.569	20
137	319	455	AGTATCCTCGCAGTCGGAAA	59.836	20
148	2	149	TGGTTCTCCAAATTCTTCCTC	58.227	21
258	44	301	AGGAATGGACGCAAGATCAC	60.081	20
134	387	520	TACATCTCCCAAGACCCCAA	60.309	20
202	5	206	GGTTCATGTAGCCGACCCTA	59.955	20
276	2001	2276	TGCAGGAAACTGTCGTTTGA	60.427	20
251	571	821	CTATTGCAATTGCTAGGGCG	60.73	20
184	853	1036	CCGTTTTGTTACCATTTTGC	58.071	20
224	1908	2131	AGGATACATGACACCCGTCC	59.661	20
154	351	504	AAATCAAACCAACCCCAACA	60.066	20
271	2892	3162	TCCCAAGTCTGAGCTTTTCTG	59.601	21

102	0	101	CATCAAACCCAAACCAACCT	59.688	20
206	29	234	CACATGATTTGGGTTTGTGC	59.823	20
272	17	288	TGGTTCATGTAGCCGACCTC	61.067	20
267	32	298	AATTGAGAGGTGGGACGATG	59.927	20
202	1652	1853	TTCAACTTGGCGCACTGTAT	59.347	20
143	1234	1376	CAATTTCTTTTTCCCCCTCC	59.75	20
265	79	343	TTTGGTGCGAGAATGATTTG	59.664	20
176	27	202	TCGTCACTTTCCTCTTCCTCA	59.974	21
234	309	542	CACGATAAAACAATTTTGGAA	60.108	24
230	975	1204	AGATAGGGGGACAGCGTAGG	60.476	20
193	1059	1251	ATGAATGGTTGGTCGCTTTC	59.939	20
260	818	1077	GGGAGGAGTACGAAAACGGT	60.361	20
110	7	116	TGTAGCCGACCCCAATTTAT	59.297	20
205	92	296	ATTCAAAATCGACTGCGCTC	60.361	20
257	23	279	AAAGAAAATTCAGGGGGTGG	60.159	20
207	662	868	TGCCTGAGGTCTTACCCTTG	60.246	20
280	694	973	CGTAATTTTCAACCCCAACC	59.178	20
143	2264	2406	GGCAGTACATCGGAGCTTGT	60.285	20
167	1455	1621	AAGGCGTTTTCTAAGGCACA	59.883	20
234	1979	2212	TGCTGACTGGTCAAGGAATG	59.831	20
231	956	1186	CTCTTCGCCTTCAACCTCAC	59.989	20
278	24	301	TTCTCTGCCAACAATGAAATC	57.806	21
108	12	119	ATGTAGCCGACCCCAATTTA	59.297	20
115	8	122	TCGAAGTCATGCACCTCTTG	59.984	20
137	2267	2403	GGCGTTCAATCCTATGGAGA	60.036	20
269	856	1124	CCAATCAAATTGGGGTCAA	59.16	19
241	2233	2473	GGGGAGAAAAACACGAACAG	59.569	20
275	297	571	CTTGGGTTGTGCCAAAGTCT	60.149	20
203	35	237	CCAGGTCGCTCAAATCTCTC	59.95	20
247	2828	3074	TCCGTTACCACTTCCTCCAG	60.103	20
118	2537	2654	CGGTTTTGGGTGGTAAAAGA	59.833	20
199	1469	1667	GAGGACTCCGTGGAATGTGT	59.969	20
218	3	220	GTCTCAATGGGGACATCTGG	60.326	20
236	375	610	CCCATCCTTGTGATATGCAAC	60.207	21
267	240	506	TGTCACCACTCCCAAACTCA	60.129	20
280	998	1277	TGCCCTTCCCGATTATAGTG	59.916	20
205	535	739	GGGTGATATTGATGGAGGGA	59.563	20
257	35	291	GCGATGGATTTTTCCTTTCA	60.016	20
163	31	193	GAGCTAGCACACCATCCCC	60.639	19
272	3263	3534	AGGTGAAGCCCAGTCTGCTA	60.012	20
251	397	647	GCCACCATTCTTTTGACAGC	60.646	20
279	17	295	GTGAAGATTAGCTCCGCCTG	59.978	20
217	253	469	ATTCCACTTCATTGCACACG	59.572	20
265	152	416	TCGGAAACGAACTCTTCGAG	60.508	20
222	62	283	GGATGAGTATTGCCTGACGAA	60.088	21
207	638	844	TGTTTTCCTGCCCAAAAGTT	59.587	20
140	26	165	TGATTTATGTAGCCGACCCC	59.784	20
207	803	1009	GCAACTGAAAAACGGTTGGT	60.015	20
223	1202	1424	CTGCACTGTATCGGGAACCT	60.134	20
261	158	418	ACAGTAAAGCCCGGTTGATG	59.993	20
278	261	538	TGAGCACCAAATTTATTATCG	58.687	23
207	937	1143	GAGTGGTGGAGCAGAAAGGA	60.386	20
237	966	1202	ACTTGCTCGGTATGCCATTT	59.597	20
170	68	237	GACATGGTTGTGGTTTGTGC	59.862	20
102	719	820	CTTGTGTAGGGGTGGGATTG	60.224	20
268	673	940	TTGGCTTGATCTTTGAGATGG	60.199	21
189	835	1023	CCGCCATCATCTCCATAATC	60.26	20
202	53	254	GGAACCAACACAAACACACG	59.897	20

169	263	431	AATCTTGGCGCCTCACTTTA	59.845	20
276	265	540	GCCACATCACATCGAAAAGA	59.654	20
228	259	486	CCACAGCTTCCCAAACAAAT	59.971	20
230	348	577	TGCAGAACCCATGTACATCAA	59.98	21
191	746	936	CCATTTCGCACAAAAGACAA	59.706	20
199	236	434	CATACAGTCGGCATCCAATG	59.948	20
278	72	349	ACGCCATTTACGTCTTCGTT	59.637	20
167	712	878	CAATTTCGGGTGGTAAGAGC	59.569	20
277	706	982	TTGTTCATTCTCCCGAGTTG	58.695	20
267	680	946	TTGTCCCGTCAAGAAAAAGG	60.081	20
224	57	280	TTCGCCACTGATGACAAATC	59.654	20
136	492	627	AAACGCGGTGATTTATCCAG	59.96	20
145	92	236	CGTGATTTCTTTTTGGGCTC	59.685	20
109	1775	1883	ATGGTCAGGCTCCAGGTATG	59.95	20
193	1914	2106	TAGAATCGGATTTATCGCCG	60.019	20
230	461	690	CCCTTGAGTAGCCAGCAGAG	60.149	20
223	4	226	CCCAAGACCCCAATTTGATT	60.91	20
280	4	283	TTTGATTGGGAATAATTGGG	57.289	20
220	1608	1827	CCCCCACCCTACAAGTATGA	59.665	20
246	215	460	AAAACCGAGAGCAGAGTCCA	59.989	20
258	29	286	CTTGTTGCTCAGCACAGTGG	60.651	20
272	1167	1438	GTCGATTTCCTTTCCAGCCT	60.578	20
280	1330	1609	CCCAATTTGAAAACAAGCCA	60.836	20
119	473	591	CCTTGCTAGGGCAGTACGAC	59.898	20
260	1024	1283	TTGTGGACATCCCGGATACT	60.195	20
229	355	583	GTCACCAAATACAAAGCCGC	60.511	20
206	159	364	TATGAGAGGCTTGCGTGATG	59.972	20
141	400	540	TAAGAATTGAATCGCAGGGC	60.175	20
140	57	196	GGGTATACTTTTCCGGCCAC	60.562	20
176	1235	1410	CTTCTTCCCCTCCCAAACTT	59.548	20
200	415	614	ACCTCTAGCCCGGTGAACTT	60.132	20
183	7	189	CCCAAGACCCCAATTTGAT	59.59	19
252	386	637	TGATTTCCAAACATACGTTGTC	60.271	23
110	9	118	CCCAAGACCCCAATTTGATT	60.91	20
199	396	594	AGCTCTCGACATCAAATCGG	60.362	20
272	25	296	AAGCAAAAGCATGGTTGGTT	59.615	20
177	1157	1333	GATGATGCCGGTTATGAGGT	59.78	20
115	47	161	GCCGGATAAGCGATTTCTTT	60.536	20
181	68	248	ACACCCAACTTCCAAGGTTC	58.891	20
185	413	597	ATTCAGCATCCCCCAAGTTT	60.693	20
238	247	484	GGGATGCATCAAAGTTGTCA	59.502	20
270	510	779	TCCTTAGTCAAGGGGAAATGA	59.939	22
174	147	320	AATGTGGCCATTCTGGAAAA	60.309	20
278	538	815	ACTTTGAACCCATCTCACCG	59.966	20
254	399	652	CTGGTTCGCAACACAGAAAA	59.881	20
187	492	678	AGGATCCTAAAATTTGAAGGG	59.692	22
213	541	753	CCCTAGCAAAAGAGAGAGGG	59.963	21
195	33	227	GAGATTCCGTGTGTGGGATT	59.786	20
174	3607	3780	GCTATTGAGCAATATCAGAAA	59.67	24
250	1385	1634	CAGCAAGAATAAAGTGTGCCA	58.978	21
264	762	1025	AAGATTGCTCTCGCCTCAAC	59.579	20
162	3	164	TGTAGCCGACCCCAATTTAT	59.297	20
257	56	312	TGATTCTAAAATGAATCCAATC	59.693	24
240	49	288	GCCGACATGACCTTAGCAGT	60.285	20
257	154	410	AACACAGACACGGACACGAA	60.203	20
189	542	730	ACAAAATGGGCATGAACACA	59.823	20
253	589	841	TCGTTAATTGGTTCCATTTTGA	59.341	22
252	563	814	GTGGGGTGAATTGTGTGTTG	59.701	20

168	83	250	GGTGGAGACTTAGGTGGGG	59.365	19
207	175	381	TGCAGCTTGCTGCTGTTACT	59.958	20
165	789	953	TCATGCTTCTTGTTGGGAAA	59.247	20
267	143	409	ATGAAATCCGAAACGCCAT	60.289	19
256	146	401	TTGTCAAAGAACACGTTCACA	58.266	23
257	3026	3282	TTACGGAGTGGATGGTGGTT	60.232	20
190	420	609	CCTTATACGTTCACCCCAAG	57.1	20
250	429	678	CAACCGAAATTTTTGGAAGG	59.424	20
187	735	921	GATTCCGTTGATTGTTGCCT	59.939	20
178	606	783	GCCCAGGGATTCAAAGTACA	59.933	20
156	4964	5119	ACGCAAACGCTCTTTTAGGA	60.018	20
204	125	328	TTGAGCCACTTATCATCTTTCA	58.888	23
202	1083	1284	CGGAGGTAGTTGGCATTTGT	59.993	20
222	429	650	AATGTAGAGCAGAGAGGCGG	59.598	20
127	191	317	TTTGCCGACTTTCCTTCTGT	59.853	20
245	266	510	CCATAAACCATTGGTCCAACA	60.466	21
200	19	218	CAATAAATTGGGGTCGGCTA	59.789	20
262	9	270	CCCAAGACCCCAATTTGATT	60.91	20
175	3790	3964	CAATGGCTTTGAGGGGTAAA	59.931	20
132	683	814	TTCTGCAGGTTTTCCTCCAC	60.232	20
232	3076	3307	ATAGTGCAGCAAGATTGGGG	60.096	20
146	596	741	CATACCTGTCCCGACCATCT	59.803	20
250	201	450	GGCTATGTCCACATGCAGAA	59.679	20
203	131	333	AGAAGCAAGTGGAGAGGCAC	59.604	20
136	1594	1729	TCCACTACTCCAATGTCTGCC	60.126	21
227	1293	1519	ATTGTCTACCAATCGGGGTG	59.67	20
108	428	535	GTCAAGTTTGAGACGTTGCG	59.49	20
163	563	725	GCATGTCGGTCGAATTGTAA	59.548	20
219	17	235	GGTTGACTCACACGTGGAAA	59.571	20
117	343	459	CCAGTAAATCAACGAAACGAA	59.162	22
231	2921	3151	CGTTGAAATCTGTTCCTCCC	59.526	20
191	42	232	ATGTAGCCGACCCCAATTTA	59.297	20
256	4791	5046	AACCACCCATCAGCAATGTT	60.24	20
187	6	192	ATGTAGCCGACCCCAATTTA	59.297	20
241	495	735	CACGAAGTTTGGTGACAACC	59.034	20
172	1970	2141	TACACACCGAGTGCAAATCC	59.572	20
204	617	820	GGGTTTGCGTTTGATTTGTT	59.845	20
255	257	511	TCTTTGGAATTGGAAGGACG	60.044	20
271	384	654	GGAGAAGAGGGTATAGCGGC	60.194	20
220	818	1037	AAATCCAAAATGGCCTACCA	59.273	20
165	112	276	CATCTTCCCACGAGAGTTTTT	58.305	21
221	558	778	TAGAACTGACGGGCAAATGAT	59.583	21
233	180	412	TGCATTGACCGTGTTTGACT	60.16	20
273	609	881	GCGGGGAAAAATAAATTCAA	58.914	20
205	6	210	ATGTAGCCGACCCCAATTTAT	59.585	21
150	991	1140	TCTTCAACTTGCTCGGAACC	60.375	20
214	274	487	CAAAAATGGTTGAGGGATGG	60.162	20
276	4728	5003	GCATTGGCATCATCATCATC	59.855	20
170	0	169	AATCATGAAAACCGAAACCA	57.916	20
224	320	543	ACTACCACGCCAATTATGCC	59.851	20
279	86	364	AAAAGAAAGAACCGAACCCG	60.455	20
162	651	812	TAGCTGACATTCTGGCTCCC	60.362	20
228	529	756	ATAACACTCGAACAAGCGGC	60.278	20
249	191	439	CGGGTGTGACATGATTGTTC	59.812	20
249	477	725	TGTGTACCACCAATCTCAATTA	60.042	24
272	0	271	CCAGCAGTTGGCTCTATTTT	57.125	20
274	1	274	GTTTTGGCCGGAATTGAAC	60.303	19
137	68	204	CATTCGGGAAAAAGGATCAA	59.872	20

225	1173	1397	ACGCGTTAGAAACGTACGAA	58.515	20
246	461	706	TTGTATCGAACGAGCATCCA	60.22	20
220	474	693	CATGACACAATTCGTTCTGC	57.671	20
279	899	1177	ATAAATTGGGGTCGGCTACA	59.297	20
277	8	284	CCCAAGACCCCAATTTGAT	59.59	19
194	75	268	TGTCCGGCAGAATACAAGGT	60.517	20
214	3390	3603	AGACGCAGCAGAACTTGGAC	60.599	20
180	219	398	TTTCATTCGTGTTTTTCGGC	60.98	20
276	3264	3539	GCAAGAGGCATGTTTATTTG	59.537	23
176	1783	1958	TGAAATTTGGGGGTGTGTTT	60.066	20
165	3545	3709	AAAGCTTAAGCCACGTCCAA	59.883	20
209	3	211	ATGTAGCCGACCCCAATTTA	59.297	20
272	697	968	GTCGAAAACTCAATGGGGAA	59.91	20
215	1597	1811	AGTTGGTGTCACCCTTGGAC	59.859	20
267	518	784	TTGCCATTGAAAACTCCACA	60.088	20
214	630	843	GTGAGATCAAGAATTATGGCA	59.635	24
279	8218	8496	AAAAAGGTCGATGCTTTCAA	57.487	20
258	712	969	GTCTCGTAGCTTTGGCTGCT	59.786	20
273	174	446	AAAAGCATATGGAAGAGCGG	59.32	20
272	540	811	CTGAGGCAGCAACTTCAGTG	59.77	20
259	6185	6443	GTGTGGAAAAGGGAGTGCAT	59.973	20
261	431	691	GAGTTGAAAGGCATGCAAGA	60.38	21
271	3	273	ATGTAGCCGACCCCAATTTA	59.297	20
266	2321	2586	TCCAAGCAAGCACATTTTTG	59.849	20
188	732	919	CACCAACGAAGCCACCTATT	59.993	20
268	199	466	GGTTCACGGTTTTGGGAATA	59.662	20
215	1004	1218	TTTAGTGGGAGTCAAACGGG	59.964	20
252	253	504	GGCTTAAAGACAACGGTGGA	60.11	20
186	428	613	CTCTCCCAATTCTGCCTCTG	59.943	20
246	663	908	TGCATGGAAACATATGCACC	60.352	20
231	778	1008	CGAATGACCAGCCAAGAATC	60.603	20
139	1410	1548	GTTAGCAGGTCGGGTTTTGA	60.11	20
254	1656	1909	GGTGAGGTCTGGTCAGGTGT	60.006	20
223	501	723	ACAGATGAGATGAGGCTGGC	60.381	20
230	3607	3836	GATCCTCAGCAAAGTCCGTC	59.81	20
248	2675	2922	GCTATCACACACACTGCACG	58.899	20
168	220	387	TTAAACCTCCACCAGTTGGC	59.971	20
219	64	282	CTGTGGCGTTGTAATAGGAGC	59.783	21
110	5	114	TGTAGCCGACCCCAATTTAT	59.297	20
243	572	814	CGTTGTCGCCTACATCATTC	59.152	20
215	4406	4620	TGCGTCCTGGCTTCTTTTAT	59.845	20
125	681	805	GTCTTCCGAGCAAGGAGCTA	59.717	20
160	509	668	GATCCTCTGGGCCAAATGTA	59.894	20
103	281	383	GATCCGAAATGAAAACCCAA	59.739	20
191	456	646	CAAAATCATCCACCGGAAAA	60.671	20
173	981	1153	TGCTTAGGTTGCTGTGATGG	59.864	20
278	1260	1537	GTTCGATGTGCAGATGAGGA	59.794	20
251	889	1139	ATACCCGGTAGCGAAGGAAT	59.82	20
211	92	302	CGCCGCCTAAATAGTCAAAA	60.218	20
185	452	636	ATGCAGCAATTGGACATTGA	60.08	20
268	288	555	CTCAACTTTCTTTCGAGCTGC	59.392	21
180	1298	1477	TGTAGCCGACCCCACAGTAT	60.397	20
157	151	307	CAGTCGAGTCCGCACATTAG	59.465	20
156	237	392	GGCAATTAGCCAAACCATGT	59.829	20
270	1076	1345	AATTGTAAAACACCCCAATTT	59.528	23
243	907	1149	GATGGTCGCCACAGACCTAC	60.542	20
209	1	209	TACCGCTCGTCCCTTACTTG	60.262	20
142	1248	1389	GATTGGGGCATCATAGTCGT	59.78	20

168	2181	2348	AAGAAAGATGTGGGGGATCA	59.336	20
169	312	480	ATGAAATGAAGCTTCCACCG	60.074	20
253	92	344	AGAGAGAGTGGAGTGCGTGG	60.608	20
233	1269	1501	TAGAAGCCCATGGAGGAATG	60.029	20
123	1890	2012	ACTTGGTGCGTTGTGATTTG	59.615	20
158	719	876	CTGTCACGTGTTGCAGTCCT	59.94	20
130	62	191	CAAGGACGCTATTGAGAGGG	59.83	20
131	629	759	AAACCTTAGGCTTCCTTGGC	59.725	20
269	424	692	TCATGGAGAGAGGAGAGGGA	59.871	20
183	60	242	CGGCTTAATACGTGTGTTGC	59.254	20
256	442	697	GGTTCATTTAACCGACCCAA	59.662	20
232	186	417	GTGGGCAATCTTGTTGTGTG	60.008	20
244	229	472	GGGTAGCACTGCATCTGTCC	60.688	20
276	341	616	AAACGGTGAAAAACATAATG	60.276	23
224	5	228	CCCAAGACCCCAATTTGATT	60.91	20
132	71	202	CGTTTCTTCATCATCATCCG	59.075	20
180	3299	3478	ACACCAAAATGCATGAGACG	59.572	20
232	574	805	GGGCAAAGGGAAGATAAAGC	60.041	20
211	2	212	CCTTCTTTTCAAGCACTGGG	59.846	20
215	41	255	GGGGAGAGAGAACCGAAGA	60.328	20
261	188	448	GCTGGTTGATCTTAGCACGA	59.028	20
127	810	936	GCAGGATTTTGCCTATCTGC	59.813	20
109	128	236	ACTCCGAGGACCTCAATTCC	60.456	20
253	3733	3985	AAACGCCCTCCTTCTCTAGC	59.983	20
154	11	164	TCGGTCCGATTAATCAAGAAT	58.521	21
251	1951	2201	AGCTGGTAGGCAAAATGGTG	60.132	20
108	979	1086	GAAAAATCACAGCGCCAAAC	60.626	20
133	3641	3773	TTTTCCGAGCTTGTGTTGTG	59.881	20
232	127	358	TGGATTCAGGTCAGTCGTCA	60.246	20
142	4	145	ATGTAGCCGACCCCAATTTA	59.297	20
255	535	789	CAAATGCGATTCAAGTGACCT	60.125	21
215	307	521	TTTCGGACCATTGATATCTTTT	58.914	23
230	111	340	GCCAAGGGAGTTGTTACGAA	60.11	20
233	2425	2657	AAATGAACGTATGGCCTTGG	59.823	20
261	2185	2445	AAGAGAGACGGAGGGAGGA	59.945	20
116	841	956	GAAGGCCATGTTTTGTATTGC	59.47	21
280	150	429	TGTGGATGAAGATGAAGATTT	59.077	23
264	27	290	TGATGGTGTGACTGAAAGCC	59.682	20
217	1409	1625	TTTCTAGTTGGCCCTCCAAA	59.679	20
268	240	507	CACAACAAAAACAATAAAAG	59.116	23
259	280	538	CTCAACACGGCCTGGATACT	60.134	20
101	824	924	CTTGGCATTCGACATTTCCT	60.074	20
113	1208	1320	GGCGCAGTTCGATTATCTTC	59.813	20
208	141	348	AAGATCACTGCAACAAGGGG	60.111	20
246	1180	1425	TGTGTAACCCATCTGACGGA	59.96	20
257	350	606	CATCGACAAAATCATAGTCCG	58.107	21
228	505	732	CAGTGGGCAGCAGTTTGTAA	59.904	20
149	90	238	ACCACCATCGACTGATAGCC	59.957	20
152	1749	1900	ACCAGTTGTTGAGTCTGCCC	60.159	20
139	5008	5146	TGCTTCAACACACCAAAACA	58.729	20
210	226	435	CTTTATTAAAATTTCTTTCACC	57.99	27
110	13	122	TTTGGTTCATGTAGCCGACC	60.894	20
125	2	126	TCTATTGGGCCGTACCTCTC	59.15	20
165	364	528	ACCATGCCAGACTTTGGTTC	59.973	20
214	416	629	TGCAAATACCTAAAGGTTGGG	58.997	21
171	31	201	CCCTACCCTCCTCAGGGTTAC	61.079	21
172	254	425	TTTTGCATATCTCCATTCGGT	59.424	21
265	791	1055	TGCTTTTCAGGGAGTTGGTC	60.232	20

227	251	477	GTCATACGACCCGCAAAAAC	60.374	20
276	874	1149	TTCAATCACTTTTTCTCGACG	58.013	21
242	2652	2893	AGCTCGAATATGCAACGACA	59.449	20
234	448	681	GGAAGGGAAGCATTCCAAAC	60.807	20
252	13	264	TTTGGTTCATGTAGCCGACC	60.894	20
140	1080	1219	GGGTTGACAAGACCAGCATT	59.973	20
185	1361	1545	CCGTTGATATTTGGCCTGTC	60.331	20
277	331	607	AGTGTTTTAACTGCGGCCAG	60.305	20
207	555	761	TGGGTGTGTGAGTGGTGTTT	59.89	20
147	112	258	AAATAGCCGATTGCATCACA	59.14	20
209	578	786	TCAATTCCCCGATACACAAA	58.818	20
120	543	662	CGCTTCGTACGCTTTTAACC	59.911	20
212	1157	1368	TTTTGTCGAGCTTCTTTGGG	60.357	20
135	989	1123	TAGAGCTTTTTGCGGTGGTC	60.386	20
116	123	238	CACCAGCATTTCCATCTCCT	60.073	20
273	812	1084	ACATGCGATCTAGAGTGTGGT	60.201	22
246	1976	2221	GGAGCGAGAGGGAGAAGATT	59.919	20
277	49	325	CGAGAATTTCCTCGGATTCA	60.148	20
214	81	294	TCGAGTCTCCATCCTCGTTC	60.349	20
262	415	676	CACTCCATCAAAGAGCAGGC	60.945	20
277	1638	1914	TCAACTCATGCAAATGCAGC	60.969	20
280	1043	1322	GCTCCGGAGTTTTGAATGAA	60.192	20
242	104	345	CCTCACATGGTGGGAAAAAG	60.345	20
222	2470	2691	AGGTTGCGTACATCTGACCC	59.997	20
118	2066	2183	CACGGCAGAGCAATTCAATA	59.833	20
138	478	615	CCGGATTGACACCCCTAATA	59.64	20
279	909	1187	ACCCACTCCCACTTCTCAAC	59	20
263	92	354	AGACCCACCAATCTCAGCAC	60.12	20
214	543	756	TTGAATCCTCAGCGTGCATA	60.366	20
153	2331	2483	TGCAAGGGTTTGAATAAGCC	60.074	20
268	53	320	CACAACTTGATCAAAATTGCA	60.159	23
204	8	211	ATGTAGCCGACCCCAATTTA	59.297	20
260	1470	1729	AGTCAGGGTGAGGTCGAAGA	59.835	20
244	1324	1567	ACCTGAAGCTGTCCCAGGTA	59.721	20
113	1656	1768	GAAAACATCCAAAGGGCTTG	59.546	20
180	783	962	GATAGATGCCTGTTGGGGTC	59.366	20
187	943	1129	ATCCTGAGTTGCACACCCTT	59.579	20
254	1081	1334	CGCGTCGCCTAAATAAAAAT	59.262	20
242	23	264	ATGTAGCCGACCCCAATTTA	59.297	20
172	1008	1179	TCTGGAATGGGAGTTTCAGC	60.195	20
229	665	893	CAAACACTTCCACGCTGTTG	60.338	20
278	319	596	ACATACGCGTGCTTCACAAG	59.935	20
278	1	278	TGTAGCCGACCCCAATTTAT	59.297	20
259	260	518	TGGAATCCTGTCCTCTGGTT	59.505	20
266	279	544	TTCCGGCCCTTCAATAATC	59.848	19
245	2165	2409	TGATGTTGGTATTTTGGCTACC	58.878	22
173	0	172	TGCAGCTCTTAACTCTATCGG	59.271	22
161	4	164	GCAATATCAATGTAAGATCAT	57.778	27
229	462	690	CTATACGTGTGAGGAGCCAGC	59.912	21
253	134	386	TAAGGAGGCGAGAGAATGGA	59.91	20
270	1791	2060	CTAAGCGAGATACCAAGCCG	59.996	20
266	313	578	GGTTGGTTGTACAAAGAAACG	59.955	23
280	1880	2159	TGCTTTGTCATTGGGATTTTT	59.442	21
272	355	626	GATTCCATGCATTTCCAACA	59.33	20
222	319	540	GAGAACCCTAAACCGAAGGG	59.934	20
182	301	482	TCTACTCCAATGCTTCCCTTC	58.398	21
247	5639	5885	CTAGGCCAATTTGATTGGGA	59.894	20
125	557	681	CTCCCTCCACTTTCTCACCA	60.229	20

227	1145	1371	GCATTGCTTGACTGAGTTGC	59.602	20
146	669	814	GGTCGTGCTATTAACCACCC	59.316	20
223	4	226	CCCAAGACCCCAATTTGATT	60.91	20
266	364	629	TGTCTCGACGGACTGACACT	59.442	20
256	567	822	GGAGACCTAAGGATGCACCA	60.073	20
194	209	402	GCTGTTCTGAGGTTGGTTGG	60.69	20
233	342	574	TGGGTAGCTTACAAGTCCAGC	59.392	21
167	953	1119	TGGATCATCATCTGGCTTTG	59.604	20
241	5924	6164	CCGCTACAATCTTTGGTGCT	60.27	20
156	1806	1961	TCAGAAGAGAGTTTGCCATTG	59.993	22
165	61	225	ATTCAAAGCATATGCCCTCC	59.001	20
187	60	246	GCCGTTTCGATTGTATTTTCTT	59.525	22
161	1900	2060	CCGTTTCTCCAGTTGACGTT	60.149	20
242	572	813	AACCTAATCCATCCCAACTTTT	57.96	22
250	622	871	TAGAAGGAGATGGGTCCTGC	59.239	20
266	13	278	CAAACAGCGATTTTGAGTCG	59.464	20
277	907	1183	AGCTCATCGCAGGTTGGATA	60.765	20
270	2895	3164	TTTAGGCGTGGAGGAGAAAA	59.817	20
112	589	700	TGTCGAATAATTGACCGCAA	60.073	20
155	22	176	TCACATCACTAGTCCGTGGG	59.545	20
228	538	765	ATAAACGCAACTCAAACCCG	59.996	20
209	258	466	CCCTACTTCTGCACTGCCTC	60.012	20
279	359	637	GGGAACGTACAGATCCCCAT	60.97	20
128	3	130	ATGTAGCCGACCCCAATTTAT	59.585	21
106	248	353	CAAACCCACCAACAAACAAA	59.313	20
275	53	327	GCGTGTTTTCCAGAATCCAT	59.939	20
230	427	656	GGTGATGGTGATGGGTTTTC	60.034	20
236	851	1086	ACATGAGAGCCTTGCATCCT	59.834	20
224	961	1184	ACAAACGATTTCCCGTCTTG	59.971	20
254	3324	3577	CACGACGGAAACATGTAGTG	59.624	21
103	1654	1756	ATAAGCTCGTTGGTTAGCCG	59.384	20
147	497	643	CTTGATTGATCTTGGTGCGA	59.799	20
254	5	258	TTTTAAAACCGATCCCCTCC	60.123	20
126	213	338	AGGAGGAGGAGGTGGTGACT	60.112	20
230	969	1198	AGGGAAGTGGAAATAAGCCC	59.42	20
219	2522	2740	TGCGAACAATCTCTCCTCCT	59.95	20
215	30	244	TTGGTTCATGTAGCCAACCTC	59.985	21
232	796	1027	AAGCAAACAGCTCCCATCAT	59.7	20
263	848	1110	GGGAAATGGCTTGCATAAAA	59.907	20
208	281	488	AGGGTACAGGTGGATGGTAA	59.751	22
125	292	416	GGTTTGCACCCGATTACACT	59.859	20
274	463	736	TCAGCCCACACAAATTATCG	59.542	20
185	11	195	GAATTGGAGGCGGAGGAG	60.703	18
272	16	287	CCCCATCTCCTTAAAGCTCC	60.032	20
131	1935	2065	AGGTCCCCGGATTTGTTATC	60.017	20
168	209	376	GATGTATCATTGGGACCATGC	60.036	21
197	333	529	ACGCCTCATCGTCAAAACTC	60.263	20
231	5162	5392	CCTTATGCCAGGTTTTCTGG	59.564	20
193	535	727	AAGCTATCCCAAGGTCTTGAA	57.943	21
244	716	959	CCCAAACTGATTTCGCAACT	60.11	20
227	1098	1324	CTTTGGAATCTTCCCTTCCC	59.875	20
251	1372	1622	AAGAAGAGGGTTCGCTGTCA	59.989	20
228	893	1120	TCGGCAAAACCCTTTTATCA	60.427	20
225	1532	1756	CGAAGGGACCACAAAAGGTA	59.964	20
190	503	692	GCGGAAATTGTGTTGTTGG	59.956	19
266	742	1007	GCCAAGCTTATATTATTGGTG	57.892	22
227	54	280	GCTAACGACGTAAGGCAAAT	59.793	21
251	2927	3177	ACCGAGTGCAACTTCCTCAC	60.307	20

168	854	1021	GCCACGGTAATGTGAATCCT	59.82	20
261	1370	1630	TTCGCTCTGTGTTTTCCTCA	59.566	20
181	1389	1569	CAATGAACTCCAAGGGGAGA	60.042	20
200	156	355	GGTAATGTCGAAGAGGCTCG	59.836	20
263	11	273	ATGTAGCCGACCCCAATTTA	59.297	20
250	1277	1526	CCCAGACTGAGTTATTATTTGA	59.335	25
233	276	508	GGGAAACCCCCAAAGTTCTA	60.159	20
247	29	275	CCAGAGCGCACTCGAATAGT	60.559	20
132	607	738	TGATGTTCTTTGGGTGCTGA	60.24	20
230	513	742	AACAATAATATCGTCCGCCG	59.816	20
189	1224	1412	AGCCACTGCTTTTGTTGCTT	60.059	20
217	910	1126	AGTGTCAACAAAGTGCGTGC	59.953	20
246	1330	1575	TTGCTTCAGCACCTTGAAGA	59.716	20
263	793	1055	CGCACAGCATTCTCCATAAA	59.833	20
271	33	303	GCAAGGGTTTCTTCAACCAG	59.711	20
241	1001	1241	GGCATGATTGCCACAAATTC	61.251	20
133	367	499	CTGCTCAGCCTCAACTCCTT	59.745	20
210	511	720	AATATGGCATGAGACGAGGC	60.066	20
209	288	496	GGATCGTGTGTGGGATCAAT	60.61	20
170	87	256	CTCAACCAGCATCGCTATCA	59.972	20
174	933	1106	CCCCAAATCTGAATCCCTTT	60.124	20
167	711	877	CAGCCTTCCAGTTGGGATAA	60.066	20
187	414	600	ATCTCCTGTTCACACCACCC	59.817	20
170	9	178	CCCAAGACCCCAATTTGATT	60.91	20
140	819	958	CCCAGGTGTTGTTTTTCAGC	60.529	20
242	1667	1908	AAATGTATATTTCGTTCTTTCTT	57.286	27
249	64	312	GAGCACGTTGTGTTCCACAG	60.357	20
232	614	845	GATGCAGGGATACTGATTCCA	59.909	21
193	1187	1379	ATGGCAAACAAAGGATGTCAG	59.985	21
278	726	1003	GAAAGGATCCCATAATTCCCA	59.971	21
214	691	904	TGCTCACCCACATTCACATT	59.967	20
203	2326	2528	TCATATTTCCCCACCCCATA	59.834	20
205	1066	1270	ATGTGGTCACCTGGGGAATA	60.05	20
213	957	1169	GGAACCACTGATCGCATTCT	60.081	20
241	767	1007	AAAATCTTGCCGCCTTGTTA	59.72	20
274	111	384	CGGAGGTGATACCCAACATT	59.67	20
118	258	375	CTCCACGTTTTAACAACCGA	58.673	20
156	111	266	TGAACAAGGTTTCGATCTATGC	59.229	22
161	816	976	GAGGATTGGGGGTTTTCATT	59.996	20
198	803	1000	GGCATTATCAGAATTTGGCG	60.424	20
203	567	769	TTATGCTGCATTGCTTGAAA	58.092	20
224	6	229	CCCAAGACCCCAATTTGATT	60.91	20
116	2517	2632	TCCTTGGAACTCTCAATCCA	58.201	20
242	283	524	TTAACTTGTCCCCGTTGGTG	60.776	20
226	919	1144	CACCTCATCTTGCTTCGTCA	59.984	20
257	359	615	GCAACGAAAAATACAAGCCAA	60.123	21
182	1966	2147	TACAGTGACGGTGTCCTCCA	60.154	20
115	3440	3554	TATTGGAGAGGGAAGCAGGA	59.767	20
279	0	278	CCCAAGACCCCAATTTGATT	60.91	20
251	46	296	GTCAGAAGGTCCCCCATCTC	60.86	20
275	4497	4771	CGCCTCTTGAATAACCTCCA	60.206	20
206	198	403	TTTCTCAGTATGCGGCAGTG	60.011	20
217	1681	1897	CGAGGAAGACGATGTAACCC	59.55	20
148	9	156	TAGCCGACCCCAACTTATTG	59.953	20
180	1835	2014	TTTTAAAACGCCTGAAAAAGTA	57.409	23
277	406	682	CGTGCGGCGATTAAAATAAC	60.464	20
213	962	1174	GGCAAATTTGAATCGGTGAT	59.768	20
267	678	944	GGCCCTACATTACAGCTTGC	59.736	20

207	69	275	TTGATTCATGTAGCTGACCCC	59.947	21
276	666	941	CGAAGGATCAACTTCATAGTC	59.666	23
259	391	649	TCCCCCACAACGTTATTCAT	60.051	20
238	252	489	AATGTTGGCAGCAACTACGA	59.347	20
148	227	374	TGTTTCCCGAGTTCTTTGCT	59.853	20
133	1359	1491	GGTCATCAATTCAGGAAGCC	59.488	20
271	407	677	CACACTATCAACCGAACCGA	59.566	20
224	991	1214	TCAGAACCATGATCTGCCTG	59.787	20
227	196	422	CCCATTATCACGACAGACGA	59.522	20
179	400	578	TGACAAATAAAAACCTACAAA	59.231	26
227	648	874	AAGAGGAGGACGAGCATGAA	59.95	20
165	370	534	CATAGGGCAAGTACGGGAAA	59.953	20
232	487	718	CACCGGTTTTGGATTTGACT	59.83	20
193	754	946	CAAATTTAAGTGAGCTTTGCTT	59.957	24
152	928	1079	CCCGATTGGACTCTCAACAT	59.927	20
112	2141	2252	CTGCACACTTTGGTCCATTG	60.152	20
197	67	263	CCTACCGGAACTCAATAACCA	58.96	21
133	2444	2576	TGCTTAGACTTGGCGTGAGA	59.74	20
141	439	579	TGATCCATCAACTTGTCCCA	59.893	20
236	495	730	TGGAATCAAGAACCCCAAAG	59.903	20
146	104	249	CACATAGTGGGAAACGGCTT	59.993	20
176	697	872	GCAAAAACAGCAAGGAGAGG	59.993	20
108	4843	4950	GAGAAATGTTTCCGGCGATA	60.038	20
180	209	388	AGTTCAGCGAGAACAAGGGA	59.989	20
270	436	705	CATCAACATTCCTGGGCTCT	60.073	20
262	1360	1621	TTGTTTCTTGAACCCCTTGG	59.942	20
261	17	277	TTTGGTTCATGTAGTCGACCC	59.845	21
267	1755	2021	AACGAGCCAAGTGAAAGCAT	59.882	20
126	541	666	ACATCCTCAACCATGGCAGT	60.395	20
186	1375	1560	GGAATTGCCCGAAATACTGA	59.901	20
250	1864	2113	CGTACGTTGTACGGGTTCATA	58.502	21
104	2536	2639	GAGTGGTAAAACTCCGCCAC	59.598	20
149	252	400	ATTTTCTCCCTTCATCGGGT	59.766	20
119	1318	1436	TCACCCGATTACTACCAGCC	59.955	20
176	0	175	TATTTCCGACAATTCGGTCC	59.762	20
155	7	161	TTCACATTTCAGTTTACTGGGA	59.016	25
279	2179	2457	GTTGGAACCTCGAGCATTGA	61.188	20
278	612	889	GTGGCGACATGAATTTCCA	60.474	19
251	847	1097	CATAATCTTGCACCTCCACG	59.148	20
255	196	450	CAAACGACGAGCATCAAGAA	59.988	20
266	195	460	TCATACACGTGGACACCTCAT	58.869	21
236	2519	2754	AACAGAAGCAGAGGGACGAA	59.989	20
182	1550	1731	CACCAATTTCCCCTTTTCCT	60.159	20
237	660	896	CATTTGGCTTGTTAGGAGGC	59.708	20
254	596	849	CGAGGGAGGTGAGGGACTAT	60.468	20
223	678	900	TTTTCAAAAGCACCCGAATC	60.053	20
191	2276	2466	TGTCTGAATTTGGTGGAGGA	59.059	20
150	1068	1217	CTCTGTTGTTGGTCGTGGTG	60.194	20
113	2593	2705	TCAAACCCAAACCAACCTTT	59.308	20
244	66	309	TAGGTCTGAGGGTTGGATGG	59.92	20
208	1	208	TCACGTTGTCCACGTTCCTA	60.152	20
199	2109	2307	AGGCTTGGTTTTGATTGCAC	60.118	20
278	655	932	TTTCCTTTTCTTTTGCTACCCA	60.102	22
264	166	429	TATGGTTTGGTCCGATGGAT	60.014	20
110	1104	1213	GGGTGATTGAGTTTCCTCCTC	59.927	21
109	2377	2485	TGGCCTAATCGTTCCTCAAC	60.074	20
102	1884	1985	TCTAAAGCCTCCCACGAAGA	59.948	20
239	996	1234	TGAAACCCTAGCGAACCAAC	60.11	20

280	1081	1360	TTCGTTGTTCCACACTTCCA	60.128	20
170	152	321	CTCTGTAGGCTTCTCCGCAT	59.598	20
193	1505	1697	TCTTGGTGGTTCTGGTAGGG	59.959	20
276	7551	7826	TGTCCACGCGTAATTCTCAG	59.864	20
228	203	430	TCTCAGTTTTGGGTTTGGGT	59.425	20
100	463	562	AGGACTAGGGAAAACGGCAC	60.496	20
170	9	178	CAACAACTCGTCACCCCTTT	60.005	20
223	104	326	TGGAGCAACTTCTTCGATCA	59.522	20
248	89	336	TGCACTGATCATACACATGAC	60.05	23
243	6146	6388	TTGGGGTCTTGGAGTCAGAT	59.505	20
112	0	111	TGTAGCCGACCCCAATTTAT	59.297	20
203	44	246	TGTAGCCGACCCCAATTTAT	59.297	20
187	940	1126	GTGCAAGAGATTGGGTTGAAA	60.103	21
186	11	196	AAGCAGAAATCGGGATTGAA	59.645	20
168	61	228	GACGAGGACCAGATTTGCAT	60.081	20
173	95	267	TTTTTGATTGGGAATAATTGGG	59.895	22
158	1516	1673	TTCTTGCAAAACGTGAGCC	59.98	19
167	1291	1457	CGAAAAGATGTATGGCGAAA	58.769	20
278	632	909	GGATTCGTGACTTTCAGGGA	60.05	20
189	7	195	ATGTAGCCGACCCCAATTTA	59.297	20
129	584	712	ACCAAAGCAAAAACATCCCA	60.344	20
276	54	329	ACAATTTCGGTTTCGAGCTG	60.249	20
172	167	338	TTTGCCATGAAAAACAAGGA	59.133	20
151	591	741	TTAATCAACCACCACACCCA	59.667	20
279	2871	3149	AAATCCTCCCTCGTGATTCC	60.272	20
272	2023	2294	GCTGCCTCTGGACAACTCTC	60.143	20
109	2039	2147	GAAGCTGCTGTTGCCGTAGT	60.602	20
103	577	679	TGATCTCCTCTTTCTTGCCG	60.474	20
213	43	255	ATCTCGGGTTGCAGTCGATA	60.624	20
268	1669	1936	GGGAAGGGGGTACATGCTAT	60.039	20
149	411	559	TCAGCAGCAGCAAATACAGC	60.31	20
263	2509	2771	AGACAACGAGGGATGACGAC	60.12	20
242	2771	3012	AGCTGTCGATTTCTGCCACT	60.02	20
196	149	344	TCACTCAGGGGCTTTACCAC	60.111	20
272	756	1027	CGGGATGTAGTAGGAAAGCG	59.724	20
128	2	129	TGTAGCCGACCCCAATTTAT	59.297	20
188	145	332	ACCTCATGAGCACAATTCCC	59.934	20
188	33	220	GGAAAATTTTTGGCCTCTCA	59.135	20
198	393	590	AGGGCTTAAAACTTGCCACA	59.747	20
135	1549	1683	TGCATGCACAATTATTTCCC	59.381	20
269	338	606	ATGAATGAATGGTTCGACTCA	59.434	22
267	1468	1734	AACTGGACCATATTCGTCGC	59.962	20
266	281	546	TTTACCAAATTCTGCCGCTT	59.72	20
244	835	1078	ATTCTGGCAAATCATCGGAC	59.9	20
184	496	679	CACCACCCTCTCATGTCCTT	59.962	20
262	661	922	AGGAAATCACGACGGTGTTC	59.973	20
213	1382	1594	CCCACACGTTTTTCCTCATT	59.83	20
167	375	541	GCAACTTTCAAGGAAGCCAA	60.365	20
185	495	679	CTGGAACGTGTACGACAGGA	59.745	20
268	20	287	GGTTCCCACGTCATCAAAAA	60.734	20
245	3222	3466	CCCACTTCATGCAGTTTCCT	60.111	20
271	897	1167	ACTTGCATGTTGTGCCATGT	60.04	20
145	1061	1205	AAACCCTTCCTTCTGCGATT	60.074	20
187	2089	2275	TTTGGATTCGATATGGATTGA	57.895	21
198	85	282	CCTCCAAACAAATACCCCCT	60.046	20
234	1404	1637	GATGCTCTACCACTGCACCA	59.862	20
135	626	760	CAAGCAAACGCAAAAATCAA	59.858	20
280	206	485	CTGACTGACGTGGTTTGCAG	60.5	20

240	719	958	GCTGGGATCTGTCAACTTCC	59.661	20
238	525	762	AACTCCCACCTTCCATCACA	60.363	20
250	102	351	TTCCAATTGTGCGTAGCCTT	60.637	20
211	5	215	CCAATTTATTGGGATTAAGGC	57.539	21
214	1268	1481	CCTCCATGTAAAGAAAAAGAG	60.045	25
268	86	353	TGCCGAATAAAGCTAAATCCT	58.055	21
170	36	205	CTCAGCTCAATCCTTCGCTC	60.24	20
198	640	837	CGTCGAATTTCGCTGATCTT	60.352	20
204	446	649	AAAGTCAAGTGCCGCTCATT	59.882	20
214	86	299	TGACAATTCGAGCTTGATCCT	59.828	21
260	863	1122	TAGGCGATGTACCTTGGGTC	59.955	20
262	812	1073	TTGGAATGCGACAGAGACAG	59.984	20
250	272	521	GACACCATTGACTGTGCTGG	60.162	20
265	7	271	TGTAGCCGACCCCAATTTAT	59.297	20
239	19	257	AGCAACAGGCACACTGGAAT	60.721	20
138	715	852	GCAAACTCGAAGAATAGCGG	59.982	20
218	397	614	CTCCAAAGTCCCTTCTTCCC	60.045	20
133	942	1074	TGAAATGCCAAATCAGTTGC	59.67	20
146	999	1144	CAAATGCCAGCTCAAGATCA	59.948	20
190	200	389	AGATTGTCGTCGTTCCATTGT	59.468	21
252	884	1135	GGGAACCTTCTCTGTTCCCT	59.534	20
153	105	257	CCAGTCCGGCTTGAAAACTA	60.241	20
173	1156	1328	CAGCAAGCAATTCAAGGACA	59.988	20
170	5	174	CCCAAGACCCCAATTTGATT	60.91	20
163	462	624	GTTTCATACTCACCTCCGGC	59.556	20
213	826	1038	GCAGGAGAAGAGGTGGTCTG	59.986	20
280	458	737	GAAAAGGGGAATGCAAATGA	59.878	20
161	10	170	AGTGTGTCGAAATTGAGAAGA	58.048	23
248	1035	1282	TGAGGGAGGAGGCTCAGTTA	59.943	20
278	572	849	TCTCACACTCTCAAAATGGCA	59.43	21
206	0	205	TGTAGCCGACCCCAATTTAT	59.297	20
217	1205	1421	CCCGACCCAACTCAGTAGAA	60.103	20
246	8	253	TGTAGCCGACCCCAATTTAT	59.297	20
260	4337	4596	AGTTTCGTGTTCTTTGTGACG	57.927	21
237	521	757	TTCATGACGTGGAAGCAAAA	60.234	20
269	87	355	CCATCTAGTTCCTCACCGGA	60.065	20
202	1200	1401	TAAAACCCCCTTCAAATCCC	59.992	20
264	863	1126	TCATCTCAAGACCACCCTCC	60.048	20
162	474	635	GTGAAATGGGAAGGACTTCAT	57.96	21
237	3691	3927	CCACCTCCGTACCGTTACAC	60.291	20
189	1917	2105	AAAAGTGTCATGGCGAAACC	59.978	20
205	507	711	CAGGTTCAAATCCCACCAAC	60.21	20
128	53	180	TGCATATACACACATGTTGAC	59.79	23
217	502	718	GGCTGGGTAATAGCCTTTCC	59.93	20
164	155	318	AGCTTAGCACAGCAGCATCA	59.918	20
209	476	684	ACAGATCCGAATGTGCGTCT	60.688	20
201	160	360	CCCAATTCATTCCATGTTCA	59.175	20
115	1071	1185	TCTTTGTGTAGCACCCCCTC	60.111	20
243	922	1164	AAGGAGGGTCAGTGAGCAAA	59.844	20
263	224	486	AGGTTTGAAGATGCCATTCG	60.074	20
148	2980	3127	ATGGGTCTCTGCCTTTTCAA	59.67	20
137	1985	2121	TACCTGGGACATGCCAGACT	60.533	20
201	2365	2565	TTTCTTCAAACTCCCACCGT	59.569	20
243	847	1089	TGATGGAACTTGTGTGCATGT	60.024	21
139	2977	3115	CTCAGCTGCTGCTCTCAGTG	60.227	20
167	525	691	ACTTTTCCTGCCATGAGTGG	60.111	20
226	702	927	CTCCTCTCTCTCATCCCCCT	59.76	20
234	557	790	GCTTCCAGCAGAAATCATCC	59.78	20

271	2066	2336	AATGCAGTCCGGGTTCATAG	59.955	20
267	8	274	ATGTAGCCGACCCCAATTTA	59.297	20
112	4	115	CCCAAGACCCCAATTTGAT	59.59	19
182	6	187	ATGTAGCCGACCCCAATTTA	59.297	20
233	2215	2447	TTCGGGTAAACCTTTGCTGT	59.609	20
247	346	592	TAGCATTTCGTTGGGACTGG	61.021	20
268	658	925	CATTCAATTCGAAATTATGCAT	60.102	24
214	759	972	AGGATTTGCAGGGTTCCATT	60.693	20
220	283	502	CTGCAAGTCACATTCCACCA	60.722	20
208	3603	3810	CGAGTATGGTGTTGGTGGTG	59.873	20
265	477	741	GAGGGATCATCGGAGGTTCT	60.421	20
270	225	494	TTCAAATCCGGGTCTCTCAC	60.05	20
199	2200	2398	TTGTCGTGATGGGTGAATGT	59.812	20
265	3	267	CGCATGACACTGATCTATCG	57.804	20
213	5	217	CCCAAGACCCCAATTTGATT	60.91	20
269	1502	1770	AACCCCAACTCACATCAACA	58.827	20
193	5760	5952	TTCTTGTTTTCCCTCACTGGA	59.697	21
207	1107	1313	TCCAGATTCAAGACCAAGCAC	60.248	21
227	1181	1407	CGTCGCCAAAGTGTTCAATA	59.729	20
257	422	678	TATCAACACCCCAGCATGAG	59.522	20
279	1069	1347	TCGTGTTCGCCACATATTTT	59.041	20
206	3750	3955	TGGAACGATTGTGTGGAAAG	59.541	20
262	516	777	GATGCAGAACAATTTGCGTG	60.265	20
108	3209	3316	TTTTGGGTGGAGAAATGGAG	59.903	20
187	13	199	TTTGGTTCATGTAGCCGACC	60.894	20
246	392	637	CCCATGCCGAATGTTATTCT	59.784	20
200	624	823	CATTATACCACGGAGGAAGGA	58.914	21
265	221	485	CCCCACACACTCATCCTCTT	59.962	20
219	384	602	TTGGGTTGGATTTGAGCATT	60.309	20
251	586	836	TGAAACATCCATTCTCCAAAGA	59.546	22
197	3346	3542	TAGATAACAGGCAATGCCGC	61.124	20
263	678	940	CTCTTCAGCTCCCACTCCAC	59.986	20
242	660	901	GTTCCTAGCTGTCGGCACTC	60.02	20
222	291	512	AAAAGAGGGGGAAAAATTCG	59.415	20
272	1341	1612	CATATAAAGAGGGCAGCCGA	60.188	20
225	1805	2029	CCTGATGAGGCTAAGGATGG	59.647	20
234	728	961	CCGAAAATGTCCTTCATTGC	60.448	20
165	756	920	GAGGACCGGACTGACTTCAC	59.688	20
264	471	734	CAGCATGAGGCAGATTGATG	60.376	20
180	308	487	CGAATTCTGCTTCTTCCAGG	59.948	20
258	563	820	CCCCTTGGGATATGTGTTTG	60.044	20
171	285	455	TCCAATAACCAGGGTTCCAG	59.784	20
276	3222	3497	CTTGTCACTAAGCCAACACCA	58.837	21
244	1085	1328	AGGAAATGATTGTTCTCCTAG	59.073	24
247	242	488	TGTTTGCTTTTCTTCATGCG	59.992	20
280	3209	3488	CATCAGTTTGCCCCTATCTCA	60.081	21
167	2004	2170	GCTTTGCTTCGTGCTTGAAT	60.531	20
190	1398	1587	AGGGGACTCGTCAGGAAACT	60.111	20
277	164	440	TCTTTTTCCATTGCTCACGA	59.395	20
264	2979	3242	TACTGCATCGGTGTCTCACA	58.813	20
277	291	567	CACGACCGTATTCTCCACCT	59.989	20
179	710	888	GGAGGAAGCATCTACGCAAC	59.843	20
223	601	823	TAAAAGTGCCCGATTTCAGC	60.209	20
225	125	349	GTAAAGGAATCCGCCAACAA	59.938	20
105	1040	1144	TGCACGATCCATATCTGCTG	60.801	20
259	3223	3481	GGGCTGTTGGTTGTGAAGAT	59.973	20
268	1288	1555	AACAAAATCCCTCCCCATTC	59.996	20
212	1243	1454	TGCCTTAACACAAAGGGGAA	60.472	20

272	3	274	AGCTTTGGTTCATGTAGCCG	60.27	20
268	2318	2585	TACACGTTCAGACTGTGCCC	59.751	20
231	248	478	TGTTATTTGAAACTGGACCTGC	58.994	22
219	933	1151	AATCTCGTTGCCGTTGGTAG	60.132	20
269	567	835	TCCTTCCTTTTCATTTCCCA	59.476	20
210	5720	5929	CGTTTTGCTTCTGCACTTCA	60.172	20
215	5360	5574	AGGGACAAGCTATCACACAGC	59.222	21
198	237	434	CCCCAAGACCCAATTTGATT	60.91	20
204	1019	1222	CACCTGGTCCTTCCTCTTCA	60.229	20
263	441	703	TGCTTAACACGTTACTCCTCCA	59.807	22
271	1828	2098	CTCCGGCTTATGTCCAACTG	60.647	20
257	38	294	GCACTCGAAGAGTAGCGGTT	59.644	20
224	1153	1376	TCTGGAAAAGAGAAGGCCAA	59.926	20
268	30	297	TGTGGGAAAAACATCGATCA	59.9	20
277	1303	1579	ATTCGGCAACTTTTGGAAGA	59.685	20
261	631	891	TTTCTCGCCTAATGCCATGT	60.606	20
217	1393	1609	TTCTACGTCGAGAGGCGAAT	59.978	20
208	2986	3193	CCCTCAATTTTGTACCCGAA	59.795	20
239	6	244	CCCAAGACCCCAATTTGATT	60.91	20
258	372	629	GCCAAAAGTAAAGGAAGGGG	59.939	20
102	2017	2118	TTTCAAAAGTCATCCCCTGG	59.903	20
266	1133	1398	AAGTCCGCAGAACAACAACC	60.156	20
210	867	1076	CTCCAATCTCTCTCCCACCA	60.191	20
156	2254	2409	ATTTGAACGGTTCTGTTCGG	59.971	20
275	1	275	CCCAAGACCCCAATTTGATT	60.91	20
174	1120	1293	CCCATCCTCAGATTTACCGT	58.861	20
110	1193	1302	TCTGGAAAAGAGAAGGCCAA	59.926	20
276	957	1232	GCATTGCTTGACTGAGTTGC	59.602	20
217	1167	1383	TACATCACCCTCCCATCTGC	60.893	20
277	503	779	CTTCCCTGCAACCAACTCAT	60.111	20
233	125	357	TCCTCCAGCTGTTCTTTCGT	59.989	20
108	81	188	AGTGAACAGCATGGTCTGGA	59.261	20
229	2277	2505	TAAGGGGATTGATTGGCAGA	60.405	20
185	1071	1255	AGCCACGAGAGAATTTGCAT	59.843	20
204	1132	1335	TGCCCTCACAAACAAATTCA	60.088	20
158	2070	2227	AAGGATCTTGATCGCTGTGTC	59.303	21
279	556	834	TTGCACACATCTCCCTCTCA	60.402	20
214	1749	1962	TATGCTGATCCACCCTTTGA	59.075	20
142	521	662	GCAGCTGAGCTAGGTGCATT	60.709	20
280	422	701	TGGATTTGCAATTTTCAAGG	58.6	20
278	2496	2773	ATCTCACTCGGACATGGGAC	59.928	20
236	2770	3005	AGGCAAAGAATTTCCAGCAA	59.823	20
182	2241	2422	TGCAAAAGAACACCAAAGCA	60.415	20
191	563	753	AGGACTCGCCTTCACTGAGA	60.135	20
115	6	120	TGTAGCCGACCCCAATTTAT	59.297	20
259	293	551	TCGGCATGTTGCTCTTTATG	59.833	20
280	981	1260	GCGCTGAAAGAGGATGAGAT	59.537	20
234	2476	2709	GTCCTCCTCGTCATCGTCAT	60.08	20
130	571	700	TGCACTTGCACTCATTTTTGT	59.381	21
199	273	471	TTGCAGAATGCAAGATGTGC	60.969	20
222	474	695	CTCACCAGAAACTCCCTTGC	59.844	20
270	1857	2126	GGATGATTGGGAATAATTGGG	60.213	21
280	139	418	ATAAGATTTGCACGCTGGGA	60.606	20
269	831	1099	CGTTGCTTGGCAATTCTACA	59.872	20
268	193	460	ACTCAGATCTGGCCTGGAGA	59.945	20
139	0	138	TGGTAGATCTGCTCCTTGTAGT	60.315	24
190	53	242	CTGAAAGGGAGTTGGAAGCA	60.366	20
258	1	258	CCCAAGACCCCAATTTGATT	60.91	20

241	967	1207	ACGCCAATTTGGATTTTGAC	59.807	20
201	13	213	GGTCCTTCGTCGCATATGAA	61.003	20
259	4978	5236	CAAATGTCATATACCCGCCC	60.038	20
267	2	268	GCACAGGCAGCTAAGACACA	60.207	20
272	68	339	CAAGTCCAATGCATCACCAT	59.374	20
205	12	216	ATGTAGCCGACCCCAATTTA	59.297	20
202	1803	2004	CAGGGAGCCCTTGGATTTAG	60.938	20
164	12	175	TTGGGATTAAGGCTTTGGTG	59.931	20
234	433	666	TGTATGTTTTGCGAGTGGGA	60.111	20
144	654	797	AAATTGTGGGATAAAATCCCC	59.8	22
242	511	752	CAGAGCAGTTGTAGACGGCA	60.199	20
263	2139	2401	CAGTGCATGCAAGCTGATTT	60.019	20
167	1575	1741	TGCAGATAGGGTTTTGGGAG	60.066	20
130	7	136	GTTTATGTAGCCGACCCCAA	59.823	20
258	340	597	CCGATAAGCAGAGCTCCATC	59.939	20
279	347	625	TGGTGAAAAATCAAACACTTG	59.876	22
211	1301	1511	AAACGATGATTTTGAACGGC	59.945	20
241	1615	1855	TTTGATTAAATCGGGCTATGA	57.306	21
164	646	809	TTCTTCCTCCGACGACAACT	59.844	20
158	359	516	ATGCTTCTCCCCCTTGAAAT	59.903	20
204	1748	1951	TCAGTTATAGCCGACCCCAC	59.955	20
248	1729	1976	CGTGACAGCATGCTCCAATA	60.834	20
240	4759	4998	CCTCAGGATTCCTCATCCAA	60.003	20
136	1459	1594	CTTGGAACAAACAAACAAGCA	58.856	21
148	1065	1212	TTTTGTTCTGGTCCGCTCTT	59.853	20
144	4460	4603	CCCATTTTGACGCTCTGATT	60.074	20
275	433	707	GATTGATTCCGGTAGGCAAA	59.901	20
280	4617	4896	GACTCAGTTGAGCCCCTCAC	59.841	20
160	1579	1738	GCATAACCCGAACCCAATAA	59.66	20
256	619	874	TTGGGAAGATTCGTGTTTCA	59.097	20
238	5869	6106	TGACAGATGAATGGACCAACA	59.951	21
126	4	129	CCCAAGACCCCAATTTGATT	60.91	20
118	3768	3885	CATTAGCTCCGTGATGCAGA	59.972	20
264	1608	1871	CTTTCGACCGTTCGTGTTTC	60.668	20
154	459	612	TATCCAATATAGGGCACGGC	59.779	20
259	1596	1854	CGTTGATTCTTCAAAATCCCA	59.924	21
214	4606	4819	AGGCGAGGGAGACCATCTAT	60.059	20
277	495	771	CAGCCCGTTTCTGAAAGACT	59.473	20
185	802	986	ATTCCCACCACCATTTTCAA	60.029	20
183	327	509	ACTAGCGTGGCTTATTCCCA	59.73	20
184	356	539	TTACCTCCGAAGGAACGAGA	59.807	20
261	5	265	CCCAAGACCCCAATTTGATT	60.91	20
278	1818	2095	CCATCACCATCACTTCCAGA	59.473	20
257	397	653	GCGTACACGCGTATGACAAG	60.346	20
165	9	173	CCCAAGACCCCAATTTGATT	60.91	20
280	1389	1668	TCTCCCTCCTCCTCCTCTTC	59.883	20
206	1202	1407	CCTCCCTCTAAAAACCCGAA	60.415	20
210	4	213	TTCATGATACTTTGGGAGTTCG	59.087	22
206	1675	1880	GCGTATTATTTTTCTCTCAATA	58.762	25
241	78	318	TGATCATCCTCCTCATTCTCTG	60.088	23
169	904	1072	ACAAATCGGAAAAGAGCAGC	59.457	20
239	1927	2165	TGAAGGTGAATACCGATTACG	59.474	22
255	1772	2026	ATCGGAAGCTTCAAGTCCAA	59.813	20
108	1944	2051	CTTCACATCATTCCCAGGCT	60.073	20
279	687	965	CGGAGAGGAAGAGGAAGAAG	60.074	21
227	1963	2189	GGTTAGATTGGAGATGCCGA	60.036	20
187	2578	2764	AAGAAGCAACCATCAACCGT	59.598	20
208	907	1114	CTGCAGAATCAACTGCTTGG	59.591	20

225	1	225	TTGGTTCATGTAGCCGACCT	60.517	20
276	4928	5203	TTCGTCCATATCAAGGCTCA	59.226	20
220	309	528	AAAATGGATGGGGTGATTGA	59.991	20
223	2948	3170	TTGTTTGCAGTGTGTTGCCT	60.347	20
118	5314	5431	AGTATTCTTGCCGTTGGGAG	59.195	20
156	6	161	ATGTAGCCGACCCCAATTTA	59.297	20
230	1431	1660	AAATTCGAACCAACGGTCAC	59.836	20
277	1672	1948	GGAGGAAATTGGCATCAGAA	60.014	20
227	0	226	AAACAGCTTCTCTCTCCGGG	60.892	20
181	837	1017	AAAAATAATGATAACGGCGG	60.179	21
250	624	873	TGGTGAGCTTGAGGAGGTCT	59.986	20
238	6	243	TGTAGCCGACCCCAATTTAT	59.297	20
263	7	269	CCGAGACCCCAATTTGATT	59.735	19
261	29	289	TGTAGCCGACCCCAATAAAT	59.297	20
134	3	136	ATGTAGCCGACCCCAATTTAT	59.585	21
153	2	154	TGTAGCCGACCCCAATTTAT	59.297	20
119	2994	3112	AAACCATCTTTCCCCAAACC	60.032	20
186	3154	3339	CCTCCCTTCTTTTGTACCCA	59.024	20
199	635	833	TGATTCGGGTTCGAATATCA	58.917	20
280	59	338	CCCACATCCAGCTTTCGTAT	59.955	20
132	794	925	CAGTTTCAAGGGGAATCGAA	60.044	20
231	3653	3883	GTGAGGATGATGGTGGAGGT	59.774	20
170	1898	2067	AAGCTGCATGAGGTGATTGA	59.399	20
263	5695	5957	CCCGTACTACGTGCATGAGA	59.74	20
140	605	744	CAAGGCCTGTGTGTTCTTGA	59.873	20
191	2121	2311	AGCCGACTTCACATAGTGGG	60.134	20
250	1099	1348	AGCTTCCAAGACGTAATCGG	59.336	20
153	904	1056	AAATACAAAGCCAGCCAACG	60.131	20
273	8	280	TGTAGCCGACCCCAATTTAT	59.297	20
192	30	221	ACGTGTATTGGGTGGTCCAT	59.973	20
184	2227	2410	GCAGAAGGCTCCACTCTTGT	59.604	20
170	1570	1739	AACTTTTGCCTGAAACGCAT	59.752	20
234	717	950	ACCATGAAGATGAAGCTGCC	60.226	20
177	675	851	CTCGTTTTCTTTCTCGGTGC	59.993	20
139	23	161	TTGGGATTAAGGCTTTGGTG	59.931	20
114	2240	2353	TATTTCTCATACGTGCCTGCC	60.11	21
191	1065	1255	TTACCAAGGACTGAGTCGCC	60.255	20
156	2835	2990	GATGCGGGGGATTTAAAGTT	60.15	20
275	280	554	AACCATTCCCCAAGTCATCA	60.173	20
235	3769	4003	ACTCTTACGAGGGACGGGTT	59.994	20
146	118	263	AATAAAGTATGTGGGAAAGTC	57.317	24
218	140	357	GTGAAACACCATCTTTCCCG	60.353	20
151	6	156	ATGTAGCCGACCCCAATTTA	59.297	20
150	217	366	TTAGGGCTGTTATCGGATGC	60.06	20
164	226	389	GATTCCCTATCTTGCTCCCC	59.866	20
226	3486	3711	CGAGCGTCTTCATTCTCCTC	60.096	20
180	1755	1934	AATCTATGCTTCCAATGCCG	60.06	20
226	3101	3326	AAGAAAATGCCGTTGGTGAG	60.11	20
232	3804	4035	TTGCGTACATTTGATTGGGA	59.93	20
242	2565	2806	TTTTGCATGTTCAGAGGCAG	59.988	20
152	1770	1921	TTAGGCTCTCCAAAGGACGA	59.948	20
179	501	679	CATTTCGACCTCCACATCCT	59.927	20
116	3712	3827	AGAGAAGTTGTGGGGTGGTG	60.002	20
217	2724	2940	GGGGTTTGGTCAGCATTTT	59.782	19
201	612	812	GATCAATGAAGGGGACATGC	60.289	20
267	3815	4081	CATCGGCTGTTACTCCTTCC	59.694	20
238	502	739	GGCTGAAAAGGATGCTCAAA	60.331	20
239	20	258	GTGTAAGTCGCGGTCTCGAT	60.285	20

155	1229	1383	TCCATCAACCTAACAGCAACA	59.184	21
225	157	381	TGGCAACGAAAATGAACAGA	60.234	20
200	784	983	GACGGAGATCCCAATGAAGA	60.011	20
141	2	142	TGTAGCCGACCCCAATTTAT	59.297	20
266	2779	3044	CTCATTGACGACATCCAACG	60.112	20
156	3318	3473	AGCGGGATAATGGAACAGTG	59.955	20
267	667	933	ACTCGTCATTTAACGCGCTC	60.416	20
237	487	723	TGCAACTTGAGGCTGAGAAA	59.716	20
260	134	393	GTTTATGTAGCCGACCCCAA	59.823	20
157	1573	1729	GATGCTTAGTTGCCCATTCG	60.606	20
279	1271	1549	CTAGTGGCTCTGGTTTTCGG	59.869	20
240	743	982	GAGAAGGAGGGGATGGAGAG	60.149	20
241	2936	3176	GCAGGAATGTGATTTTAGCCA	60.089	21
256	562	817	AAATCCCAGAATTGGTTCGAT	59.658	21
157	2335	2491	CCGTAGGTTTCGTCTTCGTC	59.734	20
256	140	395	TAAGCTCAAATGGGGTTCCA	60.439	20
258	1781	2038	CAACTGCACTTGGATCCTGA	59.831	20
189	497	685	TTGAGGTATGGATGATCGGA	58.873	20
165	1310	1474	TCTCCTACCCAAAACTCCCA	59.521	20
259	327	585	CACATCCGGGTTTTCATTCT	59.79	20
208	1913	2120	CTTTTGGGGAAACCTGGACT	60.332	20
264	1012	1275	GGGGCCCTGTCTAAAAATTG	60.664	20
197	1756	1952	ATTGCATACATCTGACCCCC	59.635	20
123	604	726	TCTCCTTCTCCCTCCTCACA	59.913	20
137	171	307	CTACCCACAACAGCATGACG	60.175	20
223	5	227	ATGTAGCCGACCCCAATTTA	59.297	20
242	10	251	CCCAAGACCCCAATTTGAT	59.59	19
168	6	173	TGTAGCCGACCCCAATTTAT	59.297	20
266	128	393	TTTAAGTGGAGGCGGTGTTT	59.609	20
192	600	791	CCATTTTTGGCGATTCTTGT	59.938	20
274	897	1170	AACCGGGGAAATATCGTCTC	60.152	20
232	390	621	TTGGTATGCGCAACAATGATA	59.972	21
233	5624	5856	TGTGGTCTCATAACAAACCTGA	58.132	22
199	2363	2561	TGCCATGCGTAAACTAAAACC	60.013	21
259	3070	3328	CACACCCTTACTTTCCCCAA	59.824	20
261	41	301	AAAAGTGGCATTTTGCCCTA	59.586	20
237	2601	2837	TGTGAATCCCAAATGCTTCA	60.049	20
275	18	292	TTTTGGCATGAGAAACTCCC	60.051	20
280	866	1145	AAGGCGAATTCTTGGGAACT	60.074	20
229	1674	1902	TTTGTTGACGACGGAACTGA	60.278	20
164	2972	3135	ACAAGAAGCTGAGAGGGCAA	60.134	20
157	2	158	TTATAAAACCGACCCACCCC	60.773	20
279	734	1012	TGGTCTTCTTGCATGTCTCG	59.984	20
258	16	273	TTCTTATCTCTGCGCCGATT	59.945	20
279	311	589	GCATTTTCCTCAAAAAGGGA	59.135	20
106	4	109	ACGGAGTTGTGAAGGAATGA	58.129	20
184	21	204	AGTCTAAGGGAGCACATGGTT	57.802	21
238	5	242	ATGTAGCCGACCCCAATTTAT	59.585	21
188	86	273	TTCTTCCACCAATTACCCCA	60.162	20
270	430	699	AATTGGTGCTCAAGAATCCG	60.074	20
214	594	807	GCACACTCGAACAAAGCAAA	60.035	20
241	2396	2636	TTTTCACGCACAACACACAC	59.191	20
151	488	638	AAGGCAAATGCAGAAAGCAT	59.851	20
266	687	952	TGCAGTAAATCTGTGACCCG	59.716	20
240	2637	2876	TTGGATAACTGATGAGGGGG	59.744	20
274	1265	1538	CCGTAAGAGCATTTTGGCTC	59.845	20
180	1699	1878	TGGTCGGTTGGTAAGAAAGG	59.964	20
124	3224	3347	AGGCTCAGTGGTCTCTTGGA	59.986	20

273	1164	1436	AATTGTGCAGTCCGGCTAAG	60.27	20
257	1648	1904	TTTCGATGTCGAATTACAACAA	59.524	23
228	1193	1420	ATGTCGATTTTATCCCTCGC	59.001	20
131	425	555	GACATCATCCACCGAGAACC	60.335	20
257	1364	1620	AAGGGAGGGAATGAAGTGGT	59.795	20
244	2070	2313	CAAACGAAGGAGGAGGATGA	60.187	20
214	1297	1510	TCAAAGAATTCCAACCCCAA	60.28	20
177	1904	2080	AAACAAGCCATTCCAGCAAC	60.118	20
189	2138	2326	AGGGCATTACCTTTGCATCA	60.469	20
137	13	149	TGTAGCCGACCCCAATTTAT	59.297	20
257	3323	3579	TGTAAGCTCACCAGCATTCG	60.011	20
218	217	434	CCAGCTTCAGGTTCTCTGTTG	60.036	21
148	2741	2888	GGGGAGGAGAGAGGAGAGAA	59.883	20
128	1513	1640	TGACTCATCACCACCACCAC	60.44	20
143	308	450	CCCGAAGCGAATTTATTTCA	60.033	20
274	3711	3984	AGTTGGGAAGGTAATTGGGG	60.046	20
272	2380	2651	AGTCCAAGGAATGAGCATCG	60.218	20
257	371	627	TACATCGCACAAAATCACGG	60.523	20
166	2660	2825	AATTATTTTGGGATTCACCCAT	59.702	23
268	2764	3031	CCACTGTGTTGATGATGTGGA	60.433	21
261	9	269	CCCAAGACCCCAATTTGATT	60.91	20
274	26	299	TTGGGATTAAGGCTTTGGTG	59.931	20
279	112	390	CGATTAACCCGTGAAATACGA	59.84	21
210	1361	1570	AAGAGGTGCATTTCAATCGG	60.074	20
168	4478	4645	TCCGCCAAAATGGTAAGAAC	59.938	20
201	3171	3371	GGCGTCAGAGAGATCGAAAG	60.096	20
238	1110	1347	ATCAATGGGCATTGGATGAT	59.982	20
263	2595	2857	CTTCACCAAGCCGTTAAAGC	59.883	20
273	1155	1427	CCTACACAAATGGATGACCG	58.847	20
227	533	759	TTTTCGTCACCTTTTGAGGC	60.227	20
178	6	183	ATGTAGCCGACCCCAATTTA	59.297	20
119	1078	1196	TTGAAATTTTTGTGTGGCAA	57.666	20
114	3430	3543	ACCATGCAGTCACAGATCCA	60.121	20
237	2776	3012	AAAAGTCGTGACCAAACAAAA	59.445	23
173	142	314	ATCTGGTGGATTCAGGCAAG	60.073	20
110	323	432	CCGGAATCATGCTAACTGGT	59.955	20
212	837	1048	TCAATGGTTGGGCTACACTTC	59.985	21
144	643	786	ACACAGTACGATCCCGACCT	59.455	20
209	8	216	CCCAAGACCCCAATTTGATT	60.91	20
137	5246	5382	CGACCTCACATAGTGGAAAAA	59.978	21
208	137	344	AGCCAGGTAAACACCAATGC	60	20
256	2686	2941	GAATGCATTTGAGGACCCC	60.274	19
219	2576	2794	TTGAAAATGGGGTGGTTGAT	60.029	20
270	1685	1954	TTATTGCCCGGGATAAGTTG	59.789	20
230	122	351	TCCCTTTCAATTACATCGCA	59.112	20
153	692	844	AGGTCGGTTGAAAAGATGGA	59.526	20
255	870	1124	ATGGGTTTTGCCATCAATTT	59.138	20
229	1848	2076	AAAGATCCAGTGTTGGCAGG	60.111	20
280	3699	3978	TTCAGAAAAATGGCGAGACC	60.192	20
250	6027	6276	CAAGTGTTCGAAGACGGGTT	60.149	20
240	5	244	TTTGATTGGGAATAATTGGG	57.289	20
161	1796	1956	GAGAAAAACAGAGGAGCAAC	59.92	23
163	1898	2060	GAAAAATGCTGCATCAACCA	59.67	20
199	1974	2172	TCAAGGTGTCCTCGATTTGA	59.215	20
215	1513	1727	TTCCAACATGCTGCCTAAAA	59.301	20
215	1060	1274	AGAGGCCAACAAAGAGACGA	59.989	20
272	3803	4074	CTGTTCGCATGGTTGAAGAA	59.84	20
168	6	173	ATGTAGCCGACCCCAATTTAT	59.585	21

245	462	706	GGATTAAGAAAGACATTGGAC	59.493	23
246	148	393	TCCCATATTTGGAGTCCAGG	59.744	20
147	2076	2222	AGTTGGGATTTGCCAGTTTG	59.971	20
205	0	204	TGTAGCCGACCCCAATTTAT	59.297	20
146	4419	4564	ATTTGGTGTCGCCTAAATCG	59.96	20
100	12	111	TTTGGTTCATGTAGCCGACC	60.894	20
264	3314	3577	AAGCCTTTCATGTCACCAGG	60.111	20
261	5351	5611	TACCTGATGGGCTATGGGAA	60.288	20
150	1581	1730	CCATATAGCCAACCCCACAT	59.528	20
280	8566	8845	CGGAAAGAGTTTTGCTCAGG	59.986	20
175	7	181	TGTAGCCGACCCCAATTTAT	59.297	20
198	1964	2161	TCGAAAAAGTGCGTCATCAG	59.988	20
218	2772	2989	TATCCCTGTGCGCGTTTAAT	60.476	20
163	2185	2347	AAAGCCCTCCAATTCCATTT	59.777	20
201	16	216	GGAAGATGCTCCAACTCCTG	59.803	20
246	1028	1273	TCTAACCCCACCATTTCTGC	59.933	20
223	111	333	ATAAGATCGGGGGCTTGATT	59.761	20
248	955	1202	AATGCTATGTGATGTTGGCTTG	60.025	22
206	2434	2639	AATCCGAAATGCAAAACTCG	60.074	20
225	8	232	TTTGGTTCATGTAGCCGACC	60.894	20
229	3093	3321	ACACCCAGTTTGAATTTTAGCA	59.926	23
268	2874	3141	GGTCCAAAAACTCAGGCAAG	59.711	20
206	4337	4542	ACTGGGCAACATAATCCAGC	59.962	20
243	0	242	TGTAGCCGACCCCAATTTAT	59.297	20
146	35	180	AAAATTATGTAATAGTTTGCCG	59.748	25
267	3229	3495	CAAAGCGAGACCTAATGGCT	59.476	20
240	112	351	ATATGTTTCGCCTCTCCCCT	59.925	20
221	316	536	CGGAGATTATCCACCATTGC	60.296	20
276	521	796	ATCCAGACGTCGGAACTCAC	60.12	20
252	818	1069	GACCAAATCCAGCCCATAAA	59.762	20
162	616	777	AGCAGTGTCATTTGCTCCAA	59.445	20
166	1264	1429	TCACATACCTGCAACCATGAA	59.98	21
225	1511	1735	AATGCTCCAACTTCGACTGG	60.255	20
162	755	916	CACCTGGATTCGAATGGTTT	59.79	20
271	934	1204	CACAGCACAAACTGATCGCT	60.056	20
271	263	533	GGCCTTCAAAAGCATAACCA	60.074	20
159	35	193	GCACGAAACAAGGGTAATCG	60.502	20
217	1129	1345	TTGTGGTCTCACTCCTCCAA	59.23	20
269	1178	1446	TGGTGTCTTGTGGTCTTGAAA	59.172	21
143	11	153	GGTGTTTATTTCGGCTGGTG	60.365	20
245	594	838	GATTGAGAATGACATGGGCA	59.456	20
245	385	629	AGGGAGGAAGAGTTTCGGAT	59.139	20
259	2709	2967	GACACGTGGATTTTAAATGGG	59.192	21
270	2282	2551	GGTGCATAATGGCTCTGACA	59.679	20
184	1458	1641	TCCACACACGTCTTCACATTT	59.049	21
144	1201	1344	TCAGCATTATGTGCTCTGCC	59.979	20
259	997	1255	TCAGCAGAGATCATCCACCA	60.363	20
271	261	531	GAAGCACAACCAACCAACCT	60.012	20
276	924	1199	CGGTTTCATAAGGTTGTCGG	60.357	20
260	796	1055	TACATTGTGCCTCCTCCCTC	60.073	20
145	739	883	CCACTCATTTTTCCACACGA	59.541	20
269	3825	4093	ACTCCTGGGCTCGAGTTGAT	61.192	20
255	322	576	GATTTCTTCGGAATCGTTGG	59.505	20
213	130	342	CCTATCGTTCCACATGCCTT	59.955	20
107	378	484	ACCACCCTCTTAGACGACGA	59.721	20
213	1337	1549	AATTGTAGTCCTTAAATTCCCG	58.165	23
186	322	507	ATCGCACTCATCATGCAAGT	59.276	20
241	801	1041	TGTTCGGAGCTTGTGTTGAG	60.025	20

146	576	721	TCTCTCATTGGTGGCCCTTA	60.594	20
171	301	471	CAACAAAGCAAACCAAACCA	59.603	20
163	504	666	CCATGACACTGAATATCCCAG	59.813	22
260	20	279	GTAGAAATCCCGTGCGAGAG	59.836	20
228	106	333	TTTCCCACTTGGTTTTGGAC	59.807	20
184	737	920	TTTCTGTTAGTCAAAATCGAGA	57.41	24
208	1357	1564	GCGTATTGTTGTCTCGTTCG	59.347	20
104	612	715	TTGCACCTACAACATGCACA	59.746	20
104	1006	1109	CCTAGCAAAAACCTTCCAGC	58.973	20
238	89	326	TCTCAGATATGGGCGTCACA	60.225	20
260	719	978	AAAACCAGCAGTTTTGGCAC	60.154	20
271	1985	2255	TGTGGTTTGCCTCACTCTTCT	59.899	21
202	50	251	TGGGTATGGGACTCAGTTGG	60.769	20
266	543	808	TTGATTTGCAACTCCCTTTT	57.338	20
171	291	461	TTTGGCCGAGTGACTAGAATTT	60.129	22
174	798	971	CGTGGAATGTGGATGATGTT	59.219	20
211	33	243	GTATTTTTCCGACTTTGGCA	57.754	20
131	256	386	TGGAATTGACGACTCCATTG	59.496	20
232	8	239	CAAATTAAAATGCGCCACG	60.081	19
217	396	612	CCGGATGGCTTATGAGTAGG	59.546	20
184	256	439	TGGCGAGAAAACTCAGATCC	60.34	20
198	337	534	AAACACACGCAGGCAGAATA	59.347	20
242	8	249	TGAAGATTGCTTCCTTATGAAT	59.644	24
185	1611	1795	TGCAGAGCAAATTCATGTCC	59.805	20
232	25	256	TGTTGGAAGAAACAAAACTGG	59.9	23
177	4408	4584	AAATCAAATGCGAATCGCTC	60.182	20
244	334	577	GTCTTGGGAAGCGAAATGAA	60.192	20
184	253	436	TTCTTTGAGCCTGTGGTGTG	59.873	20
180	865	1044	TCTTGTTTTCTCCCCAAACC	59.003	20
197	132	328	TGGGCTTCTTCAGCTTCTTTT	60.489	21
280	381	660	CCTTCTTGGTTTGAGCTTGC	59.993	20
253	2205	2457	TGTTGCAATAATCAAGTTCAAC	59.311	23
280	5772	6051	CTCTCGTTTGGACTCTTGGG	59.837	20
258	1260	1517	CCCCTATAACTCTCGGGGTG	60.694	20
264	871	1134	GAACTGCTCGGATCTCGATT	59.39	20
254	755	1008	GCAGAACATGAAACCCACAA	59.547	20
104	3060	3163	TCCAATCTCATCCCCTCATC	59.821	20
200	6510	6709	GAAGCAAGAGAGACGTTGGG	59.989	20
266	634	899	GCCTTATCCAACACCACACC	60.24	20
118	1506	1623	AGGAGGGTAGGTGGTCTGGT	59.848	20
226	5	230	GCCTTCTTTTCACGCATTTC	59.829	20
235	648	882	ATATATGGGGGAGAGGGACG	59.996	20
147	389	535	ACACCCGGAAATGGTAGACA	60.232	20
228	11	238	TACATGGCTGGCGTAGTTTG	59.752	20
147	196	342	ATGGGTGTTACCGTCTCTGG	59.844	20
222	193	414	GTCGAAGTTCCCGTGAAGAG	59.844	20
202	32	233	TTATGAGCTTGGACTTGGGC	60.214	20
279	1929	2207	GGCATAAGAAAGGATGAATGT	57.372	23
147	706	852	GTATGGTGTGGAGAACCACG	58.854	20
169	349	517	GATGAAGGCTGCATTTGTGA	59.805	20
251	2091	2341	AAATAAAACCAAAACCGGGG	59.923	20
196	118	313	CTGAGAGGTCCCAGGTTCAA	60.229	20
277	533	809	GCCCGATATTTATCAAGGCA	59.892	20
150	697	846	GAGGGCATGTCGATTTCACT	60.081	20
270	2031	2300	CACATGTCCCAAGTGATTTCAA	60.786	22
209	168	376	AAGCAACAAATGAATTGGGC	59.945	20
253	507	759	TTTTGGGAGGGAAAACGACT	60.826	20
202	1858	2059	AAATCTCCGAGGCAAGCATA	59.807	20

273	79	351	GGCTTGTCGTGGTTCAACTTA	60.161	21
184	25	208	TTTGCCTATTTAAAGCCCCC	60.267	20
227	901	1127	GGACGAAATTGATCGAAGGA	60.014	20
271	2500	2770	CAGTGGATACGAGCAAGGGT	60.134	20
274	65	338	GAGCAGACGATGATGCAGAG	59.688	20
103	42	144	TGAAAAGAAAAGGCGTGAATC	60.229	21
262	2650	2911	TTAGGAAAGCAGGCAACCTT	58.973	20
239	610	848	AGCACTAGCACCTCATGGCT	60.043	20
135	1732	1866	GCCATTCACCATCTCTCGTT	60.081	20
221	375	595	TCATCAAATTTGGGGGAAAC	59.599	20
265	1069	1333	CAAATAATTGCCGGACCAAA	60.671	20
229	118	346	CCCCCATGAAAAGTCAAAAA	59.772	20
250	13	262	CAAGTCAAATACCCGTGTCC	57.923	20
228	224	451	TCAGCAATCACCGACCAATA	60.073	20
237	177	413	CGTGTCATGTCGACTCGTG	59.868	19
203	570	772	TCTAAGTCCACCTTTCTCGCA	60.001	21
269	1	269	GACGCAGGTACGGATATTTGA	59.974	21
253	109	361	TCTTTTGTTTCGGAAATCGG	60.046	20
108	460	567	TGAGATTTGGTCAAGGGAGC	60.195	20
190	2685	2874	GTCCAAGATGGGATTGGTTG	60.173	20
273	1431	1703	TATCATTCGGCATTTTCGGA	61.294	20
222	6802	7023	TCAAATGCAAACCTGTCGAA	60.234	20
118	450	567	TCCATTATCTGGCCCTTTTG	59.894	20
211	125	335	AAAAAGCCAGGGCCTACCTA	60.089	20
162	528	689	TGCAACCCTAAGAAAAGGGA	59.679	20
198	1067	1264	GCTAGTAGGGCAAAGTTGATT	57.418	24
254	786	1039	AAATTGATTGGAGCATTGCC	59.907	20
164	965	1128	TGCAATTCCACCAACTTTGA	60.088	20
120	227	346	CCGGAATCTGAGAGAGATCG	59.903	20
245	1663	1907	ACAAGCAATGGGGAATGAAA	60.309	20
247	5	251	TTTGTCCCTAAACCCCCTCT	59.799	20
207	227	433	ACACATTTGGCTGGAAGGAC	59.973	20
264	1579	1842	GGGAAAAGGACAATTCCTCG	60.797	20
125	0	124	GCATTTCACATGTAGAGTATAT	57.153	27
247	184	430	TGATTCCTGCTTCTCCCCTA	59.767	20
239	82	320	TAGCACTTGGGATGAAGCGT	60.796	20
108	562	669	GCAATTTCATTTAACAATCACG	59.037	23
193	332	524	ACTCTCCATGGACGTAGGTGT	58.534	21
278	126	403	GGAGGATTCGGATTTCCTGT	60.272	20
220	76	295	TGGGTTTGGTCCATCTTCAT	60.173	20
239	49	287	TGTTTCTGCAGGTTGCAAAG	60.027	20
153	389	541	AATATCCCCTGGAGCCATGT	60.546	20
234	1331	1564	TGAGTCGGACTTGCATTTGA	60.39	20
161	647	807	TTCCTAAACCAGCCCAACAG	60.103	20
237	1416	1652	TCAATGTGCCATGATTTAGCA	60.088	21
187	695	881	CAATCCGCACTTGGATTTTT	59.938	20
172	13	184	ACCCATTCCCAAGAGATGCT	60.853	20
234	513	746	GCATTTCTCACACGGGAAAG	60.636	20
278	307	584	TCCTGTGCCAAGTTGAATAAG	59.747	22
111	107	217	GGTATACCCAAAGCGCACTC	59.597	20
259	877	1135	CAACTCATGGTTGTCGGTTG	60.001	20
254	1387	1640	GAAGAGCGTCCAAATCTCCA	60.34	20
189	378	566	ATACATGGCAACCTCGTCGT	60.406	20
196	1350	1545	TCTGTTTATAGTCCCCCGGA	59.382	20
204	180	383	GAAGTTTTGGGGATCCGAC	59.326	19
174	10	183	TGAAGAAATCAAATCCCACAA	59.429	22
233	1721	1953	CCTGATTAGCCACAAGGGAA	60.066	20
247	337	583	GTTGTGCTCGTACACTCGACA	59.962	21

204	2517	2720	TGTGGATGCTTGTATTTTGGA	59.027	21
250	1348	1597	GCACAAGAGGAGGCAACTTC	59.997	20
274	718	991	AGTTTCTCCGGGTGGAAGAT	59.935	20
159	1036	1194	GAATTGGTGAGGGCATCATT	59.756	20
132	0	131	GAGTTCGTTGACTAATTAAAAT	57.683	25
158	0	157	CAGAGCGCACTCGAAGAGTA	59.49	20
176	730	905	ACAATCCTGTAATTCGCGTCT	58.734	21
273	0	272	TTTTGCACCCGAATGGTTAT	60.188	20
248	323	570	TGGAATTTGTCCACCATAACA	58.733	21
191	483	673	ACATTTTACGTGCGAGAGGG	60.132	20
236	1177	1412	GCAATGCATATTTAGGAAGTG	59.432	23
224	397	620	GCGAAACGAAATTTGGGAA	60.936	19
149	712	860	TTAAGTGAGTTAAGTTTTGACC	58.424	25
252	160	411	GTCATTTCTCGTTTCGCGTT	60.257	20
203	621	823	TCCCATTCATCATGATTCCTT	59.19	21
265	686	950	TATTCCGCAATTAGCCTCGT	59.704	20
151	496	646	ATGATGGCGTCATGTTTTCA	59.931	20
151	17	167	TAAAATGTGCCACGTGGATT	58.895	20
181	187	367	CTCGAACGAACACCCAATCT	60.111	20
278	534	811	GCTGGCAACCAAGCTCTAAA	60.523	20
244	130	373	CCAATTTTTCAATCACCGGA	60.671	20
220	224	443	GCCACGGATAAGTAACACCG	60.386	20
279	1740	2018	AGCACGACCAGAAGCTGACT	60.205	20
144	248	391	CCATTCCTGAGACCAAAAGG	59.521	20
212	1189	1400	ACGCTCAAGCCATTCAAGTC	60.406	20
138	2	139	TGACGTACGATCGAGTCCAG	59.855	20
159	0	158	TGGGAATTTAGGAATCGAGAG	60.034	22
184	232	415	CATCTTCAAGTCTGCAACGG	59.44	20
271	1598	1868	CTATTTGTTGGTGGGTCGGT	59.711	20
268	444	711	TGATGGGAGGCAACTCATTC	61.016	20
222	375	596	TCACGTTGACAAGTCCAAGC	59.88	20
185	609	793	CTCTTCTTCCCACAACTGCC	59.844	20
275	38	312	GACTATAATGGCCAGCACCG	60.49	20
227	585	811	TGGCCTGATTAATTGTGTGG	59.395	20
274	592	865	GTCAATTTCCCTCCCAAAAA	58.855	20
237	1385	1621	CAGGCGGAACTAGAGAGGAA	59.569	20
272	229	500	CCAGAAAGTCCAATTATGGTG	60.584	22
245	918	1162	CGTCGCATGGATCTAGTTGA	59.823	20
175	2104	2278	TAACGGGTAGGGCAGATCAT	59.41	20
237	2438	2674	CGTTCTTCCTCAGCTTCTGG	60.126	20
215	1136	1350	GGAAAGATGAAATGCTGGGA	60.014	20
256	815	1070	GGCAGCTCCCACATACATTT	59.962	20
248	353	600	TCTCGCAAAATCAAGAAGCC	60.469	20
155	2446	2600	TATCTGCCTGCATATGCCCT	60.594	20
230	6	235	GGTCGGCTACATGAACCAAA	60.894	20
249	308	556	CCGTCCACCTCTCAATCTCT	59.254	20
249	142	390	CCTGGAAAAATGTGGGTGAA	60.724	20
265	549	813	AGTTATTGGCCGAAAATCCA	59.411	20
148	1795	1942	ATTGGCTTTCCCGAGAACTT	60.074	20
279	835	1113	AGTCTTGTGGCCCAGAGAAA	59.844	20
183	692	874	GCTAGTAGGGCAAAGTTGATT	57.418	24
260	121	380	TTGTTTGCCACTTGCTTCAC	59.888	20
210	4585	4794	AGTGGGGAGTTTAGTTCCCG	60.353	20
157	222	378	GCTGCAGATGGACTCACAAA	59.992	20
126	291	416	TGTGTTATTTCATATCTTTGTGC	59.092	26
279	814	1092	GACTTCGTGGGCTTGGACTT	61.59	20
229	115	343	AAGTTTCTTTGGGACACCCC	60.204	20
207	37	243	CGTGTGCTGGGCTATTTTCT	60.27	20

226	2882	3107	TGGGTTTGAACTGAAACTGC	58.749	20
235	219	453	ACTGCGAGATTCAAAACGGT	59.74	20
158	253	410	TATGCAAAGGGAAAAGCGAG	60.335	20
270	3272	3541	AGATTGAAGAAAAAGGGGGC	59.532	20
271	949	1219	GCGTCTCCGATGACATTCTT	60.226	20
134	3151	3284	CTTCATGTATGCTTGGTCGG	59.148	20
222	507	728	ATTATTCCGACGATCTCCCC	60.117	20
275	1086	1360	ACAATTTCCAGATGGAACGG	59.79	20
181	233	413	TGGTTTGACATGTGATGGGA	60.795	20
209	139	347	AGCTGCACCATCCATATTCA	59.105	20
139	1682	1820	CATAGCAAAACCCCCACCTA	59.817	20
236	101	336	GGGATGTGTGTACCTGAGGC	60.395	20
238	150	387	TGGATTTTCTTCCCATGTCC	59.727	20
273	827	1099	ATCCAAAATCTGGTTGCTTGA	59.56	21
209	719	927	GATTGCTTCCATTTGTGAAGAT	58.188	22
166	684	849	CTCTCCATTTGGAGGCGTAA	60.206	20
245	56	300	GCAGAATTCCGAATGACGAT	60.043	20
280	1443	1722	AGTCTCCGGGGACAAATTCT	59.935	20
128	49	176	CGTGCTTGAACAAAAGCAAA	60.029	20
182	5343	5524	CTAGACAATGCACAGCCCAA	59.864	20
204	825	1028	TCCACCATGGAACACAGAAA	59.935	20
249	201	449	CACGAGAATTGGACCAGTCA	59.676	20
211	2175	2385	CGAGCTGAAAAAGACCAAGG	59.986	20
271	1141	1411	TTGAACGAAAATTGATGGTCC	59.793	21
158	399	556	CTGTGGACCTTCATTGCTGA	59.831	20
193	616	808	TTATTGGCCGCAAAAGTTTC	60.075	20
265	1674	1938	CGGATTGCCAAGCCTATTTT	61.281	20
137	3007	3143	ACGCGTTTTAGTGGTGGAAG	60.168	20
239	1406	1644	GAAGGCAACAAGAGATGGGA	60.195	20
280	844	1123	TGGTCTCTATTTGTAGAGAATT	58.898	27
149	1129	1277	AAACAAACCTGCAAAATGCC	59.982	20
256	6398	6653	GGGATTTTCGTTTCGTTTGA	59.916	20
271	3241	3511	AAATGGCTCAGTAAACAATGG	60.237	22
179	1079	1257	AACCTCGATTCCTGTGGATG	59.927	20
191	2130	2320	TTGCATCTTCATGTGCAATTC	59.685	21
235	3	237	TGCTCCCTCCAATTAAGACG	60.206	20
278	74	351	AAAGCCTAAATCCGACCTCC	59.554	20
262	8	269	CCGACTTTTATGGCTGCTGT	60.27	20
221	400	620	TGCGAATTGAATAAGGCAAA	59.286	20
258	636	893	GGCAACAAACAGAATCCCAA	60.874	20
202	185	386	AGCCGGGTCTAGTGAATGAA	59.694	20
172	5	176	ATTTGGTTCGGTTCGGTTTT	60.573	20
251	43	293	GAGTATTCATTGTACACAATAA	57.132	27
267	345	611	TTGTCATGACTTCGGCTTGA	60.39	20
274	0	273	CATGGGTAAAAATGATAAGTA	57.379	26
246	0	245	TTTGAGGAGCTTTGCGTTTT	59.996	20
264	40	303	AAAGAGCAATGTGGCATCAA	59.276	20
235	150	384	TCAAACCAGGTTCTTCAATGG	59.956	21
227	1904	2130	AATGACAACCAAACATGCCC	60.624	20
217	1371	1587	AGGAATAATGGAGGCGGAAG	60.411	20
170	0	169	AAACGGGGTTGGGTTGTG	61.616	18
235	360	594	AACGATAACGGTAACGATAAC	57.743	23
169	0	168	GGAAGGAAAGCTAAAAAGGAT	57.242	22
205	161	365	TGCAAAAGCACTCTTCCTGA	59.716	20
259	1202	1460	TGGCATGCGAGTGCTATTAC	59.862	20
280	1868	2147	GCAGACCATAATGCTTTTGTGA	60.138	22
264	960	1223	GAAGAAGATGTCAAGCCGGA	60.34	20
150	72	221	AGCTCAATCGCCATCTCAAT	59.803	20

233	81	313	TCTGGAAGCCAGAAAACCAT	59.67	20
205	77	281	GAGACCGAACCACTAAACGG	59.592	20
239	1241	1479	TTGCAACAATTTTTGGTATATA	58.562	27
250	201	450	TATTGCACAGCTTCATGCCA	61.367	20
192	308	499	AAAGCTTTGTCCCACATAGGA	60.001	22
224	174	397	ACTAGTGGGACTGCTCCTGC	59.48	20
275	878	1152	AAACATACCAACTCACCACTC	57.963	22
164	127	290	GAGAAACTGCAGCAAAAGGC	60.14	20
116	316	431	TCGAGTTGGCGTTATTGTGA	60.257	20
264	71	334	TCAAGGATTTGGATGGGTTT	59.22	20
273	820	1092	TTGGTCAGATCAAACCGAATC	59.925	21
101	47	147	GACAATCCATCTCCATCTGGT	58.806	21
280	1118	1397	TCTGGTTTTGGGTTTTCTGC	60.088	20
272	335	606	CCGATCGAATGGACCTTACA	60.853	20
221	1211	1431	GCAACGTAAATCTGCCACTG	59.347	20

REVERSE PRIMER3 (5'-3')	Tm(C°)	size	PRODUCT3 size (bp)	start (bp)	end (bp)
TACCCCTACCCTTTGGGAAC	60.046	20	207	1433	1639
ACGATCCCCTTACCACCCTA	60.569	20	174	21	194
AAACACGACCATTTTCAGGC	59.978	20	243	116	358
TCTCATACTAAAAGGTCTTTCT	58.534	26	164	23	186
ATTTCCCGGCTTCTTGCTAT	60.061	20	133	598	730
ATGGGGTTTATTGGCTCTCC	60.152	20	188	361	548
CTATGCTTGCATTCACCCAA	59.688	20	257	14958	15214
ATAAACGTGCCAAAAACCGA	60.356	20	186	19	204
CCACGAAAAACTGATACGCA	59.729	20	255	485	739
TGATTCTCCCTCTAATCTGTTTT	57.985	24	273	12	284
GCGTCTACGGTGCAGAAAAT	60.278	20	227	83	309
TGCGTGAAAAACAGATGGTG	60.699	20	175	18	192
CATCGATTCTCTCTCCTCGG	59.903	20	208	162	369
CAATCTCGAAAATGGATGGC	60.414	20	208	257	464
CGTGAGAAGCAACCAAATGA	59.84	20	239	254	492
TTATCCTTACGCAATCCCAA	58.109	20	196	414	609
CCCACACCCTCATTCTCTCA	61.071	20	164	437	600
CAACACAAGAACTCACCTCCC	59.607	21	244	381	624
ATTTCCACCGGTGTTCTTGA	60.353	20	230	6	235
GAGATTGTTGGGGTTGAGGA	59.903	20	251	16	266
GCATGTATTTGGGCTAAGTGG	59.488	21	159	13	171
CCGATTGTTAAAATTCCGGT	58.807	20	210	16	225
TGTTGACTTGCTTTCTTGGCT	60.045	21	113	661	773
GCTTAATCTTTCAACGCCGA	60.343	20	213	29	241
CAAATATGCTTTCTTGATCATC	58.646	25	241	621	861
GGTGCATGACACAGACCATC	59.97	20	265	52	316
AATGCCTAAGTGGCCATGAT	59.415	20	271	3	273
CTCCACTCACCTAAACCCGA	60.103	20	230	8	237
CCGCATATTTGAGAGTTGCAT	60.11	21	130	14	143
CGCGAACTTTACAGGGCTAC	59.904	20	236	88	323
ACGGTTGAAAATGGGTTCAC	59.694	20	209	121	329
CTCAGGGGCATATGTGTCAA	59.522	20	196	13	208
TCCAGCCAATTTTATCCCAA	60.26	20	209	1	209
GACTCGTAATGATCCCCCAA	59.75	20	124	337	460
GTTTTAACGGTTTTGGCCG	60.342	19	262	214	475
GCTTGATAGGGAGGAGAGGG	60.169	20	157	66	222
CTTTGGATGGATGAACTTGGA	59.918	21	176	132	307
CAAAACCAACAGCCGAGATT	60.11	20	258	238	495
ACCGATATGCTATGCTTTTGC	59.251	21	164	76	239
CCATGTTGTAATTAATGTAGGG	57.155	24	103	2174	2276
GGTCACGAGAACACGCATAC	59.169	20	187	2294	2480
CCACTCGCATCACAAAGTTC	59.293	20	170	24	193
TGATGGATTGCATTTGAGGA	60.009	20	246	193	438
ACGGAAACAAGCAACTACAGC	59.438	21	147	29	175
ATGGATGCCGATATTTGAGC	59.891	20	125	154	278
TCCCAAATTTTGTCCAAAGC	59.916	20	179	1034	1212
ACCCCACTAAACCCAAACTT	57.435	20	160	28	187
AAGCCATTTTCCAAGAGCTTA	58.151	21	275	28	302
AACGACACGAACGGTTTAGG	60.03	20	165	132	296
CTTGACTTCAAACCCCAACG	60.52	20	201	331	531
GAGGCATTCCATGAGGAAGA	60.158	20	163	30	192
TCAGTGGTTGTAACATTGGCA	60.019	21	241	381	621
CACCCGAAAACCGAATAAGA	59.931	20	101	782	882
AATGCAGGGTTTGCAAGAGT	59.74	20	149	17	165
GCGCAGATTGAGTGTGAGAG	59.733	20	270	16	285

TGAGGCTGGTTGTGAGAGAA	59.545	20	279	264	542
ACAATCTGGATCGTTTGATACC	57.928	22	164	0	163
TCCAAAAATCAAAGCTTGAAG	58.987	22	195	90	284
ACGTCAGCATTTACCCCAAC	59.859	20	272	951	1222
CATTTTACGAACGAACCACG	59.083	20	275	136	410
TGGTTGCACATGAATCATCC	60.339	20	237	1268	1504
TTCCTCTCCAACAACAACCC	59.943	20	207	3118	3324
CCAAATCCCTCGTGTTCTTC	59.526	20	176	8	183
ACCGTCCATCTTAATGCAGC	60.103	20	199	914	1112
CGATCCTTTGCGTTTGTTTC	60.617	20	188	0	187
GGTTGTATGAAACCGTTAGTT	59.826	23	269	430	698
TCAGAAACGCTATTACCAAGC	59.911	22	278	166	443
GTTTGTGGTGTTCATGTGGC	59.862	20	248	1842	2089
TTGGCGCTTCTTTTGTATCC	60.209	20	105	0	104
CAAAATCCGAGGCAAGAGAC	59.813	20	131	12	142
TCGAAGGATTTTATCTGCCC	59.115	20	263	2467	2729
ATTCAAGCATGGAATCGCTC	60.185	20	201	13	213
CCCATTCCCAAATCCCTTAT	59.846	20	151	932	1082
TCTTGCACGATTCTCCACAA	60.39	20	157	654	810
CCTACCAACCAGCCAACATT	59.853	20	177	4195	4371
CACATAAATGGGTTATCAATG	59.851	24	211	301	511
TCCAACAATCTCCCACTTGA	59.059	20	139	148	286
GATGTTCGTCTTCGTCCTCC	59.661	20	213	59	271
CTACGATCCCAACGGTATGC	60.352	20	185	61	245
TCTCTCTCGGTTGCTACTGCT	59.391	21	155	25	179
ACTGTGGCGAACGAGAGAAG	60.589	20	208	315	522
CGGTTTTGGTTTGTTCCTACA	59.884	21	278	1137	1414
TGAGCCTCGAACTGGTTTTT	59.853	20	172	33	204
CTGGGGCAGATAAGGTGAGA	60.21	20	221	422	642
ACATTTTTGTGTTGCTCCCC	59.836	20	194	481	674
CCATACCTAACCTGTACCGTC	60.652	22	261	420	680
ATCGAAACAACCCCAGATGA	60.317	20	261	189	449
CCTTTTTCTTGCAAGGATTGA	59.325	21	247	269	515
CGACCTGAAGGAGGCTAGAG	59.183	20	169	1215	1383
GGAACAGCAGATTGACAGCA	59.992	20	278	1546	1823
TCATTAGCCATGTGTTCCCA	59.924	20	280	826	1105
CATGAGCCGCTAGATTGACA	59.972	20	173	128	300
TGCGTGCCATTTATAAAACA	57.749	20	104	9	112
TATCAGCCGAAAGAAGCAGG	60.481	20	275	1394	1668
TACGGGATCTCTTTGGTTCG	60.066	20	272	855	1126
TCCTCTTCCTTCTCTCACGC	59.679	20	270	1	270
TCACACTGACGTTTCTTGGG	59.72	20	166	225	390
ATGTGCAAAGCTGCTGAAGA	59.746	20	259	294	552
TGGACGTAAATACCCTTTTACC	59.667	23	124	237	360
GGAAACCCACAATCATCACC	60.034	20	238	12	249
ATGCGCGCTGCTTTAATAAT	59.873	20	108	40	147
TACAGGGCTGCTTTGTCCTT	59.875	20	214	84	297
TTTTGTTTGGGACAAAAATGAA	60.115	23	280	90	369
TTCGAGTGACACAAGGCAAG	60.025	20	240	20	259
ACACTTGCGAGGTTGTCAAA	59.339	20	196	714	909
AGACGGCAGAAGGTGAGAAG	59.598	20	210	1263	1472
ATGTCATTCTGTTGCGGGTT	60.384	20	228	10	237
GAACCTCGAATCCAAAACCC	60.673	20	135	5018	5152
TGAAGTTAGGAAATAAGGAGG	58.743	25	132	320	451
TTTCTGGGCCCAAATCAATA	60.26	20	158	26	183
TGGCCTTGCCATGTATATCTT	59.447	21	277	249	525
GGGAAGCTATGATGGGGAAT	60.117	20	233	2155	2387
TTGGGCTTTCATTTTTCAGC	60.188	20	140	572	711

CAACAGTTTGGCATCAGAGC	59.445	20	203	30	232
TGCAGCCTGAGTGAGAGGTA	59.726	20	265	2098	2362
TTGGTTATGGACATACGGTCA	58.759	21	170	650	819
ATGCATCTCGGATCACATCA	60.039	20	191	10	200
CTCTCTCAATGTGGCAACGA	59.984	20	189	580	768
ATTCCACCGTTGAAAGATCA	57.991	20	152	48	199
GGAGTGGCTTTAGGTTGTCG	59.734	20	212	621	832
ATACGTGTGCGAAACAACCC	60.817	20	124	315	438
ATTCCCTCCTCAACACCCTT	59.795	20	217	100	316
CACCCCACTCCCTACATTTC	59.259	20	220	902	1121
AGGAGATGACACCTAAACCCA	58.511	21	155	12	166
TGGCTGTCATTATTTCTCATTTC	59.188	24	150	368	517
GGAAATAATAAACACAAACAC	59.233	24	251	884	1134
TTGAACCATTCCATCATTTCA	58.806	21	113	149	261
CGAAGACAAAACACAATGGG	59.021	20	280	76	355
TCTACGTGGCATGTGGACTC	59.707	20	199	21	219
TTTGAAGCTTGAATTGAATTGG	59.231	22	241	20	260
GAGTATAACCGTCGGCTTGC	59.736	20	257	17	273
TCATATCCACGAGAATGGCA	60.033	20	222	1237	1458
GGTGTAAGATGGAGGCAAGC	59.7	20	141	23	163
CCCAAGACCCCAATTTGATT	60.91	20	255	69	323
CATCGACACCACTCATCGTC	60.121	20	241	8	248
TTTGCTGCAGTCTGTCATGG	61.023	20	245	242	486
CGCATGTACTGAACACGGTC	60.183	20	225	29	253
GATGTTGGGTCTGCAGAGGT	60.12	20	189	614	802
TCCTCATCTCCGTTGTAGCC	60.218	20	212	411	622
TTAGCTTCACACCAGCAACG	60.05	20	280	14	293
TGCCTAAAAAGTTGCTCCCA	60.742	20	256	978	1233
AAATTTACCGACGTCTCACCA	59.485	21	158	18	175
GAAGGTGTCTTCAATGGAGGT	59.484	22	151	163	313
GCCATAACTCGACCATGTCA	59.527	20	246	6	251
TCAGATTTACGAGCAATAATTT	59.558	27	124	312	435
AACTTAGCCCCCAAGTTTTCA	59.987	21	271	314	584
AAAGGCGACAAAACCATCAC	59.978	20	199	568	766
TGATCACGAGTACCTCCACG	59.701	20	198	8	205
TGACACAATCGTGGAGACAAA	60.144	21	166	1875	2040
GGGAGCTGAACAAAAGGTGT	59.187	20	225	1248	1472
CGGACCGTTTTAACGGATTT	61.055	20	272	166	437
GGATCAGTAAAATAATAGGCA	59.934	26	239	542	780
ATCCGTGCCCTATCAGGAAT	60.682	20	257	503	759
CCACATCCTCAGCTCAGACA	59.98	20	169	201	369
GCGATCCTCCTCCTTCACAT	61.542	20	245	1542	1786
AAGGACTCAAGCCCCTCAAT	60.074	20	154	22	175
CAGCAGAGGTGTGCATCAAT	59.862	20	199	96	294
TGAAACGGAACAAGATTTGC	58.747	20	134	16	149
CAACGCAGATCTAAAGACCCA	60.256	21	230	796	1025
CGTGTCAACTGTGACGAGAAA	59.93	21	242	1809	2050
GAAACCCTAACCTGATGCCA	59.933	20	264	435	698
AGCTATGCATCAACGCACAA	60.432	20	254	409	662
CCACTCCTTTCGAGGCATTA	60.206	20	210	938	1147
ATGGCTAACCATCAATTGCC	59.791	20	244	525	768
GGCCTAAGGCACTCATGACA	61.208	20	236	221	456
TTTGACTACCTTGCCAAGCA	59.464	20	169	1185	1353
CACAATATCAAGAACCCCCAA	59.671	21	277	9	285
TTGCATCATCCAGGCATTTA	60.035	20	271	2060	2330
ATTTCAGCACCCCCAACA	59.893	18	108	1024	1131
TAGCCCACTAATCCCAAACC	58.903	20	115	15	129
GAACCTTCCATCTTCCACCA	59.903	20	157	2192	2348

ACCCCCAATTCTTGATAGCC	60.152	20	112	259	370
GAGCTCCACATCAACACCAA	59.682	20	170	11	180
TGCGTTTTGATGATATATAGGT	57.703	24	214	561	774
GGCCGTATTAGCAGCGTAAA	60.246	20	278	481	758
AGCCACGTGTGTTCATTGAG	59.751	20	237	519	755
ATCTGCCATAGCACCAAACC	59.962	20	256	375	630
CCAGATAGTTTGGCCCGTTA	59.953	20	259	495	753
TGAAAGCCTACCTTGCTTCC	59.452	20	248	1	248
CTCGGTTGAGCTCGGATAAG	59.971	20	162	80	241
CCTGACTTCGCTGTGGGTAT	60.134	20	168	2288	2455
CCCACTCCTATTTCCTCTCATCT	59.975	23	143	175	317
TCAATGCTCTTTTCAACCCT	57.393	20	164	19	182
GTGGTATGGTGTGGAGGACC	60.096	20	139	106	244
GGCATCAGAGCCAAGTTAGG	59.836	20	188	12	199
GGCACGATTCAAAAGTCACA	59.697	20	279	117	395
TGACAAAGGGTGTGTTGGAA	59.976	20	135	93	227
AACGAGGGGAGTGACACTTG	60.151	20	279	6	284
TGTGAGCGTGTAGCCATTTC	59.871	20	153	47	199
CTCCCCATTGAGACTCGAAC	59.655	20	187	75	261
AATGCCTCTCACATGCAACA	60.272	20	256	308	563
CACGCAATCCACATCAAGTC	60.12	20	246	77	322
GAGAATGTTCGAGCGTGTGA	59.992	20	168	436	603
TACGACTCTTTCAAGGGGGA	59.665	20	234	1963	2196
CATGCATTAACATAGTTGGGCT	59.036	22	245	20	264
CTGCTGGAGTTGGACTGGTT	60.298	20	185	1421	1605
AAATCAAAACAAATACTAACAT	60.107	27	195	1073	1267
TTGAGAGGATTTGAGTTGGC	57.864	20	251	157	407
TTGCGACATGACACAATCAA	59.676	20	167	430	596
TGATTTCCTAGATACGGGGC	58.998	20	125	52	176
TGCGAGAACTTAGTCAACGG	59.072	20	185	15	199
AGAAGACACTTGGGCCTGAA	59.844	20	204	221	424
CTCCTCTCTGCTGAGCCAGT	59.883	20	120	337	456
GCCTAGCCTATTTGAACCCAG	60.102	21	163	233	395
TTTTTAAGGTGGGGAGAATGT	57.596	21	276	1065	1340
CAACCCAAGTTTACATGTGAC	60.318	22	279	48	326
TTGAAGAATGTTTCGGCTCA	59.395	20	253	9	261
ACCATCCCGTTTCAAACTCA	60.353	20	177	8	184
ATTTCATTTCATGGGTTTCG	57.399	20	176	15	190
AACAACCCTCCCCTCATTTC	60.169	20	121	92	212
TAGAGGAAATCATGCGGGTC	60.036	20	280	926	1205
CCGCCATAGAACCAGGAAT	59.902	19	215	547	761
CCGAAAGCTGCAAGTCCTAC	60.015	20	182	250	431
GTGAACCCTCCAATTCCAAG	59.381	20	210	356	565
CGACGGAGGAGAATGTGAGT	60.261	20	190	1128	1317
GTGTGGGCTACCAAACACAG	59.06	20	192	765	956
TGGTTCAACCTAGCATTCCC	59.933	20	162	84	245
AGAGGTTAAGGGGGCAGACT	59.207	20	257	561	817
CCACCTAGTCTTTCAGCAGCA	60.577	21	101	19	119
GAATGAAGAATGGTTTGTCCGT	60.228	22	254	690	943
TCTGTTGCTTTCCCTTTTCG	60.357	20	244	1842	2085
TGATCAAACACCAATCGCTC	59.654	20	134	3643	3776
CGGTTAAGATTCAGCAAGCG	60.895	20	216	78	293
ATACGCACTCACACACGCAT	60.215	20	210	2608	2817
ATATCCCGCGGTCATTTTT	59.244	19	253	3	255
ATGGTTCCGATGAGATCCTG	59.886	20	174	48	221
GATAAAAATGGCACACGGCT	59.967	20	248	225	472
GAAATCCCACTGCCAACTTT	59.031	20	277	82	358
TGCACATTGAGACGACAAAA	58.835	20	272	428	699

GCTGTCCCGTTCTCTCTCTG	60.135	20	278	3	280
ATAAATAAATGCCGCCATGC	59.795	20	270	16	285
TGAAGTTAGGAAATAAGGAGG	58.743	25	278	829	1106
GTTGAGCTCGGATAAGCTGC	60.125	20	196	0	195
GCCAAACTTCACTAAACGAGC	59.034	21	261	6852	7112
CAACCCCACACATTCAACAC	59.701	20	193	140	332
TTTCTGTTGTGCTGCTGCTT	59.788	20	185	389	573
TGCCATTAAGGCCAGGTTAG	60.089	20	253	25	277
CCACCGAGCACCATGTATTA	59.42	20	170	38	207
TGGTTGAATTTTGTCCCACA	59.792	20	258	1361	1618
GGCTGTTCAGAGTGTGATGG	59.261	20	263	26	288
GCCTTTCATCATCTTCCTCAA	59.259	21	131	112	242
AAGTGGATAAACCCTGCGAA	59.569	20	148	0	147
GTCCTCATCATCGAACCACC	60.335	20	209	15	223
ACAAATTCCCACCCCTGTCT	60.607	20	215	23	237
GGAGATCGAGAGGGAGAGGT	59.766	20	225	552	776
ATAATGGGGTTTCAGTCCGA	59.244	20	256	158	413
CAAAATCCTCTCCCTCTCCC	60.008	20	264	3541	3804
TTTCTCCATCCCATCTCCAA	60.395	20	271	576	846
CGATTTGAAGCCCGAGTAAG	59.839	20	119	1574	1692
AGATGCAGTGCCAGATAGGC	60.393	20	250	172	421
AGCCGTTTTGAGACGTTGTT	59.78	20	218	89	306
ATGCTTAAAACAAAGGGGCA	59.586	20	139	28	166
CCCCGGTTTCATTTATAGCA	59.789	20	199	1	199
AGGAGAGTACGAGAGTGAGG/	60.437	23	137	174	310
CTACCGTCAAATCCTGGCTC	59.694	20	251	698	948
TAGAGCCGGGTTTAAAGCAA	59.847	20	148	24	171
TCCCCGTTTTTACTCGTCTG	60.103	20	169	24	192
CCTCCAGAAATTGGGAGTGA	60.042	20	246	3371	3616
TTGTTGGCGTCGAGTTAATG	59.729	20	223	282	504
GATGAAAAAGGGAGCAAAAC/	59.192	21	275	40	314
TCTCCACTCTCTCCCACGAT	59.792	20	260	2963	3222
TAACCACCTCTTGGGTCCAC	59.82	20	169	1475	1643
GTATGGGCGGATACAATGGA	60.553	20	248	30	277
GCTAATCCCGCTGAAAATGA	60.175	20	200	2	201
TAGCTGCTGCTACCATCGTG	60.18	20	241	96	336
CACCGTACGTCGAACACTTT	58.701	20	254	54	307
CTTTAGGGCCCTTGATTTCC	59.903	20	169	197	365
TCGACCTTAACCACCTCGAC	60.111	20	131	30	160
CACAAAAGGACGATTGGGAT	59.79	20	203	267	469
TCGAAAATGTCCGACTCTCC	60.195	20	222	28	249
GGGCTTTGAGTAACTGAGGTG	58.851	21	258	331	588
ACATAACTCTCCGGCCAATG	59.955	20	196	45	240
TCTCGAAATGCAGTGGTTGA	60.39	20	247	4	250
CGGAATATCGAGAAGGTTATT/	57.056	24	266	69	334
ATGAAATCACCCCACTCGTC	59.786	20	264	151	414
GAATCTTCCATCCATCGAGC	59.592	20	114	497	610
TCAGGGTATGTCCGGTATGC	60.744	20	275	2944	3218
CCACCACCTAATTCTCTGGC	59.55	20	170	1139	1308
TCAAGACTAAAATTGGTAAAG/	58.241	27	185	363	547
CGAGTGTGTACATGGGCATT	59.445	20	279	6001	6279
GCAACGGAATACCACTCGTT	60	20	240	98	337
TCTCCATTTTCAATCCTGTGC	60.066	21	101	9	109
CAAGTTGATGCTAGTCCTCCG	59.883	21	222	3219	3440
CAAGCCGAAAATCGTCTCAT	60.214	20	258	429	686
CCCCTTACTTAATGGGCGA	59.902	19	195	186	380
TGGGAATGAAAAAGCCATGT	60.309	20	229	739	967
CATTTCTTGGCTGGAGCAAT	60.214	20	246	453	698

TCAATCCCAGCCATCAATTT	60.274	20	268	616	883
ATCAAGCCCAATACGTCGTC	59.962	20	228	409	636
TCAAGGAATGGGGTACAACC	59.647	20	163	19	181
CCCACTTTTGGGTTATTACCTG	59.641	22	274	81	354
TTGTGTGATCGAACTACGTTAA	57.469	23	185	199	383
TGGCGAGGTGTTGAGTTACA	60.301	20	279	255	533
GCACTGCTGTTGGAATTTGT	58.777	20	235	203	437
CTTTGCCCCCTTTCTCTCTT	59.821	20	207	374	580
TTGAATCAAAGCATGTCATTTC	57.752	22	196	919	1114
TAGCCCCAATTTTTGTACCC	58.807	20	240	236	475
TGTCGGGTACGACAAAACAA	60.004	20	212	728	939
CCGTAGGCTTCCATTACGAA	60.089	20	154	3	156
ACCTCCTCCTCTTCTCTCCG	59.945	20	180	20	199
CGAATTAACAACATGCAACCA	59.476	21	200	1	200
AGGTTCTGCGACGGAATTTA	59.708	20	178	165	342
TGACGGTGTAAATATGGGTTTT	59.997	23	214	7	220
GAGTTTGTTCCATCATTCGGA	59.925	21	272	2	273
TTTTTATCCCATGTTTGTGCAT	59.234	22	261	226	486
GTGCACACAAGACTTTGCCA	60.917	20	197	938	1134
CAAACAAGAAAAGGAGTTAGT	60.529	24	222	59	280
GGATGATCACCATTCGAACC	60.143	20	143	1	143
ATCGAGTTCCCTTCCGTTTT	59.94	20	167	724	890
ACTGACAAAATTTCGGGACG	59.971	20	252	22	273
GGAGTGGCTCTGGCTAATTG	59.836	20	179	22	200
GGACACCAGGGTGAGAATTG	60.363	20	278	280	557
AACATGATACGGCCGAAAAC	59.829	20	166	1	166
AACGTAGACCTGGCGTCTGT	59.792	20	273	426	698
TCGACTTTTGATCGGGAAAA	60.555	20	195	20	214
ATGCCCCACTTCACAACCTA	60.375	20	176	49	224
GAAGACAGTGTGGAGGAGGC	59.841	20	180	228	407
GCGTGTATCCGCCAAAAATA	60.831	20	251	49	299
TACCCCAACCCACTAACACC	59.569	20	103	2	104
ATGTCACCGGAAAATATCGC	59.791	20	246	18	263
GCCAAACTCTCTCCCTCCTC	60.336	20	226	15	240
TGAGGAACCAATTATCCCGA	60.266	20	266	17	282
ATAAAGGACACGTTGGACCG	59.853	20	171	130	300
CAATGATGGAACATGTAAAAA	58.785	24	203	1807	2009
GGATGGTAAAAACTTCAACGT	60.263	23	164	569	732
TCAGATAGCCCTCTCAGACCA	59.958	21	231	23	253
TTCCATCTTTCAACCTCATCG	60.059	21	163	511	673
TAAAGGGAATTTGACGGTGG	59.795	20	202	1365	1566
CCGAAATGAAGAAATGAGTTC	59.945	22	232	1410	1641
TGACGGGATTTAGGTGTTTTG	59.847	21	101	302	402
TTGATGATGGAATGAAAATGA	59.291	23	278	43	320
CAAGCATAAGGATTTTCGGA	57.845	20	230	3426	3655
ACCAGAAGGTGCAGTGGTATG	60.043	21	214	3539	3752
AAATCAACTGAGACCGTCCG	60.111	20	267	5779	6045
GGAGGTGCCCCTACTTCTTT	59.576	20	265	42	306
CAACAGCATGATGAGAATTGT	59.541	24	277	368	644
TATTTTTCCATGTGGCATCG	59.377	20	276	1995	2270
ATGAGGGGCCTCACTAACAA	59.55	20	197	810	1006
TGATGCTCCTCAGAAAGCAC	59.116	20	123	19	141
CTTGGTGTGGCATGATGAAC	59.967	20	150	147	296
TTGCCATTACCACAAACTGC	59.59	20	210	32	241
TGTTGCGTAGGGGCTAATTT	59.609	20	272	176	447
GGAGGTATATGCCACCTGGA	59.773	20	197	396	592
ACGTTTACGGTCCTTACCGA	59.494	20	166	447	612
CTTGCAACTGGTCGAAATCA	59.84	20	223	1900	2122

GCCTTCTTGCCTGTTTCTTG	59.993	20	251	306	556
CAGCAACGGTTGTGATTTGT	59.615	20	133	432	564
ATGGGGATGGTTATGCATGG	62.641	20	126	409	534
AATGGCCACAAATGTTTCCT	59.292	20	110	739	848
GTCCGCGGTTATCAGAACTT	59.198	20	242	23	264
TTTATATCGCCGAAAATGCC	59.898	20	179	72	250
TGCACCCACAAATGGAATAA	59.786	20	180	695	874
TGTGGATTAATATAGTGGTTCA	57.953	26	187	191	377
ATGAATGCACCGGATTTGTT	60.199	20	111	20	130
AATCCAACCCCGAGACAAAT	60.558	20	193	1598	1790
CTCGGATTCGTCACCTTTGT	60.111	20	273	71	343
TTTGTGGTGACCTTGAGGAA	59.109	20	157	15	171
TGTTTGATTCATTCCATTTCCA	60.167	22	261	1137	1397
CACGACTTGCAATCCGTTTA	59.729	20	207	31	237
TCCCAATCCGGTTCTATCAC	59.75	20	273	3165	3437
TTTAGTAGCGGAATTTGCGG	60.218	20	202	2742	2943
AATGCCCCGTTTTTCTTGTA	59.451	20	279	47	325
GGAAGATGAGTTCGTGGAGG	59.655	20	248	24	271
TTGGAAACCCATGGGATATAG	58.634	21	258	843	1100
GACCTTAGCTTGCGACTTGC	60.162	20	176	18	193
TGGCATCAGTAAATCCTGGC	61.003	20	198	92	289
TCTTGGGGACTTGCCATATC	59.894	20	254	478	731
CAGCGTAAGAAAATAATTGAT	59.557	24	238	4	241
CTCTTTCCGCACCTTCACTTA	59.503	21	280	94	373
GTGTGAAGTTGGTGATTGCG	60.16	20	173	96	268
CGTTTGGATCCGATTTGGTA	60.692	20	214	584	797
CAGAGCAAAAACGAGGCTCT	59.757	20	170	19	188
AGCGATTTTAATCTCCCGTG	59.182	20	122	8	129
TCGATTGGTTTGTGAATTGTG	59.43	21	271	2823	3093
TCCCTTTCGGTCTCCTAACA	59.665	20	280	57	336
TTCTGCCTTCATTTCCATCA	59.2	20	122	132	253
TCGGTTTTACCGGTTTTGAC	59.839	20	180	14	193
CCGCGAACTTAGAGGAGCTA	59.747	20	186	18	203
GGATGAAGTTGAATTGTTGGG	59.278	21	255	60	314
GTTTGGTGTTTGCTGTTGGA	59.591	20	121	464	584
CGTGGTTCGATCGTAATTGA	59.542	20	259	1	259
ACCCAACCCTTGAGAACTTG	59.037	20	279	222	500
TCTAAACGCCGGTGATGTAA	59.182	20	102	44	145
TGCTGGGAGAGATTCAAAGG	60.331	20	184	245	428
ATGTGTAAAGTTGGTGGGGG	59.569	20	243	2644	2886
CCGGTGAAGTTGGATTATCG	60.323	20	193	3062	3254
TTGTGGAAAAACCGTTCAAA	59.034	20	251	245	495
TCTCTCCCTTTCCACACTCG	60.377	20	167	61	227
GCTAAACTTTAAAGGTGATGC	59.692	23	222	85	306
ATGGGAAGGGCATTTTCAG	59.879	19	167	6	172
TCCTTCAAGGCCAGATTGAG	60.331	20	245	74	318
TTTCTCTCCAACCCACAACTCT	60.146	22	278	190	467
TTCATCCTCTTGGCCCATTA	60.405	20	184	221	404
TCAAAAACCGGTGAAAAACC	59.817	20	279	1498	1776
TTGTTTCTCTCGTGGAAGTCCT	60.281	22	232	379	610
AAGATTTGATCATGGGCGTC	59.9	20	208	526	733
TGAGTCGAACTCAATAATCAA	59.569	25	196	1134	1329
CAGACAAATCTTCGTTATCCCA	59.087	22	152	1049	1200
GAGTCTCGCAAGTCACAACG	59.622	20	217	609	825
TCAAATGGTAACCAATCACTA	59.328	24	268	989	1256
CACCTGAATCCACTCACCCT	59.962	20	187	1427	1613
TACCAAGGGCATTTTTGTCC	59.801	20	246	1684	1929
TGAGTCATCTACAGGTCAATG	57.671	22	228	483	710

TATAGTGCGTCCAGCAGCAA	60.566	20	204	17	220
GGTAGTGGGGAGTGGGATTT	60.052	20	159	449	607
TCATGTACGTTGCTTATGGCA	60.148	21	228	31	258
CATATGGGAAGGGCATTTTC	59.23	20	214	1132	1345
AACGGTTACCGGTTTGGATA	59.202	20	199	293	491
AAATTCGTGAGAGTTCCCCC	60.306	20	252	71	322
GCCTCCATCTTGGCACTATC	59.658	20	194	29	222
CAGATCTGATGGCCCAGATT	60.034	20	132	1	132
ACTGACATTCACAGGCATTG	57.067	20	119	53	171
AAAAAGTTGATGCCAAAATTA	59.605	25	146	252	397
AATTCCCCCAATTTCTGCAT	60.511	20	143	14	156
AAACCCAAAACATGAAACGG	59.702	20	233	475	707
CCATCACCAGCTTTGTTGTG	60.152	20	160	34	193
ATTTTTGCCATGCATGAACC	60.711	20	275	834	1108
ATTATCGCCACAAATCTGCC	59.929	20	205	929	1133
GAGGGTCAACCAGGAAGTTG	59.549	20	135	26	160
TTTCATGTTTCATCCCCCTT	59.22	20	195	67	261
TCACGCTCGAGAAAGAGGTC	60.678	20	233	51	283
AAATTTGGCCCCGTCTAAAA	60.645	20	239	87	325
GCCAAAATTTCAAAATGGGA	59.751	20	177	99	275
TCTAAGAGATGATTGCACCTG	58.986	23	131	486	616
ACCCCAAATGGTTAACGGA	60.037	19	195	1553	1747
AATATTGCTCCACGAATGCC	59.929	20	252	250	501
CCCCCATAACTCCTTTCCTG	60.674	20	142	548	689
TTGAATCAACCCTTATCGCC	59.901	20	104	567	670
CTGAAAGCCATGTTTCAGCA	59.988	20	220	491	710
CACCCCTTAATCCCGATCTT	60.145	20	231	1900	2130
TGATGAGTTTTGTGGGTCTTGA	60.529	22	219	7	225
CTGACATCCACTTGGCAAAA	59.691	20	268	8	275
GGGTATATGCCACAGGATCG	60.177	20	259	100	358
TTCGCATACTGAACCCAAAA	59.157	20	228	27	254
GCCAGCCCAATAACTCAACC	61.759	20	160	12	171
TCAGCGTGTGTAAACGATTTG	59.784	21	236	5	240
CCCTCGTATGCTGTGGTTTT	59.993	20	267	650	916
GGGCCGAGATTTGTTAGAGG	60.949	20	216	715	930
GCCACCTTCTCCGATGTCT	60.215	19	262	390	651
AAAGCTGCTGTCCATTTTGG	60.249	20	235	14	248
CCACTTCTCGCCACTACCAC	60.711	20	144	3	146
GCATCAGAGCCACGGTTAG	59.41	19	165	151	315
GAACGACGACGAAGAACGAT	60.263	20	201	28	228
CATGGACCCCACATGTCATA	60.048	20	173	21	193
CAGATCCAACGGCCATAAGT	59.955	20	244	890	1133
CAAAGGCCCACAATGGTTAT	59.685	20	169	37	205
ATGATTTTGGTGTGTTGGCA	59.823	20	157	311	467
TTTTTCAGGGAGGGAGATGA	59.6	20	128	285	412
ACCAAGCTTTGTGAATTTTTGA	60.03	23	268	1271	1538
TCAACTCTATCATATAAATTTTT	58.025	27	224	9	232
ACCTATGGTGGTATGGCGTG	60.657	20	162	747	908
GGATTCGAACCCTCACACTT	58.992	20	211	11	221
TTCCCGCTGATTTCTTCTCT	59.006	20	278	3538	3815
TGGGTATCCAAAAACCAAAA	57.847	20	268	1540	1807
CCAAAACATACGTTGCGCT	59.744	19	148	173	320
GCGTGAAATTATTAAGCCGC	59.722	20	229	853	1081
CGCTCATATAGGGCGAAGAA	60.323	20	270	973	1242
CCCACACTCTCCACAATCCT	59.962	20	256	1349	1604
GCATTGAAGTCTGCTGTGCT	59.195	20	231	20	250
CACCACCGTCTCACACTCAC	60.207	20	183	12	194
ACCAAATCAAGAACCCCCA	60.157	19	275	10	284

TCACCTCCGTCTAAATTGCC	60.074	20	234	42	275
CGTAAAATTCCGGTGCAAAT	59.832	20	146	812	957
TAGAGGACACTTGGACCTGAA	57.374	21	100	6	105
GTCGACATGCCCTAAAAACC	59.434	20	227	610	836
AGCGAGACCTTCTATCACGC	59.603	20	191	7	197
ACCGGACCGTTATGCAATTA	60.209	20	168	21	188
AGGTACCCCCACACAAACAA	60.126	20	210	209	418
TGACTCTTCTAGCTCCATTTGC	58.745	22	119	2843	2961
TCTCAAGGGGTCAAAGAAGG	59.255	20	239	66	304
CCTTTCATTGGATGTAGCCC	59.387	20	191	545	735
AGCCACTGAACCAAATGACC	59.973	20	273	2102	2374
CAGTGCCAGATGACGATGAC	60.279	20	195	2049	2243
TTAGGGACGATAATGTGGGC	59.784	20	124	394	517
TCCGTCATCTATTAGCACCATC	60	23	137	106	242
CACTACTAGGGTTTGGGAGGG	59.866	21	207	105	311
GATAAAAATGGCACCCGATG	60.153	20	264	176	439
TCAATTCTTCATCGCTGCTG	60.096	20	278	1647	1924
AGCGGTGAAGAAGAAATCCA	59.813	20	196	909	1104
CTCCGCCTTGACTCCTTCTA	59.569	20	210	68	277
GCAAGGATTTAGCCCCATCT	60.419	20	272	2127	2398
TTAAAAGTTCACTAAAACTGCC	57.511	25	200	95	294
TTGTGTGATCGAACCACGTT	60.008	20	109	23	131
AATCCAAAATCGCCATAGCA	60.424	20	134	1031	1164
CCACCGAGCTTCTACACGTT	60.312	20	188	6	193
ATGTTGGCTCCGATTGAAAC	59.939	20	278	27	304
GCCCAAGTGGGAGATTGTT	59.918	19	207	149	355
CCCAACAATTCCACTTCCTC	59.381	20	103	8	110
CTTGAAGCCTTGTTCCTTGC	59.993	20	210	167	376
TAAGGTGGTGACGATAGGGC	59.955	20	222	377	598
GACAGCTGTGATGAAGGCAA	59.992	20	186	2710	2895
AGAGGAGAGGAGGTTGGAGC	59.952	20	250	8	257
GAAGATTGTGGGGCGAGTAA	60.074	20	219	1725	1943
TCATGGATCAGGAATCTGGA	58.958	20	261	442	702
TTTGGTAAATACAACATAATTG	58.757	26	176	347	522
ATTGCATTGCATGTGTGGAC	60.409	20	280	394	673
AAGGAGGTGTTATGAAGGGAT	58.028	22	145	1419	1563
CGCGACCACGAAGTACATAA	59.752	20	226	87	312
TGAGCAAAAGTAATAAGAGCA	58.341	24	207	225	431
CTCTACAACCCAAACGCATGT	60.045	21	203	229	431
AATCCCAAAATCTATGGGGC	59.984	20	177	26	202
GCAGCCACTATCCTTTCACC	59.7	20	199	677	875
ACAATTTCAAGAACCCCCAA	59.264	20	241	5	245
GAGAGTGCAGCAGCAAAAAG	58.952	20	120	2	121
CCAAAATCCCAGAACGAAAA	59.91	20	180	129	308
GCGGAAGAATGAATACGGAA	60.038	20	163	2	164
CTCACACAGGCTAGACGCAC	59.648	20	177	33	209
TCCATTTTCCTCACCCCATA	60.126	20	101	452	552
TGGTAGGTGGGTTTAGGTGG	59.705	20	130	20	149
GTGGTCAATTCACAATCCGA	59.348	20	266	71	336
TTTTGAATCTTTGTCCCCAA	58.039	20	223	285	507
TCACCTAAACCACTTTTGAAGA	57.979	23	239	67	305
CGTGGTTCGATCGTAATTGA	59.542	20	100	1	100
ATGGGTTCGAGTCTCAATGG	59.927	20	280	793	1072
TCAATTGTCACACGTGATTGAG	59.615	22	189	1048	1236
TCTGGACACATCCTTGTTTATCA	59.485	23	212	1073	1284
TCATCTTTTGGGAATGGTTTG	59.787	21	243	216	458
TCACCTCATGGGGAAATTTTAG	60.177	22	102	1	102
CTCACTCACCCTCTGTTCCAC	59.741	21	234	19	252

GGTGGAGCATGGGAAAAATA	59.762	20	233	868	1100
CTTTCCTCAACCGAGCTCAC	59.989	20	255	13	267
GAGAAAGCCACAAATCTTTCC	58.894	22	262	3612	3873
CAAAAGGCCCACAATGGTTA	60.722	20	149	281	429
TAGGGATCGCTCCAGAAAAA	59.778	20	278	1962	2239
AAATGCGCAATTTTAAACCC	58.982	20	247	149	395
TTCCACTCCCACCAACCTAC	59.82	20	244	257	500
CTCATTTACACCGCCTCAAA	58.771	20	273	699	971
TTAGTTTTGACATGAAAATTGA	59.039	26	246	480	725
TCCTTCATTCCTAAATGATTAA	57.79	25	276	668	943
CCGAATCCATCATCACAACA	60.33	20	271	39	309
TGGAAAGGGCATTAAATGAAA	59.42	21	192	318	509
GATCGACCGATCCACTTTTG	60.461	20	215	83	297
AAAGTGGAATTTGCTTCCCA	59.546	20	240	194	433
TTGGTCCCTTTCTTTCTCCA	59.641	20	197	124	320
CCCTGGGACACATAAGCCT	59.935	19	259	494	752
AATCTTGGCCGTTTATTTCG	59.078	20	267	171	437
GGACGAGCCAAAATCAAATG	60.448	20	156	1138	1293
TCGCATCATCAACCTTCTGA	60.353	20	256	561	816
GAGAGGATGGAGTTGATCGG	59.612	20	259	223	481
AGACTAGCACGTGACCGGAT	59.751	20	263	252	514
CCAACCCAGAATTCGTCCTA	59.926	20	206	985	1190
TGACGAAAACTGCTTAAATCC	57.064	21	142	4	145
CACATCGACGACGCTACCTA	59.888	20	198	216	413
CCATTTCATCTTCAGCCCAA	60.972	20	196	813	1008
AGGAAATAAGGAGGTGTTATG	60.131	25	187	1222	1408
TGGACAAAATGAGTGGAGAGA	58.272	21	113	1145	1257
CGTCGAGTCTCCTCCAACTC	59.986	20	220	845	1064
ATGGGTGTGGGTGTTAGTGG	60.545	20	126	272	397
TTTGTCGGGTCATTGCTACA	60.111	20	175	836	1010
GTAATGGTGATGCCAGGGTT	59.676	20	159	1220	1378
GGGAATGAGGGATGGAATTT	59.959	20	146	2305	2450
AAATTCAGCAGGTCCACGAC	60.119	20	253	100	352
GTTGGTTGATGAGGTGGCTT	59.973	20	217	612	828
CGTTAAATCTCTTGCGAGGC	59.982	20	161	132	292
CCATCTCCAATTCGTCACCT	59.927	20	268	246	513
TGGACAGGTGGCGTTAATCT	60.517	20	253	592	844
CGTATACCCTCAAACATCCGA	59.831	21	179	787	965
TGCATGGTTTGAGTTTTGTGA	60.142	21	142	35	176
ACGGTACCACCCCAATACAA	59.971	20	196	2189	2384
AATTGCCATCTTCAACCGAC	59.939	20	177	535	711
CTCCTCTCCTATTCGCTCCC	60.306	20	264	147	410
GCATACGCGCTCATAAATCA	59.832	20	199	18	216
TCTCCATTTGTCTCCCTGCT	59.803	20	192	2251	2442
GAACCACCACACCAAATTCC	60.073	20	223	395	617
CATCTTGGCATTCTGTGCAT	59.679	20	204	118	321
AACCCTTGACGTGAATGTCC	59.827	20	231	5	235
CCAAAAAGAAGCCAAGGATG	59.679	20	212	60	271
CACAAACCATCATTGCAACC	59.823	20	273	968	1240
TGGACTGAACTGCAATGCTC	59.992	20	271	921	1191
CAGAGTGATGCGTGAAGGAA	59.984	20	189	340	528
ACCGAACCGATTTTGTCCTA	59.429	20	135	154	288
AGAATAGTGGGCTTTGGCAC	59.198	20	119	1	119
ACATCTGAAAATTTGACGCAT	57.226	21	258	157	414
GGGGTTATCACTGGATCACG	60.195	20	104	592	695
AACCATCTTCGGAGAGAGCA	59.95	20	116	248	363
TCCATGACAGGAACCAAACA	59.935	20	174	1335	1508
AAGCTCATCCATTGGTTTGG	59.933	20	147	344	490

TGGCAGAAAGATTTTAGATATA	59.31	26	133	214	346
TTTCGAAGATCAACGAACGA	59.395	20	125	221	345
AGACCGAAACCGTTCAAAAA	59.587	20	266	625	890
AGACCACCAAGTCAGCACCT	59.756	20	246	1073	1318
CGGCAAGGAGAAAGAGGATA	60.214	21	271	82	352
AACATGTAACCTGTAATCTGTA	57.047	27	226	182	407
TACCACTGCCATCCAATTCA	59.924	20	118	49	166
TCAGTCGGCCTAAATATCCCT	59.938	21	267	763	1029
ACGGGAGCATGAAATGAAAC	59.939	20	269	489	757
CACCAATTTCGATTTCCTCC	59.363	20	274	0	273
ACTGATTTTTGCGATGGAGG	60.074	20	236	1340	1575
GCGGCCACGTATTCTCTTTA	60.23	20	188	567	754
CATACATTCACACGGGGGAG	61.176	20	139	2374	2512
TCATCGACCCCATCTCTTTC	60.011	20	143	383	525
GACTTGAGCACCAAGAATCCA	60.248	21	141	84	224
CAAGCCCAGCCTAATGAAGA	60.344	20	152	414	565
TCCTTCAAAATAGGCATAACCC	60.317	22	154	46	199
TCCAAAGGCTCCATCTATGC	60.177	20	223	15	237
TGAATCGATTAGGCTTATCTTG	58.055	23	203	30	232
GAAGTTGGGGGTGGAATACA	59.647	20	272	392	663
CGATGACCTTGAGGTTCGTT	60.111	20	209	3411	3619
GATGTGATACCCGGAGTCGT	59.81	20	112	86	197
AGGACACGTTGGACCTGAAG	60.151	20	106	23	128
GTGGTTGTATGTCATTTAGCGG	59.406	22	248	303	550
GGCTTTCACATTAAGCCCTG	59.708	20	145	6498	6642
ATGGTGGTATGGTGTGGGG	61.339	19	103	18	120
TTTACCAAATAGGGTAAGCCG	58.212	21	244	1178	1421
ATCGGGCATTTCGACTACAG	60.096	20	211	779	989
GACAGCCCAAGATTGAGAGG	59.803	20	276	7	282
TCCAAGGCAAATTGAACTCC	60.051	20	261	226	486
CCAAAAGCGACAAAGTGTGA	59.881	20	174	120	293
GAATTGGTGGAAAGATTTGAG	58.162	22	244	15	258
GGCACTCTTATGGCCTTTGA	60.214	20	135	22	156
CCCACCAACCCAGATCATAG	60.187	20	244	2483	2726
AATCAATCCAGCTCCAGCAT	59.658	20	149	2000	2148
CAGCACGCGCACTACATAAT	59.925	20	270	148	417
GGACCAATTGGCACTTTGAT	59.797	20	218	787	1004
TCTCCCTTTCCTCTCTCGTG	59.525	20	168	443	610
TTACCAAACACCCAAACCGT	60.125	20	149	1110	1258
CTTCCCACCAGTAGTCTGCC	59.721	20	233	3447	3679
TGCGAATTAGCAGCTTTGAA	59.725	20	250	873	1122
CCCAACCAACAAGAACCCTA	59.824	20	131	441	571
CCCAGTTGCTCACAATGACA	60.722	20	211	363	573
AATCCCAAAATCTATGGGGC	59.984	20	193	26	218
TGGTAGGGTGGTAAACCAGG	59.705	20	211	101	311
CAATTCTCTCAACCAACCCC	59.381	20	193	28	220
CATCATGTAGTAGCGGGCTG	59.322	20	144	44	187
CGTCGTCAAACAAGACATGC	60.31	20	180	30	209
GCTGGGTTTGGTGTTGAATC	60.362	20	277	104	380
TGGACCGTTGAAATACAGAAA	58.134	21	152	24	175
GAGTTCGTCGAGGTCATCGT	60.269	20	240	28	267
CTCATCTCTCTCGCCACTCC	60.096	20	265	1686	1950
AAGCCCACCTGATATGCTTC	59.154	20	183	24	206
AACATTCGAACCAAAATGCG	60.866	20	209	493	701
TGACAAAATATGGAACCACAA	59.37	23	152	27	178
AACAGTGCAGAACACGCATC	59.912	20	156	204	359
GCGCGCAATCACTCTCTT	60.257	18	227	755	981
ATGCGGTTCAAAGGTAGGAA	59.569	20	208	42	249

CATCCTCCTTTTCCCAATCA	59.864	20	273	26	298
GGTTGACACACTCGAACCAA	59.571	20	223	7	229
TCAGGTCCGAATGCTGGTAT	60.483	20	162	3143	3304
GGGGATTTGATTGATGATCG	60.096	20	278	99	376
TAGACTGCGGATCACCACAC	59.707	20	241	256	496
TTTGTCCCCACAAATGTCCT	60.21	20	156	2464	2619
CGATGATGGAGAGGAGGAAG	59.755	20	197	295	491
CCCTTTAACAGACGCCACAT	59.993	20	153	4237	4389
TGACATGTCCTTTCACTCCAA	59.124	21	228	3124	3351
GCCTAACCGTGGCTCTGAT	60.233	19	128	64	191
TCATTAAACCCGAATCCGTC	59.762	20	107	583	689
GGCACAGCTCCACTTTCTTC	59.997	20	197	118	314
TTTCCAAATCTTTGTTCCGAG	59.188	21	228	321	548
CAGAAAGTGCTTGTTCAGCG	59.781	20	144	1182	1325
CTCTGCGACGTAATTCCCAT	60.096	20	277	79	355
AAGAAAAACGTGTGAACCATC	59.517	22	136	439	574
AATCGCGTAAAGGGTTTGAA	59.586	20	120	269	388
CGTGTTGTTTTGCTTGTTTCA	59.801	21	135	15	149
TCTTGGGGGTTCAATGTACG	60.745	20	278	236	513
GGAAGGATTAGGCGAAGGAG	60.166	20	223	13	235
TGCATATCAAATGGTGTTTGG	59.291	21	204	96	299
TTGGTTCACACAACCACTCC	59.415	20	179	70	248
ATTTGATCTCTCGCTTTCGC	59.556	20	159	3	161
TGATTCTGGCACCTCCTCAT	60.622	20	191	1451	1641
CTTGGAGCTGTTTTCTTGGC	59.993	20	237	2562	2798
TGAAATACAAAAAGGGTGCG	58.674	20	252	688	939
ACATTTGGTGAAATGGGAGG	59.647	20	276	40	315
GGAAAATGCACTTCTGGATCA	60.066	21	143	3	145
AAAAACCCTTCATTGTGGAAA	58.454	21	277	44	320
TTGTCAAAATCTCCTTCATTTG	59.038	24	268	644	911
GAGGTTTTGACGGGATTTAGG	59.822	21	265	924	1188
CGGTACGGTAAGTGCGGTAT	59.904	20	137	592	728
TCACACCATATTTTTCCCCC	59.481	20	220	754	973
TGCGTGTCTAAATGTGCCTC	59.871	20	141	380	520
TGGATTTTTCAATGGATGGC	60.649	20	154	21	174
TGATCTTTTCGCCATTAGAGAG	58.605	22	112	204	315
TCCCAGTCTAAAAGTCCATGC	59.184	21	175	201	375
CCTTCTCTCCCGACACACAC	60.713	20	119	100	218
TCAAGTCGCTACTCACCATCA	59.455	21	121	881	1001
ACAATGGAACGAGATCCAGG	59.927	20	207	314	520
TTTTTCTTGCTTTTGCTGTGA	58.736	21	230	27	256
GTCCCGACGAGAAGTACCTG	59.721	20	233	15	247
CAAGCTCAGTCTCAATGGGG	60.791	20	133	232	364
CTCTAGGGTTCAATTGGGCA	60.066	20	173	2928	3100
TGCGATAGTTAACAGGCAGAA	58.595	21	161	359	519
AAACGCTGCCTCAAAAGCTA	60.152	20	234	689	922
GTTTTGGTGTCTAATCCATTTG	59.687	24	136	46	181
CCCAAGGTACATTGCGTCAT	60.776	20	239	569	807
TGAGAAACCGTAACCCAAGC	60.11	20	239	10	248
GCTGCAGCAATAAAATTCCC	59.688	20	230	2704	2933
TCGCTCTGAACCAAAAACCT	59.853	20	205	263	467
GCACTCATCAGAGTTATCGGT	59.763	22	160	3162	3321
AATTCAAACACGAGTCGCAA	59.322	20	245	313	557
TCACAGGAGGGTTCACACAA	60.129	20	128	230	357
TTGGGGCTTGTAATAGCTGG	60.089	20	271	7153	7423
CCATCTCCACAGCCAATTTT	59.933	20	256	318	573
CACAGCAGCAATTCAACCAA	60.844	20	269	224	492
CATGCCAACACAAAAACACC	59.864	20	214	189	402

TGATTGATTACGAATCCTCGC	60.052	21	273	83	355
TTAGTGTGGCCGGTTTAATTG	59.876	21	181	82	262
CCGATATAAGCGCCATCCTA	60.04	20	185	297	481
TGTTTGATTGCATTAAAATCGG	59.84	22	164	1050	1213
TCAATCAGAGACGGTGAACG	59.831	20	230	2204	2433
TGCAATTTGTTTCTCTCCCA	59.247	20	199	1735	1933
TGTGGATATGTAGATAATTTTT	57.748	26	228	72	299
TGGTAAAGGGACGGCATTAG	59.953	20	159	740	898
TCCTTCTTCACTTTTGCTCACA	60.03	22	149	9	157
GCCCAAAAGGCCCTAAAGTA	60.432	20	226	1393	1618
CGAATTTACTGAAATACCCCC	60.069	22	229	21	249
TCACCCCATTTCAATCCTGT	60.173	20	160	0	159
CCATGTCTCTGGACTGGGAT	59.92	20	255	3438	3692
ATCTTTTATGTGCACAATGCG	58.715	21	171	359	529
GCTCCCACTACCTTTTTCGTT	59.645	21	162	77	238
TCCTCCTCTTCCACTTCCAC	59.228	20	189	62	250
ACCAGTAGATGCCCCTCCTAA	59.969	21	279	450	728
CCATGCTTCCATGTTTTCAA	59.518	20	249	6	254
CAGCTCCGACTCCTTCCTTA	59.569	20	117	103	219
TCGCATAATTTTTGTGAGAGG	57.913	21	241	56	296
TCGTTGCTCTCCATATTCCC	60.036	20	154	301	454
TTGGAACTCCGGTGAGAAAC	60.088	20	201	1443	1643
TGTGACTGCTCTGGTTGAGG	60.022	20	102	19	120
ATTTTGGGTTTGTTTGCTGG	59.839	20	263	539	801
TGAGTTGAACCCCCTCTCAC	60.088	20	182	1525	1706
TAAGGGCCGATCCTATCAAA	59.502	20	242	2810	3051
CATGCGCCTAGATAACGACA	59.856	20	247	681	927
CGCAGATATGCGTTTCTCAT	58.897	20	153	33	185
ATATACCGGTGCAAACGAGC	59.988	20	202	1170	1371
ATTGGGGAAGAAAGGGAGAA	59.875	20	115	432	546
CAGCAGAGCAGCCATATCAT	59.005	20	107	155	261
CCTCAAATTGTTGAAAAACCG	59.478	21	221	416	636
CCGTCCATCTCAAAAATGAA	58.546	20	225	887	1111
CAGCACCAGATTTGCACCTA	59.864	20	228	277	504
TGAATTTCAGTCATGGATTCTC	59.136	24	166	24	189
CAGCATACACACTCCGCATT	59.746	20	241	5	245
GGCCATTCAAATTTCAAATCA	59.765	21	232	310	541
GGACGCTCCAGATTGTTTCT	59.288	20	167	1	167
CCGAATATTCAGACGAAGCC	59.668	20	275	92	366
AACGGGATTTACTGTTTTGACA	58.539	22	255	184	438
AGCCCGTACCCGGTCTATAA	60.702	20	239	42	280
GGTGCATTGATTTCGCAAG	60.213	19	169	658	826
ATCCCCGACAAATTTTCACA	60.17	20	130	37	166
GACAAATCCAAGTGGGAGGA	59.903	20	227	1803	2029
ACCATTTTCATTTCGGGCTA	59.411	20	239	353	591
TTATGATGGGAAGAGGGGGT	60.517	20	251	143	393
CAGTCGGGGGTAACACTCTT	59.062	20	110	2153	2262
CCCTAGCTTTGCCCTCTTTC	60.332	20	274	591	864
TAAACCCTAAAAACGCGTGC	60.13	20	252	10	261
TTTCCCCTTTGCCCTCTATT	59.903	20	157	34	190
TTTTCTGTTTTTGACAGCCG	58.939	20	183	5	187
GCACTCTGCGAGTCTCCTTG	61.3	20	277	69	345
TGAGGAGTGTGAGGATCGTG	59.82	20	212	9	220
AATCGCTGTATCTCCATCGC	60.207	20	162	1503	1664
TGTCGCAATCTCCGTACACT	59.318	20	111	349	459
GCAAGCACTTTTTGCCTTTT	59.519	20	275	344	618
AAGGTGACGAAATGGGAATG	59.79	20	204	72	275
CTAAGGTAGCAACCACCCCA	59.986	20	224	31	254

GCCGAAAACAAAGTCCAGTT	59.218	20	278	24	301
CCTTATTTCCTATTCCCGCC	59.767	20	148	586	733
TTCATATACACGTGCGTCTTTT	57.425	22	158	586	743
TGCTTTCTGGTTCATTGTGG	59.691	20	279	35	313
GGTAGCAGCGATGAAGGAAC	59.843	20	230	1427	1656
GCTTGTTACCGGTGGAGAAA	60.11	20	188	35	222
TTTTAAAATAATTCCTCACCCC	59.494	23	127	988	1114
TTGTGGGATTTGAATGTGGA	59.75	20	216	31	246
CGCAGGAGGACAAAAGAAAG	59.986	20	226	2501	2726
TTCAAAGGAGGATTGTGTTAA	59.527	23	133	60	192
GACAGCCTTTTTGTTTTGCC	59.73	20	198	18	215
TGTTTGAGATTCAGTGGGGA	59.059	20	245	2669	2913
GCAGTAAAATACGGCTGCGT	60.293	20	280	12	291
CCCACGTAGCAATTGACAAA	59.585	20	263	684	946
GATTACGTCGATCCAACGGT	59.82	20	127	151	277
ATGCTTTCCCTCTCCATCAA	59.629	20	192	0	191
ATATTCGAGTCATCCGCAGC	60.207	20	261	2705	2965
TTCCCGAGTTGATACCCAAG	59.926	20	150	169	318
GTTGATTGATTGTGGTTGGG	58.67	20	180	91	270
ACTTCGGCAAATACCACTCG	60.132	20	148	94	241
TCAAAACTCACCGGAATCCT	59.526	20	260	1454	1713
GATGCGATCACTGCCCTATT	60.066	20	210	664	873
AGGTGGCATGCTATCTACCC	59.034	20	234	1745	1978
CCTTTGTCAACTTGGGCAGT	60.149	20	137	3056	3192
AAGACAGGGGTATAACGGTCA	59.762	22	190	1145	1334
CCAGAAGGATTCTTCGGCTA	59.406	20	273	132	404
ACCCGGGACCTTTCAATTAC	60.053	20	142	779	920
ACATGTGATTGCGCGTATGT	60.026	20	125	44	168
TTTTGCCTTGCATGTTGAGT	59.322	20	228	1919	2146
CGAGTGGTGTGTGAGGTGAG	60.358	20	245	70	314
TTGGCAGAACCAGAAGATCA	59.369	20	262	194	455
CGGGATTTGGTCTTTTCCTT	60.291	20	228	766	993
TATGTGCGGCTTCTTACACG	59.895	20	237	197	433
GAAACATGCCTCCACATCCT	59.934	20	261	312	572
TTTGAAGTGTTTCGGGGAAT	59.406	20	273	1281	1553
GAGGCCTTGAGGCAGACTTA	59.574	20	278	846	1123
GGCTGGTATCACCATAACGC	60.361	20	118	91	208
AGGCTGTGAAAGCTCCATCT	59.043	20	145	43	187
ATTGTTATATGGCTGGGGCT	58.419	20	162	177	338
TGCAACACCAAGTAACCATCA	60.019	21	146	212	357
TAGGCACAAGTTCGAAACCC	60.11	20	270	21	290
ATTTCATTTCATGGGTTTCG	57.399	20	156	37	192
CACGAGTGAGAAAGGGAGAG	59.583	21	115	150	264
GGTTCGGTTTTTCGGTTTTC	60.683	20	204	178	381
ATGCAGCAGAGCCAATTTTT	59.851	20	202	8	209
CCTGCTTTCCAGTTTAGTTGC	59.031	21	270	449	718
TCATGATGCTTGATGCAGGT	60.233	20	128	74	201
TTTGGGTTTCTGGGTGTGTT	60.246	20	266	797	1062
TGCTGAATCTTAACCGTCCC	60.074	20	134	760	893
CGTTTTGCTTTAGGTTACAAGG	59.722	23	259	224	482
TCAACCACCAACATTGTTTCTC	59.875	22	147	237	383
TTTTCCCTCTTCTGGGATCA	59.6	20	276	384	659
GTTGAGGAAGAAGAGCGGTG	59.989	20	177	141	317
CATCATCCTCCTCTTCTCGG	59.755	20	231	311	541
TATTCCCTCAGACCACTCGC	60.218	20	274	825	1098
AGCTGGTTACCTTCGAGCAA	60.015	20	193	29	221
AATCTTGTTTCAGGTTATCGTC	58.793	26	220	43	262
CGATAAAAGCGAATTCGGAG	59.81	20	262	578	839

GGGCTGCTTCAGCAAAATAC	59.851	20	140	3573	3712
GGATCATCCGGTGCTACAAT	59.78	20	160	592	751
CAGCTTGCATGTAAGGTCCA	59.864	20	194	471	664
GAAAACCCAAAACACATGCC	60.214	20	242	5	246
TCATCAACATGCAACCATCA	59.469	20	221	88	308
TCAAGTCAACATAAACATAAA	58.978	26	134	95	228
GGCTCCGTATGCTTGGAAT	60.051	19	139	18	156
CGTGATTCGCAACTCTGATT	58.877	20	274	71	344
GTAATGTCAAATGCGCAACG	60.14	20	114	294	407
ATGGGTTAGCGTGTGATCGT	60.406	20	268	194	461
GTTCAAAAATCAAAAGGTCGA	58.274	22	273	3	275
GGGCCGAGATTTGTTAGAGG	60.949	20	165	1569	1733
CATATATTTCATTGGCCCCG	59.998	20	138	1460	1597
AGCACTACATAAAATGAACAT	59.095	26	270	1530	1799
CCACAAACCCTTCATCACCT	59.82	20	108	49	156
TCGAATGTGGAGACGAGATG	59.787	20	178	1160	1337
TTTATCTTGCCCATGGAACG	60.827	20	273	5585	5857
GTCCAGCTCTTCCAACCAAA	60.232	20	159	316	474
GGGTTTTAAATTGGGGATTTT	58.176	21	204	142	345
TTAGCCGATGAGAGGAGGAA	59.91	20	273	4675	4947
CTTTTTCTTCGTCACGGGTC	59.711	20	214	663	876
TACGAAGGAGGCTTGGAAAA	59.817	20	248	1020	1267
AACAATCAACCAAGGATGACA	57.908	21	215	1765	1979
AGATTCTCGCAGATCAACGG	60.362	20	240	549	788
CAAACGCAACAAACTGTTATC	60.082	23	273	354	626
GTGAAGCAAGGGAACCATTT	59.031	20	273	545	817
TGTGGCTATTTTAGCTCTTTGG	58.589	22	156	8	163
CAATATTACAATGGGCAAGAG	57.725	23	123	1665	1787
CAAAATGCCTATGGAGGTTGA	59.946	21	254	0	253
CCTTGCTATGCAATACGGAGA	60.237	21	278	96	373
TCCTTCCTTGACCATCCAAG	60.042	20	280	199	478
TGCTTGTTGGCACCAGTAGA	60.449	20	211	190	400
CTGTGACGGTGCGTGTCTAT	59.776	20	160	135	294
CTTTGAGGCGCAGAAAAGTT	59.632	20	260	2030	2289
CCATGCACTTCTTTCTTTGC	58.502	20	264	231	494
TCCTGTTATCTGCCCAGAAG	57.894	20	178	719	896
GGCAAGGACCACTAGCAAAA	60.249	20	267	1281	1547
CAAGGCACCGACATCAAGTT	61.096	20	261	93	353
GGGTGGGTTTGGAAAAGAGT	60.204	20	259	597	855
GCGTGTTCTTGGTGTTCTTG	59.339	20	219	88	306
ACAAATTCGAGATCGAACGG	60.074	20	277	555	831
AGCATCTGGAATGCAGGAAG	60.362	20	234	688	921
TTTTGGGCTAATGGGATGAA	60.26	20	220	23	242
AATAGGAGAATAGGGGCGTG	58.162	20	196	57	252
CCTTCAGATGGAACAGTTGGA	60.096	21	218	121	338
ATCCTCATCTTCACCATCGC	60.042	20	268	455	722
GATGCAAATCCGAGTAGCTTG	59.859	21	244	226	469
CGAAACAATAAGATGCTGTGT	60.18	23	210	60	269
GATGGAATTGGGTGTTGGAT	59.464	20	153	24	176
CACACAACCACTCCACAAAGA	59.626	21	119	274	392
CACCCGTATGGGACAAAATC	60.051	20	176	232	407
GGTGGAGGATTTTCCTTTCC	59.744	20	196	19	214
CGTGGACAGTTTCCCAAAGT	60.005	20	204	49	252
ATTACTCACACGCACACCCA	60.032	20	131	211	341
GGAATAAAAGCCCCGATTTC	59.751	20	190	0	189
CGTGTCTATCCTCACCCCAT	59.803	20	172	65	236
TCTGGTGAAGATCGATGCAG	59.942	20	132	2658	2789
TCACCACAAACCACCACAAC	60.309	20	276	396	671

TCACCAAATTTGAGGGTTATTA	59.149	25	230	147	376
GAAGGGTATTTCTGGAAATCAT	60.076	24	200	68	267
TGGTAATTTTCGCACCCACT	60.365	20	275	150	424
GCAAACACAGGTCACAATGG	60.008	20	205	1182	1386
AAAGGGCATAATCTATGATCG	60.076	23	175	44	218
TGTGTTTTTCAGTGTGTGGGA	60.033	21	157	49	205
AATTGCACGGTAGTTTGCAC	58.703	20	280	1578	1857
CAGATGTGGACGGGTCACTA	59.545	20	279	20	298
TTGCGATACGTGGCTGATTA	60.237	20	229	75	303
TCAGACCCAGGCTTTTCAGT	59.844	20	218	158	375
TGATGAAGAGAACAAGACTGC	60.045	23	260	107	366
TGATGGTGGTTTTCAGATGC	59.502	20	214	52	265
CCTGCGTTGTCAAGATGAAA	59.84	20	206	157	362
GATCGAAGCATTTTGATTTGC	59.679	21	245	127	371
GCCATTGTGAGGAAGGTTGT	59.973	20	176	4	179
TGATCAACTGCTCTGTGGGA	60.402	20	228	3338	3565
TTGCGTTGCTCTGATAATCG	59.976	20	273	549	821
AGGCAGACAGATAAGGGCTG	59.454	20	246	428	673
AAAAGATGCATGTGTTCCCC	59.797	20	154	366	519
CCCTCACTTCTCTTCTGCGT	59.598	20	274	72	345
CCTTCCCCGTTTGTACTCAT	58.909	20	267	429	695
ACGGATTTAAGGGTTATTACCT	57.667	23	208	682	889
TAAATTGCACCCATCAACCA	59.786	20	226	881	1106
CCAAGTACACTCCTCCTCCTG	58.804	21	256	3977	4232
TGATTTGAGTGTAAACACGTCC	58.688	23	156	100	255
GAGCGAGTGGTTGTGAGGTT	60.307	20	104	7	110
AAAATGGCACATGGGTTGTT	60.096	20	256	1652	1907
TAAAACCTCGTGCTTCCCTG	60.241	20	183	2272	2454
AGCCGACTCCATTTATTGCT	58.814	20	277	1043	1319
CCTGTGGCTCAAACCTGAAT	60.111	20	277	11	287
AAGCCGATCGAGTTTGTCAG	60.397	20	159	32	190
AGGGAGTGCTCTCACCTGAA	59.986	20	215	168	382
AGATCCAACGGCTCACACTC	60.269	20	261	442	702
TTTGCTTGATCCAATGGTGT	58.976	20	257	387	643
GCTGGATAGTTGGGAAACGA	60.074	20	227	9	235
GAGAGGAAGGTGTGGAGCAA	60.386	20	266	326	591
TGAAAATATCATCGGCCACA	59.891	20	189	390	578
AGCACTCTGCGAGTCTCCTT	59.355	20	280	70	349
GGAATAAAGCCGTTTGAATTTG	59.851	22	213	15	227
TGCGTTTTGACAATATATAGGT	60.083	26	180	61	240
CCGTACACCACCCTTAATCC	59.17	20	273	1310	1582
CAAAATTACAAATGGCCAAGA	60.342	23	132	51	182
CCACTACATTCAGGGCCATT	59.813	20	142	842	983
TGCTCACCACACTCTTTTCG	60.025	20	204	226	429
ATGAACGAATCAAGTTCCGC	60.081	20	110	238	347
TCTGGCCACTTGTTTCTCCT	59.844	20	253	595	847
CAACTCGCATACCCAAAAGA	58.771	20	232	26	257
GCAAATTTCGCCGTTCTTT	60.203	19	249	2008	2256
TCCGTCTTATTGGTCCGTTT	59.429	20	280	402	681
TCTGCAGGTTCATGTTGCTT	59.445	20	180	632	811
GCTGAGCATTTTTAGCACCC	59.851	20	257	29	285
CGCTGTATAATGGGGATCTCA	59.93	21	162	2339	2500
CGCATGCTCGTTTTCTTTCT	60.523	20	182	40	221
TTCGGACCATTCAAACTCGT	60.495	20	191	4159	4349
TTATCCTCACCCGTTTTTCG	59.931	20	272	288	559
GTCCTCAACCTCTCAATCGC	59.81	20	170	73	242
CATTAAATCCTGTCCACATACA	58.008	24	170	579	748
TGATGGTTGCAAGAGAATGG	59.648	20	236	1762	1997

GCACTGCATACGGCTCAATA	59.862	20	230	12	241
GGCAAATGGCATAACAAACC	60.196	20	198	331	528
TCGGTACCATCATCTGTTTCTT	58.579	22	258	138	395
CTTTTCTTTTCCTTTTATGCTCG	58.685	23	161	22	182
GCCTATTCATTGCAGCCTTC	59.813	20	161	1031	1191
CTCATAGTTGACGCCCTTCG	60.786	20	170	10	179
TGAAGACGATGCGATGAAGA	60.504	20	113	43	155
GCAAATTGTGGCTCTGACAA	59.847	20	250	212	461
TCGTTGTGAATTACCCAAGAA	59.492	22	156	133	288
ACATGTGATTGCGCGTATGT	60.026	20	133	44	176
ATGGGAGCTCATGAACGAAC	60.081	20	203	943	1145
ATCGTGTTCCTCAAGGTTGC	60.119	20	140	2557	2696
ACTTCTCTCCCCCTCCCTTT	60.43	20	210	19	228
CCTACCAACCCACCATGATT	59.526	20	174	33	206
TGAGTGCTCAGGCACAGAAG	60.333	20	179	92	270
ACATGGCATCACTTCAACCC	60.79	20	264	398	661
CAATTTCTGCTCTAATAAATCC	58.809	25	114	13	126
CACATTCGTGCATGTTTTGA	59.124	20	259	3377	3635
ATCATAGTTGACGCCCTTCG	60.096	20	103	2	104
ACCGACCGGAATTTTTATCC	60.02	20	253	878	1130
AACCTAATCCTTTCGCGGAG	60.573	20	184	1024	1207
TTTTCGTTTTTCCGGTTGAA	60.439	20	245	28	272
ACATTGTCACGTCCTCCGTT	60.431	20	209	3	211
TGCTCCCATTTAAACAACCC	59.801	20	274	707	980
TTGGAAGAATCATAATCAAGA	58.395	25	105	183	287
CTAACCGCAGAAAAGCCAAA	60.368	20	125	2225	2349
AACCGTCCGCTTACTTCTGA	59.875	20	274	190	463
ATGCCAAACTGTTGGGAAAC	59.836	20	181	45	225
TTATCATGCCAATCCACCAC	59.205	20	184	334	517
TTTCCCATGTTGTAATTAATGT	58.388	25	193	15	207
CTCGCACCACTCCTCTTTCT	59.598	20	279	4	282
ATGCATGGCCAAGTGTCAAC	61.947	20	279	109	387
CTGGTGACTCTTGTCCTCCC	59.682	20	203	155	357
TGAGTTGGTTGTTAGTCCGGT	59.506	21	165	36	200
TTGTCTGCTCGCGTTACTTG	60.195	20	204	179	382
TGGTGAACTCGTCTCCCTTC	60.238	20	227	73	299
GAGCTGGAGTTGAGAAACGG	59.989	20	235	39	273
GCCCGGAATTCTTAACAGTG	59.569	20	158	268	425
AATCGCTTCCGCATTTAAGA	59.816	20	184	591	774
CCCAAAAAGCAACAAACCAT	59.839	20	140	2425	2564
GCAGGAGGTCTCAGGAAACA	60.386	20	168	363	530
CGTCATGTTTTCAATCGCAG	60.257	20	253	18	270
ATCTTGGATCGACACTTGCC	60.081	20	179	16	194
GGCTGGTTTCCAGACTTTTG	59.711	20	102	66	167
CGGACATGGTACATTTTCTGC	60.38	21	176	578	753
AAAGTTGATGGAAAAGGGGG	60.159	20	139	2043	2181
TTTTTCTGCATTGTCGAAGAGA	59.996	22	247	483	729
TGAGGAAAAAGCCGATCAAA	60.692	20	271	105	375
ATGCCAGTCAGATCCTGTCC	60.08	20	221	263	483
CCGTTACCTTCATCCCCTTC	60.683	20	184	15	198
TCTGTGTCAGCATGTGTGTGA	59.922	21	249	1879	2127
GAGAGAGAAAGGCTACGGGG	60.34	20	147	89	235
ATCTTTTGCACGAGATGCCT	59.843	20	210	8	217
GGGATAAGTGAGCTCGGGAT	60.431	20	223	433	655
TCCGGGTTTGATACCTGAAT	59.244	20	249	1216	1464
CCCTCCTCCTTGCCTAAAGA	60.694	20	158	169	326
CTGTGCATGAAACATGGAGG	60.112	20	279	162	440
ACTGAATGTCACGACCGACA	60.162	20	239	606	844

CGAGGACATTTACTCATGGGA	59.94	21	234	464	697
CTCGTCGTGAACTCCCTGAT	60.261	20	275	401	675
CCATATACCCACCTCCTCCC	60.401	20	257	114	370
TCAGAAACAACTTGCCCTCA	59.415	20	229	29	257
AATCGAGGAAGAGGGCAAAT	60.039	20	209	3089	3297
TCTCTTTTGGTTGGTGAAGAAA	58.856	22	227	1723	1949
TGGGGTTGTCTATTTTTGGG	59.657	20	248	227	474
AGACAGGGGTTGGGGTTAAG	60.218	20	234	62	295
GTTTAGGATGGGATCGAGCA	60.036	20	241	27	267
TATCCCTTGCAGTCCCTTTG	60.066	20	254	0	253
AATGCATGCACCTGATTACAA	59.055	21	178	219	396
CCATCCGGGATTTGTTAGAG	59.382	20	186	222	407
TTTCGAAATTATGAGGCTCCA	59.668	21	189	37	225
AGCAGATCAGGTCAGGGTTG	60.261	20	258	106	363
CCAAATAATTTTGTTTCCACCA	59.974	23	123	98	220
GACCGAAAACCGTTCAAAAA	59.953	20	105	105	209
TCCTTCCACCCAACAAAAAG	59.942	20	280	1194	1473
TACTGCATTGCGACCCTACA	60.28	20	244	326	569
TTCCCCTTTTGTAAGTCCCC	60.159	20	176	1	176
AAACATCGATCAGTCCCACC	59.786	20	116	195	310
AATGGCTGGATTTAGTCCCT	57.611	20	273	26	298
CCAAGAAGTCGCATACCTCG	60.786	20	280	53	332
TTTGGGAAATTCTTGCACCT	59.546	20	100	0	99
ATTCCAAGATGGCAACTGCT	59.7	20	195	6	200
ATTCAAGGGGCATTTTCGTC	61.184	20	177	511	687
GGTCCCAAAACCAAGCCTAT	60.187	20	137	3	139
TGCCTGCTCAGGTCTCAAAT	60.945	20	168	26	193
ACCAACCAAGAAGTCGAACG	60.149	20	278	1841	2118
CATCATCCATCTCTCCCTCA	58.53	20	120	170	289
AAAATCGGACTGGACCATTG	59.79	20	269	246	514
AAGAATGACGGAAATCACGC	60.081	20	171	492	662
AAGGGTTGATTTTCGTCCCTA	59.822	21	169	89	257
TGTCTTGAGTTTGTATCTAAGA	59.365	27	193	167	359
CAACTCACCCTCACATTTCTCT	60.16	23	180	390	569
AAATATTTCTAGCACATGAAAT	57.859	25	232	59	290
GGTGAGAGCTTGAAGAAGAG	58.417	21	134	392	525
ACTTACATCTCCCACACCCG	59.844	20	264	554	817
TTACCATATGTGCCGAGCTG	59.712	20	245	17	261
GTCAACTTGGGCAGTGGAAT	59.973	20	273	764	1036
CCATTAACGCCCCTGATTTA	59.789	20	172	247	418
AGTCGGCATTCAAGTAGTCG	57.98	20	218	194	411
GAAGTTGTAGCATGGGCTTGT	59.256	21	229	83	311
AATTGAGCTGCTTGGTTTGC	60.395	20	258	363	620
TGAAGCAGAATGCAAGCAAG	60.28	20	170	526	695
CAGCCTGATAAATGGGACAA	58.572	20	211	177	387
TTAAGCGCACGCCAATACTT	60.768	20	215	206	420
TGTCCTTCTCCCACTCCTCT	58.819	20	200	164	363
TCAAAACAACACCCAACCAA	59.834	20	251	94	344
CAACAGCCTTGTCTCTGCAC	59.622	20	241	337	577
TCATTGTACCGCAGCAAGAG	60.011	20	273	3743	4015
TTGAAATTTCCCAACATTCG	58.454	20	172	392	563
TCCCTACTGAAGCTCGAACC	59.43	20	241	78	318
CATCTCCTATCACTCCCCCA	59.879	20	154	339	492
TCCACCACCTCCAAGTTTTT	59.425	20	257	455	711
CCTCCTCACCCTTTCCTTTC	60.045	20	103	50	152
TTTTGAAAAAGTCGGCTGAAA	59.855	21	236	953	1188
TGGTGGACGAATTTGGATTT	60.17	20	265	646	910
AGCTTGACAAGGCAGTACCC	59.357	20	173	2	174

GCTCGGAAGCTTCTACACCA	60.538	20	152	3636	3787
TCAATTTGTCATAGCCAACCC	59.815	21	228	364	591
TCGTGCGACATAGTATGGGA	60.096	20	159	49	207
CCTCCATTTCCAATCTGCTT	59.126	20	257	87	343
ATGGAAAGATTGAGATGGGAT	58.781	22	261	842	1102
TAGTGAACGTTGGGGACACA	60.001	20	184	102	285
AAGAGGAAACAGGAGAGGGG	59.671	20	233	521	753
GCATTCTCTTGTAATCCCATAC	58.15	23	267	53	319
TCCAGAGACCTACATGGGCT	59.679	20	217	1290	1506
CCAGATATACCCCCACATGC	60.036	20	240	17	256
TCTCAGGGCAAATAGGGACA	60.594	20	280	4152	4431
GGCGCCTTACCAGTTAGATG	59.73	20	158	136	293
AATGAAATCCTTTGGGGTCC	59.996	20	124	2513	2636
CAATGGGGCTTGGTTTTCTA	59.931	20	268	1306	1573
GACCCCAATTTCAACTGCTG	60.495	20	200	1628	1827
GTGGACGTCCCAGATTGTTT	59.827	20	141	1218	1358
CGAGTAGATCACAACGGCAA	59.864	20	268	268	535
AAGATCTTGGTTGTTGGGTTG	58.945	21	157	577	733
TCTCTTCGAAACTCGAATCGT	59.066	21	159	2	160
GTTGTAGATCAAAGGGCCGA	60.074	20	214	52	265
TATATCAATGGCAGCCCACA	59.914	20	162	1906	2067
CCGATACGAGCTAAAGCGAG	60.131	20	188	14	201
AAATCGAAAGAGTTGACGAAT	58.378	22	251	88	338
TGGTACCAAAATGCCCTTGT	60.227	20	212	393	604
CCCGGCATACAAATAAGGATT	60.049	21	278	145	422
CGGAACTGATAGGGATGGAA	59.887	20	137	230	366
ACCTATCGTCTCCTCCCGAT	59.919	20	263	64	326
ATCCCATACCCTAATTCGCC	60.006	20	263	343	605
TATCGGGATTGGTGGAACAT	60.014	20	177	796	972
TGTTCTCGCAAACAATGCTC	59.995	20	276	149	424
CGAAAATTTAAGCCCCGAA	60.019	19	242	2165	2406
GGAAAAACACTTGAAAGCGG	59.724	20	225	983	1207
CAGCCTTCCTTCTCCTCAGA	59.673	20	163	418	580
GATGGATAGCGCCACAATCT	60.066	20	190	176	365
TTCGGGTTCGAATTTACCAG	59.931	20	259	1823	2081
TCATGCTTCAGCAGCAGATT	59.704	20	247	950	1196
AAAACATACTCAGCCACCGC	60.14	20	179	1348	1526
ATGTAGGGTTCCTGTGGCTG	59.989	20	258	335	592
AAAAGACCCTAAGCACTCACA	58.061	22	231	4325	4555
TCGATTGTGTATGGCATTCTG	59.557	21	255	38	292
CTCTCTTCCTTGCCTTGCTG	60.269	20	116	625	740
ATTAAACGGGTAACTCGGGC	60.204	20	219	1934	2152
GACACGTGGTAGCACGAGAAT	60.194	21	160	263	422
GAGATGCAGCGTCAACAAGA	60.144	20	250	335	584
CCGAAGCAGCTATTCACTCC	59.978	20	245	1270	1514
AGCTTTAAATGTGTTACAAAAT	59.159	26	278	247	524
GTAGTGGCTACGGTTTCCCA	59.993	20	136	3835	3970
CCCATTTTTCTAGGCACCTTT	59.489	21	137	323	459
TACGGTTCCACTTTTTCGGA	60.472	20	199	41	239
CATGAGCGAGTAAACCACCA	59.716	20	131	53	183
TGGCATCAAATCTAGCCATT	58.187	20	234	333	566
GTGACACGTCACACATTGGA	58.931	20	280	337	616
TTCACGCATTTCCACACATT	59.972	20	100	39	138
CACACAATACGCACACACCA	60.071	20	179	236	414
AGCTCTCTATCGGGAGGACC	59.801	20	258	249	506
GATTCTCCAAATCTGACGGC	59.635	20	191	284	474
GGGGCCTTACCTTCAATACC	59.666	20	259	28	286
CAACCGATATCCCCTCCTCT	60.285	20	155	8	162

AAGGTGGGAATTGTGGAAGA	59.381	20	224	75	298
TCCCCATTTTTCAAAAGCAT	59.388	20	244	1544	1787
TGCTAAGAGAAAGCCCCTCA	60.088	20	202	545	746
GTGGGAGACAGCAAAAGCTC	59.997	20	180	420	599
AGCCACACATGTCACAAATGA	60.024	21	239	81	319
CGTGAGGAACCCTAGTTTGG	59.587	20	199	232	430
TTCGTCCGAAATACTCCCAC	59.933	20	205	2	206
GCACAACCACTCCACAAAGA	59.726	20	263	84	346
CCGATTGGGCCTATCCTATC	60.623	20	196	99	294
CCAAATGTGAGACCCTTAACC	58.423	21	124	48	171
TGATGATCGGATGTTGATGG	60.291	20	211	205	415
TCAATCTAAAACCCGTGCAA	59.157	20	172	204	375
TTCAAGATTGTGCGAGCTGA	60.687	20	210	18	227
ACCTGCACCAAAATGGAGAG	60.111	20	150	278	427
CGTGGTTCGATCGTAATTGA	59.542	20	108	99	206
AGGGTAGACATGGGTTTCCC	60.052	20	219	242	460
GAGGCGGTAGGAAACCCTAA	60.443	20	210	15	224
AAGATCCGGCTCACAGAATG	60.218	20	132	297	428
GGCGTTGGACCAGTGTAGAT	59.997	20	277	67	343
GGATGACACGCATCAAAATG	59.931	20	155	1298	1452
CTCTTCATATGGGAAGGGCA	60.029	20	198	9	206
AGCATTTCATCCTCTTCCCA	59.629	20	107	544	650
CTGCGAACCAACATCACTGT	59.751	20	149	132	280
TTCTCAGCTCGGGTTCCTAA	59.948	20	244	146	389
ATTAAATGCGCCTCCCACTT	60.821	20	162	615	776
CGGTCACATAAGCGTCCTCT	60.277	20	241	630	870
TGATGATGACAATGATATCGTG	60.217	24	174	72	245
TTAGGCCATGTTTGTCTGCTT	59.761	21	218	198	415
AAGGTCATCACCCACAGAGC	60.12	20	206	3022	3227
TCAGCCGAAGTAACAAAGACG	60.426	21	214	2104	2317
ACTTGTGTCCCCATTTCAGG	59.82	20	196	944	1139
CGTCCACTTCATTGAATTTCTT	58.239	22	280	3919	4198
ATTGCATTACATGCTCCCATT	59.314	21	248	225	472
AATGCACACCAAAGTGAAACC	59.89	21	237	103	339
CAACAAAGCATTGCAAAGTGA	59.903	21	224	0	223
TCAAATACTAGCATATCGATGA	57.269	25	174	88	261
ATGTGATCCACCACAAAGCA	59.967	20	267	86	352
TTCCACCCATATTGCACTCA	59.924	20	128	87	214
TGTGAGAACCATCTCGGTGA	60.246	20	117	23	139
CCCAGATAGCAATAAGGGCA	60.053	20	161	730	890
CATTGTCAGAAAGTGCCGAG	59.44	20	202	96	297
TTTTCAAGAGCATTCACGGA	59.395	20	237	2174	2410
CGACAAAGACTTAACTACTTGT	60.049	27	279	852	1130
TTGAGACCCACCAACCAAGT	60.399	20	277	642	918
ATTTGTTTGATATTCAACCACTT	57.224	24	103	268	370
AACGAGTAGTGGTGGCCAGT	59.646	20	226	4467	4692
GCGTGGAAAGGCTGAATAAG	59.845	20	256	652	907
TAACCCCAACTAACCACCCC	60.826	20	106	1	106
TTGTCCAGCTCTTCCAAACA	59.415	20	190	365	554
CCAGCCCAATAACTTGACCT	59.052	20	236	69	304
CGGAAGAATTATACACGGCA	58.651	20	263	571	833
TTATGGGTCCAAACAACCTTTT	59.625	22	170	257	426
CGTGTTAATTCCCCTTCCAA	59.795	20	193	1497	1689
CAAATTTGATAGCGGTCTAATG	58.344	23	170	1463	1632
CTCAGGGACTAGTTGAGCGG	60.005	20	189	64	252
TCGCACCCGATAATTACCTC	59.923	20	278	106	383
ATTTTCCCTCCAGTTGACCC	60.169	20	195	4537	4731
CACCTAGAAATGGCATGAGGA	60.081	21	276	647	922

TGCACAGAAAATGAAAAGCG	59.992	20	227	283	509
GCCATGTGAGAGGGAGAGAG	59.945	20	253	91	343
TCCAATGGATGTAATGAGTTAT	57.297	26	280	261	540
AGCCGTCGTATTCTAAACGC	59.388	20	167	60	226
TCAAAGAGCTTTCTCTGTTTGC	58.906	22	210	66	275
GTTGGGTGAAGATCATGGCT	59.934	20	234	82	315
CTCGTCCTAACCCATCCAAA	59.926	20	278	2936	3213
GCTATGGTATGCTGTCTGCG	59.474	20	214	146	359
TGCAGGACAATATCCATCACA	59.94	21	179	7	185
CTCGTTTCAAGCCCAAAACT	59.355	20	148	35	182
TGATGACGATCTTTTGAAACCA	60.481	22	233	18	250
TTTGGGCTAAAGTGGGATGA	60.439	20	200	109	308
TTAGGGTTTAAAATCGCGCA	60.564	20	188	2366	2553
GCAATGTAAATCCTCTGCCG	60.606	20	279	1072	1350
TGTGCACAAGCTTGGAAAAAT	60.663	21	206	1578	1783
GTGCTCGCCTTTCATTTCAT	60.221	20	268	2202	2469
GACCATGAGCACAGGATTTG	59.09	20	245	265	509
TTAGATGGGGACGGATCACT	59.361	20	277	74	350
ATGGAGGTATGGTGTATGGG	57.047	20	170	2555	2724
GCATCCAAAGTGTGACCAAA	59.547	20	259	683	941
TTGACGATATATAGTGTTTTGA	58.972	27	186	287	472
CATGGGTGGTATGGTGTGG	60.517	19	151	10	160
AGCTGTTAGGGTTGTATAGTGA	57.436	27	133	370	502
GCCTTTGCCCTTTTTCTCTC	60.32	20	112	315	426
TCAAAAACGAATTTGGCGTT	60.468	20	177	231	407
GCCATGCATGTAAGGTGCTA	59.718	20	161	1059	1219
TCCTCTCGTGTTCATCCTCA	59.34	20	175	40	214
CGTCGATCTCAGTATCTTCGC	59.992	21	153	166	318
GGTAAATGGTTACCGGTTTGG	60.33	21	245	18	262
ATCACGTTGCAAAAATAGCG	58.844	20	273	46	318
GTCATGGAATCTTGTTGGGG	60.173	20	255	599	853
GTGAGGCATCAAGATGGACA	59.637	20	148	166	313
AGCCACCTCCTAGCCATCTC	60.756	20	112	340	451
CCCATGTTTGTAATTATTGTAG	58.675	24	168	1909	2076
GCCCATGATTCTGTAGTTTTGG	60.721	22	254	180	433
TTTTGTGATTTCCCATGTTTGT	59.225	22	163	67	229
TGGAAAGTGGTGTGTTCGAG	59.72	20	268	203	470
TTTGAAGGCCGGAATATGAG	60.031	20	135	90	224
CGGAGATCAAATGAGTGAGC	58.388	20	122	3	124
GTCATGCCCATTTTGAGACC	60.326	20	206	145	350
ACTGACATTCACAGGCATTG	57.067	20	188	107	294
CTCTCTCCTGGGATCTGTGG	59.785	20	197	187	383
ACATGCATGATCAATGTTGTAA	59.411	24	159	7	165
TCATGATAATGCATGTCTCTGA	59.614	24	101	429	529
AGTGGGTTTCGCGTATTGAA	60.502	20	123	29	151
GACTAGTTTTCTGCGACGGC	60.022	20	203	863	1065
TGTTTTCTGCTCTCCCCTCC	61.67	20	264	108	371
TCAACGCATCTACAGGTTGC	59.871	20	183	226	408
TCCAATTGTTGTCTTCCATCTG	59.971	22	155	286	440
CAGGTTTTGATGGTTGTGATTT	58.858	22	187	98	284
TGTGGTTGATGAGTTGGCAT	59.967	20	279	4092	4370
GCCTGAACAGTCGAGGTGAT	60.269	20	170	3	172
TGCCCAAAAAGATACAGTTGG	59.982	21	136	33	168
TGGTCGTGAGATAGAGTGCG	60.008	20	204	3	206
TGGCATCTTCTCTCAAATTCAA	59.823	22	223	328	550
TGTTTCGATGTGCATGGAGT	60.12	20	128	253	380
ACCTGTGAAAGCGATCGTG	59.846	19	220	2427	2646
CAAAGGCCCACAATGGTTAT	59.685	20	101	1700	1800

TAAAAAGATGAGCCCACCCA	60.439	20	243	103	345
TGGAATGTTATCAAGGGTGGT	59.16	21	272	42	313
GAGCTCTGGTTCCCACAGAC	59.841	20	242	828	1069
CGAAAATGCCCTTTTATGCT	59.212	20	235	1190	1424
CATCAAGAGTCGGCTGTCAA	59.984	20	197	39	235
AGAGGAAGAAGGGGGTGAAA	60.045	20	220	464	683
TCATCCCGTTTCAAACTCAA	59.097	20	154	43	196
TGGCTTCCAAGCTCTCAACT	60.134	20	202	831	1032
AACCCACCAAGTATCGGTCC	60.999	20	269	107	375
TGATGAAAAACAATTGACCAA	59.372	23	219	5	223
GCTCTGATACCATAAAAGGGG	61.005	22	159	95	253
TCACACCTAAACCATTGCGA	60.111	20	102	100	201
TGTTGCGATTTTCATTTTCC	58.601	20	203	33	235
CCCTCATAACTCCTGACTGCT	58.417	21	191	592	782
TTCAACCATCAACTCCACCA	59.935	20	256	238	493
ACCATCGATGCATTCACAAA	59.931	20	147	1700	1846
CATGTTCCGTCCCAAGATTT	59.79	20	239	45	283
TCAGTTTCGAGTTATGAAGTTA	59.749	26	190	73	262
CGCCGATTTGGAGATCTATG	60.564	20	269	39	307
TTAAATGGCCTCGGTATTCG	59.922	20	242	24	265
CGAACTGGAAGAGTTGGGAG	59.837	20	171	30	200
GGTGAAGGAGAGGGAGGAAG	60.186	20	227	73	299
CATCCGCAATTCTGCTTACA	59.833	20	274	4547	4820
TCTCGGGTCCAAAACAATTC	59.91	20	223	146	368
TGGTTATCGTTGTTGGGGAT	60.051	20	199	3585	3783
CGTCACGGTTATCCTTCGTT	59.993	20	110	226	335
TTTAGCAGAGTTGGTGAAATC	57.952	23	226	566	791
GTTTGGAATTTTGGACGCAT	59.807	20	182	314	495
GAGATTGGGGACTTGGTGAA	59.903	20	123	545	667
GGTGGGGAGAATGTAACAGC	59.41	20	133	20	152
ATGCACCAAAAATTGACACG	59.444	20	193	728	920
GGTGATTGTATCGCCACCTC	60.348	20	254	2321	2574
GACCGCTAAAAACCGTGAAA	60.11	20	266	454	719
TGATTGGGCTTTGTCTTTTTG	60.096	21	173	55	227
AAAGCCGTACATGAAAGACAA	60.05	23	220	142	361
GGGAGATTTGAAATGTGGGA	59.727	20	119	275	393
CATAACCAGCTGCCATCTCC	60.624	20	236	2	237
CTCAACTCAGAGCTCCATGC	58.699	20	167	610	776
GCGAATGAAACCCAAGAAAT	59.022	20	187	205	391
GATTTAGGCCAAGGCAATCA	60.038	20	228	50	277
ATGCGAATCAATTATCCCAAA	59.272	21	275	52	326
GGGTGTTTTGACAATATCACG	59.73	22	234	1939	2172
AAAGATCTCTGCAAGTCCGC	59.579	20	261	240	500
GCTCTCAACCATACCTGGTCA	60.126	21	266	272	537
AAATTTTCGTTCATGCCCAA	60.302	20	219	218	436
TGAGCTGTTATGCGTTTTGA	58.075	20	147	83	229
TACATCCGATTAGCTCGCAA	59.425	20	257	215	471
TTGGTGGGTTGAATGCTATG	59.395	20	204	442	645
CAAACGAACTTCCAACGTGA	59.734	20	204	41	244
TAACCCAAACCCACCCAATA	59.91	20	104	19	122
AGCTGGATTGAGCTCAGGTG	60.555	20	213	14	226
AGACGTCATGCAGTTCCTCC	60.269	20	235	461	695
AGAAACTTTCGCCTGATCCC	60.578	20	270	1	270
TGCAAGCATCCAAAAACAAC	59.712	20	193	46	238
GCTCTCATTGTAATCTCTCCCA	59.739	23	117	1	117
CAGCTCCAATCCATCTCCAT	60.034	20	228	308	535
TCTAGCACGGTTGCAATCAA	60.401	20	265	70	334
GCTAATTCGGCAGCTTCTTG	60.117	20	148	437	584

ACCCTGCAATGCTCTGATTC	60.226	20	278	1227	1504
TTCAAAAATGAGTGGACCAGA	58.187	21	127	1215	1341
CCAACTGCTGCTCATGTAGG	59.465	20	176	999	1174
CCTAAATGTGGGAAGTGGGA	59.784	20	168	1492	1659
TGTGGAAGCAAATGGTTAGC	58.773	20	189	473	661
TGGGACCACAGGATAGGAGT	59.38	20	246	4	249
CACCTTTTCTCCCTCTTCCC	60.045	20	218	78	295
GATGATCCGTTCGCACTTCT	60.226	20	225	134	358
GACGAAATTGATGTGTTGGC	58.979	20	227	228	454
TCAGGGAAAAGAGGGTTCG	60.172	19	261	968	1228
TCCAACATCCAACCTCCATT	60.173	20	170	442	611
TTCTGGTACCATACGCGAAA	59.182	20	226	188	413
ATCAATCTTACGGACTGGCG	60.096	20	229	288	516
GATCGTGCAAAATTTGAAAAG	57.444	21	247	28	274
GGCGGTTGAGATTTGTTCTT	59.174	20	110	12	121
TCAGTTTGGTTTATGAGTAGGA	59.15	25	263	946	1208
CGTGGCAGGCTAATATCCAT	59.945	20	142	107	248
ATGGAAGCTGCCCACATCTA	60.624	20	157	31	187
GCGCTTTTTGCCTGATATTT	59.349	20	212	559	770
ATGTGTACTGTGCAGGGCAT	59.041	20	252	3928	4179
TTGTGACGCACACATTCCTT	60.16	20	278	140	417
AGGAGGAGCAAGAGAGGACC	59.952	20	255	39	293
TATGGGTCAGAAAAGCCCAC	59.933	20	243	187	429
AAGAATTGATCATGCGCGTT	60.615	20	262	714	975
TTTGGGGTGAGCTTCACAAT	60.495	20	237	241	477
CATTGTGAGTGTGGGACAGG	59.997	20	182	2398	2579
CGTTAAATCTCTGTGTTGAATC	58.016	24	242	187	428
CTTGTCACTTTCTCCCTCGC	59.989	20	188	6	193
AAATGCATCGGAGGTGAAAG	60.074	20	215	51	265
ATGGACCACCCACCAAAATA	59.91	20	242	82	323
TCATTCATCCATTCCCAACA	59.707	20	200	752	951
TTGGGCTTTCACACACTTCA	60.278	20	164	314	477
CCCGATTCCCTCTCTTTTTC	60.011	20	139	507	645
TTTGCTGCTGATGTTTGTCC	59.847	20	253	2	254
TTGACTAAAACATGGAAATAA	58.939	26	160	19	178
GCAGTTTTGCTCCCACTCTC	59.997	20	153	1315	1467
GGGATTTTCGAATTTTGTTCC	59.651	21	131	713	843
GGTCGATACATCAGGCAACA	59.527	20	237	965	1201
TGCATGATGAGGTCTTCGAG	59.942	20	197	6054	6250
TTCGACTTAATCAATAAAGATA	57	27	266	92	357
TCCAATCTCCAATCCATGC	59.394	19	242	500	741
CGTGGTTCGATCGTAAATGA	59.542	20	192	88	279
GGGTACCGAAGGGATAGGAT	59.128	20	168	26	193
GAACTTGCTGTTTTGGATGGA	60.103	21	160	97	256
CACGAAATTGATGGAAGAGGA	60.059	21	197	345	541
TGAATAAGAGTTCAATGAATTT	59.912	26	223	48	270
CGAAATAAGGAGGTGTTATGA	60.238	24	127	222	348
ACACGCTTGTCAAACATTTCT	57.402	21	210	688	897
TGTGCAGAGGGACTTTAATGC	60.264	21	113	384	496
TAAGTTGATGTGTGCAGGGG	59.566	20	249	769	1017
ACAAACTAATCAAGTTCCGCA	57.439	21	260	79	338
AATTAAAAATGATTGAATTGG	58.312	24	201	458	658
GACATGATTACTCGTCCCCC	59.218	20	216	1401	1616
TTTGAACAATGGTACCTCCTCC	60.221	22	145	497	641
GTTTGGGGTATGGAGAAGCA	59.933	20	137	701	837
GACCAAGGGCTAGTTCACCA	60.111	20	193	5647	5839
TTCTCTCTTCTATTTCTTTCCTT	58.425	27	256	57	312
CGGACCGGGTGGTCTAAATA	61.972	20	102	2076	2177

CATTTGGATCCTCAAGTGGG	60.309	20	276	2469	2744
GCCTGGTAATCCATTCTTCG	59.528	20	257	219	475
TGTTGCCGTCAGTTCATGTC	60.733	20	159	1	159
TGGGATATCCGTTTCTTGGA	60.266	20	255	320	574
AAACTTCTTTCCAACCGGAAT	58.991	21	229	34	262
CATGATTTGAGTTTGAGTCTAC	60.055	24	273	491	763
AATGACCGATCTCTCTATCCCA	59.925	22	100	344	443
GTACTCCAACATCGAGCCGT	60.142	20	144	318	461
ACAAAAGCTCGGTTTAATCTGC	59.799	22	249	149	397
ATTGGGGATGGAAAATTGGT	60.245	20	142	47	188
AGGAATTGTCCCCTTCGTTT	59.805	20	244	104	347
GCATGATCAGGGTAAAATCCA	59.776	21	278	470	747
TCAGGGTTTTAGCCACAAGG	60.103	20	159	346	504
GCTCCAATTCACGTTTTTCAA	60.103	21	231	0	230
CGACTACGGAGAATCCGAAA	60.206	20	259	1	259
CCCATTTCCCTTCCTTTCTC	59.875	20	230	2112	2341
ATCGAACCCACGAGAGCTAA	59.836	20	266	2097	2362
AAAATGCTGACATTGGAGGC	60.081	20	197	2475	2671
TGAAGCAAAAGAACCAGAATC	59.861	22	194	226	419
CACCCACGAACTTTAAACCC	59.331	20	173	166	338
ATGTTGTCACCCCTACCTGC	59.851	20	268	45	312
TTGCCTCAACTACCCAAACC	59.971	20	108	11	118
CCGAACCACGTACATCCTCT	59.989	20	209	481	689
CTAACAGGGTCGGCTCATTT	59.195	20	257	5	261
GGCTATTTCCACAGTACGGG	59.452	20	275	393	667
TCCCATTTCGCTTTCCTTTAT	59.922	21	279	5594	5872
TATTGATGGCCTATTTGCCC	59.757	20	186	579	764
ATCATCCAACATCCACCCAT	59.869	20	107	429	535
CAGTTTTCGAGTTATGAAGTTA	58.177	25	101	384	484
GGCTCCGCAACCAACTAATA	60.096	20	236	657	892
CCTAAGAGATTTGATTGAAAAC	59.236	25	167	39	205
AATGCGCCTCCCACTTTAAT	60.821	20	239	101	339
CCGAGCCCTCTCTCTTCTCT	60.23	20	260	454	713
CAATGGTGCTGAAGTTGTGG	60.152	20	188	2	189
TCGTTGCCGAATCTACCATT	60.469	20	231	1	231
CGGGGTGTAACTTGCTTGAT	59.993	20	242	1050	1291
TTTTGAGGTGAGAATTGCCC	60.051	20	245	108	352
GTTATGCGTTTTGACGGGAT	59.829	20	280	995	1274
ACACTGAAACCGAACCGAGA	60.69	20	255	34	288
GCGTGACTATCCACCGTTTT	60	20	112	44	155
CACATGTACGCGCTCTTGAT	59.895	20	165	13	177
CAATCCCAATTAATTTCGCC	59.259	20	108	456	563
CACCCTCAATCACTCACACG	60.154	20	163	369	531
TCAAGGACGATGGCTTTTGT	60.636	20	191	598	788
TGGATGGTGTTTGTGGCTT	59.951	19	149	171	319
TGATCTTGGTGGGACAAGAA	59.059	20	201	12	212
GGTAAACGAGACCCAGCAAT	59.056	20	279	776	1054
TGTTCCCTGGCAGCTACTCT	60.012	20	240	400	639
TTGTAGGTTCCTAAGCAGCCA	59.89	21	260	104	363
CAAAGGCCCACAATGGTTAT	59.685	20	189	288	476
AGAAAATATCGGCAAGTGGG	59.043	20	179	16	194
AAATTGGGATTTGTGGCAAG	59.801	20	154	343	496
AGGACTCGTAAACGACACGAA	59.788	21	105	9	113
GGAGTTTCATGCCCCTTTTT	60.299	20	210	435	644
TTTTGCCCTCGAATGCTATC	60.175	20	197	688	884
TTCTTGCTGGGTCCTTTCTT	58.909	20	280	180	459
TCATTTGCAACCAAAATCCA	59.907	20	173	0	172
CGGAAATTATTTTTAACACCCG	59.633	22	256	587	842

CGTGCAATTAAATTCAAATCTT	59.476	24	251	216	466
TGCGTTTTGATGATATATAGGT	58.933	25	121	520	640
GAATAAACAACAATGAAGTGG	57.333	24	165	148	312
GAAAGCCAGCATTGAAACCT	59.316	20	257	81	337
TCGGGTTAAACAAACATAGATT	57.292	23	274	773	1046
TTGTTACGGAGATTGCCTCA	59.272	20	150	240	389
TGAAATTTGGCCTTGGAAAC	59.916	20	271	170	440
ATCATTTATTTCGGCAACGC	59.935	20	169	135	303
GTTTTGAACGGTCTGGTTCG	60.529	20	275	18	292
GAAGAACAATTACAATGTTTAT	57.771	26	190	89	278
GTACGTTGGAACACGTGGC	60.024	19	223	845	1067
TTTGCGAGGATTTTGGACAT	60.448	20	201	102	302
CAATTGGATAAGTGAGTTAATT	57.84	25	137	135	271
ATGGCGGTTACCTATCCTCA	59.41	20	206	13	218
TAGCACTTCTGCCTGGGTTT	59.875	20	276	562	837
TTTCGTGATTAAGCTTGCCC	60.209	20	280	6250	6529
ATTAAATGCGCCTCCCTCTT	60.061	20	155	186	340
GAATTGAGTTTTTCAACTCTAT	59.17	26	251	1547	1797
ACCCAAAAAGGGATAACATGC	60.068	21	241	1003	1243
ACCCGCATCACTTGAACTCT	59.727	20	239	9	247
ATGATCTACGTCCACGGGAG	59.95	20	266	182	447
TCAATTTGACGTGATTTAACGT	60.662	24	241	369	609
GACCCTTCACTCTTTTCCCC	59.912	20	274	148	421
GGAGGAATTGGGATTTTTGG	60.482	20	100	193	292
TCAAAGAAGGGTTGTGGCTC	60.232	20	241	45	285
TTTTCACCTTCAAATGTCGCT	59.738	21	219	453	671
CCTCCATGTTCCTCATCGTC	60.475	20	250	459	708
CCGCCATGTTTCGATGATTA	61.747	20	270	2175	2444
TCCCCATTTTTGATCACCTC	59.727	20	243	37	279
AAAGAGGCCGAGTGAAAACC	60.61	20	142	203	344
GGGGTTGTACTCGTGGGATA	59.67	20	264	86	349
TTTTCCGGAGTTCACCTCAC	60.088	20	280	149	428
AGGACTTCACAAAGGCCAAA	59.711	20	264	2280	2543
ACCACACGTGTTGGCTAGGA	61.572	20	279	1312	1590
ACCAATATTTTGCGGTCGAT	59.301	20	268	32	299
ATCTTGCTGCTCCAAGGTGT	59.874	20	130	161	290
GTTGTATTCGGGCTGGTCTC	59.556	20	183	210	392
CATGCTGCATATATAAATGTCT	57.652	27	100	107	206
AATAGATTGTCCCTCGAACGC	60.465	21	219	37	255
TCGGAGCGATAAGGAATCTG	60.309	20	274	9	282
GGCGTCGCTGTAATAGTCCT	59.364	20	181	328	508
CCCAATCACTCTCACCCATT	59.779	20	174	341	514
ACGGACTCCCTTCCTCAACT	60.111	20	239	92	330
ACCACTCACTTCCTCCGTCA	60.713	20	168	584	751
AGGGCATCACTAGAAAGCCA	59.836	20	223	33	255
TCATTTTCCGCACCCATATT	60.153	20	242	19	260
CAAATTGATTATGAAGAAATTG	58.222	25	272	575	846
GACATGGCTTTGCCCATTAT	59.791	20	239	394	632
AGCTAGGGTTTTTCTGGGGA	60.068	20	266	3	268
CACACACACTCTATAAAATGCA	60.501	26	230	304	533
GGTGGTTCGTGATGTCCTTT	59.827	20	245	840	1084
GAACGAGGAGAAGGACATGC	59.81	20	174	40	213
TTGTCCACTTTGTTTCTGCTG	58.96	21	102	311	412
ACCGCTTGTCTTCACCTCTC	59.455	20	195	7	201
TGCATATCTTGGTGAGTGTATG	59.897	23	150	331	480
TGGGGTTCTGCCTATCAGAC	60.073	20	221	193	413
TCATCGAATCACATGCTTGC	60.79	20	199	1469	1667
ACGGTCAGCCACTCAATCTT	59.727	20	245	53	297

TTGGGAGAATTTTCAACTCTTG	58.352	22	199	69	267
CACAAAGGCAGCACTTGTTC	59.49	20	246	7	252
AAATCAAATGGGAATGTCGG	59.622	20	128	24	151
TTCCTTTCCCTCCAAAACAA	59.518	20	253	811	1063
GCCTTTGCCTCTTTCTCTATTTC	59.886	23	123	159	281
CCACGGTTCCTTGGTAATTG	60.22	20	208	489	696
CGAGTGTGGAAAGGGAGAGA	60.377	20	158	59	216
TTCGAATTATCTTCAGGCCG	60.167	20	278	9	286
TTCCGGTCCAAACCAAATTA	60.16	20	244	119	362
CATTGCCAAAGTCATCCTCC	60.461	20	248	1	248
CGATACCATCATCCCAATCC	59.975	20	188	560	747
GTTTGGTCCGGTGTTGTTCT	59.867	20	264	247	510
GTTGAGTCGAGGAAGATCGG	59.803	20	130	688	817
ATTGGCAAATATGCGAGGAC	59.929	20	125	36	160
ATCGGTTATCACCGGATCG	60.697	19	197	273	469
CTCGAGTGAGACCGAAGTGAC	60.041	21	239	76	314
TATTCAAAGGGCATTTTCGTC	59.068	21	159	340	498
TTTTTATACAAGGGGCGGAA	59.429	20	149	72	220
CTCTGCTGTGAGCATTCGAT	59.143	20	138	69	206
CATGTAAGGCCCATAATCGC	60.31	20	132	699	830
TGATAACCTTGAGGAAACTTG	58.378	22	277	10	286
AGGGTGGGTTTGGAAAAGAG	60.332	20	273	78	350
AAATGCCAAATAAAGCTAAAT	57.912	23	153	2880	3032
CTATGCATGGGTTCCGTTCT	59.955	20	166	24	189
CAATGAAACATTGGCTGGTTT	59.853	21	143	80	222
TTTCGCCCCTTCTAGAGTCA	59.948	20	213	5	217
GGGTCAAGGAGGGTGTATGA	59.779	20	270	5	274
CCATGTTTGTAATTATTGTAGG	58.388	25	135	60	194
ACCTAGAACTGGCCTCACGA	59.867	20	166	65	230
GAGAGAGAGGCAGACATCGG	60.096	20	195	89	283
GGCCCTATGCATGTGAAGTT	59.962	20	267	433	699
TCACTCTCGAGCCTAACCGT	60.012	20	211	441	651
ATGTTGGAAACCCTTCCCAT	60.422	20	280	2976	3255
TTTGCCAATTTGAGCTCCTC	60.331	20	100	116	215
TGAGAACCCGGTTTGATTTC	59.91	20	241	6533	6773
CTTAGGGAATCGAACCTGGG	60.807	20	179	10	188
GAATCACACCAACGCCTTTT	59.978	20	168	4057	4224
AGGTTTTGACATAACTTAGGTG	60.129	27	120	0	119
AAGAGCTTCTGCGTCTTTCG	59.898	20	187	224	410
TGCACCACGTCATCTTCTTC	59.837	20	154	1190	1343
AGCCGAATGAAGGTGGAATA	59.528	20	176	10	185
AAATTGGCATTTGTGAAGCC	59.945	20	187	743	929
CCCTAGATGACAACCTTCGG	59.545	20	155	64	218
TTCTCACCAGTCTGTCAACCA	59.294	21	244	1008	1251
TGTGCGAGGAGAATCATCAG	59.942	20	171	0	170
AAATGAGGGCTGCAAATTGA	60.585	20	268	972	1239
CCTACCCGATAAAAATGGCA	59.789	20	265	134	398
TGGCTACAATACAACGCCAA	60.133	20	277	9	285
AAAATCGTCCCAAATCCCTC	60.131	20	172	2	173
TTCTGGTTTCCGTCAGATCC	60.05	20	153	85	237
GGGTTTTGCTGTCTTTTCCA	60.088	20	164	19	182
GGGGTTAAGATTTGGGGAAC	59.51	20	259	66	324
GTCATAGGCTTGGGAAAGCA	60.214	20	279	408	686
ATAAATGGTTGACGGCTTGG	59.823	20	227	233	459
CCGACCTAGCATAGTGGGAA	60.088	20	139	1527	1665
CCTCTGCAGCTTCCAAAGAC	60.134	20	152	1045	1196
CGCATCATGTTGTTGGAAGT	59.572	20	161	1060	1220
AATCTCACGGTCGGAACAAC	59.973	20	264	701	964

GTCACTTGCGGGTATTGGAC	60.384	20	148	44	191
AGTTCATTCAAAAATGTCGAG	57.927	23	207	689	895
ATTTTAAACTGACGGCCGAG	59.225	20	163	68	230
CATTGCGAGAATGACAAGGA	59.799	20	115	278	392
CCCAAAAATTGAACATATCGA	58.848	22	247	493	739
GGGCTGGTTTGTTTGTTGTT	59.875	20	173	249	421
AGCCTTCTAGCATCTCTTGCTC	59.42	22	109	302	410
GATGATGATTGCCCCATTTT	59.587	20	125	307	431
GCAAACGATCAATCCCTGTT	59.939	20	270	741	1010
GGTTAAAGATCAAACCAAACA	59.801	23	278	97	374
TCCGCACACATGGATAGAAG	59.673	20	198	898	1095
TTTGGATCCGAACATCCATT	60.133	20	234	1614	1847
CTTCGGGCATACTCCAAAAC	59.569	20	270	42	311
GCCATCCCAGATTTGAGAGA	60.158	20	219	12	230
AACCTCATTGCTCTCCGCTA	59.978	20	149	318	466
CGCCTTTATGTGACGTGGTA	59.609	20	257	2451	2707
TAAGACTGGTGGGAGTTGGG	59.959	20	262	200	461
GGCGGTGTTACAATTTCACC	60.235	20	276	86	361
CCGTCCAACCTCTACAAATCA	59.978	21	233	496	728
CCAAAACCCCTCGTACTTCA	59.964	20	279	349	627
GGACTTTTGGCCTTTGTAACC	59.864	21	173	332	504
TCTCACGTCTCACACCCTTG	59.864	20	254	16	269
CGTGTTCTATATTCCCGTATCG	58.543	22	101	957	1057
TTGACCACAGCAGTACGACC	59.751	20	214	327	540
GGGACCTTTCAGTCACCAGA	60.088	20	138	318	455
CATGTCACAAGTCACTCGCC	60.319	20	207	211	417
GGCGAGCCATATGTCATTTT	59.929	20	237	3480	3716
TGTGGATCTTGGTTTGGTGTT	60.262	21	254	205	458
GAGCATCAATCTCCTCCTGC	59.917	20	141	45	185
CCCAACTGTTTCAGCCATTT	59.971	20	237	429	665
TCATCGACGCCATATCTTTG	59.646	20	142	475	616
TGGAGAGGGTTGTTGGTGAT	60.363	20	104	104	207
GGGTATTTATGATATTTCCAAC	57.935	26	238	1	238
CCACTAGGGGTGGCAATCTA	59.948	20	226	1238	1463
GGGCGAGTTAAGCTCGAATA	59.456	20	243	23	265
GAACTCAAACTGGTTGGGGA	59.943	20	246	331	576
TTTATCCATGGCGCATTTTT	60.282	20	165	107	271
GCTTGATTTTCCTTCCTCCC	60.017	20	168	21	188
CCAGTCCGGTCCAGTCTAAA	60.103	20	266	32	297
GGTTGAGAATGGCGAAGAAA	60.192	20	275	41	315
TGTTTTCTAAAAATAGGACACA	59.056	25	236	143	378
ATCAGGTCGTTGTGGTGTGA	60.005	20	144	34	177
TGCGCCTCCTTCACTTTAAT	59.845	20	277	73	349
AAGTTGGTTTCCCACAGACG	60.005	20	162	114	275
TCCACTTGCAGCATTTAACAA	59.359	21	176	486	661
TTGGACAAAAGTACCAGGGC	59.971	20	274	1491	1764
TGTCATCTCCGAGCTGTTTG	59.984	20	271	1522	1792
GCACCACACCGAACTCAATA	59.572	20	208	37	244
TCATATGTCACGTTAAGACATG	59.406	24	229	376	604
GACGACAACGTTGGTGTTTG	60.049	20	185	957	1141
CCATGTGTATGCTGCTGGTC	60.144	20	188	323	510
AAGAACTCCCTTGGGTGAGG	60.48	20	152	28	179
GCCAACGCAAATCCTAACAG	60.637	20	258	1082	1339
GGGGGAAGGAGAAGTAGTGG	59.928	20	190	31	220
GGATGTCCGAGGTGGAGTAG	59.53	20	183	338	520
AGACGGAATACGATTCGGAG	59.15	20	274	1	274
CCAAACTCTCGTCTGGTCCT	59.3	20	190	213	402
ATCTCTTTTATCATCGCCGC	59.281	20	136	21	156

CTCTGTCACCCCAGAAAACC	59.549	20	102	1576	1677
GCCCTCATGACTCTCAGCA	60.088	19	280	824	1103
AACACCTTAAAATGTCGCCG	59.996	20	222	77	298
CATGTGTCTTATGTTCGCAGG	59.209	21	237	2509	2745
GCTACCCTTTTTGACCTACGG	60.008	21	253	27	279
AGTCGTCGAGATTTGGCAAT	59.7	20	227	48	274
GAGTTTGGGAGTTGAGCTGG	59.844	20	230	568	797
GCGGAGTTGCTGTTTCAGTT	60.44	20	274	5190	5463
GGGTCTCGCATAAAATGGAA	59.901	20	142	1101	1242
TCAAAGGCCCACAATGGTTA	61.254	20	111	17	127
TCCCCAGTGTCACACAGACT	59.113	20	121	3	123
AGTGACCACCCAACCACAAT	60.135	20	216	66	281
CCACAAAATAGGGGGAAAAA	58.781	20	174	233	406
CTCTCATCTCTCTCACCTCACC	58.06	22	255	142	396
TCTTATGCCAACAAGACGAAA	58.426	21	178	25	202
TATATGCTCGCGTTTCATGC	59.832	20	146	272	417
AGCAATGTTGTTGGGTGGTT	60.277	20	136	1117	1252
ATTCATCAATGCTTACCCGC	59.929	20	207	15	221
AAATCGTGTTTCGTGCATCA	60.119	20	126	296	421
CTCTCTCTGTCCCCCTCTCC	60.336	20	179	81	259
GATTTCTTTGGGCAGAACCA	60.051	20	256	608	863
GTCGTCATCCATGGTCTGTG	59.962	20	118	6	123
GGTCTTTTGTGTTAACATCATG	58.553	23	206	309	514
TTTGGCTATCAGCTGTCCCT	59.836	20	267	155	421
GACGGAGGTGATTCTTTGGA	60.05	20	186	260	445
AAATGAAATTGATCATTTGAG	57.621	23	253	56	308
AGAGGCAACTTGGGAATTGA	59.67	20	274	2324	2597
TTGACCGGATCGAAGCTCTA	60.874	20	266	406	671
CCTTCCTTTTGCTTGTTGGA	60.22	20	177	98	274
TCACCATAGGATTCTCTCAATC	59.615	24	275	12	286
GGGTTCCCACGTCATAAAAA	59.662	20	104	1412	1515
TCTGCATTCTTGCATATCGG	59.792	20	161	1287	1447
CTCAGCCTTATCTCTTGCCG	60.11	20	197	16	212
AATGGCTGTGGAGAATCCAG	60.073	20	209	181	389
CTACGGTTCCAAATTGCTCC	59.569	20	247	357	603
AGAACTTCGAAGCCTCCAGA	59.162	20	276	76	351
ACGCCAGCCTCACTCAAAA	61.934	19	131	3	133
GTTCGTGTGCGTGAGAGTGT	59.948	20	229	705	933
ATTTACGTCACCCCTGCATC	59.82	20	230	246	475
TTACGATATGTACCGTTCCCA	57.913	21	187	36	222
ACCACGGGACCTAGTTCAGA	59.574	20	259	8	266
TCGACCTCGTGCTAATGATG	59.823	20	216	193	408
ACGGATCGGAAATCCATAAA	59.23	20	197	990	1186
GCTAATTCGGCAGCTTCTTG	60.117	20	186	7	192
AGCAGTTGCGATCAGCAGTA	59.77	20	141	328	468
GCACAATTAAATGCGCGATA	59.705	20	170	132	301
CTGTCTCTCGGGGGATAAGC	61.115	20	113	1595	1707
GGTATCAGAGCCGAGGTTGA	60.218	20	147	7	153
CTACAAAATGCGCGAGATCA	59.976	20	212	3423	3634
CATGTTGCTTCACATGGGG	60.952	19	233	398	630
CCGTTGAGCCGAATGTTTTA	60.989	20	279	45	323
TGTGTGTGCTCCAATCTGCT	60.473	20	212	790	1001
ACGAAATTGCCCTTGTATGC	59.967	20	202	85	286
ATCCTCCCCTTGCTGAAAAA	60.929	20	258	1	258
CCACTCCAAACCACCCTTTA	59.824	20	128	108	235
TGGGCAGAGTAAGGAATTGG	60.066	20	221	1857	2077
ATGCTATCGATGTGTTGGCA	60.104	20	198	246	443
TGGATTTGCAGTGTTCTTGG	59.691	20	156	2347	2502

CAACCATCACGAAATGCAGA	60.665	20	266	1280	1545
TGAAATTTGGAAATAAGGAGG	59.382	23	105	683	787
TCTTTCAGCACAAATGCGAG	60.134	20	239	3335	3573
TCCAAATCTGAAGGCCGATA	60.544	20	271	907	1177
CATGTGGACCATCGATCTTG	59.918	20	182	4	185
GTCAGACCAGCTCCCCTTC	59.783	19	226	968	1193
TTGACCAAGGTGAGAATTTGA	59.587	22	118	125	242
TGGATTTCATCATCAAGTCTCC	58.984	22	208	51	258
AACGGCAGCTTCTCTCATGT	60.02	20	214	816	1029
ATTGATTGTTAGCGGATGGC	59.929	20	227	827	1053
GCGGTTATACTATTCTGGCTTG	59.677	23	222	13	234
AAAATCTCAAACCGTGAGATG	59.645	23	187	962	1148
TTTTCCGTTTGAACTTTTCATTT	59.098	23	279	194	472
CGGATTTAAAGGTTATTACCTG	58.157	25	224	888	1111
GCCTTTGCCCCTTTCTCTAT	59.688	20	271	77	347
TTTCCGAATATGAAAACCGC	59.907	20	258	103	360
TGGATATGGTTTTTGCAGGG	60.692	20	169	88	256
TCGTCCAACCAAATTGTTGAT	60.22	21	276	599	874
TGACAATGTTATCGATGGCG	60.488	20	170	4	173
GGAAAACAGAGCACCCCATA	59.933	20	150	2171	2320
TGTCGAGACAATCGTGGAGA	60.402	20	243	468	710
GGGTTTAAAATAGCGCGTTG	59.624	20	159	323	481
AATTAAGATTTCGGGAAATTA	57.21	25	247	163	409
ACCAGTGCACATCAAAATTCC	59.851	21	189	11	199
GCAACTCCAATAAAGAATTTG	59.512	23	253	26	278
CGAACAAGGGAAAACAATGG	60.336	20	263	277	539
CAATCAACATGCAAGCATCA	59.232	20	174	24	197
AAACAGCCGTTATCAGCCAC	60.14	20	247	87	333
CCTTGGCTATAAAAAGGGGC	59.93	20	216	477	692
AGCGGGTAAATATCAGTTTTTG	59.101	23	238	191	428
TTTGTGATGCTCCATGCTTC	59.805	20	263	283	545
ATTCAAGGGTTAGGGCTTGC	60.451	20	188	195	382
AATTGAATGGCAAGGATTGG	59.762	20	148	2152	2299
TGGAACTCTTCTTCATCGCA	59.522	20	208	104	311
TGGGTTCAAAGGGAATTCTG	59.903	20	272	57	328
CTTCGGACAGCAAAAACCTC	59.853	20	230	238	467
CTGGAAGTGCGGTAGAGAGG	60.005	20	116	561	676
GTACGGTTGCTCATCAGCCT	60.285	20	276	1879	2154
TTCCCACCGAAAGCTACAGT	59.734	20	254	2060	2313
CTCTGAGCTTGGGAAACCAG	59.982	20	101	372	472
CCCAAGACCCCAATTTGATT	60.91	20	247	394	640
AGGAGTGTAATCAAATGAGAG	59.329	24	179	67	245
TTTGTGCTTTGTGTTGGTGG	60.587	20	246	487	732
TGTTTCATGTGTCCATGTTTCA	59.864	22	231	2571	2801
AGATGAAACTGCGTTCCCAC	60.119	20	248	530	777
ACAGGAGGGTTCACACAACC	59.859	20	170	53	222
TGTACTGCATAGGTTGTTTCAT	59.58	24	270	243	512
TATGTTTTTCGGATCCCTTCC	60.137	21	229	10	238
AGTGGGGAGCCTTACCTTGT	59.994	20	258	187	444
GCCCAAATAAGTTGGAGTGG	59.429	20	219	9	227
AGGCCTAAAATGCAAGCTCA	59.982	20	190	2092	2281
CTACCTATGGCCTGCTTCCA	60.227	20	237	2553	2789
ATTCCAATTTCTTGCCTCCA	59.505	20	241	632	872
CCGGGGTCAAGAACATGTAG	60.366	20	171	1366	1536
TTGTCTCCCACATTCATGGTT	60.225	21	179	632	810
AAAGCCTACCTTGCTTCCGT	60.262	20	234	34	267
GTCTTACCGGAGCTTGGTTG	59.734	20	261	23	283
TGTGGATGAAATTTGGAAGAG	59.546	22	272	10	281

TCACCAAAATCTATAGTTATCA	59.412	27	168	344	511
GGAGGAGCAGCAAGAACAAG	60.134	20	257	770	1026
AGAACATCAGCGGGCATATC	60.066	20	172	237	408
ATTTCTCACTGACTTGGGCG	60.255	20	103	195	297
TTGTGTGTGTCCAGTAGGGC	59.597	20	277	788	1064
TTAAACCCTAAAAACGCGCA	60.593	20	280	322	601
ATGCAGTGGATTTTTGGTGA	58.976	20	214	1637	1850
CGGCCGTGTAGTTAACCATT	59.883	20	241	80	320
AAACCCAGTAATCTCAGCCG	59.195	20	117	9	125
TGTTTATTGACGCGTTTTGG	59.603	20	227	134	360
TGACGTGGCATTTTCAGAGA	60.39	20	186	95	280
CTTCGTTTGGCATGTTTGTG	60.149	20	268	296	563
CATTGTACTACATGGATGAATG	60.03	26	221	390	610
TTGACGTTTCACCTAACCCAC	59.883	21	208	258	465
ATCACAGCAAGACCTCCACA	59.261	20	280	234	513
TGAAAATCAAAAGGCCCTCA	60.555	20	142	3020	3161
CGCTTCGGACAAATATGACA	59.688	20	213	466	678
TATTTCGAGAAATGGCACCC	59.901	20	275	141	415
TGCGTTTTGACAATATATAGGT	60.083	26	234	2845	3078
CCACCTCAACCCTCATCTTC	59.505	20	271	775	1045
CGGAGTAGATCTCAACACGC	58.47	20	238	43	280
TAAACGCCGGTGAGGTAATC	59.96	20	175	277	451
CTTAAACTTCAGCCCGTACCC	60.008	21	230	0	229
TCGAAACACATCCCCAAAAT	60.17	20	221	352	572
TCAACCTCGCAGATTGATTC	58.799	20	107	1216	1322
AAAAACCAATGGTGGAGCAA	60.344	20	237	896	1132
CTCAAATGCTCGAGGGCTAA	60.481	20	212	138	349
TTGATCGATTGTTTTCTTGGC	60.067	21	149	666	814
GCAATAAGTGAGTGACTTCCC	60.004	22	236	0	235
TTGTGTTTTTGAAGTGTTATGCC	60.082	23	213	59	271
TGAGTTATGAAGTGTTATGAAG	59.11	25	167	174	340
AAGCCGATCGAGTTTGTCAG	60.397	20	177	29	205
CACTCTCCTGCTCCAGCTCT	59.883	20	185	25	209
CGGTTAGTCCAGCCATCTCT	59.308	20	188	171	358
ACCAATGGTGGTATGGTGTG	58.984	20	101	18	118
ATTTCATTTCATGGGTTTCG	57.399	20	177	45	221
TGCGCTAACAAGGTCCCTAT	59.73	20	151	214	364
TTGAAGATCAACGGTCCACA	60.088	20	163	61	223
TGGGTTGAAATGTTTACATGG	58.254	21	194	152	345
GAAACGCCACTTCAAACCAT	59.978	20	121	307	427
CACCAAATTTGAGGGTTATTAT	59.905	25	258	189	446
TTACGGATTTAAGGGTTATTAC	59.633	25	215	36	250
TGAAATTAGATTCGAAATTGCA	57.936	24	184	151	334
ACCCAACACAAACCCAAAAG	59.728	20	267	535	801
CATTCTCAAGCCACTCCCTC	59.803	20	149	116	264
CCGGTTTCGTGAGCTTTCTA	60.378	20	239	31	269
ACAATTTCCCCTTGGTGATG	59.647	20	136	680	815
ACGGGAGAGGCATACAAATG	59.955	20	211	2142	2352
CGATCACACTCCAAATGCAC	60.12	20	242	768	1009
CGAGGAGCGTGGTTTTAAGT	59.378	20	182	35	216
TGGAACCATGGGTAAAACAA	58.719	20	228	141	368
CCACACGACATACGATACACG	59.92	21	127	245	371
ATGCAAACGGGATGTCAAAT	60.199	20	247	2095	2341
TGTTACTTTTCATCGCACTCAA	58.489	22	240	1258	1497
TGCGTGATTTACACCCGATA	59.953	20	115	180	294
CGGTGATCGTAATCGGAGAT	59.917	20	208	36	243
TGGAATGGGGATTTTTCAAC	59.599	20	224	48	271
ACTTGTCCACCCACATGACA	59.846	20	238	1126	1363

CCCATAAACAATCCCCTCAA	59.617	20	236	1148	1383
ACCCAAGATTTTTGCCACAG	59.971	20	272	102	373
TCACTCGCGCTAGATTCTCA	59.847	20	130	271	400
TTGATTCTGGAATATCCCGC	59.862	20	242	2	243
TCGTTGTAAACCCGTAAGGC	59.996	20	225	76	300
CATCACACAAAACCAGTGGG	59.848	20	196	290	485
CCGGTATGCTGACGATAACA	59.566	20	253	1001	1253
CATCACCAAAGACAACCACG	60.001	20	261	189	449
CAACATGACAGCAACCCTCA	60.722	20	238	7	244
ACACTAATATGAAGCGGGCG	60.117	20	133	6	138
GAGATGGTTGCACCATAACG	59.002	20	201	42	242
TTTGTGACGAGATCATGGCT	59.245	20	169	99	267
AAATATTTCTAGCACATGAAAT	58.583	26	114	1	114
GGTTTTGACCATATTTACTGTTT	59.631	26	188	278	465
CATCACGCTTGCCCTAATTC	60.606	20	190	100	289
GACTGTGGACTCCGGTTCAT	59.969	20	219	87	305
CTGAAAAGCTTTGAGTGTGCC	60.045	21	159	657	815
TTCGTTATACAAATATCAGGCA	59.061	25	157	693	849
CAGCATATTCTTTGGACGGAA	60.081	21	242	129	370
ATCGCTCCACATGACACGTA	60.144	20	245	130	374
GTTGGTCCATTTGCCATTGT	60.624	20	218	46	263
TGAAATTGTCATCTCCCCCT	59.336	20	212	68	279
TCTTTTACTTTGCATGCTACTTT	58.354	25	279	275	553
GTCTGGAAAGATGGTGGCAA	61.046	20	280	248	527
GAGGGAGGGAGGAGAGAGAA	59.883	20	218	244	461
GAGACCCGGGTTTACCTCTC	59.935	20	135	85	219
ACCATCGTTACCGATTTCCA	60.192	20	192	33	224
AATCAACACCATTCAACGCA	59.972	20	280	91	370
AAAAACCCTGATGTGGATGC	59.797	20	272	29	300
TTGGACCAAAATAGCCTCCA	60.439	20	167	9	175
GATTTCCACTCCTGCTTTCG	59.813	20	268	3	270
CCAAGTCTTGCATTTGGTTGT	60.023	21	217	1568	1784
CTTCCCCAACTCAAGGACAC	59.549	20	260	356	615
GAATCATGCTACTACACGTCG	59.803	22	262	493	754
CCCATTAATAGCGATATATGTA	58.562	27	144	147	290
TGGACATGGACACCTAACCC	60.634	20	253	49	301
TTACCGCTGGGATCATTTTC	59.901	20	251	28	278
AGGATGGGTTATCACTTGAATA	59.65	24	103	153	255
AATCCCTTCATAACACCTCCTT	58.028	22	274	352	625
CCCTCCAAGGAATCTGATGA	60.003	20	157	96	252
CAAGAAGTCCTGCGTCAACA	60.025	20	151	23	173
AGGGATAATTAATGCGATTGT	59.726	23	275	540	814
AATTGAGATTTTGCCCATCG	59.901	20	136	47	182
GCTCCTTGTGCATCACTCAA	59.992	20	261	233	493
GAAGTCTCAAGTCAATGTATGA	57.445	25	116	569	684
AGAACGGAGAAAATATCACGA	59.175	23	238	576	813
CGCTCCACAAAGATCTCACA	59.984	20	200	781	980
TCTCAGCTTCCCCACCATTA	60.594	20	271	1772	2042
TCTTTTTGTTTGTGGCATGG	59.561	20	277	293	569
TCGCCTTGCTAGTTGGTTTC	60.386	20	182	29	210
TGATGAGAGGCATGAAGTGG	59.787	20	141	77	217
TGCATCAAACGTGGAAGAAA	60.234	20	222	2	223
CCATTTCACCACCTCCATTC	60.173	20	276	65	340
TCGGTCCACTAGCACAATGA	60.263	20	234	103	336
TGTGGAAGGGTGTGTGATGT	59.846	20	276	1386	1661
ATGATCTTCACCTTAAATCTGCA	58.248	24	260	70	329
AGTTTGGGGGAGGAGAAAAA	59.912	20	278	66	343
AAGGAGGTGTTATGAAGGGAT	58.028	22	147	161	307

AAGGTTGGAGAGGGGACAAC	60.349	20	222	12	233
GCTCGACGGAGGTTTGATAG	59.836	20	159	395	553
ACCTCAACAAACCACCCAAA	60.246	20	205	25	229
AAAATCACTAACCCACCCCAC	59.969	21	191	34	224
TATCCTCCCTCATTCCCTCC	60.228	20	258	318	575
GTGCCCCTGCCCTCTATATT	60.307	20	249	1144	1392
ACCTATGGTGGTATGGTGTAG	57.448	23	221	393	613
TTGTGAGTGAAAGTGGTGGG	59.565	20	217	617	833
AAGGAAACCCATTGTGGTCA	60.21	20	241	2392	2632
GTCCATGAGAAATGGGGTTG	60.173	20	183	32	214
TGCACAATACAAGCACCCAT	59.995	20	188	815	1002
TCTCGTGTTTTATCCTCCCC	58.981	20	108	4	111
ATGGTGGTTTGGTGGAAGAA	60.21	20	171	618	788
ATTATGGCGCCGCTATTGTA	60.452	20	220	185	404
CATTGCCTGCAAATCACATT	59.548	20	143	243	385
TCCACGGTGATGCTAGAGTG	59.855	20	219	445	663
TCCGTTTCGAACCTAAAACTG	59.254	21	221	3	223
TGTTCTGAAACATGATGGCG	60.665	20	241	1371	1611
CCAAGTCAATTGTCGATGGTA	58.488	21	269	815	1083
AGCTTCCATGGAGGTTGATG	60.073	20	222	180	401
TGGAAGCACTTTTTGAACGG	61.165	20	255	395	649
TCAGCCGACTTTTTAATGGC	60.209	20	166	63	228
TTTTTAAATGGACGGTGATGAT	59.616	23	117	14	130
TCCCTTTCTCCCAACCTTTC	60.414	20	152	566	717
CAGCAGAGCAAAAGGGTCTT	59.615	20	264	1757	2020
GCATAAACACATACCCTCACA	59.677	24	215	24	238
GGGATGAGTTATCACTTGAAT	59.765	25	158	348	505
ACCTATGGTGGTATGGTGTGG	59.463	21	249	214	462
CCTGCCTCAAGGCTAAACAA	60.378	20	250	44	293
GAAAATTCCATTTTGCAGGG	59.388	20	164	751	914
CATGAAAATCATGTTCCGCA	60.466	20	243	228	470
TCCAAAATGGTGCAGTCCTT	60.495	20	203	423	625
TGATGGATGTTGGATACACGA	59.79	21	142	177	318
ACAAACAAGACCAAGTGGGG	59.861	20	220	195	414
ACTTGTGTGGGGAATGGATG	60.634	20	271	364	634
ACCGACGTGGCCTAACATAG	60.015	20	254	247	500
CAAATGTTGCACAATCATTGA	58.945	22	218	70	287
GTTTGGATATCGAGATCGGG	59.344	20	149	64	212
ATCATAGTTGACGCCCTTCG	60.096	20	104	18	121
CACAACAATTCGCGAAACAA	60.677	20	223	79	301
AGTTGACTGCTTTGGCTTGG	60.431	20	231	1103	1333
TCGGAGTTCATCATGACACAA	60.104	21	191	341	531
TGTGGTTCGATATTTTGTTTGG	59.736	22	148	192	339
ATTGGCTTGCTGAACCAGAG	60.397	20	270	679	948
TCCTAACTTCATAACTCGAAG	58.246	25	279	0	278
ATTAACCGTGAAAATGGCGA	60.323	20	195	290	484
GCAAACCATACACGAACACG	60.035	20	227	85	311
ACAGGATGGACTCGAACGAA	60.656	20	145	9	153
TTTGTCACAGTATTTCATCATT	59.826	25	192	4755	4946
ACCGTCTGCGCTGTAGATTC	60.428	20	136	259	394
TATCACCCGCCGGAGATTAT	61.537	20	280	83	362
AAGGCCGAGATTTGTTAGAGG	59.733	21	184	1779	1962
ATGGCTTGGAAAAGATGGTG	59.933	20	270	926	1195
AAATCCTGTCAATGAAAAAGC	58.742	22	272	89	360
GCTTTGCCTAGTCAATGATGG	59.722	21	164	368	531
TTGCAATGGACCTAAGCATTC	60.089	21	192	874	1065
AGGTTGATCATTTCCATCGC	59.9	20	273	925	1197
GAGATTCCAAGTGCTCTGGC	59.957	20	258	637	894

CACCCATTCATTCCCTCATT	59.605	20	100	146	245
GATTGAGCGACGGAGTTTCT	59.434	20	219	13	231
AGTTGGAGCCCAACAAATGA	60.495	20	279	2124	2402
TCTTCCCCAAATTGGTTTCC	61.023	20	139	247	385
CCCCAAACGAAAATCAAGAA	59.91	20	217	484	700
CATGGAATGGCTGTCAGATG	60.072	20	107	19	125
AGGACGAATATGCCCTTGC	60.051	19	190	2	191
AAAAGAAAAGAAAGGACCGA	59.282	22	245	17	261
GGCTACGAGAAATGGATGGA	60.036	20	148	701	848
GAAGGCATCAACGACGTGTA	59.722	20	113	69	181
TCCCGTCTAATCTCCACAGC	60.218	20	237	20	256
TTGTTTGACGGAAATGACCC	60.734	20	264	253	516
GCAGCTACGTTTGTGTGCAT	59.942	20	177	1181	1357
AGATCCATGTTCATCTCCCC	58.741	20	152	65	216
AGATGATCACGATGAAGCCA	59.197	20	173	77	249
CCATTCTACAAGAACCCCCA	59.784	20	201	727	927
TTGTGTACCCACATCCTCCA	59.806	20	180	364	543
CACTATAGGAGGCATTATCACT	59.949	26	275	349	623
CATATGGTGAATGCCCCTTT	59.645	20	187	230	416
TCGGCGTGAATGAACTTACA	60.257	20	277	660	936
CTGTTGGCCGTTGTTTTACA	59.627	20	256	1083	1338
CATTGACACGCGAAAAATGA	60.644	20	280	145	424
GCTTTCTTTGCGAAAAATGAT	58.509	21	250	29	278
TATGGAATTCCGACGAGCAT	60.435	20	274	480	753
TGTGCAACTTGTCTGGTCTCA	60.494	21	201	640	840
CAGTTCTGGCCGTGCATT	60.84	18	205	660	864
TGGAATCCGAGAAAATCAGG	60.006	20	190	895	1084
CCTCCGTATTTTGGGTAGCA	59.953	20	204	1000	1203
ATGTGCGCGTGTACTTATCG	59.782	20	272	585	856
TATTGGGGGAAGAAGCACTG	60.066	20	155	2096	2250
TTGAATCCATTGGTGAAGCA	60.049	20	200	222	421
GAGAGAAACATTAATTCCTTCA	59.9	25	181	47	227
AAATGGGTGGTGGAAAGACC	60.979	20	279	0	278
AATCAAAATAGGGCAGGGGT	59.666	20	214	31	244
CTTTTGCTGTGGCTTGTGAA	60.027	20	255	203	457
GCCGGTCATTTGTCTTTTTG	60.481	20	166	2796	2961
TACAGCCGCTCTTGGAACTC	60.538	20	125	74	198
CTCCCTCACCTCAGGATTCA	60.191	20	207	188	394
CCGTGTATTCTCATCCGCTT	60.096	20	276	3289	3564
ACCATATTTAAGGGTTATCACC	57.552	24	276	256	531
CACTTGCTTCTTGTGGGGTT	60.149	20	188	1179	1366
TGGAGGAAGGTGACAGTGTG	59.705	20	261	249	509
AACCGAGAAAGAAACATTTCA	57.914	22	200	1102	1301
TTGTTAGTGCGTGTTTTGGG	59.627	20	181	27	207
TAGAAGGGCCACTGTTCCC	60.058	19	229	20	248
TCTTTTGGTTGGTGAAGGAAA	59.573	21	164	290	453
CCTTGTGTGATCAAGGGTCC	60.363	20	245	1702	1946
GCTAATGGTGCCACAGTTGA	59.722	20	263	38	300
ATCAGGGCTTGAAACCGAAT	60.826	20	272	97	368
AACTTCTTGCTGGTTGAGGC	59.478	20	262	49	310
GGTTATCACCGGATCACGA	59.311	19	207	603	809
ACTCCCTTCCCCATCTCAAT	59.755	20	279	1191	1469
GTTAGCATGGGAAGGGGAGT	60.328	20	205	400	604
AGGAGCTTAGGGGTGGAATG	60.455	20	110	263	372
CCGTACCCACTTTTATGGGA	59.679	20	198	11	208
TTTTAACGAATAAACATGTTCC	57.778	24	107	103	209
TTTTCACGAATAAACATGTTAC	59.098	26	274	131	404
ATCCATCATCTTCCGTGAGC	60.042	20	189	716	904

GGTTTTCAACCCATGTTTTTGT	60.001	22	273	1565	1837
CTTCCGCGCGTATAGAAATC	59.838	20	162	1032	1193
GGTTATTAGTTATTACGGATTT	57.055	27	115	327	441
TCCTTTCTGCAAACTGACGA	59.566	20	272	91	362
TCCCTTGTCACACCACACAC	60.479	20	101	440	540
TCTTCTCAAGTTGACCGAGTGA	60.028	22	251	3285	3535
CGAGAAAACTTATGCGGTGG	60.628	20	232	941	1172
TAGCATCAAAACATGGCAGC	59.839	20	206	9	214
CCGGATCAGCTCTCTTTCTC	59.116	20	180	1608	1787
TCTGTCGTCTATCACCTTCCG	60.262	21	193	63	255
TTGATTCCTTTTGTTCCCTATTT	58.142	23	183	312	494
AAGGGAGCTTCAGTCTTTCATC	58.991	22	120	14	133
TTAGAGTTCCAAGAGGGGGC	60.569	20	203	5	207
TCAACCTCACTCGCAACCTA	59.44	20	260	418	677
TCTACGACCGAAATTCACTCC	59.184	21	105	22	126
ACGAACAAGGGAAAAACAAT	58.983	21	127	90	216
AAGGGGAGAGAGGTCAATGG	60.447	20	265	425	689
ATCAACTTTTGACGGTCCGA	60.495	20	275	146	420
CACGAACGATTTAGGATCGG	60.46	20	233	201	433
TTCTGACTTTGTTTTTGTGCAG	58.135	22	197	26	222
TGACTTTGATCAAGTGATAACA	60.287	27	174	386	559
CGGATAATCTGAAAGCGAAGA	59.442	21	262	1083	1344
ATGCAATCACCAACCAACAA	59.823	20	242	478	719
CATGTCAAAAATGCCCCTTC	60.309	20	267	484	750
CCCTCCTCACCTCCTCTCTT	59.801	20	265	931	1195
ACCAAAATGGAGAGGAATAAT	57.132	22	280	31	310
GACGAAGGAACAGCTTCACC	59.851	20	268	2765	3032
TTGTGTTTCGGAGTGTTTGG	59.585	20	249	150	398
CCACTCCACAAAGATCTCACA	59.622	22	104	212	315
ATGTCCGTCGTTGGTTCTTC	59.973	20	174	23	196
TGCAATGCTTCAATTCATCC	59.628	20	230	0	229
ATTTGCCATCCAATTTTCCA	60.132	20	266	16	281
GAGGGGAGTTGTTGGGTAAA	58.884	20	276	620	895
TATGTTGGCGAACACAGGTC	59.572	20	164	169	332
TCCCTTTTCCTCTCCCATTC	60.38	20	144	245	388
TTGAATGGTTATCACCTGATCG	59.823	22	128	107	234
GGAAATTACTTACAGCCATCG	59.864	22	176	295	470
GAATCCATGCAAACAGCAAA	59.67	20	152	2340	2491
AATGCGCGTTTTTAGGGTTT	60.825	20	152	394	545
CATGTTTGGTGACTTGGTCG	60.001	20	253	7	259
CCTCAACATCCAGGAACCAC	60.363	20	271	225	495
CAGCCCCCATTTTTCATTTT	61.011	20	147	253	399
TCTGCAGTCTCCGTTTTTCA	59.566	20	218	326	543
CAAAACTCCACTCCTCCGAA	60.224	20	257	298	554
GGACCGGACCGTTAGGTAAT	60.074	20	276	220	495
TGGTTGGAGATTAAAAGTGGG	58.936	21	211	148	358
GACGAGATTTAGGTGTTTTGAC	59.059	23	134	391	524
ATGGTGGTATGGTGTGGAGG	60.51	20	190	167	356
GAGCGAGTGGTTGTGAGGTT	60.307	20	118	189	306
CGAAAATGAGCTTCCACACC	60.636	20	241	162	402
TTTGATTCTTGAGTACACCATC	59.144	23	172	56	227
TGAGTTACCCTTGAATCACCC	58.898	21	226	20	245
TTATGGTACCAACGCCAACC	60.617	20	250	74	323
TTTCATGTTTTGGAGCATGATT	59.456	22	210	302	511
CGTTCCTCTCTCTCTCGGTG	60.127	20	169	58	226
GGCTTGAAGAATGATGAAGAT	60.576	23	113	132	244
CATCATTGTTTCGCAAGCAG	60.401	20	210	1006	1215
TGTGGATTAATGTGTATCCCGA	60.074	22	183	698	880

TGAGAGAGATGGGATTTTAGAT	59.539	25	231	303	533
ATGCGTTTTGACGGGATTTA	60.323	20	112	209	320
CGGCCGGTTTGTAACCTT	60.883	18	259	2166	2424
TGCACCCTTTGACATCAGTT	59.139	20	181	49	229
TTTTTGTTTGTTCCCAGGTTG	59.862	21	102	24	125
TCGTGTTCCGATCCTAGCTT	59.836	20	218	16	233
AGCGGAAGGCATTTAAAACA	59.72	20	167	41	207
TGGTGTGTACTTTTGTAGCAAT	59.618	24	195	170	364
CAAAAGAGCTGTGGGAGAGC	60.134	20	195	107	301
GATGATGCATGTATACTATCAA	57.305	26	246	1335	1580
GGGAGGGTGGTTTGGTTAGT	60.088	20	259	24	282
TCACACTCACGCACTCACAA	60.07	20	122	2	123
TCGTAGCATGATTTAAATGGTT	60.136	25	241	575	815
CCAAGTGCACAAGTGTTTCC	59.187	20	274	295	568
ATGATTGGGACACGTGTTTG	59.267	20	277	1537	1813
GTGCAGTAGGGGTTGTCGTT	60.035	20	231	104	334
AAGGAGGTGTTATGAAGGGAT	58.028	22	132	808	939
CGCACAATTATTGCGAACTC	59.329	20	131	62	192
TACGAAGGGTATTTTGGGAAA	58.483	21	180	208	387
TAAACCGTCACCCCAAAACA	61.145	20	124	53	176
ATTCCGTCGACAAGCTCAGA	60.945	20	193	4	196
TGTATCACACAACGGTTCATCA	59.888	22	244	243	486
TAACCCATAATCCCCACCAA	59.872	20	120	53	172
GGGTGGTTATGGTTTGTAGGTG	60.385	22	176	1332	1507
CTCCGCCTTGACTCCTTCTA	59.569	20	110	307	416
CGACCAAAATTTAAAAGTCCTA	59.842	25	272	834	1105
TGTGGATATGTAGATGATTTTT	59.637	25	179	16	194
GGAGGTCAGGATCTGGTCAA	60.048	20	159	800	958
CCCATCACACTAACCTCCCT	58.866	20	260	150	409
AAATATCGGCCGTCAGATTG	59.923	20	188	2	189
CAAACCTTGGCACTTGCATA	59.729	20	103	91	193
TTGTGGACAGTGCATAGGCT	59.318	20	237	108	344
ATGGTGCATGAGACGAGAAT	58.1	20	164	177	340
AATTGGAATTGGAACCAGCTT	59.828	21	274	88	361
GAGAAGGTAGGGGGCTAAGG	59.191	20	201	8	208
TGGAGTTGGAGCAACGTAAA	59.317	20	266	1015	1280
TTGGCAAAAGAAAATAAGTTCA	60.038	24	153	219	371
TGGTATTGGTCCACCTGTGA	59.806	20	211	356	566
AAAGTCAGCCGAGAAATTCAA	58.962	21	109	786	894
TGACAATATTTAGTGTTTTGACA	57.78	26	186	63	248
TGTCAAAATCTCATTCATTTGCT	60.01	24	125	50	174
CACACGAGCCTTCTTCTTCC	59.989	20	275	69	343
TGAGGACTTCTTGGGGTTCA	60.624	20	115	67	181
GTCCTGGCACTTTGCTTGA	59.976	19	273	540	812
GTCCTCCGAACTCATGGTGT	59.969	20	161	91	251
TGGGATACGCATCAACACAC	60.399	20	223	52	274
TTTAGGGTTGGTTTTGCAGC	60.11	20	277	1084	1360
GCGGACTGCTCTCAACTCTT	59.751	20	277	200	476
AAATTATCGAATGAGGGGGC	60.116	20	132	534	665
GAAAGCCTACCTCGCTTCCT	59.983	20	174	646	819
AACCGGTTAAAAACCGAACC	60.089	20	116	396	511
AGGGAGATCTTGCAGGATAGG	59.682	21	257	6	262
CATTCACCGGATGAAAAAGG	60.301	20	270	67	336
GACGACCGATATTTGCTCCT	59.154	20	153	924	1076
TTCATGAAATCAAGCAAACCA	59.147	21	102	12	113
TGAGTGAGGAGGGGGAGATA	59.606	20	116	339	454
TCAAGACAACCGAGCAAGTG	60.025	20	159	191	349
CCAACCCATTCTTCACCAAC	60.21	20	205	191	395

TGGAAAATGAGGAATGGGAA	60.244	20	268	225	492
GACAGGGGTTCGTTGTTAGC	59.598	20	273	284	556
TTTCCAGAGTTGTTACGCCC	60.11	20	215	1143	1357
TGGATCCCAATGAAAATGAA	58.742	20	276	390	665
TGAAGAATGAAGGGAATGGG	59.864	20	161	773	933
AAGAGCGAGAGATGGACGAT	58.995	20	212	75	286
CAGAACTTGTCGTGGTGGTG	60.194	20	249	110	358
CCGGCCATAGTTTCTCACAA	61.021	20	124	95	218
AATTGATTGTGGATGGATTTTT	57.355	22	270	582	851
AAGAGGTGTTATGAAGGGACA	57.724	22	219	18	236
GCACACAATAACCAAAGTATT	58.919	25	151	64	214
CTCTCCCACTTGCTTGTTGA	59.007	20	189	39	227
CCAGCTTCGAACGTTGTATGT	60.183	21	228	1904	2131
TCAAGGAGTTGTACCTGATAG	59.666	23	244	1487	1730
TTAGCAGCAGATGCAAAGGA	59.712	20	123	540	662
CATGAAATCAGGCCATCTCC	60.426	20	223	7	229
CTGTGCTGCTGGAAAATTGA	59.988	20	240	335	574
CATCGTACATCGCAACCATC	59.955	20	202	23	224
TGAGGGGGAAAAGAGAGGAT	60.008	20	186	183	368
CTTCAGCTGACATTGGGTTG	59.288	20	270	1372	1641
CATTATTGACGCAAATGTCCC	60.203	21	191	355	545
TTGGGAAAGCACTATGGACC	59.933	20	208	86	293
TCACTCATTCAAGAACATAGC	59.761	23	178	374	551
TGACATGCTCTTAAGGATGGG	60.875	22	100	217	316
CTCATAGTCAAACACGATTGC	58.464	23	175	79	253
GGACATGAAGTAACTGCACAT	60.052	23	272	200	471
AAGAAGTGGGTGTGTGCTGA	59.31	20	175	274	448
TTCCAGGAAATCGGGAGAT	59.425	19	273	387	659
ACGCGCAGAGGAGATCTATG	60.526	20	270	512	781
ACATTGCACGTACTTAACCAA	58.669	23	270	17	286
GGGGTGAATGATCAAGATGG	60.135	20	181	7	187
AGAAGGCGGATAAGGTTGGT	59.962	20	250	3639	3888
CCCACTAACCCCTTCATCAC	59.259	20	260	171	430
AGGGAGTTGTTTAATTGTCGG	58.111	21	275	97	371
ATTTCCAAATCGGTACATGC	57.424	20	264	890	1153
AAACCCATTTATAACGGCGA	59.323	20	197	272	468
GACTTACGTTCCGCCAACTC	59.74	20	217	1961	2177
CTCGTCAACAGCTCGGTACA	60.049	20	248	146	393
CCATCTTCGTCCACCTCTTC	59.655	20	113	8	120
CTAGGGTTAGCATGCTTGGG	59.724	20	164	58	221
AGCTTCACATGACCTCCTCC	59.258	20	163	317	479
TGCTGGGTAAAACTGAATAAT	60.916	25	110	129	238
TGCCTCTCCATCTCCATCTT	59.761	20	275	5	279
GCAAAACTTAGGAACGAAGCA	59.527	21	225	17	241
ATCCTTGAACCGTGTCATCA	58.933	20	148	150	297
CCATCTCGGGTTGTAGTGCT	60.134	20	162	630	791
GCTTTATGTTGTTGATCCGTCA	60.003	22	132	50	181
CAGCAGATGCTTTCATCCAA	59.948	20	134	920	1053
CCGTCGTCGTTATGAAGAAAA	60.117	21	150	105	254
GTGAAATTATTCGTTGATAAAC	57.681	27	216	322	537
TGGTGGGTTGAATGCTATGA	59.924	20	196	1492	1687
ACATGGACGTCCCAGATTGT	60.246	20	133	0	132
GGTAGGGTGGGGATGAGATT	60.015	20	261	121	381
GAAGCGTGTACGTCCCCTAA	60.132	20	272	210	481
GTTTCATGACTCCGAAACCC	59.386	20	107	0	106
CGTTTTCCCTATTTTGTGCATT	60.232	22	251	81	331
TAAAACAATAAGGTCGCCCG	59.958	20	248	864	1111
GAATAGGCAGTGACGGATGG	60.483	20	269	99	367

GCGAGCGAGTAGGTTGTGA	60.152	19	110	2	111
ATTCTATGGTGGGGCGATTA	59.254	20	198	830	1027
ATGGTTCGCCATAAAAATGC	59.801	20	163	36	198
TTCACCCCCTACTCCATCAC	59.779	20	265	393	657
TCGCTATGCACACTTTCTGG	60.011	20	123	650	772
GGATGAAGGTGTTCGTTCACA	60.95	21	269	201	469
CGCGCCTCTACTTTTTAATTAC	60.473	23	169	818	986
TCGACATTGTTTGAGTGCAAC	59.755	21	174	211	384
GGGCGTCACAAATTTTCAA	59.509	19	229	1885	2113
GCCATTTAAAAAGTCGGCTG	59.72	20	227	1108	1334
CTGGTGAGTGAAGGCTACGG	60.843	20	190	82	271
TAAACGGGCCAATTTAAACG	59.835	20	189	169	357
AAATAATCGAGCTTGCACCC	59.186	20	177	0	176
AACACTGACCATCCCCCTTA	59.259	20	124	3919	4042
CTTCGCCACTGTTACCCTTC	59.734	20	274	767	1040
CGTGTCCGAGTGTGTTGAAA	60.757	20	118	79	196
CGGGTATTTTTCTGAGCCAA	60.067	20	269	810	1078
CTGGGCTGAGATGACTTCGT	60.408	20	242	27	268
CATGATGAGGTTTTCGGTGA	59.496	20	273	111	383
CTATCGGATTAAATGGAATAA	58.656	24	101	9	109
TCGGTGTATGCTGTAAACGAA	59.24	21	132	114	245
CAGTCACGACTTGCCAAAAA	59.881	20	220	853	1072
TCGTATGAATTTTTGTATGGAC	58.927	23	192	607	798
TTTACCCATAGCGCACTCG	59.841	19	154	809	962
CTCTACACTGAATGCGCGG	60.568	19	217	378	594
TTGAATCCTCACAATATAACCT	59.283	27	224	95	318
AGCCAAATTTGCAACCTCAG	60.249	20	243	1251	1493
TCAATTATGTCATGAATGTTCA	57.148	24	235	65	299
TTGTCGTGGTTCGGTATTCA	59.964	20	280	45	324
ACTGACATCCACAGGCATTG	59.551	20	126	72	197
CTGCTCCCCTCCTCTTCTTT	59.95	20	196	607	802
TTTGCAAATCCAAAGGTCAA	59.133	20	130	7	136
TGTACCTATCCAACGGGGTC	59.67	20	229	8	236
AGGGCTCCACCGATAAATCT	59.925	20	255	1336	1590
GCGAATCAAGTCATGAATGAA	59.713	22	277	260	536
AATCAACGACCGCAATTTGT	60.374	20	143	320	462
GCGAAGTGGCAAACTTGATT	60.257	20	134	483	616
GTTATCATAGGATCACCCTCCC	58.668	22	155	59	213
AAATGCCCCTGTATGCAGTC	59.962	20	278	642	919
TCCAAATTACAATCGTCGCC	60.837	20	276	145	420
ACGTTCGGCTCGAGAGTAAA	60.015	20	235	13	247
TGTCGACCTCGATGCATTT	60.217	19	274	818	1091
TACGATTTTTCCCCCGTATG	59.655	20	248	608	855
CGAACTTAGTCGACCTACATG	59.595	23	260	398	657
CAACCTCTGCAAACCCAAAT	59.971	20	273	375	647
AAAGAGACGAACCGACCAAA	59.711	20	163	71	233
GGCTTCCATGGTGGTTTAGA	59.933	20	104	15	118
CATTCATCAACCATCCCAAA	59.175	20	164	333	496
ATCGGTTATCACCAGATCGC	59.923	20	154	30	183
AGCCACTAAGCCACCTTCAA	59.875	20	278	589	866
ACCAAATTTAAGGGTTATCAC	59.579	24	152	98	249
AGAGAAGGGTTATCACTTGAA	57.097	25	150	70	219
AATTCGGATGGGAAAACACA	60.17	20	258	81	338
GCGGAATACGAAGAGTCACC	59.7	20	254	4	257
CGAAGTAATGCTCACACGGA	59.864	20	208	110	317
AAACACCGATTCACATTGGC	60.765	20	166	269	434
TTGCTGGTGGAAACTCCTTT	59.711	20	280	1697	1976
TTGGCATCCATCGTAACAGA	60.073	20	168	12	179

TTGAGAAGTGCTTGGCAAAA	59.585	20	256	23	278
ACTTGTTCCTATTGCCAACGA	59.623	21	178	87	264
TGTGTTTGCCAACAGTCCTC	59.726	20	273	1374	1646
CTGAGATTTGTACTGCGCCA	60.011	20	209	17	225
CCCAAACCCATTCCCTAATC	60.37	20	189	158	346
CGCTTTGTTTTCGTGTTTGA	59.888	20	256	393	648
ATTAGGGGTAGGCACGGTTC	60.208	20	274	441	714
TGCGCGATTTTAAACCCTAA	60.564	20	174	5005	5178
TGGTCTCAACGATATGCTCG	59.823	20	278	31	308
CAACACAAGGACATCCATCG	59.96	20	233	796	1028
AAAGGGCGATGACACAAAAC	59.978	20	259	9	267
ATCACGAGATGGGGACTCAG	60.072	20	164	1304	1467
372	372	372	372	372	372
GAGACTCACCCACCATTGCT	60.12	20	248	999	1246
TCGAGATCAAAACTCGCCTC	60.483	20	271	58	328
TCCAATGGCCTAAGTTGGTC	59.933	20	227	55	281
AATTGAGAAGGGGGAGAGGA	60.008	20	189	2	190
AATCCTTTCCTCTTTCCCCA	59.875	20	229	140	368
CACCTCTCCGATTAAACCCA	59.926	20	160	334	493
TTTCTTTGAGTGGGATGCAA	59.247	20	267	113	379
GGATGAGACATACTTACTTGCT	58.964	26	221	5	225
AAACGAAAAAATTGGGGTTCA	59.292	20	219	37	255
AAAACCGTAGTGGGTTAAAATT	60.041	24	278	0	277
TTGGGTGATGTGCTTGAAGA	60.24	20	130	159	288
AGAATAGCCATAGCCGATGC	59.305	20	147	352	498
TCGTGTTCTTCGTCGTGTTC	59.88	20	229	3483	3711
GGAATGAAGGTGAAGGGAGA	59.065	20	101	108	208
GAAGAAATTCCAATAGAGTTGA	57.932	25	253	19	271
TGCCTAATTTATAGATAATGGA	59.68	25	270	1074	1343
AAAATATGATCTTACTCCCACT	60.035	26	201	615	815
GGGGTAACTTGTCATCCCCT	60.052	20	137	13	149
TTATTGTCGCTGAAATCCTGG	60.081	21	183	192	374
TTTGTCCAAACAAATGAAAACA	58.097	22	189	321	509
CTGTAATCCCGATTGCTGCT	60.235	20	117	806	922
CTTCTTCGGTATGCTGACGG	60.786	20	207	149	355
AGAAGACCGAGAGACACACAA	58.991	22	157	0	156
GAGAAAAGACAATTCGGCCA	60.192	20	204	43	246
GCACACGAGCTCTCACTCAC	59.771	20	232	415	646
TAGCCGATAAAAATGGCACC	59.928	20	269	62	330
CTCGCATCCAATAACAAGCA	59.833	20	254	274	527
AATTTGTACACACGTCCACCA	58.813	21	241	90	330
GTATGCTGATCCACCTGCAA	59.679	20	258	149	406
CATGATCCAACCTTATTCCTCC	59.666	22	206	65	270
AGTCATGCGATCTGAACGTG	59.862	20	224	47	270
GCATGCTCTGTTTTCTGCAA	60.142	20	280	1	280
TCTGCAAAATGATGAACCGT	59.127	20	200	304	503
CAATTTTGTCTGCTGCATGG	60.257	20	179	426	604
TTTGCAATATTCAACTACGAGC	59.802	23	187	57	243
TGCAGATCCTCGGTACCTTT	59.694	20	230	386	615
TTACGAAAATACACGTTCGGG	59.876	21	124	110	233
TCCCCAGTGTCACACAGACT	59.113	20	255	262	516
AGCCTCAATTCGGATGATTT	58.598	20	277	1101	1377
TTTAGGATCGGAATATCGAGAA	57.857	22	280	5	284
ACTTTGGCAAATCACACAGAT	57.186	21	168	272	439
ATGTTTTGTGAAAGTCCCGC	59.978	20	113	527	639
CATGGTAAAGAAACGGTGGA	58.475	20	161	122	282
GATAATTAGTGGAGGCGGCA	60.06	20	101	1557	1657
TGAAGAGAAGAGGTCGGGAA	59.92	20	212	31	242

TCGTGTTTGGGCATTACTCA	60.111	20	280	779	1058
TTGGTACCTCGAGGCATTTC	60.074	20	230	507	736
ATTTCTCAGTCCCTGCCTCC	60.596	20	252	1293	1544
TGTTCAATCTGCCACCAAAA	60.088	20	257	1077	1333
ATGGTGGTATGGTGTGGAGG	60.51	20	188	86	273
ACACAATCCCAACAAAAAGAA	59.78	23	239	2	240
AACGAAGGGATAAAGCCGTC	60.451	20	139	153	291
AGTTGCTTAGCGACCCCATA	59.73	20	268	4016	4283
GGTTCGGGTATTCACGTTGT	59.717	20	260	684	943
GGAGTTGCAGTTTTGGATGAA	60.103	21	192	208	399
CCAATTGTCTTGGGAGCCTA	60.066	20	182	23	204
TGGAGACACCTAAGCCCATT	59.55	20	156	27	182
CGGTTTGTTGGCTAACAGGT	60.03	20	126	32	157
CAAAAACCGAAAAACCGAAA	59.951	20	252	439	690
ACCCACTAACCCAAACCCAT	60.34	20	134	63	196
CCTAACCCCACTAATGACCC	58.24	20	155	645	799
TTCGTGATTATTGCTGCTGG	59.833	20	137	517	653
CCCCACCAAAAGTCCAACTA	59.824	20	260	138	397
TATTACAGGGGCCAGTCGTT	59.452	20	242	2901	3142
ACCACCATCTTCTACGACCG	59.989	20	154	370	523
GAAGCCTCAAATCACAACCC	59.532	20	212	358	569
CCAACTCTTGTTTTAAACCGC	58.798	21	248	610	857
AGCCATTTAAAAGTCGGCTG	59.361	20	107	77	183
TGCTCTCTTGATTCATGGCT	58.544	20	251	1121	1371
GAGGCTTCAAAATCCTCCATC	60.032	21	240	216	455
CCCCATGCATGTAAAACTGA	59.395	20	270	312	581
CCTAGCTCCTTCCCCTTCAC	60.204	20	178	1073	1250
GGCGGCTACGAAAATAGGTT	60.459	20	233	162	394
GAAGCATTATAACCACCGCAA	59.978	21	253	74	326
GAGTAGGAGTCCGGAGCAAA	59.43	20	159	321	479
TGACCGGACGAAAATACTCC	59.933	20	188	196	383
TTGGCCTGTTACGACTCAAG	58.923	20	160	146	305
TACAGTCGACCTCAGCTCCC	60.408	20	219	10	228
AGCTGGAAGACAAGGTGTGG	60.298	20	210	21	230
CATTTGGAAAATCAATGGATG	59.638	22	279	678	956
TTCAATACTTTGAGGATAGATT	59.474	27	276	11	286
GTGTGTCACTCCCCGATCTT	59.969	20	157	64	220
GGAGAGAAGTTTCGGTGGTG	59.697	20	205	10	214
CCTCTTTCTGGGTGTTGTCC	59.549	20	268	274	541
TTTGTTCCAATACCGCTTCC	59.938	20	152	2858	3009
AGCGGTTATTACCGGATCG	59.93	19	223	53	275
TCACGCACTCACGATCTCTC	60.146	20	235	915	1149
TGACTTGCCATTCGAACTACT	57.496	21	188	708	895
GAGGGAGAGAGAGATAGGATC	58.526	22	107	176	282
TCTCTGAACTCGGTGACGAA	59.545	20	205	4	208
GTGATCTTGTTGGGGGAGAA	59.903	20	162	1091	1252
AAGATTCGCCCTTTCACAAA	59.685	20	177	6	182
CCGATCCCATCCCTTAATTT	59.978	20	256	249	504
GTCAAATCACGTTCACGCTC	59.297	20	241	26	266
GATGGGCATTAAAGACGACG	60.469	20	149	31	179
CATTCCTTTTTATGTGTTTGTTTC	59.38	25	242	1125	1366
GTGGGTTAGCATTTGATCGC	60.478	20	241	622	862
TGTACCTCTCGCTGCTCTGA	59.88	20	266	494	759
GGTTAAAAACCGGACTGCAC	59.476	20	139	52	190
CCACAATTTTAGGCAGTTTCG	59.634	21	166	480	645
AGCCCTCTTCCCATTTTCTC	59.651	20	150	224	373
TCAAAATCTTACACCTGGAGCC	60.483	22	278	232	509
ATTTTTCGCCGAAGAGGATT	60.041	20	235	588	822

TGGCTTTACTGGTGTTGTAGGA	59.671	22	271	181	451
GCGTTTTGATGATATATAGATG	59.327	27	182	313	494
TCCATCTTAATGCAGCAACG	59.833	20	122	2921	3042
AGGAAAATGTGTCGAGAGGG	59.137	20	268	141	408
TTTCCTCCCAACATTCGTGT	60.353	20	227	85	311
TGAGGAGCGTTGATCTTGTG	59.984	20	205	266	470
ACGGTATTGCCCTTCAGCTT	61.006	20	241	1175	1415
ACAAGGGTGACCCATTTTGA	60.21	20	173	26	198
AATTCTGCAAAAATGAACAAA	57.101	23	181	12	192
CACGAGTGAAGAAAGGGAGA	58.001	20	143	41	183
GTCCGCGAAGAAACACTCAT	60.263	20	197	175	371
CGGTAACACAAAATTGCAGAA	58.736	21	242	2177	2418
AACATGCTTCACCATATCCAAG	59.781	23	280	928	1207
CCTCTTGAGCTCTGCCTTGT	59.745	20	247	405	651
ATATGTTCACCAAGCCGCTC	60.103	20	226	6	231
TGCTACGAGAATGCATGGTG	60.834	20	234	99	332
CGCGAAGACAATGTTGAAAA	59.849	20	253	37	289
CCTTGTTTTGTAAAGGGGTCG	60.727	21	249	845	1093
TGCAAGAAAGTGGACTGCAA	60.574	20	186	530	715
CTCTCAATGGACCAGCACCT	60.261	20	258	1472	1729
CGACACAATTAACCAAAAACA	60.517	24	243	332	574
TTTGTCTGCGTGGACAAGTT	59.339	20	225	232	456
TTAATGCATTCGCCAACTGA	60.215	20	214	125	338
TCGTCGTCGCTTTCATCATA	60.366	20	167	2432	2598
TCGAATGCACTCAAACTCCA	60.39	20	146	261	406
GGTGCCCCTACTTCTTTGGT	60.361	20	212	33	244
TGTTGGCATTCAAATCAACC	59.375	20	232	659	890
CGACGGATATTTGTTCTTGTG	58.161	21	262	91	352
TCCCATCTAATCTCGTCCGT	59.508	20	182	746	927
TTGGGAGACAAACACACTCTC	58.843	22	271	53	323
CCACCCACACCTAAGGAAGA	59.959	20	120	1	120
ACCCACTAACCCCCAACTAA	58.292	20	103	1	103
CATCATTGTGATGTGTGGGAA	60.232	21	221	874	1094
CGACTTGTCGTTGTTCGGTA	59.758	20	274	212	485
GAGGGACAGCCTAGAACTTTG	59.886	22	135	293	427
GTGCATCTCGGCTACGAAGT	60.428	20	180	38	217
CCTTGAGAACTCCCACCTGA	60.229	20	277	218	494
CCACACATTTGAGGGAAGAAA	59.956	21	233	253	485
TTAACCAAAATTTCGGGACG	59.805	20	221	350	570
AAAATGACACGCAAAAAGGG	59.975	20	100	176	275
CAATCTGACGGCCGATATTT	59.923	20	168	966	1133
TTGTCACACATTTACACACACG	58.016	22	223	134	356
TGGACTTAACTGGTAGCCCG	60.125	20	270	96	365
GTGGATGTGTAGATGATTTTTG	60.116	24	170	43	212
AGCGATCCTTACAGGCAGAC	59.459	20	229	61	289
CACACACGATGGATCGAAAC	59.967	20	233	97	329
GCATCTCTTGCTCTCTCATTG	57.78	21	160	1	160
CCATTTTTACATGCCGCAAT	60.7	20	184	824	1007
GGATAAGTGGGGTGAGGGAT	60.015	20	275	35	309
ATGGTGGTTTGGTGGAAGAA	60.21	20	136	169	304
AGGTGCTGTGTGATGTTGGA	60.162	20	203	45	247
TTTCACCGTCCAAAACACAA	59.981	20	214	379	592
GCATGCAGAAGATGTGGAGA	59.95	20	217	1568	1784
ATGCAAGCTAACCGCTAGAAT	58.2	21	266	52	317
ACACGTGTCAAAATTTGCTTG	58.739	21	247	91	337
GGATGGGAGTACATTGGTGG	60.05	20	239	75	313
GTTTGGGGGTGAGGTGTAAA	59.688	20	216	522	737
CGTTTTGATGATATATAGGTGT	59.637	27	155	384	538

GACTTTTGATTCGGCTTGGA	60.192	20	103	342	444
CACTTAGCTCATTGATTTTCAT	59.24	25	132	623	754
AGAACTAGGGCACTCCATCG	59.308	20	276	80	355
CGAACCACCACACCAAATTC	61.196	20	145	496	640
CTCAACAGTCAACAAGCACAC	59.986	22	211	314	524
TTTAAGGGTTATCACCTGATTT	58.625	25	278	55	332
AACCAAGCTCTTGCGATGAT	59.843	20	129	2030	2158
TCTGTAACTCCCCCAAAAGC	59.17	20	162	578	739
CCATTCACACACACACTCAGA	59.074	22	258	183	440
CATGAAAATGGGGACACACA	60.216	20	132	355	486
CCTCATCGTCGGATTTTAGG	59.523	20	280	79	358
TGGCTGCTGTGTGAGGTAAA	60.449	20	221	171	391
ATTTCATTTCATGGGTTTCG	57.399	20	108	11	118
ACTCACACGCTTACACGCAC	59.977	20	116	1060	1175
CGGTCGTCAGATTGAGAAAA	58.847	20	221	2067	2287
GCCTCCTTTTCTCTTCTTGACA	59.998	22	192	2405	2596
TGTATTTGGGCTAAAGTGGC	57.781	20	146	18	163
TTTACCCGTTGCATGTGTGT	59.888	20	246	1418	1663
ATCGAACAGCATGAAAACCC	59.939	20	270	157	426
CAAATCCCATCAACCCAAAC	60.029	20	109	18	126
GGAGAAGAGATCGGAGACGA	59.486	20	187	39	225
TGCGAAGGTGTAGTCCATTG	59.716	20	262	846	1107
GTGGCCTGAGATAGCCGTTA	60.235	20	181	30	210
ATTTTCCCTCTGCTCCGTCT	60.212	20	156	2182	2337
GGGGTTCAAGTGTGAGGAGA	60.088	20	223	476	698
ACAAATGCATTCAAAAGCCA	59.161	20	233	418	650
GACCGCGAAGTTTACATGGT	60	20	211	80	290
AGACTGGGGTGACAGACCAC	60.006	20	163	3649	3811
TCTCCAATTAACGTTCCATTCA	59.451	22	228	2381	2608
TTTCTACTCCCTTCCCCTGC	60.569	20	168	1079	1246
GGTGGCTTCTCTCTTCGTTT	58.525	20	221	10	230
CTTCGACCCAACACCATATTC	59.302	21	100	30	129
TTTGTAAATTGGCGTAAACGG	59.883	21	266	5	270
CATCTTGTCAATTTCGCCAAT	59.952	21	187	204	390
GAGCGGTTATTACCGGATCG	61.686	20	226	72	297
ATCTAACGGCTGGCATTTGT	59.597	20	237	7	243
TTTGAGCTAATGCTCTCTCGC	59.881	21	100	99	198
TATGGGTTATCACCGGATCG	60.544	20	279	639	917
ATTAGGGTTCCTCCTTCCCC	60.497	20	113	2	114
TGATTTTAAAGCAGGATCTTTT	57.669	23	185	4	188
ACCATCCCTCACACGCTTAG	60.134	20	268	96	363
TATGGGTTATCACCGGATCG	60.544	20	210	216	425
CTCTCTCACACCGAACACCC	60.713	20	107	778	884
AACACACACGCACTCACACA	59.818	20	162	247	408
TTGTCCAGTGTGTGTTTTTGG	59.495	21	223	60	282
GGGATCCCAAGCCACATACT	61.106	20	278	1242	1519
ATGATGGTTTCCGAAAGTGG	59.79	20	259	1689	1947
TTGGGCTCAGTAAACTGCTCT	59.135	21	245	95	339
CCCAAACATTTGAGGGTTGT	59.688	20	212	551	762
TTTTATGTAAATTGTCGTGCGT	57.373	22	251	69	319
GGTGCTTGGTGAAGGAAGTG	60.69	20	125	24	148
TCCTTTATTTTGATGTAGCAAC	59.904	24	252	718	969
CCTTTGATGTTATACACGACTT	59.958	24	205	534	738
TGGAGGTCGGAGAGAGAGAA	60.064	20	268	28	295
GTGGTGACTTGAAGAAATTTG	60.379	23	160	50	209
TTTAAGTGGGGTGTGGGTTT	59.191	20	100	76	175
CGACCCAGATTCAAACCCTA	59.926	20	279	69	347
ATGATTCCTTGGCACTTGGA	60.461	20	159	490	648

ATATGCTGAGAGCCACCAGG	60.24	20	279	446	724
GTACCGGTCTGAAGTGCCTC	59.727	20	100	12	111
GAATAATGGTGGCAGCTGTG	59.152	20	203	484	686
TTCCTTTTGGCGTAGTGAGG	60.241	20	165	13	177
ATTGAATCTACGTCCACGGG	59.813	20	258	67	324
GCAGCTTCCTGCAGATTCTC	60.249	20	253	37	289
CGCTCCACAAAGATCTCACA	59.984	20	116	179	294
AGCTGAATTTCAAAGAGGCG	59.592	20	267	376	642
GCCAATTTGTTAACCGGAAA	59.81	20	142	40	181
TCTGCATGTACGCTACCTACC	57.946	21	218	42	259
CGGAGTGATAAGGTGCTGTG	59.314	20	229	0	228
ATTTCTGTCCCGTTTTCCCT	59.805	20	279	48	326
AAGGAATGGTTTGATGGGTG	59.647	20	217	144	360
AACTGCCCGTTGGTAAGAGA	59.734	20	156	3313	3468
GACAAATTGACAGCGATGGA	59.654	20	174	109	282
AGGGGTTATCACCTGAATGC	58.864	20	166	474	639
TGCAGTTGCTGGATTACAGG	59.864	20	210	5835	6044
TGAGAGAAGACCAACTCGGC	60.533	20	119	12	130
CATTGTTCATGAAAGCGTGG	60.111	20	225	223	447
ATCCGCCTACATTGGATGAC	59.78	20	247	1389	1635
ACTGGCTCAAAAGGTTGCAG	60.431	20	257	390	646
GGGCACCTACTTGTTTGTGAA	60.023	21	268	22	289
GCCTCGTCTGGTTAGTTGGT	59.212	20	225	29	253
ATCCTCCTAAGTTGCCCCAT	59.789	20	115	24	138
TGCATTCACCTTCTCTTTGC	59.002	20	201	156	356
TGGTGTAATAATTTGGTTTCAT	60.006	24	245	254	498
GCCGTCGTGTTCTTTCCTAA	60.249	20	243	23	265
GTTTACAACTCACAACGCGG	59.245	20	215	100	314
CCATATTTAAGGGTTATCACAT	59.713	27	249	835	1083
TTCCTCCCTCGTTTTTCGAT	60.929	20	263	3296	3558
TTTGTCTTCCCGTTTGTTCC	59.948	20	277	147	423
ATAACCCGGTCAACAAGCTG	59.993	20	255	19	273
AAAATGTACCAAAGACGGGC	58.952	20	221	399	619
TGTTGCAGTTGTGGGTGATT	60.008	20	180	354	533
AGAGTTCATCCCACCCAAAT	58.297	20	177	7	183
CGTAGGACAACGACGGTTTT	60.03	20	127	3	129
GGTTGCGTAAGTTTTGGTGC	60.543	20	263	168	430
ATTGGCCCTAAAATAACCCG	60.036	20	253	244	496
GAGCTGCGGTTTTGATCTGT	60.406	20	264	199	462
TGCTGTGGGGAGTAAACACA	60.152	20	271	7	277
TGCCTCACCACCAATGTAAA	59.964	20	226	528	753
CAGGCCCAATACCTTGACAT	59.813	20	135	20	154
CCTCCGAACTCATGGTGTTA	58.569	20	190	261	450
CAGATGAGGATTGGGGCATA	60.822	20	212	29	240
GTCAACTTGGGCAGTGGAAT	59.973	20	169	182	350
CATGCAAGCATCAAACAACA	59.28	20	181	3	183
TCGTTTTAATTTTCGGGAAGC	60.415	21	235	613	847
TGACTAAGGTCCCATCACGA	59.086	20	235	50	284
CATCAACCGCCAGGATTATT	59.784	20	119	20	138
AAATCTACCTCTGCCACCCC	60.328	20	221	214	434
GTCACGAGGTTGAATTGTGC	59.143	20	180	1548	1727
CGGAAGGAAGTAGAAAGGGG	60.061	20	139	121	259
TCTGCTTTTTGAGAGAATGCC	59.583	21	155	143	297
CCTGAATATGGCCGATCCTA	59.878	20	210	3	212
TTTTGGCAATGTCAGGATCA	60.049	20	217	416	632
CCCAAACTTCGGGTTCATAA	59.795	20	106	2834	2939
TGCACGTGACTTGCTTCTTC	60.183	20	117	232	348
TTGAGCTTGATCCTTGCTTG	59.148	20	127	194	320

TGTTGAGTCATTGATTGAGCAG	58.926	22	181	2128	2308
TTTGGGTGAAAAATGATTCAGA	59.429	22	131	71	201
TGATGCGAGGATCCTTTTTC	60.155	20	180	164	343
TGCGTTTTGACAATATATAGGT	60.083	26	264	37	300
CACCACTCTTCGATGGAACC	60.51	20	250	80	329
AGCGGTTATTACCGGATCG	59.93	19	231	146	376
ATTTCTTACCCGTCCGTCG	59.94	19	203	32	234
TGCAATATTCAACTACGAGCAT	59.292	23	103	27	129
AGTGGCGTTATTGGGTTCAT	59.316	20	269	4	272
TTCAGCCTAGTCGCGATTTT	59.982	20	277	195	471
ATGAAAGTTTGTGGGGATGG	59.647	20	179	507	685
CAACAGAGAATGCAAGCGAA	60.134	20	171	12	182
TATGCACGAAGCCAATTCAC	59.694	20	266	1978	2243
TCGTCCCATCTTTTACCCTC	58.981	20	249	344	592
TTTTTGAACTCTCGGCCTCT	59.052	20	251	79	329
AACCGGCGGATTTAAAAAGT	59.844	20	222	2252	2473
ATAAAATGTACGGGCGCTGT	59.501	20	157	23	179
CGAGTGTGAGGCTGTGAGAG	59.757	20	132	59	190
CACACGCACACACATCCATA	60.029	20	146	18	163
TCTTACGGAATTCCACTGGG	59.926	20	262	44	305
TCATAGTCAAAGCAACCGCT	58.529	20	279	72	350
AGGGCCTGGTCATTCCTTAG	60.455	20	263	1982	2244
CGTAGCATTCAAAGGGCATT	60.096	20	179	126	304
AACACTTGAGGAAGGATGATG	58.646	22	102	425	526
GCTTTTTCGACTTTGATCCG	59.823	20	190	62	251
CCCATTTTCGATCACCCTTA	59.756	20	213	31	243
TCGTCCGAAAATCCTTTCAC	60.051	20	272	246	517
ATCGGTTATTACCGGATCGC	61.031	20	257	293	549
ATGTTTGAAATATCGGGGCA	60.153	20	100	8	107
TGGCACAATAGGAAAGCAAG	58.917	20	142	443	584
ACAAACTTATGGACCGCTGG	59.993	20	135	555	689
GACGTCACCCCACTTGGTAA	60.812	20	200	1708	1907
TGAGGTTACGCCAAACATGC	62	20	235	64	298
TATAACCGATCCCACCCCTT	60.391	20	127	93	219
CTGGCAGTTGGGGAATTAGA	60.066	20	162	311	472
TGGACGGTTTGTGAGAAATG	59.541	20	244	1135	1378
CCATGTCTCATGTCTATGGCA	59.537	21	275	901	1175
GCTACGACATTGCCCTATGAG	59.744	21	119	35	153
TTGGATTAAATTAAAATTATGG	58.805	26	265	3636	3900
CCATGGATGTCAGTCATTGC	59.925	20	171	1606	1776
CCGTCGATTTCTAGTGTTTGG	59.618	21	191	392	582
TTTTTCCGACTCAAGGCATC	60.192	20	249	186	434
TCTTGCACATCTTGGTGAGTG	59.889	21	228	19	246
ACCTGTAGAATCTCTTACTCTAT	57.215	27	225	591	815
GGGGTGAATGATCAAGATGG	60.135	20	187	5	191
TAGCGATCGGCATCCTATTT	59.666	20	256	24	279
TAGAAGGCCGATTGACGAAC	60.214	20	158	64	221
TGAACCTTGAATCGAGTTTACA	57.814	23	179	16	194
TGGGCAATCATTTGCTTGTA	60.073	20	247	3460	3706
CACCACACATGGACCACTTT	59.283	20	156	320	475
GACAGCGTACTCCCCACTGT	60.182	20	276	371	646
TCAGCTCGTGAGGTTTCAGA	59.701	20	230	445	674
GCCTCGGTTGCTTATTTGTT	59.229	20	280	377	656
CTACGTCAACGGTGGTTTGA	59.609	20	182	44	225
ACTCACCGTGCTCTCCTCAT	59.866	20	270	4176	4445
TCCCGTTTTACCCTTGAATG	59.795	20	194	91	284
CCTCACTCTTTTACGCCTTCC	60.248	21	101	17	117
CCTGTTCTCCGCTGTATTCC	59.694	20	151	2770	2920

CATGCAAACATGGAACATTG	58.389	20	270	295	564
TTGATCAAGACCTTTTGGGG	59.903	20	229	79	307
CGACCCAACTCCTCTACTCG	59.861	20	227	73	299
GATGTTCCACAAAACCACCC	60.073	20	172	541	712
GACCGCGAACTTAGAGGAGTT	59.899	21	269	107	375
TGAAACAATGCCTGGAAACA	60.088	20	274	547	820
GATGATTGCACCATAACGCA	60.498	20	144	483	626
ATGTTGTCATAACAAAAATGA	60.089	25	101	352	452
AACCAACAATCAAGATCGCC	59.939	20	250	180	429
GTTGAGCTCGGAATACCTGG	59.694	20	278	1	278
GGTGTTGGCCGAAAGTTTTA	59.975	20	158	16	173
GATCGCATGTTGATTTTCCA	59.48	20	280	853	1132
TCGGCATGACGTAGTTTGAA	60.257	20	225	1764	1988
AGAACCATACCGAGGAGCAA	59.694	20	280	106	385
ACCATATTTAAGGGTTATCACC	57.552	24	269	309	577
AGCACCACACAAATCACCAC	59.446	20	148	528	675
AAGTCCCCATTAAAGATGTAA	57.81	25	280	229	508
TCATAAGTTAACATAAACCAA	59.079	27	111	77	187
AGGGTGGGTTTGGAGAAGAG	60.48	20	239	32	270
AAAATACGACGGCGAAGAAA	59.72	20	241	25	265
TTGGACTATCGGGTTCCAAA	60.301	20	236	38	273
ACCGCCATTCACATTCCTTA	60.331	20	265	673	937
CATCCCAGTTGTCTTGGGAG	60.501	20	180	19	198
ATGTCACACCCTCCCCAATA	60.05	20	165	239	403
ACATCATGTAGTCGCGTGCT	59.349	20	163	829	991
TTTTTCGAGTTTCTTGTTCTCCA	60.255	23	247	321	567
TCGAGAGCTGAGAGACAAAG	58.044	21	278	535	812
CCTCCTTCAGCCAAAAATGA	60.184	20	242	1284	1525
CACTTTTAACTCCAAACCAGG	58.619	23	220	105	324
CTTTCGTTGGCGATTTTCAT	60.074	20	212	64	275
CAGACAACGCCATCATCATC	60.08	20	184	9	192
AACGGTTATCACTGGATCGC	59.962	20	206	422	627
ATACCCGTCGGTGTTCTCTG	59.989	20	213	156	368
ATTTGCTTAAAATGAATCAATG	57.325	23	154	312	465
TTTGTTTTCATTAACAAGACCA	59.809	25	221	1066	1286
TCCGTCATCGACCACTATCA	60.072	20	143	612	754
CGGCCGGTTTTTAATGTTTA	59.835	20	209	2188	2396
TGAGTGGAACGATCCATATAA	57.137	22	259	679	937
CGGCTATTAGCACAAGCCA	59.984	19	229	1163	1391
AATAGGATGGGGCAGAAACC	60.152	20	257	265	521
TGCAATGCAAATCTGACGAG	60.958	20	195	4	198
TATGATAGGCCGGAAAGAGC	59.277	20	266	480	745
CGCCTGCATTGTTTCTCATT	61.168	20	188	104	291
CCCGTACCTCAATTAAAAGGG	59.719	21	264	715	978
CCGAATTCCTCTACCGTCAA	60.066	20	199	386	584
TGCACACTGTCACACTCCAA	59.905	20	134	2110	2243
CTATTGGAGCAGCTGGGAAA	60.344	20	254	202	455
CACCCTCACATCTCTTGCAT	58.671	20	115	228	342
ATAAGAGGTATTTTGACAGTAT	57.206	25	115	98	212
TGCTATCGATGTGTTGGCAT	60.104	20	254	225	478
CCACCCGTGTATGTCATGTG	60.722	20	223	400	622
ACGAAATTGACGGAAGAGGA	59.67	20	243	103	345
GCCGGATTTAGAGCAATCAA	60.175	20	214	182	395
TGACGGAAAAAGGTAGTGGG	59.964	20	280	14	293
GGATGAAAATCATTGTTCGC	58.009	20	274	583	856
TGGACTTCTCCAATCCATGC	61.016	20	229	244	472
CCTGCAATTCCTTCTGAACC	59.67	20	234	108	341
CTCGTTCTCTTCTTCATCTAAA	57.05	24	147	257	403

GCCTCAATAATTCGCTTCCA	60.175	20	267	213	479
ATCATCAAATTGCCAGGGAC	59.756	20	241	3248	3488
CAACACTCAATTATAGGAAAA	59.318	27	251	209	459
TCCAATCAGAGGTAGACGGC	60.218	20	265	235	499
GGGGAAGAGAATCAAGAGGG	60.008	20	109	363	471
ACTGATTCGCACAAGGATTG	58.724	20	189	98	286
AACATATTCCATGGTCCCCA	59.871	20	111	4452	4562
AAATGTGGCCTTTCCATTTG	59.801	20	259	1120	1378
TGCATCACATTTGTTCATATCG	59.448	22	254	29	282
TCACTCTCGAGCTTGCTGAA	60.008	20	252	1004	1255
TTTTTGCCCTTGTATGCTCC	60.074	20	275	3148	3422
TGGGTTTTTACGAAAGGCAG	60.103	20	212	20	231
CGTTCATTTCGTACCTTTAGAA	60.307	26	229	5	233
TTTTGGATTGTCGGAGTTGG	60.863	20	280	147	426
AAGGAAGGCGTTGACATTTG	60.11	20	261	93	353
ATGTTGTCCCGGACTCCTC	59.912	19	122	36	157
TGGTAGTGAAATAAACATAAA	59.645	26	142	95	236
AGGTTTTACGAACCACAATCC	60.623	22	131	151	281
TACATTTCCCCAACCACTCC	59.647	20	172	13	184
AAAAATGGTTATTATTGGATCA	57.553	24	141	97	237
GGAGGCGATTTTGTGTCAGT	60.119	20	243	1247	1489
AGGCGGACGAATATACCCTT	59.82	20	211	166	376
GGCATATGAGGCTTGGTCAT	59.923	20	177	177	353
TCCTCACCTTTCAAATCATGG	59.918	21	209	734	942
TGTTAGGTTCATTGCCACCC	60.755	20	248	88	335
TGTTGCGTAATAGGCGAGAA	59.467	20	209	330	538
ACGATTACAACGCAACATCG	59.614	20	111	372	482
CCATTCAATTTAACTTCGGCA	59.95	21	128	186	313
GTTGGCAACCAGATATGCCT	59.962	20	219	212	430
TCCAATGGATGGAAATGGTT	59.991	20	274	293	566
AAAGGACAGTAGGTGATCGGA	58.658	21	220	9	228
GGGTGAAATAGCATGCAAGG	60.469	20	255	585	839
GATCAATGCCGCTGAACATA	59.652	20	174	684	857
TTTCTGTCCCGTCTTCTTCG	60.366	20	171	13	183
CCCTAATACCACTAACCCCAA	57.876	21	101	511	611
CCTTCAACAAATGGTTCATGC	60.359	21	215	1693	1907
TTTCCAGGATCGAATTGAGAA	59.631	21	265	232	496
TTCAAACCTGGTTCTCGTCC	60.088	20	244	69	312
CCCTAGCTTTGCCCTCTTTC	60.332	20	102	8	109
TCATCATTTCATTTTATAAGCTT	58.806	25	188	107	294
TGGTTGGTGGAAGAAATCAA	58.947	20	261	13	273
CAATGTTTCCATGTTCCGTG	59.816	20	262	1324	1585
TCCATGGGAGGTTAAAATCG	59.756	20	263	249	511
GTCCGATTTGCCGTTCTATC	59.533	20	216	1027	1242
TCCAGCATTTGTATGTCCCA	59.924	20	215	1440	1654
CATGAACCTGAAACAGCGTG	60.301	20	228	2156	2383
ACAAGAGCTGAAATGCCCTT	58.936	20	216	29	244
TTGAATCATTTGCGTTGCAT	60.081	20	141	4439	4579
GCCAAAAAGTCAAGGCGTTA	60.244	20	243	22	264
GATGTCGAGATCCAACCCAT	59.744	20	240	354	593
TTAGGTGTTTTGACATGTTCAC	58.225	24	220	181	400
AAATTCAAACGCCCACTCAG	60.11	20	269	536	804
TGTTGTAATGAGGCTTTTGGAA	59.625	22	230	22	251
AATAGCGCTTTTTGCCAGAT	58.992	20	152	242	393
TTTTCCCCATCACCATCACT	60.173	20	168	111	278
CAACCGCCTGATTTGTTTCT	60.11	20	130	159	288
CCACCAGGTTTTGTAGTTCTGG	60.792	22	251	5522	5772
ACTTTCCGTATATGTCGCCG	59.982	20	244	290	533

ATACACAATGCCAAACATGGG	60.496	21	266	5399	5664
CATGAATCATAGTTGGCCCC	60.155	20	110	6	115
AATGGCGGTGAAGATGGTAA	60.331	20	274	100	373
CCTTGGCGGTTCATATCAGT	59.955	20	187	49	235
GAGAAGTTGTCGGTTTGGGA	60.088	20	165	687	851
GGTAAAAACCACGGGACCTT	60.089	20	161	87	247
CATACTCTCACCAATCCCCG	60.331	20	143	2	144
TCCCAGCATTCTTGAACACA	60.24	20	137	72	208
ATCATGTTGCTACACGTTGCT	58.324	21	150	175	324
CTCGGGTAGTCAAGTTTGCTTT	59.82	22	256	20	275
TGTACAAAAGCTTGTGGTGAA	59.836	23	182	94	275
CATTTGCCTGTGCATTTGAC	60.119	20	268	1466	1733
CACACTCGAAGAGTAGCGACC	60.066	21	215	776	990
AAATACCAAAGTCGATTATCC	58.11	24	161	39	199
TATGGGTTATCACCGGATCG	60.544	20	120	103	222
AAAAAGCATTTCACACGTTCT	60.089	23	179	294	472
AAATAATTTCCGAAACCGCC	60.148	20	234	914	1147
CACACGTTATATTTATAGTTTT	59.19	27	120	227	346
GCGAATTCAGCTAGAACAACA	58.187	21	180	1836	2015
TAGCTTATCACTATCACCCTCT	59.255	25	100	29	128
ACGGTTCACATACTCCTGCC	59.997	20	230	155	384
TGCAACCAACAAAAACAACA	58.626	20	184	31	214
TCCTTGGAACCTAGAAATGGTT	59.001	22	231	34	264
CATGGCCTCCTCTCTTTCAG	59.943	20	119	309	427
ATCCTTTTCGCCATCTTGAA	59.645	20	191	126	316
GATGGAATTGGGTGTTGGAT	59.464	20	116	132	247
TCTAATAGCAAGAGAGACCGG	59.871	22	252	63	314
TTTCAGCATTGAAACCAGCA	60.379	20	202	660	861
TGATTTCCCACCCTTCTTCTT	59.926	21	212	53	264
TGCCTCTAATGCACACAAGAA	59.775	22	279	67	345
CGGAATCAACCCTCAAACTC	59.526	20	215	1022	1236
CAAGGGTGATTGTAGCCAGC	60.657	20	156	892	1047
CTCGCTAACGGCACTAAACC	59.904	20	102	152	253
GGTATTGTCGGAACTTCGCT	59.198	20	197	67	263
TGCAGAAAGCAGGCAGTAGA	59.888	20	189	4389	4577
AGACGATTGAGAGAAAGCGG	59.574	20	222	387	608
AAATTTATTGTAATCTTCCCTC	59.594	26	188	604	791
CCCAACCCACTAACCCATAA	59.541	20	114	11	124
ATCAATGGTCCACATCGGTT	60.057	20	157	85	241
TTCCTCTTGTCGCCATTTTT	59.685	20	279	320	598
AACAATTACAATGTTTATGAAA	58.707	27	104	25	128
TGGTTGTGTGAACCAACTCTG	59.626	21	216	197	412
AGCTTCACCAAGCTTTTCCA	59.993	20	258	2	259
TGCTCAATCATCTCCGTCAG	59.942	20	177	248	424
CAAGCTCATTTTGTGTCCCA	59.691	20	251	1048	1298
ATCGATGTGTTGGCATTCAA	59.931	20	215	9	223
AATGAAAGCGATCGTATGCC	60.067	20	157	920	1076
CTCTGATGGAAGGGACGAAG	59.797	20	203	18	220
CTCCATCATCACACAGCACC	60.121	20	189	107	295
AGAATTTGGAGAGGGAGGGA	60.008	20	104	27	130
GAAAGGGATTCACCTGCCTT	60.443	20	170	1151	1320
TTGATCCTGCAATCTCTCGT	58.388	20	187	9	195
GACTCTTCACAACTTCTACACA	57.679	26	275	822	1096
AAACCCAACTACCCAAACCC	59.955	20	165	5	169
ATTTGCGTCGCCTAATGAAC	60.103	20	245	69	313
TGCTGAGAGTGTGTTGGCAT	60.473	20	107	1219	1325
GTCGTTAGCCCCATACCAAA	59.823	20	199	498	696
GATCCCGTGTGTGAACTGTG	60.005	20	180	17	196

TTTGGTTCAATGGGTTATTCG	59.685	21	196	81	276
GCATGATCAGGGTAAAATCCA	59.776	21	195	42	236
ACAGCCACCATAATCGAAGG	59.955	20	223	324	546
AAGAACGGGCAGCAGTCTAA	60.015	20	159	58	216
AGCTCGGACCTTCAGCATT	59.965	19	110	6	115
ATCTCCTCTGCTCACCTTCG	59.555	20	222	47	268
ATTTCTTGGTGGGAGGGAAT	59.629	20	242	1961	2202
TGTGTTTTATCCCTCGCACA	60.111	20	164	83	246
AGAACATGGTTTCCGAGCTG	60.255	20	166	98	263
TCTCCCCCTCTTCCCTCTTA	60.139	20	233	4123	4355
TCACCTTCTCTCCACTCTCTCA	59.175	22	230	7	236
CCTGCCTCAAGGCTAAACAA	60.378	20	248	128	375
CAGAAATTGCCTCTGTTGTTC	57.468	21	259	22	280
TAATTTCGGCCAACACCTTC	59.938	20	181	1379	1559
TGCCTCAAGGCTAAACAAGG	60.378	20	261	85	345
CCTCTCGTGTTTCTTCGTCC	59.844	20	117	43	159
CGAAGGATATCCCCAAAACA	59.756	20	261	285	545
CAAGTGTGTTTGTGAGTGGG	57.54	20	144	385	528
TTTTGTCCGAAACATCCCTC	59.91	20	187	195	381
AACTCTGCCGGAGAATGTGT	59.727	20	233	1258	1490
GATTCTGGATTATCCTGCGG	59.486	20	221	200	420
GGTTAAATTTTGTCCCTAGTTA	59.109	25	209	35	243
ATTTCTTGGCGTGGTGTTGT	60.419	20	191	442	632
GAAGACACGGTTGGACAAAAA	60.001	21	259	238	496
TGTAGTGGTTCGTGGACTGC	59.751	20	210	41	250
AGCTTCCATGGAGGTTGATG	60.073	20	128	61	188
ATGGGCTCAAATATCGGACA	60.296	20	264	12	275
GATCCGACCCGGATTTTAAG	60.633	20	207	276	482
TCGTGGAGAAACTATCCAAGG	59.998	22	244	762	1005
CCCCTACGTTGAAATTGTCG	60.357	20	231	369	599
TTTCGTTGATTTGAAACTCTAAA	60.167	25	160	341	500
TGACATCGGACCATTTTCTG	59.496	20	221	78	298
TACCTCATCACCATCCCCAT	60.011	20	151	39	189
TCCCGTTGTTGCTTTCTCTC	60.375	20	147	261	407
TAGGAAAATCATGCACGTCG	59.688	20	249	1259	1507
AGGGGTTATCACCTGAATGC	58.864	20	247	269	515
GTGGGCATAAGAGACGGAGA	60.218	20	178	2113	2290
GCGGAGATAGAGACAAGGCA	60.504	20	196	185	380
TTTATGAAGCAAGGGGGATG	59.894	20	240	20	259
AATCAATCCAACCACATCTCG	59.805	21	126	9	134
CATAGCGCCGGAATACTTGT	60.117	20	237	1895	2131
CATTTCCCCCAACTTCACAT	59.647	20	225	3	227
ACTTTCTCGCCTGGATTTTG	59.312	20	142	137	278
GCTGCGAATTTCCATTTTTC	59.666	20	274	187	460
TTGATGGTTTTTGGACTCACA	59.01	21	162	145	306
CGTGTTCATGGAATTTGAAAG	58.134	21	280	713	992
GGAGATTGAGCATCAGGAGC	59.917	20	227	31	257
GGGGATGACTCGTGAGAAGA	60.199	20	274	209	482
TTATTTGCCTCGTCCGAGAT	59.668	20	255	1669	1923
GTGGAAGAGAAGATGCTCGG	59.95	20	178	33	210
TTTGCTAGCGATTCCAACTG	59.062	20	254	447	700
GTAAAACCCGACACCTGCAA	60.924	20	244	88	331
GGGAAAGATTATTGGAACCTT	58.864	22	216	0	215
ATCGAAAATGCCAAAAATCG	59.907	20	185	3196	3380
TCTTGCAATGAAGAACGTCG	59.988	20	148	65	212
GCAAGGCCAATGGAAATATG	60.289	20	156	1715	1870
TCATCTTCAACCCCCAACTC	59.903	20	250	1537	1786
TGCTGGTGTTGAATGGAAAA	60.088	20	160	338	497

AAACGCTCGTAGTGTCCCAG	60.312	20	133	199	331
TGCGTGGTTCAGATTGAGTTAT	59.637	22	280	1131	1410
TCCTCATGTACGTTGTTTATGG	59.393	23	136	92	227
GTGATTGAGGGTGATTGGTT	57.257	20	101	29	129
CAGTCAACGTGCGCATTTAT	59.759	20	247	68	314
CTACCCGATGCCAATTTTTG	60.315	20	257	216	472
AACTCCCCCACGAACTCC	59.896	18	100	42	141
TTTGATGATATATAGGTGTTTT	57.624	26	135	2035	2169
ACGACTTGTCGTGGTTCGAT	60.577	20	243	233	475
TCTCACCTCTTTTTCCAGCC	59.405	20	255	1	255
GGCTGAAAATAGTGGTGGGA	59.933	20	237	34	270
GCTGCCTGTACAGAGGATGA	58.987	20	278	667	944
GGGATGGCTTGTTCACTCTC	59.661	20	214	19	232
TTCAGCCGTTTGGTTTTGTT	60.514	20	273	312	584
CGTTTCCGACTACCCTTGAA	60.103	20	260	3	262
TTTCGTCCAACTGAATGGCT	60.636	20	278	393	670
CGGGATCCCTTTGTATGTGT	59.67	20	203	1887	2089
TATTTGCGTGAACAATGGTG	58.046	20	274	178	451
CATGATAATGCATGTCTCCGA	59.514	21	231	1122	1352
ATCTGTTGGCAAACACAGGTC	60.028	21	109	63	171
TCACACACACGCACTGTCAC	60.437	20	115	17	131
TGAACGGTACGAGCACAAAC	59.764	20	187	419	605
TTGATCCTGTGTGCCTGTGT	60.162	20	141	70	210
TGGCAGAAGTGGGAGTCTTT	59.844	20	192	19	210
TGTGAAAATTTGGTTGCAGAA	59.192	21	187	198	384
AAAATCAAAGGCCCACAATG	59.801	20	218	104	321
GAAGAAAGAGGGGGAGATGC	60.154	20	129	482	610
CCAACTATCCATGAGAAATGA	59.843	23	103	0	102
GGAATCATCACCATGCAACA	60.339	20	201	76	276
GAAAACCTTCGGCTTGAAAA	59.315	20	279	60	338
CCAATCTCAACAACACACGC	60.16	20	204	21	224
GGACGCCACAAATTGTTTCT	59.978	20	246	49	294
CAAATTGCCCCCGTATGTAG	60.202	20	208	453	660
GTGGGGAAAGAGTTTGCGTA	60.11	20	116	84	199
AGTCGCTGCAATTTCCAGTT	59.882	20	166	52	217
GCAGGCAGCTGATATGTTCA	59.979	20	201	12	212
CCCTAGCCTTTGCCTCTTTC	60.332	20	161	108	268
TTTTTCGTGGCATCAATAAAT	57.219	21	207	53	259
ATGATCGACCAACCCTGTTC	59.786	20	155	25	179
CTCGAACCCATGACCTTTTG	60.486	20	134	839	972
GCGACGTTACCCACTTTCA	59.707	19	129	82	210
TGGCAACAAGATACCCACAA	59.964	20	126	569	694
GGGAATCGGAAACCTTGTCT	60.306	20	196	1191	1386
ACAGTTGAACCAAACACCCC	59.721	20	279	280	558
AGATGCGGGGATATATGTGG	59.628	20	278	403	680
CAACGCCATGCATTTATCCT	60.857	20	153	16	168
TCTGTTGCTCCAAATCATTCA	59.262	21	236	1481	1716
CTAACCTTGGGCTCTGATGC	59.836	20	135	77	211
TGTCGCGTTGCAGATCTAGT	59.621	20	209	43	251
GGGATGGGAAGAGCATTTAAG	59.917	21	277	1049	1325
CGAAACATGTAGTCCGCCTC	60.657	20	273	132	404
CGAGTTACAATGAGCTCGCA	60.157	20	238	684	921
TTTGAAGGAATTCGAGTGGG	60.044	20	237	302	538
CGGTATCACCCTCCTTTTCA	59.926	20	129	86	214
TCATTGGGGTGGTAGCTCTC	60.073	20	196	3663	3858
TTCTCTTTCTCACACCCTTTTCA	60.261	23	213	355	567
TTACATTCTCCGACATGGGG	60.713	20	255	339	593
GGTTCGTTTTCGTCGTGATT	59.978	20	112	485	596

CAGCAATTTCGATTTCAACG	59.301	20	149	108	256
CCCCAAACCATCTCATTCAC	60.173	20	228	2075	2302
TGGTCCCCCTTTCTCTCTCT	60.186	20	216	59	274
CATGAATCCAACGTACGCAT	59.425	20	250	1406	1655
CCTTATGCGGTTCTTGGAAA	60.067	20	257	1	257
AGGTCGGAGTGTCTCTGTGC	60.467	20	259	795	1053
TGAAGTTAGGAAATAAGGAGG	58.743	25	108	656	763
TCAACATCCCCTTAAGCCC	59.879	19	112	2938	3049
ATCTCCTCTGAATGCCTTGC	59.39	20	178	63	240
TCAATGCATGATACGCCCTA	60.058	20	237	2147	2383
AATGCTCGACTTATGCGGTC	60.243	20	276	414	689
ACAAACCAAAGTTGCGATCC	59.978	20	185	702	886
GATCGCTCATGCATCAAGAA	59.914	20	274	217	490
TTACCATATTTAAGGGTTATCA	58.789	26	238	262	499
TTGAAACATGAGGCCTTGCT	60.776	20	159	562	720
AGTGGTATGGAGTGGGGGAC	61.032	20	139	45	183
CGTGGATGCCCTAGATTGTT	59.955	20	258	371	628
GGACCGGTTAGACCGAATTT	60.187	20	123	268	390
CCAAGGAGAGTGAGCCAAAA	60.366	20	222	4	225
CGACACGGATTGAATCACAC	59.967	20	191	315	505
CAAGGCATGCAATCAAATGT	59.548	20	261	498	758
AGGCCGGCATAAATAAAAGC	60.417	20	185	223	407
CCACAAATCATGATGAGCAAA	59.533	21	185	2680	2864
CCTCAACACCATCCCACTTC	60.363	20	259	10	268
GACACCATTGGCATTCTTCC	60.326	20	278	1393	1670
TTCGAAAATCAATGGATGGG	60.64	20	229	1370	1598
GAGCTCGGTTGTGGAAAAAT	59.174	20	122	51	172
GTGTACTCTGCACTGAGGCG	59.648	20	150	189	338
GGGAAGCAAAGGAGGTAGGT	59.576	20	135	189	323
AGAAAATTCCGTTTACCGGC	60.312	20	271	26	296
TCTTCCCCCTTTTCTCTCGT	60.183	20	169	869	1037
AGTTGAAGGTGACGCTCAAAA	59.906	21	280	26	305
CGTAAAATTCCGGTGCAAAT	59.832	20	215	13	227
GAACTGTGGAAAGGGAGCTG	59.844	20	117	657	773
AGCAAGTTCGATATATTAAAA	57.104	24	203	31	233
GCGATTCTCATTCCAATTCAA	60.031	21	110	704	813
AAACCCCAAACCCATTCTCT	59.668	20	131	88	218
ACGCCTATCACGGAATATCG	59.945	20	203	1001	1203
TGCAAGAAGGATACAAGGCA	59.42	20	220	180	399
GCGTTCACACCCTCATTTTT	59.978	20	191	27	217
TTTCCACTCACTCATCCAAGAA	59.711	22	202	1	202
ACAAACTAATCAAGTTCCGCA	57.439	21	216	347	562
GTTATATCTATAGGGAGGGTTA	57.293	26	177	1243	1419
TTCGATGATAACTATGGGTTTG	57.589	23	250	401	650
ATGGAAAGAAGGGAAAGTCAA	57.773	21	258	1356	1613
CGAGCCCTTCCTAGGACATT	60.59	20	233	26	258
CCCAAGAACCGAAGAGTCAA	60.224	20	202	5	206
TTCAAACCGAGCTTGAGATGT	59.867	21	255	42	296
CACTTACACACGCACACACG	59.848	20	271	204	474
AGCCCAACGGCTGATTATAC	59.07	20	138	49	186
TCAGGATCTCACCTTCACCC	60.048	20	243	51	293
TTCCTCCTCCTCACACTGCT	59.986	20	203	696	898
CTCTGACCTTGAGGGCTTTG	59.982	20	278	140	417
ATTTGCGATTTATGATGGCG	60.802	20	265	1032	1296
ACTCGTGAGGAAAAACCGTG	60.149	20	258	370	627
GCTCAGCCCAACTTCCTAAAC	60.256	21	242	30	271
AAAATGCACGCGAGACAACT	60.837	20	128	239	366
TTCTGTCCCGTCTTCTTCGT	59.844	20	175	19	193

ATGGCCGAACATATCAGAGG	59.917	20	159	789	947
TGTTTGCAGAGAAATGAAATG	59.75	23	221	66	286
TTTGCATGTGTTGCAAATGA	59.691	20	249	38	286
TGGCTCCAACATCACAAAAA	60.088	20	205	250	454
AAGGAGGTGTTATGAAGGGAT	58.028	22	141	72	212
CTCCGATTTCTTGGTGTGGT	59.966	20	198	101	298
TGGTCCCAAGTAGGGCTAGA	59.688	20	226	1919	2144
ATTACAGCTCCTACCCGCAA	59.73	20	231	296	526
CGAAAAATTTAAAATCAAACG	60.521	25	223	0	222
GTCCCGGGAATGAAGAAGTT	60.306	20	264	326	589
TTGGTGAGGTGGCATCATAA	59.924	20	182	235	416
TGCAGATTGACGAAGGAAGA	59.522	20	140	969	1108
TGGGAGGAGGCTTAGGATCT	60.169	20	112	3	114
TAGGGGCAAGCCCTTAAAAT	59.93	20	158	920	1077
CACTTATAGATGGGTTAGCGT	59.972	24	254	148	401
AGCCTAACCTTGGGTTCTGA	58.789	20	246	150	395
AATTTTCGACTTTGCCGTGT	59.615	20	240	15	254
TGGAAATGAAGCACCAGAAA	59.247	20	107	18	124
TTGTGAGGTGATGTTGGAGTG	59.581	21	159	17	175
ATGTGGTTTTGGTCCCACAG	60.668	20	271	7	277
CGGTAGCCATCACAATTTTT	57.635	20	264	436	699
CTTGGTCCAATGGGTTCATC	60.173	20	249	193	441
GCCGATCATGTCCTCAAAGA	61.159	20	259	97	355
CCACGCCAGTCAGGTAAACT	60.171	20	143	67	209
CCAATGACACGACACAAACA	58.974	20	187	568	754
GAGGCTTCAATCCGTCACTC	59.81	20	115	710	824
TGGTGTAAAAGGGGGTTAATG	58.727	21	226	145	370
TGGACACCCCAGATTGTTTT	60.21	20	177	261	437
TGCTTACTGTTGTATGGGGTGT	59.424	22	238	166	403
ATCGGATCTGCGATCTAACG	60.199	20	232	720	951
TTGTCCCCAAACAACGAAAT	60.206	20	231	838	1068
AATACGAGACCGAAAGGAAA	59.163	22	210	2	211
GTTCATGACGGGCTAACCAT	59.82	20	180	3078	3257
ACCAATCCACTGCATGAACA	59.967	20	180	74	253
GAAGCAAATGGGGTGATGAG	60.461	20	239	2566	2804
AGATTCAGACGCATTTTGGC	60.221	20	254	2109	2362
GCCCCTACTACCCAGTTGCT	60.517	20	163	1113	1275
TGATCTGGAATCTGCGATGT	59.197	20	191	24	214
TTGAGGACATTTATTCGTCGG	59.946	21	160	406	565
CACTCATACCCTCCCTCCAC	59.38	20	272	304	575
TGCAACGCCAACTACAAAAG	59.911	20	165	9032	9196
TGCCTAACGTTAAATGGGCT	59.609	20	248	1	248
GGCTTCCAAAGCTTCCACTT	60.743	20	280	260	539
CCACTAACCCAAACCCATCA	60.605	20	118	13	130
TGCTGTGAATTGTCCAGCTC	59.992	20	248	915	1162
ACTTAGCCAAAACCCCCAAC	60.221	20	123	6	128
AGAATTGGTGGAAAGATTAGA	57.58	24	267	7	273
TTCCTTCAATCCATGCAACA	60.049	20	205	513	717
TCCCCTGCATGTGTTCATTA	59.924	20	269	150	418
ACAACAAAAGGCAAAGGCTG	60.284	20	215	818	1032
GGCTTGCCCTTAACCCTATC	59.93	20	225	405	629
CCCCAAGAACACTCAAGAACA	60.133	21	274	317	590
CCACCTTGTAGCTTTTCCCA	60.103	20	219	1130	1348
CACTTTTCCAGTCTGCTCCC	59.844	20	147	398	544
ATCGGACCGGATCGTTAATA	59.254	20	209	134	342
TTAAACAAAGCGTGCAGACG	60.052	20	269	2511	2779
GAAGATGTGGCGAAGGTTTG	60.636	20	192	112	303
AGATTTCGATTTCCCCGAAC	60.265	20	194	208	401

TCCTTTGTTTGCCCCAGTAA	60.472	20	174	399	572
CAATATTCTCCGAAGCGGTG	60.597	20	256	43	298
TATCAGAGAAGGGCAGCACA	59.547	20	239	42	280
TGATCCGTAGACATGCTGTTG	59.731	21	197	154	350
GCCTCTCACCGAGTGAAAAC	59.851	20	249	87	335
TTTGACCGAACCGTTGTGTA	60.004	20	189	2312	2500
TGCTATGATGCAAATCACCTTC	60.103	22	276	105	380
GTGGACGGCCATAAGAAGTC	59.556	20	220	233	452
TCGGGGTATCAGAAATCGAG	60.029	20	234	12	245
TAGGCTCGAAAAAGTGCTGG	60.514	20	232	48	279
GGCGCCATCTTTTTCTTACA	60.209	20	158	625	782
CAATTTTTCGATCATGTGGG	58.818	20	157	13	169
TCGTGTGTGTGAATTAAAATGA	58.136	23	259	103	361
TATATATGGGTTATCACCTGAT	57.071	24	147	465	611
CATTCTGTGTTCTCTGTTTTCGA	59.696	24	267	909	1175
GTGCATGGCGTTGTATTTGT	59.474	20	202	1999	2200
AAGAAACCGAAAAATGTGCG	60.11	20	278	1323	1600
CACCCTCTCTTCTGGTCAGC	59.986	20	230	537	766
ACCTGCACCAAAATGGAGAG	60.111	20	134	52	185
ACCTCCCAGCTCACGTTCTA	59.867	20	272	4	275
CATTCCATGGTCCCGTTTAT	59.505	20	213	74	286
TGCCGTATATGGTGCTCATTT	60.358	21	280	202	481
AAACTGCTTTCCTTCATGGG	59.17	20	204	100	303
CCTTCAGCTGCTTCTCCTGT	59.745	20	257	252	508
CCAACAGTTTGGCATCAGAG	59.288	20	252	87	338
GTGACAGTGCGTGTGTGTGA	60.437	20	207	57	263
TCACGTCAGGTTCACCATGT	60.005	20	214	229	442
GAGAAGGGGAGAGGGACTGT	59.661	20	189	54	242
TCAACAGAGAATGCAAGCAAA	59.6	21	164	80	243
TTGAGTTCGGATTAGCCACG	61.157	20	264	174	437
CTCCACTCCAAACCACCATT	59.82	20	210	371	580
TTGTCCGTATTCATTCCGTG	59.395	20	263	511	773
GGTAAGGGTAGGGTACGGGT	59.101	20	254	64	317
CCTTAACATGTCGGGTTCGT	59.853	20	197	9	205
TCCATTCCGAAAATCAAAGG	59.872	20	161	176	336
GACTTCCGCCTTGTTCTTTG	59.853	20	205	239	443
CGCTGAGGGAGACAAAAGAG	60.126	20	222	439	660
CAATACGGGACACTTGACCA	59.415	20	257	717	973
AAAATCAAAGGCCCACAATG	59.801	20	116	1085	1200
GACATCTCCCTCTCCGACC	59.583	19	273	249	521
CTCTGTCTCTCGCTCTCGCT	60.182	20	276	428	703
GACTGTGAGGAAACGTGCAA	59.88	20	258	465	722
GGGGAGAATGTAATATCCCGA	59.992	21	222	24	245
TAGCCCTAACTCGACCCAGA	59.83	20	224	41	264
GCAGCCGTTAATCTTCGAGT	59.481	20	171	1109	1279
TTGGAGGTGAAGAGAGGGAG	59.375	20	254	167	420
CCGCCAAATGATATGGGATA	60.496	20	132	210	341
AATTCAAGGATTCAAGCCCA	59.505	20	101	21	121
GATGCCCAAAAAGAACACTCA	60.103	21	280	50	329
AAAACTCACACGGCACATGA	60.16	20	243	91	333
CGTTAATGAAAGTGATTCCCC	58.43	21	183	6	188
AGGAAATAAGGAGGCGTTATG	59.145	22	128	184	311
GTTGGACTCAAGTCATGCGA	59.837	20	181	273	453
CCCCTTCATTCAACACCAAC	60.21	20	102	9	110
ATGTCTCAGCCGATCGATTT	59.658	20	172	1955	2126
GTGTGCAATGCAACAGGTTT	59.621	20	154	2217	2370
TTGCCTTTAATCGATCCTGG	60.031	20	154	26	179
CCGTACTAGCCGACGAACTC	59.898	20	250	513	762

GCTTGGTCAGTAGCCACCAT	60.142	20	214	285	498
TGGTTTTGGATGATGGATGA	59.707	20	158	23	180
CACTAACCCACCAACCCAAC	60.126	20	222	47	268
CCCCTTGAACTCCAGCAATA	60.066	20	205	199	403
CAGCCACACTTTGTCCACTG	60.348	20	104	2886	2989
CCAGTCTCCCCAAATGAAAG	59.521	20	196	243	438
AGGATTTTCCGACTCGCTTT	60.208	20	252	20	271
CGAATTCTCTCTCTGCAAACC	59.066	21	104	288	391
GGCGGCAGAGAGAGAGAATA	59.676	20	218	159	376
TGTCCGAAAAGGCAAAAATC	60.053	20	173	25	197
GAAAAATGGGTTCCTCACCA	59.767	20	280	302	581
ACCCCGAACAGAGTCAAATG	59.966	20	276	599	874
TGCTCATGAGGAATAACAAGC	57.985	21	261	1440	1700
TTTGAATGGGCACTCTTGTG	59.691	20	267	1211	1477
GTTAGCCACCAATGAGGCAT	59.962	20	108	606	713
GTCTAGTGATGACGGGGAGG	59.53	20	199	0	198
CTCCACTTGAATTCCTTCGG	59.665	20	232	320	551
TTCTGGGAACTTGAACTTGGA	59.697	21	250	351	600
ACGTCTTTGTGTCGAAACCC	60.012	20	175	176	350
TCGATAAAACTTTACCAACACC	58.6	23	250	15	264
CAGCGGAGGAAGAAGATCAC	59.95	20	262	198	459
GGACGTCTTTCTTGAGCAGC	60.142	20	201	6	206
GAAAACAAAATGGGGAGCAA	59.916	20	242	18	259
CACGACGCAACATGATTTTT	59.59	20	107	4	110
AGGGGAAAGAGGAGAGGATG	59.63	20	244	555	798
TCCCATTTGTGTGTTCTTCG	59.541	20	101	10	110
CAACTTCGGCAACGGAATA	59.673	19	154	42	195
TGTGTTTTGACAATATTTAGTGT	58.633	27	275	189	463
ATTCTCGGTGATCATTTGGC	59.9	20	211	4527	4737
GAGGACGTTGTGGTGGTCTT	60.009	20	187	200	386
CTGCACTAACGCCATTCCTT	60.27	20	174	320	493
AAATAAGGAGGTGTTATGAAG	59.323	24	133	95	227
AATTGGGAGGGATAAATGGG	59.846	20	248	1358	1605
TGTGGCTTGAGATCGTGTATAG	57.933	22	245	136	380
ATGATGGGCGATTGAACACT	60.348	20	210	159	368
TTTTATGTAAATTGTCGTGCGT	57.373	22	225	210	434
GTTTGCCCAAAATGACCCTA	59.801	20	256	1	256
GAGAGAAGAGACTGCGGTGC	60.292	20	271	1453	1723
TTCAACCAGGCAAAGACCAC	61.075	20	190	135	324
ACCGGAATAGCATCAGTTGG	59.955	20	222	6	227
TGGCTGTCAGATGATGTAAGTT	59.256	23	174	355	528
GCATTCGGTTGATTATGCAGT	59.981	21	243	953	1195
TCAGATTGGCTCCATCCTCT	59.761	20	257	385	641
GAACTCCCCTCTCTCTCGGT	59.807	20	192	17	208
CTTTCTTCTTCATTTCGCCG	59.953	20	127	4	130
AAACAGGTCCATGCATTGTG	59.42	20	257	534	790
GCACTATCTCTCCCTCACCG	59.827	20	119	323	441
ATGCAGTGGATTTGGTGGAT	60.203	20	194	179	372
GAAGCCTCAAATCACAAGCC	59.82	20	141	107	247
TGTTCGCTCGAGAATATCCC	60.177	20	278	0	277
ATGAGTCGTAGTTGACGCCC	60.142	20	199	42	240
CAAGAGCTGAAGATGTGATTG	60.022	22	193	264	456
GTTCGAATGGATTTGTTGGG	60.17	20	158	393	550
GTTGTCTGAAACCCTTCCCA	59.943	20	114	246	359
CAGCAAACCAGCTAAATGAAG	59.536	22	215	130	344
GCGAAGAAGAGGGGAAGAAT	59.789	20	255	38	292
TCTACAGCGAATGATGCCC	59.772	19	228	844	1071
AATCATTCCATTCCCCGATT	60.345	20	245	38	282

AAATAAGGAGGTGTTATGAAG	59.323	24	242	34	275
TGGCAAACACAGGTCACAAT	60.008	20	134	34	167
GGTCGTCGGATTTCATTTTG	60.309	20	257	2760	3016
GTGTCGGAAACTCAGGCATC	60.667	20	262	1391	1652
GGCTTCAACCTTGACGAAAC	59.717	20	211	4	214
GATGAGCAGAAATGAGGCGT	60.37	20	152	14	165
TGTAAATACGGTCTGTGCATGT	59.46	23	183	289	471
TGCTTTGATTTGATGGTTATGG	59.832	22	164	4300	4463
TGGGGAAGAGACCAAGACAG	60.229	20	137	254	390
AAAATAACCAAAATCAGCATG	59.788	24	216	109	324
ATAACCCGTGTGTGGGTTTA	57.729	20	243	89	331
AGCCGTTTAAAGTGTGGGAA	59.609	20	219	32	250
CCGTTGTCATAACCCACCTC	60.232	20	176	268	443
GTGGAACTTGTGTTTGTACCCA	59.797	22	200	18	217
CATGCGCAAGTACAACAACA	59.354	20	274	235	508
AACTTGTATCACTGGAAGAATT	58.329	25	273	104	376
CAATTTTCATTGCCCCTCAC	60.309	20	153	69	221
GACGAGAATGCCCCTGTATG	60.483	20	201	330	530
TAGCGATGGTGAGATGTTGG	59.673	20	170	2	171
AGAGCCACGTTAGGCTCAAG	59.639	20	262	96	357
TCAACAGAGAATGCAAGCAAA	59.6	21	152	45	196
GGGTTCTGAGACCGGGATAG	60.842	20	274	0	273
AAGGAAGCGAGGTAGGCTTT	59.504	20	191	199	389
GATCTTAGTGATTTTTCTTCGT	60.02	25	249	666	914
AAACGTGCGCTACTACCCAT	59.66	20	252	571	822
CGTGTGTCAGCGTGTCTCTC	60.685	20	133	1661	1793
TGGTTCATGCCATTGTGAAT	59.781	20	123	40	162
GAAATTTCACGAAACAACGAA	59.877	23	253	304	556
TCTTCCAAGATGGGAATGGA	60.395	20	188	111	298
AACCGTCTGGTCATCCCTTT	60.746	20	262	558	819
TTCTCTCTTGGTTGGTGAAGAA	58.955	22	170	53	222
CCCTCTGAAACCTCGTAGCA	60.388	20	236	1627	1862
GGCCTAATATGCCTGCCT	57.733	18	269	429	697
ATTCCAAGCTTTAATTGCGG	59.212	20	135	441	575
TATCCCGTGGGTCAAATACG	60.576	20	242	954	1195
TGGTTATCATGGATGCGAAA	59.891	20	197	596	792
TTTCACCACCGCCTTAATTC	59.938	20	250	27	276
TTGATATCCCCATCCTCCAA	60.088	20	218	3803	4020
CCTTTCAGGCATTTAAGTGGA	60.122	22	275	1747	2021
GGTTTCAAAGGGAGGGAGAC	59.912	20	246	879	1124
TCAGTTTCTGAGTTTTGAGGTT	59.835	24	108	747	854
TAACCCCCGGAGTGAAGAAC	61.238	20	221	9	229
ACCTCATTTATTGTCGGCCA	60.331	20	158	1333	1490
GAGATGTGGTGGTGGTGATG	59.801	20	140	384	523
AAAGTCCAAATGTTGGCGAG	60.11	20	128	1545	1672
TAAATCACAAAACCCACGCA	59.969	20	131	347	477
CCCAGCAACTGTTGGCTACT	60.312	20	259	285	543
TTTTTAGTAGGGTTTTCAAGTT	59.564	26	266	355	620
CATGCTTGAATGAAAACCACA	59.576	21	126	268	393
TGTAGGGGCAATGATGTAAAA	59.363	22	228	29	256
CAGCCCAATAACTCAACCTAC	59.892	22	145	0	144
GGAGCCTCCGAACTTTGAA	60.324	19	187	57	243
TCCACTGTCTTGTGCCTCAG	60.022	20	259	759	1017
CGTGAGAGAGAGGCTGTGTG	59.757	20	202	9	210
GGAAAGAAAGGGCGAGAAAG	60.312	20	160	765	924
ATCCTTTGAATTGCAGCTCG	60.352	20	270	1127	1396
TCTTGTGTGTGTGCATGTGTC	59.171	21	280	69	348
TACGAATCTCAAGGGGCAAC	60.074	20	212	99	310

CGTAGTTTGTGGGGGAAATAA	58.862	21	280	915	1194
ATCAATGGGTCCAAATGGTT	58.959	20	230	28	257
AATTGACAGCGAGACCGAAT	59.7	20	115	2	116
TGCGCAACCAATGTAATAGC	59.731	20	233	786	1018
CGTGTCCGGTTTGTGTATTC	58.9	20	248	104	351
CACATTGTCACCCTCACCAC	59.846	20	164	215	378
TCGAAGGTGACTATCCCGAC	60.073	20	242	107	348
GCAGCATCCTTCACCATTTT	60.081	20	217	17	233
TTGAGTTTGCAGTAGGGTTGG	60.154	21	271	7	277
TGAAACAACATGGTCCGCTA	60.111	20	270	679	948
GCATAGAGGGCAAGAAGACG	59.978	20	194	425	618
CGTTTTGATGATATATAGGTGTT	59.637	27	237	378	614
CCCTTAATCTTTGTGGTTGTGA	58.994	22	264	1905	2168
TTTGAGTTTGCATCTAAGAAGG	59.828	24	148	804	951
TTTGGTTTTATCGAAGAGGCA	59.707	21	255	850	1104
GAGGGAATGGGAGGTGATTT	60.133	20	198	243	440
ACAGGAGCACTACAGTTCACG	59.976	22	265	2128	2392
CACGTGCTGTAATCTGTGCC	60.333	20	234	380	613
ACATTCGGTTGAACCCTCAG	59.966	20	108	191	298
GGATTGATGAATTTCCATTCG	59.221	21	192	1759	1950
AAATCCCAAATGATGGGTCA	59.991	20	197	1977	2173
TTGACCAAGATACACCTTGCAT	59.499	22	188	14	201
GCTCTTTTATTTACCTTTTATGC	60.067	26	213	337	549
AATGACGGTTGTGGGACTGT	60.284	20	232	0	231
GAGAAATTTCGATGTTTCCACA	59.067	22	269	735	1003
TATGTTTCGGCCCGGTATTA	60.165	20	136	63	198
GGGTTCAATTTGGACGTTTG	60.206	20	269	530	798
ATGAATCTCATGTTATTGAGTG	58.057	26	207	671	877
TTTTTCAACGTTTGCCATCC	60.846	20	166	206	371
CTGAATGCCCTCCAAATCTC	59.629	20	268	17	284
CTTGTGAACTCCGATGGACA	59.676	20	155	449	603
TCTCGAGCAACAGAGCTCAA	60.008	20	269	105	373
GATGGTGGGTGAGAAAATGG	60.173	20	239	396	634
TCGGCAGAAAAGAAGAAGGA	60.066	20	112	430	541
GATGGCCCAGATTTGTTTTG	60.309	20	101	107	207
GGCGAACATGATGAATGAACT	59.954	21	279	24	302
GAGAGAAGTAGCAAGCGCGA	60.955	20	182	9	190
GCACACTTTTGGCCTTTGAT	60.118	20	176	3	178
CACACAAGCCTCGCTCTTTT	60.571	20	222	658	879
AAACCGTTCAAGAAAAGGGA	58.669	20	227	1855	2081
CTATCGAGCGTGTGGCAATA	59.856	20	150	20	169
CTTGTGGCTTGCAAACATCT	58.926	20	163	72	234
TCCCCAAAATACCCTTTATGC	60.029	21	264	210	473
GCATTTGAAAGGTTTTATATGA	60.438	27	200	451	650
CTTACGGAATTCCACTGGGT	58.909	20	228	33	260
TTGTATGCTTTCCGATGCTG	59.833	20	139	563	701
AGGTGACCCATTCCACACTC	59.817	20	265	123	387
TCAATGGAGGTTGGGTGTTT	60.21	20	247	267	513
AGAGCGAAGAAAGCAGATGG	59.717	20	163	1337	1499
AATGTGGAGCAACGTGAACA	60.16	20	265	2148	2412
AAAATTCTGGCATGCCTCTG	60.214	20	168	4810	4977
GGTGGTAAATGAAGAGGCTCC	59.954	21	187	5	191
AAATGCTGGTAGAGGCAACG	60.27	20	238	341	578
TGATACAGGTGTTCCAAACAAT	59.777	23	246	6311	6556
AGGGAGAGGCTTTGGATGAC	60.596	20	236	35	270
TGCATGTGTGGGGCTATTTA	59.953	20	220	1003	1222
AAATTCCGTTTTTGCCTTCC	60.292	20	179	197	375
AGAAGTCGGCAACCCTGATA	59.694	20	159	1170	1328

TCGGGCAACTGGAGCTAATA	60.732	20	213	1	213
TGCCACCCTAGATCCGTTAC	59.955	20	120	572	691
AACAAAAATATAGCTAATGCG	58.112	24	270	385	654
GGTCAAGGGAATCCCATTCT	60.133	20	182	14	195
GGGAGAGGATCAAGAGAGGA	59.763	21	199	39	237
TGTATCGCCCAAAGGAGAAC	60.074	20	223	2484	2706
TGCTTCATAACTGCCTTCCA	59.42	20	277	453	729
AATGGGACTGGCGATTGTAG	59.955	20	256	106	361
ACCGGTTGGACTGGTTGTAA	60.269	20	270	1311	1580
TGTGAATGGAGGACAAACCA	59.935	20	171	186	356
CTGGCAACAAATATGACTGCA	60.025	22	117	341	457
CGAGAAAGATGATTTGTTGGG	59.555	21	250	4000	4249
TTATCTTTGAATTCAGCACGC	58.057	21	143	35	177
TTTTGATGATATATAGGTGTTT	58.782	27	151	615	765
CCGCAAGTACGAAAACAAGG	60.659	20	244	554	797
TTCAAGAATTCCGCCATCTC	60.155	20	132	1756	1887
CCCATTTCTAACTACCCAAATC	59.962	23	211	232	442
TGGCTTCTTTAGGGCTCTTG	59.587	20	186	1103	1288
AATGCCTCTGCAAAAAGCTG	60.523	20	213	2850	3062
CCCACCCCACTACTCAAGAA	59.959	20	115	9	123
GCTTTCCCATTTTGCTTTTTAAT	59.88	23	280	646	925
TTCAGATTTTGTGATTTGGTGT	59.89	23	257	247	503
AAACGGCTTGGATTCTTTCC	60.431	20	148	397	544
TATCCCTTGCACGACGAACT	60.657	20	273	523	795
GCTAAGTGGGGTGGAGGATT	60.328	20	196	1575	1770
GCCTCTGCTATTACATGCCAC	59.75	21	210	967	1176
TGGAGAAACGAACTGGAACC	60.088	20	253	204	456
TGTGGCAGGTTATTCATGCT	59.152	20	200	432	631
CACCATGACGGCAGATGTAT	59.399	20	260	627	886
ACGGCTTCACCAGTTTCTTTT	60.158	21	139	246	384
TCGATCTTGCGAAATCAATG	59.769	20	114	27	140
TCACACGTTCTTCCCCAGAT	60.51	20	144	45	188
TGCGCTCTGATGAAAAATCA	60.488	20	227	756	982
GATGATTGCACCATAATGCG	59.921	20	166	2638	2803
CCATGATGTGACCGAGATTG	59.918	20	235	1036	1270
GTGCATCCATCTGAGCATTG	60.233	20	247	185	431
GAAGTCGTTCTGAGCTGCCT	59.751	20	240	2257	2496
CTATTTGAGGGTCCCACCAC	59.259	20	240	567	806
TCCCTTAGACCTTACATAATGA	60.001	26	253	13	265
AGATGCTGGAATCTTCGTGG	60.218	20	127	162	288
ACTTCCAAAACTGGGAACCA	59.425	20	143	325	467
TCCATTAAGAATTTCCCATGC	58.888	21	180	1621	1800
ACGGTTAAGATTCAGCACGC	60.278	20	198	21	218
GAAGCTGGTGCAATTGTTTG	59.322	20	251	92	342
CCAATTTTGAAACGGACGAG	60.472	20	148	1	148
TGACGATGAGACGTGTAGGG	59.701	20	277	305	581
CTTTCTTCACTACTGGAACTTT	57.353	25	223	53	275
GATAAGAACTCTGGCTCCAAG	59.371	22	159	450	608
GGGTCAGACAATTTGAACGG	60.353	20	231	184	414
AAAAATCTCAGGGACGGGAC	60.306	20	260	3363	3622
TGCTTCCACGGCTAAACCTA	60.762	20	265	1205	1469
GTGTCGATTGTGTTCATGCC	59.975	20	223	61	283
ATACTTTGGCCCAGTTCGTG	59.993	20	191	3050	3240
TCGAGTGTTCGTTAGTTAGTGA	59.876	24	217	30	246
CTACGTCCACGGGAGTTTGT	60.028	20	102	1	102
TTCGAAGATCAACGGACGAT	60.603	20	204	195	398
TTCCCATCGATTGAAACAAA	58.94	20	225	16	240
CGTTCTTAATTAGCGCCGAA	60.347	20	111	1023	1133

CGTCGATCTGGTGAAATCAA	59.648	20	250	385	634
CGAGAGTGAGGAAAAGAGCG	60.269	20	193	1068	1260
AGTCGGGAGAAATTCCCTGT	59.935	20	162	35	196
TGACGTTAAGAGAGTTTTCACT	59.855	24	157	1026	1182
TTTGGCAAGGGTTTGAAAAG	60.081	20	205	205	409
CAATTCCGAGGAATCGAGTG	60.594	20	189	221	409
AACATCACCTGATGGAACGG	60.78	20	254	58	311
TTCCTCACACATTCAGCCCT	60.656	20	278	144	421
CCACCTCTACGTGCCATCTT	60.134	20	209	191	399
GCAAACGGTATAGGATCGGA	59.923	20	201	238	438
TGGCTCTCACACTCACTCTCA	59.747	21	182	111	292
CTGGCAGTTGGTTTGGAGTT	60.149	20	166	61	226
TTGCAGAAGTCGAAATGGTG	59.84	20	254	417	670
AACACGTGGAGATGACACCA	60.005	20	176	556	731
TCACCCAGATTTTGCAAGTTT	59.601	21	208	158	365
TCACACAGATTAAACACTGAA	60.128	26	223	597	819
TGGAAATTTCGACACGCTTTA	60.605	21	252	566	817
CGCGAAGTACCTGCGTTAT	58.956	19	176	133	308
AACTGCTGGACCTCCACAAC	60.159	20	194	308	501
GACAATATCAGCCGAGGGAG	59.653	20	215	15	229
ATGAATCAATCACGTTTCGC	58.575	20	219	14	232
GCGGTGATGGTAAGGTGTTT	59.859	20	189	67	255
CTAGTCTTTCTCCCGTGCGT	59.496	20	275	19	293
CAGCAAGAAAAATACACCAGC	60.298	22	121	108	228
CCTTGGCCTTCTGACATCAT	60.073	20	191	134	324
GCCTGCCCTCCTATCTTCTT	59.811	20	205	740	944
CGTTGGAGCGATGTATGTGT	59.596	20	230	84	313
TACCTATTTCGAAGCCCGAG	59.315	20	277	285	561
CCCCCTTAACTACCACTTATGA	57.22	22	213	368	580
TGGACTAAATCCCGTTCTGG	59.926	20	279	1635	1913
AGGGATTTGGGACGATTTTC	60.131	20	148	199	346
TGATCGGGTTAGAAACGGAG	60.066	20	148	14	161
TGAGCCTATCTTGGAGCACA	59.547	20	187	413	599
TCTTCCCTCTCATCTCTCTCG	58.703	21	121	87	207
ATTGTTCGGCGTTAGGAGAA	59.708	20	179	51	229
GTTTCATCCCTCGCACATTT	59.939	20	263	197	459
ACGTTAAGGAGGGGATCCAT	59.651	20	255	22	276
CGTCCACGGAGAGGTTAGAG	59.861	20	249	184	432
ACGAGCGCATAGCCTTTTTA	60.006	20	119	1375	1493
ACCTTAGTTGCGAAGACGGA	59.875	20	183	28	210
GGTTTCTTACTCGGGCTCCT	59.713	20	216	212	427
GAAAAATCAAAGGCCCACAA	59.916	20	265	74	338
GAGTTTATCAGCGGTCTCGC	59.985	20	231	3401	3631
GGCTTTCTTAACTTGTTGGAAC	60.376	23	207	1	207
GTGATCAACATCCGTGATCG	59.925	20	123	663	785
GAATTCGGGAGATGTTCCAG	59.483	20	172	190	361
CCTGACCCTTTTTGAGATGG	59.521	20	208	71	278
TATACTTACCCACTGCGCCC	59.982	20	239	254	492
TTTTCCTGGAACGTGAAAATCT	59.98	22	279	162	440
TTGTACCTAAAAAGTTGTTCCC	57.805	23	280	443	722
CATCCCACCTACACCACTCC	60.238	20	158	3416	3573
CGTCACAGCCTCTTCAACAA	60.025	20	119	648	766
GGTCTTTGTCGTGGTTTCGT	60.012	20	257	508	764
TGAGCCCGTAAATCACACAA	60.111	20	178	298	475
TTCTTCCACGTCCTCTAGGTG	59.338	21	158	228	385
TCTCTCACGCACTCTCACAAA	59.76	21	167	65	231
TTTCGTCGTTCATTGCAGTT	59.322	20	124	7	130
AAGGAGGTGTTATGAAGGGAT	58.028	22	238	209	446

TCGAAAATTGAATGACAAGGA	58.201	21	180	255	434
ATTCCAGCAATGAATGGCA	60.025	19	199	96	294
TTTCTCATTGGCAGTCACCA	60.24	20	129	87	215
TTACAGATCCGTTCCCATCC	59.75	20	139	14	152
TTCGGACATGAGCAATTGAG	59.799	20	272	67	338
TGTGTTTTCTTCCCCACACA	59.976	20	187	287	473
CTTGGAGCTTTGATCCTTGC	59.955	20	153	26	178
GGGGGCATTTTGCACTATTA	59.795	20	239	259	497
GCAACTTGCCATCTCCTCAT	60.226	20	195	420	614
AAATTCAAGAATGCTGCCCA	60.585	20	268	247	514
TCACTGGAATGCTATGGTGC	59.679	20	208	2	209
ACGGATTTAAGGGTTATTACCT	59.498	25	117	136	252
TTTGCGCATAAATATTGGTTTC	59.89	23	264	0	263
GAGGCGTGACCGAACATAGT	60.142	20	245	29	273
TTAGTTATATGTATGGGGATGG	57.868	27	154	75	228
TCTTTTTCCTGAACGATGAGC	59.443	21	273	1474	1746
TTTCTTTCCTTTGAGCATACG	57.213	21	188	11	198
GAAATGAGAGAGAGCTGCCG	60.24	20	144	379	522
CCAGGCAAATAGCTACCGAG	59.861	20	201	133	333
ATCAATCTTGGGCTCCTCCT	60.037	20	184	2995	3178
ACTCGGAGGTGAAGGTGAGA	59.835	20	265	3	267
GGATCTTAATTGGTTCGATTTT	58.914	23	154	665	818
TTATGGTGGCTGCGGTTAAT	60.343	20	262	509	770
TGAACTTTCTCAGCCACCCT	59.844	20	280	211	490
CCTATGGTTGTATGGTTTGGAG	58.377	22	156	53	208
CCATCCATTTGCAACCATAA	59.232	20	225	34	258
AACTGGACCGAAAAATGCAC	59.978	20	212	460	671
TTGTTCAAAATTCGTCCAAAA	58.175	21	242	175	416
TTCTCTAACTGTCCCGTCCC	59.137	20	171	42	212
AAGAGGTTATCCCTCGTCCA	58.594	20	246	457	702
CAGCCCACTTTGACCAACTT	60.149	20	254	429	682
AACCGCCTGCATTGTTTCTA	60.637	20	140	5	144
CATTCGAACATCATCATCCG	59.883	20	251	362	612
TTCCTTGGACCAAAATAGCC	59.019	20	187	38	224
AATTGATCGCATTCAGGGAA	60.414	20	261	380	640
AAACAATTTTCTGGCCATGC	59.945	20	258	137	394
CTTCATACCATCCCACCAGC	60.34	20	133	154	286
AGTTAAGGGCCATCAGGGAT	59.789	20	127	166	292
CGCTGATGTGATCTCAATGG	60.225	20	244	96	339
CTGGTGCTCAATGCTACTGG	59.465	20	279	602	880
GGGTCAATCGGCAAAAATAA	59.773	20	218	492	709
TAAATTGCTCCGTCTCCAGC	60.352	20	156	88	243
GCCGTGCAAGATCGATAATA	58.748	20	198	1	198
GGGTTGCCAGGTTGAATAAA	59.801	20	209	263	471
TGTAAGCAGGTATCATCATAA	58.854	24	111	109	219
GATGCCGCCTAAAGTGAAAA	60.209	20	210	10	219
TTACACTCCCACTCCCGTTC	59.966	20	277	277	553
GTGTAAAGCATGGGGAAGGA	59.933	20	198	350	547
AAGGCATGAGGATTTTAGAAA	59.175	23	121	183	303
CAAGGTACTCGCTACGAGCC	60.037	20	267	142	408
TGCCCTCATATGTTGTGGTG	60.39	20	250	91	340
AACTCGGATAACACGGGATG	59.813	20	193	55	247
AATTGCCTTTCAAGGTTTGG	59.064	20	188	581	768
TGACTCACTATGGGCACAGC	59.862	20	108	375	482
GAGTGTATGGTGCTTGGTGG	59.01	20	191	35	225
CGGTTTGTTTTCGTGTTTGA	59.603	20	158	509	666
TGCCTACGCATCAAGACAAC	59.871	20	205	0	204
CGAGGAGAGGAGAGACATCG	60.088	20	132	151	282

AAAACCGGAAAAGTGGAAGA	59.967	21	194	348	541
AGGTGGGCTTAGTTGAGGTG	59.208	20	191	41	231
TCAATCAAACCAACGAAACAA	59.048	21	202	655	856
TCAATGTAAATGCCAATCTCTT	57.835	23	197	298	494
TGCCCTTATTTGCTGAGGAT	59.668	20	182	759	940
CACATTCTGAGGATGGAAATC	59.933	22	280	2118	2397
TGGCAGTAGATTCATTCTATCT	57.69	25	250	7	256
ACTTTCCTGGCTCCCAAGTT	60.11	20	264	56	319
AATCTCTGCCACCTTTCCCT	60.074	20	144	670	813
TTCACAACTCCACCTGACATA	58.132	22	174	547	720
GATTATGGCATACGTGTGGG	58.723	20	153	387	539
CCATTATGTCGATATCCATCCA	59.507	22	234	104	337
CCTATGGTTGTATGGTGTGGA	59.238	22	174	37	210
ATTCTGAACCAACTGGCACC	59.973	20	142	1827	1968
AAAAGCAAGGAAAAAGCCAA	58.987	20	259	2819	3077
ACAACAGGCCAACTTGCATA	59.199	20	249	5328	5576
GTGGCCATTTGGTTCTGAAT	59.797	20	177	96	272
AAGCAAATTCCAAGATGACGA	59.699	21	271	4642	4912
CAACCCTACCTCCTTCTCCC	59.928	20	170	900	1069
AGTGCAACACAATTTCGACCT	59.653	21	269	21	289
AACACTATCACAAGGTTCCGA	60.047	23	235	71	305
CTCCCCATTGTTCTACCCAA	59.784	20	261	4182	4442
TTTCTGAGACCGGAAGGTTG	60.224	20	141	446	586
ATGTTGTGAAGCACATGGGA	59.967	20	220	1008	1227
CAAATCCCTCTTTTCTTATTCTC	59.919	26	250	174	423
TCTCCATTCCACCATCATCA	59.85	20	238	513	750
TGCATTTATCAGCTTTATCAGC	59.895	23	239	533	771
GCCAAATTAAAGACCATATTTT	58.556	24	215	2643	2857
TGCATCCATGATATGGCG	59.988	18	214	386	599
TGTAAACCGACCTCCCACTC	59.966	20	169	1830	1998
CAACGGTTTTGGTTTGTTCC	60.241	20	212	1300	1511
GGGAGAAAAGGGGAAATAAG	60.173	22	213	57	269
TTGATGAACTCTCTTGGGTGG	60.096	21	115	262	376
CGACTACTCCCTGCTCCAAC	59.867	20	152	107	258
TTCTCATTTCCCAAATGTCG	58.546	20	276	489	764
AGGGTGTTTTCTCTGCATCA	58.287	20	250	31	280
AAAATGGTGACGAGAGAGCG	60.397	20	188	321	508
CTTCGCATGCTTATTTGGAA	58.912	20	195	41	235
AAGCTGGAGTGCCTTCTCAA	60.134	20	179	528	706
ACCGGGATAAAATAGGGCAA	60.508	20	234	1631	1864
ATTATCATATTTAAGGGTTATC	57.31	27	160	305	464
TTTTCACTCTTCACGTTTGCAC	60.326	22	183	10	192
AAAACCCTAAACAACCAGTGA	58.663	23	252	49	300
TCAAAATTGCGTCATTGCAT	60.081	20	215	232	446
AACAACAATACAATCCCGTGC	59.744	21	249	3	251
TTGCAAAAGTCACACTCTGTC	59.534	22	247	53	299
TGCGAAATCAACAAATCGAA	60.193	20	213	192	404
GACCCAACTACCAAACCCAC	59.162	20	113	8	120
TAAAGGATCACGTTGGGAGC	60.074	20	262	171	432
CCGTTTATTTTTCACACGTTCA	59.904	22	177	1118	1294
GGCTACTTCGCTGCAAACTT	59.66	20	271	31	301
CTGTGGCCACCACTACACAC	60.072	20	242	1244	1485
ATTGTTGGGTGTGGGAAAAT	59.006	20	145	987	1131
GATCTAAGGGCCGAGATTTGT	59.568	21	101	171	271
ATTCGAATTCCTAAGCGCAA	59.816	20	130	230	359
GTGGTACTTGCACGCACATT	59.646	20	240	83	322
AACATGTAGTCATGCGGGCT	60.547	20	225	313	537
TGAGGTGAAGTGTGGAGTGTG	59.766	21	176	32	207

CGCTACGAGCCACAGCTAC	59.779	19	273	29	301
CGATCCTGTGTGTGCATTTC	60.12	20	184	5	188
TCCATTTATCGGAGTTACGGTT	59.737	22	204	252	455
CCTCACGCACTCCACTAACA	59.897	20	233	8	240
AAAATTGATGGAACGGGGAT	60.378	20	265	83	347
TTGTCACATTTTTGGTGTTTCAC	59.799	23	239	1619	1857
GGGATTCTTGATGAATGGGA	59.685	20	126	47	172
GATCCAAATTTCAACCCCG	60.118	19	165	1422	1586
AGGCCTATAAATGCGTTTGGT	59.877	21	228	34	261
AGAGAGACGACAGCGAGAGG	59.883	20	139	2602	2740
TGCAAGCAGCACTTCAATTT	59.614	20	276	109	384
GGTAGCTGGGAGGAGGAGAA	60.725	20	185	16	200
GCGTAGTTTAATTGGCCGTG	60.508	20	271	137	407
AATCATGAAATTGTTGGGGG	59.481	20	194	195	388
TCTTCACCTATTATTTCAACAA	57.674	26	153	41	193
TCTTCGAGTACGCTCTGGGT	60.012	20	213	13	225
GTGCGTGACGGTTGGTATAAT	59.766	21	280	64	343
GCCCCTGATTCTCAGCATAC	59.658	20	199	15	213
TGCACGTAGGCATGTTCAAT	60.142	20	166	158	323
CTTGAGTTTGTGGGGGATGT	59.82	20	263	343	605
CGATGTTTTCGAGGATGAGAA	60.199	21	265	204	468
CATCGGCTACTTTGAAGGGA	60.206	20	239	228	466
TGAATTGTTCTTGCACTTGTGA	59.366	22	274	1016	1289
TGCCACAGCAGAAAACTCAC	60.032	20	180	861	1040
AAAATTTTTGGGCTTATCATGT	59.256	24	143	2982	3124
GCTTTCACGGGAGAAAGTTG	59.853	20	253	2641	2893
GGATCAATAACTGTCAGAATC	59.376	24	204	37	240
TTAAGGTTGGCTTGGGTTTG	59.968	20	187	2252	2438
TCTTGAGGTTTCAGATCGCA	59.522	20	220	41	260
TTAAGAGATAGTACCGGATCG	57.575	22	214	42	255
CTGAGGTCGGGTTCGTGTAG	60.701	20	129	17	145
CCACTCTTTTGGGGCAATAC	59.429	20	190	73	262
TCCACGCATGTTTCTGTCAT	60.12	20	129	920	1048
GGAAACCACTCACCGTGTCT	60.009	20	163	448	610
TCCATAGCCGATAAAATGGC	59.892	20	256	1046	1301
TCTGTACCACACTTGCTCGG	59.897	20	261	26	286
TGCACTGCATAACAAGCGTA	59.086	20	237	29	265
CGTATGAGCTCTGAGAGTGAG	60.138	24	233	1002	1234
TAATGAGGGTCATGCGTGTG	60.539	20	180	231	410
CTCTCCAACATCCAACCTCC	59.505	20	223	624	846
TGGTGGGGCTTAATTAGGTG	59.817	20	276	1319	1594
CACATTGGTAGAAGGCCGAT	59.955	20	238	398	635
GCAGTTAGCAGGATAAGGGG	58.812	20	123	2	124
TGGTTAACCGAAAACCGAAG	59.968	20	199	634	832
TCTTTGAGGTAGGGCTGGAA	59.807	20	249	465	713
AAAATTTCACGGCAATGAGG	59.938	20	223	538	760
GCCATGACCAACTTTCTTTTC	58.684	21	105	27	131
AGACGAGCTTCTCGTTCCAA	60.134	20	247	928	1174
TTGCTTCTTGAAAACTTTCTTCA	59.84	25	214	866	1079
GAATAGCTTGTGTTGCAGCG	59.638	20	165	294	458
AATTGCTTCAATGTCACCCC	59.797	20	270	119	388
ACCCTCATATGCTGGGAGAT	58.421	20	237	0	236
TGGAAAAGAATTCGTCCTCG	60.184	20	217	83	299
TGCATACACGAGTGGAAAGA	57.836	20	215	449	663
TCGGAGATGGCTTCCTTATG	60.17	20	120	425	544
GCCCCTTTGAGCTAAGGTAGT	58.927	21	274	110	383
CTCTTATCGCAGCAAGGAGC	60.257	20	149	1868	2016
CTTTGGCAAGTCGCTCTTCT	59.757	20	201	18	218

TTGCAAAACGATTCCTTCCT	59.685	20	258	61	318
TCTTTGCACAGGTCCCTAGC	60.397	20	268	11	278
TGAAATGAAGAAAAAGAAATT	57.512	23	143	103	245
GGTGATGAATGGAGAAGGGA	59.862	20	191	191	381
CCAATATCCAACGGCAAGAA	60.827	20	182	1278	1459
TTTCAAAATTCCCCACAAGC	59.916	20	175	2760	2934
TGAAGGTTGGAGGAATGGAG	60.042	20	275	147	421
ACCAGCTTGAAGGGGAGTCT	60.252	20	252	0	251
TGTAGTGTGTCACGGGCAAT	60.032	20	257	590	846
TATGGGTTATCACCGGATCG	60.544	20	150	750	899
TGAAGTTAGGAAATAAGGAGG	58.743	25	180	341	520
AATTGTATTCTCCCGAGCCC	60.286	20	224	589	812
TGTAGCCGTTATAGTGTGGGA	58.187	21	264	12	275
CCTGTTCAGCTATCTTTTGCG	60.025	21	254	79	332
TTTCGTCGGAAAAATTCACC	59.916	20	263	230	492
TCACACTACCCTCCTCGTCC	60.112	20	213	72	284
CAGGTAATGCTAGCCGGAAA	60.223	20	198	379	576
TATAGAGACCGGCCGAGAAA	59.801	20	280	20	299
ATTCCCTGATGTTGCGTTGT	60.384	20	259	2566	2824
GTTAGGAAATAAGGAGGTGTT	57.059	25	229	94	322
ATGGGTTATTTTGGCCCATT	60.26	20	263	17	279
TGCAAAATTGGCTGAGTTGT	59.322	20	100	709	808
ATGCACGTGTTGGATGGAAT	61.2	20	157	79	235
TGGGCTCATGGTGATTACTG	59.522	20	247	770	1016
TTAGATGAATGAAGTACGGCG	59.742	22	164	0	163
TATCCTGTGGAGCGTGTGAG	59.855	20	223	429	651
TTCTATTCTTTATAATTGCCATA	57.525	26	270	6	275
TTGCAGTTGCAGTTGGTGAT	60.31	20	186	820	1005
GGGCACCGCTAATGTAGATG	60.49	20	143	80	222
CTTTGTCGGTTTCTCCATCG	60.626	20	185	52	236
CCAAGTTACTCCCAGCGAGA	60.388	20	116	1	116
GCAAGAAATGGCTCCCTACA	60.214	20	257	797	1053
ACCATAGATTGAAGGCCCAA	59.387	20	233	4	236
TGAAGTCACAGCGAGGTTTG	60.025	20	107	5	111
TGACGGTCAAGATTTGCTCA	60.39	20	131	0	130
TCCATCCTTCTTTGCTGCTT	59.955	20	180	630	809
TTAACCTCCCGTGGACGTAG	59.986	20	183	370	552
TTGTCCATCTTTTTCCGTCC	59.91	20	261	50	310
TCCAATGGATGTGAATGGTT	58.617	20	268	73	340
CCTGCTTTTGTGCATAGGTT	57.906	20	174	254	427
AAATGATAGGGCACACAGCC	59.962	20	183	82	264
AAGTCGCGCAAACTTGAGAT	60.022	20	179	3812	3990
AAACCTGGCTGGACTGATGT	59.579	20	217	1759	1975
AAGTGAAACTGCTGTATGCTG	58.737	23	172	548	719
TTGGGGATGAATCTGACGAT	60.281	20	212	9	220
TAGCCGAAGCGAGCTGTTAT	60.138	20	120	71	190
TAGCCTGGTCGTTTTGGAAG	60.241	20	278	990	1267
AAATGCATGCACCTGATTACA	59.055	21	216	1	216
CCCTACCTGAATCGCAACAT	59.955	20	100	1540	1639
GCGTTTTGACAATATATAGGTG	58.944	26	104	290	393
ATGGCTGGGCTCTGAAATTA	59.668	20	280	312	591
TTGTGGATGAAAGCACGGTA	60.111	20	273	8	280
CCCCACCACTTTCTCATCAC	60.363	20	174	1762	1935
ATTACAAATGGCCAAGAGAGT	58.282	23	103	8	110
TTTTTGACAGCGAAAGTCCC	60.227	20	269	4170	4438
TTTCCCCTTTGCTCTCTATTTC	58.887	22	210	200	409
CAAATCAAATCGCCACACAA	60.501	20	252	35	286
CAACTCCAACTGAAGAACACG	60.326	22	262	1220	1481

ATCCATTCCGTACAAGGCAA	60.331	20	245	21	265
ATCGACGCCTCAGATTTGTT	59.7	20	168	948	1115
CCTCTAGCATCTCTTGCTCTCA	58.983	22	182	343	524
AGCAAGATTGATCCTCCTCG	59.386	20	278	20	297
GCAGGGCTGAGTACAGGGTA	60.277	20	221	17	237
GAGCATATTTCCACGAAGCA	58.872	20	275	239	513
TTTCCAACTATCCAAACGGC	59.938	20	212	672	883
CACACTATTAGGGTTTGGGAG	59.757	22	116	4	119
AAAGATCCCCCGAAAAACC	60.117	19	261	2290	2550
CGAGCTCGGACCTTCAGTAT	59.454	20	111	22	132
GGCAAAAATAACCAACCCAC	59.182	20	270	83	352
CCAAAAAGAGACGACCGAAC	59.711	20	119	1	119
CATGGTGATGCCTTCTAATGTG	60.386	22	211	28	238
CAATGGTGGCTTCATTTCCT	59.933	20	201	561	761
TCGTGTACAAAAGCCGTGAA	60.293	20	107	0	106
TGCACGTAGGCATGTTCAAT	60.142	20	245	15	259
GTTGGGGTCTTGGCGTACTA	59.993	20	109	17	125
TAAGGGATGTTTGCACCTGA	59.123	20	162	50	211
TGAAGTTAGGAAATAAGGAGG	58.743	25	160	949	1108
GAGTTTTCATCTTACCTTGAGG	58.333	23	244	12	255
TTGTGGGGTTGTGGTGAATA	59.667	20	188	34	221
CAGATACAGTGGCCGGAGTT	60.134	20	275	43	317
TTTTTAAAGAGCTGGGGGCT	60.197	20	185	981	1165
AACAGCCAGAGGATTCGATG	60.218	20	199	0	198
CTCATGCATTTCCCCATCTC	60.426	20	240	899	1138
CTGGCTATTTTGGTTTCTACAA	59.613	24	237	64	300
TATCAGGCTTGATGATGGCA	60.182	20	267	227	493
CGCAGCAGGTCAAGATTACA	60.011	20	263	539	801
GAAGCATCGTTTGTGTTTTCA	58.81	21	270	6	275
ATGGTTTATATTTCGTTGATTTG	58.457	24	259	31	289
TTAGGGGTGTTCATGGTTCG	60.745	20	278	31	308
TCGAGTCCAATGTTGAAAGAA	59.724	22	277	441	717
CTCACGAGATGGTGAAGCTG	59.571	20	190	22	211
TCCTTTTTGTCATTCACCTTTGT	59.9	23	232	488	719
TGGACTGCGTTAGGGACTTT	59.734	20	195	189	383
GTAGGTGGACTGACCAACCC	59.279	20	280	468	747
ATGGGTTTGAACTCGGACAT	59.263	20	175	2432	2606
TCTCCTTCTCCTCCTCCTCC	59.883	20	280	716	995
AATTGACGTGAAAAACGGGA	60.344	20	194	113	306
CTCACACAATTTCACTCTTCAC	59.023	25	170	97	266
CGAGTTCATGGACTTCGTCA	59.831	20	132	269	400
GACGGAGCAGAAATGGAAAA	60.192	20	107	3075	3181
GAGTGCGCATTCCTTACTCC	59.843	20	224	23	246
AAAAACCGCCACATCAGAAG	60.11	20	264	1883	2146
GATTAAGGATGGGCCACTCA	59.894	20	154	18	171
GTCAAACACGAGTAGAAAGGA	57.975	24	162	66	227
CCTTCCTTTCTCCTTCACCC	60.045	20	134	815	948
AAATTTGGGCCCTTAGATCG	60.272	20	192	55	246
TGAAGTTAGGAAATAAGGAGG	57.525	24	188	136	323
TCTGATTCTGGGATTTTGGC	60.014	20	263	576	838
GAACTCTCATGCCCTGGAAA	60.195	20	161	112	272
CATTATTTAAAGCACGCGCA	59.872	20	219	449	667
CAAAAATGGATGCAAATACGG	60.192	21	111	9	119
ATGGTTTCGCTCTCTGTGGT	59.727	20	193	19	211
TGCTCTTCACCTTTGTGTGC	60.032	20	192	469	660
TTAATCGTCCATTTCGTCGG	60.827	20	267	244	510
AGGGCCTCTTTTTGTCTGAA	58.909	20	205	11	215
ATGCAATGACAAGCACTCCC	61.078	20	242	75	316

TCACCATCACCATCCTCACA	60.982	20	151	1389	1539
CCCTTCAATGGTGTTTCCTG	60.345	20	127	439	565
TAGGGGTCAGTGTGGGTTGT	60.275	20	174	298	471
GCACTGACCATTTCACAAGG	59.139	20	258	764	1021
TGAACACGTTGCCAAAACAT	60.011	20	118	78	195
TAAAAACTCGACCCGATGCT	59.708	20	145	143	287
TCAAATCAGGAAAACCCCTT	58.477	20	201	55	255
TGTTTTTGGAGGGAAAATGG	59.772	20	123	37	159
GGAAGGGCTCAACAACACAA	61.075	20	217	7	223
CATGTTTTGTTTGGCTGTGG	60.004	20	263	208	470
CGGTTAGAAAATGGACCGTTA	59.893	22	279	11	289
GGGGTGGGAATGATGTGATA	60.404	20	204	79	282
TTTGATTTGTGTTGGCAAGG	59.561	20	108	359	466
ACCACGAGATGGAGACCAAC	59.969	20	201	428	628
GCTGAATCTTAACCGTTCGC	59.851	20	232	69	300
TTGATACAGATGGTACGCCG	59.566	20	279	43	321
TCAACAGAGAATGCAAGCAA	58.129	20	217	89	305
TCAGCATTCGGAAAGGGTAT	59.528	20	185	43	227
AGATGGCGGTAAACATGGAG	59.955	20	214	134	347
CCCTAATTGAGTAGAAAACCA	57.399	23	261	1343	1603
TGCTGACTTGATTTTCGAGC	59.152	20	187	0	186
GAACCATTGGGCATGAAGTC	60.326	20	259	2	260
TCACCCAAAAAGGTTATTATTT	59.149	25	280	308	587
AATTTACTCGCCTCTTCCGC	60.711	20	260	2428	2687
TTTTCCACGCACATAATTCG	59.562	20	176	485	660
TTGGTTATCGCTTGAACGAG	58.917	20	170	83	252
GCGTTTTGACAGGATTTGCT	60.257	20	105	2	106
TCTCAAAAGTCTCATTTTCACA	59.799	24	179	2347	2525
CCACACCTTGTCTCCCAAAT	59.82	20	220	2314	2533
CTTATTCGCCTCGATCTCCA	60.309	20	244	1654	1897
TAAATTGCCCTCGGATGCTA	60.548	20	189	2434	2622
GGCTTAGCTGTTCGTGGTTC	59.882	20	155	14	168
ATCATATCATGGCCGAAACC	59.61	20	175	316	490
CAACTCATTTCGCAGACCAG	59.44	20	182	165	346
GCGTTCACACCCTCATTTTT	59.978	20	228	499	726
GCTGGAATACAACTACCCCAA	60.237	22	272	1439	1710
AGGCAAGCTCGATGTCTTATG	59.49	21	279	2078	2356
TTAAGTTTGGGGGTGCAGAG	60.103	20	105	211	315
GCCGTTGAATGTGATATCTTG	58.106	21	115	13	127
GAGAAGGGGTGGGTTTTACG	60.714	20	175	3	177
AAGTGGCGGACACTCATGTT	60.577	20	119	18	136
TTTGTCACCCTCTCCCAGTT	59.549	20	265	710	974
TTTTTCTGACAAGGGTGGGA	60.465	20	275	1156	1430
CTCGTGCTTGTCTTCCACAA	60.025	20	217	1134	1350
CAAGAAGGCGTTGATGGAAT	60.074	20	154	622	775
GGGAACTTAGGATTAGCGCC	60.061	20	144	335	478
AACAGAGGGATGGGGAGATT	59.755	20	113	156	268
ACACACAGAAGTTGTGGGAGG	60.057	21	162	13	174
CCTTTGAGGATGGATTGATGA	59.879	21	207	87	293
CGCCTTGTCGGGATATTAAA	59.922	20	228	295	522
TTTTTCCGAGCAAATGAAAAT	58.728	21	239	1103	1341
CCACCTAGCAATGGTTTCCA	60.883	20	264	4	267
CCGAGGACCACCTTGTATGT	59.844	20	144	690	833
AGCGTTCGAAGTTTGGTGTT	59.78	20	204	78	281
ACTGCAATGATCCCACCTCT	59.535	20	216	954	1169
ACCTTGACGAGGTGGTTGAC	60.009	20	267	15	281
TTCTCTCTTGGTTGGTGAAGAA	58.955	22	196	153	348
AAGTGAGCCCCAAATCTCCT	60.074	20	274	532	805

CCGTTAGGTCCGTCTCGAT	60.081	19	127	44	170
CCATGAAGCACATCACAGGA	60.688	20	235	1825	2059
TGCCTTGACAAGCAGGTAGA	59.591	20	219	18	236
TTCCGTCTACCCCTTTTCCT	59.934	20	177	838	1014
ATTGCCTCTCAACCTCCAAA	59.67	20	175	0	174
AAAAATAGAGTTATCACAGGA	58.199	26	135	216	350
GTCACCCCGGGCTAGATATT	60.173	20	263	4162	4424
CCCCTTAGGGCAAGGTAGAA	60.435	20	267	28	294
TATGGGTTATCACCGGATCG	60.544	20	252	762	1013
ATTGAACACAGCCCTCTTGG	60.111	20	220	361	580
TTTGTTAGAGGTTTTGAGGGGA	59.974	22	236	321	556
CGCCCTAATAAACCTGCAAA	60.089	20	118	585	702
GAGGCAAATTATTCGGATTTTC	58.99	22	228	1198	1425
CCCCATCAACCTCCATACTG	60.187	20	182	1270	1451
CATCCCTTCCAAGTGTGTCA	59.52	20	203	41	243
GCACTTCACAGGTACCACCA	59.597	20	246	3	248
TGCTTTGTTTCCATCACGAA	60.234	20	236	149	384
GGTCCACGTATTTTCCCAAA	59.662	20	114	441	554
TCTTTGCCGATGAAGAGGAG	60.474	20	266	18	283
GGGTTATTACCTGATTACCTCC	59.052	23	175	317	491
GTGGTTCGGAGCAAAGAAAA	60.227	20	216	4	219
GCTTCCACTGCCTACTTTGC	60.022	20	246	175	420
AATTTGGCAGCTTCTTGTGC	60.395	20	121	68	188
TCCTCCTCTTTACGGCATGT	59.694	20	245	693	937
TCCACCGTGGTTAGTTGACA	60.001	20	237	110	346
TCAGCTCAGGGTGGAGAAAA	60.913	20	229	167	395
ATGCATGGAAGTAAGAGGCG	60.235	20	187	59	245
ATAGTTGGTGTGAGACGGGC	59.997	20	279	80	358
CACAATATTTGAGGGTTATCAT	58.787	25	195	466	660
TGCGTAGAACAGAGAGCGAG	59.49	20	266	9	274
AGGACATCGCGGAGAGTCTA	59.973	20	204	9	212
ACGCTGGTAGGATTTCAACG	60.132	20	224	1168	1391
GAGGCACTCGATTTTCTGTGA	60.39	21	202	62	263
AAGGACTGTCGAAAATGGGA	59.526	20	191	742	932
CGGAAGAATTAGAAACGGCA	60.202	20	241	97	337
TTCAAAGGCCGAGATTTGTT	59.685	20	145	140	284
GGTCCAACAACCTAATCATCC	58.227	21	228	230	457
CACTCCTTTCGGGACGACTA	60.246	20	235	1982	2216
CAGGCTTCACATTTCCCATC	60.461	20	230	52	281
ATTTTTGCGAGGGAGAATGT	58.647	20	126	0	125
CGGACGATATCGGTTATTGG	60.167	20	123	0	122
CCTGGTGAATGGCAAAGTCT	60.111	20	196	22	217
TTTGGTTTCTGGTGGGATGT	60.21	20	188	616	803
TATGGTGGTATGGTGTGGGG	61.296	20	242	158	399
CTGGTGTCACAACGGATGTC	60.005	20	193	41	233
GTGGTTGCTCCAAGTGAACA	59.726	20	270	192	461
CTTCTATTCCCTTCCCCACC	59.761	20	146	43	188
GCGAGCATCATACACGAGAA	59.979	20	253	2437	2689
TTCTCAGTGCATCCATTTCG	59.799	20	135	820	954
GGAGTTTGCTGTTGAGACCC	59.703	20	230	331	560
TGTCGTGGTTCGGATATTCA	59.924	20	276	16	291
GCCTAAACACACACACCTCA	57.137	20	102	105	206
GCAAGGGGCAAGTGTTATTT	59.091	20	222	514	735
CACATGCCATTCAGTCCAAG	60.112	20	232	1794	2025
GCTATAGAGCCGTTGTGGGA	60.235	20	132	1117	1248
TGGCTAATATAATTTATCTCCA	57.853	25	216	235	450
GTCGCATTGGATCTCTGGTT	60.081	20	276	5744	6019
AAAAGCAGGTTCATGCCATC	60.081	20	152	778	929

GAAAGCCTACTTGGCGATCTT	59.87	21	115	440	554
AGCCTACCTCGCTTCCGTAG	60.904	20	179	5	183
TTATGATGGGAAGAGGGGGT	60.517	20	115	2109	2223
TCCAAGAAACGTGGAATGTG	59.541	20	207	285	491
TCTCTATCTTTTTGGTTGGTGAA	59.203	24	230	4	233
TGCTCAGCATACAGGAAGGA	59.547	20	172	12	183
TGACTGTTGGACGGTTATCG	59.566	20	153	87	239
GCGCGATTTTAAACCCTAAA	59.24	20	212	31	242
CCGAAAATCTCCGTCAAGAA	60.184	20	184	266	449
TGGTTTGGGTTTAATTTGGG	59.537	20	230	8	237
ATCACTTCGAACCTTCTGCAA	59.867	21	186	7	192
CAAGCAGCAGCAGCAGTTAT	59.396	20	261	98	358
CCAAAATTTATGGTTATCACAG	59.191	24	237	14	250
CCCATGTGGGGAGATATGAT	59.44	20	118	874	991
TTTTGTGGAAGATGCAGGTG	59.691	20	179	2897	3075
TTCTCGCATGCCACTAAAAA	59.443	20	216	20	235
GAAGTCGGATTGTGGATTGG	60.317	20	185	204	388
TGGACAATAGAAAAACCACGC	59.989	21	184	159	342
TCCCGTGTTGTTATTGCTGA	60.111	20	112	15	126
AAAATTTCACATATTTGATCGG	57.59	23	192	34	225
TGCCCCATTACCACTAAACC	59.685	20	144	82	225
AAATTCCAACAACTGTCCGC	59.978	20	270	995	1264
GGGGCTGCCAGAATAAAAAG	60.92	20	280	497	776
TTGGTGATGCCAGAACAGAA	60.24	20	232	279	510
ATTTAGGGGCTTTTGAGCGT	60.095	20	270	770	1039
CGGTTTTGGTTTGTTCCTACA	59.884	21	149	76	224
GGTGATGCCGAAGGTATTTC	59.391	20	184	370	553
GACTCACGGTTTTTCGGAAG	59.711	20	250	487	736
TGTTCGATGCAAGTTTCGTT	59.322	20	160	94	253
ATTGCATACGAGGGGCTAAA	59.569	20	208	396	603
TGAACAATTGAACACCGGAA	59.941	20	180	64	243
CGCGACAGAGTGGTATCAGA	60.008	20	253	369	621
GGTGAATCTGTAAAAGGTCAT	59.885	23	236	336	571
GAGAGCCATTTGTGGACGTT	60.119	20	254	12	265
TGTGGAGAACGAACTCGAAG	59.007	20	206	262	467
ACATGTGCTGTGAGAGTGGG	59.738	20	262	501	762
AAAACCGTTCCACATTCAAA	57.972	20	165	1271	1435
TCAAACAGAACACACCTTCCC	59.997	21	118	164	281
CAACCGCATAGGCACAGTAG	59.366	20	122	14	135
GCAAATTTCTTCGAGACCCA	60.192	20	110	175	284
CAGTTTGACATCAGAGCCGA	59.984	20	179	12	190
TTGAATGGTTATCACCTGATCTT	59.376	24	111	230	340
ATTAACGACTTGAACCCATTTTT	58.084	23	280	305	584
TAGACGTCAATCCTCGGCTC	60.362	20	160	21	180
TGAATCGATTTCGGTTTTCG	60.941	20	234	408	641
TGTGATTTCTACCATTTATTCTT	59.708	26	246	2	247
GTTCTTGACGCACCATTTCA	59.697	20	148	50	197
TTGTTTGCATCCCACACAAC	60.413	20	157	265	421
TTGAGAATGTGAGACATCATCA	59.059	24	154	228	381
ATTTCACAGAACACAACGATCA	58.132	22	261	10	270
TTGATGATGAAATGACATGGAA	58.82	22	132	81	212
TAGGAGAACCAAACCGCATT	59.569	20	218	1781	1998
ACCACTCCCCACTGCAATAA	60.375	20	218	243	460
TCTTTGCCAGAGCAAAAACA	59.585	20	123	1105	1227
GTGTTCTCGTGAGAGTGCGT	59.051	20	206	4	209
TTCCAAACCTTTGTTCCGAG	60.081	20	228	823	1050
TGGTTCTGTATGTCAACGGC	59.572	20	108	4	111
TGATTAATATCAGGGGGCGA	60.247	20	272	10549	10820

TGAACAACGACTCCGATCAC	59.682	20	280	883	1162
GAACAGCATGAAAACCCGAT	59.939	20	269	0	268
AGGCCTTGATGTCCCTTCTT	60.074	20	138	177	314
TCAGATTCGAACTCTTGCCA	59.522	20	173	249	421
CTAAAGCACGATAGGGGCAC	59.73	20	266	17	282
AGAACCCGGCAGAGAAAGAT	60.212	20	186	239	424
TACGACAGTGGACAAGGGAA	59.135	20	232	88	319
AGCATCAAGCCGAATTGAAA	60.721	20	103	490	592
TCTGTTTGCCTTTCGAATCC	60.192	20	219	470	688
GCAGACTTTAAGGCAGCCAA	60.523	20	271	5293	5563
CGGGTCCACTCGTCATAAAA	60.883	20	262	373	634
TGCTTCCTTTTGCTGCTACA	59.752	20	270	220	489
GGTTTTCTCGCAATCCACTT	59.174	20	264	2250	2513
TGCAGGTACCTTCGGAACTT	59.734	20	274	47	320
AAAATAGGGGAAAAGGGGAA	60.006	21	156	242	397
ACGCAGTCTAGAGATATATGTT	57.442	26	242	300	541
AATTTTTGATCGATCTCGGG	58.974	20	221	659	879
TCGGACGTGAAGAATGAGTG	59.831	20	274	1499	1772
CTGCCGTCCAATCCATTTAT	59.784	20	125	47	171
TAACCAAAGGCTGAGTCGGT	59.734	20	221	87	307
TAGCCGTTCCTCGGTTTTTA	59.715	20	177	2865	3041
TCCTTCAACCAGTTGTTCCC	59.943	20	180	68	247
GCCAACTTTGGGTAAATGGA	59.801	20	214	188	401
AACGATAACGATTAACGATAA	57.033	24	100	591	690
CCCTCCCATATCTTCCAGTTG	60.689	21	176	724	899
TCTCCCTAAGGTGTGAGTCCA	59.706	21	273	541	813
ACACGAGATTTACATGGTTCG	59.781	23	108	1	108
AGATTCCTCGTGGGATTGAA	59.483	20	271	48	318
GATTGTAACGTTATTTGGCCG	59.376	21	134	1278	1411
AGTTTTGAGGGAGAACTGCG	59.473	20	199	16	214
AACTGAGTCCCCTACCCGAT	59.817	20	225	301	525
TTTGAGGCGAATCGAAATCT	59.784	20	201	1047	1247
TAAAAGGTTCCCCACAGACG	59.964	20	128	75	202
CTCGATCCAACGGTTCTTGT	60.111	20	159	169	327
ATGCACATGCTACTTCCACG	59.746	20	239	571	809
GCCATTGCCGGATAATAGAT	58.88	20	161	42	202
ATATCTCCCTTTTCGGCCAT	59.761	20	184	16	199
GTCAAGTCAAACTTGCCAAAC	57.373	21	253	960	1212
GCATCAGAGAGTCGGTGAGA	59.078	20	225	1112	1336
TCTTCCCCAACTACTTTCCAGT	59.144	22	280	264	543
TACCCATTGGTGCTCAAACTC	59.985	21	243	450	692
TCTTCATTTGCTTCAGAGGTGA	59.993	22	167	250	416
TCAATTCAACTGCTGCAACC	59.847	20	233	1105	1337
GCGCGTGACCAAATAGAAGT	60.278	20	243	73	315
CAGCCGTCAATCATTTAGGAA	60.081	21	144	6	149
ATCCATCCATCTCCACCTCC	61.094	20	116	1902	2017
AGATCATACACGTGGACGCC	60.956	20	280	147	426
ACTTGACCGAACCATTTTGG	59.83	20	273	191	463
GCATATACGAAGGGTATTTTG	59.289	23	203	478	680
CACACCGGGTACCAAAAGTT	59.751	20	133	178	310
AATTAATGTGGCATGGGGAA	60.016	20	238	62	299
AATCAGCTCCATTTCTTGCC	59.273	20	211	289	499
TCCGACAACGAAAGATGAAG	58.847	20	207	511	717
AGCAGTAGTGCCCCTGAAGA	60.012	20	182	1088	1269
CACTCTGTGTTGTTGGGAAA	57.109	20	268	72	339
CGGGGCTTCACCTAGTCTAA	59.331	20	220	144	363
CTTTTGATTCCCCATTAAAAAG	57.746	23	224	257	480
AACAAGAATCGCCTGCAAAG	60.386	20	253	1152	1404

CAAGATTTGATCATGGGCGT	60.864	20	159	35	193
ACACACACGAGCAAGGATTG	59.751	20	178	694	871
CTTCATTACCCATGAGCGAG	58.325	20	212	106	317
TGCCCCTTAAAACTCTCCTTG	60.589	21	265	382	646
TCGAACTCATGCATTCATTTTT	59.592	22	234	2082	2315
CACCCGAAAACCGAATAAGA	59.931	20	129	156	284
TGCAAGCTCAGCCTAATGAA	59.712	20	171	18	188
CTAAACCACCCGTGAAGCAC	60.55	20	258	140	397
GGCTCGTCACGATCTCTCTC	60.104	20	102	2005	2106
GATTGGCATCATTTTACGGG	60.153	20	234	377	610
ATATTGGGTGATGTGCAACG	59.276	20	165	1163	1327
CGAAAAATGTATTGGGGCAT	59.66	20	179	5	183
TTTCCCCGTGGACGTAGAT	60.324	19	257	219	475
ATCGGTTATTACCGGATCGC	61.031	20	151	234	384
TCTGCCTTTCTACAGCGACA	59.74	20	123	414	536
CCCCCATGCTATGAAGAAAC	59.387	20	242	16	257
ACATTACACCACCCTTCCCA	60.088	20	202	332	533
GAGGTTTCCAACTTGCTTCG	59.853	20	181	201	381
TTGTGAGAACCAACTCGGTG	59.72	20	273	233	505
GGGTTGTTGCCGCTTCTACT	61.557	20	265	0	264
GAGATGGTTCGAGAACGAGG	59.803	20	112	476	587
TGGAGAGGGGAGGTATTCAA	59.478	20	279	28	306
TTTGGAGATAGAATGAGATAGA	57.629	26	169	218	386
CAACCCTACCTCCTTCTCCC	59.928	20	203	171	373
CAAGAGCTCTCATTCTCTCCCT	59.23	22	223	646	868
GCATCAAAATTCAAAAGCGAG	59.846	21	269	382	650
ATCCGGCCATGTTGCTATTA	60.31	20	243	1550	1792
AAACCTAGCATTGGGGAAGG	60.312	20	244	55	298
AATTGATGGAACGGGGATTT	60.378	20	156	9	164
GACAAAACTTCATGGGAGCG	60.636	20	275	317	591
TTCATGATTCAAAAGCATCAAA	59.595	23	138	64	201
TTTTTCACATGCCATACACCA	59.841	21	184	25	208
TCTCACCTTCGGTCAGAACC	60.238	20	261	291	551
GGAAGAGAGAGAAGGGGTGG	60.186	20	272	193	464
AATGGAAGGGACGAGTTTGA	59.526	20	134	293	426
TTAAAAACCGAACTGGACCG	59.968	20	132	2874	3005
TCCACTCTCCCTCTCAGTACTTT	59.823	24	279	95	373
TGGAGATCGAAGGAGCTGAT	59.91	20	222	313	534
GGGTTATCACTTGAACGCGA	61.032	20	218	54	271
ATTTATAATCCCGGGTCCGA	60.349	20	280	9	288
TGGAGCTCTTGTTCCTCACA	59.545	20	136	72	207
GAATACCCCCTACTTTGCCC	59.666	20	161	77	237
AACAACTTTGAACCTGCGCT	59.92	20	217	18	234
TCGTCTGGCTAGTTGGTTCC	60.255	20	235	1	235
AGCTGGAGCTGAGAACATCG	60.7	20	119	10	128
CAATATTGCAAATGGCCAAG	59.029	20	232	35	266
CACCCAGATCGGTTTCTACG	60.508	20	244	49	292
ACATGCATGGCCATAACTCA	59.955	20	272	166	437
AGCAGATCTGGTGAGGCAAT	59.834	20	198	1861	2058
GGCTCAACAGGTTTTTCCCT	60.476	20	179	27	205
AGCATACACACCATCATTCTCG	60.022	22	238	17	254
ACACTCTCGTCTCTCTCGCC	59.738	20	237	0	236
CACCCTCACTCACTCACACG	60.358	20	106	106	211
TTGTTAAGACCTCGTGGGGA	60.486	20	254	2263	2516
ATAAGGAAGGATTCGCGACC	60.419	20	275	77	351
TGTTGGGGTTGTTGTAGGGT	60.126	20	193	1801	1993
ACAAAATTGTGCCCAAGGAG	59.971	20	184	23	206
CTGATTCGCACAAATGATCG	60.22	20	169	98	266

GGGACGAAAATAACCCTCGT	60.187	20	199	85	283
GGCAACGTCCCTCTCACTTA	60.255	20	134	1884	2017
TATCTGTGGCCGATGCTATG	59.67	20	255	2368	2622
TCCAATTGCATGCCTCTAAA	59.257	20	206	2	207
AACGGACGAACAACGAAAAC	60.015	20	228	327	554
AAACGACATCCTGACGCAAC	61.107	20	274	225	498
TTATCATTGCTCGTTTTGGG	58.625	20	255	190	444
TGAGCATCATACCCTTTTGAGA	59.708	22	242	39	280
TATTGTGGTTTAGGGCCACC	59.685	20	224	30	253
TTGCATCATCAAGTCTCCTCA	59.384	21	200	0	199
TTCGAAGTTACAAAAGGGCG	60.236	20	260	552	811
TCCTTGCACTCTTGCCCTAT	59.836	20	250	13	262
TGTTTGAATCCGAGTTTCCC	59.91	20	229	53	281
GAAGTTGAGCCATATTCATTTG	59.989	23	181	440	620
TTTCTTGGGAGGGAAAATGA	59.476	20	187	448	634
CCTGTTGGACTTTTTGAGGG	59.563	20	254	615	868
TCCAAAATGTTAGGGGTTGC	59.801	20	212	55	266
TGAGATGAGGATGCAAGCC	59.891	19	237	3038	3274
CTGATAAGCCAGGGTATGGC	59.551	20	258	98	355
AAGCTGGTGGATTGAATGCT	59.7	20	178	169	346
AATTCCCCACCCTTGTTTGT	60.455	20	208	90	297
TTGGGCACATTGATAAACCA	59.786	20	228	434	661
CAGGTCATATTTCCTGCGCT	60.235	20	225	146	370
TCAACGGCTCAAAAAGTTTC	57.999	20	158	260	417
CTCGTGGTGCAGTGGTAGAG	59.487	20	254	28	281
TTTGCATGAGCTAACATGCC	59.839	20	207	649	855
CATTCCCATCATTTCGGCTA	60.797	20	239	1799	2037
AACGAATGTAACAATACGTAC	57.736	25	214	401	614
AGCACTCGTGGATTCTGGAC	60.269	20	209	905	1113
TTACAAAAATGCCCTTTCGC	60.075	20	250	426	675
GCAGCTTCACATTTCCATGA	59.805	20	239	215	453
AAGAACACAACGAGGATGGC	60.119	20	256	258	513
GTTTTTCGATCCTGTGTGCC	60.504	20	136	293	428
ATCAGTTCGTTGATTGGGCT	59.556	20	242	3767	4008
CGATTTGGAATCGATAAGCA	58.721	20	268	561	828
CTCTTCCACGGCCTCTATTG	59.83	20	128	85	212
GGCCAATGGAATGGAGATAC	59.204	20	273	283	555
AATCTCACCAAGATGCCCAA	60.461	20	100	8	107
TGTAATGGAGGGGGAATCTG	59.744	20	106	292	397
ACAAACTTATGGACCGCTGG	59.993	20	173	488	660
GTGCACGAAATTGGAGGAAG	60.636	20	181	2072	2252
ACCTATGGTGGTATGGTGTGG	59.463	21	239	231	469
CAGTGGCTCAAATGATCGAA	59.799	20	207	328	534
AAAAATCGACAAATTATCAGT	58.166	25	276	432	707
CACCTTTGCAAAAGGGAGAA	60.22	20	215	49	263
TTGCAGCCTGAGTCAAGAAG	59.314	20	203	1291	1493
CTTCTTCAAAGGCGATTTGG	59.817	20	235	1437	1671
TGGATTCCCAATTTTTCATGT	59.125	21	268	2247	2514
TGGCGAATATTTTGTTTTTGAC	59.025	22	145	281	425
TTGCCTAGAAAATCCACACAA	59.625	22	278	1138	1415
AATTCAATCCCCAAAAACCC	59.867	20	183	449	631
AAGCCACTTTTGTCAAGGTGA	59.766	21	234	1097	1330
TCTCACCAACCAACCAATCA	59.935	20	194	363	556
AGGAATCAACCCCGACCTAC	60.19	20	233	28	260
GGAGATGCTGATTGCCTTGT	60.226	20	211	46	256
CTATGGTCGATTGGGTGAGC	60.483	20	200	4617	4816
AACAGAAAAATTCCCCTTCATC	58.493	22	263	4454	4716
GCGCATAGACAACGGTGATT	61.063	20	225	38	262

AGGGTGGTAGAAAACCACGA	59.449	20	262	2162	2423
TCACGCTAAAGAGGTGTTTTGA	59.92	22	250	214	463
TCGTGCTCATTTGTGTTGGT	60.16	20	182	8	189
GCCAGCCAGGAAAACACTAA	60.249	20	128	345	472
AAAAATTCACGTGTTAGAGTTG	59.112	26	233	911	1143
CCGTGCTTACATCAAGCAGA	60.011	20	235	7	241
ATCCCCTTCATTCAGCACAC	59.934	20	126	6	131
TCAAGAGTTGCATGTGAGCC	59.992	20	264	1457	1720
ACTGACATTCACAGGCATTG	57.067	20	198	63	260
TTAAACCCTAAAAACGCGCA	60.593	20	241	104	344
CATAAACAGCAAAGCAGCCA	60.014	20	250	375	624
CCGAAAAGCTGAAAGAAACC	58.949	20	139	795	933
CCTGTTGTGCCCATCAATTA	59.395	20	206	9105	9310
TAGGATGATTGGCAACACGA	60.073	20	195	1	195
TCCAATCAAGGCAAAGATCA	59.2	20	186	5483	5668
GGGAGAAGGGCTGTGTGATA	60.073	20	192	105	296
AGGGTTCACAGCGAATGAAA	60.636	20	123	700	822
AACTCACCGGAGAAGGAGGT	60.111	20	227	1229	1455
TTCCAAGTCTTCCCCTTCCT	60.045	20	176	3	178
TTTGTTTTCCATCGTATTCCA	58.005	21	141	4093	4233
ATACCCTTCCCTCGATGTCC	60.154	20	232	42	273
GTGGAATTCGCCCATAAACA	60.701	20	112	24	135
CTAGGCATGGAATCCGAGAA	60.17	20	268	60	327
GTTTGATATGGCAGGGGTTC	59.249	20	215	634	848
CATGCAAGTGCATATCAATGAA	59.59	22	137	1314	1450
TGAGACATAGCGGACTGCAA	60.562	20	166	228	393
GGTGGGTTCGACGACAATAG	60.375	20	130	542	671
TCAACTTCTTCAACAGGCCA	59.415	20	209	2221	2429
CAACCTAGAATGAGCATTGGC	59.722	21	212	698	909
CACGGGTCTTTCTTCTTCCA	60.224	20	201	9	209
AAGCCAGTGCTGGTTGACTT	59.914	20	240	1155	1394
TTGGATCTGCAATGTGGATG	60.481	20	262	233	494
GCTTCTCCACGTATTCCAGC	59.843	20	267	176	442
GCGTGATCTTGGTGTTCTTG	59.293	20	275	1841	2115
TCGATTGATTTCCCTACCGA	60.405	20	195	333	527
TCCTCCGTTTTTGGATTCTG	60.044	20	274	358	631
CCAAAACCGAACCGAATTTA	59.805	20	249	334	582
TGTTGGAGTCTTGAACAAGGG	60.133	21	227	343	569
TTGACTGTCACAATCCCGAA	60.088	20	249	1013	1261
TTAGGGTTTAAAATCGCGCA	60.564	20	214	7623	7836
CAAGCCATGGGTCTTTGATT	59.933	20	234	186	419
ATGAGATTGGTGGTTGTGGG	60.634	20	197	0	196
CTTTGCAGTAAGAGACGGGG	59.869	20	239	650	888
TCTTAATCCTTTGGCATTCAA	57.388	21	219	1117	1335
GAGGGTGCACATCTCTTTCG	60.801	20	267	2	268
CGCGGATGGTTAAGATTCAG	60.597	20	229	1397	1625
CAAAATCAGGCACCAGCTAA	58.917	20	222	919	1140
TCGAGTCTCCATCCTCGTTC	60.349	20	276	54	329
TACCAAGGGCATTTTTGTCC	59.801	20	210	24	233
GCCTCAAATCCTATTCTATTTTC	59.549	24	246	77	322
TCCGGGGAGGGTTCTATTAT	59.622	20	263	1333	1595
CTACCACCGATCCCTCTGAA	60.065	20	199	1102	1300
CCACACAGACGAAACGTCAC	60.203	20	185	21	205
CACCCCTGAGCTCACTTTTC	59.844	20	279	583	861
TGTCCACTGATGTGGCATTT	59.967	20	228	258	485
TGCTTGGCTCTATCCCTTTG	60.344	20	187	710	896
ACTTGTTGAAATTCACCGGC	59.978	20	277	529	805
TGAACTGGAAAATGGAACCC	59.767	20	159	987	1145

CGGCATGTTTTATGTTTCAATC	59.367	22	177	485	661
CACTAAAGTGTGCTGTCATCGT	57.969	22	184	19	202
ACTCCCCCTCGAAGTTTTGT	59.972	20	277	203	479
TCATCAATTCTTTCTGCGCT	58.6	20	279	1240	1518
AAATCTCCCGTAATTTGGCG	61.155	20	176	44	219
TTATGCGTTTTGACGGGATT	60.323	20	199	514	712
TCCCCCTTCTCCTCTACCAT	59.89	20	173	324	496
AAAGTAGAGAAGGGGAAGGG	59.948	21	170	469	638
CGGTGAAGGTGTTCGTTCTT	60.149	20	150	166	315
GAAACTTGCTAGCCCATGAAA	59.352	21	245	665	909
TTGGATTGAGAAAGCGATCC	60.155	20	279	14	292
AGCCCACAGAGTTGGAAAAA	59.711	20	102	1081	1182
AAAATCAAAGGCCCACAATG	59.801	20	127	11	137
TTCAAATGTTTTTGTAATTTCCC	59.653	24	101	29	129
TTCGCTCTCTAGCGGATCTT	59.316	20	199	1217	1415
AATGTAGGTATAAGACTGTGA	57.779	27	279	5	283
TCCTGACCGGATCTCTCACT	59.792	20	254	133	386
TACATTGATCTGCGTGCTGG	60.834	20	243	32	274
TTCCTCTCGTGTTTCATCCC	60.05	20	179	22	200
TTAGCCCATCAAAGTCCAGG	60.066	20	150	231	380
TCGAATGGCCATAAGGAGAG	60.17	20	277	2736	3012
AAATGTCCTTCATCACGCAA	59.127	20	190	21	210
AACCTTATAGGATGTCCGGC	58.019	20	216	825	1040
CCGAGTGCCTATTTTGCCTA	60.223	20	165	6863	7027
CGCGTCTATCGATACTGATCC	59.705	21	255	3228	3482
AAAAGGTCTGCCCTTGCTTA	58.973	20	132	364	495
TTAGATAAAGGCGGTGGAGG	59.178	20	277	900	1176
CACAGTCCACACATGAAGCC	60.162	20	177	1078	1254
AGGGGTTATCATGGGATCAA	59.055	20	212	6	217
TATTTCAAGTCCGGTCCGAT	59.387	20	266	380	645
ACGAAGTTAGAAAATAAGGAG	57.269	24	153	115	267
CTACTGCCTTCGTCCCATTC	59.694	20	149	1336	1484
TCGCGTCTGACTCCTCACTA	59.726	20	164	34	197
GTCCACGGTGGTGCTAGAGT	60.182	20	105	31	135
GCAGGTCCATCTGAGGTAGG	59.679	20	135	937	1071
AAAAGGGGAGAAAAGAACGG	59.566	20	232	41	272
TCCTCAGCTGAAAAGGGCTA	60.088	20	103	488	590
TTTCTCTCGTGCCATTCTCA	59.522	20	266	311	576
TGGTAAAACTCGAAGGATGGA	59.555	21	192	32	223
TGTTGCACTTTTGAACAATGG	59.618	21	178	67	244
GAGAGACGAAGGGGATGATG	59.612	20	280	224	503
TCAGAACCGAGGTTGGACTC	60.238	20	141	235	375
AAACATAAAAGCCACCTGCC	59.091	20	154	66	219
TAGCATCGTGAGTAGCGTCG	60.18	20	152	15	166
TGTGGCATCACATGGTCTCT	60.121	20	238	34	271
GCCGATCGAGTTTTGGATAA	60.038	20	153	214	366
AGGCAGAAAAGAGGAGGGAG	59.95	20	153	895	1047
GAACACTATTCCCATCCCCC	60.388	20	169	5	173
AATAGACCCAGACACGGGC	59.942	19	198	27	224
TGCTCAATGAACTCCTTTGGT	59.726	21	138	11	148
GCATTGTCGGCTGAACTTTT	60.257	20	208	1213	1420
TGCTTCATTTCACCTTCCAA	59.247	20	160	12	171
AAAGAAAAGGACGGGAGGAA	60.046	20	106	88	193
GTTATGCGTTTTGACGGGAT	59.829	20	215	883	1097
TGTGCGTGTAAAGCTGGTTC	59.911	20	238	740	977
TACTTTTGGGCAATCCTTGG	59.931	20	156	3158	3313
TTGCCAAACACACATTTTCA	58.573	20	268	1298	1565
TGGTCTCAGGAAAGGTGCTT	59.844	20	213	12	224

CGCTTATCCATGGTTGGTTT	59.823	20	232	221	452
TGCCTATTTTGAATTTTGGTGT	58.543	22	146	367	512
GCTCATCCATTGATTTGGTTG	60.324	21	276	1096	1371
TCGATCATAAGAGCATCCCC	59.998	20	261	367	627
CGTCCCACAAAATATGTCCT	57.393	20	128	129	256
CAGTGACATGGCCAAAACTG	60.152	20	214	111	324
CGCTTAAAAACCGGACCATA	59.958	20	163	878	1040
ATGTTATGTGTATGCCGCGT	58.948	20	204	23	226
ATGCAAGGGGGTGACCTTAT	60.578	20	196	0	195
CGCATTTAAAGCGGAAAAAG	59.855	20	197	105	301
TGCTATGATTTTCCCCCAAA	60.26	20	239	230	468
AAAATGCACCATTTCTTGCC	59.945	20	274	1245	1518
TTCGGAGTGAGAGGTTTTCG	60.366	20	279	24	302
GAGCGAGGGTTTTATTTTGC	58.833	20	265	38	302
CCGGCTACTTCGAACTTTCT	58.602	20	260	565	824
AACATGGGCAAGAAACAACC	59.836	20	256	870	1125
CCTCAATTGTTGCATGGTGA	60.517	20	267	1039	1305
TCATTGGAAAGTTAGGGCGT	59.569	20	132	365	496
GAACAACCAAGGCAATTTCAG	59.601	21	237	23	259
CTGAATCGCGAAACATGAAA	59.809	20	276	400	675
CCATGATGAATGTGAGGCAC	59.925	20	266	31	296
TTATTGGAACAATACTATACAA	58.07	27	137	87	223
TTCTTGATGTGTTGGCAAGC	59.847	20	139	169	307
GGTCCATGGCCTGTTATGTC	60.203	20	258	248	505
TTAGTGGGCTAAGTGGGGTG	59.986	20	178	199	376
TTGCATCAAGTTTTAGAGCAGC	59.674	22	226	36	261
ACTGAATCAGCGCTCCAGAT	59.981	20	154	204	357
CTTCCCTGCACAAAAGTCGT	60.291	20	263	72	334
AAGGTCAGGAAAACCCAAGG	60.332	20	250	2787	3036
TACAGGTTCACCCTTCTGGG	59.959	20	222	114	335
AAAGAAGGAAGGAAAGGGGG	60.755	20	111	252	362
TCTTTTCTTTTCTTTCCATTTCA	57.27	23	274	101	374
TGCAGGTTGTTTTCCATTTG	59.561	20	271	2214	2484
CGGCTATTTGAGACGACATT	57.849	20	280	1	280
ACCCTACCCACCCAAAATTC	59.919	20	190	184	373
GTGGTGGGAGAAGAGAAGGA	59.228	20	205	84	288
AAATGTCAGCCACACACGAA	60.16	20	135	351	485
AGTGTCGCGAACGGTATAGG	60.154	20	234	79	312
AAAATCAAAGGCCCACAATG	59.801	20	222	29	250
ACAATGCTGTCTATGCCACG	59.746	20	214	449	662
TGAGGCAAACTGAAAAACCA	59.293	20	261	308	568
CGATCCCACAGAGATTGGTC	60.475	20	254	324	577
CTGTGCATTTGCAGACCACT	59.905	20	144	459	602
CAAGTTTGGGATTGCTCCAA	61.001	20	271	206	476
CACCCCTTATCTTCCACAGC	59.55	20	256	148	403
GTACCTGCACGTTGCGTAGA	59.935	20	252	4226	4477
GGGCAAGTTGGCTATTTTCA	60.074	20	181	2577	2757
ATCCTTTTGGACGAGCAATG	60.074	20	245	2315	2559
TGATTGCATTATCAAGAACCAA	59.485	23	224	18	241
TTGCTCCTAGTTGGCACAAA	59.464	20	199	445	643
AAAACTTCCTAAGCCCCCAA	59.939	20	161	710	870
CCCAATTGTCGTGTGTGTTC	59.855	20	205	10	214
CCACCTATCTGCATCCACCT	59.95	20	125	1480	1604
GGCGGTGAAACGATAAACAT	59.829	20	233	224	456
GACCCCAATGGATCGTAGG	60.142	19	280	162	441
TTGGTGTTGGTGTTGTTGCT	60.049	20	227	43	269
TTCGTTTTTCCTTCCCAGG	60.029	19	139	51	189
AGGTTGAGTCGGACGAGTTG	60.298	20	254	592	845

AGCATCAATGGAGTATTGAAA	57.835	23	246	351	596
CACCAACCCAACCCACTAAC	60.126	20	144	85	228
GAGCTCGGATCAGTCCGATA	60.326	20	160	27	186
TGGTAAATCACTAGACCCAAG	59.879	23	238	49	286
GCTAAAACTCCTGATTGCGG	59.845	20	165	60	224
TGAATTCTGTGGGAAGAGCA	59.369	20	194	19	212
TCATAATGGAGGACCAAGGC	59.894	20	219	87	305
TGATGGATGGATGGTCTTGA	59.85	20	105	91	195
TATGTATCGTCCGCGCTGTA	60.259	20	257	631	887
TAGTGCCGTATTGTTTCCCC	59.823	20	258	76	333
CTTTGCAGTTCGCTGATGTC	59.596	20	274	575	848
TGAAGTAGGAAATAAGGAGGT	57.525	24	216	262	477
AGCGTAAACACGTCCCCATA	60.386	20	230	156	385
GCTTGCAGCCTTCTGTGTTA	59.224	20	226	2	227
ATAACCCCACCAACCTAGCC	60.074	20	103	28	130
GGAGTATCACTTGAATGCACC	60	22	204	91	294
GTAGGCAGCAAGTTGGTGGT	60.179	20	153	115	267
AGCTGATCCTGCGACATTG	59.959	19	207	415	621
CAAAACACTCCCCCGTAAAA	59.833	20	277	370	646
TCGAACCACGTACATCTTGC	59.722	20	165	21	185
CGGTTCATTCCCATCCTAAA	59.756	20	161	276	436
GCCGTGTTAGCCAACGTAAT	60.025	20	188	115	302
TGGAAGTGACAGCGAAGACA	60.593	20	166	284	449
ACCTTTTGCATTGTCAGCAA	59.322	20	187	431	617
ACCACAAGCAAGCATTTCCT	59.74	20	203	179	381
GCTTCCGCATCGTTCTTACT	59.481	20	237	3	239
TGCATACGGAATTTCAGCAA	60.215	20	220	531	750
ATTCGAAAATGCTCGTGAAA	58.361	20	195	1950	2144
CAACAAAGCTGGAACGTGAA	59.881	20	158	82	239
ATCTCCAAAACCCGACAACA	60.353	20	271	110	380
TGTTATGCATTTTGACGGGA	59.93	20	264	5	268
AAGGGGGTTATCATTGGAGT	57.316	20	204	99	302
TCGTAAAACGACATGAACGG	59.585	20	267	158	424
AGCCTCGGTGCTTGAAAATA	59.845	20	243	287	529
TGGAGAGGACCTTGGAACAC	60.088	20	233	2566	2798
CAAGCTGTTCGGGAGAAAAA	60.357	20	213	482	694
AAAATTGAAGCGCCAGAAAG	59.474	20	266	104	369
TCCGTTAAGCAGTAAAGACGA	57.733	21	194	435	628
CCTACTCCACCCCTTCATCA	59.92	20	220	2682	2901
CGCGTGTGAAACTCTAGCAA	60.195	20	136	195	330
TGAATGAATCACAAAAGGGG	58.395	20	228	24	251
TTTCAATTTCGTGTGCCAAA	60.088	20	278	23	300
AGCTCTTTCTCCACAGACGG	59.598	20	220	2189	2408
TGAATCCTCCCGTTTTCTTG	60.044	20	221	182	402
CCTTGTGGTTCTACAAAATAGC	59.613	24	130	168	297
CACACCCACACGCACTTTAC	60.072	20	191	382	572
GTACGCATGGAATGGACAGA	59.527	20	249	445	693
CCGATCTTAATCTTCGCTGC	59.945	20	201	165	365
GGAAATTGATGGATTTGGGA	59.558	20	196	665	860
ATCTCAGATCCAAACGCCTAG	60.228	22	170	199	368
TTCGGGGCATACATGTGTTA	59.809	20	234	3054	3287
TGTGTGATGTTGGAGTTGGG	60.416	20	177	120	296
GCTCCTAAAATATTGGTTTCTA	58.015	26	146	406	551
CAGCATTGCTTGCACTTCTAA	59.264	21	193	1104	1296
TGTTTTGTAATTTCCCATGTTTG	58.816	23	103	22	124
CGAGTATTGGTTCAATAGAATT	60.143	26	276	309	584
TGTGTACCGCAGTTCAGAGG	59.897	20	242	96	337
TTTGATCTACCTCGGCCATC	60.036	20	250	2196	2445

CCTACCTCGAGACCGAACAA	60.246	20	272	158	429
TGAAAAGTCACACGAAAACGA	59.352	21	182	238	419
TGGTTGTTGTGAGGGTTTCA	59.976	20	246	20	265
AGAAACACCATTGCAGTCCC	59.973	20	183	2222	2404
GGGGTTATCATGGGATCAAGT	59.895	21	262	275	536
GAACCAGAACTACCCCACCC	60.607	20	202	1325	1526
AGAACCGGAACCGGAATTAG	60.312	20	224	322	545
TGTGTTTTGACAATATTTAGTGT	58.633	27	104	148	251
GATCAGCCATCAACCCCTTA	59.894	20	179	0	178
TCCGCACACCATATTCAGAC	59.527	20	255	555	809
GCAAATATTGGCCGTCAGAT	59.929	20	245	380	624
ATGGTGGTATGGTGTGGAGG	60.51	20	135	128	262
TGATGGAACGGGGATTGTAT	60.014	20	269	538	806
CTTGGGTCTACCCTTTTGCC	60.846	20	200	3383	3582
GAGGCTGCTGAACATTCGTA	59.028	20	108	77	184
GAGGTTTTGACGGGATTTAGG	59.822	21	111	367	477
AGAACGAGAGAAATCGACGG	59.43	20	186	91	276
CAGCCCCTTTTTCATTTTCA	60.046	20	258	183	440
TGGACGTCCCAGATTGTTTT	60.353	20	163	3	165
TGAGCTTGTTTTCAATTGCG	59.992	20	248	74	321
CCTGAAACCCTAAGTTCCCC	59.799	20	199	1053	1251
TCGACCTACGAGAGTGAGGG	60.399	20	271	371	641
GCGAATGACACCTTTTGGTT	59.978	20	176	855	1030
GGGATGAAATGAAGTGGGTG	60.173	20	157	507	663
TCTTCGATGAACTCTGAAATGC	59.457	22	169	301	469
TGGCTACGGACAAACTCTCA	59.44	20	179	293	471
TTTTCTTCAAAATGCACAATAAT	58.319	25	237	97	333
CCATCGTCGCTATCACATTG	60.096	20	205	39	243
TGCAACAAATGGATGGTTGT	59.823	20	119	17	135
GGCATCAAAGTTGTCGATCAT	59.954	21	104	10	113
ATCCCACATTGGTTGGAGAT	59.068	20	248	26	273
CCCACCAACAAATTTGAACC	60.066	20	113	3669	3781
TCGGTCACATTCAATAAGGC	58.574	20	243	1047	1289
TGCAAACCCATGATTGACAC	60.376	20	170	676	845
GTCTCAATGGGGACATCTGG	60.326	20	256	732	987
CAGCCCACTTCTAAAACGGT	59.238	20	164	826	989
TGGAGGAATGGGTAGAGGTG	59.92	20	243	0	242
ATGATCCCAACGAAATCCTG	59.75	20	186	65	250
AACCGATCATTTCATCAGCC	59.9	20	232	2754	2985
GAGGCCTCGATCTTCTGTCA	60.497	20	103	12	114
CCGTGAAACCAATCTGATCC	60.317	20	253	250	502
TGGGCTAATCACTCTCAGCA	59.547	20	179	10	188
CAATTTGAGAATGGGATGGG	60.126	20	234	778	1011
CGCACGTGAATGCATCTAAA	60.807	20	218	583	800
AACATTGCGGACTTGGTACAC	59.912	21	265	774	1038
TGAGATGATATTATGAACTGCA	60.24	26	264	208	471
CGTGATGCAACGCATTCTTA	60.807	20	250	225	474
TCCGAGAATCTGTTAGAGGAGA	59.491	23	256	102	357
TCAACCTTTTGCAAGCACTG	60.027	20	200	533	732
TGAAAAGGGGTGAGAGGATG	60.042	20	275	101	375
CAGCTCTCTACAATGGCGGT	60.419	20	147	51	197
TTTGAATGGCAAGGATTGGT	60.309	20	240	344	583
GGCATTCTCATCTCCACCAT	59.893	20	270	4473	4742
TGCTAATGCAGATTGAGCGT	59.596	20	273	645	917
TGGTTATTTGCCCGAAATTG	60.671	20	223	65	287
GTACAAAGTCGCTGGCACAA	59.911	20	272	68	339
TCAAAAATATCCTCGCTGCAT	59.696	21	124	8	131
ACTATGCGCATGGGAGAGAG	60.384	20	227	103	329

AATGACCGTCTCGACGAAAG	60.255	20	228	343	570
GGCATGCAAAGATGAAGGTT	60.081	20	231	199	429
TTGCGTATGATAGGGTTAGCAC	59.298	22	240	26	265
CATGCTACATTCCGTGATGG	59.948	20	246	547	792
TTTCTTATTTCCCGGCTCCT	60.034	20	134	556	689
AAGACGGTGAGTTGAGGGTG	60.151	20	226	593	818
AATCCTTGCTCTGGCTGCTA	60.118	20	260	2	261
AGGGATGTTTGTACCTGAATGC	60.249	22	122	3	124
ATAAAAATGGCACCTGGCTG	59.96	20	206	172	377
CAAGAGGCAATCACGTTGAA	59.84	20	220	293	512
TTCCTTGCGTGGCATTATTT	60.456	20	184	1027	1210
TCAAGAGCAAGCAAAGATCTA	59.7	24	163	7	169
TACTGACTTGTTGTGCGGGA	60.301	20	241	411	651
AACCCGAAAACCGGTTAAAA	60.549	20	126	769	894
GGAACCGGCTAAGATGATGA	60.036	20	231	240	470
CCCGCATGTCATAACCACTA	59.42	20	272	270	541
CCAATGGCGATATTTCCTGT	59.784	20	191	190	380
TGTGGTGTCTATGTATGGGTGG	60.55	22	212	651	862
TTTATTTGGACATGGAGCAAT	57.121	21	146	667	812
ATAAATGCCTACGTCCACGG	59.845	20	215	167	381
CACCCTCCTTCCTCAAACAA	60.081	20	211	470	680
AACAAAGGGGGTTGGAGAAT	59.668	20	231	3178	3408
CGCGTGCTCCTAACTCTTTC	60.154	20	119	28	146
AGTTCGTCAAACCTCCCAAA	59.569	20	226	146	371
AAAACGGAAAACCAACATCG	59.839	20	205	46	250
TCTCTCTTTTTGGTAGGTCAATC	57.564	23	260	144	403
TGGATGGTTGAGACCCAAAT	60.173	20	156	23	178
TGTGAAGTGTTGCTGATGTGA	58.855	21	228	1160	1387
GCGGATCCCCCTTAATTTTT	61.291	20	280	302	581
TCCACGAGATTTGAAAATTAGA	57.946	23	271	779	1049
CGTGGTGTCCATTCATTGTC	59.812	20	208	3006	3213
TCCGGACGGAAAGATTACAC	59.933	20	184	76	259
GACTCGTCAGGTCGTGGATT	60.12	20	223	1066	1288
TAATTCCGATTTGGCAAGGA	60.395	20	189	430	618
ATGGCGCCTTCTATTCTCCT	60.194	20	152	342	493
ACCCGTACAATATCAACCACA	57.742	21	181	61	241
GAAGTGTTATGCGTTTTGACAA	58.249	23	234	1790	2023
ATCTCACGATATCCCGCATC	59.884	20	273	63	335
TCCCAATTCACATTCTGATGA	58.912	21	268	14	281
TGAGACGAAACTCATGCGAC	59.992	20	231	63	293
CCACATATGCAAGATTTCAGC	58.254	21	124	50	173
TCGATGAATCCATGTCTTGC	59.61	20	128	203	330
TCTCAGCATTTGGGAAGGAT	59.629	20	187	23	209
AATCCACACCCGAAATATGC	59.651	20	246	286	531
CAAATGGTTTGGGGTTTTTG	60.06	20	267	120	386
TGTTGATTAATCGGCATAGATG	59.468	23	216	1453	1668
CAACCGAAGCAATAAGAGGG	59.702	20	256	16	271
TCAGTTGGTCCCTCACACTG	59.705	20	270	553	822
AGAAAACTCACCCTGCCTCC	60.628	20	271	113	383
TTTAAGGGTTATCACCTGATTTT	57.757	24	216	825	1040
TTCGGTGAAGATTGGAGGAG	60.187	20	224	31	254
AACCAAGATCAGGCTGCAAT	59.7	20	168	672	839
GACGCCCACGTGTAAAGACT	60.179	20	253	382	634
GACTCGCAAAGACTTGAGGG	59.989	20	151	36	186
GTGACGTGCTGGTTGTCCTA	59.751	20	217	1035	1251
TGACAATTGCAAATATGGCG	60.474	20	218	2	219
GCTGCATCGATGTATTGTGG	60.104	20	197	1931	2127
ACCCTGACCATTTTCTCCCT	59.795	20	240	692	931

ATTCCAAAGCCTGGAGACCT	60.074	20	279	12	290
ATCAAACACAGCGCTATCCC	60.103	20	210	3	212
GCGACTTTTCAGTTTCCAGC	60	20	224	733	956
CATTTGCAGATGCTGATGCT	59.979	20	204	1078	1281
GTTAATGCGTGTGAGTGCGT	59.794	20	200	47	246
GCAAAATACCCTGAGTGGGA	59.933	20	176	284	459
CTGACATGGAAAGCACCCTA	58.722	20	267	266	532
ATTCATCAAACCCAGTTCGC	59.939	20	220	29	248
ATAGCCAAGGCAGCTCTCAA	60.118	20	268	1830	2097
ACCCATGAGCTGGAAGACAA	60.656	20	208	263	470
CTAGGCGGATCTAGGCAGGT	60.743	20	206	23	228
CATCGCTCCCAAAAATGTCT	60.074	20	191	212	402
AAAGCGCGATTTTAAACCCT	60.095	20	236	2182	2417
ATGGGACATTTTTAATTTTGCC	59.972	23	233	1480	1712
TTTTCGTGGATATAATTGGGC	58.817	21	174	64	237
AGACCTCCGCCACCATCTAC	61.449	20	236	4779	5014
GAAGGGAAAGAACCTTTGGG	59.912	20	257	1283	1539
TCGCTCTTAACCCACAACCT	59.734	20	118	271	388
GCATGCATCTGTCGGATCTA	59.788	20	169	338	506
GGAAATAAGGAGTTGTTATGA	60.434	25	135	2767	2901
TTATTTTCTCTGTTGCGGGC	60.209	20	254	53	306
TTTTACTTTGGCCGAATTGTCT	60.004	22	118	290	407
TTAAATTTTCGAACGCCTGC	60.205	20	180	161	340
ATTTTTGGCATTGAAGCTGG	60.074	20	234	98	331
AGCTCCAATAGTTGCTTCGG	59.476	20	191	1	191
ACTGCGCACACTTTGTTTTG	59.951	20	245	2114	2358
GCCGATTTCTTTCACTCCCT	60.578	20	140	120	259
CAAAGGCCCACAATGGTTAT	59.685	20	137	2168	2304
GGAAACACGTTGTGGTAGGG	60.269	20	273	1444	1716
TGGCTTTGGTAGGCTTTCAT	59.708	20	195	1702	1896
CGTGGAATATTTGCATTGCC	61.218	20	147	177	323
CGTCATCTCATACGTTGCCA	60.687	20	242	456	697
TCACATTTGGATGGGAAACA	59.75	20	258	2010	2267
TGCAAATGATTCCCACCTTT	60.309	20	250	3997	4246
AAATGAAGATCGGTTGCCAG	60.074	20	214	21	234
GCGGAAATTAACCACAACCA	60.732	20	148	7	154
CGCGTTACGAATCCAAGTTT	60.131	20	192	607	798
GCATGTTGTAACGACCCAAA	59.444	20	267	4	270
GGCGGAATCACATTAGCATT	59.929	20	217	281	497
TTTCTCTCTTTTGGTTGGTGAA	58.856	22	185	210	394
GGACGCATCAGGTATAAAAGG	58.593	21	241	5	245
CGCATCTGATTTTTGCAATC	59.261	20	240	1616	1855
GAAGAAACCCCTTTTTCTTCTC	59.682	24	250	590	839
TCTTTATTTTAGCCGCACCC	59.212	20	127	333	459
ATGGATGGTGGTGATTCCAT	59.869	20	263	295	557
TGTTCATACGCATTGGAAAAA	59.063	21	271	73	343
TTGAACTCCCCTCTCTCTCG	59.525	20	164	117	280
CGCCCCGTATTTTGAATTTAT	60.05	21	277	1431	1707
AGTTTGGCCTTGCATTTGAT	59.574	20	162	1952	2113
TCCACCAAGCTTACACAACA	57.736	20	176	608	783
AAGCGTTGTCGTTTCTTTGG	60.284	20	239	252	490
ATTGGCCTAGCCTTTTGTGA	59.708	20	272	1638	1909
TTGCTTTTCCGAATCTGTGA	59.395	20	251	540	790
TTCGTGTTTGTTCTTGTCGG	59.734	20	269	249	517
CCCCCTAAACCGTAAATCAA	58.805	20	201	9	209
TGAAGTTGATCAAGCAAGGG	58.847	20	213	1175	1387
TCAACATTAATGGCGTCGAA	60.073	20	266	4526	4791
CGATCGTAATTGATCTACGTCC	61.213	23	264	93	356

GTTGGTGCCAAAATTGCTCT	60.118	20	223	5	227
ATTACGAGCCACGGCTACAG	60.292	20	234	66	299
CGTAATCGGCAACTCATTCA	59.688	20	250	1081	1330
GAAAAGCCGAATGCAGAAAG	59.96	20	172	1116	1287
AGGATAAAGGGGGCGAATG	61.15	19	280	175	454
GATAGAAAAGATGGCGACGG	59.668	20	113	58	170
TGTTTGGGGCTTCTTCTCAT	59.67	20	185	3659	3843
AAGGCTATCGTTGCTTTCCC	60.582	20	244	283	526
TACAAGGCCCGACTTGAGTT	59.734	20	224	32	255
GAACCAGTAGTTCCGAAGCG	59.875	20	265	499	763
ACACCCTCACCTCCCCTC	59.888	18	173	90	262
ATATAGAAGCAGGGCGCAAA	59.838	20	272	388	659
ATTACGTAAAAATGGGTTATTA	57.717	27	165	491	655
AACGTGACATGTTGCTGAGG	59.751	20	201	837	1037
GGATCCGATGTGGGATCATA	60.514	20	122	358	479
TTCGAAGATCAACGGACGAT	60.603	20	138	9	146
AAATAAGGAGGTGTTATGAAG	59.323	24	253	120	372
CCCATGTAAATAGCCGTTGG	60.202	20	253	24	276
TGATTTGTTGGGGCTTTAGG	59.931	20	254	468	721
AAACAAGAATTCGGCATCGT	59.574	20	181	283	463
CCACCATCTTGTAGGTCGCT	60.134	20	145	1786	1930
TGAGTTTGCATCTAAGGAGGT	59.378	22	272	500	771
TGAGGATACTCGATTTCACGG	60.081	21	233	264	496
GAGAAGGGTTATCACTTGAAT	57.473	24	277	77	353
CTGCAATAATGGCTGCATTG	60.237	20	278	2703	2980
CGTTTAAGCCAATATCATTGTT	60.247	24	278	478	755
TCTCCTTCTGCGCACTTTTT	60.132	20	200	269	468
TGAGTCCATTCCGCATTAAA	59.112	20	200	120	319
TCAGAGGAAAACAGAGGCTG	58.158	20	141	84	224
ACCTTGATTTCTTTGTGGCG	60.11	20	236	109	344
CGTTAGGCTCAGGAGTGAAGA	59.624	21	100	4	103
CAGGATTTCGTATCGCTTCC	59.668	20	234	5	238
CCCAAATGAGCATCTCAGAAA	60.199	21	216	310	525
TCTTTTGGGGCAGTGAATCT	59.67	20	194	577	770
TGTTTAACTCCCACTAATGCAA	58.731	23	207	25	231
TTTCCATTTCCATGGTACGTT	59.192	21	259	2248	2506
GATGATAGAAGGGGGCATGA	59.854	20	247	1937	2183
AATCCAGCAATTTGCCTTGT	59.574	20	158	2621	2778
AATAGTTTGTCACCCGCACC	59.859	20	190	343	532
GTCCCAAAACATGCAACTCC	60.362	20	274	773	1046
ACAATTTGGTGATTGCATGG	59.251	20	239	1266	1504
CATCTCATTCCAAGTCTCCCA	60.058	21	218	630	847
ATGGTGGGAGCCTATAGCAA	59.551	20	255	18	272
GCATTGGGACACCTAAGCAT	59.962	20	241	513	753
CAATATTACAATGGCCAAGAG	57.725	23	154	93	246
AGAAACTCCCTTGGGTGAGAG	59.725	21	126	314	439
GGTTTGTTTTAGGCCCACG	60.35	19	197	4	200
TCTTGATGCATTTTGGAGCTT	59.837	21	212	37	248
TGAAACGGACAAACGATGAA	60.088	20	228	77	304
AAAAGGGAAAAACCCTCAGC	59.571	20	273	287	559
CCCGAAATACCCTTCGTGTA	59.817	20	275	83	357
AAGGGTGATGTCGCACTTCT	59.727	20	267	55	321
GGATGATGCCTTCAAGGGTA	59.894	20	230	466	695
CACCCAACTCAGTCAAGGCT	60.298	20	236	587	822
ACATGCTAGAGGTGACGTTTT	59.309	22	232	1631	1862
TTTTGTCTTTTGGGATTCGG	59.91	20	208	2086	2293
TGGCAATAAATCCAACCCAT	60.016	20	249	371	619
ATGAGTAGCAGCAACGAGCA	59.77	20	143	592	734

TGGTGTACAGAGTGCATGTGA	58.719	21	195	258	452
GCGAATATAACCCGCTCTGA	60.196	20	220	43	262
CCTTGGGCGTTGATCTTAAA	60.067	20	131	87	217
GCAGGAGAGATAGGGGGAAG	60.169	20	264	18	281
TTCAGTTGGTCAGCAAAACG	59.881	20	150	42	191
GCGCAGATCTAATGGTCCAG	60.765	20	178	205	382
GGCAACATAATCAGCCATCC	60.304	20	145	9	153
TTTCGCACGCATTAAATCAG	59.842	20	171	331	501
TGTGTGATGTTGGAGTTGGG	60.416	20	187	94	280
GAATCAGTGGCTTCCACGTT	60.119	20	243	239	481
TTATATTTCAGGGGGAGGGG	59.971	20	187	243	429
CCTTCACTCCCCCTCTCTCT	59.801	20	219	1849	2067
TTCTTATTTCTCACTTTAAGACC	58.093	27	215	452	666
AAAAACCCTTCTGAAACCCG	60.324	20	172	413	584
TTTTGGGTGTTATGCACACG	60.415	20	245	71	315
ATGGGATTCACCTGCCTTC	59.878	19	138	8	145
TAAACAGGCTTCGGGCTAAA	59.847	20	269	200	468
ACCCACCAACATCACCAAAT	59.95	20	218	58	275
TATGGGGCGTTTTATTTCCC	60.848	20	247	157	403
ATAGTCCCGCTTGTGCTTGT	59.763	20	250	44	293
TCGCCTAACTTATGCAATGAAA	59.753	22	159	228	386
GATGGTTACATCGTCCACCC	60.057	20	279	147	425
TCGTGTGGTTTTGAAGCAAG	59.881	20	242	260	501
ACCACCGGCTAAACCAGTC	59.981	19	211	14	224
GATATGATTTTGCGCGGAGT	60.067	20	225	33	257
CAATTTTCGGCAGCATTACA	59.702	20	230	358	587
AGGGGGTTATCACCTGATCG	61.095	20	135	1262	1396
TAGAGTTCCAAGAGGGGGCT	60.204	20	199	14	212
GGCAACAAGAAGAAAATCGC	59.829	20	252	391	642
CACTACTCATCATCCTCTCTTTC	57.758	25	165	883	1047
CTGCAGACGTTTCAAGGTGA	60.025	20	216	731	946
TCATTTATGAAGCAAGGGGG	59.894	20	106	32	137
AAGTTGGGGATGTAGGGGTC	60.052	20	144	3881	4024
AGCGAGATCTTCGTCCATTT	58.889	20	130	126	255
AAATGGCGTCTGTTCCCTTA	59.569	20	201	23	223
ATGATCATTCGTTCATGCCA	59.89	20	210	2461	2670
TCTGAAAATTTTTGCCCACC	59.916	20	205	39	243
GGGGCCACAAAATATTCCTT	60.02	20	163	499	661
TCATGATCGGTGAAGATTGG	59.451	20	215	10	224
GCGAAAGACATACGGGGTTA	59.96	20	262	32	293
ACTCGAAGAGTAGCGGCTGT	59.261	20	268	63	330
ATCACGTGCACCGTCATCTA	60.144	20	184	321	504
CCACGAGATCAAGAATGGAA	58.643	20	239	12	250
CCTTTCAGTCAACAGGCCAT	60.111	20	273	1097	1369
TTCAGCCCACATATGTTCCA	59.924	20	105	35	139
CCCAACCCACGCAATAATTT	61.799	20	271	20	290
CGGAGAACCTGAATTGATCTG	59.679	21	275	737	1011
TGGATCTGGATCATCAATGC	59.409	20	245	117	361
TTGGGTTGCTGAAAATAGGC	60.074	20	240	24	263
AGGCCCGAGCTAAAAACATT	60.095	20	151	57	207
GAATATTGTGCCTAGGTGGCT	58.226	21	177	30	206
TGTGATTCTGAAAAATAGATCG	57.059	24	203	321	523
ATCGAAAGACGAACACGCTT	59.882	20	219	586	804
GAAGATACTTCATGCTTGTAAA	58.527	25	172	371	542
TTGTGGGACAAGCAAATGAA	60.088	20	273	474	746
AACATGCACTTTCATTCGTGTT	59.545	22	231	47	277
TAGCGGGGTCTTTGTGGATA	60.46	20	112	334	445
AAGGGAATCCACAATGCAAG	59.933	20	248	202	449

CCTAACCCCACTAATGACCC	58.24	20	146	0	145
ACATGGAACAACATTGACGC	59.425	20	256	146	401
ATTTGGTCTCTTCCCCTCGT	59.935	20	271	678	948
TGTTCCGAATCTTCGTCCAT	60.461	20	169	4	172
ACCTCCGGATATCTGGTTCC	60.154	20	201	28	228
CAGTCGGCCGTTGTTTATTC	60.502	20	160	269	428
AAACCCTTGAAACAAATAAAAT	58.86	25	259	45	303
AGTTGGTGGAGGGTTTTCCT	59.834	20	216	102	317
TCGAATTGAAGTTAAAGCTTAG	59.062	26	132	275	406
CACGTGATTTGCTTGGAGAA	59.84	20	132	47	178
TGAAGCCTTTAAATGGGCAC	60.074	20	205	376	580
CACCCATTCATTCCCTCATT	59.605	20	138	196	333
GGACACAACAGAGGGGAGAA	60.088	20	240	349	588
GGCGAATGCTATGCATTTTT	60.068	20	253	690	942
TTCTTGGTGGCGGTAGGTAG	60.125	20	223	178	400
GGTGTTGGCCGAAAGTTTTA	59.975	20	101	6	106
TGCTCTCTCATTGTAATCTCTCT	59.688	25	229	760	988
TTGTTGTGGTGCGTTTTCAT	60.011	20	235	415	649
CATTGTCGAATCCTTCCGTT	59.933	20	132	1163	1294
TGCTATTCTTGTGAGGGGGT	59.55	20	241	211	451
TCACGCAACACAAACCCTAC	59.615	20	239	131	369
GCCTTCCCCATTGCTAAGTT	60.451	20	157	13	169
AAAGAGAGCTGCAAATGGGA	59.955	20	132	64	195
ATTGGGGAGGATAAAGGACG	60.145	20	112	65	176
CCTGGAAACAAAGAAGCACC	59.711	20	280	701	980
CGTCGTTCTTCAGAGCCCTA	60.529	20	168	12	179
CTCCAGCAATTTCAGCTTCC	59.955	20	172	75	246
ACACTTAAGGGGGTTATTAGTG	59.26	24	151	1203	1353
GCTGCTGTATTAAACCGAACG	59.793	21	257	511	767
TAAGGGTTATCACCGGATCG	59.778	20	238	1	238
TTTCTCAGTCAAAGTACAACCT	59.861	24	237	14	250
TGGACGCACAAAGTATGGAA	60.111	20	243	49	291
TGAGGGCAGTCAAAAAATTCG	61.137	20	215	2	216
GTGGTTGAAACCAGATCGAAA	59.963	21	276	1348	1623
TCCACGGGAGAGAATGAGAG	60.34	20	177	5	181
CCCCAAACAACGAAATGAAT	59.662	20	193	221	413
AGAACGGAAAATAGGGCGAG	60.573	20	194	194	387
TTGTGGCATTCTTGACCAAA	60.088	20	176	232	407
ATTTTATTGCAGCAACCCCA	60.323	20	194	732	925
TCCCCTCCACCCTCTATTTC	60.264	20	280	322	601
TTGTAATCGGACCGGTTTTC	59.801	20	237	360	596
CACCTTCTGGACTCAGACGA	58.964	20	267	250	516
GTTTACGGTTGGCGTTGTTT	59.904	20	138	240	377
ATATCGGCCGTCAGATTGAG	60.059	20	270	271	540
ATAGGGTCATGCGTGTGTGA	59.992	20	193	74	266
TGCGTTTTGACGATATATAGTG	60.194	26	169	1279	1447
CCCAAATTTTCTACCGCCTT	60.305	20	243	1027	1269
GAGCGATGTCGAATCACAAG	59.399	20	230	69	298
AAGTAGTCCTTTCCTCGGGC	59.713	20	242	124	365
TAGCCGAGAAGAACCTTGGA	59.948	20	182	80	261
TCCTGCCACATGTAATGGAA	59.924	20	175	6012	6186
AATCGCTCAATCACTTCATGG	60.088	21	240	2790	3029
AACAAACAAGCCCCCTCTTC	60.476	20	202	529	730
TTGGCCTGTTACGAATCAAGT	59.623	21	161	12	172
CTTTGCATCTTAGCGAGTTGG	60.025	21	254	936	1189
ACCAACTATGGCCAACCAAC	59.717	20	260	237	496
TGGAATTTGGTTTTTGTAACTTC	59.797	24	250	267	516
TTAGTAGCTTCGGGGTGCAT	59.73	20	239	196	434

TCATCAAACCTGCACCAAAA	60.088	20	256	470	725
CGAGGAATACGAAGAGTCGC	59.978	20	203	39	241
CATCGAGCCCACTTAGTGCT	60.419	20	249	990	1238
TGAATTCTGTGGGAAGAGCA	59.369	20	200	19	218
TCGTATGCATGTCATGGAGG	60.504	20	199	706	904
GTTAGGAAATAAGGAGGTGTT	57.059	25	133	1309	1441
GGTTTTCTTGCCAAAAATGG	59.429	20	206	432	637
TCGATCCATATGGCAAGAGAA	60.559	21	227	12	238
TTCATTCCATTTTGTCCGAA	58.94	20	272	20	291
TTGCGAATATAAAAATGAGAA	59.158	25	237	22	258
AAGTAGAGGCGGTCGGAGTT	60.268	20	234	1398	1631
GGTGTGTTGGCATTGCTAGA	59.722	20	194	1014	1207
AAGGAGGTGTTATGAAGGGAT	58.028	22	199	235	433
TTTTCCTCTCCCCTCTTGGT	60.045	20	272	321	592
CGCTGGTCTTGGAGATCAAT	60.218	20	254	1137	1390
TCAATTACATTCCCGTGGGT	60.051	20	234	1253	1486
TCAACAGCAATGAATTTGTGG	59.576	21	245	132	376
TCAGCTGCGATGTCAATTTC	59.955	20	174	30	203
CGGTGACGGTTGAGAATGA	60.671	19	152	51	202
TTGAAGTAGAGGGAGGGGCT	60.204	20	184	3737	3920
AGCGTATTTCTTGATTGCCG	60.23	20	138	687	824
AGCGTTCCCTATTCCCACTC	60.464	20	196	657	852
TGCGTCTCTCGACGTTACAC	60.056	20	226	64	289
TGTGACGTGGAAGAGAGAGAA	59.64	22	256	2123	2378
TCAGTGTTATCGAGCCTCTCA	58.61	21	278	17	294
CACTCAATCGGTTGTACCACAT	59.78	22	229	220	448
GAATGGAGGAGGATGCTTGA	60.158	20	227	4	230
CCAAAACAAAACACACACGG	59.898	20	240	5852	6091
TGAAAAGAGAAGCCCTCCAA	59.926	20	232	551	782
ACGAAAAAGCAAATTCCATCA	59.578	21	274	9	282
CGAGTGGTTTGGGAAGAAGA	60.224	20	262	0	261
AGGGCCAGAAAAACCAAGAT	59.94	20	272	345	616
TGCTGGGATACACAGGGTTT	60.375	20	171	97	267
GCCCTTGATTTCCAAGATCC	60.777	20	125	16	140
TTCATGATCAAATCTTATGAAC	58.497	24	155	30	184
GTTTGGTAGGCCGAGTCTGA	60.255	20	205	532	736
TGTTGGTGGATTGTGCATTT	59.823	20	253	46	298
ACCATATTTAAGGGTTATCACC	57.552	24	218	569	786
GGGCAAAACAAAGAAAGACG	59.724	20	279	3943	4221
AGGTCTTGACAGGTTGTGGG	60.002	20	272	17	288
GATGAGATCAATGCCCCAGT	59.893	20	137	3188	3324
CCAGTTCAAAAGCATCACCA	59.691	20	235	1252	1486
AAAAACAACATCCAGCCCAC	59.836	20	168	3047	3214
TGCCATGTTCTGCTTCTCTT	58.597	20	239	1053	1291
TTCAACCTTTTGTTTTGCCA	59.178	20	241	645	885
CAAGTTTCACGAACGAATGC	59.322	20	271	886	1156
CAGAACCCTCAAATCCCTCA	60.042	20	246	8135	8380
TGAAGAAATGGGGTCGACAT	60.317	20	235	43	277
CAACGAAGGATTTGGTGTTGT	59.883	21	274	3247	3520
GATTGGACTTGTTTCTCGGC	59.676	20	227	31	257
TCTTCCAAGAATGGAGCAGC	60.483	20	204	941	1144
TCATTTGCCCCCGTATTTTA	60.144	20	176	1	176
CCACGAATCATGATCGAAAA	59.474	20	230	2330	2559
AAGATATATAATTCATTGAGCT	57.982	27	104	176	279
TGATTTCGAGAAGCAGTAGGT	59.517	22	117	234	350
TTAACCCACCAGAACCGAAG	59.964	20	245	627	871
AATGGAGGCACTGGAGAATG	60.073	20	100	1926	2025
CACCTTAAGATCTGCTCCGC	59.978	20	238	127	364

GGCAGTCACTGGAAGGAAGA	60.386	20	268	1168	1435
CACCCGAAAATGAGTTATTATT	60.438	25	130	278	407
GGCATTGCAGAGTTGAGAAA	59.002	20	210	4712	4921
TGCGTTTTGACGATATATAGTG	59.092	25	217	302	518
AAATAGCTTATTGAATTTGATTT	58.677	26	280	22	301
CCAGATGTGAATGGGTCACT	58.349	20	183	130	312
CCATTTCCATTTCCAAACCA	60.535	20	154	494	647
CACCACGGAAGAGAGGTAGG	59.715	20	160	73	232
TCCATTCAAATGCGAATACAA	59.018	21	275	1550	1824
TTTTGCCTGATATTTGTATAACC	57.88	24	272	891	1162
TGGAGTAAGGAGGTTGAGGG	59.133	20	188	13	200
GCTGACTAATCCACAATTGCC	59.588	21	234	9	242
CTCTCCCTCTCTCTCTTCGG	58.285	20	149	122	270
TTAATCTTGCATTGGACGCA	60.215	20	122	2	123
TGGAAGATCCGAGAACCACT	59.655	20	257	1129	1385
TTGTTGAACCGTGTGCAAAT	60.011	20	207	41	247
GCTGACATGGCTTCGTATCA	59.83	20	180	1791	1970
AACAACTGCACCACACCGT	60.063	19	216	837	1052
CTTCCATCTGCACCTTCCAT	60.073	20	217	51	267
CTGTGTGCTTTATTGGAGCG	59.488	20	278	10	287
CCGTTGAAACACGAGATGTG	60.152	20	120	217	336
GAACCGCCGGAAAAGAATTA	61.263	20	267	6	272
ACACTTTTCAGCCATCTCCG	60.255	20	220	954	1173
GCCTAAGTAATGGCGCAGAC	59.873	20	144	228	371
GAAGCCGGGTGTCAAATAAA	59.938	20	266	518	783
CAATGCCTAGTTTACCCCCA	59.817	20	209	687	895
TCCGGCCAAATTAAAAGAAA	59.538	20	102	781	882
ACCAACCTCCATTGAAGAGC	59.141	20	224	66	289
TATGCTCGCTGGATTACGTG	59.856	20	251	506	756
TTCCGTCTTTAGGCATGAGC	60.352	20	267	5	271
AATCCCTTTCTCCTTTCCCA	59.875	20	101	57	157
GCCGTAAACAATGGTCGCTA	61.019	20	190	203	392
CAGATGTGGACGGGTCACTA	59.545	20	219	30	248
AACGCAATTATCCATTTGCC	59.801	20	257	226	482
TGGTTCGATCGTAATTGATCT	57.168	21	131	18	148
TGAGATTTCTGGGTTGCTCC	60.195	20	249	162	410
GAGTTTGGCACTCTTGCACA	60.032	20	107	89	195
ACCCCAGGTCTCTTCAACCT	59.968	20	198	155	352
TGCAACCATTTTGTTGGAAA	59.946	20	241	43	283
CGGATCGGAAATCCATAAAT	58.714	20	211	270	480
CGATGGAGTTCCCTCCTAGA	59.234	20	184	7	190
ATGGGGTGAGACAAAGCAAG	60.111	20	251	142	392
GAGTTCCCGCGTCATAAAAA	60.074	20	269	772	1040
CCGACACAAGCTGAAGTGAG	59.616	20	151	43	193
TCAAATCAGCGCATGAAATC	59.775	20	116	2854	2969
GTTTTGGCATGCTAGTGGGT	60	20	145	71	215
AGTCCCAATCTTTTCCACCC	60.169	20	148	86	233
TTGACAAATTCCCGAAGAGC	60.192	20	263	49	311
TTCTCTGTTCTGGCAGTGGA	59.545	20	207	106	312
GGGCATGCCAAAAATATCAC	60.161	20	273	969	1241
CTGTGAAATTGCACGGCTTA	59.872	20	214	4	217
TTCAAGTTTGGGGGTGTGAT	60.21	20	279	251	529
TCAAGATTTAGGGGTTATCATTT	58.508	24	112	171	282
TTCACTTTCCTTGGGGACTG	60.081	20	199	5224	5422
TTTTGGCGGGAAAAATAGC	60.026	19	257	224	480
CTGAATTTGGAAGGAACGGA	60.044	20	276	495	770
CCTATGGTGGTATGGTGTGG	58.569	20	268	32	299
GTTCCATGTTACCCGTGGAC	60.096	20	157	63	219

GTATTGGGAGCAAGGCAAGA	60.214	20	275	195	469
CACATCCTCACACACTCACACA	60.697	22	242	2629	2870
CCAACACAAATGAACCTGGA	59.389	20	213	21	233
CCCACATCCCACTCTCTCTC	59.638	20	186	783	968
CACGAACGGTATAACATCGG	58.917	20	270	708	977
CCCTCGTATGCAATGAATCTG	60.475	21	254	369	622
GAGGGGGTGACAGAAATGTG	60.363	20	266	39	304
CTGATTCGCTAGCTTCCCAC	59.978	20	118	21	138
GGAACCAAGTCTTCAGATGC	57.288	20	237	67	303
ACCGACAAAAGGTAGGCTCA	59.734	20	227	269	495
GCATCGTGTGAAGCATTGAT	59.685	20	141	216	356
AGTATGGATAGAAGGGGCGG	60.299	20	234	51	284
AATGCGTCTTGGATTCCATC	59.9	20	170	60	229
TCATTGGAATTTTCCGGGT	60.118	19	268	914	1181
GAGCATTTGATGGAGGATCG	60.57	20	242	27	268
ACTGCCCATTTTACCCTTTTT	58.919	21	112	866	977
GCACACCACCATCGTTGTAA	60.436	20	235	102	336
CCCACACTAATTCTAATTTTCG	58.974	23	248	352	599
GAAATTTTCTGGCGACGGTA	60.074	20	161	1833	1993
AAACCACCTCCGAAAACTTG	59.073	20	262	169	430
TCCCAATGATTGTTTGGTCA	59.75	20	215	748	962
CACTCACAGCCAACAGGGTA	59.745	20	130	1286	1415
TTCCAATTGCGAAAAGATTTG	60.061	21	165	77	241
ACTCCCAATGGATCGCTATG	59.917	20	189	58	246
GCATAAGCATGGTTGAGGGT	59.962	20	135	1304	1438
ATCTGGAAAACACGCCACA	60.104	19	209	168	376
ATCCAAACGGCGAAGTGATA	60.469	20	192	55	246
TCCGGCAATCTCCTTAATTG	60.031	20	153	297	449
TCAATCCACCAATGCTTCTG	59.648	20	179	1444	1622
TTGCAAACATTTTGAAGGACA	59.192	21	200	265	464
ACTGGACGGAAATCGGAAG	60.058	19	140	391	530
ACCACTGCATTCACTTTCCC	59.973	20	261	952	1212
TTGCTCGCGAGATTTCTTTT	60.096	20	270	648	917
CATGCCAAGTGGTGTGATCT	59.551	20	265	341	605
GGATGAGGTTGTATTGAAACT	59.891	23	142	59	200
ACCCTAGCCTTTGCCTCTTT	59.371	20	165	190	354
AGCGTTATTTTGCAAGGTCG	60.264	20	116	7	122
AACACAGGCCACAAATGGAT	60.24	20	280	14	293
GGGTGGCCCTCAATTTTATT	60.02	20	267	35	301
AAGGGGAGCATTGAATGTGA	60.461	20	271	896	1166
GAGCCTGACTTGCTTTCACC	59.997	20	175	380	554
TTCTCTCTTGGTTGGTGAAGAA	58.955	22	210	22	231
GCACCTATATACGCACGCAC	59.238	20	266	3	268
TTGACCGATCTCATTTGAAAAA	59.564	22	253	61	313
TCATAATCATCCAATCCAAACA	57.817	22	270	6193	6462
ACTTGCGGGGTTGTTAAAGA	59.609	20	218	657	874
TGAAATAGTAACCGCCGACC	59.96	20	245	173	417
GGAAGGATACAAAGGCTCGG	60.949	20	158	0	157
TCAATGTTTGACGTCTCGAA	57.806	20	224	94	317
AACCCAACCCACTACCCATT	60.34	20	147	0	146
GGACTATTTGCCACCCAGAA	59.933	20	247	548	794
TTGAGCGAAAAGCCAAAGAT	59.96	20	192	3401	3592
CGTATCAACTTTCGGAAGCG	60.762	20	117	8	124
TTTCTGTCCCGTTTTCCTTG	60.081	20	246	117	362
CGAACATCGTTGCTGCTCTA	60.157	20	223	443	665
GAGGACGCCCAATGATAAAA	59.901	20	219	925	1143
ACCAAACATGCTTCTCATGCT	59.755	21	211	21	231
ACTGGAAGAATTGGAGGGCT	60.074	20	208	104	311

TTAAGCATGCACGACTCCC	59.814	19	261	745	1005
CTTCTTCCCCGTTTTGTTCA	60.081	20	235	1026	1260
ATTCCTCCTTTTCAGCACCC	60.443	20	280	5	284
TCCGTCTGCTTGGAGAACTT	59.989	20	235	863	1097
CCACTCTCTCTCCTCTTTCTCTC	57.98	23	172	620	791
CGTGCAGTTTCAGGAGCTTT	60.571	20	147	258	404
TTCGCACGCTATAAAACAAGA	59.916	22	128	670	797
AGCAGCAGAAACCCTTGTTG	60.431	20	268	1494	1761
TGCCTCATTTGTGTTAATTTGG	59.868	22	236	36	271
AGGAAGATTGTGGTGGGGTT	60.607	20	182	73	254
TGAATGGCGACAAGTTGATG	60.665	20	251	1611	1861
TTGCGCCTAAGGAGGAGTTA	59.975	20	246	1939	2184
GGATAGGCTAGATGACGTAGA	57.925	24	217	111	327
TGCATTGGAAAAAGTTGTGG	59.561	20	238	311	548
TGGAGTTTTTGCTTTCTGGG	60.22	20	137	1856	1992
TCAGCATTTTTCGGGAGTCT	59.813	20	169	230	398
GTTCCTCATGCACCTTGGAT	59.934	20	259	859	1117
TTGCAACATCTTGATCTCCATC	60.081	22	260	98	357
GTGTGGTGTGTTAAATGCGTG	59.943	21	276	3166	3441
ACACCGTGCATTACAAGATGA	59.065	21	183	8	190
CAACCCTACCTCCTTCTCCC	59.928	20	179	38	216
TCTGAAGTTGTTCCCGAAATC	59.16	21	252	69	320
GTACATGACCGTGTTGGTCG	59.88	20	201	47	247
TCTGAAAATCAAAGGCCCAC	60.051	20	113	2115	2227
TATTATGGGGGTGGTTCAGC	59.645	20	227	275	501
CTGCGTCCTTCGTCGTTTAT	60.27	20	133	10	142
AAAGAGGCATTCGATCCTTG	59.269	20	187	248	434
TCTCCATCATTGCTCCTCAA	59.322	20	162	2405	2566
CTGTGTGATGTTGGAGGTGG	59.997	20	117	8	124
CAAGGCTGCAGAAGTGTTGA	60.175	20	204	4485	4688
CTGTTCAGCTATGTTTGCCG	59.488	20	145	88	232
GTTGGGGGTTGGGTTATCTC	60.422	20	225	10	234
CCCAAACTTGGGGAAGAAAT	60.159	20	241	680	920
CGATCGTGAGAGGGAGAGAG	60.088	20	269	100	368
GGTGGGTGCCTAGGTTTTCT	60.361	20	249	19	267
ATACGAACACTGCACCACCA	60.032	20	218	430	647
TCAAAATTAGTGTCAGCACCG	58.833	21	149	1493	1641
ACTGAAGTCTCTCCTCCGCA	60.135	20	271	162	432
CCATTCCATGTCACAAACGA	60.367	20	280	658	937
CCATCGACGACAAAACAACA	60.552	20	110	492	601
TTACCTGGACTCGAACTCGG	60.246	20	247	43	289
AAGGGAAGGGGAAGTGAAGA	60.045	20	267	48	314
GAAAGGAAGAATGCGAGTGG	59.813	20	256	236	491
TAAGTTGGAGTGGAGTCGCC	60.255	20	226	19	244
CGGGAAAAAATCGAAGGAAAT	60.252	20	241	362	602
TTAGCCTTAGCCCCAAAACA	59.715	20	252	231	482
ATCACGAACAGGATTGGGAG	59.927	20	233	43	275
TTCATGACGGCAAAGTCTTG	59.84	20	193	5	197
GTCCCTAGTTAGCTCCTAGATA	59.881	27	205	192	396
CCCTCCAAGTGATGTCACAA	59.52	20	132	2759	2890
GCACCACTGCAGAGATTTCA	59.992	20	151	16	166
ACCTATGGTGGTATGGTGTAG	57.076	23	177	101	277
TTCACCCATTTCCACCAACT	60.21	20	203	42	244
AGGGAAAATAGCTACTCCCAT	57.42	22	268	588	855
TCTTGAAAACTCCAAGCCCA	60.745	20	120	16	135
GGATTTCACCTTTGGATGGA	59.727	20	162	18	179
TTATTTGCACGCGCAGTAAT	59.379	20	252	37	288
CACGCTTTCTCTATCGGCTT	59.615	20	254	8	261

CCTCACCACCTCAAGCTTTC	59.844	20	200	118	317
ACCCACGTTACCCACGTCTA	60.291	20	184	1094	1277
CACCAACTGCTTTATTGCCA	59.729	20	236	468	703
TGATGAACTCGTCAATTGGAA	59.112	21	242	429	670
TGTTGGGTTGGTTTGACAGA	59.976	20	238	23	260
CACGTGTGGACATCCATATCA	60.256	21	267	91	357
TGCCGTGTAAATCCATCAAT	58.846	20	280	444	723
CATTGCATACGATGGGCTAA	59.543	20	232	22	253
TTCCTTGCCAAGAACAGACC	60.232	20	119	84	202
GCAAACCCTACTTCACTCACCT	59.682	22	246	52	297
AGTTTCTTGTTTCCTACCCCC	58.5	21	133	2	134
GGTGAAAAGCTGCCCTATCA	60.214	20	277	370	646
GTGTTTTCGCCCCAGTAAAC	59.476	20	233	0	232
TCGAAATCAGCATATCAAAAC	59.616	23	271	39	309
CTTTTGCTGGCACTTCCACT	60.431	20	144	1	144
TTGTGTGCATGGAATTTTTG	58.018	20	243	3	245
CACAAATTTGGGTTGCCAG	59.949	19	160	136	295
GAATAAATGCAATCACGCCC	60.297	20	250	410	659
GCAATGAATTAGCACCCACA	59.548	20	208	17	224
CCAGGCTTGAGTTTCCTCAC	59.844	20	127	5	131
AGGGAGTTGGCACCATATCA	60.34	20	137	597	733
TTACATCAACCCGTCAACCC	60.615	20	276	797	1072
CCCAGCGCAGACAGAATAC	59.41	19	280	41	320
TATGATCGTCGTCGTCCAAG	59.673	20	268	90	357
AAGGTCACGGCTTTTGAAAT	58.695	20	177	654	830
AGCCAGAGACTCGGATTCAA	59.95	20	216	879	1094
CACCAGGCAGCACTAAAAGA	59.072	20	141	1045	1185
CCAACCTCCATTAACAACCC	59.146	20	231	4	234
CCGATCGTGAGGCTTTTAGA	60.344	20	253	397	649
GGAGCTGCTCTTTGAGATCG	60.24	20	256	1024	1279
CCCGTATATTCACGACTCGTTT	60.257	22	228	317	544
AAATTATTCACACCCGCTGC	59.967	20	142	5421	5562
TCGACACATTCAGGCAAATC	59.654	20	156	13	168
GCCGTCAGTAGCTTAATCGG	59.867	20	219	1977	2195
CACCATTTTGTTGAGGGGTC	60.21	20	278	2458	2735
TTTGCTTAAAATGGATCAATGG	58.98	22	262	87	348
CAAATTCTGCCCTCCTCAAC	59.67	20	225	219	443
CTTATATACGGGGGCGGTTC	60.528	20	220	402	621
CCAAGCCACACATCTCTCAA	59.831	20	261	246	506
TTCCGCACCAAGATTTAACC	59.938	20	272	44	315
TGCGTTTTGACGATATATAGTG	59.092	25	101	658	758
CCTTTGATTTGCGTTGATTG	59.157	20	206	12	217
TTGCAGTAGCTTGTGAACGG	60.05	20	242	14	255
TGATTGAAATATGCCACCGA	59.891	20	259	186	444
AGGCAGCATACCCATCACTC	60.104	20	141	1983	2123
GGAATCGTTCCATTCTTGTGA	59.925	21	162	96	257
TCTACCCATGCAAATCAAGTG	58.637	21	120	65	184
GATGGCTCATTTGTTCCGTT	59.939	20	265	45	309
TGGATATTGTTGCCGTTTGA	59.93	20	264	1	264
TTCACTCTCACACACGCACA	60.07	20	120	828	947
ATGCCAACTTTTCCTCATGC	60.081	20	278	1772	2049
CAGCATACAGCAGTTTCGTTT	58.121	21	198	997	1194
ATTTCACCAAGATGTCCAAGA	57.096	21	101	20	120
AGCTTTTGCGAGTTTTGGTG	60.42	20	204	50	253
GGCAAGATATTTTCCGATGC	59.512	20	195	185	379
CGTTGCCGGTTAAAGCTAGT	59.424	20	241	30	270
GTGAGCACCCCAGATTGTTT	59.973	20	239	1493	1731
ATTTTATGGGACGGAGGGAG	60.145	20	249	368	616

AGAATCCAGAAGGGCAGTTG	59.284	20	183	3235	3417
CGCGCGTTTTTAGGGTTTA	61.09	19	123	300	422
CCTCGACTTGACAACTTTGCT	59.529	21	280	105	384
TTCAAACGATTGCCATAGAGG	60.081	21	190	702	891
TCCGGTGAATACCTCTTTGG	59.926	20	261	2194	2454
GCAATCATCCAACCACAATG	59.781	20	208	523	730
TTTAAGGGTTATCACCTGATTT	57.757	24	145	71	215
CCAATCTTGTTCGGGTTCTT	59.028	20	202	9	210
TGAAAGCGATTGTAAGCGTG	60.014	20	242	80	321
TGCGTTTTGACGATATATAGTG	59.092	25	272	1012	1283
TACATTATTGCGCAGACGGA	60.237	20	217	3204	3420
AAACTCCAAAGTCCAAACTCC	60.012	22	128	0	127
CTTTCCCTCTCCATCTCTAGCA	59.976	22	264	1095	1358
CAAAAGATTTGGCTTTCGGA	60.181	20	276	449	724
CCATCGTCACCTTTCTCCAC	60.51	20	153	48	200
CCCGTTTTTCCTATTTCGTG	59.447	20	178	78	255
AGGTGGTGGAGTGGTGTGA	59.984	19	227	111	337
GAGGCCAGGAGAATCACAGA	60.349	20	221	539	759
TTTTGATGATATATAGGTGTTTT	58.782	27	230	404	633
ACACGATAAGCGACGGAAGT	59.763	20	157	3243	3399
TTTGGAAAATCTTTGGTGGG	59.772	20	227	4254	4480
CCTTTCTCACCTAATTACAACC	58.153	23	183	3349	3531
TGCACGATTTGACTTGCCTA	60.401	20	243	645	887
TCTACGACCACAATTTGTCCC	59.845	21	171	515	685
AGTGTGCCAACAAGCATCAG	59.905	20	143	481	623
CAAATATTAGGCCAAAAACGC	58.687	21	209	2449	2657
TGAATTTCCATCGTTGATTTG	58.468	21	141	133	273
TGGAGGAGAGAGAGGTGACG	60.54	20	106	469	574
TTTCATCATAATATTGATTTTTG	58.504	26	118	896	1013
CAAACTAATAGCAATGGCCGA	60.102	21	136	3806	3941
GGGATATCTCTTGGGGCTTC	59.866	20	218	1439	1656
GGCTCAAAAGACAAGTCCCA	60.232	20	211	163	373
CGCAGTTAGCAGGATAAGGG	59.861	20	260	1137	1396
GCCATCGTCACAGGTTTCTT	60.119	20	177	17	193
ACTTGTTTTGTCGTCTCCGC	60.299	20	103	2433	2535
ATTTTGTGAATTTGGCCGTT	59.32	20	143	353	495
CCCCTCCACTAATTCTCCCT	59.392	20	219	589	807
GAATCCAGGTTGAGGAGTGG	59.505	20	181	30	210
AACCCAATTTCACCATCCTTC	60.046	21	180	168	347
TGAGGGGTGGTTGAAATGAT	60.173	20	174	70	243
CCAACGGGTAGATACCCAAG	59.308	20	279	686	964
GTTTGAGGTCGGAGATTGGA	60.05	20	173	570	742
CCAATTCCATCAAATCCAGG	60.126	20	188	82	269
GGTTCGGAAAAGGTTAGGCT	59.593	20	226	78	303
CGACTTGTCGTGGTTCGATA	59.716	20	264	62	325
CGAGAAAAACAAAATTATACG	59.565	26	250	589	838
GTTTTTGCGTCGAGAACTCA	59.05	20	163	80	242
TGAGGATGTTTGTGGGTCAA	59.935	20	134	1804	1937
CAAGAGACGCATTAAGACGC	58.677	20	218	1326	1543
TCCATTCACACCAAGAAGGG	60.892	20	209	108	316
CTTCGCATTCTCTCATTCCC	59.773	20	202	83	284
TGCGTGAAATCGAAAGTGAG	59.988	20	186	465	650
GCTCGAGTTTTAGTGTGGGG	59.734	20	273	149	421
AAAATCGAATGTCGAATCGG	59.901	20	239	26	264
CACAAGAAAATTATTGTCGCT	60.063	24	270	584	853
GCCCATAGTGCCTTCAACTT	59.198	20	172	630	801
TCTCCCCTCCATTTTCACAC	59.903	20	141	1551	1691
GGTCTCACGGGTGGTTTTTA	59.83	20	244	1558	1801

CACCGCGTCTTTTCACTACA	59.904	20	245	2283	2527
AATCATGGTGCACGAAATTG	59.4	20	182	412	593
GGTTGTGGTGGAGCAAAGTT	60.012	20	156	4431	4586
CTCTTGACTTCTGATCCGGC	59.95	20	223	26	248
CGAGATTCTCTCTCGCTCTCA	59.981	21	148	343	490
TGCCTCATCTGGATCACATC	59.591	20	229	2	230
CGTTCGATTTGCGGTTCTAT	60.096	20	209	585	793
GTGTTGGTGCTTGATGGTTG	60.008	20	135	2022	2156
CCAAACGACATTATGACGCA	60.523	20	265	176	440
TTCAATATCCGCCAGAGTCC	60.036	20	199	2270	2468
TGTGTCGCGAATTTTGAACA	61.233	20	211	9	219
CCCATTTTTCTTCTCCTCTCA	58.372	21	279	100	378
TAGCTTTTGTGCCGCTTGTA	59.648	20	242	43	284
ATGTCACCTGCTCATGTTGC	59.714	20	205	268	472
TGGCTCTGGTTTTTGGTAGG	60.103	20	276	0	275
AATTCTTGGGGTTGATGACG	59.79	20	222	556	777
AACACATCGTTTCCTGGGG	60.764	19	249	76	324
GCCTTGTACGCACTTCCTTC	59.882	20	271	954	1224
CCCAACCCTTGATTACGTTG	60.22	20	132	19	150
CAAAAGCACAAATTGGGAAA	58.649	20	234	53	286
TTAACCTGCAACGGTCAAAA	59.202	20	218	1469	1686
TGCTCAACACTCACGACTGC	61.258	20	272	88	359
ACGTGGAGTTCCAAATGCTC	60.119	20	272	1	272
GTATGCCGTTTTTCCTCCAA	59.938	20	277	1321	1597
CTCCTCTCCGTCGCTAGTCA	60.69	20	250	2	251
TCTCTCCCTTTTCTCACGGA	59.92	20	133	835	967
GCATACCGCGGTTTCATTTA	60.831	20	189	784	972
CGACTGGGAGGAGAAGAAAA	59.401	20	275	67	341
CCCGGGTTTTCTTTTTGTTT	60.19	20	200	1398	1597
CCCCAAATGGAGACGATAAA	59.756	20	178	4641	4818
AAGGTGACAATTGTGATAGCC	59.499	22	279	125	403
ATTTGTACGGCGTTTCCTCA	60.502	20	260	555	814
GGTCAACTTTCTGCACACCA	59.726	20	211	607	817
GAGGTGGTGGTATTTGGTCC	59.116	20	263	31	293
AACGCTCCAGATTTCATGCT	59.843	20	269	436	704
CAAGCAGACTAAGCATGGCA	60.157	20	235	83	317
CGCTTTAACTCAAACCCACC	59.609	20	115	149	263
TCCACCTCATATTTCGCAGA	59.226	20	179	19	197
ATTTTCCCAAATGCAAGCTG	60.074	20	256	246	501
AACCCGCTTATATCGTGTCG	59.982	20	104	36	139
CCACAGCTATGCCTAAGTGC	58.555	20	181	3276	3456
GGCATTCAAATCAACCATTG	58.82	20	239	75	313
GGTCGGCTACATGAACCAAA	60.894	20	107	41	147
ATAGAGGAGGACGCGGAGAG	60.883	20	177	737	913
TCAACAGCCGCAAAAATCTA	59.443	20	172	278	449
TTGAGCAGTTATCACCGGAT	58.173	20	239	29	267
AAAACGGGGCTAAGGATTGT	59.835	20	277	246	522
GAACTCACAAAGTATGGGGCA	59.985	21	127	3	129
AGGGATTCGAGTTGCTTTGA	59.813	20	264	5192	5455
CCCCATGAAGCAGAGATGAT	60.034	20	133	741	873
TATGCACGTGAATGCTTTATTT	57.456	22	191	34	224
ACATTCTGGAATGGTTCCCA	60.173	20	181	1251	1431
CTTTTGGCATGACCATTGCT	61.032	20	176	1936	2111
AGGACTCACTGAAGGAGGCA	59.986	20	278	663	940
TGCGTTTGATTCGTTGAGTT	59.322	20	224	367	590
GGAGCAAGAACTTGAGGCAT	59.434	20	241	169	409
CCGATTTTGTTCCTTTTCAAAT	59.374	22	230	642	871
TCAAATGTCCCTCGTCTCATT	59.541	21	238	317	554

GTGACATTTTTAGGCGGGAA	59.938	20	196	1182	1377
TCGTATGTACCGAATGCGAG	59.712	20	184	17	200
AAGCCTAACAAGTGGATATTA	58.116	26	164	1301	1464
GATAGGCCCTAACTCGACCC	59.925	20	190	9	198
CAGGTAAAACCTAAAATAGCG	60.36	23	236	4927	5162
TGGTTATTACTGGAACGCGA	59.182	20	182	1112	1293
GGCATACTTGGTTGATCCGT	59.82	20	257	10	266
ACACTAGGGCTTTGCTGCTG	60.592	20	162	2868	3029
AGCACTCCCTTTTACCACCA	59.592	20	250	64	313
TCTTCGATTGGAGTTCAGGC	60.34	20	242	551	792
TCAACTCCATTTGTATACTTCA	59.068	26	279	26	304
CAGATCTGATGGCCCAGATT	60.034	20	106	17	122
CCTTCTCTGGCTGTTGTTCA	59.007	20	102	1483	1584
TGAACTAATCAAGTTCCGCGT	59.761	21	182	41	222
GAATTTCACCCTGATTCCAA	57.426	20	280	43	322
TCTTCGCTGTCTCTCAGCAA	60.008	20	162	1292	1453
AAAGGGAACTTCCTGTTTTAGC	58.034	22	201	66	266
AACGAATCAAAACCTGAGCG	60.249	20	100	84	183
ATCGGTTATTACCGGATCGC	61.031	20	151	79	229
CCATCTGTCCACGCTTTTCT	60.255	20	163	159	321
CCTCTCTGCAACACCATTCA	59.831	20	195	507	701
ACCATCGAACCCCACAAATA	60.051	20	210	20	229
GGGGTGGGGGTATGTTAGTT	59.805	20	147	81	227
ATCATCCCCACAATTGCATC	60.557	20	116	261	376
CGAATCAGAAAGAACGTAGC	60.025	21	179	32	210
GCAAATCAAACCCTTGTCAAA	59.967	21	248	682	929
AACAACTTCCTCTGGCATCG	60.255	20	156	1045	1200
AGCAGTTGGAGAGGGTGAGA	59.986	20	207	119	325
TTGTTGCACCTTGTGCAGAT	60.31	20	179	598	776
ACGGTTTGGGCTTAATTTTT	57.688	20	278	467	744
AAATCAAAAGCCCACAATGG	59.801	20	124	68	191
ACATGCACAGATTCCGTCAC	59.557	20	216	303	518
TGCATGAAATTGGAGCAAGA	60.343	20	125	134	258
GGCCATTCAAGAAAGCTACG	59.845	20	157	471	627
ATGTGCGTGTGAGTGTTCGT	60.236	20	211	93	303
TCACATGAGATGATTAATTGG	59.343	24	181	64	244
TGGAATAACCCAAGCCAAAG	59.931	20	266	2535	2800
TGATTCGGAGGAATACGAGG	60.029	20	202	418	619
AACAGCAAATCCGAGACACA	59.293	20	253	449	701
CATTTTCAGGTCCTCACCAA	58.541	20	124	31	154
GAGTCGGAGATCAGCTACGG	59.973	20	243	43	285
TGAAACTGCTGTATGCTGAGTT	59.424	25	169	313	481
TTTGCTTGATCCAATGGTGT	58.976	20	118	37	154
TCACAAAGAAATCAGCACGAA	59.454	21	255	0	254
TCAACGGTTTAAAATTGTTCCT	57.74	22	169	131	299
AAAACTTCGGGGAAGCAACT	60.11	20	131	342	472
CCTCTTTCACTTCGATCCCA	60.187	20	132	65	196
TGAGATTCTGGTTTCGGCTT	59.813	20	208	133	340
AGTTGCCCAACTGGAGACAG	60.298	20	208	15	222
CATTGGGTGGAAGTGTAAAGA	59.914	23	172	540	711
TTTGAGGAGGAAGAGGAGGA	59.936	21	153	31	183
TTGGTCAGTTTGTCCGAATCT	59.583	21	107	256	362
CGCTGAAATTAGTTGAGGCAC	59.897	21	272	133	404
CCCCCACATGTCATAACCAC	60.903	20	268	283	550
TTGGGTGTAAGACATAGAAGG	57.815	23	195	856	1050
GCGAAAAACTCGAAAAACCA	60.223	20	264	1546	1809
GAGGAAAACTCACTGCTCTCTT	59.608	24	156	11	166
TCCTATGGAAACTCAAATCCG	59.03	21	277	43	319

TGATCTCAACGGTATGCTCG	59.823	20	239	490	728
GAAAACCTGGAGTCAGCTCG	59.989	20	266	426	691
GAGAGGAGAACTGCGTGAGG	60.135	20	162	73	234
CGCTTCTTCGCTATGGCTAC	60.138	20	219	392	610
GGGGGTTTTTAGTGCCATTC	60.542	20	240	3301	3540
AAGCCGATCGAGTTTTTCCT	60.208	20	265	36	300
GGAGAGCCACAAAACAAAGG	59.711	20	158	1310	1467
ACAATAGCGTGTGTTTTGCG	59.799	20	274	587	860
GCTTGATTATCCCGGTTTTG	59.411	20	161	450	610
ACCCTCGAATGATATGCTGC	60.066	20	164	31	194
CGGTTAAAAATCGGACCAGA	59.931	20	245	208	452
GCATGGCATGAAATTGTTGA	60.476	20	274	117	390
TTTCCGGTGATGGATGAGTT	60.317	20	148	474	621
TTGTCTAGCAATCTTCGAGTTTT	58.302	25	280	135	414
CGACAATGTTAAAAATCAAATA	59.631	27	170	65	234
TCAAGGAGTCACAACGTGAAA	59.324	21	139	172	310
CTGATGAACAAGCCGAACAA	59.84	20	231	579	809
ACACGATCGTAAGGCGAAAT	59.597	20	106	4	109
TTACCCAACCCACTAACCCA	60.081	20	172	136	307
TCCCTTCATCACACTTTCAGC	60.248	21	132	0	131
GTGCTGCAAATGCAATGACT	59.878	20	214	30	243
AGCGGTTATTACCGGATCG	59.93	19	250	2230	2479
AGGAATGTGGAAAACAACCG	59.83	20	279	2251	2529
CCAAGATCAATGGTTCCTAAGT	59.879	23	136	1264	1399
ACAATGCGAGTGCATTTTTG	59.735	20	185	112	296
GTGCAGTGTTTTGCAAGGAA	59.888	20	208	79	286
TTGGGCTCGAAAATTGAAGT	59.685	20	132	14	145
GAACCCAGCTGAAAGGAGC	59.942	19	280	44	323
TATATTTGCTCTGGCAGGGG	60.053	20	216	682	897
AGCTCAAGGATTTTCGCAGA	60.096	20	246	28	273
CGAAGAATTCTGTGCTGCTG	59.74	20	196	1248	1443
TCATAGGTAAAGCCGCAACC	60.096	20	212	22	233
AAATGTCACCCCACATGCTT	60.24	20	124	91	214
GGCTCAACAACACAATTCCA	59.547	20	250	28	277
CTTCATGAATGGCATGACTGAT	59.962	22	246	44	289
TTTGCCTCATTTGTTTGGCT	60.617	20	111	1134	1244
AAGAAACAAACAGGGTACGA	59.56	22	162	364	525
ACTTTGGTAGGGGTCAGCAC	59.065	20	228	115	342
TTCGTTATTTGATTGGGGGA	60.124	20	188	1246	1433
AGGTATCGTTCGCGCTGTAG	60.428	20	261	14	274
AAGCAAGAAGGTTGCAACTGA	60.045	21	148	355	502
TCATGTCAACTGTCGAAGGG	59.676	20	124	3	126
CCTGTCTCAATCCGCTCACT	60.408	20	187	1434	1620
TGGCTACTGTTCTTCAGCCC	60.397	20	156	2	157
TTAGCCTAAGTCGGGACAGG	59.331	20	257	600	856
GCATGATGCAGCCCTAGATT	60.207	20	240	1903	2142
AGCGTGAGATTGAGAGAGCG	60.844	20	241	61	301
TATCCTTCTTTTCCTCCCCG	60.382	20	234	8	241
TCGACTTGTGCAATCAGTCC	59.837	20	228	771	998
AAAAATGCCCTCGTATGCAG	60.096	20	239	22	260
TTTTACCCTTTCCGCTTCAC	59.202	20	209	48	256
GAAGAGGGGAAAGAAAACGT	60.096	21	190	193	382
ATGTGTGTGTGCGTGAGTGA	59.772	20	179	433	611
TTACTAGCCGTTGGTGGGAG	60.125	20	151	463	613
CCACAACTATGTGGGAAAA	58.325	20	208	405	612
CACTCGAAAAAGGCATCCAT	60.074	20	198	2583	2780
TCGTTTTAGTTGGCCATAATCT	57.848	22	202	286	487
TTTTTCAGCACCACTTCACA	57.867	20	169	126	294

GCAGACCAGCTTTTACTGGG	59.875	20	190	456	645
AGGGATGACAGAATGAATGTG	59.41	22	204	507	710
CACGGGAGTTGGAGATTAACA	59.978	21	265	134	398
ATCGTTTTCAAAATCAGGCG	60.074	20	237	208	444
ACAGCGCGGAAGTTACAGAT	59.904	20	241	25	265
CTAAATGCCCTGCTGTAGGAA	59.37	21	211	372	582
GTTGTGTTGTGCAGTGGAGG	60.203	20	254	1109	1362
ATGCTTAATGTGCATGTGCG	60.697	20	143	2069	2211
CGCTCACAATGATGGATACG	60.096	20	220	4937	5156
ATTATGTTGTGGGGTCAGGG	59.526	20	140	468	607
GAACAAATTACACAAACAAAA	59.299	25	128	521	648
CAAGCAAACAACCAGCACAA	60.876	20	177	1587	1763
TCGTGGAGTGAGTGGAAGTG	59.864	20	272	113	384
TGGGAGAAGGGAGTTTCAGA	59.773	20	270	847	1116
TATCGTCCCCTTTCGATGAC	59.894	20	156	221	376
TAATCCAAGCCATCCATTCC	59.722	20	128	24	151
ACGTGTGCGATTAGGGTCA	60.128	19	105	28	132
CAGGTGAGTGTTCCATGCAG	60.309	20	196	2967	3162
GACAGCCACGTGGAATTGTA	59.572	20	207	20	226
TGAGCCAACTGAAAACACACA	60.331	21	125	2843	2967
ATGCGGACGGCATTTATTTA	60.303	20	209	199	407
GCTGAAACCAAGGCAAAGAA	60.365	20	225	302	526
TCCCTGTCCTTTTTCCCTTT	59.912	20	254	474	727
TGCAAGCATCTTTTGTCTCG	60.134	20	214	12	225
AGGAGCGGTTTGAACAATTC	59.174	20	114	19	132
TAAGGGAGTTGGTAGGGCAA	59.564	20	229	46	274
TTTGGTTGTGGTTTGGTTTCT	59.364	21	224	1	224
ATCATCTCGGGGTGCAATAG	59.917	20	215	17	231
CGGGGTATTACATAAATGATGC	58.285	22	192	41	232
AGGTGGAGTTTTAGGCGGTC	60.496	20	272	5	276
GAGTCTGCCACGTGTACCAA	59.751	20	158	414	571
TTTTTGATGAGCTGGAGCCT	59.955	20	259	3988	4246
GGGCCGAGATTTGTAGAGGT	60.464	20	147	189	335
AAGAAGTGTGTGGGGGTGTC	59.859	20	204	994	1197
GGGCTTAACAAAGTCACGGA	60.11	20	183	397	579
AATGCGCGTCTTATTTCCTT	58.857	20	236	970	1205
AAAAATGAAATGTGGGGTGC	59.668	20	264	1949	2212
TGGGTATCTCTCGCTGCTTT	59.978	20	279	805	1083
GCCAGCTTGTTTTGGGATAA	60.074	20	199	255	453
TGGTGTCTGAACAGCAGAGG	60.022	20	271	165	435
TGACTTCGCCATTTTCCACT	60.636	20	280	215	494
TGTCCCAAAATCGTGTCTCA	60.088	20	265	14	278
GGATAGGTTGAAACTGCCCA	59.933	20	279	48	326
TGCGCATCTAGCTTGAGAGA	59.995	20	277	526	802
TCCCCGATTCTTTTAGCCTT	60.034	20	148	121	268
GCCTTTGGGTCAAAATCTGT	59.031	20	226	1758	1983
TTGTCTCTTGCAAGGTCGG	59.968	19	245	1	245
GGGTTTGCTTCGATGAAGAG	59.813	20	111	14	124
CCCTCTTCAACCTTTTTAGCG	60.236	21	243	97	339
CCTAAAACACGACAGGGGAA	59.964	20	261	60	320
GACACGCATAAAGGGACCAC	60.384	20	238	249	486
ACCCAATGACACGACACAAA	59.855	20	133	6	138
TCGTTAGGAGGTGCCTGTCT	59.867	20	171	34	204
AGATAACCGTTCCCGCTCTT	60.096	20	221	44	264
CATAAAATGGACACGCACCT	58.502	20	172	39	210
CACACACGCGCATATACAAA	59.211	20	106	1638	1743
AAGTTAAGCGTGTTTGCGCT	60.082	20	251	1235	1485
TCGGATTTTTATAGGCTTCTTCA	59.285	23	278	1344	1621

TCAATCATGAGCGTCCGTAA	60.22	20	145	7	151
CGAAAATAGCCAAGTCGGAA	60.202	20	266	3	268
GCTTTCAGGGTTTAAAATCGC	60.089	21	204	295	498
TTCATGATAGGATGGGGCTT	59.344	20	225	2507	2731
TGGAAGGAGAAACGATGACC	60.05	20	200	49	248
CCACCTTTTCATTCCGACTC	59.526	20	151	41	191
GTGAGAGCATCTCCAACGCT	60.564	20	196	418	613
AACACAGCAGGTTTCGATCC	60.119	20	244	12	255
ACTTCCCTTCATCAGCCCTT	60.074	20	249	1206	1454
TGCGATCTGAACGTGTTTTC	59.847	20	234	233	466
CCATGGTAGAAACGCACAGA	59.716	20	172	414	585
TGTTCGGAATTGCACTCTCA	60.39	20	101	82	182
TGGAGGATGGAGGTTGAATC	59.862	20	210	334	543
TCGAATTTGTCGTTTGACCA	60.088	20	272	1004	1275
TCGTCCTCCTTCGACACTTT	59.844	20	264	808	1071
CGGGTTATTGTTGGAAATCCT	60.061	21	211	9	219
CAAGCTTACCCGAGCTGAAC	60.015	20	243	16	258
GACCGATCATTGCTATCCTCA	60.051	21	185	542	726
TTTTCTCGAGTTTCACGCCT	59.993	20	178	4759	4936
TTTTGGTTCAGGGGTGGATA	60.162	20	122	167	288
CGTATCCCTCCTCCACACAT	59.803	20	160	1271	1430
ACAAGTGTTGCGGGATCAAT	60.384	20	276	84	359
TAACTGCCTCTTTGCACCTG	59.072	20	220	14	233
AATACCAGGCAAAAGAAGCG	59.361	20	239	962	1200
TTGAAACGGACGAACAATGA	60.088	20	155	23	177
AGAATGTTGCCAATCGTGTG	59.572	20	186	45	230
ACTGCACAAAAACAAACGCA	60.338	20	248	127	374
ATGGAGGATCACACCACGAA	61.356	20	240	558	797
AGCCCCCATTTTTCATTTTC	60.13	20	213	974	1186
GACATCACTTTCGTCGCTGA	59.992	20	101	307	407
GAGTCGCAAGACACAATTCG	59.445	20	137	1488	1624
ACATGTGAGATTCCACGCTG	59.707	20	260	304	563
AAAAATGACGAATGGGAGGG	61.042	20	124	235	358
AAACTTGAGCAATGTTGGGC	60.118	20	265	431	695
TTCGTATCTTGCCCATGGAT	60.296	20	248	242	489
GGACAGTTTGTCCGAATCTTG	59.583	21	271	138	408
AAGGAGGTGTTATGAAGGGAT	58.028	22	196	1222	1417
CCAAACGGCCGATAAGAATA	59.922	20	184	16	199
TGCACCAACATTCAGACAAAA	60.142	21	180	502	681
AAATTTTGTTTCCCACCAAATA	58.744	23	107	280	386
TTTGATCACCACCCTCCATT	60.173	20	254	876	1129
TGACTTGTTCCGGTATGCTG	59.716	20	118	0	117
TTATCCCGTGTAGCCCATTT	59.297	20	236	4	239
CCGCATTTATGTGTGCAAAA	60.508	20	279	39	317
CTTCATCTTGGATTGGAGGC	59.629	20	155	513	667
CGACGTGCTTTTGGTAATTGT	60.046	21	139	1307	1445
GGAATTTTGTGATTGGGTGG	60.029	20	251	1200	1450
TTTTCAGTTGATGCCTGATGA	59.262	21	187	1471	1657
CTTCCAGAAACCTGAGCAGC	60.134	20	245	1910	2154
ATGCCGTCTCACACATTAGAA	59.637	22	165	2303	2467
CCCACCAATTTTGAGACGTT	59.83	20	263	69	331
TTTAACGAATGCTCCAGCG	59.961	19	280	111	390
CGCACTTGGCTCCTTTTTAG	60.011	20	275	1009	1283
AGTGTTTTGACATGATTACTCG	57.373	24	110	2138	2247
CGATTTGGATTCGAATTTTGT	58.932	21	169	58	226
GGTTTGCGAGCATAAAAATGA	60.089	21	235	549	783
AGGCCATGCAAAATAAACCA	60.323	20	261	11	271
AGCGCACTCAAACAATAGCC	60.416	20	278	687	964

GCAATGCCTAGTTTACCCCC	60.692	20	243	0	242
TTGAAGGTTCACGGTGTTGA	60.128	20	276	206	481
ACACACACTCACGCACACATT	60.137	21	161	408	568
TCTACCCAAAGTGCCCTTCA	60.626	20	201	19	219
GCCATACATCCCACAAATGA	59.205	20	210	693	902
CTAGGCATGGAATCCGAGAA	60.17	20	251	15	265
ACCAACCTTGGCCACATAAC	59.717	20	235	3	237
CCCACAATTAGGTCCCCTTT	60.046	20	165	257	421
AGCGGTTATTACCGGATCG	59.93	19	188	1608	1795
GTGGCGACATCCGAATAACT	59.962	20	202	192	393
CATAGCCGATAAAAATGGCG	60.424	20	200	79	278
TTCGAAATCCCCTTTTTCAA	59.497	20	226	1029	1254
CAATGTTGGCATTGGAGCTA	59.688	20	265	461	725
AGAATATTCATGGGGTCCGA	59.2	20	193	1204	1396
TTAACCCGGATCGGAAAAAT	60.489	20	276	835	1110
GCGGCTAGAGTGGATAGTGG	59.859	20	258	323	580
TGGGCACATTGCTCATTAAA	60.073	20	262	2809	3070
TGTTTGTCGGGCCTAAATAA	58.162	20	264	547	810
TCTTGATGTGTGATGCCTCC	59.637	20	263	710	972
TTGTGATGCGTTTCGTGAAG	60.844	20	259	1468	1726
GGGTCACGGGTTGACCTATT	60.999	20	257	210	466
CTACGTAGCCCCCAAATCAA	59.953	20	205	217	421
AGGGCAGTCAAGACCATCAT	59.535	20	239	11	249
CACCAGTGGCAAACACAAAT	59.465	20	172	69	240
CGAATATCCCCCAATTCAAA	59.593	20	259	2295	2553
GCCTGCCTATTAAACTCCCC	59.93	20	211	0	210
TTTTTGTTATGATAGGATAAAA	60.04	27	260	466	725
CACCATGCTCAGGAATGCTA	59.823	20	223	2212	2434
AACCCTAACCCGACTCGTTT	59.864	20	211	87	297
CTGTCCATTGTGAGAAGCCA	59.831	20	257	218	474
CTCAATGATGAAACGGGGAT	59.75	20	135	80	214
ACTCACCCACACACACACGA	61.157	20	273	4	276
ATGGAGAAAAGGTACGCACG	60.132	20	160	6	165
TGCGTATCTTGGCATTGTGT	60.142	20	189	1332	1520
CATGAAAGGAAACAAAATCGA	59.098	22	119	762	880
TTTGTTATGCGTTTTGACGA	57.846	20	269	103	371
CCTTCTTCCACCGTTCTTCA	60.224	20	117	4324	4440
TCCAAAAATGCAAAATCCAA	58.98	20	239	7	245
AGGCTCAGACCAAGATGACG	60.408	20	256	873	1128
GGCTGCACACGAATGATTAAA	61.014	21	149	673	821
GGGAGGATAAACCGAGGAAG	59.897	20	279	2145	2423
TTCTCATCCACAGACCCCTC	60.048	20	142	1905	2046
TCCAGCAAGAAAATCGGAAT	59.645	20	211	27	237
TTTTTGGTTGAATAGGGGTGA	59.302	21	271	107	377
TCCGAATTCCTACTCCATGC	60.036	20	202	198	399
GCGATCAGCAAGGAACTGAT	60.37	20	181	1327	1507
GGATGTGGGGGTAAATTAGGA	59.896	21	247	1737	1983
CCCAGAGCGTACTCGAAGAG	60.149	20	107	524	630
TTTTTCAATCATACTTCCGGTTT	60.107	24	221	57	277
TTTTGACCAATCCTTTTGGG	59.772	20	274	258	531
CGGCCAAATCAAAAGAAAAA	60.047	20	212	374	585
CCTCCATTCAAGCAGAAAGC	59.955	20	190	925	1114
TTGCAATAGCATGCCAACAT	60.103	20	235	180	414
TTCGGCATTATAGGAGGACG	60.053	20	273	40	312
GCCGTAGATCTAACGACCGA	60.235	20	128	1313	1440
TTCTTGATGTGTTGGCAAGC	59.847	20	277	63	339
TAGATTTGGGCAGTGTGGTG	59.566	20	167	278	444
CAATATGAGAATGGCCGAAAG	59.556	21	159	428	586

GTGGACGTCCCAGATTGTTT	59.827	20	190	731	920
CACGTGGCATTTAACTGGTG	60.027	20	259	1216	1474
AAGGGGAAGTTATTATTTGATC	59.882	25	166	306	471
GAACGGCGTACAAAAGGAAA	60.11	20	143	186	328
CGTTGATGAAGCACCGTATG	60.134	20	168	663	830
TTCCTACGCACTCACATTAAGA	57.601	22	179	234	412
CCCAAATGAAGAGGTTTGGA	59.903	20	117	1325	1441
CGATGACATTAACAATAACAA	60.095	26	280	270	549
CACCCTTCGATACTCCGAAA	60.066	20	252	61	312
CAGATCAATGGCCCAGATTT	59.894	20	228	506	733
CCAATCAAAGCAGATCCTCC	59.629	20	258	565	822
CTTCTTCTTCCCCATCATGC	59.629	20	254	5	258
CGCCTGCACATCTACAAAAT	58.799	20	225	6155	6379
TCTGTGGTTCCATTCCATCA	59.893	20	212	508	719
TCATTATCACAGGAGATTGGCA	60.469	22	237	487	723
GCCTGAACCACCAACCTTGT	62.297	20	277	121	397
ACCTCGCCTCCGTAGATACA	59.717	20	228	67	294
ATCTATGACGCCGGTGAAAG	60.096	20	261	1040	1300
GCACCTAGGCCAAATTGAAG	59.708	20	195	59	253
GGCTGGTTGAAGATCAACTG	58.287	20	259	2706	2964
GAGAGGGGGTGAGGTTGTTT	60.349	20	270	258	527
TGCAGTTTTTGCATGGTTCT	59.322	20	270	1428	1697
TTCGAAGATCAACGGACGAT	60.603	20	122	34	155
AGAGAGACGACGGATCGAAA	59.95	20	238	15	252
GCAACGGAATACCACTCGTT	60	20	119	141	259
AAACAAAAGGCAACTGATTCG	60.042	22	273	19	291
ATGCCCAGACGCACTAAAAC	60.14	20	226	42	267
TTGGAGGGAGAAAATTGTGC	60.051	20	114	1236	1349
ATTCTCAACAAGGGGCTGAA	59.67	20	220	229	448
AATTGCCACGTTGAGGAATC	59.939	20	270	2	271
GCGTTGGGATCGTGTTAAGT	60	20	194	3371	3564
TGAGCTTCCAACGTAAGTTTCA	60.176	23	178	3150	3327
GCATGATACCAATGCTGCAC	60.112	20	243	46	288
GGATTGGAACTCCAAAACGA	59.91	20	279	348	626
TCTGACGCCTCTGTAGTGGA	59.571	20	186	1396	1581
CCCTTACATTCCCGTTGTGT	59.711	20	251	57	307
CCAGAGCTCAGCACGGTTAT	60.419	20	113	583	695
TAATTTGGCAAACTCTGGGC	60.074	20	129	784	912
CAACCCGTTTATATGCGGTC	60.209	20	158	67	224
CCACGTCTTGTTTTCCATCTC	59.583	21	117	4438	4554
AACATTGTTTGGGAAAAACCT	57.508	21	162	828	989
TCGAAGGTCAATGGTTCACA	60.088	20	218	115	332
GCGCGGAGTTTAAGAAATGT	59.365	20	185	344	528
GCCATCAGATCTGCACTGAA	59.95	20	209	1231	1439
CTCGTTTCTTGCTAGCTCGG	60.284	20	231	664	894
GCAATATTACCATGACGGGC	60.182	20	275	2013	2287
GCCGGCAACTCACTTAACTC	59.882	20	101	51	151
TGATAAGGGGAGAATGTCGAA	59.514	21	141	264	404
TTGCCGGAGAAGACTTTGAT	59.813	20	254	101	354
GATCTAACTAGGCCCGTCCC	59.925	20	245	159	403
GAAAAACCCTAATCCGCCTC	59.909	20	211	10	220
AGCAAACCCGTGTTCTTCAG	60.291	20	246	213	458
GTCCATGAAAGATTGGGGTG	60.173	20	241	1734	1974
AAGAACCCACACAATCTGCC	59.973	20	188	1001	1188
CACCCCGAGATAACTTTCCA	59.926	20	223	17	239
CTGTTCACCAAGTTCGCAAG	59.485	20	163	115	277
TCATTGGGTTCAAATCGTCT	57.991	20	263	104	366
CTACCATCTCGGGATGCAGT	60.096	20	241	1340	1580

TGTGTAATTGTGTTGTGTCATG	57.923	24	210	309	518
GACAAACAACAGCGGATCAA	59.697	20	205	1223	1427
GCTATGAGCATGTCATCAACA	57.291	21	123	2	124
CCTTCCATTCCGAAAATCAA	59.872	20	142	1	142
TGGGATCTCAACGATTCACC	60.871	20	240	678	917
CCTTGTAGATCGACAGCCTTG	59.883	21	212	59	270
TGCATAACACGGGTGGAGTA	59.988	20	253	1363	1615
GAGGTCACCCTTTGTCCGTA	59.966	20	262	217	478
TTAAAATGTGCTGCTGGTGC	59.879	20	263	283	545
GTAGATCTGGCGGGTAGGTG	59.574	20	277	373	649
TTGACTTAACAAACCCCAAGG	58.98	21	257	88	344
AGCTGAAATTGAGTTCGGGA	59.813	20	277	18	294
TTGAAGTGCGGGGTATTACA	59.037	20	223	3	225
TCTACGAATGTTGACGGAAAA	59.625	22	183	465	647
GATACGTGATGCGTTGATCG	60.104	20	255	68	322
TTAAATCTCCCCACAAACGG	59.795	20	223	29	251
GGGTACAGAGCGAAAACGAG	59.875	20	245	193	437
AAGCATGAGTTGTGTGCTGG	59.905	20	236	8	243
AATGGTCCGAAAATGCTTCA	60.448	20	148	11	158
GAGCGACCTTCAATGGTGAC	60.667	20	158	694	851
AGTGGTTATTACCGGATCGC	58.93	20	208	2694	2901
TGATGGTGAATACGATTGGC	59.355	20	168	219	386
ACGACGCGTGTAGTTGTTTG	59.829	20	275	203	477
CTTCCCAGCAGAGAATCGAG	60.088	20	149	5	153
CGGGGTAATCTCAAAACCTG	59.424	20	246	540	785
GGCCATTCCTATTTCCTTCC	59.74	20	145	409	553
AGCCCATTCGTGATTTATGG	59.784	20	261	15	275
CAGTTGGCGACATAATCTGC	59.301	20	256	18	273
TGCAGCCCAATGTATGAGTT	59.152	20	233	205	437
GCAGTTAGAAAGAGGAGCGG	59.218	20	224	3	226
GGGAGAAACAACCACCATTG	60.21	20	240	612	851
CATGAGCCTCCAAACCCTAA	60.066	20	153	1054	1206
AGCACGAGAAAAAGACCAGC	59.621	20	170	1624	1793
AGCAAGAACTCACGCCTTTC	59.621	20	277	96	372
TTTTGCTGTGGTCCCCTTAC	59.971	20	149	446	594
TTTGGGTAGGCCTGAGTCTG	60.246	20	275	3282	3556
AGCTTCAAACATTGATGGCA	59.276	20	252	238	489
TGAAAGGTCTATCCGCTTCG	60.344	20	255	46	300
CTCCAACCTGCCACAAAAAT	59.971	20	189	2461	2649
GGGATGTGTGGGATTGATTC	59.995	20	240	935	1174
CACAGATCACGATTTTCGGA	59.648	20	260	1049	1308
GTAGGGGTGAAAATTCGTGC	59.434	20	191	109	299
TCGCGTAGAAATCCTTATGC	58.017	20	191	16	206
TGAAAGAAAACAAGAAAGAAT	60.499	26	250	4228	4477
TAGCGAGGGAATTAGGAGGA	58.879	20	258	2	259
TCCAAAGAAATTGAGGTGCC	60.051	20	251	254	504
AAATAAACATGGTTCGGGCA	60.188	20	275	946	1220
TTATCTGTCCTCTGGCCTTGA	59.822	21	239	4	242
TGCGTTTTGATGATATATAGGT	60.054	26	261	1896	2156
TGGGGGATTATTTGCAGAAC	59.762	20	190	3	192
TGGGATCTGATCTTCAGCCT	59.761	20	183	11	193
TTGCCTATTTTGGAGGATCG	60.031	20	220	51	270
GGTTGTGAGAACCAACTCTGT	59.664	22	185	120	304
CTGCTTATCGCCACTGTCAA	60.011	20	109	164	272
CAACCACGTACAACCTGCAC	60.072	20	237	738	974
CCTCCGAGGACGATAGTGGT	61.436	20	192	355	546
CATGGTTGAATGGATATGGC	58.646	20	272	140	411
GGGGCGTGACAAGGATACTA	59.955	20	265	64	328

TAGGGAGCTGTCAATTTCGG	60.206	20	253	1066	1318
ACAGATGGGAGGAGAGAACG	59.254	20	237	1	237
AGGCAATATCAATCTCGGTGA	59.542	21	149	129	277
AGGGGGAAGCACAGTCTAGG	60.64	20	279	77	355
GGTGTTGTGTGATGTCGGAG	60.005	20	163	115	277
GTTTAGTGATGGAACGGGGA	59.79	20	147	44	190
AATTCCTGATCCCACACCTG	59.779	20	224	112	335
CTGAAGTGAGCGAGCAACAG	59.922	20	244	1663	1906
TTCACCTCCATTTTCGATCC	59.871	20	198	31	228
CAAAAATGCCACGTATCCCT	59.823	20	211	6	216
ATCTCCAATCACGTTCCACC	59.786	20	258	783	1040
TTGCAGGTGCTAACCAAAAA	59.344	20	124	19	142
AAAATGACCCTCCTTCAGCC	60.443	20	262	76	337
AGTGTCTCCAGTCTCCACCG	60.306	20	229	2946	3174
GGGCTGAAAAGCCAATTAAA	59.189	20	279	10	288
CCTTATGGCATTGGACATCA	59.35	20	193	72	264
TTCGGCTCCTCAGACACTTT	59.989	20	224	105	328
TCGACCGAAGAGCTATCCAT	59.797	20	217	313	529
GTAGAGGCGGAGTGCTTTTT	58.604	20	231	2	232
GCTGCTCTAAGGCGTGTTCT	59.786	20	248	2776	3023
CAAACCGGACTGGACCATTA	60.745	20	273	7	279
CAAACCGGACTGGACCATTA	60.745	20	268	8	275
AATCTTTGAGGACCCCCTTT	58.896	20	128	10	137
CCTATGGTGGTATGGTGTGGA	60.501	21	259	53	311
CTCTGCATGTTTGTTGGGTG	60.152	20	248	1832	2079
TGGGCTAATCACTCTCAGCA	59.547	20	251	222	472
AAAATCAAAGGCCCACAATG	59.801	20	225	208	432
GGGAGTTATCATTGGATCAAG	59.805	22	189	527	715
GGTCGACATTAAATCTTGGCA	59.952	21	186	659	844
CCAAAGAACTGATATCCTCAC	57.668	22	145	525	669
TTATCAAGGGCCCTACCTCC	60.278	20	211	598	808
CTGACCACCCCAACATCTCT	59.962	20	261	89	349
CTTTTTAATCCACCTGGCGA	60.067	20	203	15	217
TCATGTGCCTGGATTGGATA	59.883	20	150	121	270
TGAACGAGTAATTCTTGGTGAT	57.814	23	279	558	836
TTGGAGAACTGGTAGCGGTC	60.255	20	149	6	154
TAGAGAAAACCCGGCTCGTA	59.839	20	241	184	424
TTCAAAACTGCATTTCTGGGT	59.601	21	249	641	889
ACATGATTGCCATCCTCCTC	59.893	20	142	659	800
AGAGCAAAACCCATCAGTGG	60.111	20	103	1723	1825
CAGCATGTGCGGTGACTAAG	60.472	20	228	0	227
TGAGTGACAAGACCCTGCTG	60.022	20	240	597	836
GTCAACATCGAAGGCAATGA	59.654	20	225	38	262
CACGAGATTTACGTGGTTCG	59.195	20	139	18	156
GGCTTTAGGTCTGGCCTTCT	59.848	20	159	2757	2915
GTGGGCTGTGGCTTTTGTAT	60	20	269	272	540
GAAAGAAGGGTGCCGTGTTA	60.11	20	271	4147	4417
TTGATCTGATGCACGAAAGG	59.799	20	148	1	148
TTAATGGCCCCCAAGAAAAT	60.489	20	271	123	393
AGCTGCATGCCTTCTCTTTC	59.723	20	253	4214	4466
TCCATCCCATCACTACCCAT	60.011	20	194	110	303
GTTTTCCCCAAATTGGTTCC	60.391	20	251	209	459
ATCCTCATCTTTCCCCAACC	60.133	20	146	1424	1569
CTATCTCTCCCTCCCACACG	59.673	20	100	1	100
TAGTTGGGGGTATTTTCGGC	61.029	20	238	49	286
GAACACCCACCACACCTCAT	60.701	20	199	118	316
AAATTGCCTCCATACCTCCC	60.152	20	226	258	483
TCTCCTCCCCTTTTAATTCCT	58.212	21	220	49	268

ATTCAGCAAGCATTAGGCGT	59.873	20	265	0	264
GGTGAACCAAGCGGATAAGA	60.074	20	143	285	427
CGTTAGGCTCGAGAGTGAAGA	60.04	22	161	3	163
TTGGGGTTGGAATAGGTCAG	59.784	20	243	125	367
CCCACCAGTGCCATACTTCT	59.989	20	113	660	772
TCTTCAATCCTTCTTCCCCA	59.6	20	151	40	190
TTCGAAAATGGAGGGATGAG	60.006	20	252	58	309
TTCTGTAAATGGCCCTCGTC	60.074	20	127	753	879
GCCCTCCCAAAAGTAACTCC	59.94	20	196	55	250
CCAGTCCACTTTTGAATGGC	60.495	20	208	25	232
CAGGCACATGCAAAAAGAAA	59.849	20	155	124	278
TGTCTTCATCCCATTGACCC	60.725	20	266	112	377
GGATTCCGATTGCAAGAAAA	60.016	20	278	282	559
TCATCATCTTCCCTTTCTGCT	58.875	21	175	64	238
CCATACTGCCAAAACGGAAC	60.365	20	248	228	475
GTCTCTTCCTGGGAGGGTTC	60.05	20	123	32	154
GGTCATTTTAGCTTGATCAACA	57.952	23	176	522	697
GATTGTTTCTCGATAGCCCG	59.668	20	246	1913	2158
TCGTTTTGAGAACCGGAGAT	59.67	20	216	9710	9925
CACAAAGAATGCCCCATTTC	60.309	20	226	2480	2705
GGTCGGCTACATGAACCAAA	60.894	20	158	1	158
CGAAGGTGTTGATGAGCAAG	59.44	20	230	84	313
CGCTTCTTCTTCTTGTTCGG	60.125	20	189	2773	2961
AATTCCTCAAGCTCGTCACC	59.288	20	152	7	158
AAGGAGGTGTTATGAAGGGAT	58.028	22	266	975	1240
TTGATTCTGGAATATCCCGC	59.862	20	152	91	242
GACCTAAGCCACTCGCTACG	60.037	20	237	297	533
AAGTTGTGGCTGCAAATTCC	60.118	20	110	194	303
TTCTCATTCTCTCGGCTCTAGG	60.11	22	142	1149	1290
TTCCTCATTGTTTGTGTGGAA	59.01	21	207	56	262
CTGTAACTCCCCAAAAGCCA	60.103	20	200	986	1185
TTGTAATTTCCAAATCGGGG	59.633	20	265	1	265
GACGCTCCACATGATGACAC	60.13	20	154	229	382
AAAACTGCGAAATGAGGAAGA	58.962	21	205	202	406
TTGCTACAAAACCAGTGGCA	60.293	20	204	1061	1264
CAGCAAGAGGCTCGATGTTT	60.538	20	237	73	309
GAACGTCGTCATTGTACTTGGT	59.032	22	195	243	437
CAGTCAAACCCACGAGCTTT	60.291	20	168	2319	2486
AATTCCCACAAATCCAACCA	60.029	20	205	427	631
GATTTTGGATCGGGTTTTGA	59.739	20	115	4045	4159
TTTGCCCCTTCTGACTCTGT	59.844	20	232	193	424
ACTGCCCAACAATGGCTTAC	60	20	192	3	194
TCTCCATGATTTCCTTTAATTCG	59.47	23	118	217	334
TGTTTTGCCCGTACGTTGTA	60.029	20	249	190	438
TTGAGCTGGCAGAGACCTTT	60.134	20	135	209	343
TTAGGCCCCTCCCTACATCT	59.919	20	209	273	481
CATATATGCACCCCCAACCCT	59.528	20	234	1216	1449
TCCCAACAAAACGAAAAAGT	57.25	20	172	1264	1435
CGCTCTCTCATTGTAATCTCTCT	58.83	24	124	357	480
CACTTCGACGATGGAGAACC	60.656	20	242	736	977
TGAAAATGTCAGGCTTGTGC	59.847	20	223	1678	1900
TCCGTGAGTTTACCCAAAGC	60.11	20	136	1176	1311
GAGGAGAGCGAGCTTGGAT	59.652	19	208	118	325
CATGGCAACAATGGATAGCA	60.488	20	133	409	541
AAAATCCTTTGCACAACCCA	60.344	20	112	48	159
TTCTTGGCAATCATGTCCCT	60.461	20	190	59	248
TCACACTCACGCACTCACAA	60.07	20	121	15	135
TTTGTACCAAAAAGTATATAAA	57.58	27	262	595	856

TCGTTCAAGTCGGTCACATT	59.139	20	206	35	240
CAGATCTGATGGCCCAGATT	60.034	20	141	278	418
CCCTCGACTCGAAATCAAAA	60.184	20	211	22	232
CTTTTCCCCCTCTTCCAGTC	60.045	20	270	64	333
TAACCACCCAATCTTCGCTC	60.074	20	186	91	276
TCGTGAGAGATAGATATGGAG	57.233	24	273	76	348
AGGGGTCTGACATTGTAATAA	59.685	24	274	31	304
ACTCAAGCCCCAAATTCTGT	58.646	20	213	318	530
GGGTGTATGTGAACCAACCA	59.112	20	205	626	830
AATTTGGCTTGTTACAGCGG	60.131	20	250	566	815
CCTCCATTATCCACTCTCGC	59.653	20	277	720	996
TCTTCAAGAGCAGAAAGGGG	59.545	20	253	32	284
TTAACAAATCGCCGTTCCAT	60.323	20	271	792	1062
TGTCGAAATGGGAGTCACAA	60.088	20	180	1151	1330
TCAGAACATGGGCAAATTCA	60.049	20	157	503	659
AGGGACATCTTGGTGGGAAT	60.575	20	280	35	314
GGGAACATTCGAGCCATAAC	59.391	20	168	36	203
ATTGCGATGTGGAAGCTTTT	59.713	20	126	19	144
ATTGGTCATGAAATCCGAGG	59.75	20	227	121	347
ATCGTCCCCTCTCTTGCAG	60.356	19	110	469	578
TCAGTGTGTGAACCAGAGCC	59.872	20	155	48	202
AGCCAATGGTAACATCTCTGC	59.212	21	236	303	538
GGATAGGAATCTCAAGAGTAT	60.007	25	187	1011	1197
TCTCTCTTTCTTGGTTGGTGAA	58.955	22	208	124	331
ATTCGGACATCGAGATTTGG	59.894	20	248	59	306
CGAATACTCCAAATGACACCA	58.488	21	238	53	290
TTGAATATGCAATCACCAAAG	59.485	23	214	31	244
GGTGCACCACCCCTATCTT	59.794	19	139	702	840
GAAAACAGAGGTAGTGAATTG	57.489	24	229	287	515
ATTATGCATGAATTGCAACATT	57.112	22	129	116	244
TTCACCATGATTTCGATACACA	58.895	22	231	655	885
CAGGTTCATTCTTTGCATGTG	59.184	21	169	798	966
AGAGGGAAAACAGGGGTAGC	59.576	20	125	6	130
ATAAGCAACGAAGGGAGTGC	59.34	20	216	275	490
CGGACAAAAGAGTGGAGAGG	59.837	20	206	1585	1790
TAAGGCACGCATAAAACACG	59.764	20	154	457	610
TTTGCTGTTTGCACATGGAT	60.119	20	271	20	290
TGGAAAATGTGGTGTTGGAG	59.389	20	213	0	212
ATCACCATAACGCACCCCTA	60.214	20	246	127	372
CCAGGTGGAGTTACACCCAT	59.697	20	210	730	939
TGGCCATGTTTTTGGATGTA	59.786	20	201	651	851
GAATCACTTTGCAAGCACCA	59.847	20	184	220	403
CAAACCGTTCCTCAGATCGT	60.111	20	200	66	265
TGGAGTGTGAATTGAATCGC	59.654	20	134	194	327
GCTGTCCAGGATTTGGGATA	59.894	20	248	5	252
GAGCAAGCATGGTGTGAGAA	59.992	20	214	369	582
TTTTGAACCCTAGAGGGGGT	59.799	20	195	805	999
TGAGATTTTCCTGCCAAACC	60.051	20	233	1550	1782
CTCTTCAGCTGCTCTCCGTT	59.891	20	242	306	547
CGCTGTTTGTTTGATGGCTA	59.872	20	172	39	210
ACGGCATTGAAGAAATGAGG	60.074	20	272	52	323
TGGGTTAAAGTTGGGAACCA	60.198	20	200	836	1035
CGACGCGATAGACTGCTGTA	60.18	20	258	717	974
CTTTTCAAACACGACCGACA	59.734	20	228	1	228
TTATCAGGGGTCAACTTCGC	60.074	20	152	917	1068
ATACGGTTGCATACAAGGGC	59.851	20	238	3	240
GAACCGTTTAAACAACCCGA	59.839	20	254	124	377
CATCTCTTTGTCTCCCCCAC	59.505	20	257	197	453

AAAGAAGATTCCGGCGAAGT	60.208	20	219	229	447
TACCGTGTGTGTGCATGTGT	59.486	20	103	1210	1312
GAACACGAGGAACTTGGGAC	59.555	20	137	0	136
GTCGGGAGAGAGGGGTAAAT	59.397	20	232	67	298
TTTATGGGTACATCGGGGTG	60.439	20	258	486	743
TGGCAATGTGGTGGTAAAGA	59.964	20	186	165	350
CCATCGTTGTCGAAATCCTT	59.933	20	209	272	480
ATGAATGGATTCCGGTCAAA	60.133	20	275	7	281
TTGTGTATACTCCACGGCGA	60.134	20	225	28	252
ACTTCCTCCATAGGATGCCC	60.293	20	278	311	588
TCCGTTGTTATTGCCTGAGA	59.272	20	271	83	353
TTGGTTAGCACCAAATAGCCA	60.494	21	195	50	244
GCACTTGCTTGGATTGTCAG	59.445	20	203	12	214
CCCAGCTGAGAGCTATACCG	59.993	20	263	386	648
AACACACAGAAGGGAGTGGG	60.002	20	219	656	874
TCGTTTGCAAGAAAATGGGT	60.481	20	194	26	219
ATTTCCTTGGCCTTCTTCGT	60.074	20	207	1414	1620
GTGAATCCCACTGTCCCATC	60.184	20	238	2444	2681
AGGCAAACCTTGAAGAAGGG	60.601	20	254	816	1069
TGGAGCAAACATTACCGAAT	58.093	20	241	551	791
CCATGTCAAGGGTTCGAAGT	59.966	20	220	133	352
AGTTCATCAGCAAAGGTGCC	60.263	20	103	1873	1975
CATTTGTGTGGAAACCATCG	59.816	20	254	6	259
ACTTCCCCCATTCTTCATCC	60.133	20	252	256	507
CTTAAACCCTTGAGCCATGC	59.708	20	197	142	338
AGAAATTCCCCCAAGACCAG	60.298	20	276	1814	2089
TGTGTTTGGTTTTGGCTGCT	61.636	20	219	94	312
TGTGGTTGAAATCTAGCCCTT	58.707	21	149	10	158
TGGTGCTTCTATGCACTGCT	59.621	20	212	270	481
TGACACAGATTTGGTGCTTGT	59.202	21	238	385	622
GAGGTGTCGGTGTGTGTTTG	60.047	20	247	761	1007
TTTCATGCCACCTCCAATTT	60.309	20	125	134	258
CACCCAGAAACACACGCATA	60.574	20	101	28	128
GTGTTTTGACAATATTTAGTGTT	57.875	27	100	756	855
GTTAGGGATACCGCTAGGCA	59.205	20	272	73	344
TTCGCAATGCTTTGATTGAG	59.953	20	149	52	200
GCTCAACTGTTCTGAATGCG	59.596	20	243	5	247
TCAAAAGAGCACCTCCTGCT	60.134	20	199	9	207
CCTCCCGAATTTCTGTGTGT	59.966	20	236	794	1029
TCAATGGAGGGTGGGAGTTA	60.309	20	238	544	781
GTTGGATGTTAAGGATGCCG	60.331	20	181	231	411
AGCCAACAAAACCTTCCAGA	59.711	20	271	492	762
GGGTTGTGGTGAAGGAGAGA	60.088	20	195	22	216
GAGCGTCTGCTTAAAATGGG	59.845	20	227	169	395
TCAATGACCACACAACCACA	59.376	20	271	124	394
CACTAAATAAATATTTTGGCAT	57.149	27	245	21	265
TCAGATGAAAAGCCTACAGGA	58.973	22	136	214	349
TCGCCATTGATTCTCTCTCC	60.303	20	253	251	503
GTTGGGCCGACACTGTAAAT	59.859	20	141	65	205
TGTGCATTTGTGTTCCTTGTG	60.603	21	211	57	267
AATCTCGCATCCCAATTCTG	60.036	20	122	71	192
GCGACTGGCACCTTATCTTC	59.843	20	181	2074	2254
TGGAACCCATCAACACAAAA	59.792	20	236	406	641
ACGGGTTTCGCTATTCATCA	60.469	20	154	12	165
GTTTTTAATCGTGGCCGCT	60.089	19	155	135	289
AAACCTTTTACGGGGAAGGA	59.808	20	193	81	273
GGAGTGTTGGAGGAGGAGTG	59.682	20	276	6	281
CGTGGTTCGATCGTAAATGA	59.542	20	256	75	330

GAACAAGTCAAGGAGGGCAG	59.844	20	279	4	282
TGCATTTATCCGATTTATCAAA	58.561	23	240	781	1020
GTCGTGGATATGGGCTGACT	59.957	20	195	1106	1300
TCATGTTAATTGGTGGTATCAT	59.898	25	214	3374	3587
TGAAACTGAAGATTTGGGGC	60.051	20	167	1243	1409
TCAATTTGTGACAGGGCTTG	59.691	20	262	1885	2146
CCAGTTTTACCACCGCCTTA	59.99	20	173	802	974
GTGTGTATGACCGTGCGTGT	60.52	20	157	81	237
ATTTGTGCGAGTCTCGTGTG	59.905	20	242	704	945
TTCCGGGACATTTCTCTCTC	59.213	20	137	510	646
TCATGTGTCTTCCACCATGAA	59.951	21	188	5026	5213
TCTTTCTTTCCCTTGCTCCA	59.926	20	223	121	343
CCAATGCATTACGAGTTGGT	58.502	20	275	367	641
TCCTAGCCCTCAATCTCGAA	59.91	20	257	603	859
CCACGGAGAGACGACAAGAT	60.261	20	266	977	1242
AGTACTAGCAACGGAGATGCG	59.553	21	216	41	256
ACCCGACGTATTCGAGTTTG	59.993	20	248	176	423
CTTCTTGCCGATGAAGATGAG	59.963	21	271	477	747
TTCATCATCAGCTGCTGTCC	59.95	20	185	1070	1254
TGCCACAGTTTCATCTTCCA	60.24	20	214	4586	4799
GTTGAGGACTTAACGGTGGC	59.598	20	245	109	353
CTGCCTGAGTTTTTGGGAAC	59.711	20	279	324	602
CCGATTGTAGAAAAAGGATTA	59.098	23	203	14	216
TTTGGGGGAGAATTGTTTGA	60.28	20	249	84	332
CGAACCTGATTTTCGTTTCAA	60.096	21	238	113	350
ATCATAATTGACGCCCTTCG	59.923	20	106	10	115
ATGGACCCTTGTTGGTTTGA	60.21	20	253	192	444
GTCAATCGTGTGAGGGGAGT	59.969	20	136	84	219
CCGCACACCCCTATCTTTTA	59.953	20	232	353	584
TGCTTTGACACCACCACAAC	60.616	20	277	47	323
GACGAAAATTGCCCGTAAAA	59.943	20	245	105	349
CCCCGAATTTCCCATAACTC	60.502	20	144	25	168
AGAACATCGACTCACTGTATT	58.344	25	167	233	399
TCCTCAGCTTCTGCTTCACA	59.855	20	237	107	343
ATGGGATCCCTCAAAACAGA	59.336	20	213	663	875
TTGCCCCCGTATACTACGAC	59.845	20	171	38	208
TCCGACATCATTCTCGTTTG	59.648	20	279	24	302
GTTGCACCGTGTGTTTCAAG	60.199	20	235	2	236
AGTTGGAACGAGCGAAAAAG	59.494	20	238	87	324
ATCTCCACATTCTCCCTCCA	59.46	20	201	594	794
GGCCCAGTAGCATGAATATG	58.065	20	267	108	374
AACGTAGTTGCTACATGTTAA	58.933	27	280	23	302
CAAAGGCCCACAATGGTTAT	59.685	20	272	2	273
GCCCCCAGCAAAATAAAAAG	60.77	20	163	4425	4587
TCTTTGACCCCAAGAGAGGA	59.773	20	269	15	283
TCGTTTCTTCACTCCAACCC	60.088	20	254	149	402
CAATATGAAAATGGGCGAGA	58.576	20	229	231	459
TTGGGATTGAGCCCAAATAA	60.26	20	280	13	292
CCAATGACACGTTATGCTCAA	59.6	21	200	90	289
GTTGTTTTTGTCGCGGATTT	59.982	20	279	2	280
ACAGAAATTTCCTTGGTTGCTC	59.637	22	168	262	429
CGGGATTTAGGTGTTTTGACCT	61.417	22	280	1935	2214
ATCGATAATTCGCACCCAAG	59.923	20	232	962	1193
TCATCGAAAATCTGATCTGGG	60.021	21	230	774	1003
GAGGAGGAAGAGGGGAGATG	60.149	20	266	196	461
GGCAATTTGTTAATTGTTTGAG	58.236	23	233	222	454
CTTTGAATTGCAGCTCGACA	60.134	20	268	655	922
CCATTCCGAAAATCAAAGGA	59.872	20	191	67	257

CCAAATGATTTCCCTTTGATG	59.26	21	221	68	288
AAGATTTGGGGTTTAGGGGA	59.639	20	229	888	1116
GCTGACGACAACCATCATCA	60.698	20	129	4	132
ATGTAGGGAAAGATGGCACG	59.955	20	277	410	686
TTTGAAACACGGGTTCTAACAT	59.801	23	240	896	1135
ATTGCTCTCCAACCCACAAC	59.973	20	262	125	386
ATTTCGAAAATCAACGGACG	59.938	20	151	232	382
TGGTGTTGGGAGAGAGATGA	59.18	20	210	507	716
GATTACGTCGATCCAACGGT	59.82	20	136	2	137
CCCAGTCGTATCACTTTGGC	60.517	20	202	21	222
GCGAATGAAAAGACACAACG	59.322	20	261	131	391
ACATTGAAAACCAGCCGTTC	59.978	20	145	114	258
ACGGATTTGTCGATCGGTTA	60.331	20	233	1327	1559
AGCCTCCGGCTTTGTCTACT	60.403	20	225	53	277
ATCGTAGTTGACGCCCTTTG	60.132	20	171	92	262
TGTAGGGAGTGGGATGTGTG	59.388	20	277	115	391
GGGAAATTTCAGTTGCAAACA	59.967	21	251	1	251
AAGTGCACAAGCACTCGCTA	59.812	20	126	17	142
ACGTAGTGGGAAAAAGGGCT	59.998	20	260	140	399
CTTATTGCCTCCATCGTCGT	60.096	20	221	85	305
ACTTGATTCATGGCACACCA	59.967	20	233	333	565
AATTGGGGTGCAGTTCAAAG	59.971	20	182	108	289
CACTTAGGGGGTTATTAGTGG	57.22	22	279	7706	7984
ACTCGTTCATGCAGACGAAA	59.445	20	169	2394	2562
AAAACAAATATGGCCTCCCA	59.273	20	197	584	780
ATGACAACCCACCAGAAAGC	59.973	20	173	949	1121
AGACCGAGCGCAATGAATTA	60.742	20	227	263	489
GTAGCCAAACATGCGGTCAT	60.925	20	146	0	145
TTAAATGCCGGTCAAAGCAC	60.999	20	266	150	415
TAAGATCGAACGATCCAGCC	60.177	20	217	88	304
GAAACTGACCACCACGGAAT	59.827	20	239	416	654
GAAAAGAGAAAGAGGGCCGA	60.817	20	215	16	230
AAAAACACGAAACTTGATTGT	58.71	23	270	102	371
TTTATTTGCGGGAGCTGAAT	59.682	20	205	27	231
TGTTTGGTTGCTTGCTTGTT	59.366	20	207	1149	1355
GGGGTCTTCTTTTGGGACTC	59.912	20	271	371	641
TTGTTCCCGACAAGAAAAAGA	59.71	21	278	2015	2292
ACCAATTTGAATGGTTATTACC	59.906	25	142	581	722
TATGGATGACGAGGTCGAGA	59.193	20	255	91	345
TTTGGTTCGGAAATAGGTGG	59.795	20	273	18	290
GAGGAGCAATACTGCTTGTGG	59.89	21	147	10	156
CAACTTGGGCTAAGGATTTTG	58.751	21	149	62	210
CACCGAAATGTCCAGGCTAT	59.955	20	263	55	317
CAATGGTAAAACAACGCTCG	59.226	20	265	1	265
CTCTCCATCCACTGCAAACA	59.831	20	274	144	417
TCGAGACTTCGGTTGGTTTC	60.232	20	167	1	167
TTGTCTCCTGGGAGAATGGT	59.505	20	252	396	647
GAGATGTGTGTGTGCGTGTG	59.772	20	262	985	1246
ATCATTCCCAGCCACACATT	60.203	20	149	12	160
AACCGTCAGATTTCAAACCG	59.971	20	234	380	613
CACAACCGTCAAGACCATGT	59.441	20	226	22	247
GGGAGAGAGAGCAGCAGAGA	59.969	20	249	233	481
TCGGATGAACACCCCTACTT	59.405	20	257	1263	1519
CACAAAATTGGGATTAGGCG	60.315	20	208	129	336
GAACGATGCTGCCATGATTT	61.014	20	212	459	670
TAGGCAGAGCAACAGCAGTG	60.347	20	246	6	251
TTAACCGCCAAACTCAAACC	59.975	20	182	434	615
AGATCATACACGTGGCCGTC	60.956	20	150	416	565

CCCCCATTTTTCATTTGCTT	61.011	20	259	0	258
ATCATGGAAACATGACGTGC	59.379	20	230	38	267
GGTAAAAATTGTGCGCTGCT	60.272	20	240	1087	1326
TTGGGCCTGAATGGACTTTA	60.439	20	137	18	154
GTCCACGGTGGTGCTAGAGT	60.182	20	144	23	166
CAGCTCATGCTTCCTCCTCT	59.703	20	221	1664	1884
TTTATCGTGGCCTCTTCACC	60.074	20	220	0	219
GTGGGGGACTTATCTGTTAGA	57.621	23	278	53	330
CTATCATCGGTTGGTCGTGA	59.522	20	278	1005	1282
GGTGGTATGGTGTAGAGGACC	58.242	21	236	70	305
CCATTGGTATTGACAGCGTG	59.988	20	110	492	601
GCACTCTCACGAGCTCACAC	59.771	20	136	886	1021
TCATGCCTAAATGTTTTGATGC	59.971	22	233	229	461
GAGCTTGCCGAGAGAAAGAG	59.454	20	158	180	337
CTTCTCCAAGGCTTTTGCTG	60.125	20	241	132	372
TGTGGCTTATGGAGGTTCAAA	60.487	21	132	172	303
TGGGCCGCTTTAAAATATGA	60.405	20	253	375	627
AAATTACGGCCACAACAAGC	60.003	20	176	2202	2377
CACTCCACTACCGTCGACAA	59.745	20	161	78	238
TGTCTGTGAGAATGGCCAAG	59.831	20	205	103	307
CCAAGTCCAAGTCCGAAGAC	59.697	20	224	19	242
GCTAAAAATGTGGTTGGCGT	60.003	20	280	1309	1588
CTCCCCTCCTTGTTTTCACA	60.081	20	126	429	554
AGACCGAAAACCGTTCAAAA	59.587	20	225	221	445
AAGGGATGATTGCACCTGAA	60.461	20	224	45	268
ATAAAGGGTGGTTGGGTTCC	59.919	20	200	53	252
GTCAGAATGGATTGAGTGCG	59.245	20	140	87	226
TTTCCCTAACAAATCACACCG	59.847	21	113	142	254
TGTCCAAACAAATAAAAACAT	60.139	24	187	15	201
GAGCATGAGAAAATCCTCCC	58.667	20	112	18	129
TGGGTGGTGGAAAAGAAGTT	59.425	20	197	40	236
CACACACAATGTTGGGAGGA	60.416	20	131	27	157
ATATTGGTTTCGGATCGTGC	59.791	20	220	4328	4547
TGTGGTTGAAATCTAGCCCTT	58.707	21	153	10	162
CGCATCACTCTTTTTAGCCA	59.062	20	262	467	728
TATGCGTTTTGACGGGATTT	60.323	20	208	250	457
GATTCGGAAGGTCGACAACT	59.141	20	143	7	149
TCTGGATCTCACAGCTCACA	57.966	20	203	105	307
CTTTTATCCCCAAAATGCCC	60.489	20	214	406	619
TGGAAAGCCATGATAAATCCA	60.274	21	274	40	313
AAGCAATAATATTTGTGCCAT	58.582	23	200	74	273
CGCGGACACATCATGTAAAC	59.995	20	277	10	286
TCACACATAATTGAGTTATCAT	59.685	26	266	52	317
AACCGTAAGTGGTGGAGGTG	59.884	20	254	457	710
ACCGTGTCGGATACACATGA	59.837	20	214	30	243
GAGAGCATTCCCACAAACATT	59.045	21	106	643	748
GCAAGGACGAATTCCAAGAG	59.813	20	254	1438	1691
TCCCCTATCGGTATTTTCCC	59.978	20	236	61	296
TCTGGTGGTTCATTTAGGGC	59.933	20	223	68	290
AATTCTCCGCCACCTTTTCT	60.074	20	169	76	244
CTTCACCCGTACGTTGCAC	60.167	19	168	526	693
ACGATTTTGCCCTTGTATGC	59.967	20	214	6	219
GGGAGAGAGAGACAGCGAAA	59.679	20	145	218	362
CTCGAACTTGTACCCGAAGC	59.875	20	153	87	239
GTGCACATTTCCCTTTCACC	60.362	20	114	358	471
ACGTGCCCTATTCACATTTTT	58.504	21	140	12	151
GACCAACGTGGCCTAACCTA	59.993	20	251	442	692
CATTGCAGATTTTGATGAGCA	59.824	21	252	2068	2319

CGAAGGCATCTGCGATTTAT	60.196	20	155	136	290
TTTGATCACACACGCACAAA	59.721	20	167	13	179
TCCAACTCATCTTTCGGACC	60.05	20	279	584	862
CCCTAATTTATGAAAGAGTGG	58.576	23	183	325	507
TTGTGTGGGTCGATTCTTGA	60.088	20	198	1228	1425
AACACCAACCACGAACAACA	59.897	20	267	53	319
TCCATCCTCCATAATCCTGC	59.854	20	221	95	315
AGTCATCTCCAAATGCCTGC	60.226	20	260	2644	2903
CCCAAAACATTACCCGGAA	60.54	19	132	98	229
AGCATGCGACAACATGAATC	59.685	20	250	867	1116
GGGACCGTGATGTCTAATGG	60.195	20	186	1696	1881
TGTGGATGTGCGTGTTTTCT	60.16	20	222	620	841
AGGCTAGACCATTGTAAGGGG	59.491	21	196	70	265
TCCACGGATGTAAATTGTTCC	59.677	21	230	1621	1850
CAAGAAAGAATGTGGACGCC	60.636	20	155	91	245
ACATTTTTCCACACTCAGCG	58.775	20	279	262	540
AGCATGGGAAGGGGAGTTAG	60.455	20	111	43	153
TGACTCATACCATGGAGCACA	60.128	21	174	462	635
ACCATAGAACCACACGGCTC	59.997	20	266	147	412
ACCATAGAACCACACGGCTC	59.997	20	100	315	414
TCGTCCGAAAGAAACCTTTG	60.22	20	257	35	291
TCACAACCAAGGTTTGGACA	59.976	20	218	906	1123
CAAGAGGATGAAGGCCAGAC	59.803	20	257	78	334
GGCAGCTCTGTTCCAAGTGT	60.453	20	248	51	298
TTACAGATAACCGTTCCCGC	59.96	20	158	0	157
GACAAGTGGTGGCTTCTGGT	60.159	20	266	565	830
AAATAGAGCAAGTGGGCAGG	59.336	20	258	2212	2469
CCCCCTCTGTTTTCACGTC	60.494	19	216	234	449
TGCAACCTACTCAAAGACTTC	60.341	23	268	569	836
GCTTACAAAGTTGATGCCCC	59.574	20	256	33	288
GCTTACTGATGCAGAAGCCC	59.985	20	255	99	353
ACCCCTCACATGCTCTTCAC	60.12	20	269	636	904
TTCGTTGACCCCATATGTCA	59.774	20	202	450	651
CAGCACCAGAATTGCTCCTA	59.024	20	197	131	327
CCGACTGAACCTCATCCAAA	61.034	20	269	151	419
AATCACCCAATCATCCAACC	59.464	20	186	543	728
CACTCCATTCTTCGTCCCTC	59.655	20	112	9	120
CAGTTAAAGCGTTCCAGCAA	59.108	20	187	1056	1242
CGATCGGTCAATCGAATTTT	59.901	20	161	450	610
AAACCCTAGTTTCTGCTGCG	59.517	20	176	20	195
GGTGCAAGGCATAAAATCAAA	59.957	21	224	2654	2877
ATCATGGAAACATGACGTGC	59.379	20	232	38	269
TGCCATCTCGTTGGAATTTT	60.448	20	152	12	163
CCTTCAGAGGCATGGTTTGT	60.111	20	218	2	219
GGGAGGGAGAGAGGGTATTTC	60.27	21	253	212	464
CCATTCTTTTAGGGCCAACA	59.931	20	210	454	663
CGATCCCTCTCTCTCACGTC	59.945	20	188	83	270
AATGGATCGGAAGCAATGAG	60.036	20	169	799	967
TCCCAACCAATGACTTTCAA	58.947	20	276	3464	3739
GACACCGTTACGCAGACTCA	59.905	20	136	1472	1607
TCCCCTAATTCACGTGTTGAC	59.845	21	263	612	874
GCCGATTCCTCCTTTCTCTC	60.293	20	211	4219	4429
TCGTCGATGATCGTATAGCAA	59.295	21	278	34	311
AACACGCGTTTTTAGGGTTT	58.676	20	256	33	288
GAGTGGGAGATTGTTGGGAA	59.903	20	275	36	310
GGAAATGGGTTCTCTCTCCC	59.874	20	215	136	350
ACGTGTGAGACTTCGTGTCG	59.94	20	277	1097	1373
TGCTGGACCTCCACAACTTT	60.69	20	140	101	240

TGCCCCACCCAAGTATTTT	60.177	19	103	140	242
TGCACGCATTATTCTAAGCA	58.119	20	224	32	255
TCTTCCCACCTTACTCACGC	60.255	20	256	40	295
CTTTCCCTTCTCCCTTTTGG	60.04	20	159	45	203
CACACAAGCAACTTCCCTCA	59.873	20	253	626	878
GCTTTTGCTTGCATTTGTTG	59.49	20	211	2416	2626
CAACGAGCCTTCCTTTTGTC	59.853	20	280	333	612
TGAAGAAGGAAGCTAAAATGC	60.03	23	166	6	171
GCATTTGTTAGAGGTTTTGACC	60.389	23	112	2364	2475
TCGATCGATCCCATCTTGTT	60.426	20	178	80	257
CGAGGAATGATAGAGCCGAT	59.249	20	272	309	580
CATCTCTCCTTCTCTTTCTCGG	59.593	22	149	119	267
AAAATGAAAACGTTACTTCTGC	58.791	23	177	129	305
GTGGACTCTTGGGGTTGAGA	60.088	20	228	19	246
CCCTTTTCTCCTTCTCGCTT	59.955	20	228	248	475
GTCTCGATGGTGTGATCGG	60.063	19	151	22	172
CATATATGGGGAGCGTACCG	60.188	20	274	4	277
TATTCTGCCGAAAATACCCC	58.898	20	178	94	271
ATGCTTGCCCAGACTTTCAA	60.776	20	280	56	335
GGTGGTGGGCGAGTAATAAA	59.823	20	138	274	411
AAGTCCACACAGGTGACTCG	58.725	20	149	213	361
GATTGGCGAGGGGAGAGT	60.16	18	219	1415	1633
TCAGCTCCAGCTCCTTGATT	60.096	20	267	1034	1300
CCGGAAGGTCGACATTTATC	59.387	20	135	37	171
TTCACGCATTTCCACACACT	60.16	20	140	10	149
GGATTCTCCCTACTCCACCC	59.755	20	219	356	574
AGGAAAGCCTTTGACCGAAT	60.074	20	270	144	413
AGAGCAAACTCCGATGGCTA	59.978	20	262	1302	1563
AAGACACCTAGTTGCCCCCT	59.994	20	120	131	250
AATTAGCCGAAATCCCCATC	60.116	20	212	1040	1251
TGCAGGGTTCGATTCACATA	60.073	20	237	270	506
GAAGCCTCATCTCGGGTTC	59.753	19	143	143	285
TTCCTCCCTGTTTCACGAAC	60.088	20	151	205	355
GGTTCTGGGCCTAACTGTCA	60.111	20	250	176	425
AAGCGTGCTTGTCTTCGAGT	60.201	20	277	44	320
CGGTTATTAGTTATCACCCGAA	59.322	23	238	738	975
GCGTTTTAACTCGTCGTGGT	60.176	20	235	1094	1328
GAGCTGAAGCACTTTGACCC	59.997	20	134	1642	1775
ATCCGAAAATATGCAGTGGC	59.929	20	178	1812	1989
GAACCTGAAATGCAAGGAGC	59.82	20	130	1257	1386
GAACTAGGCGAGAACGATGC	59.985	20	177	391	567
GCTGCTTAGGAGGGTTTCCT	59.848	20	242	227	468
ACGTAAAAGGAAATGCATGAA	59.898	23	188	264	451
TGCCTTGACTCCCAAAGATT	59.67	20	207	99	305
ACATGGTGGAGTGCATTGAA	59.967	20	164	66	229
GTTGGCCCTTGATTGTTGTT	59.836	20	181	144	324
AACTAAAGGGGAAGCTCTGC	57.695	20	229	557	785
CTGGGTACGGCTAGAAGGAA	59.331	20	163	227	389
AGGGTCGTTCATGGATTACA	57.864	20	175	346	520
GGATTTGGACAGACCACCAC	60.223	20	103	482	584
AGAAGTGTAGAGCGGTCGGA	60.012	20	102	1825	1926
GGAGGCCTAAGCCAGATAGC	60.327	20	174	68	241
TGCTCCGAATTCTATTCCGT	59.668	20	272	48	319
GATGCCTTTTTGCTTTGCTC	59.967	20	185	1921	2105
TGTAACTTGATTGCTAAGAAAT	59.554	26	251	90	340
GCATATCCAGCACGCTAACA	59.862	20	276	133	408
TGTAGTGAACTCGACGCTGG	60.049	20	180	235	414
TGCATGGGTCAAAGTGAGAC	59.682	20	262	8	269

GTTTGCCGGCTATTACGCTA	60.246	20	251	65	315
GAAGATCGGGGAGTGACAGA	60.199	20	163	629	791
CGTGTCGCCATCAAAATAAA	59.562	20	248	127	374
TGTTGGGATATGAAAATGACA	60.826	23	119	295	413
CTCAGCATACGGGAAGGGTA	60.088	20	249	7	255
GTCGACCCTGACCCTCATAC	59.384	20	236	394	629
TATAGTGCAACCCCCTCACC	59.813	20	241	69	309
GCGTTGATCACGGTTAGATG	59.152	20	205	1573	1777
TGCACTATGGGAACTGCAAC	59.722	20	148	600	747
ATTCCCACAACAAAATGCAA	58.869	20	251	396	646
GTCAACAAGCTGTCAACCCA	59.726	20	274	42	315
CAGCTGAACCATCAAGAGTCA	59.022	21	276	80	355
TGGAAACAAGGGAAAGTCAAT	58.54	21	218	0	217
TTAAGAGGGAGGGAAAAGGC	59.661	20	195	832	1026
CGACGTGTAATCACCCTCAA	59.566	20	261	10	270
AACGAGGATCAGTGAGCAGC	60.564	20	238	197	434
TGCCACAATTATGGAGATATG	59.682	22	237	16	252
ATGTGAATGCACCTGAATACG	58.516	21	245	128	372
GTAACTGAGTGCCACTGCCC	60.721	20	264	6	269
TGATTCACGCTAAAGCACAAG	59.948	22	226	8	233
GATTCGTCGACTACTCATGCA	60.278	22	191	2401	2591
TCCCACCATTTAGCACTATCA	58.107	21	277	37	313
AACCCAGCAATACACCGAAC	59.859	20	235	12	246
TCAACAGAAACGCACACACA	59.912	20	242	27	268
ACGGTGGTGCAAGAGTGATT	60.577	20	143	4	146
GGGATCCCTCGTATCTTTCC	59.728	20	147	4536	4682
GAGGGTGAGTTGGCATCATT	59.934	20	234	96	329
TCGACTTTCAGTATTGCGATTG	60.264	22	262	359	620
CCCTTGTCTTTCATCCCTCA	60.042	20	206	118	323
GCACATATTTCAACGAGTGCC	60.526	21	264	8	271
TGCATGCATTGCTTAAGTCT	57.126	20	249	209	457
CATGGGGAGAGGAGTTAGCA	60.21	20	266	148	413
TTACGGTTCCCTCTACGTGC	60.132	20	223	190	412
TTCATTAAGGGAAGACGTTGG	59.871	22	273	27	299
CAGTCAGGGCCAAGAGAAAC	59.844	20	211	1167	1377
AAGCATTGATGTCTGAATTTGA	58.755	23	253	260	512
CAACAGTTTGGCATCAGAGC	59.445	20	159	228	386
TGTTGCCAGAAAAATTGTCG	59.706	20	249	21	269
TCTGGTGGAATGAGATCCAA	59.009	20	275	347	621
CCTATGATGGTATGGTGTGGA	58.159	21	252	74	325
AGGGGTGTTCAAAAATATCCG	60.061	21	170	53	222
CACTCACCGTCAAATCGTGT	59.597	20	274	49	322
CTGCCTGCTTCATGTCTTTG	59.591	20	228	115	342
TGCTGATATCGTACAACTACA	59.653	25	165	133	297
CCTTATCGATGGGGCCTATT	60.13	20	220	20	239
AAATCCCTCCCCAAGTGTTT	59.668	20	150	347	496
TTACATTGGTGCGTGCACTT	60.18	20	265	3211	3475
CGTTTTGACAATATTTAGTGTT	57.129	25	134	996	1129
CTCATATGACCACAACCCGA	59.369	20	244	37	280
CACTCAATAATGCTGCTGCC	59.449	20	207	113	319
GGCTCACCCAAATATGGAAC	59.249	20	216	2103	2318
TGCTTGGGGCCTAAAATAGA	59.677	20	233	1207	1439
AAAATCAAAGGCCCACAATG	59.801	20	116	1044	1159
CCATCTCCACGACGTTATCA	59.522	20	204	1572	1775
CACCACCTTATCACACACGC	60.032	20	181	27	207
ACGATCCATATTGGGTCAAA	57.735	20	212	9	220
AGAGCAGGGAGGAAGCAAAT	60.349	20	154	1877	2030
GATCAGTATGGCAGTTGGGG	60.34	20	138	54	191

CTGATCTGGGTTGGGAATTG	60.309	20	115	3	117
ATGTGCTGGAGCCTTGCTTA	60.934	20	258	2116	2373
GACCCACTGACCTCCGTAAA	59.966	20	266	339	604
ACCCGGAGTATTCCGAAGTC	60.328	20	194	251	444
CATGCAAGTTTGCTCCTACTG	58.592	21	277	2911	3187
TTTTTCGAGGTCCATTTTCG	60.046	20	190	65	254
CCAAAAATTCAAAATCCAAAC	58.869	22	242	39	280
AGGGTGGTTTTCCCAAGTTC	60.204	20	217	394	610
TCGCGGATTTTTGGATAAAC	59.907	20	224	2	225
GCAGCAAATCGATCCATACC	60.444	20	209	970	1178
ACGGATTTATTGGTTATTACCT	58.008	24	183	469	651
AACTGGGAAAGTGGGGAAGT	59.834	20	203	156	358
GGTAGTTGATGAAAGCCGGA	60.074	20	175	35	209
CACACTTTACACACACTGAAA	59.163	25	118	423	540
CATCAGAGCCCACGGTTAGT	60.134	20	248	139	386
AGGGTTGTGTGCCCTATCAT	59.288	20	255	8	262
TTTGTGGGTTTGGGACCTTA	60.198	20	186	4815	5000
CTCGCTCAACCAAGTAAGTCG	60.06	21	202	362	563
TTGGGAGGAGAGATTGTTGG	60.042	20	278	16	293
CCTGATGCCCTCTCTTCTCA	60.488	20	135	2114	2248
GCTAACACCACGCCACTACA	59.788	20	211	1245	1455
GCAGTTATTGTGATGTGGGTG	58.914	21	250	20	269
TTGCCTCATCTTGGTTGCTT	60.776	20	256	270	525
AACTTGTGGTGGTGGCTTGT	60.466	20	230	118	347
TTGTGCTTAATTTTGTTTCTAAT	58.884	25	176	148	323
GTGTGGAGAGGATTTTGGGA	59.903	20	202	941	1142
ATCCCCAATTTACCAAACCC	59.756	20	173	29	201
CGATCTGGTATCAGCGGTTT	60.096	20	199	344	542
ATTTTTGGATGAGGCAGTGG	59.933	20	277	1231	1507
TTTTCTGACCAACACCACCA	59.976	20	123	1368	1490
ATCCAGCAAGGAGGAAGTGA	59.803	20	239	15	253
TTGACAATATTTAGTGTTTTGA	58.99	27	139	350	488
ACCTTTCTCTTGGCCTCCTC	59.817	20	192	338	529
CGGGAGTATTTGGTCACACC	60.232	20	173	153	325
TAACATGCAACTCCCAAACG	59.585	20	271	2413	2683
CCTCAATCACCCCTTTTTGA	59.903	20	268	1137	1404
CCACATTTAAGGGTTATCACCT	59.654	23	101	232	332
TTTGGGGTGTTTGGAGTTGT	60.246	20	156	211	366
GGTGGGCTTGGTGTACTAACA	60.172	22	112	917	1028
TAATAGGCCCACACCACCTC	59.813	20	243	62	304
TGTCGCCTGAAAAATATCCC	59.901	20	271	5	275
TGTGAGGCCCATCATACTTG	59.522	20	157	1365	1521
CCAACCCTTTCTCCTCCTCT	59.671	20	259	205	463
TTCTGGATGGAAATGTGCAA	60.049	20	250	77	326
GGGTGTTTTGACAATATCACG	59.73	22	178	241	418
GCAGATGCCACAAAAGGATT	60.081	20	172	858	1029
GGATTGCTGAAAACTGGCTC	59.82	20	253	19	271
AAACAGCTGGCATCTACGGT	59.763	20	127	1157	1283
TACTACATCAACCGCCAGCA	60.28	20	100	548	647
TGCTACACTCGACAGTCCGT	59.493	20	133	7	139
GGAGGGATCGGATAGAAAGG	59.859	20	194	1415	1608
CCACGTCACCTTATTCCCAT	59.67	20	216	1	216
AACAACGTTATCTGCGACAAG	59.813	22	202	520	721
GGATCATTAGGGTTGCCAGA	59.894	20	163	264	426
AATTTCTTGGCCTACACCGA	59.569	20	279	55	333
GGTATGCACTCTGCAACCAA	59.722	20	109	963	1071
TGTTACATTTGGCTCGGTGA	60.111	20	220	470	689
TCTAGTCGATCCATCCCGTT	59.508	20	277	465	741

GGTGTCTGCAAAAGCATTCA	59.847	20	256	359	614
AGAGGAGGGGTCCATGAAAG	60.447	20	126	845	970
TGATTCCGGAAAGAAGATGG	60.006	20	141	984	1124
GGCGCACTGAATTGTTGTTA	59.735	20	212	7	218
CCAGATCCAAACGAGTTCTCA	60.239	21	219	0	218
AAAATGCCCTTGTATGCTGC	60.103	20	147	20	166
TAGGATTTGAACCTGCGACC	60.074	20	258	45	302
TCTGCTGCAAATTTGGAAGTTA	59.89	22	176	854	1029
CCGTCGATTTTCAGGTTTTG	60.472	20	187	104	290
TGCAGAGGTGGCTCAGTTAG	59.187	20	279	29	307
TTCATTCAAGCTACCCACTCTT	59.317	23	161	107	267
TGGCCATGTTGGTAGATTCA	59.924	20	153	24	176
CTTCACCACTCAATCTGCGA	59.984	20	187	1080	1266
AACGAGATCGAATGGAGAAAA	60.075	22	111	829	939
TGTCCACTTGTGTCACGGAT	60.005	20	220	68	287
TTCGAACGATAGCTCCCACT	59.836	20	139	695	833
TCATCATTTCGATCCTGTGG	59.451	20	149	0	148
CCCTCGAAATGGGTTTTTCT	60.291	20	206	612	817
TGGCAATTTGTCTTTCAATCC	59.93	21	191	28	218
TTAGAGCATCTCCAATGCCA	59.375	20	205	14	218
GTGGAACATTCATCCCCATC	59.995	20	187	1384	1570
CAGCACTTTTCATGTTGTTGC	59.381	21	211	830	1040
CGGATGACCGAGCTACTGAT	60.24	20	247	215	461
CAGCAACGATTGGAGCATTA	59.833	20	225	114	338
TTTTGTCGATGATATGGTTGTG	58.413	22	191	39	229
TGTAACAAATAAATTAACGTAC	57.577	27	166	1089	1254
GCGTGTTCTAGGTGTTCTTGG	59.788	21	226	125	350
CTCATTGTAATCTCTCCCAAAG	57.927	24	277	280	556
CATGCATGATGTGATGTCAGTC	59.999	22	165	42	206
CCATTTACTAAGAACGACATGC	60.404	24	277	1645	1921
TTTTCGGATCGAAATTAGGTT	57.759	21	204	467	670
TTTTTCTTTTGCACGACTGC	59.087	20	155	14	168
TCTCGGAAGGAATGAGATGC	60.303	20	251	4	254
CCATGGTGAGAAAACAACGA	59.541	20	274	99	372
CAGCGAGATCTTCGTCCATT	60.362	20	163	115	277
CCATTGGCTCGTTTATTTTAGA	58.331	22	280	171	450
TCGGGTCTTGAGGGTAATTG	59.926	20	262	443	704
CGGGCAGAAGAAGAACAAAT	59.312	20	263	506	768
TGCATACAAAGGTAAGGAGGC	59.238	21	142	636	777
GGGAGAAAGACACGTGGAAC	59.555	20	270	134	403
GCAACATAGTTTATGCATCCCA	59.859	22	213	81	293
ATTGTGAACCGGTGGTTCTT	59.308	20	232	140	371
CAATGAAATAAAGAAGCCGGA	59.199	21	238	266	503
ACCTTACACCTCACACCCCA	60.275	20	169	456	624
TTTCCTTCATTCCCATTATGTC	57.923	22	256	398	653
CGGCCAAATCTAACGAAATC	59.547	20	263	285	547
ATTTCAAAAAGTGGGGTCCA	59.264	20	247	18	264
GAAAGAAGAAGAGAGATAGAT	58.05	27	255	482	736
CCATCGTCCTTATGGGCTAA	59.916	20	280	191	470
CTCGGTTTCTCTCCCATCAA	60.187	20	186	9	194
CAAACTTGACGCGCTATCCT	60.407	20	251	3	253
GAAGACACCCAAGCCCATAA	59.933	20	210	21	230
TTCTCCTTGTTTCCGTGGAC	60.088	20	278	67	344
TGATTTGATTCTTCGCGTTG	59.809	20	106	2491	2596
595	595	595	595	595	595
GACCTTCCCAAACTTCATCG	59.526	20	237	50	286
CGCTTCAACTTTTCCACCAT	60.11	20	138	634	771
TCCCAGTACGCAGACTTTTCTT	60.295	22	280	34	313

TTAGGAATTTGTTCCCGTGC	59.938	20	272	59	330
CGGCTTCTCCCTATCAAATG	59.662	20	109	496	604
AAAAACCCCGACTCAAACTT	57.697	20	225	308	532
CTCGTGGACACCTTGTCAAA	59.72	20	121	27	147
TTGACAATATTTAGTGTTTTGA	58.99	27	254	606	859
CCCGATCCTAAGCAACTTCA	60.206	20	118	796	913
GTTGCCCACAAGTTCGAGTT	60.156	20	167	363	529
TGCAAAATGGGGATTTGATT	60.132	20	269	1013	1281
CACTTGGACCAGAAAAGGGA	60.081	20	109	14	122
AGACGTTGCATGTGCTTCTG	60.056	20	107	1840	1946
TGCTGAGTTTTGAGTCACGAT	58.511	21	178	131	308
AATCGAGGTGTAACGGGGAT	60.578	20	273	1861	2133
TGCTCCTGTAAGTTTGCCATT	59.761	21	264	1161	1424
GCTGATTCTGAAGGCATGGT	60.226	20	274	99	372
GCTGATTCTGAAGGCATGGT	60.226	20	280	100	379
CCAAACCAGAACCGTGAAAT	59.83	20	220	416	635
CCAACCATAATTGTTTCGGG	60.046	20	248	296	543
TAAACAGCCGGAAATGGAAG	60.067	20	234	1034	1267
CCCATAACCATGACAAACAAT	59.975	22	253	407	659
CTGCTACAATGACGATGCCA	60.834	20	131	20	150
AGGTTGGGATGGAATGAAAA	59.22	20	247	301	547
AAAATCACTAGCATGCACGG	58.799	20	137	70	206
TTCATAGTCGGCTCAATCCC	60.036	20	149	392	540
CCTTGCTAGATGGCCAAAAA	60.202	20	279	319	597
TTCCACCTCATATCATTCCCA	60.14	21	274	81	354
TTGTCCTCCTGTCCCTTCAC	60.088	20	175	706	880
CCATTGCATGCGTCAGTATC	60.104	20	234	3516	3749
TGCAGAGATGGTGATGGTGT	60.121	20	249	6	254
CTCGTCGCCTCTTATTGGAC	59.836	20	254	13	266
GAGCTTTGTATGCCCCACTC	59.7	20	265	92	356
CAAACGCCATCAACATCAAG	60.111	20	117	0	116
AATGATTGAAGCTTCCCCCT	59.903	20	153	312	464
TGTTGGATGCCTTTGATCTG	59.648	20	150	10	159
CGAGTTGCTTCTATCGTCACC	59.89	21	219	680	898
TTGGCATGTAATGCGAGTTT	59.186	20	243	1010	1252
ACAAGACGGACAAGTTGGGT	59.474	20	264	240	503
TTGGAAGCAATTGCATGATT	59.115	20	197	30	226
CACGTCAGCTTCATCTCCAA	59.984	20	238	325	562
TGCCCCTTATTCAATTTCCA	60.26	20	177	415	591
AGCACCGACTGAAAATGAGG	60.255	20	179	0	178
TGCTGCTTCAATTCGTTTCC	61.285	20	277	49	325
AACCCATCCTCTCATCGAAA	59.483	20	134	105	238
GCATCGTCTCAACCCTTGTT	60.119	20	129	104	232
AGCGATTTCATGGAGATTGG	60.036	20	247	668	914
GCACACAAATAATGGTTTCTTC	59.771	23	216	144	359
CTGTATTTGCACAGTGCCTCA	59.92	21	250	711	960
TTTTTAAATGGATCGGCCTCT	59.922	21	270	2	271
AAACGGGTGAGCAAGACAAC	60.156	20	262	1552	1813
AAATGAACCGAACCAAACCA	60.206	20	274	49	322
CATGTTTTTGGATTTTGGGG	60.024	20	170	905	1074
CTCGAACCACTTTCAAGCCT	59.473	20	274	130	403
TTGGCTTGGTTGTTGTAGATTC	59.134	22	279	992	1270
TGGGAAGATCTCTCCATTCTG	59.224	21	230	238	467
TAGGGGTTATCACCTGAATGC	58.917	21	118	159	276
CGAATTAATCCGTCCAATGA	58.429	20	247	764	1010
GAATCACTTTGCAAGCACCA	59.847	20	243	156	398
TGCAACCGAAAATTAGGGAA	60.427	20	181	138	318
TCAAATTTTTCTCATGCATATTT	59.012	25	229	517	745

TTTGTTATGCGTTTTGACGA	57.846	20	184	358	541
ACGTGCAACCAGATTCAAAA	59.174	20	141	82	222
CAAAGTGCTTTAGGGGTGGA	60.103	20	126	116	241
AAAACCCTTCTGTCCTTCCC	59.415	20	184	21	204
GAAGCGAATCGTCGAGAAAC	59.962	20	217	292	508
ATGATAGCCATGATCTCCCG	59.877	20	232	299	530
AGAGGGCTATGCTGATTTGTTC	59.752	22	260	47	306
CCTTGTGTTGCCAAGTTTCA	59.734	20	157	120	276
TCAAGGGACCAGAGGAATTG	60.042	20	262	66	327
TCGGGGTATCAGAAATCGAG	60.029	20	269	45	313
CCATATAACGATGCCATCCC	60.001	20	279	11	289
ATGGTGCAGAGGATAGACGG	60.096	20	246	1271	1516
CCCCACCAAAACTCCAACTA	59.824	20	245	15	259
TTCACGCTTCTTCCCCTCTA	59.948	20	139	292	430
TCGCTTCCAGTTTTGTCCTC	60.375	20	264	8	271
AACAACAACAACGTCGTCCA	60.049	20	200	4	203
ACCACTCTTGCATTCTCTTTCTC	59.956	24	100	13	112
GGCCGGATTGCTGATATAGA	60.023	20	141	934	1074
CAAGCCTAACACCACAAGCA	59.904	20	274	490	763
CTGCCACCATTGATGCTAGA	59.823	20	164	63	226
CTCGCTTCAGTCAGTTATCCG	60.023	21	159	11	169
TACATTCATTGGGGTGTGGA	59.623	20	105	12	116
TGGCAGATTTAATATTTACGTT	59.847	26	212	167	378
TGGAAGGGAAAAGAACCTCA	59.641	20	178	445	622
GACCTGACACAACCCTCCAT	59.817	20	262	56	317
GTGGACGCTCCAGATTGTTT	60.119	20	268	496	763
GTAGACAACGGGGATCATGC	60.348	20	136	7	142
TGATACAAGTGTTGAAGCCAA	58.688	23	203	444	646
CACCCTTCCCCTAAACCCTA	60.172	20	188	312	499
CGGTGATAACTAGGAACAAAT	59.806	24	190	576	765
CCCGGTATGCTGACGATAAT	59.807	20	201	1	201
ATGGTTGCTTGATGGAGAGG	60.073	20	147	6838	6984
GTCCAAATGGCACCAATTCT	59.797	20	201	1	201
TGGGTCCAAGAAAACCAAAG	59.942	20	120	273	392
ACACGGAGGTGATGCCTATC	59.957	20	220	541	760
TGCGTTTTGACGATATATAGTG	59.092	25	162	447	608
TTGTCCCCAAACAACGAAAT	60.206	20	211	17	227
GTGTAATCGAGGGAATCGGA	59.894	20	280	320	599
TGCCTCTTCGGATGAACTTT	59.813	20	181	4574	4754
TCCGTTGAGATTTTGCATCA	60.197	20	192	103	294
TCATGGATGGGGACTTGATT	60.135	20	256	545	800
TGTTGGGAAAGAAGAATGGA	58.117	20	270	31	300
GCGAAATGAATGTACCGGAT	59.791	20	262	673	934
GGCCATCGTTACTGGTTTTC	59.434	20	207	40	246
CCAACCAGGGCTACATTTTT	58.949	20	129	748	876
CCAACACCACAACACCAAAC	59.745	20	242	22	263
TGAAGCAAGAAAAGGGGCT	59.94	19	166	593	758
AACATGAGACGCAAACACCA	60.16	20	255	68	322
CGCGTTACGAATCCAAGTTT	60.131	20	176	278	453
AACCGAAAAATTAATCATCAC	57.085	22	202	158	359
TTTTAAGGCGTTCAACTGGG	60.103	20	201	30	230
GAGATTGGTGGTTGCAGGAT	59.934	20	266	251	516
CGTGTATGTGTGTGAGTGTATA	60.095	27	182	151	332
AGTAGCGATGTCGGCAATTT	59.736	20	231	4300	4530
CTTGCGATTAGGAATGGAGG	59.662	20	233	314	546
CAAGAAAGTTGTGGGGTTGTG	60.429	21	277	11	287
GCAACATCTAATGGTTGTGGG	60.242	21	214	126	339
TAGGATTCTCACAGCCGTCC	60.218	20	260	4	263

TCAAACATCGCATCCTCATC	59.61	20	248	268	515
GGAATTTGATTCCTTCCCCA	60.995	20	272	636	907
CCTGATTTTTCATGTTTCGGA	59.924	21	278	130	407
AAGATGACACGGAGGTTTGC	60.119	20	245	106	350
CGCAAGCATGTTAATTTTATTCA	59.213	23	270	143	412
GAATGCATTTCCGGTGACTT	59.939	20	218	1276	1493
AGTGAGAGAGAGGGCTGCTG	59.883	20	277	52	328
TCTTCATCGTTGTAACCCTCG	60.118	21	240	88	327
TGCAAAACGGATGAAAAACA	60.088	20	270	334	603
TTGGAAAAGCCATGCAAGTA	59.301	20	215	52	266
CAACACTTCACAGCTTCTCCC	59.899	21	210	436	645
GGATGGGGGTTAAGGAAGAG	59.761	20	218	69	286
AACAAAGGGGCAATATGCTG	59.96	20	150	114	263
AAGGAGGTGTTATGAAGGGAT	58.028	22	168	430	597
GCGCCACACGTTAAAGTTC	59.336	19	237	12	248
AAAGAGACAAAAGGCAGCAAA	59.144	21	256	31	286
TTGGGATTGGTCGTTTCAAT	60.17	20	217	701	917
GCCATTGTGGGCCAGTAGTA	60.914	20	280	120	399
CTTCATGAGGTGGCACAATG	60.112	20	217	766	982
TTCAATTCCTTCCAACACCG	60.863	20	173	111	283
CGTGTGTGTAACGTGTGTGTG	59.591	21	121	1212	1332
AGAAAATAACCACGTGCCCT	58.579	20	189	96	284
TCTTCCTCATTGGTAGGCGT	59.694	20	104	57	160
CCCTCGAAGTTTCGTTTGAA	60.22	20	249	324	572
TGCTTTTTATAACTCGCCCG	60.218	20	198	1333	1530
ATTGATCGGTCCTTCACCAA	60.317	20	205	49	253
TTTCCATGGCTATGCTTCTC	57.915	20	184	111	294
CATGGGTTCTTTCCTCACAA	58.541	20	278	534	811
TAGCAGCTGATATTCCCGGT	59.691	20	135	102	236
TGTGGATGTTGGTTTTGAGC	59.547	20	247	669	915
TGCCTAAAGAACGTTACACGG	60.172	21	265	3	267
GGAGAGACTCGAGATGCAATG	59.965	21	187	39	225
CGAGGTAGCAAGTTGGACAAA	60.29	21	189	391	579
GCCAATGAATTCACGAGGAA	60.983	20	249	66	314
GGCCGGATCTCACTAAATCA	60.036	20	165	2123	2287
TTGATTTGTTTAATCTAATGGAT	57.304	26	276	776	1051
GCGTTTTGATGATATATAGGTG	58.907	26	186	123	308
ATCGAAGTGACGATGGAAGC	60.226	20	266	3372	3637
AATTTGCTTGCTGAGTTGGC	60.395	20	212	248	459
AAGGTGACAACCGATCAAAA	58.048	20	279	235	513
CAACTGCGACCAGATTCAAA	59.84	20	253	526	778
ACTGTTATGAGGCGGGATTG	59.955	20	185	92	276
GCAGGATCAAGGTGAATGAGA	60.211	21	225	54	278
TGTTCTTCACGGTTCAATGC	59.697	20	262	32	293
GAGGAGAGAGAGGGAGGGAG	59.489	20	231	251	481
TAACCCCAAGTCTGGGACTG	59.959	20	187	21	207
AGAGGATCGAGAGAGACGTGA	59.142	21	267	82	348
CCAGGGGCAATCATCTCTAC	59.508	20	266	86	351
TCGATTACTGCAAATCTCGG	58.869	20	210	79	288
GGCCTCATGAACTCTTGAATG	59.685	21	163	926	1088
ATTTCGGTTTGGTATGGTGC	59.691	20	194	672	865
CACACACTTCCACACGAACA	59.15	20	240	527	766
CCAACTGAGTCCACTACCCG	60.557	20	183	25	207
GGTTATCACCGGATCGCT	58.462	18	193	1933	2125
CCCAAACATCCAACCAATTC	60.029	20	263	217	479
ACTCTATCTCTCTCACACAATCT	57.487	27	164	270	433
AAATAAGGAGGTGTTATGAAG	59.323	24	185	351	535
CCATCTTTAGCTCCGTGTCC	59.694	20	254	223	476

GCTGTGGATAATGTGGAGGC	60.492	20	247	24	270
TTCCTAAGTCGTGTTGCGTG	59.904	20	150	891	1040
CAACAGCCCGTCAAAGTACA	59.758	20	264	382	645
CGCCGTTTTAAGACCCATTA	59.958	20	187	834	1020
GATATGCGAGATGGATGCCT	60.028	20	164	3538	3701
TTCTCAGCATATGGGAAGGG	60.029	20	237	6	242
TTTTGTTATGATAGGATCAAAC	57.769	25	177	1786	1962
CGTGTGGGAAAGATATGCCT	59.955	20	258	920	1177
TCATCGATTACGTTGAGATGAA	58.241	22	280	756	1035
TCACCCACTCTCGTCACTTG	59.864	20	100	7	106
ACAGTCATTCCTGTCGCCTT	59.727	20	238	82	319
TCAACCTCCTCCACCTGAAC	60.088	20	275	507	781
CCTTATTTTTAACCCTAAAAACC	58.713	24	251	217	467
TGCAACGCTTGTTTCAAGAC	60.035	20	191	1151	1341
TTACGAGCTTGCGAGATTGA	59.712	20	231	163	393
CACCCAACCACAGCAATTTT	60.786	20	250	22	271
CTGAAAGAGAAGCAGCCGAG	60.41	20	252	66	317
TCCACGTGGCACAGTAACTC	59.751	20	171	61	231
CGGATTCGAGTTTTAATGGG	59.406	20	221	421	641
TCTTTCATGCAATCGCTTTG	59.953	20	225	508	732
CCAAGGGCAAGACAAACTTC	59.711	20	245	138	382
TCCTCAATCTGGTGCTTGTG	59.831	20	151	1846	1996
TGGTTTCCGTTTATATGACGA	58.031	21	198	9	206
TTTCGTGGAAGGATACCGAC	59.933	20	267	24	290
AATAGGGGCATCACGATGAG	59.917	20	234	2439	2672
AGCAGGATAAGGGAGTTAGCA	58.111	21	204	401	604
ATTCTGCAATAATCCCGTGC	59.929	20	253	14	266
CTTGTGGGAGGAAGAAACCA	60.081	20	154	338	491
TCCCATCCCTTAGTTTTGACC	60.173	21	220	113	332
TGGGAAGAGAGCGAGAGAAA	60.21	20	213	11	223
AATTCCAACTTTGGGGTAATCT	57.96	22	240	45	284
ATGCGACGATGATGATACGA	60.065	20	140	251	390
TTTGGACTGTATCGGTCTACCA	59.494	22	191	76	266
AGTCATGAACTAATCAAGTTCC	59.123	25	258	93	350
ATCTTGGTGGGACTACGTGC	59.997	20	155	275	429
TGACATGACTCTGATGATTGCA	60.541	23	153	245	397
TGGACCAGAGAGCCATTCTC	60.349	20	277	1259	1535
CTCATTTTGGAGCCCATTGT	59.933	20	185	60	244
CAGTGGGCAACTACAAGTGG	59.209	20	154	671	824
ATTGGAATTTCTGGGAGTGG	58.836	20	272	2038	2309
ACCTTGTCGATTTTGATGGG	59.79	20	178	1968	2145
CCGAATGTAGTGGATACGGC	60.352	20	107	330	436
ACAAATGATGGCTGGCTAGG	60.096	20	229	282	510
TTCCCAGCATGATGGTACAG	59.522	20	183	135	317
TTGATTCAAGTTGCAGGTGG	59.691	20	182	41	222
TCAATGTGGCGCAATTAAAA	60.074	20	278	289	566
CCTCTTCAAACAGAGAGCCG	60.126	20	170	840	1009
TATTTTATGGTCTTCCAACATTT	57.343	25	272	108	379
TGGTGCTCTTAGATTCATGGTG	60.132	22	199	349	547
GCCTTGCCTTGTCCATATTC	59.533	20	268	140	407
AAGGGTGAGTGGTGGGAAAT	60.607	20	279	250	528
GGCTTTTTGGTCCAGTTCAA	60.088	20	229	3632	3860
CCGGTGAGATTCTATTCATGG	59.396	21	264	101	364
GACTTGAGCTTGTTCGGAGG	59.989	20	162	245	406
GAGGACAGAACTGCTGGGAC	59.841	20	188	322	509
TTTCCAAACAGTGCACGAGA	60.427	20	194	5557	5750
AGGGACGACAAAAAGTTCCA	59.569	20	279	752	1030
TTCGTCCATTGTAAACAGTTCC	58.997	22	176	132	307

GAAAAGGGATTTGGACGGTT	60.166	20	263	63	325
TGGCTGATATGCATCAGAGG	59.781	20	152	1618	1769
ATTGCGGCATTTTACGAGAT	59.574	20	234	86	319
CTCTCAAACTCACGGCCTTC	59.989	20	149	11	159
AGACCGAGCCCATTCTTACA	59.694	20	255	3	257
TGAGTTTGATGGAGCGAGGT	60.801	20	269	308	576
ATCTTCACGAAGCAGCAGTG	59.191	20	167	0	166
GCACTCACTCTGGAACCCTT	59.305	20	258	36	293
TGGCAGCTCATAATCAGTGG	59.823	20	126	350	475
GCAGCAGTGCAACTGAAAAG	59.788	20	113	5165	5277
TTTTTGCAATAATTTCCGCC	59.913	20	265	2	266
TGCATTGAATGGACTTAGCC	58.723	20	243	25	267
ATTTTTGTCCAAATGCACCC	59.668	20	233	28	260
GGCTTGGAGGGTTCTTCTTT	59.691	20	168	300	467
TCCAGCCCCAGTCTAACAGT	59.721	20	247	673	919
GCGTGTTTTTGGCCTGATA	59.679	19	210	51	260
ATTGCCCTTTCATGCATTTG	60.837	20	204	1251	1454
GGAAAGGCTGTCGATTACCA	60.074	20	237	45	281
TTCAACAACTCATCCACATCAA	59.024	22	277	1081	1357
GAAAAGGTTCCCCTTTCTCCT	59.934	21	264	289	552
AAAAGAAAAAGTCGCTGCCA	59.996	20	276	57	332
AGGTGTCTGGGACGATGAAG	60.112	20	222	194	415
GAGCAATTGTTGGACCGAGT	60.119	20	156	531	686
ATTGCACCCCAGACCATTAC	59.676	20	140	24	163
CCGACCAAAAATCAAACCAT	59.662	20	231	414	644
TGGATCGACAATTAGCTGGA	59.226	20	168	326	493
CTACCCCCGTTGGAAAAGAT	60.18	20	223	16	238
TCCTTTGAATGGACTTGGCT	59.67	20	240	21	260
TTTTAATCTTGGCCGCTGAT	59.682	20	230	1581	1810
TGAAAATTTGAGGCTGCACA	60.379	20	238	3450	3687
ATTTCACTTGGGAGGTGGTG	59.82	20	212	121	332
TCCTTCAATGGAGGTTCAGG	60.042	20	252	291	542
ACCGATTTTCCCCCATTTTA	60.361	20	256	313	568
GTGATTTGGTGAAAGCCCAA	60.874	20	110	104	213
AAAGCAATGGAGGCTTGATG	60.214	20	169	5217	5385
GCAACAATTCGAGTGGACAA	59.697	20	269	920	1188
CCGACATAATACACCGCCTT	59.845	20	135	31	165
CCTTATGGTGGCTTGTTTGG	60.357	20	194	414	607
ACTTCCCGGACAGCATTAGA	59.694	20	228	374	601
GCGGCAGAATGAAGAAGAAA	60.469	20	122	278	399
CCATCCATGCAAGTCCATTC	61.282	20	261	89	349
ATCGGTTATCACCGGATCG	60.697	19	279	1299	1577
CCGTGTCCGTGTACATTTG	58.394	19	270	138	407
TCAACCATTTTTGTGCTCCT	58.201	20	152	259	410
GCGCGCTGTATATCTAACGAC	59.916	21	153	62	214
TTTTAGAGCATCCCCAGTGTG	60.118	21	279	213	491
TGGCTCTGGTACCATGTTGA	60.112	20	220	4	223
CCTTCACGAGTGGTGACAAA	59.72	20	128	655	782
GTGTTTTGCGTGTGTGAGGT	59.648	20	236	25	260
ACCGAACCCATTCTTACAGG	58.909	20	249	3	251
AAGCGTTTACTTTTGGGACG	59.267	20	186	426	611
TCTGGGATAAGGAGCATCAGA	59.782	21	251	920	1170
GGGTTTGGAATGTTAGCTGG	59.429	20	268	303	570
GAAAGTGAGCCCATTTGGAA	60.051	20	210	644	853
TTGCAGATCTTCATCCAACAA	59.262	21	242	34	275
TCCTCAATTCGATCCTGGAA	60.538	20	180	48	227
GAATTGCGGTCGTCTTCTTC	59.82	20	238	841	1078
CAATTTGTTTCGAATTTTGCTG	59.64	22	185	244	428

CCCTGCTTCTGAAACCCTAGT	59.759	21	141	684	824
TCTTGGGAACCCTTGAGATG	60.042	20	257	965	1221
AGGGAGTTTGCACCAGATCA	60.656	20	277	19	295
TGAATCTGCATAGCCTCTACGA	60.003	22	231	118	348
GGAAGGGTCTCGTGTGTATG	58	20	273	486	758
AGAGGATCTCAAGCCATTTCA	58.875	21	225	469	693
TTGATCGACAGCATCCTAGC	58.979	20	230	328	557
ATTTCTTGAGTCGGGGGAAT	59.766	20	278	580	857
CGGAGGACGAGCTATTTATGG	60.943	21	280	247	526
GACTGCGCCTAGAATTCGTC	59.985	20	233	259	491
TGTGTGCAGATCTAATGGCA	58.81	20	176	154	329
ACGCACGCACTCAGTTACAC	59.977	20	273	1196	1468
TACCTCCCACCGCACTATTT	59.452	20	136	45	180
TCGAATCCTTCGATTCTTGG	60.148	20	196	138	333
AATTTGGAGCGACAACGAAG	60.249	20	235	32	266
AAATGCCCTTGAATGCTACG	60.096	20	261	0	260
CAGACCAGACTAGGGGCAAA	60.246	20	192	228	419
ATTTTTAATGGGGCAGGGAT	59.512	20	277	66	342
AACCGAATGCACTCACACAA	60.16	20	145	516	660
GCACCGGAGAAGAACTACCA	60.255	20	258	507	764
TTTCTCAACCGAGCTCACC	58.945	19	125	286	410
ATCCGCCCCTTATCTCTGTT	59.925	20	218	260	477
TTCCCTCGATTCTCGTGTCT	59.803	20	269	903	1171
CCTCTGAGGTGTGCTGCTTT	60.589	20	266	84	349
CGCCGAGTCAGTGAGTTGTT	61.45	20	244	507	750
GATATTAAACGAGCGGTGGC	59.574	20	273	708	980
TCGCATCAGGAAGGGTATTT	59.528	20	272	457	728
TTCCAATGAAAGGGGAAAAA	59.36	20	201	143	343
ATTTACGTCGATCTGCGTCC	60.103	20	181	51	231
TTGCACCGTGTGCAGTTATT	60.18	20	158	284	441
ACCAGCTGCACCTGTAACAA	59.365	20	172	3366	3537
TTCAAAGAGATGGGTCAGGG	60.042	20	169	1355	1523
AAATGATCTACGTCCACGGG	59.813	20	224	438	661
CGGTTAAAACCGGACCATTA	59.693	20	175	71	245
TGTCACTTATAGGCGCATCTG	58.956	21	153	17	169
CGGCTGTGGTTTCAAATTCT	60.11	20	253	376	628
ACCATCGTAGGGTGTATGCC	59.7	20	239	13	251
GAGCTATTGGATTCATCCGC	59.633	20	220	86	305
ATATCAAAGGCGTGGATTGC	59.929	20	176	699	874
GGTAGCCATTTGAGTCGCAT	60.103	20	204	323	526
ATTCATCAACAGCCTCCTCG	60.218	20	128	2	129
ACTTCATCCCATTGAGTCCG	59.927	20	103	2	104
CGATCGAAGACTCCATCCAT	60.034	20	203	3040	3242
TTGCTCTAACAATTCTGAAACG	59.065	23	199	384	582
CGCCAGGGGAATTGTATTTA	59.789	20	224	1162	1385
GCAGCCATGGTATGGACTCT	60.104	20	280	547	826
TGTGGTTTGGTCCGGTTAAT	60.088	20	140	21	160
AGTGGATTTGGGGATGATGA	60.135	20	258	362	619
CGTGGAGTCGACGACAATTA	59.716	20	181	1020	1200
GCTGCTCTTCTTCTGCTGCT	60.187	20	198	597	794
GCCAAATGCCTACAAATTGC	60.465	20	238	1190	1427
TTGGCTTGTCGAGCTCTTTT	60.132	20	262	6192	6453
GATGGAAATGGCAAAAGCAT	59.907	20	140	323	462
TTTTTGGCTCGTTGAGCTTT	59.996	20	247	2347	2593
TGCAAAGCATACTAAAGATGCA	59.463	23	221	349	569
TGGAAGGAAGAAATCGGAGA	59.744	20	279	651	929
CGCCAGCTTTTCCAAAATAA	60.198	20	266	1570	1835
CTCGGTCTCCTTTGTCCAAC	59.697	20	160	293	452

ATGAATAGTTGCGGATGCAC	58.602	20	179	156	334
TTCCCCTTTGCCCTCTATTT	59.903	20	225	73	297
ATTGAATATGCATCACGCCA	59.921	20	241	4	244
ACGAACATGACACGACAGGA	60.162	20	248	1659	1906
CACTACCAAGGGGTCTGCAT	59.989	20	131	340	470
CCAATAATAGTTGGGAGCGG	59.429	20	256	81	336
CCGGATATACAAACTACAGGG	59.758	22	215	111	325
GGGATGAATTTCCACCATGA	60.526	20	167	580	746
AACCTACATGATGGAACGGG	59.67	20	159	2	160
GCATCTCTCTCTTGCTCTCATTC	60.665	23	108	372	479
ATCGGTTATTACCGGATCGC	61.031	20	197	200	396
GCTTGTCCGTAGAAAATGGG	59.569	20	228	543	770
AGCCGTCGGATTTAACATTG	59.96	20	161	2369	2529
AATGCTTGCCATGAGAATCC	60.043	20	278	769	1046
TGACGGAATTTCGGTGTTTT	60.344	20	118	435	552
CAGTTGGTTTTGCATCATCG	60.111	20	134	4580	4713
CCGCACTGCATTTCATACTG	60.28	20	214	869	1082
CGGGAGTAGTCTCGTTCCTG	59.861	20	252	39	290
AGGATCAATCCCCACAAAAA	59.22	20	271	159	429
GGAATTACCGAGGGAGAAGG	59.897	20	105	48	152
GGGTGGGGATCGATTTTTAT	59.852	20	200	26	225
AGGACATGCTCAATGTCTGCT	59.889	21	190	114	303
CACAGAGAATCAAACCAACAC	60.06	23	160	282	441
AATGGACCAGCCACTACAGG	59.989	20	276	1378	1653
AACATCATCCAAATCCCAGC	59.756	20	220	626	845
AAACTGTCCCTACCTGCCCT	59.994	20	258	1424	1681
ATGAACCACTCCTCGCTCTC	59.41	20	242	37	278
AGCGGCGAAACAAATAAAAA	59.732	20	279	3169	3447
AACAGCCATAAGCACAAGCTA	59.101	22	157	1713	1869
TCAAACATGCGATCCTTACA	57.702	20	186	381	566
GAGTGGAGGATTCGGTGAAA	60.05	20	225	681	905
GCCAATGGCCCAATAATTC	60.11	19	242	5	246
GCAAGTGGTCACGTGAAATG	60.16	20	277	364	640
GACGCCACATGTCTGCTAAC	59.323	20	220	251	470
GGTTCTCTGGTTGCACCATT	59.973	20	201	989	1189
CAAAACCCGTAAAGCGAAAA	60.102	20	177	915	1091
GTTCGAATCCTCTCTTCCCC	60.015	20	279	94	372
GGTAGCCTTTCATTCCCTCC	59.903	20	125	475	599
CCACCAAGTCAAGACATCCC	60.363	20	255	269	523
CTTGTCTCCATTCCATTGGC	60.461	20	224	92	315
AGGCTATAAAGGAGCGAGAGT	57.926	22	274	915	1188
ACATATTTATACGCATATAGCA	57.577	27	196	1886	2081
CCAGAGATTTCGCTCGATTC	59.917	20	109	838	946
CCGTGATGCCTGTGAAGTAA	59.716	20	192	2298	2489
GTGCGAGTGTTAACCGTTTC	58.283	20	261	0	260
CGACAATTTTAGAGACAACGTC	59.322	23	213	2507	2719
CTTCTTCCAACGAAGCCAAC	59.853	20	266	937	1202
TGTAGCCCGGTGCTAGAGTT	59.898	20	144	22	165
ACGTTGGACCTGAAAGAGGA	59.697	20	209	166	374
GGATGCCCAAAGTGTACGAT	59.82	20	233	8	240
CTTGTGAAATCAATGCACCG	60.111	20	250	50	299
AGTTCGTCAAACCTCCCAAA	59.569	20	183	259	441
ACCCTAGCCCATGAACACAC	59.851	20	245	513	757
CCACAGCAAACTCGCTAGAA	59.22	20	230	8	237
AGTTGTATACCGCCGAAGGA	59.592	20	209	103	311
TTTGGTTGGGTAGCTTTGGA	60.472	20	277	406	682
ACAATCGTCGGATTTTAGCG	60.096	20	177	2	178
CGGATGGACCGGATGTATTA	60.544	20	252	11	262

GCTCGGTATGCGAGAGAGAG	60.263	20	210	57	266
TACGGCTGCGTAAACTACCC	60.152	20	273	14	286
CCCTAGCCTTTGCCTCTTTC	60.332	20	115	287	401
GCTTGTCTGGAGTTTGCTCA	59.165	20	276	65	340
GCGTACCAAATCATGTCGAA	59.548	20	277	915	1191
CACATGGAATTGCCTGAAGA	59.648	20	276	419	694
GCCATGAACACATTGATTGG	59.781	20	254	150	403
CACCCGAAAACCGAATAAGA	59.931	20	126	393	518
CCATGTGCATTCTTGTTGATG	59.98	21	223	10	232
TAATTAGGGTTGGCTCGGTG	59.953	20	193	136	328
CATCCCAAGCCATACGAACT	59.955	20	252	54	305
ACTTCCCAGCTTGGTCCTTT	60.11	20	257	1250	1506
TTTGAGAGAAATGGACGAGGA	59.799	21	279	424	702
GTTTCCTCCACAACGCTCTC	59.851	20	167	1970	2136
TTGCAATAACAAAACTCGGG	58.674	20	255	63	317
TTCCTACTGGCTGTCCTTCG	60.388	20	194	995	1188
TTTCCTTCAGATGCTCCACC	60.195	20	265	149	413
CAATAAGAAACACGCAACACA	58.796	22	200	221	420
GGGTCCAGACTTGAGACCAA	60.088	20	199	698	896
TGTGCGCTTGAGTGTGTGTA	60.096	20	160	680	839
TGACGTTCTTGCTGCTATGG	60.011	20	147	1625	1771
CACATGTCACGAATCGGTGT	60.45	20	263	119	381
CACCGTAAACAACCATGTCG	59.881	20	237	282	518
GATCGACCAATTGTGTGACG	59.967	20	171	1003	1173
TACGTCCATGGGAGAATGTG	59.369	20	229	68	296
CAATTAGGGCCACATGATGA	59.35	20	258	60	317
GCCCGTCTCTTGGATATGAA	60.036	20	280	5580	5859
ATTTCTCTCGTCACACGCCT	59.874	20	207	947	1153
TGCATGTGATCGTTTTGACA	59.676	20	182	341	522
TGGAGGAAGAAGACAAGATG	59.42	21	187	51	237
TCATCGGATGTCTGAGATGG	59.585	20	208	69	276
TTTTGGTATCAGAGCCACGG	61.021	20	266	73	338
TAGATCACATTTGGCACGGA	60.073	20	145	284	428
GTCTTTGCGGGTGAAAAGTT	59.218	20	242	28	269
TCCAAACCAACAACACCTGA	59.976	20	141	102	242
GGGCGTACGACAATGGTTAT	59.713	20	176	2707	2882
AAGGGACATTTTCTGCTTGC	59.316	20	218	1782	1999
ACCTCTCCCTCTCCTAGCCA	60.349	20	190	1267	1456
AAACCACACCTCCACCTGTC	59.859	20	269	722	990
GATACTCCGGCCAACTGAAA	60.074	20	168	1413	1580
GAACCTAGCCGGAGAAGACA	59.43	20	235	32	266
AAACCTAGCAATGGGGGAAG	60.312	20	119	2535	2653
CTCTATCGCCCTTGCTTGAC	59.978	20	145	15	159
GGTAACACAACTAATTACATA	57.217	27	132	107	238
CTTGGACCAGATTGTCCCTC	59.505	20	228	351	578
GAAAAATATGTAAAATTCACC	57.771	26	173	356	528
ATCCATCCTACACAACCGGA	60.195	20	212	19	230
TAGCATCAGTGTTTGCCGAA	60.401	20	262	1229	1490
TCCCAATTTAAGGGTTATTACC	59.555	24	146	1017	1162
CTCGCTAATTGCATTCTCCC	59.807	20	276	268	543
AGGGCCCTGCAAATTTCTAC	60.451	20	143	1043	1185
CCATGAGCAGAAAATGTGGA	59.648	20	174	668	841
GGTGTGATGATGAATCGTGG	59.769	20	172	42	213
TGACTGCCACAGTTTCCTCA	60.44	20	237	1531	1767
CCACTTGTCTACGGGACCTG	60.557	20	204	319	522
TTGGAAAGCTGGGAAAGAGA	59.926	20	264	346	609
AAGGACCAATGAGATGGGTG	59.779	20	224	90	313
TGAAGGTGACGAGAATGGTG	59.676	20	120	697	816

GGTGTGTGAGGTGTGTGAGG	60.045	20	128	15	142
TGCTCTCTCATTGTAATCTCTCT	59.688	25	252	108	359
AATTGAAATCAGGCTTGCCA	60.585	20	201	1789	1989
TGCTGCTGAACTTCTTGTGAA	59.773	21	231	4751	4981
TGCATATCTTCGTGTGTGCAT	60.158	21	242	133	374
GCTTCTCGAGTTCAAGCGTT	59.763	20	140	303	442
GTTATGCGTTTTGACGGGAT	59.829	20	159	329	487
CAAGATCCAAGGGCTGTGATA	60.081	21	187	708	894
CGATCCGGTCTGATCCAAA	61.978	19	268	352	619
TAGAGGAACAAAACACCCGC	60.11	20	125	1076	1200
ACGAAAAAGGGCATGAAAAA	59.564	20	274	387	660
TTCACACGAGAGTGCAGATTG	60.04	21	197	536	732
GCCAGAAATAGTGGATTTTGC	58.709	21	239	2171	2409
ATTTAAGGGTTATCACCTGATT	58.08	25	185	607	791
TTTTAAAAGGAGACATTGCTGT	57.239	23	226	246	471
TGTTGCAAGTAGTAAAGTAAAC	59.475	25	175	535	709
AAGGTTATCACCGGATCGC	59.909	19	248	1159	1406
TTGTAACCGCTGTTATCCCTC	59.101	21	156	674	829
GGTTTCCACCACCATTGAAC	60.073	20	164	360	523
AACGCATTCTCCATGCTCTC	60.37	20	128	59	186
GTATGATGAGATGGTCCCCC	59.02	20	195	43	237
GGCTGGGATGTCATTCATTT	59.756	20	280	133	412
TCAAATGGTGTGGAAAAGGA	58.947	20	191	360	550
CTGTCCCTGGCTTTGTGATT	60.111	20	257	347	603
AGCTTCACCGGTTTGTTCAG	60.291	20	229	1408	1636
ATGGCTGTTTTCCAATGAGC	60.081	20	172	523	694
AACCGTTTGTTTTGCCCTAA	59.492	20	232	109	340
ATTCAAATCTTAACCGCCGA	59.547	20	268	1273	1540
TTCCGTTTTCGACATCACTG	59.691	20	226	729	954
CAACAGTTTGGCATCAGAGC	59.445	20	211	29	239
ATCTCCAATAGCAACTGCCC	59.154	20	148	582	729
GTACAGTGGTGGTGTGCTCG	60.227	20	200	406	605
GGCTAATTGTTGGCCTTTGA	60.074	20	216	32	247
CAGAATGCAGATGCCTGTGT	59.862	20	156	307	462
GCATTGGTAACTTCCCCCTT	60.187	20	275	18	292
GCACAACTAATGCTTCCTGCT	59.536	21	254	146	399
CAAGATTCAATCCCAGCCAT	59.894	20	138	346	483
AGGTGATTGTGGTGGGTCC	60.649	19	136	54	189
ATGCCAATGCCTCATCCTAA	60.435	20	165	336	500
TATCCCAACAGGAGAATGGG	59.744	20	187	2420	2606
TAACTCTTCCCATCTTGCCG	60.206	20	191	568	758
ACGTAGGATATCACTAAATTGA	57.146	27	275	1171	1445
GTGCAGCCTTATCTCTTGCC	59.985	20	206	94	299
GGGTAGCATATGTCGATGGAA	59.799	21	160	68	227
GCGTTTTGATGATATATAGGTG	58.907	26	186	555	740
TCGTGCACAAAGTGGAATGT	60.16	20	237	844	1080
ACCCTTGAAGAACTCATCCCT	59.056	21	226	2837	3062
TGGCAGAGGTTGGGTAGAAG	60.246	20	215	18	232
TCACTTTGGGAAGGTCGTTT	59.569	20	172	215	386
TATATGCATTGCGCGTTTTC	59.705	20	272	69	340
AGTTTTGTGGTCGAAGGTGC	60.156	20	123	230	352
CTCATTGACAAACCATGTCCA	59.405	21	198	200	397
AAACCCGTGTTCTTCAGTCG	60.149	20	247	28	274
GAGTGGGCATTATGGAGCAT	59.923	20	140	735	874
TTTTGGCTGAGACGAATCAA	59.395	20	183	73	255
GAGGGAAAGCCGATCAATTT	60.399	20	113	197	309
ATCGGTTATTATCGGATCGC	58.88	20	263	1243	1505
AATGCCCCATCTTCAGTTTG	59.933	20	280	54	333

GTTAGCATGGGAAGGGAAGG	60.817	20	203	426	628
TAGGAATCACACGTGGTGGG	61.777	20	242	168	409
GAGGCCCTTACAAAGCATCA	60.214	20	241	1832	2072
CAAGTTTGGCTCGATTCACC	60.636	20	214	1275	1488
ACCAATCTCGCATAGAACCG	60.096	20	267	1304	1570
CACAAATGGAGGTGATGTGG	59.806	20	250	318	567
AGGATGCCCACTGTTCATGT	60.395	20	158	0	157
CCATCGTGAAGAACAGACCA	59.676	20	160	340	499
TGACATGCCATTTTCTTGCT	59.276	20	279	1028	1306
TCTCCCCACTTCACCACTTC	60.088	20	222	142	363
TGCTCTCGCTCTGTCCTCTT	60.431	20	266	121	386
CCCGGTAAGAAACCCATTTT	60.048	20	260	118	377
TGGGAAGAAAGGACAGGATG	60.042	20	185	7	191
TCGAGATGAAAACATTGGCA	60.197	20	218	113	330
TCCACCCATATTGCACTCAA	59.924	20	155	13	167
TGACTGGGTTAAAACAATGCC	59.853	21	132	390	521
TGCAGCTGCTCTAATCATGG	60.119	20	257	1255	1511
GGGGAGTAAAACGACCGAAT	60.187	20	228	77	304
ACAATGGGTGGTTTTTGGAA	60.066	20	279	357	635
TCCAAAATGAGACCAATCTTG	59.546	22	263	149	411
GACCATGCACCAATTCCTTT	59.797	20	221	2032	2252
TCCGGTTAAGTCCGTGATTC	59.933	20	208	1086	1293
GAAACGTACGACGAGTGGGT	60.035	20	171	633	803
CAACAATGCCTTTGGTCTCA	59.691	20	153	327	479
TCCCAAGTCGAATATCTGCTG	60.22	21	180	875	1054
CCGAAAGATTAGGTTTAGCCG	60.095	21	220	113	332
CAGCCTCTTCTCTGGCTCAT	59.703	20	240	727	966
ACCAACTGCAGAGTAACGCA	59.515	20	233	2267	2499
AACTATTTTCATGAAGAGAATC	59.156	26	198	1080	1277
TCAGGTTCGTGTCGTTTTCA	60.278	20	192	165	356
GCCACTAATGCCATCACAAG	59.152	20	125	2103	2227
CCCGAATATTCTGTGCCAGT	59.955	20	239	2563	2801
AGTCAGATGGCGAGAGCATT	59.981	20	258	2496	2753
CCGCTGATGAAATGATCTGA	59.756	20	223	295	517
CTGGAGCCATTTTTGTGGAT	59.933	20	255	19	273
AAAACACTTCGTCCAATGCC	59.978	20	121	382	502
TCGATTACTCCACCCTCACC	59.927	20	234	426	659
CCACCCTCAAACAACACTCA	59.565	20	222	5	226
TAATTACGTCCCGATCCCAA	60.146	20	203	2700	2902
CACAGCAGAGGGAAACCCTA	60.246	20	271	681	951
TGAAGTATCGACGCATTCACA	60.272	21	222	561	782
AAACATTTTCAAAAACGCCA	58.187	20	198	70	267
CCATCACCAACACACCACAT	60.138	20	206	49	254
CCGAATCAAATAGCTCCGAT	59.138	20	205	165	369
CTCTCGGTTCGGGTTGATAG	59.688	20	178	765	942
GCGTGCTGAATCTTATCCGT	60.243	20	257	198	454
TATGGAGCATGATTTGGCTG	59.646	20	265	78	342
GCAAATGCTTCTTACCCATCA	60.089	21	261	60	320
CCGGTAAAAACAATTCGCAC	60.356	20	139	113	251
AGAGAGAGAGTGTGGAGAGA	58.121	24	100	464	563
TTATACCACCGCCACCCTTA	60.202	20	224	932	1155
CTTTACGACCATCCCCAGTC	59.405	20	268	81	348
AAAGCTTGCCGGAAAAACTC	60.721	20	266	19	284
AAATGTTCGTGCGAATGTGA	60.119	20	133	443	575
TCATTCAAAAATTGATCACCCA	60.167	22	146	15	160
TGCGTAAATGGATCCCTGAT	60.296	20	275	2091	2365
AAAACGATGTATGGGATTGAT	58.696	22	223	153	375
AACAATCGTGCTGAAACGTG	59.764	20	280	20	299

CCCATAGACAAAAAGGCCAA	59.931	20	277	189	465
CAAGTTGTATTCGGGTTGGG	60.22	20	107	119	225
AACACCCTGTGTATCCCAGC	59.851	20	229	1	229
AAAAACACCAACACTTCTTGC	59.961	23	276	2322	2597
CCGTTGTACATAAGCGGGTT	59.883	20	271	154	424
GACGAGGGAGAAGAAGAGGG	60.328	20	227	43	269
ACTGCATCACTCTCAAGCCC	60.418	20	221	1019	1239
AAAACTCCGGTGTTCCATTG	59.83	20	110	380	489
TTACGCTAGTCCGTGGGTTT	59.632	20	150	3	152
AGCCCATGTTATGACCTCCA	60.34	20	198	2262	2459
CCAGGTGTTATGACCCGAAC	60.232	20	199	310	508
CACCACCATCACCCTCTTCT	59.962	20	142	157	298
TGCCACTTAGAAAAGTAAAAA	60.101	25	229	329	557
AGGTGAATCGTCAAACGTCAC	60.028	21	134	299	432
CCGTACCGGAAATTAACGAA	59.826	20	253	243	495
GGAAATTCTGCAGTTCGGAG	59.813	20	194	144	337
GGGTCAGCTCTTGATTTCCA	60.195	20	250	216	465
TAGTAGGGTGCAGGGGATTG	59.948	20	238	2378	2615
CCGCTTTGCCTAGAAACATC	59.845	20	279	1370	1648
CCCTTTTGCTCCAAGACAAG	59.846	20	250	456	705
AGTCACAGGATCCAAGAGCC	59.258	20	178	273	450
CATTCCCAACTCCCAAAATTA	58.794	21	244	420	663
AGAAGGAAGAAAGGGGGACA	60.045	20	160	992	1151
ATGAAGCATGCAATTCGACA	60.228	20	236	59	294
TCCACCCGAGCTTTAGTTTTT	60.116	21	179	1996	2174
TGTCTTGTCTTGCCAGATCCT	59.859	21	263	2000	2262
TTTGATGTTCGAAAATACCCCT	59.716	22	151	102	252
ACATGCATGCTCGCAAATTA	60.245	20	134	30	163
GCAGCGTCAAATCAATAACCT	59.242	21	280	266	545
CGTGTGCAATGCATCTGGTA	61.713	20	198	97	294
TGTGGCATCCTATCAACCCT	60.34	20	259	288	546
CCCAACCCAACCACAATAAA	60.452	20	238	489	726
GCCGAGATTTGTTATGCGTT	60.103	20	105	1391	1495
TGTTTGCTTGTAGATGTTGGGT	59.54	22	182	799	980
CATTTGGCCGACTTTAGAGC	59.845	20	211	2647	2857
TGGCATGGGGAAGCTACTAT	59.551	20	229	81	309
TTCTCCCCAAAAGCTAATCG	59.292	20	278	147	424
GCGAAAACTTCTTCGATTGG	59.823	20	178	4	181
TTCGAATCCGTGAAGGACC	61	19	280	138	417
TTGTGTAATTGTGTTGTGTCGT	59.468	23	232	106	337
TCGGACGGTCTGACCTATTC	60.073	20	229	18	246
GTTCTCTCGAAGCCCCTAGC	60.484	20	267	1823	2089
ATGAATTTGCATATAAGGAGG	57.296	24	174	244	417
TGGTGTGAGTTGTACGCATGT	60.088	21	245	233	477
CCAAATTTAAGGGTTATCACCT	58.849	23	245	3668	3912
TTTCGACCGACAAAAAGGAG	60.22	20	184	640	823
CCAAAAGAAAATCTCCTGCG	59.817	20	202	700	901
GCATCGAGCTTAACGGTCTG	60.934	20	234	112	345
AAAATGCAACCAGCATTAAAA	57.417	21	269	492	760
TACCCATTTGAAAATCCCCA	59.988	20	143	161	303
TCATGAGGAGCGTCAATCAG	59.942	20	140	10	149
AGTGCTGCCTCAAAGGGTAA	59.875	20	173	91	263
CGATCCTGTGTGGCCTAAAT	59.955	20	172	160	331
ATACTCACCTTAGCCGCACG	60.292	20	225	928	1152
CACTTAGAGGGTGTTTTGACCT	57.404	22	209	914	1122
TTCCAGATCCAAAATATCCAC	60.02	22	258	260	517
TGGATCATGTAAGGAACAATG	59.738	23	139	26	164
TTCAAGGCATTTGAGATCCAC	60.066	21	279	2273	2551

AGAAGAAAAGACATTCCGGC	58.386	20	120	275	394
GTCAACCATCAGTCCCGAAG	60.51	20	182	250	431
GGTGGATTGTCCTTGATGCT	59.934	20	142	864	1005
AATGATTGAAGATCCCGGTG	59.75	20	160	15	174
TTAAACCCTAAAAGCGCACG	60.251	20	263	222	484
CCCCCTAATCCCTAAATCCC	60.678	20	132	1048	1179
TTCATATGGGGAGCCATCTC	59.854	20	265	0	264
ACGCAACCGTAAAGAACCTG	60.168	20	114	469	582
CCCGATCACCATCACTATCC	60.158	20	280	119	398
TGGTATCAGAGCCATGACGA	60.225	20	277	7	283
GCACGAAGAAGGTTAAAAGG	60.116	21	202	701	902
TATCGTGCGCAATAGACGAG	59.999	20	215	1142	1356
AACTCGATAGGAAAGGATGCA	60.095	22	121	836	956
TCTTTGGGCGTGAGAGTAGG	60.388	20	137	5	141
GTGCGTTGACCAGCATTTA	58.274	19	127	273	399
GCAATCCCATAATGGAAGGA	59.722	20	268	8	275
TTTTGGAGATCTATGGCTGTCA	59.708	22	166	252	417
TGGTTTCCACATTGTCTTGC	59.547	20	242	117	358
AAGTGGGAGTTAGGGCACATT	59.878	21	218	62	279
TTAGGTGTGTGCATCTTGGG	59.566	20	218	513	730
GGTGAACTGCCTTTGCTCTT	59.478	20	232	1485	1716
TGTGGTATACGTTGAGCGGA	60.134	20	156	31	186
GCCGAGATTTTTCCTTCCTT	59.666	20	266	1780	2045
CGGTTATTAGTTATCACCCGAA	59.322	23	150	2871	3020
CATCATCACCTCGTCCCTCT	60.072	20	275	29	303
CAACTTGTCCACCCACACAG	60.039	20	264	120	383
TCCTTCAATCTCAGCCTTTCA	59.94	21	238	975	1212
ACAATTTCGGCTGCCACTAA	60.637	20	188	145	332
CATATGGGCACAGACACTGG	59.984	20	157	17	173
CATATGGGCACAGACACTGG	59.984	20	157	17	173
AAAGGAGCTTCTTGCACTGG	59.615	20	247	1646	1892
TCCCAGAATATCGAAGGCAC	60.036	20	200	287	486
AGGGTTTTGAGGGTTTGCTT	59.976	20	213	478	690
AAATCCCAACAAATGACCCA	60.029	20	176	1155	1330
ATGCAGACGAATAAGCGAGG	60.374	20	184	153	336
GCATCCACCACCATCACATA	60.21	20	182	85	266
CAAATGGGGTCCTGATCGTA	60.713	20	172	633	804
TGAAAGCTAAAATTTGCAATCA	60.892	25	118	12	129
CAAAGGCCCACAATGGTTAT	59.685	20	140	34	173
GACAAAGCAGGCACACAACT	58.935	20	221	130	350
TTGAACGGAATCATGGACAA	59.9	20	166	80	245
TTTGTCTACCAGTTGCCCCT	59.592	20	235	797	1031
GGCATGATTCTGCTGGTTTT	60.081	20	214	1345	1558
GTTCCGCACCAAGATTTGAC	60.504	20	169	157	325
AATGGTCCCCTCATGAACAC	59.636	20	138	8	145
CAACCAGCAAACAAAAGCAA	59.888	20	247	11	257
TTTAGGAAGGATCGGGGC	59.968	18	229	171	399
TCCATTCCGAAAATCAAAGG	59.872	20	155	742	896
TTTTACACGGGACCGTCAAT	60.227	20	266	487	752
AGATGTTGGATCTGCAGCCT	59.834	20	251	593	843
CAAGCTGCTGGTAATCCTCC	59.836	20	242	4235	4476
CTTCTTTAACAACCCCGCAA	60.103	20	232	286	517
TCTTCTTCCACTCGCATCGT	60.945	20	226	875	1100
GCGTCCGACTCCTCAACTAT	59.313	20	101	73	173
TCATGTGCAAATTGTTTGGG	60.357	20	233	340	572
CAATGATGCATGGTTATGGA	57.77	20	253	177	429
TGTGTGTGTGCTCAGCAGTG	60.758	20	234	282	515
GCAGGTAAATATCAATTTTCGA	57.112	23	185	298	482

TCCTCAGATCGATGCACTGT	59.372	20	275	17	291
TACGCACGATGTTGGTGAAT	59.995	20	173	118	290
TCCACTTCTGGGGATTGAAA	60.43	20	226	105	330
CGTTGGAATTTTAGAGTTACGT	60.274	24	110	578	687
GTGGGCTTCGACTCTCAGAC	59.993	20	255	495	749
GCGCGTTGATCTACCAAAAT	60.103	20	278	800	1077
GTGCTGAGGCGTTTCTTGAC	60.986	20	256	32	287
TGTTCGGATTTGGCGATTAT	60.289	20	277	218	494
TCCCTTAATTTCCTCACCCC	60.124	20	174	290	463
TGGACTCCGTGTGTATGACTG	59.606	21	202	479	680
TGGTTAATGCCTACGCTAAAA	58.868	22	153	1119	1271
ACATGATTTGCAAGATGCCA	60.08	20	248	520	767
ATCCGATGTGGGATCGTAAC	59.635	20	196	687	882
TGGTCTTACATCTCCCAGGC	60.073	20	189	1513	1701
AACACGGTAACAAAATATATT	58.491	27	148	214	361
CGGTTTCACCAATGGAAATC	60.17	20	109	304	412
GATCTCTTTTGTCAAGGGCG	59.813	20	117	6	122
GCCTGTCCACAACAATACCC	60.24	20	241	48	288
CCAACATAGGATTGTGCACTC	60.944	22	264	198	461
TTCCTCCTTTCCTCTTATGGG	59.536	21	271	138	408
TCCCCGAATATTCCAACTCA	60.266	20	164	162	325
TGGTGAAAGGAGACGAAGGT	59.697	20	233	94	326
TGAGTGAACATGTGTGTGCG	60.373	20	109	300	408
ATCCAACTCCTGCATTTTGC	60.081	20	274	9	282
CGGTTAAAAATCGGACAGGA	59.931	20	264	1832	2095
TACGGCACCATATAATCGGG	60.548	20	104	91	194
AAAGTGGCCGACAAAAACC	59.963	19	172	662	833
TAGAAATGGAGGTTGGGTGG	59.784	20	118	39	156
TCTTTTCACTCGAGCCCAAC	60.375	20	250	93	342
CGACTGGCAAATACAAAAGTT	57.007	21	248	381	628
TGGCTCCATTCTTCCTCCTA	59.767	20	241	162	402
GGAATTGAAATCCCACCTGA	59.727	20	266	379	644
GCCAAAGCAAACATCACAAG	59.322	20	223	206	428
CTCTTTCTCCCAATGAACCAA	59.157	21	228	1614	1841
CTCGTAACATCCCCATCCAT	59.629	20	268	741	1008
ATTGTTGAAACCGGTCCAGA	60.353	20	199	316	514
ACAATTGGCCTCTCCTCCTT	60.074	20	124	230	353
AGCCTGCATTTGACTTTTGG	60.249	20	188	620	807
AGGAAGGGCGAAAAAGAGAG	59.955	20	228	76	303
TGTTTGGTTTGTGAATTGGG	59.268	20	154	1609	1762
TTCTTCTCCTTTCCGCTGAG	59.688	20	259	281	539
CCACCAAGCAGTGTTTATAGT	59.308	24	212	160	371
TATCCCCTCATGCATTCCTT	59.344	20	250	1640	1889
GATTGGACCATTTGTCCTTCA	59.782	21	229	44	272
TGGTCAATACCAGAAAAATCC	59.315	22	277	177	453
CCCCTTATTTGTGGTTCCAA	59.657	20	251	30	280
CCCAACCAGAGGATTACTGC	59.55	20	266	56	321
CTAGGCATGGAATCCGAGAA	60.17	20	249	107	355
TCCACGAATTTGACACGAAA	60.088	20	159	1465	1623
TGAATTTTGTTTCCCACCAA	58.841	20	125	9	133
TTTCAAAGAATTTGTGGTAGAA	59.119	25	165	698	862
TTGCTCCAGTTTCCTTTTGC	60.365	20	117	52	168
GGTGGCACTGCACAAGTATG	60.183	20	205	66	270
TAAACAAAGCCCCATTTTGC	59.943	20	253	3314	3566
TGGGAAGGATGAAGTTTGGA	60.43	20	118	1201	1318
GGTGCCGGTCCATAAAATAA	59.66	20	261	807	1067
CGTGAGTTTAGGTGGGGAGA	60.103	20	254	32	285
AAAAGTTGAAAAGAGCGCTGA	59.28	21	112	62	173

AGATGGAGGCCGAGAGTTTT	60.212	20	108	1642	1749
GGCAGCAATCAACGACAATA	59.694	20	261	226	486
GGATATCCAAAATATCCGAAA	57.071	22	230	1052	1281
AAAAACGATCATATCCAATTTC	59.268	23	154	156	309
TGCTCTGATCACTCCCACAG	59.98	20	239	867	1105
GTCGGATCTGCGAGATAAGC	59.946	20	232	471	702
ACCCTTGCAAATTATCGCAC	59.967	20	149	362	510
TGCAATATGTCCTTGCACCT	59.152	20	235	2340	2574
AACATGAGCGCACCAACAT	60.136	19	110	23	132
TGTGACAGGAGATGGGACAC	59.502	20	216	13	228
GGCTAATGTGTGGCAGGTTT	60	20	207	1537	1743
TCATCATAACATCTCAAACATT	58.556	25	250	1757	2006
ACGCCTCAACTAACCAAGGA	59.734	20	251	35	285
GGACTTATTACCAATCATCCCA	58.164	23	149	729	877
TCTCAGCTTTCTTGATGGGAA	59.94	21	191	1409	1599
CCCCCAAATTTTACAAGCCT	60.177	20	152	3185	3336
TTGCCTTGGCCCATTTAATA	60.275	20	277	1281	1557
CGTGTTTGTCCATTCAATCCT	59.845	21	180	9	188
TCAATTAACAATAGACTGACG	58.335	23	109	390	498
GGAAAGAGTGTGTGTTTGCG	59.339	20	219	409	627
CCGTCGTATTTTCCCAACAC	60.227	20	229	44	272
TTGTAGCCCCTTTGAGCCTA	59.839	20	238	10	247
ACAACCCCCACGGTTTTAC	59.559	19	264	68	331
ACCATTGATTTGGTTGATTGAA	59.182	22	107	56	162
GACATTGCTAGCACCGAACA	59.871	20	178	92	269
AAAATGTAACAACTTTTGATCC	59.723	25	257	625	881
GTGATGTGGCAGCTTTTCAA	59.847	20	135	114	248
AAGAATGATAGGACGTGCCG	60.096	20	116	31	146
ATCGGAGTTGATTTGATGCC	59.9	20	160	251	410
TTGCGAAATAAATGCACCAG	59.702	20	189	989	1177
ATGCGTTTTGATGATATATAGG	58.042	25	100	706	805
AAACAATGAAATTTGGAACAA	59.68	24	180	3	182
GGCTATCAGCAACAAAACCC	59.574	20	279	1010	1288
CACCCTAAAAATACGCCAACA	59.876	21	219	144	362
TTGATGGGAGGAATTGAACC	59.727	20	168	4713	4880
GGTTATCACCGGATCGCTA	58.534	19	200	117	316
TCTTTCGTGAACTGCTGTGG	60.025	20	260	986	1245
AGCCGTATGATAGTCGCACA	59.326	20	253	131	383
CCCTCTCATCTTTCGACACG	60.791	20	277	1350	1626
ACAGATGAGTGGCAGTCGGT	60.746	20	139	98	236
ATGTAATAGGGTTTGGGAAGG	57.006	21	200	819	1018
CCCGAAGAAGCCATCAAGTA	60.206	20	225	83	307
CATGACCACTCTTTCCTCCA	58.641	20	263	2343	2605
AAGGCAAGTTTCAGACCACG	60.291	20	253	219	471
AGCCATGGATACAAGCAAGG	60.096	20	110	1381	1490
ATTACATGGCTCCATTTGCC	59.791	20	217	137	353
GGTGACAAGCTTATGGACCG	60.517	20	219	132	350
CGGTGTTGGATTGGTGAGTA	59.415	20	122	1120	1241
AAGACGAAGACGACGACGAT	59.874	20	232	524	755
ACTCCTTCACTCCCAGCTCA	59.986	20	204	810	1013
GGCAGCTCATCAAGTTCACA	59.992	20	169	8	176
ATTTCTGACGAAGGCTGTGG	60.255	20	279	10	288
TCTTCACCAACTGTACGCCA	60.301	20	125	751	875
CAATTTGTTTCAGAACCCAAGA	60.362	23	246	4378	4623
AAATGCATGCACCTGATTACA	59.055	21	158	143	300
TCTTTTGCCGTAGCTTGTGA	59.609	20	245	42	286
TTTCCTTTTCCACCAACGAA	60.452	20	213	19	231
TCATATTCCGCCATCTCCAT	60.26	20	184	892	1075

TTTTGATTTTATTGGATTTGTT	58.024	24	279	14	292
TCACGAGCCAAATCTTCCTT	59.813	20	257	177	433
CGGTTATCACCGGATCGC	62.397	18	274	1198	1471
CAATTGACTCCGTCCGTTTC	60.495	20	162	338	499
CATCCAATTTGGGCCATTT	60.517	19	267	23	289
CTTTTCCGATGGTGTCGTCT	60.111	20	197	100	296
AACCCGACACGATATAAGCG	59.982	20	280	301	580
CTGCCTCCATTTCTTGCTTC	59.955	20	242	383	624
GAACTGGATTGGAGACGGAA	60.05	20	241	40	280
TTTGAAAACATGCAAAGGCA	60.229	20	187	67	253
AGGGGTTATCACCTGAATGC	58.864	20	184	162	345
GTGGACGTCCCAGATTGTTT	59.827	20	178	4	181
TGTAAGCCCATCAACCTTCA	59.123	20	239	1416	1654
TGAGCCATGAACACCAACTC	59.682	20	243	302	544
CTTGGGTTATCTTGTGGCTCA	60.118	21	115	21	135
TGTTCCGAAAAGGAAAATGA	58.187	20	166	1088	1253
TTGAATGCAGGGTCTGATTG	59.648	20	137	786	922
AAAAAGCCAAATGAATGGGG	61.011	20	128	21	148
CCAAGCATTATATTCCCCGA	59.751	20	202	906	1107
CGAGAGAAAGAGATGGAGCG	60.232	20	256	41	296
TTTCATGTTTCGGAGCATAATT	59.864	23	226	442	667
TGAGAAACATTAAATGCGGC	58.771	20	228	27	254
AAGGGAAAAGGATAACAGCC	59.952	21	142	290	431
GCTGGTTGACTGTACCAGGG	60.567	20	246	86	331
TCGATATTGTTGTTGCCGTG	60.523	20	277	573	849
GGTGGCCATATGTGAATGCT	60.754	20	250	454	703
CCGCCGTAAAGAAATCAATG	60.448	20	255	98	352
TGTTCAACCTACCTTTGCCA	59.17	20	222	1323	1544
TGGTGCTGATGACGATTCTT	59.245	20	228	124	351
CGAGCTCGAGTTTGAATTTG	58.649	20	224	735	958
CGCCCTCTCCACCTATCTC	59.77	19	169	17	185
ATGGCAAAGAGCAAGTCAAA	58.502	20	253	90	342
TTTGTGTGACCCATCTTCCA	59.935	20	202	2229	2430
GCCATCCACTACACCAAAGAA	59.985	21	267	551	817
AAATGTTCGAAATACCGGGG	60.902	20	101	277	377
GAGACGTGAGAGGGAGATCG	59.945	20	241	422	662
TAAGCTTGCTCCCCCAATTA	59.677	20	166	2798	2963
CAGAAACTACATCGCGCAAG	59.632	20	135	161	295
TGGTCCTTGTATGCATTGCT	59.152	20	274	64	337
ATGTGCATGCTGATAGGCAA	60.251	20	213	1339	1551
AGGTGATGATGGTGGAGGG	60.756	19	105	66	170
CAACATGCAAGCCCTGATAA	59.688	20	243	5	247
TGTTGTTTGGAAAGTTGGAGG	59.994	21	236	642	877
TTTCAAGTTAGAAACGGGGC	59.202	20	251	133	383
TGATCTCATTAAATCAACGGCT	59.983	23	136	97	232
GATCTACGTCCACGGTGGTT	59.851	20	148	38	185
TTGGACCTGCCACCAATTAT	60.192	20	230	738	967
AGCAATATCGATCTCGCAAA	58.483	20	176	79	254
CAGTTAATCGGGCAATCTCC	59.528	20	172	18	189
CAAAGGCCCACAATGGTTAT	59.685	20	146	403	548
TGGCACACTGTCGAGAAGAG	60.178	20	252	37	288
ACACTCACGCACACACACAA	59.818	20	206	103	308
TGAAGAGAGAGCTTCTGTCGG	59.876	21	239	216	454
GTGTTCGATACCGGGTTCTT	58.912	20	245	97	341
ACACCCCACCTCATTTTCAA	60.21	20	236	180	415
TTGGTTTTGAGATGGAACCAC	59.822	21	168	6	173
TGCAAATACGGAAAATTTGAC	60.347	22	280	681	960
CTTTCTACCATGCAAACCCC	59.429	20	280	312	591

CACCGGAGTTTTACGTGGTT	59.891	20	241	65	305
TGATCCATTCCGACTTCCTC	60.011	20	248	119	366
TCCTCCATCAAACCATTGTC	58.331	20	274	2329	2602
TGAGCTATAGTTGGAGGGTAG	59.845	24	175	6284	6458
TGGAGAAAAGGAGCTGGAAA	59.926	20	213	1316	1528
TTTAGGTGCATCTCTTGACGA	58.515	21	209	142	350
GTGATTCATGGCCGAGGTA	59.466	19	246	52	297
CTAATTTAAGCCCCATCCCC	59.637	20	235	168	402
TCAATTACCCTCAAGACCCG	59.926	20	263	50	312
GAGAGAAAACCGAGAAGCGA	59.694	20	258	43	300
CTTAGTGAAGTAGCCGCCCA	60.399	20	221	2	222
CAGATCGAGATCGATTGAAGC	59.931	21	260	21	280
CGCGTCAGATTTGTTATGTGT	58.715	21	253	90	342
CCTGGTGTGTTGGCATTCTA	59.566	20	186	0	185
ATTTGCGCGTCAATTACGTT	60.517	20	247	1831	2077
AGGGGTCAAACCTCCACTCT	59.968	20	210	129	338
GCCAAAAATTGTCATCCACA	59.375	20	226	127	352
AACTGGGCCATGATAGGTTG	59.813	20	243	3	245
GACTCCCTTCCTCAACTCCC	60.05	20	223	524	746
TACCTGGAACGCATCACAAA	60.111	20	279	3631	3909
ATTCTCCGCTGCAAACATCT	59.843	20	166	707	872
TACCTAATCTCCCGCCCTTT	59.924	20	278	147	424
GGAGGAGATGAAACGACAGC	59.81	20	108	148	255
CACATCAGAAGCAGTGGAGG	59.415	20	255	80	334
CTTCTTGAGACACAGAAGCAT	59.671	23	266	107	372
GTTCCGTGTCGGCATAGACT	60.142	20	142	2338	2479
TGCATCTTGGAGGTGAGTAGG	60.262	21	231	25	255
TGGTACCTCCAACAAGAGGG	59.959	20	195	171	365
AAACACTGCTGACTGAAGCG	59.239	20	263	509	771
CACCCCTTTCCTTTACCCAT	60.046	20	248	164	411
GTTGTAGGCAAAAGGGCGTA	60.131	20	168	357	524
TATTGTCATCCACGCAAAAA	57.635	20	266	104	369
AAAAGACATTCCGATGTGGG	59.79	20	235	477	711
TGTCATGTCCACCTCATTCA	58.389	20	181	501	681
CATCCAAGACATGATCGCAC	60.08	20	244	43	286
TAAACCCCAACACCTTCGAC	59.83	20	245	406	650
CTGGAGTGTCAAGCTGGGAT	60.261	20	195	106	300
TTCGAGGAAGTCGAGGATTG	60.331	20	222	25	246
GGTCGGCGTCTATTTCGAT	60.051	19	209	204	412
AGATTATGTCGTGGATTTTGAA	59.778	24	251	55	305
CACCCTTTGAATTTTGCCTC	59.546	20	137	151	287
CCTGGGAGATTGCTTGAGAC	59.803	20	124	1	124
TCTGAGAATTCAGCAACAAAC	59.934	24	276	320	595
TGAAAAACATGGATCCGAAA	58.94	20	223	25	247
AGGCACAATAGCCACGAATC	60.103	20	255	250	504
CGAACTTGACACGAACACGA	60.906	20	269	357	625
GAAGAGGGATATTCGGAGGG	59.859	20	212	389	600
TTTGGGGCTACGTGTTCTTC	60.11	20	248	45	292
AGAGAAACTGGAACCCCCAC	60.349	20	259	44	302
CGGTTATCACCGGATCGC	62.397	18	250	836	1085
TAGCGCATTTTTGCCTGATA	59.447	20	229	903	1131
TTTTGCATGCTCAATAAAATGG	59.968	22	253	1266	1518
AGGGGTGTGTTAATGATGGG	59.526	20	209	232	440
GAATTTCCCAGTTCCAACCA	59.767	20	137	865	1001
TGCAAGATCCAATGGTTGTG	60.517	20	280	462	741
TAAAGGTGGAATGTCGTCCC	59.79	20	181	1923	2103
CTTGCCATCCTCCTCCAATA	60.029	20	222	1782	2003
CAAGCAACAAATCGAGCATC	59.425	20	160	695	854

TGGAGATTGAGGAAAATGGG	59.864	20	192	1048	1239
AGTTTTGAATGGCTTGGTGG	59.971	20	248	585	832
AGGGAGGTGGTTGATCAGAA	59.505	20	277	124	400
ACGGCTGTGTAGTGTGTTCG	59.819	20	143	598	740
AAGCAAAAGCTGAGGTGTCAA	60.045	21	247	11	257
TAAAAATGACCCTCGTTCGG	59.931	20	252	0	251
CTTCAAGCCCGCATTAAAAC	59.72	20	211	19	229
TAGTCGGCCGATAAGTTTGG	60.089	20	203	822	1024
GACCTACGTCCACTGTGCAA	59.751	20	278	27	304
CGACGTGGAATTTCATGGTT	60.755	20	225	18	242
TCATGTCCGTCCATTTTGAA	59.9	20	227	659	885
CCCTCCCCTCTCACTTTCTC	60.186	20	150	1755	1904
AGGCAAGCCTGTGGTAGTTT	58.865	20	152	51	202
AAATCCATCCCATCCACGTA	60.014	20	209	303	511
CACAGCCAGCTAGTCGGTTT	60.453	20	167	161	327
ATCGACCCTAATTCGAACCC	60.152	20	270	1196	1465
TGCATGTGAGTTGCACTTGA	60.029	20	216	449	664
TTTGATGCAGCAACCATAAG	57.383	20	279	57	335
CATTGATTGATTCACAGCCCT	59.947	21	228	148	375
GAAAGTATGGCTGCTCCTCG	59.978	20	248	1832	2079
TTTGGGTGTTCTGTACACGG	59.46	20	233	114	346
GGGTCTCGCATAAAGTGGAA	60.074	20	273	129	401
TGATCTTGCTTGGTTGCTTG	59.988	20	158	2146	2303
CACATGTGGAGAGCTTGTGC	60.473	20	207	559	765
CGATGTCACCATCGTTGTTC	59.967	20	268	1746	2013
AGCTTTGGGCAAACATCAAT	59.574	20	261	27	287
TTGTTAAAGGTTTCGACGGG	59.968	20	102	10	111
GCCAAGACTAGAGGCTGTGA	58.187	20	111	277	387
AGTCTCGTGCGTCTCCAGTT	60.057	20	231	295	525
TGCGCGATTTTAAACCCTAA	60.564	20	269	1579	1847
TTGCAAATTTTCGGTAAGCA	59.328	20	131	407	537
GAAGATGGAGAGACGGTGGT	59.105	20	275	220	494
TGCCAATGGAATAGTGATCG	59.499	20	273	1660	1932
CCCACACTCACATGTACAAAC	60.244	23	152	324	475
ACTGGTTTTCTACCCCAGCC	60.361	20	273	36	308
TCGAACATGTAGTGGTCAAAC	60.081	23	194	293	486
TGAACAATGAGATCCACAATC	58.976	22	280	423	702
TTTTACCTTCTCCAGGGCAA	59.679	20	263	4236	4498
ATGTCACTGCCTTGCCTCTT	59.874	20	226	607	832
CGACACCGAGGTAATGAACA	59.566	20	167	742	908
CCACCGGATATACTCCTTCG	59.406	20	206	588	793
ACCCGAATTACCACCCCTAC	59.94	20	272	1896	2167
ACACACGAACACTCACCCAA	60.047	20	198	69	266
CGGCTACCCGATTCATTAAG	59.564	20	173	60	232
TTGCCTTTTGATTTTCGGTC	60.053	20	280	697	976
TGCAACCAAGTTGTCAACCA	61.159	20	252	65	316
TTGACTGAACTTCACCCATTT	57.16	21	123	251	373
TCCTCCTCACGAGTTTGGAC	60.238	20	243	377	619
AGACCGGAGTAGATGACCTTC	57.321	21	105	363	467
GATTTTGACATCAAGATAAGG	58.262	23	220	408	627
AGAAGTAAACCACGAGGCCA	59.734	20	227	33	259
TGTCCTCAACTGAAAGAATGC	57.937	21	268	1679	1946
TTCAATGCTTGTTGTCGTCC	59.697	20	231	76	306
GATCGGAGCTGAGAAAGCAG	60.24	20	229	854	1082
CGCCATTCTCTCTCTAACCTG	59.087	21	162	288	449
ATGACCTTGAAACCCCTTGA	59.381	20	275	2717	2991
CACCAACAGCTTGTCGAATG	60.301	20	161	1881	2041
CAAGGGCCGAGATTTGTTAG	59.702	20	213	1366	1578

ACCATCCATTCCGAAAATCA	60.133	20	182	176	357
CTTGGCTCCGGGTTGTAGTA	60.125	20	277	322	598
CATCGGTTCATGTCACTTGG	59.96	20	186	4	189
TCTGAGATGTACACTGCGCC	60.016	20	156	21	176
CGTAAAGCCCAATCGAGTTC	59.708	20	226	17	242
TTTCTAAATGGTGGCCGAAA	60.427	20	173	445	617
CAACGGCTATTTACATGGGG	60.202	20	255	692	946
TGCATGCTATACGGCACTGT	60.31	20	222	2774	2995
CTAATAGCAGGCAAAATGCG	58.609	20	240	3	242
TCAATATTTCCCAAACTCGGA	59.397	21	195	11	205
TGAAAAATTCAAATAGGAATAT	59.643	25	257	14	270
CAAAATTTGGGGCAAAAA	57.057	18	276	743	1018
ATTTTTCTTTTCGGTTGGGG	60.157	20	123	6149	6271
TCTTCCAACTCCCAGAGGAA	59.773	20	265	130	394
CAATTCCCAATCGAGCTGTT	60.074	20	156	1788	1943
TCAAAATCAAGTCTTCCTCCG	59.298	21	199	340	538
TAATTGGACCTCGCGAAAGA	60.712	20	277	23	299
GGCAAGACATGGTGTTGTTT	58.47	20	277	833	1109
TGTAGGGGACTCGCTTCAAC	60.255	20	178	64	241
GGGTTCCAGCGTCATAAAAA	59.938	20	278	316	593
TGGGTGATCTGAGAGGAAAAA	59.656	21	249	517	765
CCTCATCTGTTGTAACCACTAT	58.2	24	270	390	659
TGTTTGCGAGTGAGAAGGTG	60.025	20	243	1078	1320
TCACGCTAAGGGGTGGTATC	59.955	20	163	395	557
TCCGTGCATGAGAGAGAGAA	59.656	20	114	1666	1779
AGTCTGCCATTCTTGCAACC	60.263	20	225	434	658
GTTGCAGGTTGATCGAGGAT	60.081	20	211	83	293
GAGGACACTTGGACCTGGAA	60.088	20	265	745	1009
AGGCTTCGTGTCTCTGTGGT	59.907	20	205	90	294
AATTGAGGGAAATGTCAGCG	60.074	20	188	1718	1905
CTTTTCTGTATTGGGGCTGG	59.564	20	236	467	702
GGTGGAGGAGGGTATTAAGAT	60.546	23	119	568	686
CCTCTGGACCGACCATTTTA	59.926	20	210	463	672
CGCAGAATCATGAGACACAAA	59.856	21	235	17	251
GCTGCTGTGTTTGTCTTGGA	60.032	20	216	292	507
TTGGGTGAGAGAAAGATAGAT	58.914	24	239	447	685
AAATCCAGCAGGCAGATCAC	60.226	20	231	658	888
TTGGTCCACCAATCTTGTGA	59.935	20	254	900	1153
AAATCTGGGCCCTTAGATCG	60.411	20	214	19	232
ATCGTGAGGAGCGTTGATCT	59.834	20	238	354	591
TGATTTCAAAACCCGCTGTT	60.481	20	264	265	528
CATAATGCCTTCCCGTGACT	59.955	20	208	117	324
ACAATGATGGACACATGGCA	60.829	20	142	539	680
ACGCCATTGATGGAAGAAAG	60.074	20	154	134	287
ATCCTTGCACCTCCTCTTGA	59.803	20	275	2184	2458
CCACTGCTGTCAGCTCAGTC	59.764	20	241	270	510
GCACAACAATCTGCAATCTCA	59.862	21	231	1054	1284
CGCGTCCGACTCCTTAACTA	60.399	20	272	107	378
TGAAGTTTGGCAAGGAAACC	60.088	20	227	138	364
CTTGGCTCGTTAGACATGGG	60.647	20	206	95	300
ATGCAATTTTTGTGGGCAAT	60.196	20	151	863	1013
TCAGCATGATATTGCGGAGA	60.329	20	160	83	242
CAACAAATTCCAATGAAAGGG	59.302	21	254	122	375
TCACATTCAACCTCAGCGAA	60.39	20	247	1286	1532
CTCTCTCTCCTGATGCAGCC	60.246	20	240	2651	2890
TTATGTCGAGGAGGACGCTC	60.362	20	241	3047	3287
TGGGCTTTGTCAAGATTGTG	59.691	20	277	809	1085
TTCCAGCAATGGAACCAAAT	60.309	20	278	971	1248

TGCTGTGGACACGTTCAAAT	60.16	20	249	24	272
TGGGAACATTATGATGGGAAA	60.002	21	218	632	849
GCTCGAACGAGCCTATTGAA	60.49	20	214	1694	1907
AAAAATGACACCCGGTTGAA	60.206	20	270	327	596
CACGTGTAATTAATTCGGTTAC	60.057	24	267	28	294
GGGAATTGGCCCAAATAAGT	60.02	20	261	52	312
CATCAGTCTACAGCCAGGCA	60.008	20	243	740	982
GCTGAAACCAAGGCAAAGAA	60.365	20	183	261	443
TTGATTGGTCATTCCTTTCATT	58.418	22	159	103	261
ACACATGTCGCCTTCTGGTT	60.577	20	198	34	231
CGAGGAATTTGAAGAACACTT	58.88	22	250	1406	1655
CACCCCGAGATGGTAGACAT	59.803	20	216	163	378
TTGAACTCACGATCTCACGC	59.992	20	159	31	189
GCATAAATTGTGTTCCCCGA	60.701	20	276	175	450
GTTGGAGGAGAGCTGTAGCG	60.156	20	233	28	260
CAGGTGACGTTGGCAAACTA	59.758	20	253	21	273
ATGGGAAGAGGGGGTATGAG	60.147	20	240	1276	1515
TGAGGGAAGGAGAGATCGAG	59.48	20	248	151	398
GGTCAAATCGAGATGCACAA	59.654	20	202	778	979
AGGAAGAAAGAAGGGGCAAA	60.18	20	180	81	260
CATGGCTGGATCTTGCTGTA	59.823	20	230	2376	2605
TGACGGACCTTCATTTTTCC	59.91	20	206	508	713
TGAAAGGGACACGTGGAAAT	60.353	20	126	1381	1506
GGAATGGTGTGGGGAATATG	59.871	20	138	818	955
CCGTAAAAGAAGTCGTTGCC	59.747	20	223	183	405
TCACCATCACTGACTCTGCC	59.827	20	225	88	312
GGCCCCTCTACTCCTGTGAT	60.477	20	105	281	385
TGTTTCCGGCAACTTTATCA	59.157	20	199	410	608
TGATTGATTAATTCGTTTGTTA	60.124	26	215	125	339
CATGAAGGAAAAAGTCGGGA	60.044	20	240	79	318
GCTTGCCCTCATTCATGTTT	60.081	20	185	291	475
AGCTGGCTCAACTACTCCCA	60.012	20	262	2677	2938
GCTCTTGCCCCTTTCTCTCT	60.096	20	274	107	380
TTGAAGAGAATCCACTCGCC	60.34	20	254	594	847
TGTAAAGTGAACAATGGAAGC	58.346	22	215	4964	5178
TTTTGCCCCAACATGCTAGT	60.502	20	241	959	1199
CCAATTTGAATGGTTATCACCT	60.457	23	122	1267	1388
CTCAGTATGGACAGTGGCGA	59.855	20	174	241	414
GTTTTCGTTGTTTCCAGCCT	59.218	20	241	2201	2441
TTCAGTAACTTCAGTGGGCAA	59.785	22	252	4369	4620
GTGGGGTAGAAGGCAATGAG	59.55	20	259	50	308
AACATGCACACAAGCACACA	59.785	20	265	164	428
GCACCATTGCTACCTCCAAA	61.032	20	151	270	420
CAGTTGGACTTTTCGCTTCC	59.853	20	258	526	783
GCTTCAGCAAGGAAGATGCT	59.723	20	145	1414	1558
GAAACCCGTGAACTAAACGC	59.615	20	148	699	846
TGTGAACCTTTTTCAGCCGT	60.668	20	190	1442	1631
ATCCAACGTTGTAACACACAC	58.877	22	135	4	138
GTCTCCACCTCCATTGAAGC	59.661	20	261	284	544
GGAGGGGAGGAAAGAGAGAG	59.367	20	161	45	205
GGCAACTTTTGATTCTTCTCG	58.962	21	255	4357	4611
CCCAATAACTCGCAATAGTTT	58.698	22	203	412	614
TCACAATATTTGAGGGTTATCA	60.337	26	213	255	467
TCCAATAACTCACAAAACTTTA	57.144	25	184	270	453
ACTGACCTGCCCAACAGAAT	59.579	20	260	3220	3479
CGTGTACTCTGCACTGAGGC	59.648	20	158	416	573
ATCCCTCGACTTTCCCCTAA	59.897	20	188	1799	1986
CATGTTCCCAATTAAATAAATG	60.219	26	268	93	360

AAAGAAGGACCTCCCGTGAA	60.988	20	166	710	875
TCTGGTTTTTGCTGGTGATG	59.691	20	211	46	256
TTGATGGTGGTGGATATTGG	59.049	20	207	450	656
CAGTTTCGAGTTTTGAAGTTAG	60.193	25	167	150	316
TACTTTGCCACACAAGGCTG	59.904	20	113	1028	1140
TTGATAGGGCCGAAAACAAC	59.938	20	158	4	161
AAACAATCTGGTGCGTCCAC	60.966	20	258	3	260
GTGGCACCAATCAACTCCTT	59.973	20	190	435	624
TTGGAGAACAGGTAGCGGTC	60.255	20	154	36	189
TACGGGAATGCACCAAGAA	60.057	19	115	89	203
GCCCACCATTTATCTAAACCTG	59.737	22	210	95	304
TTTCATTTCCACCTTCCACC	59.767	20	166	387	552
TCCCAAAAGAGTTGGGAATG	59.903	20	274	6	279
GACAGTCAACCCACACATGC	60.013	20	220	627	846
TGAACCTCCAGGGAAGAAAA	59.641	20	279	385	663
AGCCAACACCTACACCAGGA	60.567	20	183	2977	3159
TACGATCCGATCCAACGATT	60.296	20	175	3	177
CCCAAATTCAGGCTGTTCAT	59.933	20	184	3	186
CCTCCCCGTATCGATTATCA	59.739	20	280	50	329
AAATGATCCTTCAGCAACCG	60.074	20	280	1102	1381
GCGCCTTGCATGTATGATAA	59.691	20	249	16	264
CTATCCGCTGAAAAGCATCC	59.807	20	203	79	281
TGTCCACGGCTCCTAAAAGT	59.734	20	280	1160	1439
TGGAACAACACTTCAACAACG	59.643	21	279	4149	4427
TTGCTAGAGGGTTTTGTTAATAT	59.891	27	115	1167	1281
TTGGTGGGAGATTGCTAGAG	57.894	20	151	145	295
TGTTTAATCAGGTAGAAAGTTG	58.854	25	234	1114	1347
ATGCGGCGCCTTTTTAAT	60.557	18	272	142	413
CTTCTTCCCCAATCCTCCTC	60.008	20	249	1574	1822
CATCCCATCACTACCCCATC	60.011	20	115	135	249
TTTCCCAAGGATCAGACGAC	60.05	20	258	1970	2227
CTTGCTCGTTTTATCCCTCG	59.839	20	242	410	651
GTCTTTGACAGTGGAACCCC	59.405	20	264	2	265
AATTGGACACATAGTTCATGCC	58.839	22	155	49	203
CAGAACTGCCCTCGGAATAC	59.694	20	237	115	351
AAGCATCCCGAACTCTTTCA	59.813	20	244	104	347
CATCTTCTCATCTCAACTCCCA	59.284	22	277	2	278
ATGAGTGGCGTCTACGGAAT	59.579	20	182	58	239
TGCCAAGTGTGTTGAACCAT	60.008	20	242	11	252
TGTTGAAGAAGCACAGGCAA	60.574	20	246	101	346
CGCGAGTTACTTCCATCGTC	60.796	20	133	227	359
CCGGCATCATCTGCTTTTAT	60.06	20	224	90	313
AACCCGAATTCGATACAACAA	59.329	21	135	65	199
TTTACACAATGCCGACTCAAA	59.216	21	154	34	187
ATGGTCCCTACAGCAACAGC	60.142	20	277	2202	2478
GATCGTGAATGATCTACGTCCA	59.962	22	196	157	352
AATTCCCCATGACCCACAT	59.854	19	277	88	364
GAAGAACACCCCATACGTGC	60.384	20	275	132	406
TGTGCTAGGGTTTAGGTGGG	59.986	20	166	43	208
TTTGGCTGATTGAATTTATGGA	59.433	22	186	669	854
AATCGATTACTCCCGCCTTT	59.93	20	211	91	301
GCGGTCCAGATCTGCTACTCT	60.938	21	178	313	490
AAGTGAGGATCGTGGAAGGA	59.655	20	116	2	117
TGCACACGAGCTCAATCTCT	59.733	20	226	211	436
CATCTGCACCAGCAGTCTGT	60.055	20	234	711	944
AAAGCAATGGCGGATACAAG	60.096	20	202	66	267
TTTGCCCTTGTGGATTGATT	60.309	20	249	2243	2491
TTTGGGCTTTTAGCCTTCAT	58.831	20	216	658	873

GGGATTTATTTTGGGGTACA	59.774	21	123	341	463
GGCCTTACACAGTGGCTCTC	59.874	20	213	114	326
TGATTTCCCAGCAAAATTGG	60.807	20	139	4	142
GGGAGGTGGTTCGAGTTACA	59.966	20	264	188	451
GCGGTCCAGATCTGCTACTCT	60.938	21	184	327	510
TCCCTGGGATTTTCACTCTG	60.042	20	161	112	272
CCAGTTGGTGGACCTAAAGC	59.592	20	224	1821	2044
AGGCGTGGTGATTATTCCAA	60.331	20	223	854	1076
AGGCTCTGCATGCTCTTTTT	59.222	20	168	13	180
CAGTGACATGGCCAAAACTG	60.152	20	194	3	196
CGTAAAAATGGTTATTACTGGA	60.066	25	261	440	700
TTTTGGCTGGGGAGATTAAG	59.155	20	223	117	339
AACCACAGGATCGAAAAATGA	59.42	21	251	473	723
CGATAAGGGCCTAGAAAAACA	58.397	21	111	15	125
CCTTTTGTGAGGACTGAGGG	59.691	20	121	1588	1708
TGGGTTTGATTCCCAAATGT	60.029	20	261	224	484
AATTCATGGCTGCGACTTTC	60.221	20	273	260	532
GGTTCGGTGAGATCAGCTTC	59.81	20	197	321	517
CGCTTCCGGAGTGGATAATA	60.053	20	169	75	243
ATCTCCGTTCAATGCTTCCA	60.603	20	261	0	260
GGTGTTGGGAGTTGCTGAGT	60.159	20	183	266	448
ATCGGTCAAATTCAAACTCG	57.67	20	240	1332	1571
TTGTTGGGTTGTTGGTGTTC	59.288	20	280	256	535
AGGTCTAGGCCCCTCAAATC	59.536	20	127	1140	1266
ATCGAACTCTTGCGTTGCTT	60.022	20	130	45	174
ACGTAATTTGGCGGTCTCAG	60.132	20	270	521	790
TCCACAAAAAGTGGGTGTGA	59.976	20	142	37	178
CGACCTCCCATTTTCGTTTA	59.931	20	139	22	160
GCTACCCCTCCCTACACCAT	60.212	20	214	589	802
CTTTTCACACGAGGTCACGA	59.873	20	257	24	280
GTGCAATCCAGTGAAAACTCT	59.78	22	191	48	238
TCATGTTGCATATTATTTGGCAT	59.256	23	242	59	300
AATTTCCCACCAAACAGCAA	60.344	20	192	533	724
ATCCGGCGCTCTAGATACAA	59.829	20	124	234	357
CGTGCTCACCATGAAACCTA	59.716	20	257	1109	1365
GGAGTTGGCACCAGATCACT	60.12	20	276	1303	1578
TCGTCACTATCTCGTCGTGG	59.855	20	231	1147	1377
AGCGGTTATTACCGGATCG	59.93	19	156	486	641
TGCACCTTCCACGAATCATA	60.073	20	153	27	179
CAAGGCTTGAAGCTGGTAGG	60.008	20	247	81	327
AACAACGGTATCACCTGAACG	59.906	21	203	3938	4140
CCTTTCGCGTGTCAGAGTTT	60.431	20	152	3	154
CACGGTTAGGCTCGAGAGAG	60.149	20	184	51	234
TGTGTGAAGGTTGAGTTGGC	59.726	20	253	15	267
CGAACTTGGGTACACTTGGG	60.401	20	218	11	228
GGCTGGGTACCAACTACACC	59.333	20	163	478	640
GCACGCGGAAGACTAAAAAC	59.889	20	275	20	294
GGTCTCACGGGCAGTTTTTA	60.11	20	208	1882	2089
TTCTATATAAAACGAGACCAAA	58.838	27	172	160	331
CGGCCTTCAACTCTACCTCA	60.388	20	207	2095	2301
GGGAGAATCGAGATTTGTTTTG	59.945	22	275	270	544
GGGGTTCATCCATTCATCAG	60.135	20	231	22	252
TTGTTGCCTGATCGATCCTA	59.226	20	119	369	487
ACATGAAGCGCTGATTGTTG	59.871	20	206	1376	1581
TGGTAAATATCCTCCGGTGC	59.784	20	197	91	287
TAACTTCCAAAATGCCTCCC	59.019	20	259	799	1057
GCCCGTGTGCATCACTACT	59.723	19	132	550	681
GCACCAAATAATTCGACTTGC	59.605	21	274	163	436

CGAGCTTCAGGCATTAGCTT	59.752	20	186	772	957
GCATTGATGGGATTCCACTT	59.756	20	207	1090	1296
CTGCAGCTTCTTCACCTCCT	59.745	20	234	304	537
GGTGGGTGCAACTTTCTAGC	59.74	20	166	7	172
GGGTTTGGAGGGGTATCCTA	60.011	20	230	125	354
CGACGGAACCACCAATTTTA	60.722	20	164	8	171
GATTTGCGTGGTCCATTGAT	60.733	20	265	6	270
TCAGCCTCCATCAATTATCAA	58.174	21	163	183	345
AGGGGTGACTTCATGGAATG	59.779	20	228	1915	2142
TCCGAGTTTTGTTGAGGACA	59.262	20	222	169	390
CATGCTGCCGGAAGTAATTT	60.096	20	262	150	411
TGGACATATGGAGGGAAGGA	60.272	20	257	829	1085
TCCCTCTTGAGTGAGCTTTGA	60.119	21	272	2527	2798
AAGAAGGGCGAGCTTAAAGG	59.98	20	183	1221	1403
ACCAGGCATCAGATCAACAA	59.09	20	263	146	408
ATGGACTCCGAGGATGATGA	60.439	20	224	33	256
AATTCGGGTTTGAGCTGCTA	59.845	20	231	1760	1990
TTGTCCGAAACTTCCCTCAC	60.088	20	274	1642	1915
CCGACCTCGGTAAATGCTTA	60.089	20	227	605	831
TTGGTTGGGGTTTTGTTTGT	60.103	20	168	503	670
TCCAATCGAAGATTCGGAAC	60.014	20	206	94	299
TTTGTTAGAGATCTTGACGGGA	58.834	22	203	961	1163
GTGTGTGTATGAGAGCCGCA	60.907	20	191	1350	1540
TCTTGCAACTCCTTTGGAGC	60.517	20	265	3	267
CTGGCACATCTGCAGTTCAT	59.862	20	251	264	514
AGTCGAAGCTGTGGGAGATG	60.408	20	242	646	887
GTGGATGGTCCTCAGCTGTT	60.12	20	192	279	470
TGTGGAAATTATGGTTCGCC	60.701	20	248	796	1043
TGCGTTTACATTCAAGCAGTG	59.926	21	100	43	142
CTTCTGGCTTCTCTTGCCCT	61.027	20	112	36	147
ATTTCGAAGATCAACGGACG	60.074	20	115	61	175
GTCTGTTGATTCATCGCCAA	59.654	20	279	106	384
CCCCATTAGCTTCATCCTCA	60.029	20	236	780	1015
ACTTCAAATTTTGTGCCCCA	60.344	20	133	191	323
CAATACAACTGCCGAGCTGA	60.011	20	106	80	185
ATGATCGCTCTGTTCCGATT	59.658	20	274	682	955
GCAACCAGGTACTCATTGGC	60.526	20	165	776	940
AACCCCAACGGACAGATTTA	59.288	20	173	1832	2004
TTCCACCTGATCCTGGTTTC	59.903	20	168	2082	2249
TTTTCATTCATGTTTCGCCA	60.051	20	246	655	900
GCACTGAGGCAGAGTACACG	59.648	20	133	1596	1728
GATAAAACAGGGGAAAGGGC	59.777	20	152	167	318
GGCATTTGTATACCCGTTGG	60.074	20	177	101	277
TCCATGCAAGGCTTTCTTCT	59.955	20	143	473	615
TCCATGCAAGGCTTTCTTCT	59.955	20	139	325	463
TCGACGATCACAATTTGTCC	59.502	20	197	435	631
CCCAAATTTTGACCATTTCCT	60.041	21	176	0	175
AAAACACATATGGTGACACGG	59.149	22	224	1285	1508
TGGCTGGAGAAAGTAGGAGG	59.425	20	150	2593	2742
CCCATAACTCCAAACCCAAA	59.657	20	275	46	320
TCACATGGAAACATGTGGCT	59.967	20	186	181	366
GGGAATTTAATTTCTGGCCC	59.621	20	143	2669	2811
AGACCAAAAAGCTGGGTGAA	59.711	20	195	279	473
TCTTAAAAGGGAGGGGCTAA	57.95	20	280	138	417
TCGGTTTAGGTATTTTGATGTTT	60.465	25	137	83	219
TGTCCTTAAAATGCAACCCC	59.801	20	209	117	325
TGGTTACAAGCAGTGGCGTA	60.316	20	163	3	165
GACATGGATTGTGCATTCGAC	61.338	21	280	32	311

AGGGGAGTGATCTCATGTGG	59.92	20	251	157	407
TGCTGCTGATTCACATAGCC	59.979	20	279	45	323
CCATGGCAGATTCATCCAG	60.015	19	196	165	360
AATCCCACGATTTTTGAATCC	60.013	21	262	1561	1822
GTATGTGTGGCTGTGGATGC	59.999	20	271	27	297
CCTATGGTGGTATGGTGTGG	58.569	20	191	4	194
TCTACCACTCCGAAACCTCG	60.246	20	181	139	319
AGCGAGTGGGTGACAAAACT	59.769	20	170	129	298
TGGTACCTCCTCCTAATTTCCT	58.163	22	181	258	438
TATGATGGGAAGGGTGGGTA	60.006	20	262	1167	1428
AGCGAATGTTGTGAGAAGCA	59.596	20	243	24	266
CTCGACACAAATCTGCACAA	58.409	20	212	298	509
GGTTTTTCGGTTTTCGGTTT	60.197	20	183	178	360
ACAACTCTCAGCCATCACCC	60.12	20	259	627	885
CTGCATACGAGCATGGAAGA	59.972	20	275	586	860
TTGAGTGCGTGTGTGAGTGA	60.07	20	255	133	387
GGAAAATTGGGAAGGGAATG	60.482	20	164	3705	3868
CAAACGCTAAACGACACCAG	59.386	20	279	2	280
AAGTTATGCTGGTGGTTGGG	59.853	20	262	345	606
ATGCTATGGATGCGTTGACA	60.104	20	108	171	278
TTTCAGGCAGTGGCATTAGA	59.42	20	166	167	332
GTTAACTGGGTGATCGGACG	60.375	20	177	25	201
CTCCATTTTCCCTCCTCCAT	60.264	20	278	470	747
TGCATGATCGATATTGTAAGGA	59.468	23	172	68	239
CATGCGACAGCATGAAATCT	59.83	20	193	192	384
TCCATTTCCTTTTTCGATTCC	60.246	21	199	994	1192
GATTTTAGGTTTACCGGGGC	59.68	20	253	14	266
TTGACGGCCCTAAACAAAAC	59.975	20	215	173	387
CTCCGCCTTGACACCTTCTA	60.388	20	163	0	162
TGTGAATCAAGTACCCCGAA	58.973	20	192	159	350
TCGAACCTGCCCTCATTATC	60.036	20	228	400	627
AACACCATCGCTACCTCCAA	60.517	20	116	91	206
TGAGCGTGTGTGTCAGTGTG	60.593	20	192	372	563
GTGGGCCACTTTGGTGACTA	60.954	20	254	326	579
CTCTGCTGGCCAAAAGTCAT	60.397	20	271	781	1051
CATTACAGCCGTGAGAAGCA	60.011	20	263	4	266
ATCGAACACGATGCAACTGA	60.272	20	269	1315	1583
TGGCTTCATGCAAATTCAAG	59.809	20	159	288	446
TTGTATATCGAGCAACCGGA	59.136	20	190	3828	4017
GGAGGACCTAGACAGCCCTC	60.216	20	176	1367	1542
CAGCCAAATGTTGGGTTAGC	60.502	20	269	97	365
ATTGCCCATATCAGCACTCC	59.923	20	278	796	1073
CCTCGACGTTTTCCTTCTTG	59.846	20	216	1108	1323
GAGATAGTACCGGAACGCGA	60.235	20	133	1211	1343
TTGGATGTTCCAAATACAGGC	59.815	21	275	2555	2829
TGGAAAAAGTCACCGGAAAA	60.452	20	276	49	324
TTCCCTCCTTGACCTTGCTA	59.807	20	178	113	290
TGGATTTTCTGAATTGTGGGT	59.278	21	254	846	1099
TCATGCAACAAAACCACCTT	59.024	20	259	1918	2176
AAGACCGAGGCTAGCAAGAA	59.218	20	234	79	312
ATGCATCCGTTAGATCAGGG	59.917	20	236	101	336
TGGTTTGCTTGGCCTATCTT	59.708	20	110	205	314
TCTGAATCTGATTGCGTTGC	59.955	20	262	43	304
CGAGGACACATAAGCCTCACT	59.367	21	280	163	442
AAAATCGAAAGGCCCACAAT	60.673	20	271	609	879
AACACGCGTTTGTAGGGTTT	59.54	20	229	104	332
TTTCCACCTAAGCAAGGCTG	60.378	20	213	1319	1531
TTAAAGTTCTTAAGTCCTGGCG	57.792	22	277	655	931

GATGGTTGCACCATAACGC	59.947	19	182	298	479
TCAATATAAAGGCACCAATTCT	59.871	24	152	266	417
TGGTCGCCGTGTCTGTAATA	60.134	20	196	3851	4046
CGACAGGTGGGAGAGTCATT	60.112	20	254	390	643
CACCGTTGTCTTTAAGCCGT	60.168	20	247	708	954
ATACGGATCTCTGCCTCTCG	59.41	20	157	1	157
GAGGTTTGCTTTTGGTTGGA	60.088	20	256	265	520
TCTTTCCCTACCCCCAAAAC	60.159	20	258	203	460
AAAACACGAGCAAAACGACA	59.366	20	253	95	347
GGGAAGAGGAGGTATGAGGG	59.89	20	144	636	779
AAATAAGGAGGTGTTATGAAG	59.323	24	161	291	451
GATGTTTTCCGGCTCAGTGT	60.119	20	268	92	359
GGTGACGGTTGAGAATGACG	61.527	20	270	183	452
GGGCTCAACCACATTCACTC	60.52	20	221	39	259
GAGTTTTCATCTTACCTTGAGG	58.333	23	270	71	340
CAAAACGCATAAATAGTGCAA	58.006	22	279	44	322
GCTCACATCACGGAATTGAA	59.654	20	209	158	366
TGTGTTGGGCTAAATTGGTG	59.439	20	202	4	205
GTGGGTATGTGATGTGGATGA	59.078	21	203	943	1145
GCATTTGCTGCTATCCCACT	60.243	20	204	1175	1378
GTCACTTCAGCGTCACCTCA	60.03	20	276	123	398
TTTAGCAAGCACGCCTCTCT	60.292	20	277	1222	1498
TGTTTCATGACATTTGAGGTTT	59.89	23	267	411	677
CTTCTACGCGAAGCACGTTT	60.575	20	275	1225	1499
CCGTTGCAAGAGTAATGGCT	60.27	20	186	2772	2957
AGCAGGCGAGGTGTTACAAT	59.763	20	205	94	298
TGCGATTGATTAGTTCGTGC	59.839	20	280	386	665
TTGCCATATTCACCTCCACC	60.723	20	194	1448	1641
TTTGGAGAGAGGATGTGGGT	59.505	20	278	705	982
ACACACAAATGGTTTGCCCT	60.277	20	207	80	286
TTCACTTACGGCAGTGGGTT	60.55	20	274	150	423
TTACGGGTCAAAAGAAACCA	58.121	20	249	678	926
CTTATCTCTTGCCGTGGCTT	59.476	20	198	67	264
ACGAAACCCCGGATCTAAAA	60.664	20	176	40	215
CAGTGGATATGCAATGTGGG	59.799	20	216	88	303
ATTACCATCATTCTTGGCCATT	59.576	22	245	169	413
TTCTCACAATCCTGCAAACG	59.84	20	212	1499	1710
TATCGGTTATCATCGGATCG	58.404	20	250	360	609
GGAATTTCCTTGATACACATAC	59.918	26	267	629	895
ATGGGATCTACATGCTGGGA	60.303	20	137	134	270
CTTAGATGCCATCAACCCGT	59.955	20	188	18	205
CATCAAGAAGCTGCAGCAAG	59.888	20	263	775	1037
AATCCCTATCGACACCCTCC	60.154	20	207	56	262
GGGTATTTAAAGGCACGGGA	61.029	20	279	1087	1365
CGTTAAGATCAACGCGGATA	58.794	20	207	2494	2700
GAGATCGTACGTTTCGTCCAA	60.125	21	169	2001	2169
GATCTCCGAAGCTCAAAACG	59.955	20	101	261	361
TCCACAGTTTTGTACCCACTTT	59.827	23	118	1604	1721
TACACGCATATTCGCACACA	59.741	20	182	148	329
CCGGGTAAGAAACCCATTTT	60.048	20	116	442	557
ATCAAGTCTCACACCGGACC	59.969	20	260	268	527
GGGAAGTTGAGATAATGGCG	59.528	20	274	9	282
TCTTGATGGCGGTAGGTAGC	60.235	20	234	288	521
TATAATGCCGACCCTCGTGT	60.352	20	136	13	148
GCTTCTGCTCCATCCTTTTG	59.955	20	248	1035	1282
ACCTCCCCTGCTCCATATTT	59.789	20	103	284	386
AACCATCCGTGCTCAGAAGT	59.727	20	253	130	382
TTTACGATCTTAATCCGCCG	60.054	20	212	23	234

TTTGAATTTCGTAACGGGGA	60.294	20	197	11	207
TCGGGACGAAATTTTTGTATG	59.818	21	275	1	275
GGCAACGGAACAACAACTTT	60.015	20	228	3197	3424
GTCTGCCACACAGGGTTTCT	60.159	20	216	1192	1407
CATCCCATCACTACCCCATC	60.011	20	255	18	272
AACCGAATAACCGAACCAAA	59.315	20	240	20	259
ATTCTTGGCCAAAACGTGTC	59.978	20	239	150	388
CTCATCTGCACCTCCCTCAT	60.223	20	253	1291	1543
AGAGCACCCCATTTCATTTG	59.933	20	222	1228	1449
AGTTTATCATTTGGGCCGGT	60.562	20	136	25	160
TTTCTTCACCGTTTTCCTTGA	59.71	21	242	447	688
AAATGACGACGATTCCAAGG	59.933	20	188	3077	3264
CAACAGTTTGGTTTGGCTGA	59.734	20	169	794	962
AGGCATAAAATTCTCCCGCT	60.061	20	252	20	271
GCTTCAGGGGGTGTGAAGTA	60.111	20	228	116	343
CTCTCGCCCCAAACTTAGAA	59.448	20	171	485	655
TTACCTCCTCCACCATCGAC	59.927	20	254	291	544
GCCGAATATTTTGGGCCTAT	60.135	20	223	415	637
GAAAAGAAATGAACACCGGC	59.551	20	265	7	271
TTGAAGGCAACAAGTGCAAG	60.027	20	257	585	841
TACCCCACCGACATTTTTGT	60.088	20	126	343	468
TCCGTGAATATTTAACCCGC	59.795	20	190	1222	1411
TGCAATCACCAAAGAACTGA	57.806	20	116	342	457
CAATGTCCCCTATTTGGACG	60.184	20	221	176	396
CAGCTCCTTTCCCTGCAGTA	60.529	20	138	2176	2313
CTGATGGCCCAGATTTGTTC	60.461	20	189	1360	1548
GGTGCGTGAATTGGCTTAAT	59.967	20	202	165	366
AGAGGGTTATCATGGGATCAA	59.307	22	163	470	632
AAGCTTGTGGAGTACATGAGA	58.408	23	251	40	290
TGGTCGCATGTTACGTGTTT	60.035	20	180	1341	1520
AATTGCCAAGTTTGCGAGAT	59.713	20	262	619	880
ATTGGCTGAAATGGAGTTGG	59.933	20	238	495	732
GGGCCAACCACGTTAGTTTA	59.861	20	234	449	682
GAATACGTAGATGCCCGGTT	58.93	20	166	514	679
GTCTGGGACAGACAACCGAT	59.969	20	172	87	258
TCAATCCTTTGGAAACACTCC	59.017	21	170	163	332
TGCGTTCACACCTTCATATTTT	59.519	22	194	144	337
CTCCACCAACTCGCCTACTC	59.867	20	160	445	604
ATGCATACATGACTCGAGCG	59.854	20	127	69	195
GATCGTACACGATGGCGATA	59.529	20	178	403	580
CACCATCATCGACAATCACC	59.769	20	213	387	599
ATTTAAGCTGCACTTTTATTCA	57.118	25	244	136	379
TTCCACGTTTCATGTTTCCA	59.941	20	139	65	203
CAGGCCAATTCGTATGAACC	60.331	20	276	855	1130
TCCCACTTCCCTTGAAACAG	60.081	20	205	437	641
CCCTCGGATGCTATGCTAAA	60.188	20	258	324	581
TCGTCTCTCTCGTCTCCTCC	59.663	20	176	28	203
GGGGATCGTGCATACATCTC	60.312	20	257	96	352
AAACCCCTATATCCCCATGA	58.057	20	231	1301	1531
GTTGGATTCGAGCAGCTCAT	60.37	20	277	122	398
TGTTGAGAGAGATGGAGGCA	59.499	20	102	114	215
AGTGGTATGATGTGGGGGAC	59.511	20	209	189	397
TTTGAAAAGAGGGAGAGCGA	60.066	20	114	2081	2194
AAACTCTTCCGCCCCTTCTA	60.2	20	178	108	285
AGGAATCCTGCCCCAAGTAA	60.817	20	222	248	469
TTGGTGTGGTGAATTGGTGT	59.701	20	273	71	343
CTTACCATTTTCGTCCGTCC	59.429	20	184	2175	2358
GCACCTCGTTGGAATTTTTC	59.551	20	184	899	1082

CAATGTAAGGGGGAGCAGAA	60.066	20	222	156	377
AACATGTTTGCTGGTGCTTG	59.764	20	241	3714	3954
GGCAAGCGAGTAGGTTGTGT	60.321	20	170	233	402
GGGTTGTTAAAATGTCCACCC	60.326	21	155	607	761
AAAAACCTTGGCAACAGTCG	60.147	20	241	40	280
GTTTCATCAACGGACACGGT	60.823	20	278	477	754
GGAGAAGACGGAGCTTGGTA	59.43	20	244	723	966
ATGAACATGCTCCTATTTTAATA	57.053	26	280	734	1013
ATTCCCAGTGAGGTTGTGGA	60.363	20	133	1407	1539
ACAAATTTAGGGCATGCGAA	60.456	20	191	314	504
GGGACGAAAATAACCCTCGT	60.187	20	240	38	277
CCCCCTCTCTACACATTGACA	59.974	21	216	2903	3118
TTCTGCATCAGGCCTTCAC	59.934	19	115	0	114
TGCGTGAACCAGAGAAGAGA	59.701	20	199	414	612
ACCGGTTGACCCCGAATTAT	62.535	20	189	1254	1442
TCCTCCTCTCCCTCTTCTCC	59.883	20	255	17	271
TCACTTTCACCGAGGGTTTC	60.088	20	102	143	244
CACGTTAGACCTGGAGGAGG	59.715	20	128	24	151
GGCATTGTTAGAGCCCTTGA	60.214	20	220	200	419
AGGTATTTTTGAGCAGCCCC	60.451	20	128	1044	1171
GCGATTTCAATTCCGACTTT	59.162	20	230	1304	1533
ATTTTCGGCCATGACTATCG	59.923	20	247	181	427
GAAATGTTTCTGTTGGCTGG	58.201	20	217	2862	3078
CAACGCCATAGGGAAGTGTT	59.993	20	264	1564	1827
TAGTGGTGGGATCGGAAAAA	60.301	20	189	86	274
TAATTGGGTGATCGAACGGT	60.192	20	269	10	278
TGAGGGGTTTTCATCCTCTG	60.042	20	232	74	305
TCCATTCCGAAAATCAAAGG	59.872	20	118	18	135
CGTCAGATGCCACCACTAGA	59.855	20	225	145	369
AGCGACCATCAGACCAATGT	60.542	20	172	2561	2732
TCATTGAACTCCCCATCACA	59.893	20	244	1350	1593
ACCTATGGTGGTATGGTGTGG	59.463	21	133	454	586
CACGAAGCATTGCCACTAGA	60.011	20	223	580	802
ATGATACTGACACCCGACCC	59.661	20	148	716	863
AGTTAAAATCTCCACTTGGGAA	58.259	23	135	265	399
TTTTGGGTCTTTGTCGTATCAA	59.492	22	186	1245	1430
ACATTTAATGCCCCAGCAAA	60.323	20	202	420	621
TGAACAGGTTGCATTTTAGATG	59.639	23	255	2016	2270
CAACAAACAAAGATTCGGCA	59.706	20	184	519	702
CGACAAGAGAAAGAGGGTCG	59.982	20	186	349	534
GCGTGGGATTGAGAGAAAAG	59.813	20	223	900	1122
GCTGCTCGAAATTTACCGAC	59.851	20	253	312	564
ATTGGGTGGGATAGTGCTTG	59.813	20	192	308	499
TAAGGGGCATTACCACATGC	60.721	20	191	517	707
GAGATATTCTGTCGGATAGGTC	59.13	23	245	450	694
CACCGTTAATCGCAACAAAA	59.603	20	268	185	452
AACTGTGAGGAGCGTCGATT	59.874	20	167	15	181
CCTATGGTGGTATGGTGTGG	58.569	20	193	24	216
CAAGAAAGAAAATGCAGCCC	59.823	20	192	182	373
ATCTTCCTTTTCTCGTTCACATA	57.089	23	222	198	419
TATGGGTTATCACCGGATCG	60.544	20	166	459	624
TACGCAGTTGCTCGGAAGTA	59.632	20	266	39	304
TCTTTGATCCAATGGCCCTA	60.405	20	196	1	196
GTCGCCGATATTTGCTCCTA	60.196	20	125	334	458
CACACCATGTGACGAAGGTT	59.441	20	271	627	897
TCCACCAATTTGCCATTTAAC	59.69	21	226	36	261
GGAGGCATTCGATCTTTGTG	60.603	20	147	60	206
GACCATGCCAAATTGTGTTG	59.823	20	189	129	317

AGATCTCGTTGTGGAGGTGG	60.112	20	195	1007	1201
TCGAAGATCAACGGACGATA	59.226	20	211	2224	2434
TCGCTTATTGTACTCTCCCGA	59.853	21	111	47	157
AAGCTTGCATTTTATCGGGA	59.682	20	219	249	467
TGAGGAAGAAACCAAGTATCA	60.035	24	244	586	829
TGACCGATTCAAAAGTGCTG	59.84	20	258	480	737
CTGCCAGGACGAACTTGTAA	58.923	20	276	227	502
ACGTTGTAGTTGAGGCCCTG	60.171	20	280	1064	1343
TTCACGAATTCTTCTTTCCTTTC	59.786	24	276	951	1226
TCAACTCAATAGGTTTTCGAGT	59.732	25	197	9	205
ATTTGGCACCATTCTTCACC	59.797	20	267	330	596
GTCAGACGTCCTCCTGGTGT	60.161	20	110	37	146
GTCCGCGCTGTAGATTCAA	59.964	19	126	40	165
ACTTGCGAGAGGCTGTAAGG	59.639	20	121	3909	4029
GGTTGATGGATCTGCGTTTT	59.939	20	275	119	393
AGGCTGAGATCTTTCCAACG	59.43	20	104	959	1062
AGAGAAACTCAACGGTGCGA	60.975	20	229	105	333
CCACATATGCAAAATATCAGCC	59.349	22	279	163	441
AGGCCGAGGAGTAGGAAGAA	60.34	20	187	158	344
TCTCCCAGGAAAAGCATCAT	59.629	20	210	2039	2248
GACGTGACGAAAGTGGGAAT	59.973	20	205	2	206
CTTCCCTGCCGATATCACAC	60.483	20	248	60	307
TGGGGTGGGATTGAACTTAT	59.101	20	271	23	293
AATAGATGCATGAAACATTTTG	57.786	24	279	28	306
CTTTGGAGATACAGGCGGAG	59.83	20	266	1465	1730
ATAATGTTGCGCGTGCTTTA	59.379	20	159	246	404
AGAAAATTGCAAAGCGGTGT	59.752	20	248	2	249
TCCTAGCCCTCAATCTCGAA	59.91	20	234	253	486
ATCCACCACTGCTTGGAGTT	59.579	20	215	280	494
CAGCTGTGGAGCTGATGAAG	59.726	20	215	205	419
CCCTTAGATCTACAACGCGG	59.724	20	203	171	373
GTAAAACGCTAGAAGGCCCC	60.095	20	125	8	132
AGGAACAATCCCAACTTCCC	60.169	20	206	315	520
GGAACAAGGCAGTGGAAAGA	60.232	20	272	1276	1547
TGGGGGTTGGAATGTTAATG	60.418	20	235	473	707
AGCAAATCCCCTTCTCTGCT	60.349	20	139	849	987
CATGTTGCTTTTGCATGTGA	59.28	20	152	72	223
CAGATGGGGATTTGCTTCAT	59.894	20	275	2585	2859
AAGCAAACCTTGAAGCCAAA	59.861	20	248	7	254
CCGAAATATCCGGTTTTTATT	57.141	21	258	889	1146
GGGAGGGTTTCATTCTCATTT	59.275	21	275	54	328
CTGGCTCCCTATAGTGCTGG	59.853	20	269	1362	1630
CACATCCAGCATCAACCAAC	59.967	20	254	105	358
TTGCTGTAGGCCTTTTGCTT	60.018	20	171	103	273
TTGGGCAGCTGTAAAACCTT	59.747	20	252	154	405
ACCTCCAGATTTGACAGGGA	59.505	20	262	80	341
CGATTAGTGTAGGTTGGGCTC	58.732	21	172	350	521
TGAGCAGCCTAGATCAGCAA	59.847	20	188	140	327
TGTTGATTTATGGCGGATTG	59.377	20	241	957	1197
TTTCTCATTGGCAGTCACCA	60.24	20	271	540	810
ACGGAAATCTAGGGAGCTGG	60.59	20	271	127	397
TTCCCACCCCTTCTCTCTCT	60.186	20	236	2825	3060
TTTGTGCCTAAAATGCCCTC	60.074	20	237	405	641
TTGTTGTCGCTTTAGCTCCC	60.386	20	268	430	697
GGGTTAAAAGAAACCCCCAA	60.027	20	226	264	489
TTCTTTGGACAAAAATGCCC	59.916	20	254	425	678
TGGAATGGAATTCACTCCTAAA	58.556	22	224	2847	3070
ACTGCCGCTGAAGATGAGAT	59.981	20	234	1193	1426

ATGCGAAGAAGCTCAGAAGG	59.717	20	156	44	199
GGCCTTTTTGCAATTTGTGA	60.98	20	231	1624	1854
CGGCCCAGTCTAATTGGTAA	59.953	20	256	2	257
GCATTACGTGTGTGCGTTCT	59.794	20	264	55	318
TCAATCGAGCTACAAACGTG	57.506	20	110	14	123
AAGACGAGAACAATCGCTGG	60.397	20	278	5392	5669
TTGTTGCATGTCATTGGTCA	59.516	20	223	261	483
TTTTTCGAGATGGGTCGAAT	59.505	20	179	675	853
TTCTTGATTCGTGAATTATCCA	59.851	24	163	414	576
GCGTTGGAGATGGTCTTACAA	60.125	21	193	499	691
CCAATGCGGATGCTCTTAAT	60.06	20	280	36	315
AAGCCATGCAGGTAAAACCA	60.502	20	266	35	300
GAGAGGGAGGAAAGACTGGG	60.186	20	188	608	795
CTTAGGAGACCCCTACCCCA	60.311	20	219	196	414
AGGGGGTTATCACCTGATCG	61.095	20	111	448	558
AGCCCTCAACTCTCCCTTTC	59.817	20	120	267	386
CCACCCGTTGATTTTTCACT	59.83	20	253	375	627
TGGGCCGAGATTTGTTAGAG	60.206	20	247	864	1110
TGGTTTCCATCGTTTGTTGA	59.941	20	123	471	593
GGCCGATATTTGCTCCTAGTT	59.606	21	271	146	416
ACACCTGGGTGAAACCAAAC	59.721	20	163	312	474
CACCTAAAATATTGGTTTCTAT	57.121	26	127	293	419
GTCACGTGGCATCATGAGAA	60.698	20	204	331	534
GCAAACAAGAAACATGCCCT	60.118	20	158	1622	1779
AACAGTGGGCTTGCAGGTAT	59.621	20	272	2836	3107
TGATGAGAAAGACGCCAAGA	59.522	20	269	916	1184
CATGTACCCCGGATCTACCA	60.594	20	279	828	1106
AAAAAGAAAAGAAAAGAAAG	57.177	26	252	443	694
GCAAGTTGAGGGAGAATGGA	60.195	20	264	260	523
GGTCTTTGGCTATGACCCAC	59.41	20	260	163	422
TGATTTTCATGTTTCGCGATT	60.45	21	215	82	296
TTCTCACACGATTGAAACGC	59.847	20	235	2441	2675
CATGCGTCATGAATGCTACA	59.259	20	264	88	351
GGAAAGAACTCAATGTCGGC	59.676	20	268	126	393
TCACACAGTTCATCTCCCGT	59.101	20	258	11	268
TCTCCATTGCTGTTGGGAAT	60.461	20	238	3104	3341
GGAATCCCTTGACACGAAGA	60.05	20	258	375	632
CCTATAGTGGTATGGTGTGGG	60.365	22	216	158	373
GCAACCAAGGAGACTTGAGC	59.997	20	144	171	314
GGCTAGCCTTTGAAGCAATG	59.982	20	149	23	171
CGTTGCTTCCTTCCTACTCC	58.934	20	205	185	389
GTTTTTCCCCATTGGGTTTT	59.903	20	186	162	347
AAGAGGGGGTATGAGTGGAA	59.813	21	101	126	226
GCGTTTTGACAATATTTAGTGT	60.205	26	139	329	467
TGCATATTTCTCGATCCCGT	60.435	20	250	5673	5922
TCCTCCCATCTGCAACTAGC	60.362	20	223	966	1188
GGCTTTCCCTTGCTTTTCTC	60.32	20	174	525	698
TGAACACCCCTACTTGAGCC	60.111	20	185	0	184
GCGATTAAGAGCTCGTTGGA	60.49	20	225	0	224
AGTTCCACGATAGGAGGGTG	59.014	20	274	759	1032
GGTCCAATAGCCATGTTTACG	59.352	21	257	444	700
CAACAAGATTCGATAGAAGCC	59.361	22	152	761	912
GATCTGCTGGCGGTCTTTAT	59.297	20	247	921	1167
GGCTCCTTGGATTCATCTTG	59.629	20	276	68	343
GCTGGCTGCTCAGTTCCTAT	59.603	20	119	9	127
GAGACGCGAATGTTGAGACA	59.992	20	222	3484	3705
CTTTGAGCTGATCTTGAAATGC	59.114	22	133	453	585
CTCCCTCTCTAAAGGGACGC	60.34	20	110	389	498

GCCAGTCTCTTTGGATCCTG	59.803	20	147	239	385
TGGTATCCATAGCAAAGCGA	59.281	20	250	157	406
TAAACGGATTGGATTGACGG	60.692	20	187	157	343
TTCTTACTGCCACACAAAATCA	58.346	22	247	457	703
TGGTAAAAGTGCTCAAGACGA	58.566	21	268	102	369
TATTCCGCCGTGGTCTAAAG	60.089	20	279	133	411
CACACGCACTCTCACTCTCC	59.603	20	155	1295	1449
CAAACTCGCTCAAAAAGACAC	60.453	22	221	1974	2194
GAGAAATCGCACATTCGTCA	59.805	20	245	11	255
CGAATCAAGCACCACTCAAA	59.84	20	180	257	436
CGGAACCAGACCGAATATGA	60.853	20	191	28	218
TCCGAAAATCCCAACAATAAA	59.287	21	268	271	538
ACTGATCCGAGCGATTTGAC	60.226	20	238	3256	3493
ATCTTCTAATCACCGCCCCT	59.925	20	220	203	422
TTGTTTGAGGGAGAAGTGGG	60.081	20	218	3207	3424
TTTGGAGGATCGACGTTACC	59.933	20	251	76	326
TCATTCAAGGAATTTCACCAA	58.052	21	213	918	1130
CGAATTCAAACTCTCCCGAA	60.184	20	268	12	279
CAGCTTCACAACAGGTTTCG	59.485	20	204	142	345
ATGACTGCAAGCAACCTGTG	59.905	20	151	40	190
CTCCACCCTGGTTCTAATGC	59.55	20	276	936	1211
ATGCTGCGAAGAAAATACCG	60.23	20	244	164	407
GACACGTTGGTGAAGCATTG	60.16	20	147	249	395
TCCGCTATCGAAAATATAATCC	60.469	23	273	112	384
ACATCCACGGGAGAGAATGA	60.475	20	191	25	215
AGAGGGAGGGATACACCTCTT	58.161	21	270	59	328
TTCTTCACCCAACAACCACA	59.976	20	213	169	381
AAGCAATCAAGATCCGAAGC	59.415	20	139	734	872
CTAAAATGGAAAGGGCGTGA	60.067	20	129	456	584
TGGGTGCCATATCCTCTACC	59.773	20	254	6672	6925
ACGGGTTATTACCTGATCGC	58.93	20	100	827	926
TTCCCAACTCCAATTGATCC	59.727	20	207	1016	1222
CAACCTTTTCACACCACCTTC	59.482	21	187	96	282
CCTTCATCTTCAACGCCTTC	59.813	20	182	1340	1521
ACAGAAGGAGCAAAGCTGGA	60.134	20	262	621	882
CATGTGCAGGGAAGATCAAG	59.241	20	193	7	199
GGGTGGAGTTATGGCTGAAA	59.933	20	237	148	384
CCATTTCAAGAATGCAGGGT	59.933	20	195	1511	1705
AGCCAAGGAAAATAATCCCA	58.508	20	230	1494	1723
CAACACAAGAACTCACCTCCC	59.607	21	203	561	763
GCTGCCGAATCTGCTCTATT	59.579	20	214	5760	5973
TCTCGATCACTACAATCTTTGA	59.445	25	273	159	431
TGCCGTAACCTGTCATACCA	59.988	20	208	50	257
ACGAAATGTAAATGCCCCAA	60.188	20	222	1449	1670
GAAGGAACGCTTACACGGAG	59.875	20	126	10	135
TTATCATTTCGTCCCCAAGG	59.756	20	160	116	275
TCTGTCACGTCTTCGTGTCG	61.092	20	131	300	430
AACTGTCATCACCCTTGGGA	60.363	20	259	1121	1379
ATGGAGAGGGAAAAGAGGGA	60.008	20	279	18	296
AGAAAGCCGGCAAACTGTAA	59.883	20	221	139	359
GCAGATGGCAGATTGGTACA	59.679	20	183	118	300
AACTGCCCAATCTGGATGTC	59.934	20	270	1140	1409
CAATTAGGTCATCTCCAACGC	59.583	21	257	1190	1446
TTGCCCCACCTATGCACTAT	60.352	20	274	265	538
TGAGTCCATTGTAGCGGTTG	59.716	20	253	96	348
ATATCCACCCGAATTTTCCC	59.852	20	233	2336	2568
GTCGCGTGCGATAATTTGTA	59.731	20	236	156	391
ACTCCTCGGGACGGTTTACT	59.994	20	274	115	388

CTAAGGTCGGCGATAGCTTG	59.996	20	179	860	1038
ATGGGTCCATCACTCCTCAA	60.326	20	181	308	488
ATGCACGTGTGTAGGGTTTG	59.49	20	272	1006	1277
TTGGAGTTTGGAGGGTCTGT	59.549	20	260	141	400
ATAATGTTGCGCGTGCTTTA	59.379	20	132	87	218
GGAACGAACCAAAAGTCCAA	59.948	20	218	562	779
GCAGGAGAAATGGAGACAGC	59.957	20	197	668	864
TATGGTCCTCACACCAACGA	59.96	20	166	2061	2226
GCATCATCTTGTTGTATTCGTT	59.532	23	210	15	224
CCATTGTTTAATGAATGCGTG	58.947	21	242	574	815
CCCTTGCTACCATCATCGTT	59.955	20	176	201	376
CTGTATTGTGGAAGGACGGG	60.366	20	231	276	506
TTGCAAATAACCATCACCCA	59.786	20	264	1806	2069
GGGATGACTCCAAAAGGACA	59.903	20	235	171	405
TCGAACCTTGAACCAAAAGG	60.081	20	174	9	182
CCCCAAGCTAACCATTTCAA	59.931	20	126	4143	4268
AGCCCCACATAATCCCACTT	60.578	20	211	99	309
TGTACCGCACCAAGATTTGA	60.111	20	170	0	169
AAAATACAGTGCTACGGCGG	60.152	20	146	174	319
AAAAATTTAGTATGAGGTCAC	59.925	26	271	621	891
AAGGGAGTTCTCCCAAATCAA	59.926	21	163	37	199
CATAAAGCCACCCCAACAAC	60.227	20	205	190	394
TAGCCCACTAAATGACCCCA	60.323	20	226	196	421
TCCTCTACCACCCGAAAGAA	59.665	20	211	342	552
TCCCATTTGTGTGTTCTTCG	59.541	20	270	2342	2611
AAGGTGGAGGCTTTGACTGA	59.844	20	137	889	1025
TGGAGGAGGAGAAGGAACAA	59.773	20	136	398	533
AGCTTCAAGTCCCCACTGAC	59.305	20	231	57	287
TGAGATTTGGACGGTTATGATT	59.729	23	205	202	406
GCGAACTCGGCTAGAACAAA	60.523	20	154	657	810
TCCACTTCTCGGAGCATAGC	60.504	20	161	201	361
CGAATCATCATGAGGTCGTT	58.516	20	238	529	766
GTTTGCTACATGGCATCGTG	60.142	20	185	170	354
TTTCTGGTTGCATTTTGCTG	59.849	20	241	1534	1774
TTCTTTGAATCATCTTCCACCTT	59.123	23	223	268	490
CGGTTGAGAAATGAGAGCGT	60.397	20	141	279	419
CTATTTTCGCTGGCTTGGTG	60.762	20	278	211	488
CCCTCTCCTCCCTCTTCAAT	59.63	20	221	194	414
AAGGCGGTTTTTGATACGTG	59.996	20	265	356	620
TTGTCTCAGAAACTGTAACCCT	60.198	24	261	2887	3147
GATTTCCCAACAGCACCAAT	59.797	20	195	189	383
ACACGTGGCAGATTTCAACA	60.16	20	279	624	902
CCCTTGTTGCTGAACTCTCC	59.844	20	237	2458	2694
GGACACGTTGGACCTGAAAG	60.545	20	153	37	189
TCGAAGATCAACGGACGATA	59.226	20	244	423	666
CATAAAAGCAAAAGACGGGG	59.581	20	225	3215	3439
TTTGCCAGTAATTCACAACCC	59.853	21	219	448	666
CAAGGGCTATGCAAATAAAAG	60.114	22	276	83	358
TGATGGCAATTCTATGACCCT	59.401	21	138	22	159
CCCTTTCGATTAACACCCCT	60.18	20	219	1088	1306
CTGTGTGTGAACCTGCCTGT	59.782	20	268	795	1062
ACCATATTTAAGGGTTATCACC	57.552	24	168	772	939
TGTGCATCGTGTTCTTGTGTT	60.214	21	126	0	125
GGGAAGGATGAAAGGGGTTA	60.124	20	101	180	280
TGATGGTGACGTAGAACATTT	60.414	23	165	44	208
CGTGTGTGGGAATGAAACAG	60.001	20	102	78	179
CCTCCCCCTCCATCTCTATC	59.851	20	212	334	545
CAAGTGAAACCAAACCCAGTC	59.482	21	265	214	478

TCATCTAGCATCTCTTGCTTTC	59.261	23	179	395	573
GTGGCAAGAATTGAGAGGGA	60.195	20	238	588	825
GACCACAAAATGGGAGAACC	59.239	20	151	1	151
CGGCGTTAACTAACCTGGAT	59.111	20	254	30	283
ATATCGTTGACCATTCCCGA	60.155	20	255	302	556
CAGAAAGATCAGGGGCACAT	60.073	20	232	590	821
TTAGACGATGGCGGATCTAAA	59.69	21	237	275	511
GGAAAAACCAATCATGGCTC	59.368	20	257	909	1165
CGACTTGTCGTGGTTCGATA	59.716	20	280	40	319
AAGTGAATTCCTTCCCCACC	60.169	20	239	854	1092
GACCGAAATGCCCTTCCTAT	60.286	20	243	651	893
CGATTTGACCTCGGATAATCA	59.908	21	250	165	414
TTTAGGAAATGACATGCCGC	60.971	20	196	3658	3853
CACACCTCCTCCAAAGCACT	60.298	20	148	585	732
CGGGAGGGAGAGGGAGTAT	60.419	19	110	371	480
TGGTTGCCTTACGGAACTCT	59.734	20	270	138	407
CGTCAATCGGCTTTGAAACT	60.249	20	239	2605	2843
GAAGTGCATATGCGAGGTGA	59.83	20	134	739	872
GAAAAACCTACGTTTGCGGA	60.11	20	204	107	310
AACCCGTTTGAGGTTGAACA	60.388	20	271	7	277
TCATGTATTCCCCTTGGTCC	59.605	20	224	2372	2595
TAAGCCAAAATCCTGCGAAT	59.682	20	263	40	302
AAATGAAGGGTTGAGATGGG	58.836	20	193	2020	2212
TCATTTTACCTTTCTGTTTTTGG	59.932	25	250	416	665
ATTCCTTCCCACTGGATGGT	60.575	20	152	109	260
TGTCAACCCTGTTGAGCCTAC	60.164	21	279	1856	2134
CACAAAAGCAATGAGGCAAA	59.849	20	234	3461	3694
GGTGCACACGTGGAGGTAG	60.17	19	280	409	688
AATTTCGAAAATTTAAAGGTCC	58.2	23	196	452	647
CATCGCATTCTCGATTCAAA	59.769	20	253	1478	1730
CACTGGCCAAGAATCAATCA	59.648	20	248	416	663
TCCGTTGGATTTATCTTCTCCA	60.792	22	244	3503	3746
TTTGCTCGAATTCATATTTTTAT	58.297	25	270	434	703
GTAGCCCGAGTCAGATCGTC	59.834	20	274	182	455
ACCACACACAGGGTTATCCA	58.697	20	101	169	269
AAGGGATGTGTTTGGACGGT	61.572	20	149	817	965
TCCATTCCATTGACCCATTT	59.991	20	274	114	387
TGAAAACGTGAGGCTGAAATC	60.242	21	257	137	393
ATTGATTTGGTTTTGGGGGT	60.278	20	253	12	264
TGTGGCAGTAAAATTGTGGG	59.439	20	244	80	323
CCTAGTGTGCCCCCTAGTTG	59.61	20	189	618	806
CAAGAACCCGGAAAGTGAAA	60.081	20	267	1568	1834
AGGTTATGGCGGGTGTTATG	59.708	20	118	446	563
ACTCTCCATTCCATCAACGC	60.081	20	251	284	534
CCATTCCGAAAAATCAAAGG	59.383	20	240	458	697
CTGTTTGCATGCCTTGTACG	60.316	20	236	243	478
TTTGAACATGGGACCTTTCAG	59.956	21	152	66	217
CCCTGGATTTTGATTGAGGA	59.864	20	261	90	350
AGCCAGGATCTCATCGGAAT	60.961	20	205	151	355
TGACGGGATTTAGGTGTTTTG	59.847	21	240	375	614
TTGTTTCGGTGTTGCTTCAG	59.881	20	266	356	621
GCTCTTGTTGGAGGTTGCTC	59.997	20	251	2119	2369
TGAGTTGGCCAAGAGAGTGA	59.545	20	223	343	565
GGAAAAATCAAACAAAAACAC	58.566	22	257	1243	1499
TATGGGCCCAAACAAAAATC	59.638	20	245	382	626
AATGCGATGTGAGGACATGA	60.08	20	243	1778	2020
GAGGCAGAGTAGGGGGAATC	60.037	20	137	22	158
CCTTCTGACAAAGGCGAAAG	59.986	20	204	2825	3028

TGTGCCATTTCTTGCACTTC	59.847	20	181	2249	2429
TTCTTCAACCGATCAATGAAA	58.201	21	279	843	1121
TTTCTGGATTTCAGTCCTCCTT	59.213	22	257	1466	1722
TCTTATGAAATCCGCCATTCT	58.66	21	139	757	895
GGGATTGGGATGAGAAGAGA	60.022	21	272	49	320
ACTCACGCCCTCTCACTCAC	60.467	20	266	41	306
ATGCACAAGACTCGACACCC	61.146	20	190	99	288
AGGATTTGACGATGGTGGAG	59.927	20	249	1441	1689
CGGTGTTAAAAGATGCCCTC	59.569	20	257	2314	2570
CCCCCTCTTTAACCTCCATT	59.28	20	252	193	444
CGATCGATTTTAGGGTTTTCC	59.795	21	237	733	969
CTTCTTTCCGCCTCTTTCCT	59.955	20	255	35	289
CATCAAGATCCAAGGGCTGT	60.073	20	201	4	204
TAAACCCGAACCCGATTACA	60.181	20	201	16	216
TTTCAACAAACACACACGCA	59.765	20	267	512	778
AAAACCCATGGATGCAAAAA	60.167	20	274	469	742
CCCCACAAAATAGGGAAAAA	58.781	20	121	361	481
CTTGTCTCCGTTCTGCTTCC	59.989	20	277	1245	1521
TGCACTCCCTGTCACCTAAA	59.288	20	205	966	1170
TGGAAACAAATCAATTGACCA	58.855	21	153	246	398
ACACAGCAGTAGGGTCCAAAA	59.648	21	157	7	163
CCCACCCCCAATATCAAAA	60.369	19	165	322	486
TCCACTTCAAGATTGGGGAG	60.042	20	213	561	773
TGCTCGCCTTATTTTGATCC	60.175	20	246	2977	3222
GCACCATTTTTCACTCCACC	60.362	20	115	59	173
TACTCCCACCCCATGACATC	60.6	20	231	132	362
CCAATCAACTAAACCCCCAA	59.657	20	223	1113	1335
CGGGGTACTGGTAGGTGAGA	59.982	20	235	361	595
TGCAGTGGGTTTGATTGTGT	60.008	20	171	318	488
TTTTCAGTTAATGAGGTAATGC	57.967	24	199	22	220
TGGAAAGAATCAGGAAGCCA	60.713	20	151	21	171
GGATTGATAAATGCCGCAGA	60.942	20	254	14	267
GAGGCTGGATTATAGTTGAATT	58.318	25	260	2507	2766
GCAGCCTCCTCCTCTCTCTT	60.238	20	200	7	206
TTCTTCTAAGGTGCCCATCTG	59.322	21	243	2691	2933
GCATTGGATTCCTTTTATCCG	60.63	21	193	501	693
CGTTGCCAGGTCTTGAAAGT	60.291	20	243	604	846
TTATGCCTATGTGGCTGCTT	58.414	20	279	551	829
ATACAGCCCTTTGCCTCTCA	59.836	20	274	2	275
AGATCACCAAACCAACCAGG	59.82	20	262	1670	1931
TTGGTTTAAAAGTCGTTGTTGA	57.43	22	268	219	486
AATCTAACTAATGGCGCGGA	59.704	20	175	430	604
TCCAGCAGTTTCAATCACCA	60.24	20	201	1339	1539
GGGTGCTTCACCACTCTCAT	60.12	20	113	4	116
GGGATGTAAAGCCTGCTCAA	60.214	20	155	153	307
CAGCACCAAGAATGCAACAT	59.722	20	179	4674	4852
CTAAGGTGCAAGCCACAGGT	60.312	20	276	62	337
TGATTTGAAACAGTGCTTTTGT	60.193	23	153	885	1037
TGTGCAGATTTGTTGCACTTT	59.381	21	185	20	204
TGGGATAAATCTTCAACACCG	59.809	21	234	198	431
ACGTGCCGGAAAAAGAAATA	59.586	20	199	731	929
TTCACAGTTTTCATTTGATCAC	58.986	23	209	7	215
AGTGTTTTGACATGATTACTCG	57.373	24	249	1458	1706
TCCCACCACTACACAAGTGC	59.597	20	269	121	389
AATCAATATAAGGTTGCACGAT	57.338	25	265	613	877
TGGTTCGAATCCTCCACTACA	60.501	21	264	85	348
CTATTGCTTCAACCTGCTGC	58.677	20	164	2162	2325
TCGTCTTCTCTCATGTGCGT	59.577	20	230	127	356

TTAGAGCCCTGCCAAACAAC	60.249	20	276	11	286
TGGCATTCCAGTTTTGAACA	60.088	20	272	9	280
TGCATTGTCAAAGTAGTTAACT	59.027	26	152	348	499
ATTCGTGCCAAGTTTATGCC	59.967	20	198	160	357
GTGATTTGAAATAAAATTTGAC	57.233	24	267	3473	3739
AGAGGATGGCGTGATAGGTG	60.096	20	188	93	280
CGAGTAAACCAAACACGTGAA	58.737	21	238	3099	3336
AATGGCATGCAACTGTTTGA	60.119	20	262	245	506
AGTTAAAATCGAACCGAACCA	58.616	21	244	306	549
ATTTCAACCTTTGCCAACGA	60.481	20	276	882	1157
ATCTCCACTCTGTCGGCAAC	60.269	20	275	302	576
TCCTCACCACTGTACCCCTC	59.962	20	266	411	676
CGAGATGGGGACAGTTGTTT	59.966	20	256	162	417
GGACAGCCAGCTGAAGAAAC	59.997	20	235	1312	1546
ATAGGCAAATTCGGAGGCTT	60.061	20	255	166	420
ATAGGGTGACGAACGTCGAA	60.517	20	218	385	602
GATCGAGTGGAGGAAGATGG	59.612	20	269	525	793
TTTATTTGGAAGTGCAACCCA	60.342	21	109	1909	2017
CACTCCAACTTTGCAAGAACA	58.96	21	193	1050	1242
CTTCTGTTTACTCACGCGCA	60.195	20	187	11	197
AGAAAGCTTGAACATCCCGA	59.813	20	275	2508	2782
TACCACAGGCTTTTGGAGGT	59.592	20	252	444	695
ATTGGAGAGAGAGGGTGGCT	60.216	20	150	140	289
TAAAGGTCCCTCACCCGTC	59.911	19	227	1562	1788
AAATACACAATTGAACCAACA	59.589	25	119	619	737
CACAGATTTTCTGTCGCCAA	59.84	20	231	50	280
CTCCTCACCACACTTCATCG	59.257	20	267	530	796
GGGCGAGCAATCTGTAAGTC	59.843	20	250	195	444
CCATCCATTCCGAAAATCAA	60.64	20	274	49	322
ATTGCATGTGCGAAAAGGAT	60.478	20	231	488	718
GCAGGGTTGAATCTGAATTTCT	59.598	22	280	165	444
TCCATTTGTCATTCGCCATA	59.891	20	231	704	934
CGAAGCGATCACACAGCTTA	60.157	20	159	2	160
GGGCAGGTGGCTAATCACTA	60.096	20	136	1195	1330
TGCATGCTCACGCAAAGTAT	60.432	20	275	1893	2167
TGACCATTTTGCCCTTTTCT	59.546	20	235	385	619
CCACGTGCTCCATACTTCCT	60.134	20	246	482	727
AAAGCCGACAGACAACAAGG	60.291	20	184	200	383
ATGTCGTTGAAACGAACGAA	59.174	20	279	38	316
CTCCATCCTCTTGCTTCGAG	60.088	20	273	1047	1319
GAAACATGCCACCTGACAGA	59.682	20	204	470	673
CCTACCTGCAATTGGACACA	59.566	20	261	4400	4660
AAAAATAGGCCCTTTTGCGT	59.97	20	152	1671	1822
AAAAATGAGTGGTTCATATTG	57.968	24	171	682	852
TTAGGATCCCTTGTCCCATTT	59.652	21	224	268	491
ACCCTTTGAAAGTTGATGGTTT	58.914	22	269	200	468
TTCGAGCAACATCTTGTGGG	62.175	20	136	839	974
ACGGATTCATGGAGTGGAAG	59.927	20	225	437	661
GTTTTCAATCACAGCCACCC	60.362	20	132	165	296
CCAATTGTCCATATTTCGCC	60.153	20	210	341	550
TCATGTGAAAAATTTCGAGCA	60.117	22	274	10	283
TAGTCATTGGGGAAGGCAAC	59.933	20	185	678	862
TGGAAAACAATGCCTAACAGC	60.124	21	269	121	389
TCCTACATTATTTGGGGATTAA	58.735	24	125	20	144
TCCATTATCACGCGATCAGA	60.182	20	113	6	118
TGACACGATTTCGCAAAAGA	60.379	20	218	946	1163
GTGCAGTCGATATTTGCTCC	58.326	20	121	1	121
CCCTTCTTTCCACAGCAGTC	59.844	20	271	33	303

TTTCTCGCGGTTTTCAGTTT	59.861	20	210	212	421
TGGCCTTCCTCAATCTATGG	60.029	20	148	0	147
AGCTTGCCCCTTGTAACTTG	59.378	20	193	365	557
GAATGTTCAAGGCCATGGTT	59.797	20	229	131	359
CGATCACACAGAAAACACGA	58.246	20	100	14	113
ATATTTTGGCATTTGGAGCG	59.928	20	248	2019	2266
CCAATTACACAAATCAACCTG	59.244	22	278	94	371
TGCGTTTTGACAATATATAGGT	60.083	26	163	313	475
GGCATGTGTGGGAGAAGAA	59.621	19	171	7	177
TGCCAGGGTTATCTTGATCC	59.894	20	108	261	368
TGAGGAGGACAAGAGGTTGG	60.229	20	128	170	297
GGGGAACAAACATGAGCAAT	59.797	20	255	955	1209
TTTGTTTGGGGGTGTTGAGT	60.246	20	184	2717	2900
GCACCTGAGGAGGTGTTATGA	60.126	21	128	1120	1247
TCCATACTCAACACAAGTCGA	58.283	22	280	367	646
TGGAGAGGATTCTGTCCCAG	60.191	20	229	3890	4118
TACAAATCACGGGAACGACA	59.964	20	276	697	972
TTATAATGATATTTTGGAACGC	58.472	25	227	615	841
TTCACGAGTGGTGACAAACG	60.757	20	194	274	467
AGGGTTTGGGCAGTCATAAA	59.429	20	270	137	406
ACACCATCAAGGAAAGACGC	60.119	20	211	386	596
TCTGCCCTAAGATGAAACGG	60.206	20	174	103	276
TGAATCAATCTTGTGCGTTGA	60.25	21	182	20	201
ATCGCCATAATTGACTGCAA	59.14	20	109	18	126
TGCAGTGCCTTTGGTAGTGT	59.365	20	224	141	364
AATAGCGGCTGATCTGAAGG	59.434	20	200	390	589
TAGATGATCGGAACGTGAAGC	60.228	21	212	686	897
CATCTTCTCCACCAAAGGAAA	59.157	21	277	1231	1507
TAGACGGAACCCTCCAGATG	60.065	20	242	1108	1349
ACCAGGCGTACAGTCAAAGG	60.171	20	209	180	388
TATCATTGTTTCGCGAGCAG	59.976	20	244	204	447
ATTGATTAGAAAAATGCGCGA	59.709	21	176	97	272
CAGCTGCAGAGATGGAATCA	60.096	20	257	486	742
CGCGTTACGAATCCAAGTTT	60.131	20	176	345	520
CTCCATGGTGCATTTCACAC	59.967	20	263	4	266
TGGGTCACTCCTGTTTAGTGAA	59.633	22	275	14873	15147
CAAGATTGGCCATGTGAAAA	59.518	20	210	175	384
AGCTCGGATATGTGGTAATCA	59.877	23	271	226	496
ATTGCGAATTCAGCCAGAAC	60.221	20	175	20	194
GGCCTAGGCACCAAATCTTAT	59.476	21	188	1590	1777
GGCACAAATGGGTTCAAAAC	60.214	20	190	13	202
GATCGCATGTAGGCACCATA	59.529	20	266	284	549
AATCGTTGATGGGGTGTTTC	59.653	20	250	1153	1402
TGCAACCTTGCTCACTCTTC	59.165	20	262	1459	1720
TGGTTTTATGTTTCTCTTTGGG	59.865	23	252	1527	1778
TTGAGGTTACATTAGCCGCC	60.096	20	252	144	395
TCTGTGAATCAAGCTCAAGCA	59.731	21	166	221	386
TTCTCTCTTTTGGTGGAAGAAA	58.098	22	256	213	468
ACTGTGAAAGAGACCTCCGC	59.455	20	181	1164	1344
CAGGTCGAGGATTGTCGTCT	60.261	20	162	260	421
GGAGTGCTAATTGTGTGGCA	59.722	20	165	178	342
CCCTCATAATGTGTGGCTCAT	59.828	21	271	63	333
AACAGACCAATCCCAATTAAT	59.601	23	170	1339	1508
TGAGTCCATGACCCAACTTT	57.971	20	175	753	927
AGAGATCCGTGCTTCACTTG	58.029	20	164	1438	1601
AAAGGCGGCTAAATCAATCA	59.682	20	269	283	551
GCTTGAGAGTCTTCTTCCTTGC	59.779	22	279	211	489
TTTCCCCAAGCTTCCTACAC	59.17	20	276	464	739

TTGTTTCCACGCACTCACAT	60.16	20	181	60	240
TGTTGACGTTGGATCTGTGAG	59.736	21	263	2325	2587
TTAGCATTTGACTACACTCCTC	58.151	24	233	225	457
GTTGGAAATGCAGCAGAACA	59.847	20	219	984	1202
TTTTCCCGAAAATAAAAAGAA	59.457	24	114	339	452
GATAACATGCCATCACACGC	59.963	20	277	865	1141
CCCTCACACTATCTATCGCCA	60.103	21	224	199	422
TGAACAGCCATCGAGCATAG	59.972	20	267	1203	1469
ACCTTCCACGCAAACTCAAC	60.156	20	249	1284	1532
TGTGATTTCATCCATTCGGA	59.859	20	225	264	488
TCCTCCTATTTTCCGTCGAA	59.64	20	266	182	447
CGACAAACCACCAATTTCCT	59.83	20	182	102	283
GCGCAGATCTAATGGTCCAG	60.765	20	196	9	204
GGGTTTGCCTTTAGCCTCAT	60.451	20	240	130	369
TGGCCCTTTTGTACACTTCA	59.17	20	131	317	447
GTGCAGCACTAGGTCCATTG	59.318	20	280	124	403
TCGCGAATTCAGCTAGAACA	59.712	20	122	24	145
GCCGCATTTCTTCTAACCCT	60.582	20	234	951	1184
AATATTTGCATGGCTCTGGG	59.923	20	274	1266	1539
GGGGCGTATAGACGCAAATA	59.95	20	179	627	805
AATGGCATCTTGGAATCACC	59.756	20	175	1201	1375
TGGGGTTATTAGTGGATCAAG	60.204	22	164	982	1145
GTGCACCTCCTCTTCAACAA	58.854	20	258	1022	1279
TGTTGCGCGTGCTTTAAATA	60.401	20	181	307	487
GAGCAAAGTGTTGAACTCTCG	59.942	23	120	8	127
AGTGGCAGTGGGGGTTAAG	59.974	19	267	13	279
TCGCCGTGTTTGTATTCTTG	59.729	20	259	813	1071
AAACGCGCATTTTTAGGATT	58.764	20	274	356	629
CAATCGGTAATTCAGCTCGG	60.597	20	175	609	783
CGCTATGTGACCATCTGTGG	60.136	20	238	5170	5407
GTTATACCCGTGCGTTCCAC	60.257	20	269	54	322
CGATTGAATTGGTGGGTTTC	60.17	20	173	75	247
AAGTTGCCGATCATCCAATC	59.9	20	184	1548	1731
CGGTTGTTAGGGCAATCAAG	60.493	20	143	163	305
GGGCAAAACTGTAATTGCTCA	60.124	21	261	4048	4308
CACGAGATTTACGTGGTTCG	59.195	20	109	131	239
CATGGAATTGAAACTTTCGGA	59.924	21	170	2	171
AACCTAAAACCCGACCCGAT	61.777	20	278	351	628
CGGCAATTGTTGACCACATA	60.379	20	100	289	388
GTTGGGGAATGGAAGAATGA	59.727	20	247	1032	1278
TTGGCAAATTTTCTTGCACA	60.229	20	159	1027	1185
TGTGGGTGTGTGAGTTGTGA	59.568	20	110	113	222
CGATGCAGCAGAAAGACAAA	60.134	20	245	152	396
AAGGGCTTTGTTGGTTTGTG	60.008	20	241	1080	1320
TTCATTCTTTGCATCCCTCC	60.014	20	194	3728	3921
GTGGTCGGAGAGTTGAGAGC	59.993	20	163	433	595
GGCGCTCCAATCTGAAATTA	60.175	20	211	168	378
GCTTCCGCATTTTCTTTTTG	59.832	20	280	982	1261
ACCTGACACGAACACGACAC	59.63	20	267	850	1116
GTGTGCTGGCATTGCTAGAG	59.621	20	133	43	175
TCAAATCTTACCAGCCGCTT	59.845	20	238	719	956
GCCCATCTGATGCATTCTCT	60.189	20	256	252	507
CTGGTTTTGAACGTTTGCAG	59.362	20	169	602	770
TGTTCTCGTATGATTACGCTCC	59.252	22	270	1023	1292
AGAGCAAGAAACCAGAGGCA	60.134	20	185	156	340
TTGTTATTGAGAGGGCAGGC	60.214	20	162	67	228
GATTGATGAGGGTTCCAAGC	59.488	20	254	93	346
TTTGGGCCTTTGATTCACTT	59.546	20	171	0	170

CACACCTAGTGTGCTATCATCA	57.854	23	209	75	283
ATTTCCCGGAGAGGAGAAAA	60.011	20	267	1004	1270
CCAAATTGCCCTTCTGTGTT	59.971	20	270	449	718
CCAAGATTTGATCATGGCGT	60.864	20	271	585	855
GCACAAAAATGCCTCTCGAT	60.221	20	275	27	301
ATTGCATTGCATCTTCCCTT	59.533	20	165	503	667
GTATTCGCTCTGCCACAACA	59.871	20	237	2586	2822
AAAAACGTGAAGGAGACGACA	59.766	21	203	378	580
CCACACCCTCTTCCTCTGAA	60.229	20	182	401	582
TAGGGTTGAGGTTGGAGGTG	59.959	20	243	1437	1679
TGTAAATCTGCCCGAAAACC	59.938	20	123	80	202
GGTTAACATTTCAGCGAGGC	59.713	20	180	5	184
GGTTAATGAACGCAACCCAA	60.732	20	118	66	183
TTCTCCGTCCCATAAAATGTG	59.809	21	246	824	1069
TGGTGTACAGTAAGAGGCAAA	59.989	24	239	664	902
TAAATCCTGCAATCATCACCC	59.776	21	235	259	493
ACGAAATGAGGAAATCGACG	60.074	20	243	78	320
AACCCGGACAATGAGCAATA	60.331	20	219	257	475
GAAGAGGACCCCATTTGGTT	60.169	20	143	411	553
ATCGATTGAACCAAACACCC	59.653	20	250	87	336
TGAAATAAACATTGCCACCG	59.42	20	268	1001	1268
CAAATCATGTGCGCTGAAAT	59.694	20	135	5535	5669
GGTGGGAGTGTTTTTCGTGT	59.867	20	226	138	363
GTCAAGTCGACCACCCTTGT	60.009	20	132	21	152
TAGTTCGAGGTGGAACGAGG	60.246	20	156	385	540
CCAATTTGAATGGTTATCACCT	60.457	23	272	1210	1481
TGATTACGAGATGTGGAAGCC	60.088	21	163	270	432
CAACTCCTTCCCTGCATTTC	59.67	20	218	1958	2175
TCATTTCAAAAATCAATGGATG	59.291	23	241	2324	2564
GTTTTGTAGCTCTCGTCGGC	60.022	20	241	1003	1243
TTCTTGGTTAGCTGGTCTGGA	59.861	21	223	1900	2122
CTTTTGAACAATGATACCTTCTC	58.271	24	216	36	251
TCATGGTGCTTGAAATTGGA	60.049	20	168	14	181
TGGTAACATAAAGGGCCGAA	60.315	20	237	146	382
CGAACTACGGGGTGAATGAT	59.813	20	255	82	336
GATTGGGATGGGCTAGGAA	59.839	19	280	7	286
CTTACCACCATTCACCACCC	60.088	20	236	722	957
TACCAATGCCACAAAAACGA	59.969	20	120	213	332
TGCAAGTGCAGTTTGACTCTG	60.229	21	262	29	290
ACTATTGCCAGTGGCGTCTC	60.285	20	124	914	1037
TGGAACTCGTCTTCCTCAGT	57.416	20	214	776	989
TCACGATCGAACCACGTAAA	60.111	20	171	1434	1604
ACCTCTTTTCGGTTTGATGG	59.028	20	166	230	395
CGAATGATCTGGTGATGGTG	59.918	20	201	179	379
CAATGGATTAGGCCGAAAGA	60.031	20	183	1109	1291
ACCTGGTCTCCAAGTGATGG	59.962	20	242	2464	2705
TTCCGCCTAACTCTTGGAAA	59.817	20	184	393	576
CAGCCTGCCTTGGAAACTAT	59.336	20	276	117	392
AAACTTGCGGGAATGAGTTG	60.11	20	112	753	864
GCTGCAGATCTAACGACCAAG	60.03	21	130	368	497
TTAACGGTCCGGTCTTATGG	59.817	20	263	384	646
TTAGACGTGAATTGCAAGCG	60.014	20	275	178	452
AGGCCCATCATACCACAGTC	59.81	20	169	953	1121
CATTTTGTGGCCTGTGTTTG	60.004	20	204	2214	2417
GCTCACCGGTTCTTTTGAGA	60.375	20	182	134	315
CAACGATGTGCTAGTTGTGGA	59.773	21	126	99	224
AACACAAAAGGGCTCATTCC	59.031	20	211	103	313
GGTCGTGTTTAGCCAAGGAA	60.11	20	181	535	715

TTACGGCAATTTGCATCAGA	60.215	20	160	335	494
ACTTTTCACGGACTGCCAAC	60.156	20	131	1997	2127
TTCGAAAGCCAAGATGGAAC	60.192	20	243	974	1216
GCATTTTGAGCTCGCATTTT	60.351	20	185	471	655
GTAGGAAACCCGCCATACAA	59.823	20	211	74	284
GTTCGCCAAGAAACTTACCG	59.747	20	258	691	948
CGCCAAAATGTCATCACAGA	60.665	20	144	134	277
TCACCAATCTCCCAGCTTTC	60.195	20	278	662	939
TGCAAGCATCAAAAATGGAG	59.809	20	218	757	974
CAAGTCATACATCATGTTATCT	58.628	27	219	3	221
TCATGATGCCAACTGAATTAAA	58.161	22	280	2	281
CTCGATGAGGAATGGGAAGA	60.15	20	279	68	346
TTGTGTGATTTTGACCCCAA	59.792	20	278	123	400
GACTCAAATTCACATGGCGA	59.654	20	184	4	187
CTATCGTTTTCTCCGCCTTG	59.839	20	174	351	524
CCGATTAAAAACCGAACCAG	59.447	20	232	231	462
CGATTGTTTTGAATTCGCCT	60.074	20	215	12	226
TGAAGGCTGGGAATCAGACT	59.803	20	194	1016	1209
TGCATACAACACGCAAATGA	59.716	20	249	2292	2540
TTCGGAATTTATAATATGGGCA	58.4	22	277	98	374
GCTCGTGTGTTACAGGGGAT	59.997	20	248	704	951
AAATATGCCACCTATTGCCG	59.816	20	254	24	277
AGCTGTTTGGCTACGGAAGA	60.015	20	257	159	415
ACGGCCCTTTCTCTTGAGTT	60.247	20	277	70	346
ATACCATGGCGTGCAAGAGT	60.547	20	219	172	390
GTGGGATTCACGTGGTTTTC	60.218	20	218	207	424
TTTGCATCAAACATGGCTTC	59.67	20	241	1238	1478
CAACTACTCCCTTCGCCAAA	60.241	20	169	454	622
TTCGATCTTCTTTCCTTTCCAA	60.177	22	104	8	111
TACAGGGTTCTCCAACCGAT	59.405	20	176	138	313
GGGTGGAGAGAGAAAGGGAG	60.186	20	254	5491	5744
AAAAAGGGATTATCACGGGG	60.013	20	132	1005	1136
GTGGATGAATTTATGCCGGA	60.67	20	277	465	741
ACGAGAAGCTCTGCAAATCC	59.579	20	148	1149	1296
GGATTTTGATGTATGAGTTTGC	59.297	24	266	461	726
CAACCCCGTCATTTCTCAAT	59.79	20	180	0	179
ACCCTAATTGTTTCGGGCTT	59.835	20	197	212	408
ATCATATGGGTTGGTGTTGTCA	59.978	22	179	183	361
TGTGTTTTCAAAAGCCTAGACA	57.63	22	227	217	443
CTCTAGATCGCGGGCAAGTA	60.502	20	110	9	118
CTGAGAGCGATCGACCATTT	60.362	20	240	197	436
CCGCCGTATCTCCTCACTAA	60.227	20	276	101	376
CGAGGGCCATTTACCCTAGT	60.332	20	106	512	617
TTGTAATAACCCTTATTTTCGTG	58.619	24	266	69	334
AAGAGGGGAGCTCGTACCAT	60.096	20	129	429	557
CGAACAGTGGGCGAGAAATA	61.157	20	266	2104	2369
TCCTTCGAGGAGGAGTCATT	58.816	20	226	498	723
TGCTCTCAAGAACACGCACT	59.776	20	247	374	620
ACAACGACAGAGGACGGAAG	60.298	20	127	5	131
ACCTCCATGGGTTGTCTGTG	60.84	20	273	485	757
CAAGAGCTTAGAACGGGTGG	59.869	20	158	3004	3161
GTACGGCTGAGCCTGATTG	59.41	19	218	649	866
TGTCCGATATCTAGGCCAAA	58.187	20	270	395	664
GACATTTGTGGTGGATGTGG	59.656	20	184	185	368
AGTTGGGGTTGAGTTGTGCT	59.622	20	195	570	764
ATTAATCCGATGGCCCTCAT	60.499	20	211	615	825
GTCTAGGAAAGGGCGAATCA	59.269	20	253	214	466
TTTTCTTTTACCTGTATTCAAGA	58.032	27	248	225	472

CGCCATAGCTTCTTGGTCTC	59.978	20	225	115	339
GAAAAGGGGAGGATCGGTTA	60.258	20	154	357	510
CGGATCACCAGATCCGATAG	60.439	20	252	470	721
TGAAAGAATATGAGTTTGAAC	60.004	24	191	98	288
CCAACCAAATCCGGTTACTG	60.22	20	266	62	327
AGGCCTTGCTCTCTCTGTTG	59.745	20	279	62	340
CAGCCATGGTGGTGATAAGA	59.522	20	120	4	123
ATCGAAAATGCCTCTCACCA	60.603	20	224	1218	1441
GAGTTGGTGTGTTGGCATTG	60.008	20	163	394	556
CGGTTGACAGCCGATTTTAT	59.96	20	270	567	836
GGCTGGATAGTTTTGGCTCA	60.214	20	217	649	865
TGCTCAAGTTCTTGCCATTG	59.988	20	276	493	768
TGACGAGGAAACAAAGGGAG	60.224	20	108	659	766
TGATGCAAATTGGGAAGCTA	59.257	20	240	121	360
ATGTCAAAATATGGGCATCCA	60.031	21	277	611	887
GAAAGTTTGGGGTGGGTTTT	60.068	20	171	996	1166
TTCATATATCACGTTAAGACAT	58.031	26	233	410	642
CCAAACGTATATGCCCTGGT	59.708	20	222	96	317
GCGTCGTTTCTTGAATTAGGG	60.962	21	205	1272	1476
TCAACAATACACGCCACACA	59.589	20	223	1279	1501
AATGGTGCCCAAATTTGTCT	59.292	20	239	228	466
TGCGTTTTGATGATATATATGT	58.859	26	199	971	1169
AGGGCAACCTCGAATCAATA	59.528	20	236	2961	3196
TGAGAAAAGGTTGTACATGGC	60.534	22	221	72	292
ATGTCCAAAGCTGGCAGAGT	59.874	20	166	547	712
TGCATGCACGTGAATATGG	60.088	19	139	321	459
TTTTCATGTTTTGGAGCATCA	59.147	21	172	370	541
TTCCCACCATTCACATCTTG	59.343	20	256	482	737
TGCATGTCTGCTGTCTGTGA	60.193	20	187	1729	1915
TTATCACCTGATTTCCTCCCT	57.599	21	208	595	802
AAAAATCCTTATGCCCCCAA	60.489	20	237	12	248
ACCCGGGTTTCGAAGTAGAC	60.361	20	188	1398	1585
TCCTTGCCAACAAGATAGTGC	60.264	21	220	2609	2828
AGCACAACTGCACAAGCAGA	60.812	20	239	45	283
TCGAAGGATGTGTTCATTGTG	59.556	21	249	1909	2157
AGTTGGGACGGAGGGAGTAT	59.817	20	262	219	480
CAAGCACCATAAAGTTCAACG	60.166	22	214	318	531
CAACAGGTCTCACCAATCCA	59.52	20	135	973	1107
TGACGAGTTAGAATGGCAAAG	59.883	22	108	12	119
GTGGATCCAAGCTGACCAGT	60.12	20	178	3756	3933
CGGAAGAATTAGACTCGGCA	60.344	20	265	38	302
ATGCATATATTAGGGGAAAAA	58.112	27	278	896	1173
CCTTTAACAAATTGGTGTAGTC	57.414	24	194	216	409
AGAAATTTGTGAATCGCCCA	60.448	20	228	802	1029
TGAGAGGTCTAGGGTTCGGA	59.797	20	244	641	884
TTTCATGTCCCTACTTCCGC	60.074	20	105	3	107
ATGTGGATAGCAGAGGCGAG	60.384	20	162	47	208
GTCCACGGTGGTTTGAGAGT	60.009	20	153	39	191
TGTATGACATTTGGCTCCGA	60.073	20	230	496	725
AATTCCAGCCATGTAGGTGC	59.962	20	173	824	996
TTGAGTTACAAGTGAACTACC	60.089	24	253	1193	1445
TGCCCACTAATCTGTAAAGGG	59.892	22	184	927	1110
GTGGCGGTAGGTAGCTCTTG	59.898	20	204	170	373
TCCGTGAACCGTTCTTCTTC	60.232	20	265	444	708
GAGGCTGGGTGTGAGAGAAA	60.386	20	193	1558	1750
TCCGTTCATTCAACGAGGTT	60.495	20	280	50	329
CCATCGACAGTGTTGCTCTG	60.463	20	211	719	929
TCGGAAAAACTCCTGAGTGA	58.414	20	182	380	561

GATGTGGTGTTGACGGTGAT	59.239	20	174	130	303
CCTGTAGCCATGTGATTGTTG	59.061	21	259	412	670
GGGAACATGCTTCCTGAAAA	60.051	20	159	6	164
CGTTCTTTCTGATTCGCCTC	59.955	20	147	486	632
TGGGCAATACGTGGTTTAGG	60.742	20	277	97	373
CTCCTCAACTGCAACACTCG	59.616	20	199	207	405
TCAGTTTTCGTCCCTTTTCG	60.22	20	206	852	1057
CATTCCCGAGAATCCTTCAT	58.934	20	168	792	959
GCAAAAGGTTTGAAGTCCTGA	59.345	21	237	895	1131
GCATGTTATGGTGGTGCTTG	59.995	20	241	11	251
AACATTAAATCTCATACCCTCA	59.33	27	251	224	474
CTGATCCTTTCTGGGAGTCG	59.797	20	195	210	404
TCACTCCATCTTCACACCCA	60.088	20	148	2661	2808
GTTAGAATGGCGCCGATAGA	60.196	20	160	1180	1339
GCGGGGAAAAATAGGAAGAA	60.381	20	175	179	353
TTCCTCAATTTCTTCCACCCT	59.926	21	236	164	399
ACTTTCCAAGCATCCAACCA	60.495	20	279	59	337
TCCACTTCGGTACTTTTCGC	60.249	20	124	2873	2996
AGAACCTATCTCGGTGAGCG	59.454	20	240	6	245
GGTTTTGACCATATTTACTGTTT	59.631	26	119	437	555
TTAGTTAGTACCGATTTCAGGG	57.499	24	151	1179	1329
GGAGAACGTGAAAGCCAAAG	59.853	20	188	9	196
TGACCTTTAAGGCCGATGTT	59.569	20	252	782	1033
TTGTTCTTTGGTTGCAGGAA	59.293	20	189	2814	3002
CCAACAAGGCTAGCTAAGGG	58.994	20	171	34	204
ACCCAAAACGTCCATTTTCC	60.949	20	275	572	846
GGATTGAATGGATGTTTGGA	58.187	20	101	0	100
TCACAAATACCCCTAAACCCA	59.188	21	146	358	503
TGTCATGGCATTTTTGTATGTTT	59.288	23	249	302	550
TTGCCATCGAGCTAAAACAA	59.443	20	224	22	245
AAGATTTGATCATGGGCGTT	59.391	20	234	377	610
GCTGTAATATGTACCGTCCGC	59.515	21	236	241	476
GGGCTGCCTCCTAATCCTAA	60.542	20	266	336	601
TTATATGACCCCCTCCCCTC	59.974	20	232	1110	1341
CTTAAGGCACACTGCACCAA	59.904	20	267	1191	1457
GTTTGGAGGAGCAAGTGGAG	59.844	20	260	941	1200
CCATCATTTCATTCCCAACC	59.991	20	219	3589	3807
CGACTTACGATCGTGTCTTGA	58.937	21	195	326	520
GACAACACCCTCAAATGGCT	59.973	20	229	959	1187
CCTTAACAAAAGCAAACCGC	59.758	20	250	704	953
TTTCGAATGATTTTGCCCTC	60.016	20	218	0	217
TTGTTTACACACGGTGCGAT	60.035	20	254	84	337
ATTTTCCCCAAATTTGTCCC	59.867	20	140	23	162
CTTGAATTGCTCTCCCTCCA	60.331	20	259	153	411
ACGTCCAAATTGCTCGGTAA	60.502	20	262	130	391
GTCCGAGTGCTTGTATGCAG	59.47	20	264	201	464
ATGCCACTCTTGTGCTTCCT	59.874	20	169	9	177
AAGCCACCTTCCTTTGCTTT	60.242	20	150	1059	1208
TCCTTTCTTCTTACGGCACC	59.312	20	241	800	1040
CGCGAACTCATAAATTGAACA	58.83	21	217	9	225
ATGACCGTCCGTTTTGAAGA	60.495	20	261	276	536
CCAAAAGTGTTATTTTTGTTTCC	57.875	23	145	65	209
TTGTTAATCAGTTTATGCATCTT	59.484	25	150	24	173
TGTCCTCCATTAAGCAAGCC	60.214	20	115	0	114
TGTGATGAGAGAGAGGGGCT	59.945	20	224	115	338
CGAAGGTACGGTATGCGATT	59.982	20	187	47	233
AGAATGCCGGCGATAAGAG	60.324	19	192	398	589
GCAACTGCAAGTTCAAAGCA	60.18	20	267	514	780

ATTTTGGGAGAAGTATTGGGA	57.54	21	184	56	239
CCAATTTGAATGGTTATCACCT	60.457	23	162	1853	2014
GTTATGCGTTTTGACGGGAT	59.829	20	231	285	515
TGCATGGATGCAAGTTGAAG	60.812	20	233	134	366
AATAGCTTTGGGTGCATTGG	59.96	20	242	2814	3055
AATTAATTTGGCCGGTTTGG	60.876	20	238	13	250
TTCCGAAAATATGCTCCACA	59.112	20	270	697	966
AGAGGAGCCCCATTCATTCT	60.037	20	216	222	437
TGGGTATGTCGATGTCGATG	60.353	20	207	3	209
AGAGGTTTGTGCCATTCGTC	60.119	20	236	154	389
AGGGTCCCACCCTTTTGTTA	60.581	20	145	199	343
TATGAACCCACCAGCATTCA	59.924	20	125	1963	2087
CAGCTTGCTGAGTCCAATGA	60.136	20	260	327	586
GCTAGAGGGTTTTGTTAATATG	58.796	27	173	325	497
TTAAGGCCAACTTCCCTCCT	60.068	20	249	1542	1790
AGGAATGATGGGATCTGCAA	60.426	20	240	2014	2253
GGCGGCGTGACTTATTCTAA	60.23	20	263	207	469
GGGGGAAAATTATAGTTAGGG	57.532	22	117	515	631
CGATAGATTCGATGAACCCC	59.344	20	227	664	890
GCAGTGCAATTGAAGGTTTG	59.322	20	126	5	130
GGGCCTATTGAGCCAAGACT	60.599	20	280	972	1251
GAAAGTGCATTTTTGGGAGC	59.691	20	242	96	337
CAGAAACATGTCAACGTGAGA	60.196	23	278	1114	1391
TCTCCGAGTTCTTGCTCTCC	59.679	20	209	371	579
CCTGGCTTCAAAACCAATGA	61.001	20	210	714	923
AATTGACCTTTGACGTTGGC	59.978	20	241	4	244
TTTTATTCAGGCAAACATTCTC	58.796	23	205	311	515
CGCTGGTTTTGGAGATCAAT	60.074	20	229	2293	2521
TCCGGTCCGATTACAATTTC	59.762	20	202	282	483
CAGCATTTCTTCAACTGCGA	60.134	20	100	1446	1545
CTTCCAGAGGGATACCGTCA	60.065	20	199	633	831
TCCGGATTGTCACACCTATG	59.369	20	223	90	312
TGCGACCTTAAATTTGGTGAC	59.989	21	189	21	209
TCACTTTTACAACTTCCACATG	58.721	24	204	96	299
TGGAAAGAACTAAATGCCCG	60.067	20	165	137	301
TGTGCATGTCTCATTTCGTTT	59.188	21	134	25	158
AGCCATGGTTCAATCATCAAC	59.811	21	254	3115	3368
TCACAAACCCATGTCCCTTT	60.21	20	245	1456	1700
AAGGAAACATTCTTTTGGGGA	59.801	21	248	1914	2161
TGAGGGACTTGAAGGGTTTG	60.081	20	217	169	385
AGATTGGGTACCCGACACTG	59.844	20	175	5	179
AGATTCAAGGGCCGAGATTT	60.039	20	199	814	1012
AAATTGAGCTCCATAGCCGA	59.807	20	226	6	231
AAAATCAAAGGCCCACAATG	59.801	20	145	5	149
AACTGTTCTCGACTCAGGGC	59.455	20	242	20	261
AAGGGTGGAAGGTTGATTCC	60.169	20	156	456	611
ATGTGAGTGGCACGTGATTC	59.557	20	210	1612	1821
TATCATTTTGCCCAACCTCC	59.762	20	278	1234	1511
GGATGGCAAGCTTTTAGCTG	59.982	20	193	520	712
TATCGCTGTGAGTGTGGGTG	60.745	20	219	1042	1260
GCCTTGATTGGAACATGGAA	60.843	20	251	102	352
TGTAACCCAAACCAAGCACA	60.004	20	245	2097	2341
AAAGAGAGGAGAGGCGAAGG	60.088	20	192	6	197
CCAGACCAACCAACACTGACT	60.057	21	278	90	367
GTTACTTGCGGCACTAAGCC	59.911	20	251	814	1064
CTCTTTGCTTATTCGCCCTG	59.975	20	277	451	727
CTTTGCCCCTTTACTTGCTG	59.876	20	162	467	628
CCACATTTCAGAGTCCCCAC	60.363	20	230	692	921

TCAACCATTTGTTTTTGCCA	59.946	20	245	908	1152
CCCGTGGACGTAGATTCATT	59.813	20	255	4	258
TGGTGGAGCGTCTGTTTTAAT	59.623	21	280	31	310
CTGGGAAAACCCTGTGTAGC	59.592	20	276	1943	2218
GGAGCCATGATTAGCTCCTCT	59.825	21	265	246	510
GACCGCAGGTTAATCCAGAA	60.074	20	197	1094	1290
TGTCTCCATTCTATTGGCCC	59.894	20	267	199	465
CCGAACATTTCACAATCCCT	59.79	20	243	206	448
ATTAGCGAACATGGAGGTGG	59.955	20	135	493	627
AACCCTAACGCACAACTCAA	58.283	20	160	30	189
AAAATCAAAGGCCCACAATG	59.801	20	277	379	655
TTATTGTGTGGGGCAGAGGT	60.375	20	216	149	364
GAAACGTTTTCCCTGAGCAC	59.717	20	184	404	587
GATTCTGTATCCGCCATTGAA	59.915	21	249	619	867
TGTGAAAGTCTTTGGATGGTTC	60.026	23	258	101	358
GCTTCGTTGATGATGGAATG	59.079	20	244	474	717
CCGCCGATGTGATTTTAACT	59.96	20	198	317	514
CACCAAAATTCCGACACGTA	59.439	20	186	637	822
CATTTTTCCTCATGGAATGGAT	60.02	22	188	1123	1310
GCAGCTGCGAGAGGTTTAAG	60.292	20	121	124	244
ACGGAATACAATTCGACAGAA	59.891	23	277	1051	1327
GAGGGGTGTTTCCAGACAAA	59.943	20	246	57	302
GTTGTTGAGGTGGTCTCCGT	60.009	20	227	626	852
TTCCCGGCTGAATGTTACAA	61.389	20	177	10	186
AGCTTTCAGGTAGGCACAGG	59.496	20	201	15	215
ACGAAAATCTCTGCCCAATG	60.074	20	213	173	385
AATTGCCACCCCTCACTACA	60.375	20	247	488	734
TAAGGGTTATCACCGGATCG	59.778	20	124	384	507
TGCCGATCAATGCAGTCTAC	59.83	20	273	842	1114
CGGGTCGTGTCAGAAATTG	60.096	19	278	173	450
TATGTGGCCCCAACTTTTTC	59.801	20	268	87	354
GGGTCCCACCACCTAACATA	59.526	20	197	69	265
TCACTCCAGTTTTTCACCCA	59.109	20	208	900	1107
GGAAGCAAAAATGGCAGAAG	59.823	20	181	632	812
TTGACTAAGTTGTGTGAGCAGC	59.966	23	265	739	1003
ACGTAAAAATGGTTATTATTGG	59.092	26	255	909	1163
ATGCTGATGTTAGTGCGCTG	60.042	20	188	16	203
ACCTTATCGCCCCACTCTCT	60.096	20	230	34	263
GAAGGAGGACTCCAAAGGGA	60.565	20	185	605	789
ATCGTCCATCTACGCAAACC	59.962	20	218	150	367
AATTTCCAGATTCCCGTCG	59.879	19	267	1424	1690
TTGAGCTGTTATGCGTTTTGA	59.5	21	103	1557	1659
TCTGCACGTGATTTTCTTGG	59.84	20	199	213	411
AGGGGGTTATCACCTGATCG	61.095	20	190	533	722
ATTTCTGCAATTGGGGTTCT	58.504	20	140	67	206
ACCGTGACAAGACCTTTGAA	58.187	20	187	797	983
CCACAACCCTTTCATCACCT	59.82	20	263	327	589
CTCGCAAGCTTCGATTTCTT	59.73	20	178	147	324
CAATTACACTGCATGGGCTG	60.134	20	165	78	242
CGTGATTCCTGCGTCTTTCT	60.397	20	277	118	394
CGGTTTCCAGATCTTTCGAG	59.807	20	166	2488	2653
TGGCAGAAGTCGTTGAACTG	60.025	20	205	156	360
TCGGAGCCATAATCATCACA	60.033	20	252	669	920
TTGCTCATTGATATTCAATCATT	57.735	24	220	213	432
GTTTTCATTTGATCACGCCC	60.318	20	114	16	129
ATGAGTTCGAGGCTCAATGG	60.218	20	221	463	683
CAAGCAGTGAGATTGGGACA	59.831	20	204	1667	1870
CGTCCAGTTCACTTCATTGG	59.135	20	113	1166	1278

CCTGAATTCTCCCCAACTCA	60.042	20	273	498	770
GAGTTCGTCAAACCTCCCAA	60.088	20	256	138	393
GAGGGAAATGGTGGGGTATT	59.881	20	162	1022	1183
AATCTTTGAACAGCCGATGG	60.074	20	211	574	784
GTTCGAACCCTTCATCATCG	60.461	20	103	570	672
CTCGTCCATTTCCCTTCAGA	60.187	20	227	390	616
AGAGTGCGCGTTTTCATCTT	60.022	20	148	402	549
TCACGACATTATTTCCCTCAAA	59.451	22	156	3458	3613
GTAGCCATGGAAGAATGCGT	60.103	20	205	354	558
TGCTCCCACATTAGTAGCACC	60.147	21	109	388	496
ACCCGAATCCGTTACAACAA	60.227	20	125	560	684
TGAAGTTAGGAAATAAGGAGG	58.743	25	185	659	843
AAATCATGTTTCACCGCCAC	60.765	20	133	2	134
CCAATTGGCGTTGAGTACAA	59.585	20	246	144	389
GTCTTCGAGACGGAACCACT	59.305	20	256	582	837
TCTGTAGCCCAGTAGGCCAT	59.717	20	145	2889	3033
CCACCACCAGAAGCAAACTT	60.149	20	141	249	389
GGCATTACAGAAAGTTCCGC	59.713	20	261	385	645
GAACAAGGGTAAGATGAACCC	60.221	22	196	385	580
GCGGCTTCATCTTTACTTGC	59.988	20	244	162	405
TCTTCACTGCTGACCGTGTT	59.467	20	175	167	341
CCAATTGTAAAGGGGGCAC	60.177	19	269	1643	1911
TTCGATTCAAGGCACATCAA	60.197	20	181	251	431
AGGCTGGATTTCGTCCCTAT	59.925	20	167	483	649
AAACGGTTGAAAAGCCCATA	59.451	20	248	17	264
CATGAAGGCTGCGATTAGTG	59.444	20	233	94	326
CGTCACGGTGGTTCTTCAT	59.535	19	277	555	831
ACCCACACCAAATATTCCCA	59.91	20	267	721	987
TCAAACCACAGCTGAAAACG	59.881	20	230	2448	2677
TTGATGCACGAATTTGGAAG	59.664	20	187	239	425
CAGACCGTTAGGGGTGTTCA	60.943	20	275	50	324
CCACTTATGTCGAAGATTTTTG	59.933	24	252	1598	1849
TGCACTCTAAGGGATGATTGC	60.228	21	130	322	451
AATGGCGCTATCTGGTTGTT	59.597	20	110	6947	7056
AATTTGGGCCTCCATTATCC	59.984	20	215	414	628
GTGATTGCTTCTTCATGGCA	59.805	20	193	155	347
CTTTTTGGTTGCTGTTGGGT	60.008	20	208	6954	7161
AACACACAAAGCCACCATCA	60.008	20	214	182	395
AGTGGTTATTACCGGATCGC	58.93	20	192	751	942
CGTGAGAAGCGTTGATCTTG	59.591	20	244	936	1179
AGGAAAAACGTGGCAGTCAG	60.291	20	254	567	820
TGCAGGGTATGCATGTTTGT	59.995	20	160	305	464
CTGCGTGTGAGGGCTACTTT	60.453	20	172	780	951
ACAAACAATGGGACCACAAAA	60.118	21	257	248	504
AGTAAGAACCGCGAGCTGAA	60.154	20	240	251	490
GTTTTAAACCAAGGCCTCCC	59.814	20	225	150	374
GGCAATGGACATGGAAGAAA	60.843	20	242	1835	2076
GACAAGCACTCATGTGATGGA	59.698	21	194	3082	3275
CTCCTGATCCATTACCCGAA	59.887	20	258	205	462
TGCAAGATTGCGACAGTACA	59.021	20	127	1155	1281
GTGCCGTGTACTTCCTCACC	60.577	20	244	83	326
CAGTCATTGGATTGCATTGTG	59.98	21	142	359	500
ATGAAAATACGCGGGGAAAT	60.517	20	273	84	356
CAAAGGAAGTCGGTTGGTTC	59.569	20	167	16	182
GTGCCCAAAACTACCGAAAA	59.975	20	261	3585	3845
AAACCGAATCTTTTCGTGAATC	59.485	22	243	25	267
AGATGAGGGATTTTGGGGAG	60.264	20	194	3273	3466
CCAAGTAAAGCTCGAACCCA	60.241	20	268	1294	1561

TTTCATGATCCAGATGGACG	59.451	20	236	140	375
TGTGGAGCTACTCAGCCCAT	60.823	20	273	158	430
TGCGAAAAATTTGGTTCTTG	58.792	20	280	165	444
GTGGCACGATCATTGTTGTC	59.975	20	197	325	521
GTGGCACGATCATTGTTGTC	59.975	20	197	314	510
CATCACCTTCACCATCACCA	60.378	20	260	396	655
CGTGCTCATGTCAGCAAGTC	60.627	20	186	1	186
TCGAAGATCAATGGTCCACA	60.048	20	135	117	251
TGCGTTTTGACAATATATAGGT	60.083	26	135	1390	1524
CTGGGAGCGATAACATGGAT	59.917	20	280	2377	2656
GTTGGCATAAAATCCAACCA	58.335	20	225	531	755
GCTATCAGGAACCTATGTTTGG	57.774	22	217	1207	1423
TTCAAACAAGGCATAAAACTTT	58.412	23	146	213	358
AAGAGGACAGGCATGCAGTT	59.874	20	188	876	1063
GCAAAGAAGGGACGACTGAG	59.989	20	239	884	1122
TCACGTGTCAGCACACAATTT	60.214	21	187	29	215
ATTACAGCCCAGATTCCCAA	59.387	20	278	231	508
TGATAGCGTTTTGCTGTATGCT	59.938	22	202	418	619
GAGGTTGGTGACAGTGGCTT	60.159	20	263	493	755
ATCGCTTCTTCTTTCGCAGA	60.235	20	273	222	494
CCCCTGGTTGTTATCCTTGA	59.784	20	186	37	222
TTTCGACCTTCGTAAAGCCT	58.973	20	247	916	1162
TCGATAGGACGTGTATGACGA	59.163	21	211	1692	1902
GGAGAAATTTGATTTGTTGGG	58.405	21	274	205	478
TAACCCTTGGATCTGAAGCA	58.298	20	268	49	316
TACTCTTCGATCCCGCGTAT	59.691	20	153	151	303
AGATGCTTTTTGTCGCGAAT	59.851	20	276	2433	2708
CGCCGCCATTATCTCTACTC	59.829	20	173	103	275
CCCACTTTTAAATTGCGAATG	59.481	21	280	709	988
GATTGCGTAGTCGTGTGTGG	60.183	20	266	562	827
TTAAACTACACATGTAATCCAT	58.07	27	199	923	1121
TGGTTTGGCGGTTGATAAAT	60.188	20	256	115	370
CGCGTTAACAGTGGAAAACA	59.769	20	240	96	335
AAAGTTGGGATGGAGGGAGT	59.795	20	223	13	235
ACACAGAATTCGCCCAAAAC	59.978	20	223	231	453
ACACCATCCACTCACCCAAT	60.096	20	275	90	364
TCTTTCTCATTCAACACCCCA	60.48	21	109	3	111
GCTTAAGAATCGTGGCTTCG	59.982	20	197	222	418
AGCAAAAATAAAGGGGCTGC	60.566	20	278	609	886
GGCAAATTGGGAATTAGTGG	59.273	20	267	260	526
ACGGCACATCAAACACCATA	59.847	20	190	4599	4788
GATCACGCAATTCCTCCTGT	60.081	20	182	347	528
GCGAAAATTGGGGTTTCTTT	60.292	20	133	2273	2405
GCATCAAGAATCAAGCCTCC	59.78	20	265	711	975
TGTATTTTGTCTGGCAGCGT	59.347	20	214	159	372
TTATTCGAGCTGGTCAACCC	60.074	20	203	446	648
CCTCTTCTTTCCCAAATCCC	59.875	20	109	1144	1252
GATCCCGACGACCTCTCATA	60.034	20	144	534	677
AACCCAACGTCGGTTACAAA	60.262	20	208	840	1047
ATCCCTAAAGTGCCCTCCAA	60.817	20	189	20	208
AATGGAGTGCACCTCCTCAA	60.656	20	248	1146	1393
ATGGGGTGAATTTAAAGGGG	59.882	20	261	261	521
ATTGACTAGGAGCACGCGAA	60.934	20	201	659	859
GTCTGGGGCTTTGTTTGAGA	60.232	20	237	88	324
TTGACACACTCTTTCTCAGTGG	59.938	23	244	1020	1263
TTCTTCCCGTAGTCCAGCAG	60.388	20	225	354	578
TGGCATCACATGGTCTCTTG	60.688	20	132	380	511
GTGCATGAGCTGTCTCTTGG	59.577	20	231	7	237

TTGACAATATTTAGTGTTTTGA	58.99	27	166	943	1108
GCGCAATGGATAAACCTGAT	59.929	20	238	179	416
GTCCCATTCTACTGCCCAAA	59.933	20	234	485	718
CGTAAATCCGGCTTGAATTG	60.448	20	164	353	516
GCCCTGTCACAACTATTCCC	59.41	20	222	92	313
GTAATTACATGGCCAACGGG	60.074	20	265	177	441
TCTCATCCTTTGCCTTGGTT	59.67	20	234	395	628
GAAAATTGGCAGGATCCGTA	59.901	20	135	235	369
TTCCCACCATGATTTCAACA	59.75	20	219	1308	1526
TGTTTATGCCGTTGATACAAAA	59.437	23	209	197	405
AACAGCTAGCGCCATCTACG	60.564	20	211	215	425
TTTCCTGCAACAATTTCAACC	59.967	21	242	625	866
GGTTTGAACCATGATTTATTTG	59.491	23	186	451	636
AATAGCCGTTGGGCTTTTGT	60.849	20	267	15	281
TACCCGCAGTTGGCTAGTTT	59.769	20	230	497	726
TTCGCTCATCATCCTCCTTT	59.773	20	197	1218	1414
AACTCCAAATTTTGATGCATGT	58.493	22	242	383	624
AATTGAGAGGCTGCCAAGTC	59.434	20	184	848	1031
TATCCCCGAATGTGCCTAAC	59.784	20	219	844	1062
TGTGATGAAGTTTACACAACA	58.163	25	209	1628	1836
GGGGTAGGAGTTTGGTGGTT	60.088	20	169	23	191
TTTTCGCAGAGACCTGGAAT	59.813	20	196	259	454
GGGGACTGTCAATTCATTTTGT	60.096	22	111	1388	1498
TCACTGCAATTGTTCGTTCC	59.697	20	180	90	269
TGCCTACACAAATCCACCAA	59.964	20	134	920	1053
ATTGAGCCAGGGAGAAGTGA	59.803	20	251	29	279
TCACGCCTTCTCTCTCCAAT	59.95	20	238	636	873
CCGTTATCTGCTTCGTTTCC	59.708	20	221	126	346
AACCCTCAACCCTCTCCAAT	59.795	20	202	43	244
GTGGCCCTCAGATTTCAGAT	59.094	20	150	168	317
TCGTTTCGGACCAATCTACA	59.123	20	269	214	482
TGCTTCCCTCACAACAACAA	60.278	20	267	1784	2050
CGTTTTTGGCCTGATATTTG	58.162	20	187	17	203
TGCATCTGTGAATGGAAAGC	59.805	20	180	174	353
CTGGGAGCATGTCAGTGTTG	60.309	20	220	767	986
CTTACAATGTTGCCCCCAAG	60.357	20	277	814	1090
TTTTTGTAAACCGCCTCGAT	59.586	20	195	582	776
GGATTTTCACAGGCCAAAGA	60.051	20	153	508	660
CAGAGAAAAGTCGTCGGGAA	60.366	20	180	158	337
GAGTTCCCGCGTCATAAAAA	60.074	20	265	489	753
GCATTGAAGTTAGTGGGGGA	59.933	20	183	0	182
TGATGAATGACGACACATGC	59.037	20	255	327	581
AGAGGACAACGGGACAGCTA	59.867	20	137	765	901
GCACGATCTCATGATTCCAA	59.61	20	255	21	275
TAATTTGGCCGGTTTCATTT	59.3	20	202	23	224
CAATAAACGCCCACATGAAA	59.42	20	280	357	636
AAATTCCAAACTCCGACCAA	59.406	20	203	203	405
CGAGTGCCGTACTTGAGAGA	59.187	20	212	213	424
GCGCTATTTTTAACCCCAAA	59.11	20	236	182	417
TCTCCTTTTCCACCATTGCT	59.67	20	259	980	1238
TTGTCTCTTGCATCACTCCCT	59.859	21	224	523	746
ACACATGTGGCTTTGCTTTG	59.764	20	163	191	353
ATTTCCTCCCCAGCACTTTT	59.94	20	119	113	231
GCACCATCTTCTCAACACCA	59.682	20	189	178	366
GCTTTGTTTTCCTCTGCGAC	60	20	273	609	881
GTTAACGGTCCGGTATCACG	60.249	20	258	863	1120
TCTTCGTGTTCTTCGTCGTG	60.025	20	154	938	1091
CAAATCATGTTGAAAGGAACC	59.839	22	272	728	999

AAGTAGCCATTGGTGGGTTG	59.853	20	161	242	402
TGGTCACATGCACTATCTGC	58.217	20	274	180	453
GCCTCAAGACAGAACTTCGC	60.142	20	131	59	189
TGTGAGGGACACAATTCTTGA	59.124	21	247	205	451
TGGGGTGATTGGTAATAGCTC	58.917	21	175	140	314
CATGAGCGTTCGTCATTGTC	60.272	20	130	16	145
GCTTTACGTTTCAACCCGAA	60.11	20	184	287	470
TCTTAATGAGGGCCCCTACC	60.278	20	261	127	387
ATTCCTATGGGTTTTGGGGT	59.397	20	224	74	297
GGGAGAAATCGATAATGGGG	60.47	20	254	150	403
AAAATCAAAGGCCCACAATG	59.801	20	140	995	1134
GCGCAATTGCATCTATTGAA	59.809	20	203	1985	2187
TGGGTGTAGCAGCATTTTGA	60.257	20	169	263	431
CTCAAACCCCAAGAATCGAA	60.044	20	217	490	706
AATTAGCTTCTTCGTCGCGT	59.138	20	208	1458	1665
GCGAGATCCAGAAGTCCAAT	59.243	20	261	1445	1705
TAATCTGTTCCGGCCTCTTG	60.206	20	230	3245	3474
TTTTGCTTGAATGCTTTCCC	60.188	20	155	719	873
CAAAAGGTTTATCCCAGTCTCT	58.333	23	129	3518	3646
TCGAAGATGAATTTTTGGAAAT	60.292	23	234	25	258
TAAGACACCAGGCAGTTCCC	60.111	20	228	237	464
ACACACACACGCACACACAC	60.177	20	244	307	550
ATGAAGAAAATCTGGCGCTG	60.352	20	271	588	858
TGAAGTCGTCGTAGGAAAGCA	60.948	21	224	735	958
CAAAGCTCAAGCTGATGCAA	60.28	20	210	2994	3203
GAATTCTCGACATTCCCGTC	59.488	20	277	340	616
GTGATGATTCGGCTCGTTTT	60.081	20	184	568	751
CATTCAACGCATTACGAGGA	59.688	20	279	2773	3051
TCGAAGCCATGGCCTATTTA	60.548	20	214	118	331
TGACCCTTTGTACCGTTCCT	59.449	20	277	17	293
AAGGAACGAACAAGTTTTCCA	58.73	21	246	678	923
TGAATGTTGTCGTAGCCTGTC	58.79	21	215	1251	1465
ATTGTCTCTCATTCCGAGCG	60.362	20	127	531	657
GTGGCATGGGGAAGCTACTA	60.096	20	236	50	285
GAGCACGCAGAGAAGCAATA	59.326	20	224	392	615
TCCGGCCAAATTAAAAGAAA	59.538	20	271	196	466
GTGGTGGAGATTTGGGTGTC	60.223	20	106	130	235
TTTGTCGTATCAGCAGCCAC	59.871	20	268	4780	5047
CAACATGTGGAGATCGAGGA	59.631	20	197	631	827
TCTTTAACCGCCACCAAAAC	59.975	20	208	524	731
TGAGAGCAGTTTCGGACATAA	59.883	22	278	142	419
CGAAATGCACAAAACACGAG	60.293	20	137	428	564
CTTCAGCAAACCAGCTCTCC	60.134	20	140	151	290
TGCGAAGTTTGTTCTTGTGC	60.035	20	160	557	716
TGGACGAGACGCACTAGAAA	59.591	20	242	3	244
TTGGCTTTGCAATCTCATTTT	59.712	21	267	80	346
TGTGAAAGTGGAAAACACCC	58.442	20	240	512	751
ACCATGTTTCTGCAAAGGCT	59.74	20	249	65	313
AGCTCGGTCGGGTAGAAAGT	60.268	20	242	95	336
GGGGGTTATCATGGGATCA	60.352	19	267	2403	2669
GAAAGTGAAGAATCGATTGGA	59.601	23	124	367	490
CTTCACGCAAACAAATTCCA	59.706	20	162	242	403
CCATCTGTTGTGTTGGCAAG	60.152	20	197	498	694
CCCAACTTTCTCCCCTCTTC	60.045	20	241	3344	3584
TGAAGCACAATGAAAACGGA	60.234	20	228	139	366
GCAGAGAAAATTGAAACCCC	58.622	20	229	1564	1792
TTCTCAACAGCGTGTTTGGT	59.339	20	280	1318	1597
AAATAGGTCGGGCTTTAGGC	59.593	20	191	311	501

CTGAAATGAAATCATGCCCC	60.274	20	203	799	1001
TGTTGTGTGCAAGTTCCCAT	60.008	20	218	583	800
GTGCACAACAAATAGGCAAAA	58.738	21	225	225	449
TACATTCCAATGGCAAAGCC	60.837	20	196	769	964
ACAACTCATTGTCAACCGCA	60.16	20	100	685	784
TTCCAAGATCAACGGACGAT	60.461	20	167	496	662
AGGCTGATTGTGAACTCCAGA	59.859	21	257	2084	2340
CATGTTACACGTGGACGCTC	60.183	20	134	2	135
TCTCTTCCCAGCAAGAAAGG	59.545	20	270	95	364
GGAATTGTTCATTTGCAACG	59.016	20	275	802	1076
TTAAATATTCATGGGCACGC	58.513	20	160	207	366
CTCAGGCCTATCGAACCAAA	60.206	20	248	130	377
TGACCCGCCTCATCTTCTAC	60.218	20	187	1168	1354
CAGGTTTATCAACAAGGTTTTG	59.795	23	141	23	163
CATCGCCGATTACATTTCCT	59.923	20	280	563	842
ACCTCCTCCTTTTCCTTCCA	60.045	20	248	804	1051
TGCGTAGAACAGAGAGCGAA	59.888	20	122	518	639
CGAATTCTAGGCGATTCCTG	59.801	20	202	1282	1483
CTGTCTCCTTGTCCCTCTCG	59.978	20	250	137	386
GGTTGGAGAAAGCAAGTTGG	59.711	20	183	296	478
CTTGAAAAGGGTTGCAAGGA	60.22	20	112	845	956
AAACCCTGTGTATCCCAGCA	60.375	20	222	104	325
GCCCCTCACATGCACTAAAA	61.032	20	223	3551	3773
CAATCATGTTGGGTGCAGTC	59.967	20	200	248	447
TACAAGCCTTGGACTTTGGG	60.103	20	164	1225	1388
GAGGACGTTGATTTGTTGGG	60.353	20	202	170	371
AACCATGTGCTTACACCACG	59.49	20	255	236	490
GGTGGTCGGAGACTAGGGTT	60.371	20	274	228	501
GAGCTCAGCTGAACCCAGAC	60.143	20	210	1001	1210
CTGCATGCACATAGAGTATTGC	58.346	22	273	381	653
CAATATTCTTCGGAGCGAGG	59.801	20	251	1879	2129
GGTACGTGGGGTATGGTCAA	60.495	20	276	610	885
TTTTTCCAAACAAATGAGATAA	58.586	25	278	115	392
TCTTTCTGCATCCACCACAA	60.24	20	247	121	367
TAGGCCCATAAATGCTTCCA	60.415	20	250	38	287
GGAGTGAGGATTTGAGGTGG	59.505	20	172	677	848
CAACCTCCTTTCTCACCGAG	59.837	20	146	431	576
GACAGAGTGGGCTCTCATGG	60.829	20	160	645	804
TCCCTACGAGGAAGTCAGGA	59.797	20	257	123	379
TTGGTTTTGTTTGGGATTGA	58.841	20	234	163	396
ATTTGTTGGAGGTTTGGTCG	59.83	20	216	64	279
TTTTTATTGTTTGCTCCGGG	59.937	20	175	11	185
GGTATTGTAGCCATTGGGGA	59.645	20	152	371	522
TCGATGTTTCCTTCCCATTT	59.363	20	267	237	503
GTGTGCTGGATGTCGTTGAT	59.557	20	139	19	157
CCTTGTTCCTCCATGGAAAT	58.836	20	211	935	1145
TGTTCACCTTTTGGCCATTT	60.344	20	193	32	224
CTTTCTGGTCAACACTCACGA	58.917	21	223	212	434
TGGGATAAAATAAGGGGTTTCC	60.241	22	254	967	1220
TTGGGCTGCAAATGATAAAA	59.146	20	205	88	292
CGTCTCCTCCCTCTACCTCC	60.208	20	244	843	1086
ACAAGAGCAACACATGCCAA	60.31	20	233	2586	2818
GTGGGGAAGACTGTGTGGAG	60.563	20	157	15	171
GGGGCCAATCCAAATTTAT	58.563	19	108	702	809
TGAACCGAAAGGTCAACCAC	60.934	20	232	409	640
TTCATCTTCACCCCTTTTCG	60.044	20	251	7	257
ACTATGCTCACCCACTTGGC	60.142	20	270	5679	5948
CGCCCCACATTGTTTCTTAT	59.823	20	120	69	188

CGAGACTGAGTCCTCCATCA	58.912	20	246	134	379
AAAAATGAGCGGACCAAAAT	58.557	20	256	1149	1404
TCTTAATTGGGGTGAAAGCG	60.067	20	260	6	265
CGACCATTAGCAGCCTCAGT	60.419	20	186	557	742
TATCCTCCTTCCCAGACGAA	59.623	20	251	1685	1935
GGGAAAAATCTTGGATGTAGT	58.919	23	256	239	494
TGGTTTGGAATATACCGAAGTT	60.115	23	147	4030	4176
GCGTAAGGGTGTTCGTGAGT	60.179	20	119	101	219
ATGCCATGACACGAACAATG	60.399	20	207	163	369
GGCCGAATTATGCTTTTGAA	60.04	20	261	94	354
TGTGTCATCTTACACTTTCCAC	58.201	23	135	21	155
ACAATCTGCGAAACTGGGTC	60.119	20	106	18	123
CTCGACAACCTTGCCCTATC	59.694	20	210	549	758
GAGAGTGCCTCACTTTTGTGG	59.899	21	200	180	379
CTGGGGTCCATGTTAACCAC	60.088	20	266	720	985
CTTCAATTTCTTGGCGTGGT	60.11	20	236	424	659
TCGAATTTTCATCGCCTCTC	60.296	20	271	46	316
CATTTGCAATGGAAAAAGGG	60.294	20	152	1748	1899
CGGTTATTACCGGATCGCT	59.93	19	197	60	256
TGGAATACCACTGCGTTCAA	60.111	20	177	669	845
TCAAAGTCAATAGCCCAACCA	60.487	21	239	320	558
CGATTCTTTTGTACGTTTGAGC	58.945	22	169	29	197
TCATTTAACCGCTGAGTCCC	60.074	20	132	16	147
GCATCCTCGTGTGTGGATTA	59.527	20	272	260	531
GGCAAGACTCGATCAGGAAG	59.95	20	158	179	336
CCACTGTTCAAGTGGACGAA	59.72	20	211	122	332
CCAAGCATTGTGGATGCTCT	61.208	20	108	600	707
CCAATTTGAATGGTTATCACCT	60.457	23	158	412	569
TCTCGTTTGGAGGAATTTGG	60.044	20	204	495	698
CCTCGTTTGCAGCAGTTACA	60.05	20	234	992	1225
GGCGTTACCGCATATGATCT	59.951	20	204	3193	3396
TGTTTTTCCGATTTCACCAA	58.987	20	178	32	209
TCATATTTGATGGGACCTTACG	58.831	22	274	190	463
CCCCCATATGCTATGCTTTG	60.302	20	236	369	604
ATCCCAAATTCCCAACCTCT	59.629	20	110	582	691
CGTGGCAGGCTAATATCCAT	59.945	20	244	9	252
CCCCCTACATTTCTTCATGC	59.387	20	276	748	1023
TCTTGTGGTAAGCAGCTCCA	59.591	20	211	1183	1393
TATATCGGGGGCTGAGCATA	60.403	20	173	221	393
CAAACTCCACCATAACCGCT	59.993	20	238	547	784
ACAATCTGCGAAACTGGGTC	60.119	20	108	18	125
AGGGGACTTGCACAAACAGT	59.622	20	243	100	342
CGATATTGTGCCGGTTTGA	60.473	19	271	90	360
ACGGGTGAGAATAATTTAAAG	59.774	23	180	2224	2403
CATCAGGTTCACTGGCAAAA	59.691	20	277	1118	1394
AGGTTGGCCAAGTAAGGTCA	59.592	20	245	15	259
TCAATGCAGATGGGATTCAA	60.009	20	188	434	621
GAATCAATGGTGGGCTTTGT	59.797	20	229	418	646
TTCATAATTTTGTTGCTTTTGC	57.131	22	273	1844	2116
AAATCCCAGCCACACATTTC	59.797	20	140	497	636
TCATGATCACTTAGGCACTTAG	58.415	23	280	547	826
CAGAGGCATGGTCTCAGTCA	59.98	20	243	606	848
GGGAGGACCATAGCTCATCA	60.034	20	131	523	653
AAGGCAATGGAGTGGATGAG	60.073	20	239	466	704
AGCCCACTCTTTCTAACCGTC	59.765	21	127	511	637
GCAGAAAAACCATGGGAGAG	59.67	20	104	453	556
AAAGCAAGCCTGGACTACCA	59.875	20	262	199	460
ATTTTCGATTTAGGGGCGAT	59.772	20	161	1481	1641

GGTTTTCAGATACACGTGCC	58.076	20	163	33	195
AATGAGGAGGAGGAGTTGGG	60.447	20	225	3	227
CAAAGGCCTAGAAGTGTTTTG	58.562	22	148	694	841
AGGAAATGCAGTGTTTTTCAA	57.411	21	260	215	474
GACAGTTTTCATTTGATCAAGC	60	23	131	92	222
TTGAAACGGACCAACAATGA	59.941	20	242	25	266
AGTAGCACGACCAGATGGGT	59.604	20	247	869	1115
TGTTATTTCAATTAAAGTTGAT	59.719	26	262	242	503
GAGAACCAAGGGTCAAGAAA	59.61	22	204	334	537
CAAAAATCCAACACCTCTCAG	59.513	23	260	1278	1537
TCACAATCGTCCATTTTTCG	59.518	20	272	245	516
TTGTGTGATCGAACCACGTT	60.008	20	205	92	296
AATCTGATGGGCAGTAACCG	59.955	20	251	591	841
GTGACTCAAGTCTTCAACCAA	59.291	23	274	269	542
CCCGTGCTTCAATCTCTCAT	60.218	20	273	1	273
CGGTGGAATATGTATGGTTGT	59.996	22	219	8	226
CTTCCGTGTCCTCTCCAAAG	59.837	20	195	19	213
GATCTGCCATACTTGCACCA	59.679	20	164	485	648
GAGATTTCCTCCTTCCACAGG	60.059	21	154	609	762
AAAAGAAAGAAATGCACACG	59.397	21	224	1136	1359
GAGTTGGCTGTCCCACTCAT	60.12	20	215	1128	1342
ACCATATTTAAGGGTTATCACC	57.552	24	170	621	790
GTTGAGGAATTGGGAATGGA	59.727	20	194	1462	1655
ACGTTCTTCTCCATCCCCTT	59.935	20	182	215	396
GTACTGGCGACAGCGATACA	59.895	20	234	469	702
TGAAATTAGGAAATAAGGAGG	58.625	25	246	345	590
TGCATACGGAAAACAAACCA	59.969	20	278	484	761
TCTGAGATTTTCATTTTGTCGG	59.994	23	198	713	910
CTTCAAATGCTCAAGGATCAA	57.958	21	252	1428	1679
GGCTGTGTGATCATGTTTGG	59.967	20	242	961	1202
GTACCTGCCGACAAATGGAG	60.517	20	105	90	194
AGGCCACTGAGAGTGGTGAC	60.315	20	211	3555	3765
TGGCTATAAAGGTCGCAGTT	57.543	20	263	799	1061
TCATGCTTGAATCAAAACAAC	59.206	22	194	0	193
CCTGCTTCTCAGGTTGTCCT	59.45	20	107	2203	2309
AACACACGCACACACTCTCA	58.876	20	226	361	586
TTTTGCCATTTTCGAAATCC	59.886	20	255	1272	1526
GAAATAAGGAGGTATTATGAA	58.156	25	155	837	991
ATTGCTTCCAATCGAACACG	61.032	20	147	3505	3651
TAATTAGTTCCACGAGCCGC	60.23	20	280	203	482
GTGATGCAGTGTTGCTGCTT	60.064	20	233	2259	2491
TTTTGATCGTCTATCTTGCGAA	59.853	22	270	267	536
TCTTTTACTTGCAATTTCTGTTT	59.4	25	279	1014	1292
CGCTGTCAGACCCAGGTATT	60.134	20	240	836	1075
TGCTCCATGACTTGCTTCTG	60.136	20	249	703	951
TTGATCAGCAGCTATGGAACC	60.228	21	259	83	341
TGATGGAAGCAATGCAACTT	59.276	20	173	171	343
TTGGCAAAACCCTATTCAGG	59.931	20	236	2838	3073
GTTGGTTACGGGAATTGCAT	59.691	20	198	1257	1454
AGCTGATCGAGCAGAGAAGG	59.851	20	265	2587	2851
GGCCAAAACATTGCTCCTAT	59.046	20	271	2619	2889
TGGACAAATATGGTGATGGC	59.205	20	247	185	431
GTCCGATCCAAGTTCTGGAG	59.655	20	171	2305	2475
CGATCGAGATGTGACGACAA	60.84	20	276	332	607
TCATGGAAAAAGCAAGCAGTT	59.875	21	197	25	221
AAGGTGATGGGTGTTGGAAA	60.21	20	188	251	438
ATAGTTTTGTTTGGCCGACG	59.996	20	248	198	445
CGAAGGTGGGTTCTTGTGAT	59.966	20	222	6	227

GGGATCCATTGAGGATGTGT	59.593	20	268	2683	2950
GGGAGGGAATCTATTGTGATTC	59.666	22	197	578	774
TTGGATGAGATGATGGCAAA	60.009	20	236	1	236
CACCGCCCAACCATTTATAG	60.202	20	262	639	900
GGCTGCATTTTTATCCCAAA	59.907	20	231	535	765
CGCCCTAGCAAAAGTGTTTC	59.883	20	269	474	742
ACCCCGACTTCTCCTTTGAT	59.935	20	260	1978	2237
AAGAGGCGATTGCTTAGGTG	59.476	20	270	66	335
TTCCAATGGCAAAGTTGTGT	59.024	20	189	200	388
AGACCCAAGCCTACCGAGTC	60.649	20	214	951	1164
TATACAAGCTGTGGCGGTTG	59.752	20	230	93	322
TCGTCCAGTGCCTGTGAAT	60.263	19	259	2258	2516
GGGTCGACAAGCTTGAGAAA	60.375	20	183	11	193
GCAGAGAGGGAGGGAGAGTT	59.952	20	154	206	359
GCACCCCTTTGTAATCATGC	60.339	20	268	1035	1302
CCTTCAAGATTATGGTGGGG	59.24	20	277	878	1154
CACGAATTCCCCGACTTTTA	59.931	20	225	936	1160
TCACCCGAATCTTTCGTTTC	60.051	20	206	497	702
ATTCAAATCCGGTGGTTCAA	60.17	20	192	16	207
TGTCCAAATAAATGAGGCCC	59.762	20	252	116	367
TGGAGCTGGAGGTTACTTGG	60.246	20	156	14	169
TCCCAAAGTTTCACACGTCA	60.128	20	214	503	716
TGGGATTGATCCTACCCAAA	60.126	20	217	2504	2720
CATGATTGCTGATCCACCAC	59.925	20	225	3037	3261
ATTTAATTAGGTCCACGCGCT	60.003	21	104	123	226
TCTTGACATTCCAAGAGCCC	60.195	20	216	179	394
TTGGTAGGTGTCCGTGATGA	59.96	20	248	837	1084
AGTTAGCATGGGGAAGGGTT	59.827	20	139	76	214
TCATCCCAAGTCCAGAGCAT	60.622	20	247	2738	2984
TGTACCCTACCGTGGGAAAG	59.846	20	276	690	965
CCAGCAATAGCCCTCTGTGT	60.277	20	257	4399	4655
TGCAAATGGTGATTGCTCAT	60.08	20	231	399	629
GACCGTGTGCAATGAAACAG	60.16	20	251	126	376
TGGCATGCAAACGACATTAG	60.665	20	106	2	107
GCTGCAGATCTAAGGCCGAG	62.461	20	147	974	1120
TTAAAAGTGCGGGGCATTAC	59.964	20	185	17	201
AACATGATGAGAGTTGGGCA	59.09	20	273	33	305
TGATGCCTCAAATCACAAGC	59.805	20	248	1600	1847
TGGCGATTAATTTCCCTTCA	60.395	20	160	400	559
AATGTCCAACTCAAAGAGGAA	59.165	23	262	130	391
CCACCCGATAAGGCAAATAA	59.789	20	243	1620	1862
GAGAGTCTGAGATTTGGCGG	59.95	20	206	911	1116
TGCGGAGTTCAAGACTGATG	59.984	20	220	20	239
CCGGAGATTCTCTCTCTCCC	60.292	20	216	26	241
TTGTGCATCAAAATAAACCCAA	60.218	22	145	1559	1703
GTTCCCGACTTCTGAAAGCA	60.375	20	221	270	490
TTGGGATTTCACGAAAGATTG	59.924	21	234	11	244
TTGCCGTTTTGTTCATGTTT	59.062	20	235	1925	2159
ATGGCTGAGGTGGCTAATTG	60.096	20	157	268	424
CCGGATACGGATTATATCCAA	58.659	21	248	384	631
ATGCATACATGGGGACAACA	59.654	20	228	371	598
TGCACGTAGGCATGTTCAAT	60.142	20	262	8	269
GTCGATTCGCCACCTTTAAC	59.574	20	201	227	427
AATTGCCCGAAATACGGAGT	60.692	20	169	250	418
AAGCCTACATTCACATTCCCA	59.443	21	243	416	658
TCCAGCGACTCATGTTGTTC	59.837	20	261	740	1000
AATTTTCTTGAGATCGGGCA	59.645	20	189	251	439
CCCAAGAATGGGTTATTATTTG	59.14	23	271	656	926

CGAAATGCATGATTGAGGTG	60.073	20	203	768	970
GACCCCGAAACTTTAGCGTA	59.225	20	135	274	408
GACATGGATTGTGCTTTCGAC	60.52	21	217	17	233
GGAGGGATTGAACGTAGGTC	58.447	20	173	922	1094
AAGGGTCTGCCCTTGCTTAT	60.096	20	273	502	774
ATTTGCTGGAGGGAGAGGAT	60.037	20	258	390	647
AGCGAAAGAAAATGGTTTGAA	58.865	21	279	5	283
CGCCTTACGAAGCCAAATAC	59.742	20	178	157	334
ACCTGCCGTCTGACATAAGC	60.285	20	177	459	635
TGATAGTGGAGTTGTGAGCAT	58.878	23	278	59	336
TGACGACCGATAATTGCTCC	61.003	20	185	33	217
TACTGCAGTGGAGTTGCCTG	60.049	20	255	1408	1662
CACCAAAAACTGATAAATGAT	58.556	23	255	423	677
TTTTTGGCCTTTGATCTTCG	60.181	20	219	138	356
CGTGAATAGTGCTGCCTCGT	61.394	20	233	512	744
AGTGACCCTTTGGTACGTCG	60.028	20	240	1643	1882
TGATCTCCTTTTCCCTTGGA	59.6	20	193	1025	1217
CGGTCTCGGTTTGGAATCTA	60.066	20	268	135	402
TGGGATAGTACCGGAACACG	60.766	20	187	877	1063
CTCCTCTCCTATTCGCTCCC	60.306	20	193	118	310
GAGGGAGGGAAGATATTCGG	59.859	20	272	1441	1712
TTAGTCAAGGGGTGGAAACG	59.964	20	264	1038	1301
AAAATCCGAGCCAGTTGTTG	60.11	20	245	224	468
CGCTGCAACAAATACACACC	60.18	20	238	996	1233
CTCCAACCTTGTTTTTCCGA	60.081	20	228	573	800
AAAACTCCATCCAATCACCG	59.79	20	235	162	396
ATAGGATTTCACTGCCTGCG	60.235	20	241	146	386
TTGCTTCTGGAAGGGATTTG	60.184	20	108	2699	2806
ACCTGATTTTCTCCCTCCCT	58.997	20	223	1547	1769
TGCACGCAGCATATTATGAA	58.88	20	218	576	793
GCTTATGGTTTGAGCTGCCT	59.481	20	109	713	821
ATTCCAAATCCAAACCACCA	60.029	20	228	156	383
AGATTCTGCTCGATTCCCAA	59.773	20	155	1348	1502
TTTGGAAAAACAGAGCACCC	60.088	20	276	200	475
GGCTTAATGGCCAAAAACAA	59.943	20	239	3821	4059
TGACATTTGTCTAACGATGGTG	58.554	22	273	66	338
ATGTGATGCTCAGCAGTGTTT	58.385	21	209	48	256
ATACTGTTTGGTGCAGGGGA	60.375	20	236	21	256
AAACGCGCTATTTTAAACCC	58.332	20	254	1	254
CACTGCATTAAACCTACTCCCT	59.209	23	262	3910	4171
GTGGTCTGGCAGTCGTGTTT	61.176	20	273	2751	3023
CAGACAATCCCGGAGGACTA	60.065	20	227	2616	2842
TGACACGGTGATTTACGTGG	60.427	20	249	241	489
TGAATCCTCCCCCATTGTTA	60.126	20	271	1156	1426
ATCTAATGCCCCAACACAGC	59.962	20	237	1132	1368
TGTGCGCTAAAGGTTTTCCT	59.883	20	202	19	220
ACTCCAACCCTTCTTTGGGT	59.834	20	258	5285	5542
TATGATCGGCCGAGAATCTT	59.628	20	269	787	1055
TATGTGTGTTGCATTGCGTC	59.155	20	166	383	548
GCGAAACAGGAAAAATTAGG	59.957	21	164	84	247
GCCTGCTACACAGGGTTTTC	59.74	20	199	26	224
TTACAATGGCAAATCCCACA	59.786	20	191	546	736
TGAGAAGAACACATAAATTCG	59.772	23	278	1612	1889
GGTGGAGACAGGAGGGTGTA	59.962	20	217	53	269
TCCAGCTGTTAAAACCCACC	59.971	20	236	1000	1235
TCGGAGTCTTCAGACAAATCA	59.853	22	264	1929	2192
GCTTCAGTCCTTGCATCCTC	59.957	20	274	4899	5172
TGGAATACCGGTGCAAAAAT	60.188	20	200	1558	1757

CCCCTCCAAAAACCAATCTT	60.159	20	216	51	266
TGGTCTTTTCAATCCGGTTC	59.91	20	248	213	460
GCGGCATCATCTTCTTTCTC	59.923	20	193	674	866
TATTTGCAGAATTTGCCACG	59.702	20	233	198	430
ACACCTGGGTGAGACCAAAC	59.859	20	159	764	922
TGTTAGAATGGTCCAACCCC	59.647	20	222	185	406
GGCTAGGCTTGTAGCAAAAGG	60.389	21	230	75	304
CGCATTTTTGGCCTGATATT	59.928	20	232	765	996
TATGCCCACATCTCTCTCCC	60.034	20	158	795	952
TCCTTAATTCATTAAATACATA	57.288	26	163	441	603
TGCAAACACAATGTCTGAAAT	59.632	22	271	696	966
CCCTCTCTCCCCTCACTCAT	60.605	20	197	101	297
GTGTGATTGGCAGTGACAGG	60.162	20	147	1032	1178
GCACGGCAGTGGAAGAATA	59.814	19	277	1015	1291
TCAGTACAATGGAGTGATGGC	58.585	21	167	606	772
AAGTCAGCCGAGGAAATTCA	59.813	20	278	170	447
CCTTTTGAACAAGGCCTCAA	60.22	20	200	248	447
CGGCTGTCAACAGAAGTTCA	60.025	20	203	71	273
GGCATGTGGGGGTATAGTTG	60.074	20	258	1531	1788
TTTTGAGACACCCCAAGTCC	59.943	20	279	139	417
TATTTTCGGTTTATTGGGCG	59.799	20	215	32	246
TGGGACACTGTTTTCTTTGG	58.594	20	202	277	478
TCCCCTGCTTCTAAAACCCT	60.068	20	130	20	149
TTTTCCCAACAAATTCAGCA	59.133	20	249	223	471
GAGAATGGTGGAAGAAGCCA	60.195	20	260	442	701
TGGAAAACTTGGCTTGGTCT	59.711	20	109	941	1049
GTGGGAATAATGTATGAATGA	59.487	24	272	943	1214
CACGGTTGCCCTTTGTTACT	60.03	20	205	693	897
TGTTTGTGATCCCAATTGAA	57.35	20	238	604	841
TCCTCTCCCTTTCGTTTCCT	60.183	20	122	3	124
TCCAGTGTTGCTTTGCCATA	60.257	20	251	1193	1443
AAGTCGAAATTTGGCAACAA	58.267	20	182	124	305
ATGAGCACATGCCAAAATGT	59.005	20	203	1839	2041
AGGCATGTTCAATTGGGAAA	60.309	20	271	189	459
GCTAATGGGAAAAGCATTGG	59.547	20	118	1452	1569
ACATGATAATGCTGATAAAAA	58.59	25	204	447	650
TCTTTGGCTCAATGGAGGTC	60.195	20	263	790	1052
GGAATCTGGACTCGGATTTG	59.483	20	223	15	237
CCGGCAGCATTTTTACTTCT	59.361	20	213	3487	3699
CGGGTGGGAATGTATTAGGTT	59.952	21	258	62	319
ATAAAAAGGACTGGCCTGGG	60.312	20	214	60	273
TTTGGTTGAAGGTGCATGTC	59.547	20	118	402	519
CAGTCCCCACTGCCTTTATC	59.55	20	123	279	401
TGAGGCCACTGACTTGAATG	59.831	20	178	112	289
CAAATAATGTGGCAATCCCC	60.016	20	151	35	185
TTCATCTTGTAGCGTTTGAATG	59.772	23	105	1	105
AACAAATGCATCATCTGCCA	60.08	20	197	1438	1634
TCCTGATGGACAACTGACCC	60.934	20	259	138	396
ATTTACCCATAGCGCACTCG	60.117	20	214	62	275
GGAATATGATCGGTCGCAA	59.445	19	239	2	240
AAATCACAGGAGGACGATGC	60.081	20	183	849	1031
TTATCAACCCAAAACCCCAA	60.024	20	168	113	280
GCTAAAAGGGATTCTTGGGC	60.041	20	160	1149	1308
ATTTTGGAGATGGACCGTGA	60.317	20	260	918	1177
GGTGGTAGTTGGCGTTGACT	60.035	20	248	411	658
GCTGACTAACCCATTCTTGTTT	60.048	23	119	1038	1156
ATCTGAACAAATGGGCTTGG	59.933	20	238	2861	3098
GAATTCCGGAAAGCGTACAA	60.074	20	239	1371	1609

TACCCAAACGTCCCAAAACT	59.331	20	174	531	704
AATGGTGGGGGTAACAACAA	59.948	20	201	229	429
TCTTTCTTGGAACATCTCGTCA	59.853	22	249	601	849
GACCTGGTTCATTTCAGGGA	59.903	20	157	211	367
AACACACAAACGAATGGCAA	60.011	20	212	467	678
AGGAAACCTTAAAGGGCCAA	59.939	20	267	1124	1390
CCATGAGTTTTTGTGCGATG	60.111	20	279	278	556
TGAACATGCATCCAAAGGAA	60.049	20	253	175	427
ACCTGGAAACGCATATGGAG	59.955	20	260	2	261
CCTTTTCTGCATTTGGTGCT	60.249	20	217	618	834
GGGCTATCGACCTCTTTTCC	60.039	20	243	492	734
CAATTTTCCGGTGGAGAGAG	59.665	20	215	355	569
AAAATGGAGCAGAGCGAATC	59.415	20	246	228	473
CTCACCTGCACACACATTCAC	60.219	21	280	1181	1460
ATGGGGCTGTTGTGAAAGAA	60.495	20	242	2085	2326
TCAGTCAACCAACCAACTGC	59.726	20	219	14	232
ATTGCACCTCGTAAACACCC	59.859	20	112	21	132
AACGGTGTGTCATCATTGGA	59.812	20	157	1532	1688
TTTACACCACAAAGTTGCCG	59.627	20	135	839	973
AAAGGTCCTTCTCATTGGGC	60.443	20	143	25	167
TGGTGTTGTGGACTTTACGG	59.46	20	211	22	232
CAAACTCAACAACCCGTGAA	59.585	20	227	94	320
CGCGTGACAAATTCTTGAAA	59.849	20	217	212	428
GAGAAGCCAGGCAGCATAAG	60.118	20	215	47	261
CCAAGATCAATGGTTCCTAAGT	59.879	23	109	446	554
TTGCAAATTACCAAGGGATT	57.108	20	124	162	285
ACTGAAGCTCGAACCCCTCT	60.393	20	246	240	485
GTGGCAGGAAGCATTCACTT	60.263	20	272	1157	1428
ATGGGGAGGGGATATGGTAA	60.224	20	131	238	368
CCAATCTCTTTCATCACTCTCGT	59.765	23	169	68	236
TGGTTGCATACTTGCACACAT	60.05	21	203	8	210
TGTTGCTATCCTTGGTTCCC	59.933	20	100	2913	3012
TGTGCACTCGATGATGTTTG	59.248	20	236	2656	2891
CAACTCCCTACCGAAAGTCG	59.728	20	228	481	708
ACAAGCTCTTCATCGGTTGG	60.255	20	265	334	598
CTGATGCATGTGGTAGGAGC	59.271	20	221	4027	4247
CCATACAAAAGCGCCAAACT	60.131	20	122	2033	2154
TTGTAGCTCCTCCTAATTTCCTC	58.129	23	178	416	593
AACCCAACATCATCCCTCAC	59.636	20	176	150	325
AGAGTTCGAGGTGGGCTTTT	60.247	20	280	19	298
AGCAGTTTTGATTGCTCCGT	59.882	20	150	2853	3002
TACCCTTACCTGTCTGCCGT	59.615	20	245	186	430
CAAACCACGATCAAAATCCC	60.17	20	212	445	656
AGGCGGTATGCACTCAAAGT	59.763	20	219	782	1000
TTGGGTTTTGATGATTGCTTT	59.442	21	265	1016	1280
CGTGCGCTTACGGATAAAAT	60.116	20	227	3223	3449
TGTGGCCTTTTGTCACTTCA	60.278	20	243	168	410
TGGGAGGACAAAGGAATCAA	60.43	20	212	368	579
AAGGTTGGGGTAAGCTGGAG	60.488	20	263	832	1094
ATACCAAGGACCCTCCCAAC	60.052	20	245	66	310
GGACGTCCAAAAACGGAAAT	61.08	20	205	481	685
TGTAAGCAATGACGAAGCCA	60.401	20	197	76	272
CAAGTGAAATTGGATGGTGCT	59.985	21	227	347	573
AGCTGCTGCGAGATTGAAGT	60.307	20	233	200	432
GGTGCGGGATCAATAGGTTA	59.784	20	209	4264	4472
AGGTGGGAGTGGAAACACAC	59.859	20	155	642	796
GTTGCTGTTCTGACCCGACT	60.307	20	102	503	604
CGGCATGATGCAGTAAGAGA	59.972	20	103	3408	3510

AATCCTGCCTTGTTCCTCCT	60.074	20	234	61	294
ATCGCTGACTTGTGGATTGA	59.245	20	205	619	823
AAGGAGAGGAAGGGCTTTGT	59.323	20	276	947	1222
CTGCCTCAACTTTGTGTGCT	59.086	20	265	1320	1584
TTGACATGTGGCATTGTGTG	60.003	20	154	1949	2102
CATCACCGGCCTACAAAAAT	59.823	20	210	2179	2388
ACTCCCAATTCTGAAACGGA	59.526	20	225	225	449
CCGGCTCCACATGTATTTTA	58.506	20	260	582	841
TTCACGACTCGCTGTTATGG	59.864	20	191	397	587
CACCATGGTTTCCAATGCTA	59.395	20	275	6	280
ACCGTGATGGAACAACCTTC	59.827	20	134	76	209
TTCACAAGCTCACAAAACGTAT	59.326	23	242	483	724
CCTAGCAAGGCTTCCATCTG	59.971	20	207	116	322
AAGGTGAAAGAGACATCAACC	60.026	23	103	541	643
TTTCCGCAACTTGACAATGA	60.234	20	264	246	509
CATTATCTCAAACGAGCGGC	60.742	20	249	163	411
AAAGGGGCAATGACCTATGA	59.387	20	151	210	360
CGAACAAGAGTCTTCCGAGG	59.982	20	149	582	730
TCACCTTGATTGGTGATGGA	59.893	20	222	2437	2658
TCATCCACCTCGAAGACCTC	60.199	20	159	617	775
ATTACAGGGATGGGTGGGTT	60.306	20	255	161	415
TCCTAGGCGCTATTGAGGTG	60.365	20	192	176	367
CACATAAGCGAAAACGCAAA	59.88	20	250	3681	3930
TTAGTTTCATGAATGGAAGTGA	57.035	25	100	5	104
TGATTCTCGACCAACCATGA	60.048	20	227	206	432
GCATTGACGCAAGGACATATT	59.981	21	187	623	809
TGTTGACGAACGAGACAAGG	59.873	20	197	91	287
TTCGACAAATCATTGCAACA	58.676	20	210	1310	1519
CGAGCACAAGTTCTCCACAA	60.025	20	134	2553	2686
AAGGCAGCATGCTTGAAACT	60.022	20	250	2013	2262
GAGAATGGAGTCGAACCGAA	60.195	20	221	225	445
TTTGTGGGTGAGTTTGCACT	59.187	20	140	27	166
TGGACCATTTGTGCACTTGT	60.008	20	275	1636	1910
ATGCTGACGAAAATTCAGGG	60.074	20	208	387	594
TTTGTGATTCAGGGTTCCG	59.481	19	279	221	499
TTGGGGATGAGATGGGAATA	60.088	20	238	6614	6851
ATGGCCCAGATTTGTTTTGA	60.309	20	144	30	173
TCGAGAAAAGACAAAGAAGGC	60.345	22	104	1325	1428
TGTGCATGAAGTGAAAGGGA	60.24	20	263	9	271
CGTAGTTTAATTTTGCCGGG	59.489	20	203	877	1079
CTTGCGAGCAACTTGTCAAA	60.172	20	225	279	503
TGGAGTCCATGAGCATCAGA	60.363	20	267	36	302
CACTCATGCTTGACCGAAAA	59.84	20	145	1424	1568
TGGGGAATGTTGAGAAGGAA	60.43	20	269	965	1233
GGCATCAAAATTGGTAACGG	60.188	20	180	560	739
AAGAGAGGACACCTCCGGTT	60.111	20	162	196	357
GAGTTGCATGATGGCATGAG	60.233	20	255	113	367
TTAGGGATTAAAAGCGGCAG	59.341	20	217	90	306
GTTTGCCACATGGCATCATA	60.352	20	204	535	738
CCCTCCACCGCCTTAATAAT	60.164	20	237	1129	1365
CACGCATTTGTGATTTTTGC	60.118	20	216	1	216
CCTGACGAAGGAAGGTTCTG	59.837	20	116	262	377
GACACAGTTCACCCCCATTT	59.679	20	226	198	423
AATTTTGAGGTGTGGCTGGT	59.454	20	242	214	455
AATAGTCTGCAAACCACGCC	60.14	20	260	567	826
GCCAGCAATAATCTCAGTGG	58.326	20	258	706	963
ATAGAAAGGCGAGGCTTTGG	60.702	20	228	1	228
TGCATGGCAAAGCTTCAATA	60.356	20	232	1033	1264

AGCCGATAAAAATGGCACAC	59.967	20	229	691	919
AGGGTTTTGGAGATGAGGGT	59.795	20	261	335	595
TGACAAGATGATGAAGGCCA	60.201	20	267	350	616
CAGAATGGTGGCAACAAAGA	59.691	20	241	478	718
TCGGAGACGAGAGAGGAGAG	59.81	20	157	607	763
TTTAAAAACTTGGTTGGCGG	59.972	20	197	458	654
TCCATCTCCCTCACTTCACC	60.048	20	146	786	931
CGGGGTCGTATCATATTTGG	60.031	20	115	475	589
AATTTGATTGATGGTTTCGGA	59.264	21	221	14	234
GTACCAGCAGAAGACTGGGG	59.721	20	238	1407	1644
CGAATTCGAGCATCAGTGAG	59.547	20	177	934	1110
CTTCGACTCCCTTGTGGAGA	60.377	20	278	251	528
CAATCCTTTTTGTATTCAAACT	57.468	24	205	513	717
AAATGACATGTGTCCGTCCA	59.812	20	175	3	177
GTTTGGAGCCTGGAATCTGA	60.195	20	151	2397	2547
TTTTTGACTTTTTATGGGGGT	57.539	21	258	204	461
AATAAGGGGGTGCATGTGAG	59.813	20	119	281	399
CCGATGTCCAGAGGAACAAC	60.51	20	171	146	316
TTTGTGTCGCAAGGTGAGAG	60.025	20	235	2695	2929
TTTCTTCACCCAAATTTAATCG	58.176	22	275	487	761
CGAAGAAGGTGTTGGTGGAC	60.545	20	262	197	458
TGACAATATTTAGTGTTTTGAC	57.78	26	172	543	714
ACGCGTTAACTAACCGGGAT	60.741	20	263	1132	1394
TGGGGAGATGTCAGTTGTGA	60.088	20	253	742	994
AAGGCATGTTTCGAGTTTGG	60.11	20	235	313	547
CGGTTAGAGCCAACCTCTCA	60.388	20	234	490	723
TCCCATCCTTCAAAGTCTGC	60.195	20	232	2190	2421
GGTTTCGTCATAAGGCGGTA	59.96	20	264	538	801
TCTTCATCCCCACCCCTAAC	61.076	20	269	1652	1920
AAACCCCCTCTTAAGTCCTGA	59.088	21	263	283	545
GCATGTTCTGTGTTGCCCTA	59.722	20	275	960	1234
AACATTAGAAAACGCGCCAT	59.614	20	245	29	273
ATTCATCCGCAACGAAAGAG	60.214	20	270	2942	3211
TGCTCACTCATCCTCCAGTG	59.98	20	138	780	917
ATTATCCAGTTTGGATTTTGTT	57.292	24	178	1853	2030
GTGTACCCTGAGGGACGGTA	59.844	20	150	89	238
TAATAGCGGCCGATCTGAAG	60.323	20	245	419	663
TAATGCTTTTCCGTGGGTTC	59.938	20	191	2089	2279
GTTCATGGTTGTGCGAATTG	59.972	20	206	407	612
ACCAGGAAAGCCAAAGTCCT	60.11	20	244	1859	2102
TATAACCCAGACCGGACCAA	60.184	20	184	29	212
TCATTCAACGGTATTGTCATGT	59.261	23	189	629	817
CCAATTTGAATGGTTATCACCT	60.457	23	103	627	729
CAGCTCATCGTGGATGCTAA	59.972	20	171	1186	1356
ACCATAAGGCGCACAAAAAC	60.003	20	260	1074	1333
GAGACAGGGGTTCGAATCAG	59.655	20	246	10	255
CAATCTAATGCATCCAACGC	59.14	20	151	38	188
TTTAACTAACTCCGGCCCAC	59.087	20	174	739	912
GTTTGGACAGATTGCCTGGT	59.973	20	237	1040	1276
GGCATCAGGAGGATCAAGAA	60.158	20	252	2279	2530
ACCAATGGTGGTATGGTGTG	58.984	20	176	137	312
ACTCTTGGAGCGACTCCTCA	60.135	20	247	929	1175
GTTTGCTGACGCAGGGTATT	60.14	20	212	499	710
GGACAGTCATATTTGGGCTGA	59.947	21	152	2533	2684
GGCACACATTATGGTTTGGA	59.251	20	179	235	413
CCACATCGGTGAAGGTAACA	59.415	20	147	263	409
AATGGGGATTCACACCTCAC	59.636	20	169	443	611
ATGGATCGTCAACCACAGAA	58.933	20	193	1937	2129

TGAGTCAGCACTGTGGTTCC	59.872	20	264	300	563
TTCCCTTTACTTCTTCCCCC	59.393	20	113	647	759
TACCTCCTCTGGGGACAAGA	59.649	20	231	1078	1308
AGCAGCTCGATGGAGGTAGA	60.119	20	249	2150	2398
GGGATAGTATCGGATCGCAA	59.885	20	128	70	197
GAATGGGAATCGAGATGGAA	59.831	20	133	14	146
TGCCACATTTTTCCTGATTG	59.518	20	182	742	923
TTCCTGCTATCATCAACCCC	59.894	20	204	429	632
TGGGACGCTCTATTCTGGTT	59.694	20	106	258	363
TCCGTCAACCAAACGTATTC	58.476	20	277	720	996
CTTCCATCTTCCAACTTCGC	59.813	20	213	95	307
CCAAGCCAACCAAAGCTTAC	59.747	20	249	602	850
TGCTCATGAAATATCGTTGGT	58.106	21	223	267	489
TGTCGGAAATTTCTATGCCTG	60.081	21	249	1120	1368
TTTAAATGGACGTAAATGGATT	58.012	23	125	15	139
GAGCGCTGGAAGCTATTGAT	59.579	20	238	30	267
TCGTTCCTGGGCTATGATTT	59.528	20	183	2968	3150
GGAGAGGAGAGTGGGACCTC	60.198	20	274	265	538
GATGGAAACAAGTGGATAGTT	59.799	25	116	863	978
CGCAATTATATTAACTTTGCGT	60.375	24	264	1482	1745
CCACGTGGAATTATGGGAGT	59.67	20	171	1714	1884
AGAGACTGTTGAAGCTCGGC	59.751	20	245	28	272
TCCTAGTGTCTTGTCTCCCACA	59.762	22	233	967	1199
AATCGGCAAAAACCACAAAC	59.845	20	220	741	960
AAACACCAACGTTTTCAGGG	59.869	20	187	204	390
CTACGCCGTTCTTCGTGATT	60.27	20	243	1692	1934
GTTCCTGCTTTGTGGTGGAT	59.973	20	278	965	1242
GTCCCAACTGAAGTTCCCAA	59.943	20	244	205	448
TCCACAATGGAAAAATGCAA	59.907	20	210	2755	2964
GATGCTGGTGATCAAGTGGA	59.637	20	256	367	622
CTGGAGCGGTAATCACAAGG	60.647	20	125	588	712
ACCCGAGACAAAAACCACAG	60.005	20	172	1	172
GTGAGGGAATGCTCTCCAAG	59.803	20	277	86	362
GATCCCAGAGTTGGACTTCG	59.655	20	225	2806	3030
ATACCTTTCTTTTTCCCGCC	59.442	20	130	2283	2412
AGACCAGAACCTAATCTTGGG	59.101	22	271	536	806
AAAAATCAAAGGCCCACAAT	58.418	20	265	590	854
TGTACAAGCTGCTGGAAACG	60.05	20	256	2625	2880
TACTCAATCAGCTCCAGCCC	60.362	20	206	1988	2193
CCCCTCATGTTGGTGGTAAT	59.526	20	268	258	525
AACATCATCGAGGTCGGTTC	59.934	20	194	917	1110
GAGACCAATTTTGCTATGTAAT	57.142	25	226	234	459
GAAATAAGGATGTGTTATGAA	59.894	26	149	508	656
AAAGAAAGCTTCAAGCAGCG	59.904	20	194	63	256
CCAAGCCTGGAGACCTAAGA	59.425	20	221	19	239
TGAGAATGGTGGGTGTGAAA	59.935	20	233	620	852
AATGCAAACCAGTGAAAGGG	59.971	20	244	1080	1323
CAGATTCTGGCACTGAGCAA	60.136	20	138	5493	5630
CGACCTAGATCTGACCGGAA	60.21	20	223	237	459
AATCTTGGGTCCAAACCCTC	60.169	20	179	299	477
ACCAGGTCTCCTGGGTTAAA	58.498	20	269	155	423
CGTCCATGCTCTGTTCTTCA	59.984	20	137	884	1020
AATTCAGCCTCCATTTACCTCA	59.966	22	257	2688	2944
ATCGAGATGCTCTGATGCAAT	59.818	21	277	20	296
TGTTTCCACGAAAAATTGAGC	60.103	21	267	931	1197
AGGGGAACGAAAATCTCTCC	59.513	20	171	2839	3009
GTGGGTGATCAGGAAAAATCA	59.782	21	172	60	231
TGCGAGTGTTGCATCTGAAT	60.423	20	235	315	549

CGAAGAACCTGGTTTGATCTG	59.72	21	274	866	1139
GGAGGACACCATTTCTCTGC	59.661	20	177	7752	7928
TTGAAGGGACCAAATGTGAA	58.947	20	275	672	946
TGAAGTTAGGAAATAAGGAGG	57.525	24	276	558	833
ACACAAGTATGACCAGGGGC	59.851	20	184	17	200
AGAAAGTATCAGGCGCATCTT	58.111	21	186	26	211
CCGAAGGCAACACCACTACT	60.171	20	112	2161	2272
TGTTGAACGTGTACGTTGGG	60.463	20	227	591	817
AAAGCACGTGTGAATATTGGG	59.875	21	257	299	555
CAAGCTTATTCCTGCCCAGA	60.344	20	252	660	911
TGCATGAGAATTATTGAGGGG	59.908	21	197	1600	1796
TTAGTGGCTGGAACCGAAGT	59.734	20	219	517	735
TGGCTCAAAAAGTTTCATATTT	57.534	23	119	1980	2098
GTTTGCCATGGAGATTTCGT	59.939	20	231	11	241
TTGGGTTAATCCGTGTAATCG	59.707	21	232	359	590
AAGGAGGAGGTGAAGAAGCC	59.817	20	271	17	287
AATTGGAGAGTTGGGTACAAG	59.526	22	137	176	312
TGCATGCCGCATACTATTAC	57.321	20	241	1620	1860
TTTCCTCTTCCGATTTTTGGT	59.932	21	253	918	1170
TGATGTATGTGCGATGGGAT	59.763	20	180	825	1004
CCCCCAATTTGTTTTACTCG	59.311	20	205	1399	1603
CCTAATAAAATGGCCATGCG	60.295	20	224	1546	1769
CTGCAGCTTTTTGTCAATGG	59.464	20	226	252	477
GAGGGACGAAGCTTTTAGGC	60.34	20	274	213	486
ACCGCTGACAAACATCATCA	60.12	20	231	5360	5590
CTCGATCAAGACCCTATCGC	59.797	20	185	1071	1255
CCTCGGATTAAAGCTAGGGC	60.184	20	278	1051	1328
GAAACGAATCTGTCGGTGGT	59.973	20	266	2695	2960
CAAACAAAAGGGCCTTCTCA	60.22	20	230	968	1197
AGCTGGTAGGTTTTGGAGGG	60.488	20	274	668	941
CACTCGAACCAGTCAAACGA	59.873	20	154	806	959
GACCACAACCAACCACATGA	60.27	20	161	827	987
CTCACGCGAGGTCTTTCTTC	60.134	20	155	32	186
AAATAGATCTTTTGTAAAGCCC	58.02	23	165	2917	3081
ACAAATTTGCAGATGGAGGG	59.933	20	199	40	238
GGATGAGGAAGAAAGGGAGG	60.008	20	237	1027	1263
ACGGTTGACAGCCGATTTTA	60.502	20	177	442	618
GAGAGAGGGAGGGAGAGAGG	59.489	20	258	149	406
GTCTCAACCCTTGATTGCGT	60.119	20	179	660	838
CTCCCTCCAAATCGTTGCTA	60.206	20	104	631	734
TGATAGGGCACACAACCCTT	60.375	20	280	520	799
TCCTTCCGTTTAAGTAATATGT	58.288	25	236	99	334
TCGTCCTTTCGACATTCTCC	60.195	20	167	2051	2217
GACTCCCATTCCCAAGCTCT	60.596	20	280	2373	2652
TTCAAGTAAAATTTCCCGTTCG	60.329	22	242	634	875
GTGCCTTCTTCTAACTGGCG	60.015	20	221	501	721
CCTAGGGTTTCCCTCAGCTC	60.204	20	189	272	460
TCATGTTGCTTGGATGCACT	60.272	20	187	425	611
TCCAAGTTGCCTTTCAACCT	59.711	20	185	611	795
AATTTGCATTGGGTTTCGAG	59.938	20	132	255	386
CTTCGAAGCGATGGAGTAGG	59.971	20	102	19	120
GTCTCCATGCTTGAGCCAAT	60.226	20	261	447	707
GATAATTAAGTCATAGAGCAG	60.655	25	102	24	125
TCACGATAAGCCAACATGTGA	60.127	21	239	587	825
AGGTGGAACAAGTAACGCAA	58.283	20	216	440	655
TGAACCGGGTCTCTCGTAAC	60.111	20	105	2715	2819
TGGAAATTAACCACAGCCCT	59.429	20	260	440	699
TCGGTTGACCGAAAATAGGT	59.429	20	230	55	284

TGGATGTTTCATTTTGCCTG	59.518	20	250	559	808
GATCCTCCATTTCCCACAAC	59.192	20	232	293	524
GGCACATCGTGTGAATCAAG	60.12	20	163	241	403
CGGACGTTAAACGAAGGAAA	60.103	20	262	305	566
TGTTGTAGTATGGCAAGATCCA	59.167	23	198	383	580
CCAAGGCGAGCTCTAAGTTT	58.743	20	200	139	338
CAGTGTAAAACCTTATTGGGG	59.641	22	268	123	390
CAATGCTCTTTTCAACCCTTTT	59.646	22	208	403	610
TGGAAATCGCGAAATGTAAA	59.146	20	173	805	977
GAGTAGCCATCGAGATTCGG	59.797	20	264	337	600
TCCTGAAGAATTTCGGCATC	60.155	20	161	339	499
CCCCTAATCCGAACACAAAA	59.795	20	132	804	935
ATTCCCTCCCCAAATATCCC	61.054	20	280	2457	2736
TTCAATAGAGGCAGCGGATT	59.807	20	215	797	1011
TCGAAGATGAAAAAGGGCAT	59.645	20	150	247	396
GATCTAACGGCCGAGATTTG	59.668	20	260	577	836
CGATTTCTACACCATTGTTCCA	59.861	22	212	2362	2573
GTTCGGGTGTGCAAAAATTC	60.352	20	278	358	635
CGATGATGAGCATCAGAGGA	59.9	20	172	3	174
CTCTTCCCTGCAGATGATGG	60.758	20	259	1463	1721
ATGACTTCCAGTGCCAGGAC	60.12	20	238	831	1068
GCTCCAAAATGATTACGTGGT	58.965	21	279	575	853
CCCGACAATTTCACCCATAC	60.051	20	236	237	472
GTTTGTTCAATAGGCCCCAA	59.801	20	141	8	148
TGACAGTACACTGCTCCTGG	57.367	20	238	309	546
TTGACACGAATATGACACAAA	59.003	23	152	315	466
CTGCATCACCTTGCTTCTCA	60.136	20	266	644	909
ATGGCATCATCTCAACCCTT	59.366	20	248	902	1149
AATGCTTCGGACTTGCTCAT	59.843	20	274	713	986
AAATCCTCAATGCAAAAGCAA	59.712	21	189	327	515
AAGACCCTTGTGAGTGGTGG	60.002	20	216	23	238
GGCGGTTGAGATTTGTTCTT	59.174	20	216	1491	1706
TTGTTGTGATGTGAAGAATTGT	57.312	24	178	282	459
AAAATCAAAGGCCCACAATG	59.801	20	119	1264	1382
CAACCAAACCAACCATCAAA	59.268	20	234	1730	1963
CTCGGATTTGGGTTTCTTCA	60.044	20	264	1245	1508
ACGAATCATTGATCGGCTTT	59.533	20	225	493	717
AAAACCGATGCAATTATGCC	59.801	20	279	102	380
ACCGTTTGCAACAATTGAGA	59.174	20	247	1465	1711
TCAACATGTCGGCATGATAAAT	60.217	22	247	286	532
GCATCGTTTATCCGATTGCT	60.067	20	250	14	263
TGTAAAATCAATGCACCGGA	59.93	20	276	449	724
CGTGTGCGTGAGAGAGAAAG	59.77	20	123	36	158
CGCTGGTTTTGGAGATCAAT	60.074	20	122	561	682
TATAAACGCTCGTCTGCTGC	59.234	20	200	48	247
CAAGGGTAAGGGAGGTGACA	59.959	20	152	808	959
ACCGATCTCACCCCTTTTCT	59.935	20	234	485	718
CAAACGGGAGGAAAATTGAA	59.91	20	151	679	829
AATCACGGATTTGGAGGACA	60.317	20	135	2110	2244
CCTTCATTGGGCAGTTTTGT	59.971	20	214	298	511
TGCTTTGGGTTCAAATGGTT	60.344	20	270	16	285
CACTTCAACACTCCCCACAA	59.565	20	266	2815	3080
ATCGGTTATTACCGGATCGC	61.031	20	274	484	757
TGGTTATCACCTGATCTTCTCC	58.121	22	243	450	692
TCGAGTTAGCGTGTCGTGTC	60.056	20	122	307	428
GTGGAGGGGGAGTATGGATT	60.015	20	265	140	404
CAAATGACAGAATCGCGGTA	59.688	20	278	63	340
CAGTCAAAGGAGGAAGACGG	59.837	20	268	573	840

CAACCCTGAATGCCATTTTT	59.801	20	162	690	851
GAAATGTTCACACACGTCGG	60.008	20	145	338	482
ATTGGCAATTAACCGTCAGC	59.967	20	244	274	517
TATAGTTTCTGCCCAGCCGT	59.73	20	257	1637	1893
CTTCTCCTTGGGCAACTCAC	59.844	20	267	42	308
TTCCGGCAAAAACCAAATTA	60.287	20	241	2671	2911
GTGGAGGGTTTTTGTCTCCA	59.943	20	275	3390	3664
GTCTCCAACCTTGCAACCAT	59.973	20	124	971	1094
TGCTGCTCTTTTCTGGGTTT	59.993	20	110	100	209
AGCTTCAACGGTATCCAGTAA	60.069	23	126	1000	1125
TTTGATATGATGCCAACGTCA	59.945	21	252	3625	3876
TTGGCACGAAATTAGTTGTTTG	60.034	22	216	219	434
TCCCCCTCTCTCTCCTTCTC	59.883	20	131	6	136
TGTTGCAGCTCTTGCTCTTG	60.472	20	280	136	415
AGCACACTCGAAAGGCAATC	60.406	20	168	276	443
GGCCGTTTTAAAATCGAGTG	59.586	20	246	663	908
AATGCATGCACCTGATTACAA	59.055	21	171	910	1080
AGCTGTTATGCGTTTTGATGA	58.452	21	237	1700	1936
GGTTTAACTTTTCAAATGGAAC	58.903	26	275	145	419
GAGAGCTGCTGCCGTTTACT	59.786	20	155	271	425
ATCACCTCATCACCGCCTAC	59.957	20	113	300	412
AAATGAAACACCCCCAAACA	60.066	20	210	3583	3792
ATCCGGAAGGTCCAAAACTT	59.805	20	180	605	784
TCCAACACAAAACTCTAAATTT	59.821	25	233	532	764
ACGTCGAGAGATGCAACGTA	59.47	20	107	8	114
CCTCACGTGATATTTTTAGCAC	59.197	23	187	915	1101
CGACGTTGCAAGAAAAGGTT	60.284	20	195	316	510
TGCAATGTACAGCAGAAGTGG	59.92	21	260	466	725
CCTTTCTCTCTCTTCCCCGT	59.811	20	133	60	192
CCAATTTGAATGGTTATCACCT	60.457	23	129	808	936
ATCCCCTTCTCTTTCCCGTA	59.897	20	172	1216	1387
GCAACACATTGTGAAGCCAT	59.577	20	231	254	484
TCCCCTTTTAAGGTTGATGGT	59.69	21	269	1063	1331
GTTTGGGCAATTGAAGGAAT	58.882	20	138	1269	1406
CATGACCACGCCAGACATAG	60.136	20	211	2995	3205
TTCATGCAACCATGAAAACAA	59.961	21	279	3149	3427
TGCCGGAAAACACCAAAATA	61.214	20	197	473	669
TTGAAAGCCACGTGTCAGAA	60.427	20	232	611	842
CCGGTTCTCCTATCCGATTT	60.278	20	174	629	802
ATCGCGTCCACAAATACACA	59.995	20	164	2618	2781
TAAAAGTGGCAAGCGACCTC	60.386	20	245	145	389
ACGACTGCATCAGCAAACTG	60.056	20	206	193	398
TGGAATGAAGGGGTGAGATT	59.336	20	175	167	341
TCGCTCATTTCACTCCATGA	60.353	20	221	1377	1597
TCGCCCATTTTCTCAACTTC	60.192	20	276	681	956
ATCGGTTATCACCGGATCG	60.697	19	273	3734	4006
GGGATTCAGGAAACAGGACA	59.903	20	273	3377	3649
GCCGCAAAGACTTAATCTCG	59.982	20	152	970	1121
TGTTCGGTTCAGTCGATTTG	59.691	20	265	311	575
CAATCCGCAAACAAAGTCAA	59.706	20	266	269	534
GAACCATCCGACCTTGAAGA	60.05	20	257	979	1235
AAATATTGGCCGTTTATTTCG	58.094	21	213	539	751
GCATTGAATGAATGGAGGTTC	59.382	21	172	36	207
ACGGATTTAAGGGTTATTACCT	59.498	25	232	1785	2016
TCTGTCTGGAGGAAAGCACC	60.386	20	118	19	136
TTTTCACCCGACAAATCACA	59.941	20	176	391	566
AACCTCATTGATTTGCAGGC	60.081	20	187	654	840
CTGCATCTTGTGTCCTGGAA	59.831	20	235	1404	1638

GAGATTTGGGCAAGCTTTTT	58.443	20	261	281	541
TGAAATCCAAATAGGTTAGAAT	59.664	25	199	1011	1209
TCGTTTGGCACGTTTTGTAG	59.769	20	197	2209	2405
CGCTGGTTTTGGAGATCAAT	60.074	20	156	528	683
AACAGGGAAGGCAAGGAAAC	60.476	20	277	578	854
AATTCTTGCACGCCATTTTC	60.081	20	239	651	889
AACCCTAGCTCGGAGAAGGA	60.34	20	105	10	114
TGATTCATTTTCTGCACGGA	60.197	20	185	136	320
AATCGTGCTATTTTTGCCTGA	59.734	21	237	255	491
TCCTTGGCTGACTAGGTGCT	60.012	20	163	978	1140
AAAAATATGGCATCCCGGTT	60.389	20	262	510	771
GAAGCTGAACCAGCGTTTCT	59.621	20	234	931	1164
TGTAGCAGCGAAATGCAGTC	60.165	20	267	1120	1386
TCTTCCGGATTTTAGGAGGC	60.522	20	259	7	265
AGTGAACCCAGTGGGAGATG	59.962	20	229	722	950
TCTTCCTCGTCACAGCTTCA	59.701	20	102	2265	2366
TCTAGGGGGTTGTTGCTTTG	60.103	20	231	1698	1928
TTCGGTTAATCCAATGGTCA	58.818	20	251	782	1032
GACAAAGTTGTAATTTGCGGC	59.644	21	273	904	1176
GCAAGAAACACAAGCCCATT	60.118	20	171	1116	1286
TTATCGCACAAATATTTTGATTT	57.045	24	271	403	673
TTGGAATGAATAAATGGAATGA	58.357	23	255	17	271
TATTTCAACCCCGCAACAGT	60.365	20	148	1685	1832
TGCCGACTTTGTGGATGTAG	59.716	20	116	102	217
ATAAAAATTTGGCGGCATTG	59.804	20	272	5	276
CTCCAGCTTCCCACATCATT	60.073	20	175	752	926
AGCGCAGATATGAAGGAGGA	59.939	20	210	879	1088
TTCCAAGAACGAAGTCTTCCA	59.838	21	219	16	234
TTTCTGTTCGCAAAAATGGA	59.277	20	171	2476	2646
TTCTCAGCAATCATCGCAAC	59.955	20	177	715	891
TCCAAGTTTTGAAGATGACCTC	58.293	22	268	526	793
AGCTCCAGCAACGTTACCAC	60.321	20	137	428	564
AGTGCGCTCTGGGTAAACTC	59.501	20	208	382	589
TATGGTGGTATGGTGAGGGG	60.452	20	163	112	274
ACGTGGATGTTATGCACGAA	59.995	20	122	642	763
GTGCAATCCTTCCAATCCAG	60.461	20	184	139	322
TGCATGACTGGATGAAGAGG	59.787	20	243	1150	1392
AACCAGAGACGCAGCATTTT	59.882	20	258	2358	2615
AGGAATGTCCACCGAGAATG	59.927	20	208	48	255
TAATTTCCAGGTTGATCCCG	59.756	20	240	221	460
TCTTTTTGGGATCAACGGTC	59.91	20	256	1596	1851
TGGTACCTCCTCCTAATTTCC	57.165	21	270	102	371
GCCGGTAATTTCGTGTAGGA	59.96	20	212	472	683
CTCACCTCCCCAAATACCCT	60.183	20	122	1986	2107
TGCTTCTGCTTACTGCCCTT	60.154	20	133	1097	1229
CAAGATTACAAAGGGCCCAG	59.564	20	241	747	987
TCCCGATTAAAGTTTCCATGA	59.397	21	232	431	662
GGGAGTGATACGAGTGGAGTG	59.589	21	245	1481	1725
TCAGGTACTTCAGCACTGCG	60.199	20	143	1469	1611
GTAGAGAGAAGTGGGCGGTG	59.867	20	148	22	169
GGTGAGGCCAGATTATGTGC	60.492	20	156	522	677
AGCTTTGATCTTCGCCATGT	59.843	20	234	645	878
TCGCCTGTATAAATGCCTCG	61.113	20	273	536	808
AGCACATGAAGAATGCAACA	57.834	20	258	341	598
TCAAAGATCCAACGCAGAGA	59.522	20	205	17	221
TCCATGTCTTTTTCCCTTCA	58.117	20	243	1839	2081
TGAAGTTAGGAAATAAGGAGG	57.525	24	162	562	723
CGCTTATAAGAGCGAGCAAGA	59.903	21	273	227	499

AAGCCCTCGTGAACATAGGA	59.694	20	240	3240	3479
GGTTCGGTTTTACGGATTGA	59.801	20	214	817	1030
CAGCCGAAAACCGAATAAGA	60.202	20	186	884	1069
TCTCAAACAGAGTGGGGAGG	60.229	20	229	288	516
GAAGCACTGGTTTTGGAAGG	59.711	20	274	344	617
GGCTCCCATTGTTTCTCATT	58.984	20	274	1328	1601
ACCATCATCACAAGATGCCA	59.925	20	255	206	460
GGGGACCATTTTTCCGTTAT	59.888	20	239	271	509
TTGCACATTGCATTTGAGTTT	59.22	21	254	13	266
TCGTGTGATGCCTTGGAATA	60.073	20	216	622	837
ACTTGCTTAGTTCATGGCCG	60.27	20	122	236	357
TCGTTTCTTTGGATATTTTTGTC	59.885	24	258	204	461
TGCCTTGCCTTTTAAGCACT	60.018	20	111	1707	1817
TCGTTTCATCTTCCTCTCGC	60.483	20	263	202	464
AAGGGGGTTATTAGTGGATCA	57.801	22	236	700	935
CCCACCCATGCCATTATTAG	60.031	20	241	1228	1468
TTGTTGAAACGAATCCGACA	60.088	20	268	2080	2347
CTTTTGCACCCTATTGGCTC	59.708	20	128	279	406
TCGAGGATCAATCTCGGAGT	59.761	20	261	1109	1369
TAAGTTTCTATTCGCCCCCG	61.27	20	256	522	777
CCTTTGATGCTGAGGCATTT	60.214	20	164	732	895
AAATATTGAGGTGGGGGTCC	59.881	20	128	136	263
GGAATGGGGAGTGTTGTGTT	59.679	20	237	530	766
TATTGCCCCTATCTATGCGG	59.907	20	172	572	743
TTAGCATAAATTTAGCCACCG	57.12	21	134	577	710
TAACGATGGACTAGGGGCTG	60.088	20	222	8	229
CACCTCCCTGGGGATTTTAT	60.011	20	195	2491	2685
ATGTAGCTTCGCCCATGACT	59.723	20	238	398	635
CCGAAAGGGGTGGTCTAGTT	60.353	20	220	270	489
TGGTTGTAATTGCACCAAATTT	60.045	24	167	281	447
AGCGTGAGCTCATTTTCGAT	59.985	20	226	2302	2527
GTTGGTCCATTGCCATTTCT	59.797	20	197	30	226
ATGAGTTATCACCGGATCGC	59.923	20	212	795	1006
CAACGACCTTCATTCGATCA	59.648	20	104	0	103
TTTCAATTGGCAACAAACCA	59.946	20	258	1312	1569
TGGTGAAAACCCCCAATAGA	60.162	20	214	443	656
ATCGTACGTATCGCCGTCTC	60.125	20	246	484	729
GCACTCCATTCCAAAATTCG	60.448	20	255	106	360
TGTCTGATTCTCCACCGTCA	60.246	20	210	35	244
GTGCACTTGAAATTGCATCG	60.265	20	229	179	407
TCAGAAACAATCTTTGTCTGTT	58.992	25	236	1115	1350
ACACCAAGTGGGAAATAGTGC	58.972	21	146	1727	1872
TCTACCACCGCCTCATCTTC	60.218	20	267	2380	2646
ACTGGCATATTTGTGTTGGCT	59.513	21	234	368	601
GGTAGAAGAATAGGTGCATGA	57.533	23	140	910	1049
GGACCGTGATGGACTGACTC	60.537	20	193	2890	3082
CGTATCATACAAGTATGCTGTC	59.985	25	251	5	255
CTGAATTGGCTTGTGGGTTT	59.971	20	217	688	904
GTTGAATTTTCACCCCGGTA	59.662	20	212	1569	1780
AAGGAGGTGTTATGAAGGGAT	58.028	22	166	1237	1402
TTGCAACACAAAGCACGAAT	60.302	20	151	284	434
TTTAGTCCATTCTTTCGGCG	60.202	20	191	1995	2185
AAAATTGCCCGACCTATCCT	59.799	20	222	48	269
ATCTTTAATGGTGGCCTGGA	59.387	20	220	2165	2384
GACCCAAAATGCAAGTGGTT	59.836	20	242	944	1185
GAACATGGGGAAGGGAGTTT	60.169	20	204	211	414
ATCTGCTCAAATCCTGCGAC	60.37	20	239	805	1043
ATGTAATGCCTCGCCCTATG	59.945	20	250	11	260

CCCAATACCTCCCCTCTCTC	59.89	20	241	1235	1475
CATTCGGTACGAAAAATCGG	60.315	20	269	47	315
GGTTCACGATTTGGGAAAAA	59.778	20	258	2487	2744
CACCTCCATCTCCGATCATAA	59.902	21	135	762	896
GTGAGGAATCCACTCTCCCA	60.048	20	266	39	304
CTTTCAGGCTTCAAAAATCCA	59.325	21	203	6	208
ACCGTTAAAGAAACCGGACC	60.221	20	152	1255	1406
TTGATCGCGACATTTGATTT	59.115	20	236	48	283
TGAGGCATCTCTCTCTCACA	57.05	20	249	313	561
TGAGGCAGTGTTGTTCTTCG	60.025	20	237	1329	1565
CTGCCAAGGAACCACAAAAT	59.971	20	187	1307	1493
ACGGATTTAAGGGTTATTACCT	57.667	23	256	747	1002
TTGCAGAAGGGAAGAGACAG	60.119	21	253	1489	1741
TGAAGCGTCAAATCACAAGC	59.995	20	273	306	578
CCCTTCAGTGCATCTTTCCT	59.284	20	227	1466	1692
ACCACCCGAGTAACAACGAC	59.891	20	247	1237	1483
TCGTGTCTAGTGCAGCATGA	59.141	20	115	4748	4862
TCTCATCCAACGAGCTGAAA	59.522	20	264	299	562
GATCCTGTAAGCTCCACCCA	60.073	20	256	177	432
GTAGCGAGATTCCGATGGAG	59.797	20	107	267	373
GGATTCCGAGTTTTCGATCC	60.777	20	168	552	719
GCTTGGTCATCCCTCTTGAA	60.195	20	241	859	1099
CTTCGGAAGCAAAATTCACG	60.742	20	130	2516	2645
TCAATTTCTCTCTCCTGCACC	59.42	21	260	207	466
AAAGCAGCCGCAAGAAGATA	60.117	20	214	846	1059
GCAATCGTGATAGGCAACCT	60.103	20	124	2376	2499
ACGAACGCCAAGTTCTCCTA	59.875	20	255	252	506
GATGGGTTATTGATCACGGG	60.014	20	146	3845	3990
GCATTTCTTTGACCTCCTGC	59.82	20	204	167	370
ATCGAATCGGAAAGTTCCCT	59.903	20	265	290	554
CCAAAAGTTCACATCACTCCA	59.633	22	189	4	192
AAAGAACTTTCTCCTCTGGCA	58.187	21	218	200	417
GTTAGGGGTGTGCACGATTC	60.384	20	271	4	274
CAGGCAAATCCTTGGGATATA	59.823	22	220	20	239
GGAGGCATTCGATCTTTGTG	60.603	20	200	175	374
ATTGCAGATGGATGTAGGGC	59.923	20	246	48	293
TTTTTAGGCTCTCGGAGCTG	59.724	20	237	183	419
ATCGTCCTTCGTGCAATCAT	60.492	20	199	4442	4640
AAATGGACCCATCCTCAGGT	60.575	20	162	2249	2410
TTGGAAAGGAAAGCTCGAAA	59.931	20	230	1470	1699
GAAGTGAATCAAGTGATGGCT	58.794	22	158	41	198
TGGAATGTCAAGTCAACACAA	57.556	21	139	931	1069
TTCGTCGGAGCAGGAATAGT	59.836	20	280	213	492
GTCATTGTATGGTGCGTTCG	59.995	20	273	160	432
AGTCCCATGTTGCTGCTTTT	59.74	20	227	39	265
TAGAAGGCACTGGCTTGGAT	59.836	20	219	211	429
GAGGCTTGGAACAAACATGAA	60.103	21	274	1724	1997
TGCACAAACAGACCATCTCC	59.682	20	189	1112	1300
TGAATGCTCTGAATGCTGCT	59.704	20	259	824	1082
CATGGATTTTCTGGGTCTGC	60.461	20	143	461	603
CAACCTCAAAAATGCCCACT	59.971	20	179	801	979
TCGAACCACGTAAATCCTTTG	59.982	21	261	1006	1266
CTCCAAAAACACGCACACAC	60.199	20	184	15	198
TCCCAGATGATGGTTGTGAA	59.893	20	275	208	482
TGTGAAATCCGAAAAATGGAG	59.924	21	245	224	468
CACCTTCCCCTGCAAAAATA	59.931	20	171	1338	1508
CCCAAAATTCCCCAACTTCT	60.159	20	252	323	574
CACAACAAAAAGCAACCCAA	59.603	20	168	334	501

TCTGTTGCGTGGAGCATTTA	60.401	20	229	0	228
ACCATAACGCACCCAAGAAC	59.859	20	189	2129	2317
TCTCGAGAAAACGGGATTTG	60.184	20	211	644	854
AAATGGTGTGATCTTGGACCT	58.364	21	279	1834	2112
CAACGTAACTGGCAGCAGAA	60.05	20	124	577	700
CGAAGAGTAGTGGCTGCACA	60.199	20	202	402	603
TTCGCATAGCAGTTGTTCCA	60.401	20	259	1922	2180
CTTTTAGCCAGCCCAGTTTG	59.876	20	279	43	321
TGCTTCTTGTGGAGCTGAAA	59.716	20	276	1051	1326
GAGTGAATGTGCATGGAGGA	59.637	20	190	241	430
TGTTCCTACGCACTCACATTAA	59.344	23	258	704	961
CAGTGCAAGTGTGCAACAGA	59.642	20	274	338	611
GCAAGTAACCTAGTGGCCAAG	58.917	21	188	130	317
CACCTTCGAGATTGCTAGGC	59.978	20	182	1684	1865
CGTTTACGTTTATCCATACCCA	58.806	22	163	362	524
AATTCGTTCGGGGATAGAGC	60.419	20	279	338	616
GCAGTTCATGCGATTCATTG	60.228	20	247	185	431
TGCCTACCATTTCAGCACAA	60.257	20	234	409	642
TGCAACGTTGAGACAAGAGG	60.025	20	250	1619	1868
TTCCGTAGTTGGTTTAGGTTCTT	58.328	23	244	691	934
ACCATCAGATTCATTGTGCG	59.527	20	269	898	1166
CTCCAAACCCAATATCACGG	60.184	20	242	568	809
AAGAAGCAATGGATCATGGAA	59.519	21	222	145	366
TTTTGTTCCTCCTCCCTCCT	60.045	20	233	135	367
GGCATCTCCTCTTGTCTTGG	59.803	20	233	2997	3229
GACGTCCGCTATAAAGCCC	59.682	19	257	6640	6896
AATAACCCCACCATCACCAA	59.91	20	143	88	230
TTCGGTTTCTGCAATTTTTG	58.792	20	271	58	328
CTCAGACAGCTTCAAATCCC	57.451	20	215	728	942
CTCAATCTCACACACCCACG	60.154	20	122	656	777
AAGAAATGGCCAATGTCAGC	60.081	20	178	1	178
CTCAATTACATCCAAGCCGC	60.606	20	211	760	970
ACAATCGATTTCCCAACCAC	59.653	20	172	57	228
TGATTCTGGGTTTCCAGTCC	59.903	20	153	336	488
AAAAGCAGCCATAACTTGCC	59.365	20	196	583	778
GGAATTCTATCCGAGCACCC	60.797	20	135	1664	1798
TGTCTAGGCCCCTGTAGCAT	59.717	20	152	778	929
TCTCACCGCCAACTCTCTCT	60.135	20	169	1423	1591
CAACTTCAGTGCCTCCCATT	60.111	20	212	39	250
GGAGAGTTCCAGATGCGTGT	60.269	20	126	2688	2813
ATGCCCTAAGGGGGAGGTAT	60.882	20	201	309	509
CGACTTTTCACTATTCTCCGC	58.986	21	160	10	169
AGGGGTCCTCCGTCATAAAC	60.19	20	199	1431	1629
TCCAACGACAATAATTCCATTT	59.616	23	251	589	839
AAATAAGGAGGTGTTATGAAG	59.323	24	151	1635	1785
GAAAAGCTTGGGAATGGTGA	60.051	20	188	1133	1320
GGGATAAGGCCGTCGATAAT	60.137	20	128	18	145
GTTAGATGATGCCACTGCGA	59.83	20	274	2754	3027
TCGTGCCTAGTTGGAAACAA	59.317	20	213	522	734
CTTCCCCTGCAATCAAAGAA	60.184	20	171	3643	3813
TTGCTGAAAAGCAAGCCTCT	60.27	20	134	652	785
CCCTCCTATGCACTCCAAAA	60.066	20	233	3642	3874
TGCGCTATGCCTAACAAAAC	58.985	20	275	172	446
CTCGCCATTTTCCCCTAAAC	60.792	20	264	496	759
TCTCCCATTTCCAACCTGAG	60.042	20	177	1566	1742
GCGCATAAAATCAAAGGGAA	60.04	20	196	3546	3741
TTGCTTGTGGCATGTTCTTC	59.847	20	245	748	992
TCAGATGAAGCCAAAGAGGG	60.331	20	276	2066	2341

TAGAGTAGCGGCTGCAGGTT	60.176	20	132	59	190
AGGCAGCTGTATTCACGAGG	60.419	20	118	616	733
CCAAACACCCCCTTAGTGTT	58.812	20	250	864	1113
GGGATGTTTGGAGAGACGAA	60.05	20	137	40	176
ATCAGCAGCAACCAAGTTGA	59.445	20	199	540	738
ACACGACGAACTTTTCACTTCA	59.819	22	215	559	773
GCCATTTATTCGTTGCTTGC	60.597	20	192	1436	1627
TTCGAGTTGTGGTATGGCTG	59.716	20	271	453	723
GATGACGTCAGCGAATGATG	60.233	20	174	813	986
AAGTTTGGGGGAGGAGAAAA	59.912	20	255	382	636
TTCTTCCAGAAGTGGGCATC	60.195	20	263	1167	1429
CCTCCTGAACCAAATCCAAA	59.903	20	144	567	710
CTTCTCTCACCACCGCAAAT	60.255	20	130	947	1076
CAACGGTTGCAATTTGATTC	59.016	20	227	507	733
ACTCCATCTCTCTCCCGCTT	60.358	20	240	564	803
GCAGGTGGAAGGAAGAGGA	60.333	19	222	732	953
TGCCTGATGAATTTCTCCTG	58.797	20	268	6060	6327
CAATGGTGAATATTATAAAGG	58.513	25	216	192	407
TGCACTTGTGCCCCTAAAAT	60.502	20	269	1772	2040
AATTTCCCCGCGTTATTTCT	59.808	20	176	769	944
TGTAAAAGGATTCCACGTATTT	60.053	25	259	352	610
TGACCAGCCTGACCTCAAAT	60.656	20	225	1059	1283
AGAGCTCAGGATCTTGCGAA	60.24	20	238	3314	3551
ATGTGGCATGGTGAGAAGC	59.653	19	231	1292	1522
GCTTCTCTCTCGCTCCTCCT	60.38	20	130	1079	1208
TAAAACGCGCTTTCATACCA	59.351	20	234	376	609
AACTCATCCAACTAAGCCGC	59.34	20	269	1203	1471
ATGAACCTGCTTTTTGTGGC	60.118	20	253	973	1225
GGAGAATCCGGTGGATAAAA	58.832	20	254	341	594
TTGTTCACCCACCTTTATCCTT	59.741	22	241	3097	3337
TTTCGAGAATTTCCTGTCCG	60.184	20	268	17	284
TTAAGCAAGGGGATGACTCG	60.206	20	157	3328	3484
ACCGGAGTGTGTTGATTTCC	59.827	20	275	70	344
GGCGGCTTACATTGTTTCTC	59.713	20	263	16	278
AACGTCAAACGGTCTATGCC	60	20	111	3228	3338
GCTGACCGTTGGTAGCCTTA	60.27	20	232	882	1113
CGACGCCTCAAATTTACTCC	59.708	20	207	520	726
AAGAAATCAGGAGCTGCCAA	59.955	20	270	6259	6528
CACGGTAAGTCCCGACATTT	59.853	20	188	542	729
AGCTGCTCCTTTCAAGCAAA	60.27	20	271	456	726
GGTCGTTGCTGGTTTAATGG	60.365	20	184	297	480
TGCGTTCTGAGTTTGTTTCG	60.027	20	240	2764	3003
TTGAAAATTGTTTTATTCCACAT	59.246	25	198	13	210
ATCTGCTTCGGTACAATCCG	60.096	20	136	25	160
TCAGTTATGCTCTTCTCCCCA	59.822	21	198	964	1161
CGGCCGGATTCACTATTTTA	59.922	20	121	0	120
GACTGATTCAATCTCCTCCCAT	59.401	22	212	2	213
AATATTATTGTGGGTGGCGG	59.547	20	253	367	619
GATCATGGGCTTGCAATCTT	60.043	20	275	3966	4240
AGAAAGGAGAAGCAACAGCG	59.757	20	211	444	654
CATCCTTCTGAACACCGGAT	59.927	20	173	33	205
CCACAAGAAAGCAGTCCTCC	59.844	20	262	1085	1346
GGTGGAAAAGGGGGAGTCTA	60.298	20	176	161	336
GAACACGACTCTTTCGAGGG	59.844	20	269	145	413
ACGAATAACTGCAAAAGGCA	58.439	20	202	856	1057
CGCACAATAGCTCCGATCTT	60.374	20	183	231	413
GCCATTAGCCTTGGAGATGA	60.177	20	221	151	371
GTCAAAGGGATCAAAATTCCC	59.636	21	203	3426	3628

TGAACGGTTAAAATAATTGCTG	58.731	23	277	189	465
ACCCCTTGAGTATGTCCCATC	60.067	21	237	1316	1552
TAGGAGGGAGGTTGCATTTC	59.126	20	278	296	573
GCACCATATACTTCCCAGCC	59.415	20	148	9	156
CCATGTAGGCGTAAAAATAGG	58.224	22	144	758	901
CGGCGATCATTTGATACCTC	60.435	20	267	19	285
TGAAATGCCCTCTTCACCTT	59.67	20	210	566	775
CTCACCCGGCCTCTTTATTT	60.443	20	134	1400	1533
GGAGTCGCGGAATCAAATTA	60.038	20	206	348	553
TGAAAGATGAAGGTTTGGGG	59.903	20	247	333	579
CACATGAGTCGATGATTGGC	60.08	20	140	53	192
CCACGTTTTGGGGTCCAC	62.219	18	263	589	851
GTCAAACAACGTGAATGAGCA	59.755	21	251	347	597
TAACGAGCCAAATTGTGCAG	59.872	20	170	454	623
TCGTGTTTCCTATGCTTCTGG	60.256	21	140	745	884
TTTCCTCCCCTCTCTCTCGT	60.328	20	277	1633	1909
TTTCTGTCTTCCGCGAATTT	59.823	20	147	12	158
CCCATTTCAAGCTTGCTCTC	59.955	20	228	278	505
CCCCACCCCCAAAATATTAC	60.123	20	254	3088	3341
GTGGACGCTCCAGATTGTTT	60.119	20	272	1515	1786
ACTGCCTGCATTGTTTCTCA	59.445	20	215	609	823
ACCAGCCCTTTTCTTTCCTC	59.691	20	268	4277	4544
CACCAAATTTCATCATTTTTAG	58.144	25	256	403	658
AGATTCAAGGGCCGAGATTT	60.039	20	116	57	172
TTTTGGTCTGGTCTGAGCCT	59.844	20	163	2223	2385
GCAAGTTCAACCTTCTTGGG	59.711	20	152	1505	1656
AATGCGTGCAACACACAAGT	60.23	20	161	9	169
TTAAAAGGGAGCGAGAGCAA	60.089	20	216	635	850
TGCACGTAGGCATGTTCAAT	60.142	20	256	105	360
AGTCCGATTTCAACCAGGTG	59.966	20	202	644	845
CATCCCCCAAAAAGAGGTC	59.322	19	273	838	1110
TGGTTATGCAAGTGGAACGA	60.111	20	222	246	467
TTCATGAGCTCGCTTTTATTGA	59.985	22	232	254	485
CCTATGGTAGTATGGTGTGGG	60.365	22	146	59	204
GAAGGGGCGGAATTATCTTC	59.873	20	130	2402	2531
TGCGTTTTGACAATATATAGGT	60.083	26	245	642	886
TCCCAAGCCAAACACTCTCT	59.844	20	198	3751	3948
TCTTGAATCTGGCCTTCGAT	59.773	20	253	692	944
TAATGGCGATTGCAGTTCAG	59.833	20	270	249	518
TCTCTCTCCGACCTCCGTTA	59.943	20	167	998	1164
AGACATTGCCTTGCACTTCA	59.445	20	271	235	505
TGATTCCTATGCCTCGTGGT	60.483	20	251	105	355
GGTCTCCGGTCCCTAAAATG	60.683	20	251	640	890
TGGGGATGGGTCACTTTAAT	59.101	20	270	221	490
GCTGCTGCTGATTTTTACAGG	60.032	21	278	962	1239
CAAACCGGGAAGAACTACCA	59.964	20	235	688	922
AGAAAAGGTGCTTTCCCACA	59.711	20	121	939	1059
TCATGGTTTCTCTGTTGCGA	60.39	20	274	717	990
GGCGTTGAAAATCTCCATTG	60.448	20	175	632	806
GTTGTTGGAGCTCATGGACA	59.682	20	207	609	815
GCCGATGGAATCAAGAAAAA	60.016	20	190	2354	2543
CTTTTGAACCGGGAACTTCA	60.081	20	218	1910	2127
GCACTCGAAGAGTAGCGGTT	59.644	20	280	55	334
TTTAGCTGGCAGGCATACAA	59.467	20	235	24	258
TCCCTCCCTCTTTAAAATCACA	59.939	22	176	3690	3865
TCTCAAGCCCGCGTTATTAG	60.356	20	269	963	1231
CAACAGTTTTTCTGGGGCTC	59.711	20	278	1313	1590
GCATGCTTTTGTCCTTTTCA	58.895	20	209	3419	3627

CAATGGTGGAGCAGTTTTCC	60.495	20	106	58	163
GGCATAAAATGGGTGCTGAT	59.791	20	125	234	358
CACTAAGTTGAGCGTTGCGA	60.195	20	113	925	1037
CAAAATGGTCATGAAACACGA	59.43	21	261	920	1180
ACCAAATTTGCAAAACCGAA	60.335	20	260	142	401
TTGCAAACGTCAAACAAAATG	59.634	21	222	693	914
GCCGTCTGATTGGGAGAAT	60.026	19	278	1016	1293
CATAAGATGCACCTGCGAAA	59.833	20	252	321	572
ATTGACGGGGTTCACAGTTC	59.827	20	199	262	460
CAGACCTCCAAAAGCAGGAG	59.982	20	211	1225	1435
GAATCCGAAAAATAAGGGGG	59.616	20	230	279	508
CATCTCCCCTCTCTCTCCAA	59.329	20	173	26	198
TCAATGAACAAATAGGTCACA	58.922	24	257	344	600
ACCCGAGACAAAACACGAAC	60.012	20	206	270	475
ACAAAGAGGAGGAGCGTGAA	59.989	20	272	730	1001
TTGTCTAGTTGCAACCCCCT	59.592	20	279	2221	2499
TCGAACATTTCCATAGCCCT	59.528	20	205	533	737
TGTTCATCCATGTTTTGGGA	59.75	20	175	207	381
CATGCTGTTGGCCTGTAGTG	60.324	20	106	0	105
TCGGTTCAATAAGATCACCGA	60.454	21	231	961	1191
AATACGACGACGAAGCCAAC	60.14	20	187	55	241
GAGAGGTGGGACCCTGAAAT	60.314	20	254	313	566
AGATGCAGAGGACCAGGGTA	59.679	20	150	12	161
TCTGAGGAGATTTTGGCAGG	60.331	20	242	556	797
CCGTGGGTATTCCCTACTCC	60.569	20	221	392	612
TCATGGGAATTCACGAAACA	59.9	20	190	284	473
CCAAGCATGCTCATGTCAAT	59.679	20	126	145	270
CTGAGGTGACCTGGACCATT	59.962	20	268	35	302
TGCATGAAAACTCCCTCACA	60.24	20	216	593	808
TTGAGCCCAAGAGGAAAGTG	60.366	20	208	377	584
TGAAAATCGCCCAAAGATTC	60.016	20	168	682	849
TCCATCAAATCCAGGTTGGT	60.173	20	155	786	940
GGCTAGCTGTCCATACAATGC	59.75	21	223	294	516
GATTAACATGCGGTCGGATT	59.791	20	257	1305	1561
AAGCTAGCACGTAAATGGGG	59.248	20	120	540	659
CCATCGTTCCCATATACCCA	60.405	20	227	2	228
TATTTTGGGCCTGAATGGAC	59.762	20	206	484	689
TGAGAATGTGCTCAGACCGT	59.42	20	269	1021	1289
GATTCGATTGCTTGCATCAC	59.234	20	258	278	535
GCCACCCTCTCTCGTAGTGT	59.33	20	279	196	474
TCGGTCAACATTGCTTTCAA	60.234	20	126	1334	1459
ACTGGTGCTCATGCTTTGG	59.846	19	234	2967	3200
ACACGTGGAGACAACGTGAA	60.203	20	222	112	333
TCTCCATGCAAACTTCACCA	60.24	20	200	1562	1761
AGGGAATGGAATGAGCATGA	60.426	20	278	45	322
TAACGGAACCGTGGGATAAA	60.181	20	162	316	477
GCACTCGAAGAGTAGCGGTT	59.644	20	259	2058	2316
AGGACGTCGAGGGAGAGAAT	60.216	20	207	559	765
GCTTGGCCACTTATGAATCG	60.606	20	262	32	293
CCTCCCCATGGCTAGACTAA	59.146	20	193	381	573
TTGCTCCATGTTATGCAATG	58.145	20	246	1303	1548
CATGCAACAAACCAACCAAA	60.393	20	237	397	633
GATATTGGAGAAGATATGAAA	57.823	27	260	1684	1943
ACAACAAGATGCCAAAATAAA	59.822	24	187	670	856
CTTCCTGAGTTGACCGATCC	59.655	20	136	344	479
CATCCCCATTACCTTAGTTAGC	59.424	23	264	523	786
TCTGACGACCGATATGTGCT	59.271	20	250	97	346
GTGAGGCGAGGAAATCAGAG	59.95	20	278	17	294

TTTCCTTTCATTACACGTGCC	59.989	21	266	39	304
TTGATGCAATGATCTCATTCTTT	59.976	24	246	351	596
TGCACAAGCATGTTTTTCATT	59.22	21	240	291	530
TGTAAACAGGCTAGGTCGGA	58.379	20	280	1512	1791
TTTTTGGGAATTGAAATGGC	59.751	20	219	803	1021
TCTGTTTTTGTTTTGGTTGCC	60.004	21	232	145	376
GCTAAAGCCATCTCCAATGC	59.813	20	237	323	559
CCTGGCAGCTTTTGATCTGT	60.397	20	155	73	227
ATTTCCCCAGTTTGTGTGCT	59.454	20	129	602	730
TGTTCTAGCAAAGCCCAACC	60.249	20	152	880	1031
CATCTCTTCTCCTCGCCCTA	59.526	20	185	671	855
GATGACAGAGCAATCGGGTT	60.081	20	232	321	552
TGGTGGAGGGTTTGTTTGAT	60.21	20	146	519	664
TCTTGCACCAGTTGTTGAGG	59.873	20	169	324	492
TCTGGAGATCAACTCCTCGG	60.34	20	191	370	560
ACCGATTGCGATGCTTAACT	59.736	20	222	1372	1593
AAGAAATTGGACAGTGGCGT	59.598	20	168	3918	4085
ATCTTCAACCCCCACCTCTT	59.795	20	176	642	817
TGCAATCCAAAAGGGAAAAA	60.407	20	256	52	307
GGGAAAAAGGGCTTGTTGTT	60.332	20	185	3686	3870
TTTGAACACTCAATGCGCTC	59.995	20	270	944	1213
TCAGTGTTGCTTCGATCTGG	59.984	20	280	1177	1456
ATCGTGCCACTTTTCTGTCC	60.119	20	252	335	586
TGTGGAGATAAGCAGCGAGA	59.697	20	235	28	262
AACTGAAGATGACATCCCCG	59.927	20	191	926	1116
ACTCTTCCACCGACCTCTCC	60.648	20	210	14	223
TGGGAATCCGGACACTAACT	59.405	20	245	327	571
TTTCTTTTCTTCCCCCACCT	59.912	20	273	1065	1337
CACCAGACCGGCTCATTTA	59.658	19	280	563	842
TACCCACCTCGAATATCCCC	60.901	20	138	310	447
CAACTAGGGGGTCCTGAGGT	60.363	20	148	1599	1746
TCACGTGACTTATTTGGTGGAA	60.399	22	227	2858	3084
TCATGAATCATCAATTCGAAAC	59.849	24	229	20	248
TAAATTTGCTTGGCCCTCTG	60.202	20	216	1834	2049
TCAATTCGCCCAATCTTCTC	60.155	20	242	993	1234
TGTTTAATTTTTGTTAAGCATGC	59.958	25	211	379	589
TAAATGAAACCGGGGTATGC	59.66	20	198	17	214
GACAAGGAAAAAGAGCGCAG	60.132	20	184	1566	1749
AAATGCGTGAAGATAGTGATGT	59.171	23	218	446	663
TAGGTGCTTGGTTGGGAAAC	59.971	20	209	537	745
TCCTGCTTCTCCCACATCTT	59.803	20	116	669	784
TGCTGAGGTGGAGCAGTAGA	59.726	20	278	2071	2348
CCGTGTTTTGACCCTTTGAC	60.388	20	278	0	277
AGTGGAGTGGTGGAGCAAGT	59.756	20	142	825	966
TGAGACTTTGGTACGGGAGC	60.255	20	225	339	563
GCGACTTGTGAGACAACGAG	59.622	20	140	300	439
GGAATTCCATCCATCTCGAA	59.831	20	120	219	338
GGCATCCATACTTGCCACTT	59.962	20	273	1178	1450
CATGCATACAAAACCAAACG	57.57	20	159	4358	4516
TCCTGCAATCTCTGAACCAA	59.369	20	269	371	639
GCATCATAGGACCCCAAAAA	59.762	20	210	390	599
CATTGACCGTCCTTGTATGC	59.002	20	230	108	337
CGCAATATGAAATGGCACAC	59.96	20	268	788	1055
TGTTCAGCACACAGAAACTTCA	59.534	22	260	566	825
TTTTTCTTTGGGTCATGTGATG	59.839	22	262	697	958
ATTTGATCCCCCAATTCAAA	59.067	20	155	18	172
ATTCACCAGCTCCTCCAATG	60.073	20	255	2333	2587
ATTGGTGCATGATTGCATTG	60.352	20	159	511	669

ACATGGGATTCATGGGTCAT	59.869	20	211	746	956
CTTCTTTTGGCTGTGCTGGT	60.431	20	163	831	993
TCTCCAACAACTGGTCAGCA	60.44	20	218	1980	2197
CGGAGCAAATTTATCCTTTTGA	60.421	22	127	683	809
GAGTTCAATAACGTTTTTAATA	59.561	27	280	1568	1847
AAGTTTCCATTCTGCCGTGT	59.598	20	152	74	225
GCACGAGCTGTGTTGCAG	60.357	18	229	470	698
TTGATGTTTGTATATGTTTCGTT	58.542	25	277	240	516
AATGAGGTCAATGGTCAGCC	59.934	20	151	1147	1297
GTGTGGCGTGCTAACTGCTA	60.081	20	217	239	455
TTATGAATGAAAGCCACCCC	59.762	20	153	60	212
CTGCTGTCCATTCCTCCAAT	60.073	20	279	624	902
TATTATCTCCCGCAACACCC	59.784	20	213	697	909
CCGTTCCATCAAGCATTTTT	59.938	20	151	1097	1247
AAAAGGCGGTGGAAGAAACT	60.11	20	108	7502	7609
CACCCCACGAGACAACTTTT	60.005	20	113	742	854
ACTAGTGGCAGCCATGTCCA	61.688	20	235	256	490
GCCGTTTTGCTTTGGTTTTA	60.109	20	240	377	616
CAACTGTGATGTTCTTGTTTTG	59.707	23	279	720	998
TGCCATCGTTCACTTTACCA	60.111	20	202	1271	1472
CAAGCTTCTTCCCACCAATC	59.67	20	271	996	1266
TAGTGGTCGACGGGCTTTAG	60.262	20	264	227	490
TCCAGTGTAGTTTACCCGGC	59.993	20	181	871	1051
CCATGTCCAGACCCATCAAT	60.6	20	250	1091	1340
GCCACGTCATACGAACTCCT	60.142	20	257	595	851
ATTCTGCTATTCCCGAGGGT	59.925	20	225	0	224
ATCCGTTCCGGTCTTCTACA	59.55	20	229	417	645
CTGATGAACCCTACCAACCAA	59.838	21	254	392	645
ACTTGCAAATATAAACGTAAT	59.169	26	205	226	430
AGCTCCCAAGTCTGAGTGGA	59.986	20	178	441	618
CAAAACAATTGCTCACGCAT	59.735	20	119	1029	1147
AGAGCTGTCCATCCCATTGA	60.622	20	120	1050	1169
ATAATATGGGGCGTCCACCT	60.419	20	242	205	446
ATGTCTGCCCAGCAGAGAAC	60.418	20	279	682	960
ATGCACAATCATCACACATAA	59.634	23	154	722	875
AGGAACGGGAGATTTTGCTT	60.074	20	194	259	452
TTCCGGAGCATTACCCTATG	59.916	20	277	1679	1955
AGGTGAGCCAGATGTAGCGT	59.898	20	156	738	893
GCGGACAGAAAGAGATAGCG	60.118	20	187	335	521
TGTGTTGAAACCCTCATCCA	59.935	20	249	1425	1673
CTGGTTGCCAGCTTACTGCT	60.592	20	201	326	526
TTGTCATGATTTGCGGGTTA	59.93	20	189	49	237
GGGAAGAGAGTGAGAGTTTTG	59.507	22	115	769	883
GGATCTCCAAATCTGACGGA	60.011	20	217	840	1056
GGTTCGATTCTCATTTCCCA	59.871	20	254	10	263
TGTATTCGGTTGAATTTGATGG	59.699	22	123	317	439
GCTTTGACAATATTTAGTGTTTT	59.901	27	279	3629	3907
CACACATCCATGTTCGTGCT	60.604	20	265	163	427
TCCTTGTAGAAGCCTTGGGA	59.807	20	278	53	330
GGCAGACAAGCCATCATTTT	60.081	20	154	401	554
TGATTGTGGACCAACAGCAT	59.967	20	182	167	348
TGAAGGTGTGTGGGGTGTTA	59.848	20	240	1329	1568
CGAAGGAATATGGACAAGGG	59.382	20	184	1724	1907
ATTTCCAGCGTCGAAGACAT	59.7	20	162	59	220
CTCAATTAGGTGTCCCACCG	60.366	20	198	337	534
GCCCTTCCCAACTCAAAGA	60.18	19	133	963	1095
TTCCTTCACTCTCCACCTCG	60.377	20	217	1404	1620
GGGTTCAAACTCCACTCAACA	59.997	21	178	617	794

TGTGTGTCATTTGTTTTGTTAGG	59.464	24	263	119	381
TCTGGACGATCCTCATCCTT	59.612	20	222	119	340
CGTTGTAATGCCCCGTAAAT	59.72	20	182	1277	1458
TGGAGTTCAAGCCCAAAAAT	59.546	20	280	2107	2386
GGGTCCTCCCAGTATGTGTG	60.238	20	205	1477	1681
CTAGGCCCATTGCAAGAAAA	60.202	20	272	1033	1304
CAATCTGCAAAAGAACAGGGA	60.234	21	253	302	554
TTATCCTGTGCTTTTGCACG	59.872	20	237	2664	2900
TCTCCTTCCTCCATTCCCTT	60.008	20	140	74	213
GCATGCTCTCCACCTTTGAT	60.226	20	193	246	438
TGCGTTTTGATGATATATAGGT	58.933	25	271	724	994
TCTTTCCATCTTGGACCACA	59.059	20	183	3669	3851
TTATTCTCGCAAACAGTGCC	58.92	20	279	2410	2688
TCTTGGATTTGGAGGAATGG	59.864	20	212	354	565
CCCTCGTATGCAGTGGTTTT	59.993	20	228	679	906
TCTGCTGAAGCCCTTCTCAT	60.096	20	240	12	251
TGGGAATGTGGTGTAGATTTG	58.338	21	185	221	405
ATCATGAATGACACATGGCG	60.362	20	225	11	235
TCACAAGGGTGAAAGGGAAC	59.943	20	232	71	302
ACCACAGTGGCATTACACGA	60.032	20	258	728	985
CTTTGCCGTTCTTATGCTGC	60.905	20	130	403	532
TGGAGGTTCCCATTAATCCTC	60.138	21	160	683	842
GAATAGGAATGGGGGAGAGC	59.866	20	221	959	1179
TGGTTGGAGGGTAACATCGT	60.232	20	204	1029	1232
GCGAAGCGACATCACATAAA	59.839	20	141	24	164
AACTTGTGTTGGTGGCTTCA	59.187	20	246	1904	2149
TCAATCTCGTTGAAAAATGGTT	58.605	22	261	818	1078
CCCTCCTAAGGACCCCTTCT	60.797	20	119	0	118
CGCTCGACTTTCTCGAAGAT	59.717	20	226	283	508
TAGGGAGTCACTTCCGTTCC	59.137	20	265	1649	1913
AACATTATTGCGAGCGAACA	59.329	20	184	74	257
TCTGCTTGACAAGTGGCATT	59.445	20	244	7	250
GGCCAACAAATCGTCAATCT	59.939	20	242	292	533
CGCTCAACAACCACAACAGT	59.794	20	205	76	280
CCATCGAAGCTCACTGTCAA	59.984	20	168	969	1136
TGATGTTATAGTAAGCAAACCA	57.922	25	217	716	932
ATGCTGAAGGAGCCAAAAGA	59.955	20	159	289	447
CCGTTGCCTTACCTTTTTCA	60.103	20	255	492	746
GGACACCACGTTAGCATTCA	59.572	20	225	354	578
TGGGGGAGATTTTTGTTTTG	59.772	20	238	959	1196
ATCAAGAGCTCTCACCCACG	60.408	20	102	6	107
AAACTACCACTGCGTCCCAC	60.035	20	187	751	937
ACGAGCTCTCCCCTTTATCC	59.674	20	280	335	614
GCACCTCCTGTTAGCGAGAA	60.538	20	264	392	655
CCATGATTTCGGACACACAC	59.812	20	251	603	853
TCCATACAGACACAACCCCC	60.634	20	187	281	467
TGTCTGGAATGGAATGTGGA	59.893	20	277	4264	4540
CCCCTACATTGGGAGTCAAA	59.784	20	225	896	1120
AACATGATACCGCCGAAAAT	59.301	20	226	159	384
CCATCCCAAACCAAAACCTA	59.657	20	273	1291	1563
TGGAAAGCAACTCAATTTTGG	60.096	21	149	559	707
TGGTCGAATGAGGAGTGAAA	59.215	20	256	133	388
GCCTCTGCTTCACCAATTTT	59.316	20	261	245	505
TGCAGACGAAACTCACAAGG	60.025	20	141	657	797
GAAGGTGGTGTTGCTGTGAA	59.726	20	271	201	471
TTATCACCAAAAGGAGGGGTT	59.69	21	265	711	975
GAAATGAGGGAGAAGGGGAA	60.38	20	244	6310	6553
TGGCATCTTAAAATCCCTCAC	59.033	21	248	14	261

TGCCTCTATTGGGATTGAGC	60.177	20	119	47	165
TGTCGCTTCACTGGTATTCG	59.864	20	244	1501	1744
ATGTGATGTGAGCCACGAAA	60.12	20	182	2520	2701
TGGTTCCATCTTCGAACTCC	60.05	20	257	131	387
AACACGGCTGTTTACGTGGT	60.474	20	265	599	863
TTTTCACGTGTAGGAGCCAA	59.317	20	265	410	674
CGGTTTGATTTGGTCCATTT	59.662	20	212	7	218
GCATGCGTTGTCCAAATAAA	59.567	20	180	921	1100
CTTTGGGCATTGTTCTCTGA	58.847	20	264	85	348
TTTGGTCTCGTTGTATGAACAA	59.544	23	243	433	675
AACATGGGTACTGTTTCGCA	59.05	20	135	996	1130
AAATTCATGTGTTCGTAATGAT	60.135	24	275	344	618
TGGAGATGGTGTAACCGTGA	59.96	20	203	28	230
GAAAGGGGAAGGAGAAGTGG	60.045	20	130	20	149
CCACGCTTGGCATTTAGATA	58.794	20	169	355	523
AATCCCATGTTGCTGCATTT	60.339	20	163	154	316
AATTCTCCTCCTCAGCCCTC	59.778	20	233	1022	1254
TTTTGGGAACAACCGTTCAT	60.206	20	278	613	890
TGGCAACTCCATGAACAATTT	60.359	21	254	354	607
TGTGACGAGGTTGTGGAGAG	59.864	20	214	1523	1736
CAATCCAAAACTCTACATTTTC	59.06	25	280	305	584
TGAAGTTAGGAAATAAGGAGG	58.743	25	172	802	973
CCACACCCCACACTCTCTCT	60.153	20	256	299	554
TTTTGCATGGATTAACAGCG	59.702	20	204	95	298
GAAAAATTGGCCTCACCTCA	60.051	20	145	1672	1816
GAAAAGGGGTGACCACAAAA	59.807	20	256	897	1152
TTCCACGAATACAAGCGTTCT	59.761	21	240	330	569
TTCGGGTCTTCCACCACTTA	60.486	20	271	752	1022
AGGTTACATTATGTGGCCCG	59.708	20	279	909	1187
ACAGCCAGAAGAAACCCAGA	59.844	20	207	151	357
ACCGTCGATGAAAAATCTGG	59.933	20	267	991	1257
GGAGCAGGTTCGAAGTGAGA	60.533	20	220	4969	5188
GGCCTGGCTATCTTGGTAAA	59.182	20	276	2084	2359
TCCAATATTTATGGCGATCTAA	59.744	24	225	914	1138
AACATTGTGAAGGAGGCTGC	60.263	20	264	1121	1384
TATCGGGTAAAGTCCGCATC	59.923	20	279	1688	1966
TCTTCAAAGTTGCAGCCTCA	59.716	20	266	1505	1770
CCAAAATTGCCCTTTCATGT	59.801	20	240	122	361
ATTTGCCCCACACAACTGAT	60.24	20	146	9415	9560
TACGAATCACACTATGGGCA	57.572	20	150	442	591
AAAGAAGGGTTGGCGATGTA	59.569	20	244	984	1227
CCAATTTCATTGATAACTCACC	58.865	23	219	51	269
GAGGAAGGATTTTGGTGGGT	60.169	20	256	282	537
GCCTGTTGAAGCAAACAGTCT	59.534	21	277	1158	1434
GTGCTGATGATTTTGAGCCA	59.805	20	169	2676	2844
TTTGCACATGAGCTTTTCCA	60.379	20	208	1249	1456
TCACACAAGTCCGTTGGAAA	60.128	20	229	369	597
GCCCGTGTCCATAACACAAT	60.646	20	274	1796	2069
TGCTTCTCACCAATCAGTGC	59.992	20	113	18	130
CCATGGTGGTCACAATTCAC	59.656	20	213	109	321
CCAGAATTTCGAACCTCCAA	60.044	20	155	1628	1782
GGAAGGCCTAGATTTGTCTTGA	59.725	22	201	2285	2485
CAGGACTTGTAACCTTGGGG	59.444	20	164	915	1078
TGGATTTTTGCCCTTGTTTT	59.429	20	272	322	593
GGCAAACAACAGTTGCAAAA	59.752	20	156	820	975
ACACACATGGGCTAGCTGAA	59.318	20	255	384	638
AATTGGTTTTGAGACCACGG	59.83	20	229	447	675
GCATGGGGTTGGTTCCTATT	60.94	20	228	563	790

ATGCACATTGTGTCCCAAAA	59.823	20	195	726	920
GATTTGGACCCCACCCTACT	60.052	20	109	434	542
TGACAAGATTCAATAAAGCCA	59.639	23	237	827	1063
CAGAGGAGTCCTTCACAGGG	59.828	20	159	215	373
TCTCTTGAATTTCCCCAACG	60.044	20	128	152	279
TGGTGTTTGATTGCGAGAAG	59.84	20	246	1941	2186
CCATCGCCACCTTTTGTAAT	59.823	20	184	66	249
GGAGCGCACGAGAATTTTAC	59.851	20	240	450	689
AAATGCATCTCAATTTTTGGA	57.239	21	233	534	766
AATATCACCAAGAGATGCCCA	59.401	21	274	247	520
GCAACGAGAAATGGAGTGGT	60.119	20	256	1855	2110
TCCCAAGAGTCCAGAACCAG	60.229	20	149	1480	1628
CAAAAGCTATGCTTTCACAAA	57.853	23	184	119	302
GGAGGTACCCTAGGCGAGAG	60.225	20	222	123	344
TCTGGTATGCTGCTTCTCCC	60.362	20	176	2603	2778
GTCGATGGGGCAGAAAAGTA	60.074	20	140	591	730
CGAGTATCGCTCCGACTTTC	59.978	20	275	101	375
CCGATTTGATGAGAAGTGGC	60.603	20	221	29	249
ATCTCTCAGCATTAGCCCCA	59.797	20	273	434	706
GAAATAAGGAGGTGTTATGAA	59.323	24	280	693	972
TCTCCAAAGCCCAACAACAT	60.495	20	197	239	435
TTCAGGACGCTTTACCGAGT	59.875	20	280	141	420
ACTAACCAATGCGGATGCTC	60.103	20	267	3121	3387
TATCACCAACCTCTGCACCA	60.112	20	110	677	786
CCTTCGTCACCAACGAAGTT	60.149	20	269	643	911
CAGGTGATTGAACTCAAAGCC	59.726	21	272	3202	3473
CCGGGCATCAGAACAATTTA	60.827	20	273	1781	2053
GGCCACAAGCCATTAGTGAT	59.962	20	191	389	579
GGTGAAGCATGCAAAGATGA	59.805	20	241	907	1147
CCTAAAGTGACCCCATTCCA	59.784	20	277	830	1106
TAAGTGCATGGAGGTGGTTG	59.566	20	209	232	440
CATCTATGCTCGCACATTCG	60.388	20	231	2654	2884
TGGGGTCTTCCTCAGATACG	60.065	20	123	1378	1500
TATCAAGCTTGTCAGCCCCT	59.836	20	225	1729	1953
GTTGTGATGCAATTTGAGCC	59.131	20	237	1131	1367
GAAGGTGATGGGGCTATGTG	60.34	20	135	143	277
CCCTGTAACAGTTGGTGCCT	60.028	20	264	1243	1506
CCCTTGATTTAAGAGATCCAAT	59.004	23	278	210	487
TTCAGAAATGCAATAAATTCC	59.11	22	270	1115	1384
AGCGCCTCCATATCAGAAGA	59.939	20	257	1655	1911
TGTTCGCACAGGTGAATCAT	60.12	20	214	12	225
GGCCGTTTGTTTTATTGGAA	59.81	20	165	555	719
CAAATAGGTGGGTGGTGGTT	59.569	20	234	46	279
TTCTCGCAGAGCATGTGTAT	57.013	20	280	1192	1471
CCTTGCTAAGGGGAATCAAG	58.785	20	243	476	718
CTCGAGATGGTAGATGCCCT	59.263	20	259	425	683
AGAATAGCCCAGTGGTGGAA	59.55	20	243	312	554
TTGTGTTTTGACGTTTGCATT	59.122	21	100	7	106
GACCGCAGGATAATCCAGAA	60.036	20	165	908	1072
TTGTTAGTTTTGGATGGTACGA	59.817	24	227	441	667
TGCAGGGAAAAAGCATGAAT	60.585	20	262	2329	2590
TGTGATCAAAGAAGAAAAATG	59.549	25	266	887	1152
TAGTAAACCGGACGTGGCAT	60.386	20	235	555	789
TCCTGCATATTGGAAAGGGA	60.405	20	274	1850	2123
ATGGTGTCCATCCCTCTCAA	60.326	20	275	3152	3426
GCACGTATCGACATTGCTTA	57.41	20	121	998	1118
AGCTAGGAGGAAGGGCTGAC	59.979	20	213	0	212
GCATCCAGCAGTGTAGGTGA	59.862	20	235	720	954

GCCGGAGTGATGCAGTAGTT	60.285	20	196	234	429
GCTCAATTTTAGTTGTGAAATC	60.065	26	130	2170	2299
GCGCACAAACACTCTCACTC	59.628	20	107	60	166
CGATTACGCCTCTAAGAAAAC	58.589	22	211	222	432
CAATCGTATGGTCTCCCCAG	60.331	20	271	456	726
TCCTGTATCGATTATCATTTTC	57.736	24	266	313	578
TCTCAGACAAAACCTTCGCC	60.375	20	236	1417	1652
GCTGATGTGCAAACAAAGAAA	59.797	22	264	2000	2263
TGGCTAGAGAGATTCCACGA	58.543	20	182	372	553
AAGACCGGCCATTCTACAGTT	60.012	21	135	723	857
AACCCAGTGAATGATAAGGGG	60.06	21	204	12	215
CGATATGTTACGTAGGATGAC	59.374	24	224	1593	1816
AAATGTGTTCCATTGCGGTT	60.235	20	255	1053	1307
TCTCAATAGCCCGTTTGGTC	60.074	20	158	106	263
CGAAAATCAAAAAGCCCACA	60.97	20	225	2365	2589
GAGAGAGGGTGCCATTACCA	60.073	20	274	138	411
TCTACGTCAGCACACGCTTC	60.207	20	248	577	824
CTGATTGGGTGCAACTGAGA	59.831	20	260	454	713
ACCCGTTCCACAACCTACTG	59.884	20	240	335	574
ACAGCCAGCATTGTTTCTCA	59.445	20	171	58	228
TGCACACACAAACCCTCACT	60.203	20	111	430	540
GAATGTCGTTTCAAAATAAAA	60.107	24	259	1192	1450
ACATTGCTGACATGATTGCC	59.533	20	128	148	275
TCCGAAAAGGCGATAAAATG	60.033	20	233	67	299
TGGGTATGGGCTTAAAATGC	59.795	20	159	1125	1283
AATTGTGAACAGGTGGCAAG	58.623	20	246	546	791
CCCCTGATCAAGTCCATCAC	60.326	20	183	835	1017
GATACATGCGCGAACTCAAG	59.449	20	199	602	800
GCCTCAGGCGTAGTCATTGT	60.285	20	209	484	692
AACGCACACCTCTTCTCGTT	59.914	20	160	0	159
CAAGCGGATTTGATGGATTT	59.901	20	246	128	373
AATCCCAAATCCCATCACTG	59.605	20	223	429	651
TACCCATCTCTTTGCTGTCG	58.874	20	203	484	686
AAGGTCCGTAGTCCATCACG	59.989	20	271	3372	3642
ACTAAATGTGCGTAGGGCCA	60.523	20	227	1118	1344
TAGGCTCCTGGTTTTTGTGC	60.249	20	204	966	1169
AGCGACGCATGACCTTATTC	60.243	20	263	1727	1989
AAATAAATTGGGCGACAAGG	58.943	20	249	438	686
TGCTCTCAGATCCGGCTTAT	59.939	20	161	1379	1539
ATGGGTTATCACCAGATCGC	59.78	20	129	1085	1213
CGATTTACACACGCGCAC	59.859	18	276	0	275
CGCGGAGTTTAAGGAATGTT	59.225	20	187	1983	2169
CCCGATTGACATCCCTAATG	60.148	20	227	439	665
TTTGTGGTGGAGAGGTTGTG	59.565	20	224	459	682
AGGCTGAGACTGAAACCACG	60.444	20	237	886	1122
GGCCAGAACCATGAGAGAAA	60.195	20	185	3131	3315
GTTCCTGCTTTGTGGTGGAT	59.973	20	234	35	268
GTGGCACCTTTTCATCCATT	59.797	20	182	108	289
CCCCAAATTCCTAAGAACCC	59.639	20	233	4538	4770
ATCAAATGACAAAAACGCCA	59.016	20	227	394	620
AAAAATCCGTCACTAAATGGG	57.988	21	237	964	1200
TCTAGTACGCGGGCCAATTA	60.599	20	269	2	270
GGCCGTCTAGTGACACGAAT	60.142	20	148	20	167
TGTGTTAACCTTTGGCTCCC	59.971	20	181	1213	1393
TTTTTCCAGACGTCGTCAAT	58.201	20	264	486	749
TGTTGGCATTCAAATCAACC	59.375	20	263	1192	1454
ATTGTCTTGCTTTCCAGCCT	58.936	20	127	101	227
GATTTTGGGATGGACTTGGA	59.727	20	155	111	265

TTTAAGGGTTATCACCTGATTT	57.757	24	271	1003	1273
ATCTACCCCTCATTCCCGAC	60.154	20	215	1360	1574
ACGCCTCTCTCCCTCTCTCT	59.709	20	200	854	1053
AAGGCTGGCTCTGATCTTCA	60.096	20	250	2822	3071
TTTGAAGCATGTGTTAATTGCC	60.006	22	262	246	507
ATGCACAAACAATCCACGAA	59.972	20	223	2978	3200
CTACAATGGGCAAGGCATTT	59.96	20	260	631	890
CCACTGTATCCCGAGATGGT	59.803	20	210	711	920
TCAGGCCACTTACGTTCTTACA	59.807	22	259	1237	1495
AGGGTTGAACTTTGAAGGGC	60.476	20	202	409	610
TGAAGCTGCATTCACTCTGC	60.296	20	255	1018	1272
GGCTCCAAACTTTTGGGTCTA	60.469	21	246	1456	1701
ATTCTAGCTTGTCGCAGCAC	58.283	20	222	1145	1366
GGAAATTTTCGGGTGAACCT	60.166	20	208	1167	1374
GCTATGTTTGGATCGGCATT	59.929	20	103	262	364
CAAGGAAAGCCCGTGATTAG	59.702	20	256	701	956
CTGTCTTAATGGGAAGGGCA	60.066	20	268	1690	1957
TGCGTTGTGTGTGTATGCAA	60.801	20	229	4229	4457
AGCTTGTGGAATTGTTTGGC	60.118	20	187	1175	1361
CCGCTTCCTACAGTACTCCG	59.891	20	149	1870	2018
TCGTCGAGAGTGAGGAGGAT	59.945	20	242	440	681
TCCTCTCACGCACTCTCAAA	59.701	20	267	710	976
GGGAAAATTTGTGGTTGTCG	60.206	20	137	1578	1714
GGTTTGAATGCGGTTTAAGG	59.451	20	226	1177	1402
TTGGCAGAGGTGTGAGAGTG	60.022	20	161	416	576
TTTCAGGCGAGGAAGAGACT	59.162	20	267	461	727
CACTCTCCACAAGTTCCCGT	60.151	20	115	2276	2390
TGGGAATATTGGCATTTTTGA	60.137	21	278	615	892
AAGAGAAGCAGCAGCAAACC	59.763	20	243	392	634
TTTCTGGTGAAACCGACCTC	60.088	20	212	459	670
GGATGCATGGCTCATTGATT	60.843	20	203	434	636
AGATAACGCAACGTCGATGG	61.052	20	155	1550	1704
GGTTCCCGCGTCATAAAAT	59.776	19	199	794	992
TTATGAAAACCGCAGCAGTG	59.872	20	225	290	514
ACATTATCATTTCCACCGCC	59.651	20	188	394	581
AAGTTGTGGGGCTGGAGATA	59.55	20	264	146	409
GCCTCTGATGCAAGTCCTTC	59.957	20	263	2505	2767
ATCGCAAACGATTTGGATGT	60.339	20	198	59	256
TGTTCCTAAAAACATGCCCA	59.013	20	264	2227	2490
GGTCTTCGGGTCTGGGTATT	60.19	20	184	1155	1338
ATGTCGGCATTCAAGGTTTT	59.434	20	251	1037	1287
TCAAAGCTTGAAGGCCTAGC	59.73	20	213	782	994
GGCTTCACTTTCAAAACCCA	60.088	20	271	43	313
TCAAACTCCAAATGGTGCAA	60.088	20	248	31	278
TTACGTAAAAATGGGTTATTAT	57.411	26	154	952	1105
ATATGGGACGTCCAAAAACG	59.685	20	129	2775	2903
CCTCCCAGATCTAATGGCCT	60.422	20	157	1133	1289
TAGGCGGATTGGTTTTTGAC	59.938	20	211	890	1100
ACCTTCCATAGGTTGGGAGC	60.328	20	118	80	197
CGACGGAGAGCTAAATCGTT	59.476	20	211	400	610
CCTCTGTATGCAAATGCAGC	59.449	20	139	3502	3640
GATCATTACTGGCCATGGGT	59.635	20	254	1120	1373
TTGTGTTCAAAACTTTGCGG	59.746	20	212	903	1114
GGCATTGGCATAGTCCTGAG	60.624	20	251	479	729
CCCAATTTGCTTGTACTTACTC	59.11	23	271	2706	2976
TCCCATTTCTTTTGTTCCCA	60.28	20	171	1162	1332
TTTTCTGCCCACCAGAAATC	60.051	20	190	2562	2751
TCTTTTTGCAGGATATTCGATC	59.263	23	194	410	603

TAGGTCACCGAATTCCATCG	60.853	20	278	47	324
CAAGAGCATTGTTGCTGGAA	59.988	20	272	649	920
AGGGAGGAATAGAGCCGAAA	60.166	20	254	785	1038
GTCGTTGTTTCACCATTGGA	59.394	20	164	1096	1259
CAACGGTATGCTCGGATTTT	59.96	20	182	42	223
CTTTTCGTTCTTTCTCAATTTCG	59.441	23	203	36	238
CACCAAATATTAGGGTTATCAC	60.706	25	219	836	1054
TTGAGTTTGCATCTAAGAAGGT	58.575	23	175	3217	3391
AGAGGGTGAGAGGGGACCTA	60.066	20	262	1383	1644
CGTAGATCCCTGTCGGGTAG	59.569	20	278	361	638
GGTTGTGGATTTGTGAATAAAA	57.971	23	240	2453	2692
ATGGGCCCTCTAATCTCCAT	59.75	20	269	790	1058
AACAAGGAGAGGAGCAGCAA	60.134	20	102	4224	4325
GTCCAGGTCTCCCTCTCTCC	60.198	20	142	610	751
CCCTTTTTCATGGTGGTTGT	59.688	20	154	4443	4596
TTCTAAGACCGGGATAGGCA	59.662	20	121	10	130
GGCCATAAAACATTCGAAACA	59.824	21	210	1225	1434
TTTTCGAACAACATTGCGAC	59.712	20	260	2179	2438
TGGGACCCGTCTTCTTATTG	59.926	20	168	1267	1434
TCGTAGTAGGAGCACGAAAAC	59.941	22	268	18	285
GTAGCTCCTGAATCCCCTCC	60.037	20	255	574	828
CCCCCTAACATATCCACGTTT	59.952	21	163	416	578
GGCCCTTTCCCTCTGTTTT	60.428	19	273	0	272
TAAAGAACGAAAACCACACGG	60.018	21	191	0	190
TTAGGGCCCATCCTATCACA	60.288	20	272	973	1244
TGGGGGTGGGAGTTTAAGAT	60.549	20	156	466	621
TGTAGTTGCTGGATTGCAGG	59.864	20	223	1036	1258
AGATCCACTTGCCTTGATGC	60.226	20	189	1908	2096
ATACATGCGTGTGCGTTCAT	60.026	20	268	2316	2583
TTACCAATCCGGGTGATGTT	60.051	20	213	1156	1368
ATCCCTGCTCCACTTTCTCA	59.803	20	235	368	602
TGATTTGTGCTAACCCTCGTT	59.623	21	240	392	631
AGGATGGAGCAACTCCAGAA	59.803	20	148	420	567
GCAATACCCTAATCCAGCCA	59.923	20	217	361	577
GTCCGGTAGGGTGCATAAAA	59.823	20	226	557	782
TGGATTGAAATAAGGGGTCG	59.756	20	214	153	366
GAAATCAGCACGAATCACACA	59.713	21	150	1002	1151
CCATCAAGAGGAAGAGGCAG	59.943	20	256	502	757
ACCATGGCGTCTTCTGTCAT	60.542	20	247	1394	1640
ATGTCATCCAGCACTGCAAA	60.272	20	253	941	1193
GCTGAGCGGATTTAATCGTG	60.742	20	207	394	600
CACAAACATTCCAATGCAGC	60.119	20	225	780	1004
GAATATGGCTGCTTGGCTTC	59.813	20	163	2446	2608
GAATTTGTTGACGAATGGGG	60.17	20	278	747	1024
CTGCGAGGATCTACGGACA	59.951	19	269	737	1005
GCCGTTGTGTCGTTTTCTTT	60.154	20	189	83	271
ATCTCATCAGCAAGGCCAGA	60.914	20	226	1397	1622
TTGGTCAAATCGAGAACAACC	59.963	21	253	718	970
GGATGGTGCATTTTGTGATG	59.781	20	261	523	783
TCTGTCATCGGTCCAGAGAA	59.34	20	278	2690	2967
TCAGAAATTCAGGTTTCCACC	59.017	21	257	3334	3590
AGCCATGGCCAAGAGTCTTAT	60.11	21	280	513	792
CTGCTTCCAATGGTTGCATA	59.688	20	249	9	257
AAGCTACCAATTGACGACGG	60.132	20	120	501	620
TGTAGCCGACCCCAATTTAG	59.953	20	279	181	459
ACAGGTAATTTCGGTCGCAC	60	20	257	208	464
CCACCACCATCTTACAAGCA	59.566	20	264	88	351
TCCTCAATAGCACCAGCGAT	60.765	20	265	26	290

TGCACCTTGAAGTTGTGGTT	59.187	20	216	1225	1440
GTCCCTCCAACATAAGGCAA	59.933	20	277	1872	2148
AACATGATGAAGGTCCGAGG	59.927	20	192	1113	1304
CTGTGCTTTGAGCAACTCCA	60.175	20	244	248	491
AATGCAGTCCCAAAACAAGC	60.118	20	222	201	422
TCAATTCCCCCACCAACTTA	60.162	20	260	461	720
ATAACGGGATTGAAGGAGGG	60.145	20	198	18	215
GCCTACATCCACTGGTCAAGA	60.126	21	255	2444	2698
TGTTTCGCGAGCAGAAAATA	59.585	20	177	86	262
ATCAGACCCACTTCGTGAGG	60.112	20	265	394	658
GCCTGATTTCCCCTTCCTAA	60.391	20	266	264	529
TAGTTGGGACCCCTTTCACA	60.345	20	178	1044	1221
CGAACCTGAAATGGGAAAAA	59.91	20	176	241	416
CCCCAGTTTTCCTTCCATTT	60.159	20	212	382	593
TGGAGTGTTGGATCTGTTGC	59.682	20	151	1141	1291
GCCCAAAGTTAGATGTGACCA	59.985	21	211	5	215
CGAAAGCGGAGTTGAAAGAA	60.493	20	248	484	731
AATTTCATTGCCATCGGAAC	59.768	20	267	368	634
TCCCTCCTCTCTCTCTCCCT	59.489	20	266	764	1029
GATTCGAACGCTTGATTTGG	60.585	20	223	834	1056
GACTAGCAAATTTCGGGACG	59.708	20	256	414	669
GGAAGCAAAGAGGCTGAAGA	59.694	20	215	227	441
GCAGAGGTGTATTCTGTTGCC	59.755	21	189	1349	1537
TGCCTTCCTTCTTACTCCCTC	59.835	21	148	18	165
TTTGCAAGACATCCAACATCA	60.104	21	198	1450	1647
TGACAATCACTTGCCACCAT	59.967	20	176	340	515
GTCCCTGTGCAATCACTCAA	59.682	20	170	2422	2591
CCCTCATTTGTACGGACTTGA	59.978	21	258	490	747
TAGGGACATCTGGGTGTGTG	59.388	20	176	2349	2524
AAAGGGATGTCTCAGGTCCA	59.505	20	237	2238	2474
TCCTTGAACTTCTTCGGTGG	60.224	20	198	1491	1688
ACACGCCAATTCAATCATCA	59.931	20	260	1687	1946
TGGTAAAAAGCGCTCGTACA	59.509	20	274	258	531
ACTTGGATGGGCATTAACCA	60.192	20	255	761	1015
ATTCTGGTTTGAGGGGGAGT	59.795	20	189	527	715
TCACTCTTCCGACTTCCGAT	59.803	20	111	720	830
CTCCTCTCCAGCCATCTCCT	60.891	20	157	1198	1354
TGCTGCTTCTGGTTGATGAC	59.992	20	250	72	321
ACAAAGCTCGAGTGGCATGT	60.865	20	213	5836	6048
TCAAAACTATCGACCTTTTCGG	60.462	22	272	1236	1507
TGAAGTTTCCCCGAATTTTG	59.91	20	163	474	636
CAGAGTGCCTCTCTTGGGAA	60.523	20	139	2029	2167
GTTTGGGTCGAATTTGAGGA	59.91	20	268	62	329
TCATCTTGAGAGAGCGCCTT	60.24	20	245	42	286
ACCGGCCAAAGTAAGGCTAT	59.987	20	170	220	389
AAGGTTTAAGCTCAACGGCA	59.883	20	169	666	834
ACCATCTCTCGCTCTGCAAT	59.981	20	177	1013	1189
CGGCAGGATTAAGTCCCTAGT	59.623	21	116	60	175
CACAAATGTCCCTAACATGAC	60.284	22	249	3720	3968
AAATGGTGTTTCCACTTTTTGC	60.257	22	203	641	843
TGCCGGATACAGATATGCAA	60.058	20	190	48	237
TGAAGAGGAGCAAATGGGAG	60.331	20	103	192	294
TTCTGACCCCCTTCAGTCAC	60.088	20	175	516	690
GCCCTGATTCTCGAGTTTTG	59.813	20	280	2165	2444
TTGATTTGACATTTTTGGAGAG	58.729	23	139	224	362
TTGAGATTGGGGATTGAAGG	59.864	20	248	115	362
TTTGAGTTGGGGGAATTTTG	59.772	20	240	335	574
TTTTCAGTTTCGAATCAGTTAG	57.644	23	277	539	815

CATCCACGGTTGTTGAAGTG	60.001	20	255	442	696
TCTAGGCATCGAGATGCAGTT	59.992	21	140	586	725
CTATCATGGGCTGGAGGTGT	59.95	20	276	1087	1362
TAGAGTGCGGGAGAAGGAGA	60.088	20	230	1303	1532
TGACTCCAGGGTATTCCAGG	59.92	20	174	2338	2511
TGTTCTCTAGCTGTGCCCCT	60.012	20	109	625	733
TGCGTTTTGATGATATATAAGT	58.254	26	110	2594	2703
AGGCATGAATCGGTTTGACT	59.556	20	151	26	176
AAATGTCACGCAAGATGCAA	60.265	20	197	302	498
ACTGGGCATCACTTCCCATA	60.34	20	278	5813	6090
CCAATCAGCATTAAACGGGT	59.823	20	245	505	749
CGAACCGCAGCAAATTAAGTA	60.265	21	133	501	633
TGCTGGAGCTACGATTAACCA	60.777	21	265	595	859
ATTCCTCAAGCATCATTCCG	60.036	20	132	983	1114
AACGGAGATTTGTCAAACGG	59.971	20	244	480	723
TAGGGTTGTCACGGCTAGGA	60.647	20	280	159	438
CGTGTTTGCAGTAGGGGTTT	60.03	20	200	471	670
GGGTTTAATTTCTCGCATGG	59.411	20	218	1123	1340
CTTTGCTGTGCGTCGATTT	60.003	19	224	876	1099
ATGTGGATGGACGGATTTTC	59.611	20	251	759	1009
TTGGGATTAAGGCTTTGGTG	59.931	20	189	2305	2493
GACTATGAAGGCTTGTCGGC	59.843	20	226	506	731
AACCTCTTCTCCTGCACCAA	59.844	20	270	25	294
CAGATCCAAGATCGCAAACA	59.799	20	250	464	713
TAACACCGTTAGCCACCCAC	60.807	20	268	1048	1315
TCCTTGTGCTTTGGCTTTTT	59.861	20	186	4988	5173
TTGATCTGGTTTTCCCCATC	59.727	20	200	1749	1948
GTCCCCTCTGCAGAACTTTG	59.844	20	262	889	1150
ATTTACGGGTTTGTGCTTGC	60.003	20	269	448	716
CATCCCCATTGTTCTACCCA	60.572	20	236	25	260
TGGGTGAGCCAATCACTAGA	59.241	20	267	569	835
ATGTGAGTGCATGCAAGTGG	60.756	20	228	548	775
TGTTTGCAATTATTTCGTGG	57.176	20	145	443	587
TGAAGAGTTCTTTTGCTGGGA	59.978	21	274	260	533
ATCGACATCCACCTGCAAA	60.064	19	246	1133	1378
GGCTGGTTTGCTTGAACATT	60.118	20	169	1540	1708
GCATCAGAGCAAAACGACAA	59.995	20	212	706	917
CGACCCAACACACACATTCT	59.441	20	193	509	701
TTGCATGATTGCTCCATGTC	60.641	20	217	409	625
AAGCTATTGGCGGAGTATGC	59.347	20	279	380	658
CCTCGCGTAAACCCTTGTTA	60.124	20	260	2587	2846
GTTCATCTCAACCACGGGAG	60.51	20	242	373	614
CGATTGGGCCTATCCTATCA	59.878	20	255	937	1191
ACCATGACCCTGAACAATGA	58.774	20	264	1639	1902
TGGAAACTGACGAAAAGGCT	59.853	20	258	191	448
ACAAGGCATCACTTCACACG	59.751	20	207	2290	2496
AGATTGGTGGGGAGGTTAGG	60.183	20	113	56	168
TTAACCCACCAAAAAGGTGC	59.839	20	211	455	665
ACCTAGCCCTAACCCACACC	60.247	20	142	330	471
TTATCCGAATCTTTTCGTGGA	59.533	21	227	178	404
TTGAGGCTACCATGGGAAAG	60.066	20	260	157	416
TGGAGATTACCGGGTTTTGT	59.288	20	252	414	665
AAATCAAGCCATTTCCGAGA	59.645	20	263	724	986
GCCATTACGGGTGAGGAATA	59.784	20	270	1262	1531
GGCGAGATCAATGTTTGGAT	59.9	20	202	540	741
CTGAGCTGTCCGGAGACTTT	59.598	20	175	2499	2673
TTTTGAGTTGGGATCTTCGG	60.044	20	271	791	1061
TCCTCTCTCTCTCTCCATCACA	59.127	22	238	1320	1557

TGAACGAGTTGCAGCTTGAC	60.183	20	249	62	310
TGCCTTATCTGTCAGTCCCC	60.073	20	207	1214	1420
GGGAGGGGAGAGTTTGAATC	59.874	20	255	2122	2376
CCTCCCTCACCTCCACACTA	60.104	20	121	1293	1413
ATCAAACAATGGCATCGTCA	59.931	20	169	2407	2575
CGAATTTGCAAAACCGAAAT	59.943	20	277	44	320
TACGAGCACATAGCGCTCAA	60.708	20	241	1075	1315
AAGGGCGCGACAGTTATAGA	59.867	20	177	0	176
TGGATGTGAATAGGGTGGAAA	60.177	21	241	481	721
TCCTGTGAGCAGAAGGGAGT	59.986	20	125	183	307
GCGTAAATTTTGAAAGAAGCA	57.304	21	279	3	281
CAAGCGTGATTAGCCATCAA	59.833	20	255	202	456
TTGGTGTGTTGTTTGCGAGT	60.199	20	178	6125	6302
AATGCAACGGTTTTAGTCGG	59.996	20	177	456	632
TTCATGTTTGCTTAGCCGTG	59.872	20	254	2459	2712
TGCAAAGTCATGGCTAAAGAA	58.57	21	279	2284	2562
GACCATTGGATGGATGGTTC	59.995	20	108	555	662
CGAACACAGGGCAATAGTGA	59.716	20	148	110	257
TCCATTGATTGCTTGATCCT	58.088	20	272	23	294
AGAAATGGAAGATGCCATGC	60.043	20	137	188	324
CCAAAAGCTCCTGCACTTCT	59.615	20	166	2192	2357
GGTTCGTCGGATGAAAAAGA	60.051	20	156	138	293
AAATCCCAGTCAGCAAAACG	60.11	20	223	171	393
ACTCGAGTTCGGCCTATTTAGT	59.717	23	226	167	392
TTCCAACTAAGTCATCGGGG	59.926	20	273	510	782
CGTTTTGACGATATATAGTGTTT	59.375	27	157	1871	2027
ATTGCTGGAATCAGACGACC	60.081	20	244	1604	1847
CCGTCGCCGACTTAAATACT	59.248	20	246	1909	2154
TTATGTCACTGGGGAAACGA	58.973	20	262	559	820
GGAGTTAAAAGCACCATTGAG	60.001	22	279	1109	1387
ATGATGACGCCATGTTTCAA	59.931	20	190	114	303
AATTTCCACAATGAGATTGCC	58.895	21	259	9295	9553
AAGGCAACATTCGCACTCTT	59.882	20	248	1773	2020
CGGACCGTTAGGATTAGCAT	59.067	20	247	946	1192
TTGAGTTTGCATCTAAGAAGGT	58.575	23	213	2497	2709
GCTGATCGTTGCAGTAGGGA	61.348	20	241	409	649
GGAAGTGGACACCTCCTTCA	60.088	20	261	2	262
TGAGTTTGGTGTGTTGGCAT	60.008	20	242	314	555
TGATAATGCAATGGCCGATA	59.882	20	218	113	330
TGTGTAGTCCTGTTCCTGCG	59.897	20	211	2575	2785
TGAGATGGTCACCCTTCCTC	60.048	20	214	722	935
CAGACGGCCCTCTAAGAAAA	59.448	20	144	167	310
TTGGTCATCGCAATTCGTAG	59.688	20	110	338	447
TTTGCTGCCCAAAAAGAAAA	60.701	20	280	417	696
TGCTAGAATGACCTGATGCG	59.972	20	157	60	216
CAGAAGACGGGTTCGATAGG	59.688	20	242	839	1080
TATATAAGAAACGGCGGCCA	60.424	20	110	1273	1382
CTTGTTGGGGAAGGAGAACA	60.081	20	180	553	732
CGTCAAGCAATGCCAGATAA	59.833	20	256	469	724
ATGATGCAACATCCCTTGTG	59.374	20	270	4970	5239
TGTCAAATTGTCAACCACACG	60.456	21	188	1200	1387
GAAAAATGGCAGAGTGCTCC	59.82	20	157	2289	2445
CCTGGGTTCTTGGTTTTGAA	59.942	20	239	1297	1535
TTAAATCCAAGGAGGCGAGA	59.778	20	219	8	226
ATGGAGGGAAACATGCACTT	59.41	20	143	9	151
TTTCCACAAAATCTGGGGTC	59.767	20	145	0	144
TGCTGTTTGCATTTTAAGATGA	60.186	24	187	825	1011
CACCCATTAATGCTGGTTGA	59.395	20	134	41	174

ACACAATGGGCGTAATTCGT	60.257	20	195	1769	1963
TTCAGGACGGAGGAGTTGAC	60.238	20	278	13	290
AAAGGTTTTGATTTTCCGGC	60.292	20	117	55	171
ATGGGCTTTAGTCCCCTGTT	59.827	20	207	482	688
TGGCTTCTGTTTCTCCATCA	59.369	20	252	742	993
GTCACACCGAATCTTGCCTT	60.119	20	188	1148	1335
CACCGTTCTCTGCAACAAAA	59.881	20	275	500	774
CGGTTGGAGAAGTCATGTCA	59.676	20	237	1619	1855
CACTTGCAGGACATCAATCG	60.263	20	272	1505	1776
GACGTAGCAAACGCAAGGTT	60.313	20	255	1523	1777
CTCCATTTCCATCCAAGCAT	59.894	20	147	218	364
CTGGCCATTGATTCTCCCTA	60.029	20	201	2138	2338
GTGTGTGCATGCTCTTGTCA	59.436	20	269	8334	8602
ACACATGCCTGGAGCATACA	60.144	20	208	800	1007
ATTCGCCAGTCCACGACTAC	60.142	20	210	1635	1844
TCACTGCACTCGGTGATGAT	60.279	20	266	1220	1485
CCCAATTTGGTCGTTTTTGT	59.702	20	227	2664	2890
AACGCTGGAAGAATGTGACC	60.119	20	231	879	1109
GATCTTTGCTCAGTCTGCCC	59.957	20	262	296	557
CACAGAGCGCACTCAAAGAG	59.922	20	208	304	511
TTTGCGATCCCAATTAGTCC	59.901	20	172	3986	4157
CTATCCGCAGGCCAAGATAG	59.823	20	206	337	542
CAGCATGAATCAAACAACCAA	59.576	21	207	765	971
TCGTCTTTCAATCCCACACA	60.088	20	273	126	398
TCACTGCGCTCATTGTAAGG	60.011	20	225	496	720
GAAGGTGGGTCGATGGTGTA	60.78	20	177	580	756
GAAGTTTTTGCGCAGGAATG	60.752	20	233	3370	3602
TAGCCGATAAAAATGGCACC	59.928	20	157	571	727
CCATTCCATTCTCACCCTCA	60.86	20	121	1574	1694
CACTCCCATTTGTGCTTCAA	59.691	20	190	891	1080
TGCGTTTGTTCTAACTTTATCA	59.734	24	267	2793	3059
CAGGGGGACTTTAATGGGAT	60.011	20	267	139	405
GTTCCAAGTGATCGGTGGAT	59.786	20	115	1142	1256
GCGAGCAAACTCGGTTAAAG	60.018	20	201	2709	2909
TGCTGCCTAAAAACATGTGG	59.729	20	242	227	468
TGTAATGCCTCCTTTCAGCA	59.42	20	265	944	1208
CGCTCTCCCTCTATCTTCCC	60.306	20	248	224	471
CGCAGGGCTGAGTACAAAAT	60.27	20	255	53	307
TTCGGGGCGAATAGAGACTA	59.801	20	180	317	496
GGGATTAATTCCCAGCATGA	59.722	20	222	1133	1354
GCCACGCTCTTTCATTTCAT	60.221	20	183	986	1168
ATTGCATTCTTGGTGTGTGC	59.577	20	246	1080	1325
TTTAACGATGGATCATGTAAG	58.508	23	174	1408	1581
ATTTCACTTTGCCAGCAACC	60.118	20	141	784	924
TTGGTCCGGGAGGATTTATT	60.502	20	154	1945	2098
TCTGATGGCCCAGATTTGTT	60.461	20	110	490	599
TCAGGTTTAGTTGTTAGGTGTT	60.333	26	257	4870	5126
GCACAATCAAACCTTGCCTT	60.118	20	165	2257	2421
GAAAAGAGAGGGAGATGGGG	60.008	20	268	3196	3463
TCAACTCTTGTGGATAACTATT	59.968	26	280	1208	1487
CTGGATGGTATTCTGGAGCC	59.508	20	225	6	230
TTGCACAGCTCTAACAAACAC	59.578	22	226	495	720
TTCTCAGTGCTGATGTTGGC	59.992	20	275	571	845
CTTGAAGCGCCTGTTTCTCT	59.757	20	111	362	472
TCCTTGTTACCTTTGCCAGA	58.352	20	209	2038	2246
AAGAACCACGCGTAATCGAG	60.27	20	279	1774	2052
TGCGTTTTGATGATATATAGGT	60.054	26	270	1315	1584
CAAAGTATTTTCCGGCGTGT	59.996	20	228	607	834

GGCTTATCTGAAAGGAGGGG	60.032	20	271	5715	5985
AAATCGCAAATCTCCCACAC	59.939	20	219	0	218
TGTCGGAGAGGAGCTGGTAT	59.827	20	251	1090	1340
ACCCGAGAGAGAGATCGTGA	59.945	20	122	386	507
ATGATAACAGTGAGGCCGGA	60.483	20	260	561	820
TTATGATGCCTAGTGGTTGGC	59.974	21	256	363	618
GTCTACTGGCCATGGAGGAA	60.073	20	185	552	736
ACTTGGATTGAAGCTCAGCA	58.597	20	261	441	701
AGCAAACGACTTGTTCCAGA	58.497	20	209	1661	1869
CAGATAATGGTGGGCCAAAT	59.645	20	218	418	635
TTCAAATGCCAGTTTTCACG	59.706	20	200	993	1192
TTTTTGGAGGAGATTCTTCG	57.007	20	102	1910	2011
GCGAAATCAATGCACCAGAT	61.014	20	142	1869	2010
CGTTTATCGATTAGCACCCG	60.468	20	136	793	928
TTTGCGTGTGAACATCAACC	60.562	20	266	2708	2973
ATGCAACGTCGAGGTTTTTC	60.118	20	197	270	466
GCATAGGAATGCCAATTCAA	58.577	20	264	36	299
TGGAGTAGGCAAGCCAGATT	59.836	20	172	901	1072
ACTTCCCAACCATCTACCCA	59.259	20	259	481	739
AAAATCAAAGGCCCACAATG	59.801	20	130	2	131
GATTCTTTGAATCATATTCCAC	58.865	25	275	256	530
CTCTCTCTTCCTCACCAAGCA	59.73	21	191	15	205
TTAATGGTTGATGGGAGGGA	60.126	20	156	1045	1200
GTTGGGCCCGTTAGGTTTAT	60.075	20	198	36	233
CCTCGGTCTATCTCATTTTTATC	58.715	24	274	1020	1293
ATGCCCTTATGATTGGGATG	59.605	20	185	600	784
AAATGGAGCAGTTTCATCGC	60.221	20	204	2152	2355
CTAAGAGCTGTGCACCCCAT	60.277	20	175	903	1077
CGTACATGTTGATTGCCACC	59.847	20	244	211	454
TACATTCCATTGTTTCGGCA	59.93	20	128	581	708
TGCAAATGAGAATTGGGACA	60.049	20	155	559	713
TCTCATCTTCGGCCTCTCTC	59.636	20	128	2282	2409
ACGGATTCACCAGAACAAGC	60.119	20	250	1979	2228
AGTCAACATTTGGCCCACAC	60.823	20	173	219	391
TATGCATTTTGTGTGTGGGG	60.234	20	168	68	235
TGGTGAGAAAATGGCAATCA	60.049	20	240	327	566
CAAAATGCGAAATTTAAGCCA	60.082	21	232	560	791
CCTTTGGACTAAACCACCCA	59.824	20	190	1848	2037
AATTCCCGTATTGGCTAGGG	60.164	20	275	1207	1481
GTAATCGAATCTCGCCCTCA	60.177	20	179	551	729
GGCCAACAACATGAAACTCA	59.547	20	195	1034	1228
AGCATGATCCAGCATGACAC	59.669	20	268	1529	1796
CAACTGGCCCTGATGGTAAT	59.813	20	258	245	502
ACATCCATTCTCGATCTGCC	60.042	20	201	1087	1287
TTGTTTTGTGCGTTATGTGGA	60.022	21	133	1183	1315
CTTTCGGAAGCGTACATCAA	58.917	20	267	391	657
TTCAATGCACGGTTCTTCAG	59.84	20	268	177	444
AAGGTGGAAAAGGGTTGCTT	59.976	20	260	578	837
CCGATCAAAGCCTTCTCTTG	59.948	20	151	901	1051
ACGGAAATTTCACTATGCCG	59.96	20	250	1391	1640
AAGCAAAATGGATAGCGTGG	60.096	20	142	195	336
TTCGAACTCCAATGGGGTAG	59.926	20	243	1198	1440
GGAAGTGGTCCCAGTTTGAA	59.943	20	185	322	506
TTGATTTGATTTGTAGTTTTGCG	59.204	23	278	1012	1289
TGTGACACGGAAATTTGAGA	57.642	20	190	2083	2272
TGTTGGATTTGGGATCCTCT	59.336	20	223	1494	1716
ATTTGCACATCAAACTCCCC	59.797	20	166	546	711
GCCTTTCTCGCTCTCCCTAT	59.947	20	260	5578	5837

CTCTTCGGTGGGGGTTATCT	60.319	20	224	505	728
AAAAACGGATGAGAAAGCGA	59.823	20	162	620	781
ATTTGAGAGGGAATTTGGGG	60.124	20	277	19	295
GCGTGTATATGCTCGAGATGG	60.641	21	201	2155	2355
GGAGCTTCTTCTCTCTTCAAG	60.135	23	190	1246	1435
CTGCCACTCTGCAGGTACAA	60.049	20	277	623	899
CCCTTAGCTACCCAAAAGCC	60.089	20	101	1249	1349
GTTTCACACACGCACACACA	60.26	20	252	498	749
CAACTTTCCGCTTCTCCAAC	59.853	20	143	602	744
GGGGGCCAAGAAAAGAGTAG	60.068	20	203	880	1082
TGATGGAACGTCGAAAGTTG	59.691	20	251	642	892
TCCTTGCCGCAATTACTTTT	59.72	20	157	1369	1525
AATTCCAGTTGTCCTCGCAC	60.119	20	155	613	767
ATCAATGACCACCCAACCAT	59.91	20	197	0	196
CGTCCAATTCTCTCCACTCC	59.655	20	163	1218	1380
CCTGTTTGTGATGCCTGAGA	59.831	20	214	642	855
ACAGGTTGAGGCCCCTTAGT	59.994	20	127	71	197
CCGATGAAAGGAATTTGCAC	60.448	20	263	452	714
AGCATGGCCCTGTCAATTAG	60.096	20	210	3530	3739
ACGTCTTTGATGGATAGGCG	60.096	20	253	71	323
CATGGACCCCACATGTCATA	60.048	20	182	237	418
CACAACAGGGGAACCATACC	60.088	20	224	786	1009
GACATTCGTCGTTGAGGTGA	59.682	20	212	15	226
TTCGAAAAAGGAAAAATAAAA	59.468	25	204	21	224
TTTCGAAGATCAATGGACGA	59.2	20	120	2268	2387
GCACAATGCACATACAAGGG	59.995	20	107	41	147
AAAGGAGACTAGTGGCTGCG	59.639	20	260	519	778
GGATTGGCCTAATTTTGTGTG	59.329	21	223	1613	1835
TCATACTGAGCTGAATAGTTAC	57.707	24	103	5	107
AGCAGGATGGAGTGCTTCAG	60.555	20	147	626	772
AAAAACATGAAGTCGGGCAC	59.978	20	205	24	228
CGACGGTGGGTTGTTAAGTT	59.891	20	196	697	892
TACTTCGCACTTTTCCGTTG	58.964	20	156	736	891
CCACCCACTGCATTCTCTCT	60.261	20	187	763	949
CGAGGTTTGTACCGTTCAATTT	60.269	22	181	979	1159
TTTATCGTCCTGAGGCATGG	60.992	20	261	502	762
CAAAAACAATAAAGCAATGCC	60.002	22	216	635	850
ACATCTTATAGCGTGCGGGT	59.62	20	177	1566	1742
ATCGACACAACATGACACGC	60.614	20	119	4973	5091
TTGGTGGATTGGAGATGGTT	60.173	20	279	2351	2629
ACCGTTGAGACAGTTGGGAG	60.151	20	255	1600	1854
GAGAATGTTGTCCCGGACTC	59.511	20	250	102	351
TGCGTCTGCTAATCTCCCTT	59.978	20	187	1856	2042
AATGTTCTTCAAGGTTGGCG	60.11	20	251	2841	3091
GAATGAACTACGGCTTGGGA	60.074	20	205	125	329
GCCCTAACAGACCTTGACCA	60.111	20	248	392	639
TTGGCCAGGAACTTAGAAGC	59.452	20	233	290	522
TGTTGAGATGCCTCAATCAAA	59.262	21	275	426	700
ATACGCGAGTTTGACCGAAA	60.637	20	237	3913	4149
TGGATTGGTTGAGAAGGGAG	60.042	20	280	1224	1503
TTGCCATTTTCAATGATCCA	59.867	20	188	2141	2328
GGGTGTTTTCAAGAAGCCAA	60.088	20	165	599	763
TTTGTTTTGTAAATGGTGCTTG	59.562	23	133	3061	3193
GCTCAAGTTGATTGTAGCGGT	59.397	21	260	136	395
CCGGGATATACATCTCCTCC	58.281	20	191	554	744
AGCAGGTGGTCATATGGAGG	59.95	20	237	48	284
TGATCTGTTTCTGGCTTCCA	59.369	20	224	261	484
TGCTCTGCTTTGATCAGCTC	59.425	20	238	448	685

ATCTTCTCGTTCCCAAACCC	60.306	20	233	4370	4602
GACGGGGTTTCACTTTTTGA	59.948	20	108	494	601
GGTAATCCGATTGGCTGTTG	60.331	20	159	673	831
GTCGAACCGAATTCCATGTT	59.797	20	265	607	871
AAATAAAGCGGCAACCACTC	59.229	20	230	1312	1541
GAATGCAGCCGACTCTTTCT	59.579	20	121	885	1005
AATTGCAAGTATTCTCTTCGCA	59.036	22	227	541	767
ACAAATTTGCCCTCGTATGC	59.967	20	260	2445	2704
GGGTTTATTTGCTGGCTAGG	58.718	20	271	616	886
TACTTGCCGCATCATCACTC	59.83	20	229	3185	3413
CCCGGTTGATGATGAATACC	60.014	20	160	629	788
TGGCCTTGCACAAACTAAAAA	60.635	21	280	1126	1405
TCTCGATTCAGTTTCCCCAC	60.05	20	176	323	498
ACTTTCCAAGCCACTCCTCA	59.844	20	137	1210	1346
CCATTTCAAAATCCTGGCTC	59.505	20	223	2691	2913
GCCAGAATGTTGTTCGTCTG	59.293	20	260	612	871
TTGAATATATTATCAAATCCAA	57.918	26	151	601	751
TGCGTTACGGGTTTTCTCTT	59.747	20	172	776	947
TGGATCATGGATGGTAAATCA	58.632	21	123	630	752
GTGAGAGGGAAAACGATGGA	60.05	20	108	1265	1372
TGAAATGGGCTGTGAATGAA	60.049	20	215	302	516
CTTTCCCATCCATACGCACT	59.955	20	185	1056	1240
GCTCCGTTTGACGAGCTAAA	60.523	20	211	673	883
TCACACACACTCACACGCAT	59.772	20	135	587	721
CCATATCTTGCCAATGTAGAG	58.287	23	280	654	933
CACGACGGATATTTGGCATA	59.401	20	280	623	902
TTTTAGTGTTCGGGCCAACT	59.609	20	269	224	492
AATGATGCAGTTCCCAGAGG	60.073	20	229	656	884
GAAAAAGAGTGGCTTTTGCG	59.996	20	159	4816	4974
GAATGCCGGTCTGAAAACAT	59.939	20	278	9	286
TGGGCCATTTGCTCTATTTG	60.961	20	167	1147	1313
CAGCTGCTAGGTTTGCGAAT	60.543	20	236	401	636
GGCATATTTGGGGAGAGGTT	60.152	20	279	845	1123
TTTCCTGCTTTTCTTCGTGG	60.357	20	249	48	296
GTTCTAGCCCAAAACTGCCA	60.249	20	172	1467	1638
CTGTCCGAGGTTTCGTCTTC	59.844	20	186	2345	2530
TAGAAAAGGTTCGCCATCCC	61.303	20	166	3214	3379
CTTCACCACCGTTGATTCCT	59.966	20	103	105	207
GACCAATGCACCGAGAAAAT	59.939	20	145	693	837
TCATGCAAGAAAACGTGGTT	59.174	20	277	1007	1283
AGCATCCACGTCAGCTTTTT	59.882	20	163	1360	1522
TGGAAAACCGTTTAGGGACA	60.336	20	275	88	362
TCACAAACCCTTGCTTTTCC	60.088	20	165	1542	1706
TTGAGGATGAAGTAGCGTTGG	60.256	21	186	635	820
CCTCAAGCTTTCCCTTCCTT	59.821	20	214	3901	4114
TAATGTCCTTGGAGATGGGG	59.744	20	263	1058	1320
CTCGTCGCCTCTCTTTCAAC	60.134	20	232	922	1153
CGTATTCAATAGACACATTGC	59.903	23	229	1667	1895
CCAATTTTCCCCAACTCAAA	59.772	20	248	2287	2534
AAGCAAGAAACCGCTTGAGA	60.132	20	207	4630	4836
GCACCTGCTAGTGTACGGGT	60.201	20	251	237	487
ATCTGTCAGCATTTGGACCC	59.934	20	211	1008	1218
CATTTGAAAGAATACAAAACG	58.295	24	224	311	534
TTTGTTCCACCACTCCATCA	59.935	20	241	56	296
AGATGAGTGAGGCTGGAAGC	59.56	20	206	1114	1319
GGGAGAGGGAATTGAGGGTA	60.264	20	224	9	232
CACCAAATTCAAGCAATGGA	59.518	20	239	656	894
TTTACATCATGTGGTCGCGT	59.995	20	213	1428	1640

TTGGTACCGAAGTTGTCATCC	59.845	21	227	1169	1395
ATAAAAATTGCATGCACCTGA	58.174	21	269	1788	2056
ATCTCGCACGCGATAAAAAT	59.71	20	175	4996	5170
GGCTGTTGCTGAGTGTGAGA	60.187	20	276	485	760
GAGTATCGGCTGTGGGTTTC	59.556	20	275	2940	3214
GCCACACCTGACATTGCATA	60.549	20	202	677	878
TTCCTTTTCTTGGGTGGATG	59.903	20	260	4375	4634
CTAATAAGTGCTCCGACTCCG	59.007	21	268	7	274
TTGGAGCATTGCCATTGTAG	59.688	20	249	1453	1701
TGTACTGAATGCATCAAAACCC	59.867	22	168	631	798
CCCCATTCCCTCTCTCTCTC	60.149	20	250	48	297
GGCTCTCCTCTCTCTCCACA	59.663	20	257	1398	1654
GTGGGAGAAATGGGGAGAAT	60.133	20	271	627	897
CGTGCAATAGGTAGAGAAAAG	59.407	24	204	664	867
TGTTATTATTGGAACAGCACCC	58.878	22	217	1679	1895
TGTTGACTCCCACATGTTTCA	59.992	21	251	2108	2358
ATCACGCACAGTGGTACACG	60.662	20	258	406	663
TCACCATCGATCTCTGCTTG	59.942	20	258	478	735
TTAAGTCAATTCCGTATGACAA	59.048	25	196	62	257
GCAAAAAGTTCTCCGGCTTT	60.721	20	231	1321	1551
GGAAAAACTGCTGCCTTTTG	59.861	20	236	739	974
CATCTGCACCCATTTCCTTT	59.933	20	187	707	893
AGAAAGCCGAGGAGAACTCTT	60.022	22	275	1154	1428
TGTACTGCCACTTGGGTGTC	59.597	20	154	1396	1549
TGGATTCGTCCAAAAATTCC	59.739	20	137	125	261
GGCCAGATTAATTCTTTGCG	59.682	20	101	1937	2037
TCATTTGCGCTTGTCATTTC	59.816	20	277	759	1035
GGGCGCTATCCATTATGAAA	59.892	20	191	1179	1369
TCTTTTCCATGGGGTAGCAC	59.933	20	129	638	766
TCGGCATTCTATTGTGTGAA	57.702	20	233	1126	1358
CTCATTTATGCATCACTAATTTC	57.532	25	230	111	340
GTTTCACGTTCACTCTCGCA	60.032	20	272	4672	4943
GTGGACAAGAATGGTTTGGG	60.21	20	244	1891	2134
CCATCTCCCACAAACAGTCC	60.363	20	260	1334	1593
TGAAACTCTCATCGCACACC	59.837	20	226	1528	1753
CATTCGTTTTCACTTTGCCA	59.706	20	160	740	899
AAGCGAGAAGAAAGAGCGTG	59.898	20	272	1422	1693
CGCTTTTGGATTAGCAAACA	58.958	20	269	1519	1787
CGATTTGGATTCGAATTCTGT	59.033	21	206	613	818
GGCGATGCAAATAGAGGAGA	60.318	20	181	1079	1259
GCCGACTCACCAACTTTCTC	59.851	20	214	37	250
TCTGACTCGCTTTGATGTCG	60.136	20	178	292	469
GATCCAACGGCTGAAAATGT	59.939	20	242	3175	3416
CACTCTCTGTTGCCCAATCT	57.87	20	229	99	327
TGTGAAAACGTTGGTTGTGAA	60.035	21	212	4494	4705
CTATGGACGCAATCCTTTCC	59.528	20	120	531	650
CAAGACTGGACACTCCACCA	59.705	20	115	1175	1289
CGGGAGAGCAAGTTTTGAAC	59.853	20	170	88	257
ATGATGTTGATAAAACTGATAA	57.746	26	280	627	906
TCATCCAATGGTTTGGTTTG	59.222	20	279	696	974
TGTACTGTGAAAGGTGCCCA	60.152	20	276	663	938
TTCTTTGGTTGGAGGAGACG	60.224	20	168	371	538
AGTGCCGATTGAAGTGCTG	60	19	232	1879	2110
TGAAGTTACGAAATAAGGAGG	59.526	25	235	1717	1951
CTGGTTTTTGCACGATAGCA	59.872	20	200	678	877
GCTACAGCAGCCATTGATGA	59.979	20	124	2003	2126
GGTCGACAATCAAGTTGCAG	59.293	20	260	2192	2451
GATAAATTAATCGCTGGCTGG	58.73	21	241	588	828

TGGAGGGAAAGTGGCAAAAT	61.728	20	275	1706	1980
TGAATGGTAAATGAACCGCA	59.93	20	108	3	110
TACAAAACCATAACACGCGG	59.486	20	265	211	475
TTTCCTTGCAAGTTCCGTTT	59.724	20	220	0	219
AGTCCCTTGTTGGGCAGTAA	59.592	20	261	1343	1603
TCCACCCTCAGAAATTCAAA	58.117	20	185	2047	2231
CTTGCAGCATGGTCAAAGC	60.555	19	143	1692	1834
TTCAATCACCACAACCAAACA	59.849	21	279	1075	1353
TTGCTCTCATTGTAATCTCCAC	60.497	23	162	1886	2047
GCGGTTATCACCGGATCG	62.397	18	133	3207	3339
TGGATCTCCTACTGGGTTGC	60.073	20	241	1318	1558
TCTGTCGCCTTGAATGATTG	59.799	20	230	875	1104
TTTTTGGTACTTCATCATTTAAA	59.354	27	257	733	989
TGCAGCAGGAACAAGAACAC	60.032	20	241	144	384
TAGGGCCCTTAGTTCGTGTG	60.125	20	202	471	672
GGAGCATATCTTGCAAACACA	58.787	21	174	297	470
TCCCTTACGGTCAATGTGGT	60.232	20	190	1087	1276
TTTGCCATAGATATGCACCG	59.543	20	230	210	439
GAGCTTTGGTGGAAACATCC	59.532	20	151	54	204
ATGAACAGGTCCGCGAATA	59.09	19	260	559	818
GGTTCCAATTTCGTGTTGGT	59.694	20	202	4329	4530
AAAAGAGTGGTGGTGGATGG	59.82	20	245	774	1018
CACCCATCTCCCATTTGAAC	60.173	20	198	5219	5416
ATCGGGTAAGCAACATGACC	59.82	20	278	276	553
ACATGTCATTGACCAGACCC	58.186	20	103	0	102
CTTGTTGCCACGTATCCTCA	59.716	20	216	1986	2201
CGTGAAGAGTTTCCCACCAT	59.966	20	256	2045	2300
CAACCCACGGATGGTTAAGA	60.745	20	274	1277	1550
GGCAACAGTGGGATAATGCT	59.962	20	261	1541	1801
CAGCAGCAGCTTCTTGTTCA	60.472	20	126	1976	2101
GAAACATTAAGCCTCTGGCG	59.845	20	235	66	300
CTCAACCAAGGAAGTGTTGG	58.187	20	274	621	894
AGCAAAATTGGTCTAGAGAAT	59.278	27	159	1857	2015
CGCATGTGCTTCTCAATCAG	60.562	20	265	2098	2362
GACGAGCTTGTTCTCGCTCT	59.898	20	276	5083	5358
CTTTTGCTGGGGAGGAGTT	59.269	19	260	2106	2365
TTCGTCAAATAATCCAAGCAA	58.291	21	208	753	960
ATTATTTGTGGCGTCTGGCT	59.597	20	250	416	665
TCGAGTTTCTTGCGAGTTGA	59.716	20	178	709	886
ACGAACAACAGTTTCTGGCA	59.339	20	194	372	565
AGGAGGGTCCCTTGCATAAG	60.455	20	233	41	273
TTGATTGATTTCTCTCCGCC	60.155	20	266	276	541
TGTAGCAGGAACAAATGCCA	60.257	20	249	75	323
GAGAAGGGCTGAAAGAAGGC	60.464	20	127	767	893
ATCGGTTATTACCGGATCGC	61.031	20	223	1853	2075
CACCACTCCCCTCTTGTTCT	59.149	20	280	282	561
TATGGAACACATCGGACCAA	59.774	20	246	1811	2056
GGTCACCCTAATGGCAGAAA	59.933	20	181	231	411
CGGAAATTTTCAACCAATTCA	59.797	21	238	4868	5105
TGGTAGAGGCCCTGTGTTTC	60.111	20	225	4060	4284
AACACCCCATTTTGCTGTTC	59.836	20	234	282	515
TGGATTCGGGTATGTTGCTT	60.331	20	148	8	155
TGCCAGTCTTCACGGTTATG	59.716	20	196	1862	2057
CCCATTTCCACTTCCATCAT	59.605	20	276	1457	1732
GAATTAGGGTGGGCGAAAAT	60.15	20	148	540	687
TACAATAGCATCGGCACCAA	60.096	20	280	753	1032
AGTGTTTTGACATGATTACTCC	57.599	26	261	2750	3010
AGCATCGAGAGCTTCCAAAA	60.096	20	253	803	1055

TTGCATCTCTTTTGTCGCTC	59.152	20	176	759	934
TGAAGTTAGGAAATAAGGAGG	58.743	25	224	5483	5706
CCAAGTTCGAGTCCGAAGAC	59.844	20	231	67	297
GTTGAGGAAGCCGAACAAAA	60.227	20	169	106	274
GTGTTTCTGCGGTGGAGAAT	60.119	20	183	364	546
ACGTCCAGGGTTAGAGTCCC	60.371	20	190	3169	3358
CCAGCAAGGGAAAATTAGCA	60.202	20	153	1308	1460
ACATTCAGGCTCAAAAGCAA	58.502	20	211	1158	1368
AGCAAGCATGTTCTCCCTTG	60.397	20	229	143	371
CCACCATACCCACACACCTT	60.545	20	168	703	870
AGGTGTGAGAGGGTGGTGAG	60.153	20	180	1075	1254
GGAAGGGAGCAAAGGTGTTT	60.476	20	264	6831	7094
AAACCCTAATTGTTTCGGGC	60.184	20	259	28	286
TCTAATCCTCTCCCCTGTCG	59.234	20	210	10401	10610
ACTTGGGGTTGAGTCCTTCC	60.349	20	271	150	420
GGGTACAAAGAGCTCAGCGA	60.538	20	212	835	1046
GTGCGTGCATTTTTACGTGT	59.662	20	261	755	1015
TTTCAAAGCCATGCTGTCTG	59.988	20	259	1670	1928
GGGCTTTTGAATTTTGGGAT	60.13	20	221	124	344
GGTTGGGACGGATAATCGTA	59.645	20	199	2955	3153
GCCTTCTCAAGATGCAATCC	59.78	20	170	560	729
AAAGCAGCAAAAACCCACAG	60.284	20	241	2215	2455
GCACTGAAGTGGTGAGTGGA	59.872	20	189	2758	2946
TCAAATTTAACAGGCCGACAT	59.465	21	189	585	773
CTGGCTCGAGGACTCATCTC	60.096	20	104	862	965
TACCAAAGCCGCTCCTAATG	60.223	20	249	1149	1397
AGTTCTTCTGGATGCTGGGA	59.803	20	214	1751	1964
AAAGCTAACCTCCCCACCTC	59.576	20	251	95	345
GGCATGTGGCATACCTCTCT	60.104	20	207	3991	4197
GGAAGACAAATATGGGACGG	59.244	20	166	34	199
TCCATGCATTTTTCATTATGTG	58.42	22	279	292	570
TCATTGGATAACAACCGCAA	59.93	20	267	449	715
CATCTCCGTTGTTGCTGGTA	59.716	20	251	8	258
CAGTTCACTGCGAAGCTTGA	60.324	20	234	3484	3717
CCAGAGCCTGCCTCTACTGT	59.622	20	265	781	1045
CTGCCTGGAAATGCCTTAAC	59.708	20	274	1042	1315
CCCTTGGTGCTGTTATGACC	60.375	20	260	2564	2823
CATCGGCTGGAGAAGAAGTC	59.95	20	191	46	236
CGGAAATAGTGCGTGTGATG	60.134	20	244	0	243
GGTCAAAACATTGACCATATTT	59.949	26	213	2234	2446
GGTGTGGAAGGCGAATTAGA	60.074	20	260	104	363
ACATGCCTCTTCCACAACCT	59.579	20	165	2333	2497
CTGGAAGAGCCGTTGTTTTC	59.853	20	172	8	179
AATTCATGGGCGTTTCTTGA	60.448	20	185	742	926
TAGCTGTTTGTGCGATGACC	59.871	20	214	1634	1847
ATTTCTGGTGTTCGGCGTAG	60.132	20	246	226	471
GGTCAGCCTCGACTACTTGG	59.867	20	259	1993	2251
CGAAATCAAATCATTCCCGT	59.762	20	166	34	199
TCTTGCCCGCATTTTGTTAT	60.456	20	275	44	318
GGAGGCACAAAAGACGCTAT	59.34	20	143	100	242
CAGGCGCACAAACAGAAATA	59.872	20	260	33	292
AAGAGTGCACCACACCACCT	60.631	20	201	4300	4500
GGTTTTCATAATGAGGGCGA	59.901	20	249	1620	1868
AGACATAAAAAGGGCTGGGG	60.312	20	219	432	650
GTTTCTCGCAGAAGGTGGAT	59.288	20	213	255	467
CAGATTTGCCCCTGTATGCT	60.096	20	164	859	1022
AAAAGCCTCCAAAGCATGAA	59.823	20	267	30	296
CTTTCACTCAGCATGCCATC	59.399	20	129	2	130

GCCGTACCATTCTGCATTCT	60.103	20	250	2720	2969
AAACAAGAGCCGAAAAGGGT	60.11	20	252	1745	1996
CAACAAACGTTGTCAATGGG	59.857	20	205	5381	5585
ACCATATTTAAGGTTATCACC	57.552	24	253	1763	2015
GAGGCTGGAGCAAGAGAAGA	59.827	20	256	772	1027
TTGGCTTCCATTTCTGTTCC	60.051	20	228	1313	1540
CAAAAGGTTGGGGAGTTCAA	59.942	20	228	67	294
TTCTTGCCACTTTCTCCGAT	59.813	20	164	2368	2531
GGAACACCCTTGCTTGAGTA	57.797	20	280	3477	3756
TTATCCCTTCGCTTTCTCCA	59.778	20	156	2342	2497
TTGCACATACACGCAGCATA	59.892	20	256	896	1151
CGCAACTGAAAAACCAAACA	59.746	20	157	720	876
AAGTGTAGTTCCGGGGGAGT	59.856	20	122	159	280
TGGGCAGTGATTGCTTGTAA	60.257	20	243	2205	2447
TATTCGACGATGCTCTGCAC	59.979	20	191	853	1043
TTACAATGCAATCGCCTCAC	59.694	20	213	2709	2921
ACTGCAGATATGGCGGGTTA	60.49	20	242	9	250
CTGGTTCCAGCTCCAATCTC	59.803	20	181	611	791
CCACGATAAATGCTTCGGTT	59.96	20	178	2582	2759
TCAGTTTTTGTTATGATAGGAT	57.035	25	275	1499	1773
ATCAAGGGCGTTTTTATATTTG	58.97	23	269	189	457
CATCGTTTTACCTTTTGGCG	60.48	20	278	1961	2238
AAGTACATTGAACGCCCTGC	60.14	20	229	3053	3281
TGTCAGTTGCAACATTGCTT	57.896	20	269	1025	1293
TCACTTCAAACGTCGTCCAA	60.278	20	237	2000	2236
AATGAATCGAAAATGCTCGG	60.038	20	263	228	490
TTCCGTCGTTGAAATCTGTG	59.691	20	253	1608	1860
GAATGTGGAGTTTGGTGGTG	58.827	20	246	731	976
CCAGCGTAAGTCCAACACAA	59.758	20	172	293	464
TGGGCTCTTCATCACTACCAC	60.126	21	252	1331	1582
GCTGCAGCAATGAATCTGAA	60.104	20	262	744	1005
TTTTCCGATTTGTGTTGGTT	57.972	20	213	730	942
TCACAATAAGGCCCTCCATC	59.894	20	183	840	1022
GATCCCGCACAAATGAGATT	59.9	20	232	95	326
CCTGTCTGGAACTGGAAGGA	60.229	20	275	20	294
AAATGAAACCAACACACCCC	59.55	20	249	1870	2118
GCGTGTGGACTCCGTTTATT	60	20	234	491	724
GAGAGGCATTATCCAGGTCAC	58.609	21	280	3182	3461
ACCAAAATCCCTTCTTTGTCTT	59.874	23	253	1729	1981
TTCAATTCCTCGATAGCAAGA	59.75	23	209	1767	1975
CCCAACATGCTGGTCTTTCT	60.111	20	248	208	455
TGCAAAAAGAAGCACAACCT	58.554	20	154	478	631
CAAATTAGGCATCCACAACG	59.037	20	279	1340	1618
ACGGATTCAACAGAAAACGG	59.971	20	193	269	461
CACTGGTGGTGGTAGTGGTG	59.907	20	243	338	580
AAAACCCCACCCTTTTTGAC	60.068	20	148	407	554
ACATCATCGCATCGATTTCA	60.041	20	177	1364	1540
AAAATCTTTACCGCATACACA	58.699	24	214	2135	2348
TGGTGCAGCAACCAACTAAA	60.293	20	252	382	633
GATAGACGCCTACGACCCAA	60.096	20	262	2078	2339
GCATCCAAGCAGCGTTAAA	59.968	19	273	880	1152
CTTTCGGCATTCGTAAGGTC	59.708	20	199	8	206
TAGAGGCGGATCCAGGATTT	60.92	20	268	3774	4041
TTCGGCCATATCATGTTTCA	59.891	20	280	21	300
GTGGTTGGAGTGGGAGACAT	59.817	20	198	1959	2156
CAAAACTGTGACGTAGTTCCG	58.349	21	265	367	631
CCGCATCCACTAAACCCTAA	59.953	20	175	515	689
GGGCTTCTTTTCTGGCTTTT	59.835	20	133	373	505

TGGCAAATGCTTTGTGTTTC	59.712	20	144	1087	1230
TGTGCTATTCATCTCATTGCC	58.738	21	231	1883	2113
TCTTGGATTGTGCGTCAGAG	59.984	20	277	231	507
ATGACAGTGGAGGGAGAGAG	59.871	22	162	37	198
CCCTATGTCAAAAGTGTGGGA	59.838	21	239	1042	1280
GCATTGGCTTTGCTTACTCC	59.851	20	264	160	423
CCCAGACTTCGACATAGGCT	59.308	20	220	3	222
GGGATGGTGCTACCTTTTGA	59.933	20	242	2630	2871
TCACATGTCCCAACATCTCG	60.534	20	269	897	1165
TCGACTGCCTTCAAGTAAAGC	59.646	21	280	783	1062
TGATCGCTTATGCATTCCTT	58.336	20	253	2934	3186
TGTTCCTGTGGATGGTGGTA	59.806	20	240	946	1185
GCTGTGTTTTGTGGCATGTT	59.621	20	238	2011	2248
ACGAGAAGACTTCGCCAACA	60.975	20	132	770	901
CTCGGTTTCATTGCCATACA	59.542	20	204	187	390
TTTGTATAGTTGGGCGAGGC	60.096	20	181	265	445
TTGGGGGACCATTTTGTTTA	60.024	20	142	919	1060
TTGAGGGGAGAAAACAAACG	60.081	20	193	1774	1966
AAAGTGCAACGGAACTGGTC	60.156	20	148	666	813
GGAGGACTGGCAGAGAGATG	59.945	20	223	4172	4394
TTTTATCAATTCGGGGCTTG	59.901	20	202	184	385
TTGGTGAGTTGGAGGAGAGG	60.229	20	260	909	1168
CCCTGAACAGGTATGGATAAG	59.72	22	215	1086	1300
TGGCAGCCAGTTTGTCATTA	60.257	20	238	4990	5227
TCCAACACACAAAACCTTGC	59.591	20	242	4050	4291
GTGGACGTCCCAGATTGTTT	59.827	20	229	1819	2047
AGCCCAAACTACCGAATCAA	59.569	20	267	2353	2619
ACGCGTATGCATTGGTCATA	59.983	20	234	978	1211
AAAAGGGCCTGAAAATCCAT	59.777	20	278	3175	3452
TATTAACACAAATCCGGGGC	59.66	20	241	2246	2486
ATGAGTGGCAGGGCAGATTA	60.624	20	149	2499	2647
TGACTCATAAACACCCGACG	59.566	20	178	985	1162
CAGCACTGCACTTCTGAGAG	57.4	20	254	907	1160
TTGCATCTGATGATGCCAATA	60.05	21	234	2212	2445
AGTTTGGGAGTATGGTTGGAA	59.741	22	237	1720	1956
TTGCGGAGTTTTCATTTTCC	60.053	20	154	1515	1668
TTTTCGGATTCGATGCCTTA	60.528	20	255	170	424
CCGAAAATCCCAAAGATGAA	59.872	20	116	2228	2343
TTGCATAAATGGGCCTTGA	60.02	19	258	870	1127
AAAAAGGGAATGAAGCAGCA	59.823	20	232	1380	1611
GTCTCCCTCTGCAAAATCCA	60.195	20	192	1868	2059
TGATGGCATTTTTCTGGTTG	59.518	20	148	1156	1303
CTCACCTCGAGATGGTAGGC	59.827	20	214	539	752
GCAAGCCATCAGATTCCAGT	60.226	20	263	210	472
TTCAAGGCGTTATCTGGAGC	60.352	20	270	3812	4081
AGGAGGTGGATGGAGTGTCA	60.527	20	179	1217	1395
TCCGAGGCTATTCTTTTTGC	59.433	20	225	61	285
ATTTCCTTTTCCCCACCAAC	60.032	20	279	1658	1936
ATGTATGGGCCCTTAATCCC	59.873	20	238	120	357
TCTGAACTTTGCCAGTGCAT	59.445	20	163	484	646
TCTTGTGGCTGTACTCCGTT	58.37	20	260	1268	1527
GATGCACTTAGTGGTGCCAG	59.318	20	276	729	1004
GATTTTGGGAGTAATGGGGC	60.511	20	136	360	495
CAAGAACCGGGGATGACTAA	59.926	20	211	579	789
CATGTGTATAATAACAACCGCC	59.674	23	160	8535	8694
TGCATATTGACCCACTTGTCTC	60	22	243	869	1111
AGGTTTTGGGTTTAATGGGC	60.055	20	128	430	557
ACCCCTCTTTTTCCACCATC	60.169	20	207	3239	3445

TGCTATGTTCTCATTCGTTTGC	60.272	22	274	208	481
TGAATTGAAAGCTGAATCATGT	60.124	23	237	23	259
ATCACCATAGCGTCCACTCC	59.957	20	177	1828	2004
TTCTGGTAACAAGGAATGCAA	58.28	21	206	1881	2086
TTTTCCTTCTCTTTGCAGCC	59.569	20	208	396	603
AAGGGTGGTGTTTGTTGGAG	59.861	20	273	1264	1536
TGTCGTCTGACATTGCCTACA	60.317	21	144	13	156
AGGACTTGGGAGTCTGGGAT	59.929	20	237	520	756
CCACCATTGCTAATCGTCCT	59.955	20	139	3442	3580
TGCAGTTTTAGGCATATCGAAC	59.279	22	245	104	348
ATGCATGCAGCAAGTTGTTC	59.878	20	204	946	1149
AGGTTTTCAATGCAAGGGCT	60.987	20	235	846	1080
AAGAACAAACGACTTCCACCA	59.624	21	230	2487	2716
TCTTTGATTCCAACCCCAAG	59.903	20	207	587	793
GAAGGCTGGTAACCCATCAA	59.933	20	200	218	417
TGTGTGTGGCCACTAAAATGA	60.019	21	242	160	401
CGCTTGAATTGAGGGTTCAT	60.074	20	236	741	976
CCTACAATGCCACACCTCCT	59.989	20	134	136	269
TTGTGGTGTGGAAGATCTGG	59.52	20	209	1176	1384
ATTCCCTTTTGTCCCTTTCG	60.291	20	223	993	1215
ATTCAATCTGCACCTCCTGG	60.073	20	129	192	320
GAGGTTGAGGGTGGCTGTAA	60.111	20	143	1036	1178
ATCGTGGATACGTTGAAGGC	59.962	20	271	9	279
CAAAAAGCGCTACAAGCACA	60.191	20	243	708	950
ATTGCGCTCAAAGATATGGC	60.203	20	203	2198	2400
CCAAAATTACATGGTTCGGTG	60.096	21	233	1526	1758
TCTGGTAACCGAATTGCCTC	60.074	20	209	1055	1263
TCAGGTTTATCAACATCATTTAT	57.667	25	202	14	215
GCCCATTTGCAGAATCCTAA	60.038	20	106	1527	1632
GCCATCTGTATGGCTTGACC	60.492	20	187	1950	2136
TGAAGTTAGGAAATAAGGAGG	58.743	25	272	3054	3325
AAACAGCACCAGCTTCAGGT	59.914	20	219	2380	2598
TCCACTTTTTGTTTTGGAGCA	60.634	21	238	367	604
AGCCCAACCTATTCTCACCC	60.328	20	137	1903	2039
GATTGGTCCAGCAGGTTTGT	59.973	20	276	594	869
TGCATCTCCTCCACCTATCC	60.034	20	151	454	604
GCACAGCATGTGGAGTGAAG	60.473	20	252	1403	1654
TTGTTGCGCAATGAAGACTC	59.995	20	251	17	267
CATCATTCCCCTCCTCTTGA	60.003	20	256	397	652
CATCCGTCCATTTCCAAGAT	59.75	20	246	2121	2366
TTGGGATCTTGCATGAACAA	60.049	20	234	491	724
CCCAACCCAATCACAACAAT	60.474	20	242	1039	1280
CACAGCGGTCTCGTCAACTA	60.049	20	232	1116	1347
GATGTGGAGCTTGCACAAAA	59.847	20	231	1477	1707
CCGCAAAAATCCTTCACAAT	59.938	20	257	3704	3960
TCAGCAATCAAATTGGCAAC	59.67	20	275	538	812
TGCCTTTCCATGAACAAAAAC	59.967	21	253	1565	1817
TTTCAATATTGGGCAGAGGG	59.894	20	206	1828	2033
GATCCCGGACTGAGTGAATG	60.475	20	246	322	567
AACAAGAAGGCCGGAAGAAC	60.61	20	234	325	558
GGCGTGACACTTTTTCGATT	60.118	20	252	3630	3881
CAACAATTAATTACCGCCGC	60.335	20	253	2616	2868
TATAAATTTTGGCGCCGTTG	60.797	20	267	1128	1394
CAACCCAAACATTTATTCCCC	60.279	21	226	2376	2601
CGAACAAAGCACACATGAGG	60.301	20	225	5544	5768
TGGCACAACAAAAGTAGAGAG	59.562	22	247	307	553
CCGAATTTCTCCCAACTCAA	60.044	20	208	4547	4754
TCCACATCTTTGGGATAGGG	59.744	20	247	135	381

CCGGAGAGAAAAAGACACGA	60.366	20	252	1969	2220
CGCTATGTACACGGTGTTGC	60.203	20	146	1102	1247
GTTTGCTTTGGGGTTGTGTT	59.875	20	278	1329	1606
GGAATATTTGCCTCAATCCG	59.369	20	119	9	127
TCATACTCTGGCTGCTCGAA	59.697	20	241	2233	2473
TGTGCATGCTTCAGTCTTGTC	60.048	21	207	2892	3098
GAAGCCCATATGGCATGAGT	59.923	20	239	457	695
CATCGTGTAGTGCATCCTGC	60.296	20	236	1502	1737
GTGAATCTTGGTGGCTTCAA	58.697	20	153	40	192
GGCATTTGGAATGAGTTTGG	60.309	20	231	362	592
AATCACAGAATAAACGCCCG	59.96	20	255	3642	3896
TAGCAGCAGTGTGGAACTGG	60.049	20	276	646	921
GGAGACGGTGACAAAAGCAT	60.119	20	221	108	328
AAGGACCTCAGCCTGCAGTA	60.012	20	191	2347	2537
ATATGGTGGTATGGTGCGGA	61.003	20	132	176	307
ATGCTTGATAGTGGGCATGTT	59.471	21	184	16	199
GCTGCATCCCGATATGGTAG	60.457	20	202	2217	2418
AGAAGCTGAGCACGCCTAAA	60.292	20	270	1029	1298
GGAACTAACGTCCTCCCGTT	60.361	20	163	550	712
TTCGACTTTTCAAGTTATTTTTC	59.74	26	253	94	346
TTAGGCGATGCCCTCTATTG	60.188	20	206	403	608
TGGATGTTTACTATGGGGTGTT	59.531	23	249	1183	1431
AGCAACCTCAAACCACAAGG	60.149	20	181	4	184
TCCCAGTTACCTACCACCCA	60.224	20	121	2271	2391
AGGTCAGGCTACCCAACAGA	59.721	20	258	21	278
TGCCATCAAATGCAAGTTTC	59.67	20	251	1153	1403
TATTGTTGCTGCTGATCCCC	61.003	20	242	756	997
CCCATCAGACCAGTTGACAC	58.94	20	237	914	1150
GGAAACCCTGAAGAAACGAA	59.146	20	267	1832	2098
ATTCAATCTCTGGGCTGTGG	60.073	20	163	5485	5647
AGCAGCATTAGCCAGAAAGG	59.615	20	147	2375	2521
CTTCTCTCACATCCATCGCA	59.942	20	216	1164	1379
TGAATTTCAATACACGCCCA	59.93	20	269	1211	1479
TCCCATTTCCTCCAAATTCA	60.244	20	115	3738	3852
GCAACACTAGGCAACAGCAA	60.058	20	239	1705	1943
TTGAGCTCATGTCAGCTGGT	59.577	20	260	440	699
GCCTGCTCAACCTCAATTCT	59.434	20	259	2827	3085
AACTGGTGTGTGTGGCTGTC	59.63	20	274	9341	9614
TGCATGTGGTGATTGGTAGA	58.486	20	269	1343	1611
CTCTGCTTTTTAGAGAGAGGG	59.811	24	128	4109	4236
GCTTCTCATCCTGCGAACTC	60.104	20	257	633	889
ACCCCAAGATGGAAGACAAA	59.381	20	278	3461	3738
TCCTTTTGCTTATGCCGTTC	60.209	20	213	1734	1946
TTCCTAGCTCTCCCCCTCTC	59.912	20	229	2236	2464
TCTAACACGCAGCATCAAGG	60.011	20	228	2551	2778
TTGCCTTTATTTCTTGGCAGA	59.84	21	225	1128	1352
TTAATGCAGAGCAGCCAAGA	59.712	20	129	844	972
CGAGGCATATCATGTTCGG	60.041	19	198	2234	2431
TGCTACCTCGCATTGTTGAG	60.011	20	237	327	563
CCCATCACCAAACAAAACCT	59.688	20	277	2575	2851
TGCAATCGACGGAAACAATA	60.073	20	219	1194	1412
CAAGTTTGAAGTGCAGCATGA	60.042	21	197	2802	2998
TGTCAAGAGTCTTTGCACCG	60.025	20	181	1191	1371
ATTCAACTCCAGACGCCATC	60.081	20	277	1435	1711
AGTGGGCTTCTACCTTTCCC	59.576	20	271	2236	2506
GCATACGGCTCACTCTACGG	60.817	20	180	1019	1198
CCCATTCCAACCATAGCAGT	59.813	20	227	3960	4186
GGCATTACGCATTACCACAC	58.923	20	167	73	239

CACGACCTGAATGCAAGAAA	59.84	20	222	3292	3513
TTGTTCGTGTTCCAAAGGAAG	60.132	21	277	4002	4278
TGGTTTGTGAATTGGGTTTTG	60.613	21	230	73	302
TGAGCTGTGTTTAGGGCTGA	59.591	20	107	1834	1940
TGATGGTGAGGATGCTGCTA	60.376	20	269	3297	3565
TTGTGTCCCAATAACACCAAA	58.783	21	138	2780	2917
TCCATAGCCAAGCACAACAT	59.152	20	204	3636	3839
CAGTTGGAGTTGCTTTTGGA	58.897	20	223	1310	1532
TCTGTGGGACCAACTTCCTT	59.549	20	128	5510	5637
ACCCCACAAAGAAAACACCA	60.246	20	231	534	764
GCCCCAAATTAAGCACAAAA	59.943	20	229	2251	2479
CGTTTCTTGGTAGTTTGCCC	59.609	20	269	3872	4140
TTTAAAGAAGGCCAAGCATTT	58.079	21	216	3401	3616
GCGTTGTCTTGTGTGGTGAT	59.603	20	120	14	133
TTGTTAGAGGTTTTGACGGGA	59.595	21	276	2627	2902
AGCATTAAAAAGGCCATCCA	59.547	20	112	2641	2752
TTCACTCACATTGCTTTGCC	59.847	20	188	3167	3354
TGTGCAAAATGCTACAGGTGA	60.309	21	228	4630	4857
TAGCCGTGGTTTGTCAAGTG	59.758	20	223	1256	1478
CATCATCGACTCGTCCCTTT	60.073	20	228	1318	1545
ACCAACAGTTGAATATGCCTA	60.302	23	262	710	971
CGGGAGATGGTTGTTTGAGA	61.034	20	227	3107	3333
CTGAAGCAGAAGCCCATCTC	60.096	20	256	2107	2362
CGGAGAGAGCGAATGAGTCT	59.703	20	255	1348	1602
AGCACACCAATCCGAAAATC	59.939	20	275	3885	4159
CAAGAACAATAATCGGTGCAG	60.131	22	223	2536	2758
CGCTTTGGTGCATCATCTATT	60.11	21	239	522	760
TTGGAGAAAATTTTGTGGGC	59.916	20	279	1530	1808
GAATCCAGCACACCAAGACA	59.682	20	253	1373	1625
GGAATCGGAACCCTTTTAGC	59.909	20	257	2539	2795
ATTGCACCCAGAGATGGAAG	60.073	20	229	4974	5202
TCACTCATGGCTTCACGTTC	59.837	20	246	3199	3444
GGGAGACCTCCAAAGCTAGG	60.204	20	154	2032	2185
ACTTTAAGGCGAATTAGCACC	57.615	21	222	1635	1856
CCCAAGCTGGTGGTTATGAT	59.813	20	188	2799	2986
GACTCGTGTTCCAACATTCA	57.033	20	273	397	669
GTAAGGGACCATTCACTGGC	59.41	20	223	3222	3444
GAGAAACGCCACACACACAC	60.211	20	156	772	927
GGCTAGCTGAAGGATTTCCA	59.41	20	259	2927	3185
TTTGAGCTCCCGAAAATGAC	60.192	20	276	54	329
CGTTGGCCCGATATTTAGAG	59.564	20	228	1187	1414
GTGGATGCTTATCGCAGTGA	59.83	20	214	177	390
GCTGCTGCTGTCTAAATCCA	59.178	20	252	23	274
TGAAGATGGCACCTTGAGTG	59.831	20	239	802	1040
CAATGAAGTCGTGCATCACA	59.248	20	226	1154	1379
GTCATCTCGACATCCTGCAA	59.794	20	197	103	299
CCACTTTCACCAACTCACCA	59.565	20	274	701	974
CGACAGATCCCCTCTCTCTG	59.937	20	254	1772	2025
CAAACCACAAAGCAGCACTC	59.49	20	233	142	374
TTTAAGCTCAATGCCTGGGT	59.708	20	179	2636	2814
GGGCATTTTGATGACTTCACT	59.045	21	184	4262	4445
TGACCATGTATCGGTCTTTCA	58.987	21	271	18	288
CGTGTTTGGTGGCTTTTCTT	60.147	20	242	1297	1538
TGCGTTTCTGCGTTTTTATG	59.88	20	272	2617	2888
CATTCACGGAAAACTGCACA	60.699	20	243	1281	1523
ACATGAGCTCGGTTCGAAAT	59.7	20	251	1377	1627
ATCTTGGCAATCCAAAGCTG	60.214	20	139	1	139
TTAATCTTCGTCTTCGGCGT	59.845	20	252	740	991

AAAACAACCCAGTCACGCTC	60.156	20	249	3902	4150
CTTCGTGGAGCTGCAAACTT	60.571	20	184	2061	2244
TGGAAACAGCCATTCACAGA	60.24	20	257	2556	2812
GATGATTTATCACCGAATCGC	59.387	21	272	3943	4214
CCACCATGATTTCGACACAC	59.812	20	225	5756	5980
AAAATCATTGGAATCAGCCG	59.901	20	219	6001	6219
CCTCGATGTTTGAAAACCAGA	60.096	21	156	81	236
GTGCATGTGTGTGTGTGGAA	60.053	20	229	560	788
GCAACATGCTGATGGTGGTA	60.549	20	166	1126	1291
ACGATCATCACATGAACCGA	59.925	20	172	2257	2428
CGAAACGATTAGTTGAATGTGC	59.652	22	193	2000	2192
CGGAACACAATTCGACAGAA	59.691	20	130	19	148
TAAGCCAAGCACACATGAGG	59.864	20	180	6951	7130
TCATGGCTCTCATCCAAACA	60.201	20	269	2209	2477
CCAGTCAAAGTCACCAGGAA	58.695	20	194	1935	2128
ATTCCTCACCCAAAATGGTG	59.647	20	249	1798	2046
AAACTTGCAGAGTCGGGTGA	60.833	20	243	1233	1475
CTGAATTTGTGGTGGCAGTG	60.152	20	180	475	654
AGGTTCTCACTCTCTCTCAGCC	59.249	22	271	771	1041
GACGATAATTCGTCCGTTGG	60.331	20	256	2735	2990
CCACCCACTCTCCCCTTAAC	60.736	20	217	987	1203
TTTAAGCGAAGAACAGGGGA	59.817	20	225	712	936
CTGATACCGAGGCAAACACC	60.517	20	240	1215	1454
GTCAAAACAAATGCTGTGGGT	59.89	21	266	1741	2006
TGTGACCAATATCACAGATTCG	58.502	22	276	10	285
TGCATAGCTGATATGTCCCA	57.67	20	152	1763	1914
TCGGAAGGCAAGATCACTAGA	59.963	21	280	593	872
CAAATAATGCAGAGAGCGAGC	60.131	21	262	2433	2694
ACCTTCCAATTGCTCTGTGC	60.263	20	241	330	570
AGGAAACCTTGCAAATGCTG	60.249	20	263	2972	3234
GGAATGAATGGAGCGTGAGT	60.081	20	256	5304	5559
TCTGGAATTCTCGTGCTTCA	59.522	20	231	718	948
TCGTCCCTCTCCACAAAATC	60.05	20	191	643	833
GCTTGGTACAATGGCTGGAG	60.657	20	251	9045	9295
CTTCGCTTTTCGCGATTTTA	60.456	20	231	7844	8074
ATGTCCAAAATTGTTGTCGCT	59.49	21	280	912	1191
ACTCGGCCTAGTTCGTTGAA	59.875	20	269	358	626
AAACATGTTGGCCAATTTCA	58.869	20	234	2464	2697
GATCCCTTCTTTCTCAGCGA	59.508	20	216	2007	2222
GCTTCAGTTGGCAGGTATCC	59.7	20	101	1541	1641
ATTCCGAACCTGAAGCACAG	60.255	20	250	335	584
TGCTGTACTTGCATTGGAGG	59.864	20	257	639	895
CGGTATGGTGTCGTACCGAT	60.657	20	199	7	205
TGCACAAAACAGTTCCACCT	59.187	20	269	7392	7660
TTTCACCCACAAAATCATCA	57.35	20	279	2078	2356
CAGGCGGCATTCTCTAATTC	59.807	20	267	292	558
ATTGGTGTTCTGGGTGGAAA	60.21	20	220	1979	2198
TTGTTGTTGGTGGAACTTGG	59.435	20	271	2194	2464
TGAGAAAACAAAAGTGGCCC	60.088	20	261	202	462
AGAGTCGGAAGGCATATGTGA	59.708	21	114	261	374
TGGGGAATGACTCACCACTA	58.93	20	212	4455	4666
GATTCGAGTTTTGCTTCCCA	60.192	20	153	2317	2469
TGAGCCTCCATGCTCCTATT	59.797	20	222	88	309
TGTGTTTTGACAATATTTAGTGT	58.633	27	152	4685	4836
TGGGAATAGCGATTTTCCTTT	59.922	21	186	3259	3444
CACGCACACACAAATTCACA	60.204	20	257	1306	1562
TGAATCACCACCCATCTGAA	59.893	20	199	5080	5278
TTGACTCCCCACTGTTAGCC	60.111	20	113	38	150

CGGAAAAGAAAACCCACTTG	59.581	20	224	281	504
TGTTAGCGAATTTTTGGTGG	58.674	20	265	166	430
TAACATGCCCCAGACACTGA	60.112	20	226	1026	1251
CACCCGATTCGAGTAGCTGA	61.336	20	272	2900	3171
GCGCCACCTCAAAAGTAAAA	60.244	20	203	1	203
CACCTGGAATGATAATGGGG	60.006	20	250	2307	2556
ATTGGTGCGTGCATGTATGT	59.878	20	135	20	154
AAAGCTCAGTTCGATCCCCT	60.212	20	271	6718	6988
CGATCTCCTGTTTCTTCCGT	59.284	20	223	3140	3362
GCTTTTTGCCTCCTTTCATTT	59.729	21	265	1156	1420
CAACAAAAATCAAGCCATGC	59.161	20	266	2362	2627
TGCTTTTGCTCTCCAACAGA	59.716	20	232	14	245
ACCTCAAACCCTTCTGCGTA	59.734	20	142	1835	1976
GAAGCCGAGAAACAAAGACG	59.993	20	155	1760	1914
CACCCCTACCCCTACCCTAC	59.571	20	275	2238	2512
GCTTCAAACTGGCTCTCGAT	59.579	20	228	3579	3806
CGGGTCTGCTCAAGTTTCTT	59.473	20	236	162	397
TCCTTTCGATTCATTCCTGC	60.155	20	190	2083	2272
ATGAATTTGCCTTTGTACATTTT	59.355	24	263	558	820
GAATAGCCCAAGACGAGTGC	59.843	20	194	1701	1894
CGGATTGGATCGGAGATATG	60.252	20	238	854	1091
GTGGGGTGATATAAGATGATG	58.278	22	244	58	301
CGAGAGGTGGGAAAAGTGAA	60.224	20	225	583	807
CTTTGGTTCATGTAGCCGAC	58.228	20	124	271	394
CAATATGGGAACTTCGCGTT	59.96	20	247	173	419
ATGAGTTCTTGATCGGTGGG	59.927	20	218	137	354
TAGCTTCGCATCAAGTCCCT	59.978	20	267	666	932
GGAAGCTGCTCTTGAGTTGG	60.134	20	242	274	515
TTTTGCCCCGATAGAAATCA	60.395	20	265	615	879
GGTTGCACACTCCAACACATA	59.48	21	275	196	470
TTCCATGATGCCTAGCATTG	59.646	20	100	53	152
TGGACTGATCAGCAGAGGAA	59.499	20	250	183	432
TCCTCGCCTCTTACATCTGC	60.504	20	174	51	224
TGGCATTGTCTTGGTTGTTC	59.547	20	269	1820	2088
GCCAATCCTAGCGATGAGAA	60.318	20	237	462	698
CAGGACGGTTCCTCTCTTGA	60.377	20	141	73	213
GCCAAAGAGTTGTTGGAAGC	59.859	20	251	1244	1494
ATAGGCGGTCTGGAGAGTGA	59.827	20	178	821	998
TAGAAGCATCTCCGAGGGAA	59.91	20	252	5007	5258
CTCCAAGACCCCAATTTGAT	58.836	20	243	539	781
TCCAACCCATCTCCCATTTA	60.126	20	271	1135	1405
ATGGTTGGATATTTCCCCCT	59.356	20	222	306	527
AAACAGGGTTGGGAAGAAGC	60.476	20	118	51	168
TGCCATTGCAGCTAGTCTTG	60.157	20	183	447	629
ACCACCGCGTACCACCTT	61.403	18	273	298	570
GGGAATTGGGCTGAGATTTT	60.265	20	210	67	276
GGGCAAAAATGCCACTCTTA	60.074	20	143	79	221
TTTGTCGGAATTAGGGATGC	59.901	20	127	3547	3673
TTGTTGCACCGTGGAGATTA	60.111	20	153	84	236
AATAGCAGCCAAGGCAGAAA	59.982	20	218	1510	1727
ATGCCGTTTGTGATCATTTG	59.4	20	241	7	247
TTGGTAAAGATAAATGCATCT	58.244	25	246	359	604
TTGGCAGCAACTACTACCATA	58.053	23	258	2356	2613
TGTGGTTGATTTGTGGGTGT	59.701	20	113	4	116
TGTAGCCGACCCCAATTTAT	59.297	20	228	1469	1696
TTTCGGGATGTTGCTAATGG	60.827	20	162	23	184
CTTGGTCTCGGGTTATGTTTTC	59.871	22	264	156	419
GAAATTTTGTAGCCGACCCC	60.673	20	105	91	195

CGATGCCCTTGAGAATCAAT	60.036	20	249	4233	4481
CCCACCAAGTATTAATATGCTC	59.335	24	184	0	183
CACGCTCCTCTCCTCCATAG	59.966	20	260	1772	2031
CCAGCCTAAATTCCATCACC	59.387	20	217	17	233
TTATCAGAGTCGAGCAAGCG	59.322	20	167	106	272
CCAATTTATTGGGATTAAGGC	57.539	21	202	1464	1665
GGAGAAGCAGCAGAAATCGT	59.579	20	165	407	571
CGGTTGTATGAAACCGTTAGAT	60.63	23	201	7	207
GTTTGCTGTGCTTGTTCGAG	59.64	20	250	1081	1330
GTTGAGCCGATTGACCAGTT	60.119	20	164	79	242
CTGCAGCCATCTGTTCTTGA	60.136	20	159	7	165
TGATGGGGAAATGGTTGAAT	59.991	20	247	782	1028
GTTTATTGCACCCAATTAGGAT	58.456	24	249	268	516
GAATTTGGGAAGAAATTTCAGT	59.033	25	261	192	452
TTCCAAGTTGGTTCATGTGC	59.547	20	256	30	285
CTTCACTTCCATCCTCTGCC	59.803	20	118	460	577
TTTAGACGGGCTCTTCTTGG	59.448	20	263	5702	5964
TCGACAACATCTCCGATCAC	59.637	20	247	1542	1788
ACATTTGCACGTGTTTCCCT	60.419	20	230	191	420
CAGCATCAGTGAAGCCTTTG	59.591	20	270	11	280
TAGATGCACCGGTTAGGAGG	60.088	20	277	1849	2125
TTCTGTTGGTCATTTTCCCC	59.767	20	280	627	906
CGCACTATGTTTTCCGATCA	59.688	20	132	1331	1462
TGAAATACCATCCAGTCTGTCC	58.912	22	264	12032	12295
ACTTGCCTTGTGACTAGCGTC	59.558	21	261	2360	2620
ACACCAGCCGAGAACATCAT	60.542	20	194	207	400
AGCTCAACCAAACAACCCAA	60.529	20	235	21	255
CGTACCACACGATGTTACCG	59.904	20	186	687	872
GCATATCTCACGCAAAGAACC	59.728	21	278	1353	1630
AAGCTGATCCGTTCCAAAAA	59.685	20	261	501	761
CAAAGCAACGAAACCACAAA	59.746	20	213	13	225
GGTTGAAAATGTAAAGGAAAT	58.2	24	167	29	195
AGGCCTGCACTCAAAAGAAA	59.993	20	200	2	201
GCGGACCGGCTATATACTTG	59.592	20	272	391	662
TCGATTGCTTAGATTGGTGG	58.721	20	171	14	184
GGATACATTGCATTTGGGAA	58.282	20	237	414	650
CCGGATACTGAAGATGAGGG	59.502	20	250	687	936
ATGAGTTGCAACCAAAACCA	59.024	20	112	42	153
TCAAAATGGAAACGTGGACA	59.941	20	197	0	196
CCTCAAAACCACCGAGTCAT	59.966	20	157	3	159
ATCATTCCTCTTGAATTTGGTG	59.828	23	260	58	317
GATCGGGTTTTTCGGGTATT	60.02	20	245	88	332
GTGGATGAGAGGGTTTACCG	59.405	20	249	1142	1390
GCCAACCCACCAAAGAAATA	59.801	20	263	615	877
TGTGATGTGATTGGGAGAAAT	59.797	22	205	754	958
ATCCATTTCACACCGGAGAC	59.786	20	273	299	571
TTCTCGTTCTCTTTCCTTCCC	59.813	21	243	10	252
TCTCCTTGGCCGAAAATATG	60.031	20	122	965	1086
TGCACATGCTTTAGTCCCAA	60.257	20	132	2025	2156
AGGAACATCGTTGTTTGGATG	59.845	21	226	184	409
CTGATGGTGATGGTGTTTCG	59.96	20	268	1938	2205
GCACCCCCACCTTACTTTCT	60.361	20	270	67	336
CCCAAGACCCCAATTTGATT	60.91	20	111	6	116
ACATTGGCTTGTGAGTTTCG	58.775	20	168	96	263
ATGGCATTGATGATGAACCA	59.738	20	230	166	395
CGGAGGTAGTTGGCATTTGT	59.993	20	229	326	554
GCGTAGTGAAATTTACGCCC	59.614	20	271	84	354
TGCTTAATTCTTAATGTAATAT	59.009	26	180	587	766

TAAGCCCCCAGAATCCTTTT	59.903	20	150	51	200
TCCTCCAAATTTCTCTCCCA	59.6	20	263	2804	3066
GTGAGGTGCATGTGGATCAG	60.121	20	246	240	485
TTTTTCACACCAGAAACCAAA	58.161	21	154	32	185
GGGTATGTATACTTGTGCCCG	59.238	21	142	638	779
GGGGAAAAGAGAGAGGTGGT	59.534	20	254	21	274
TGGAGTCGATGTTGATGGAA	60.048	20	170	1456	1625
TCGAACAAGTCCTCCAATGA	59.215	20	219	568	786
TTGGGCAGCCAAATATTGA	60.02	19	119	254	372
GCGTTGCTATCCCGTCTATT	59.209	20	270	301	570
ATCGCTGATGTTTGGATGTG	59.527	20	255	451	705
CCCAAGACCCCAATTTGATT	60.91	20	263	173	435
CCTCAACCAGCTTAAACCGA	60.241	20	261	406	666
AATGTGTGCACGAAGAGCTG	60.056	20	124	1799	1922
TGAAATCTGTCAACCCTCCA	59.059	20	238	202	439
AATCGAACCTCTCCACCTCA	59.655	20	103	219	321
GCGATTCGCCTTCAAATCTA	60.31	20	278	484	761
ATGATCAGTTTCCGGAGCAG	60.218	20	171	240	410
TTGGAGGATAAAATTTGTAACA	59.351	24	126	414	539
TGTAGCCGACCCCAATTTAT	59.297	20	108	1514	1621
GATGCTACTCCCACAAACCC	59.41	20	226	286	511
AGTAGATTCCGGGCCATTTC	60.286	20	202	564	765
AAGGAAACCACATCTAACCTG	59.817	24	268	8	275
TGCCCTATTTTTCCTCCTCA	59.64	20	191	17	207
TCGATCCCACGTATTGTGAA	59.924	20	105	75	179
CGATGCTCCTGTGTCAAAAA	59.84	20	193	1595	1787
CATGGGTAAGGTTGCGTACA	59.464	20	140	249	388
TCCTCATCCCCATCAACATT	60.135	20	161	155	315
AATGTTGAGCCCAACCCAAC	62.071	20	269	220	488
CCAAATCACACGCAATCAAA	60.501	20	224	1955	2178
GGTATTGGCTTTACAACTGGG	58.503	21	259	6	264
ATAACAGTCCTCGGCGTTTG	60.132	20	130	238	367
TTCGAAATTTGGTGTTAGCCT	58.753	21	177	1239	1415
TCTGAACAATTTGCAGCTCG	60.134	20	189	320	508
TAGGGTTTTGGAGGGGAGTT	59.799	20	189	86	274
CCCAAGACCCCAATTTGATT	60.91	20	200	781	980
AGTTGAATCACTTGCTCGGG	60.255	20	267	534	800
CGTCGGGTAGACCAATGACT	59.989	20	243	59	301
TGTAGCCTACCATTCCGTAGAA	58.787	22	187	1258	1444
GGTTGAAGATTCGGACGATG	60.461	20	174	1609	1782
TCGGCATAAAAATTGGTCAAG	59.95	21	266	71	336
TTGATTGCTAATTCAATTTTTAT	59.326	27	142	124	265
TGCAGACACTTCAAAGTTCCA	59.475	21	170	30	199
CCGGATCGGTCTTAACTCTG	59.688	20	233	962	1194
GGTGCAAAGGACATCGGTAG	60.517	20	196	4	199
AAATGCAGTATTGAATTACTTT	59.834	25	253	59	311
GTGGCCTGATCTACAGCCTC	59.834	20	269	86	354
TGGATGATCAAGGCTCTCAA	59.322	20	238	306	543
CTCGCGGCTAAATTTGAAAG	59.979	20	219	71	289
ATCAAGCAAGCGGAACTCAC	60.406	20	136	400	535
TGGCAACTGTACAAACAATTCA	59.132	22	251	582	832
ACATGTCAATTAAAAAGAAGGA	57.538	25	253	315	567
TTTCGTCCCTTACCCTTTGTT	59.858	21	224	3	226
CTTGCAAGGGAAGACGAAAG	59.986	20	215	245	459
ACTGCTAGACCCAGTGGTGG	60.174	20	197	0	196
ATTGAAATCAGACCGCCATC	59.9	20	280	98	377
GGTTGGGTTTAGGGTTGTCA	59.688	20	280	28	307
TGAATATCACAGAATTTGGGA	60.19	23	161	239	399

TGATGTTTCCATTGAGCGTC	59.654	20	152	44	195
ATGCATGGTGTAGGATCACG	59.399	20	224	423	646
GCCAAGGGTAAGAGAAACCC	59.94	20	205	2765	2969
CCCAAGACCCCAATTTGATT	60.91	20	267	653	919
ATATAGCCAGCCCAGCCCTA	60.93	20	237	1	237
CGCTGACACAGATGTTCCTC	59.42	20	277	758	1034
CCTTCAGCAATTCTTCCTGC	59.955	20	228	513	740
TGATGGAGAATTTGGAGGCT	59.629	20	273	4320	4592
ACTTCCTGGCCAGACCTTTT	60.11	20	190	5	194
ATTGTGCAATGGGAATGGAT	60.021	20	278	698	975
TGCAAAGCGAAGAGAGACAA	59.864	20	248	290	537
GCATGGATTCCTTGTTCGAT	59.9	20	110	397	506
CTACCCGGACTTGGATGTGT	59.844	20	202	260	461
ATGTAGCCGACCCCAATTTA	59.297	20	262	1736	1997
GAGAGAAGCCAGGGATGACA	60.349	20	190	29	218
AAACAAATGAACGATGCCGT	60.374	20	102	141	242
TGTAGCCGACCCCAATTTAT	59.297	20	275	3402	3676
ATTCTTCGGTTGGAGGTGTG	59.966	20	201	454	654
AATCAATGGAGCTGCAAAGG	60.214	20	101	154	254
TCAATCACCAATCAACAAAAC	59.708	22	203	156	358
TCGAATGAGAAAAACTGGGG	60.044	20	245	52	296
CGACGGATTGATGCTAATTG	59.136	20	250	705	954
ATCAAAAGGTCATGGGTTCG	59.79	20	125	13	137
ATGATAGTTCCGGTGACCCA	60.195	20	202	959	1160
ATGTAGCCGACCCCAATTTA	59.297	20	241	2467	2707
TGTAGCCGACCCCAATTTAT	59.297	20	105	13	117
GGGTGTTTTCTAGAGGCACG	59.734	20	163	869	1031
CAAGTAAATGCTCGGCACTG	59.488	20	188	1820	2007
TTGTGGGCTTTTAGTGCCTT	59.747	20	181	0	180
TGGACAGTAGCAAAGCCACA	60.449	20	277	329	605
AGCAAAATTGTTTGTTGTTCTG	59.183	24	109	318	426
TCAATGGAATCATTCAGGAGG	59.879	21	268	1915	2182
TAAAGAGACAAGCCAACGCA	59.609	20	269	1521	1789
TTGGAACCGCTTCTCAACTC	60.375	20	276	186	461
CATTGTCAATTTCAGCAGCG	60.401	20	246	23	268
AAGAACTTGCCCACACCATC	59.973	20	266	1230	1495
GAAGGGCAGTTGATGGAAGA	60.195	20	199	53	251
TCCCCGAATGTCACAACATA	59.774	20	104	2208	2311
ATGAAATTCCCGATAAGTTGG	60.855	23	212	0	211
GGGATTGTTATCGTGATGGC	60.163	20	246	152	397
CAGAAGAACCATGCCAAAGA	58.847	20	254	288	541
ATAGGTGAGACCGGGGAAAC	60.19	20	120	2796	2915
TGAAATATCATGTCCAGGTTTC	57.62	23	241	5	245
TCAATTTCTCCAAGCTGATGC	60.346	21	185	6	190
ATGGAAAAATTTGCAGAGCG	60.209	20	229	2918	3146
TTATCGGTTTAGCCAGCACA	59.325	20	274	762	1035
AATATGATGGTGCGGTGGTC	60.613	20	274	70	343
CCCAAGACCCCAATTTGATT	60.91	20	140	391	530
TTAAACCTACCCCTTCGCCT	59.96	20	221	1502	1722
ATCCGCCCTTGATACAGGT	59.376	19	181	2264	2444
CCTCCATCCTGGAATTGAAA	59.864	20	280	156	435
GATTGATGCAATGGGTGAGA	59.456	20	253	304	556
GGTGTTGAACAACCAGACATA	57.512	22	266	746	1011
TCAGCAGCCATCTGTTCTTG	60.136	20	244	43	286
CACCCGTGTTGAAGTTTTGA	59.585	20	197	21	217
TCGACCCGTGATACCAGACT	60.533	20	212	115	326
ACCATCACTCTGTGAACCGAC	60.025	21	129	59	187
CATTTTATGCAGCGAATGTTGT	60.027	22	164	22	185

TCTGGTGGGGCGAAATAATA	60.281	20	170	326	495
TCGATCAAAATAACACCATTG	59.838	22	239	1426	1664
GATTTTCGAGTTGCAGAGGC	59.962	20	184	1648	1831
CAGAAGGGGTTATGTCCTCA	57.582	20	262	107	368
AGGTGGTGTTTTCCACATCC	59.679	20	235	32	266
GGCAGCCTAATATTGAGCAGT	59.784	22	228	43	270
GCTCTTCAGGTGTTGGACCT	59.305	20	233	1458	1690
ACCAATGGTGGTATGGTGTG	58.984	20	130	202	331
AGGAGATGGGAGGTGGTCTT	59.929	20	183	20	202
CAAACCGGTGCTCCTTGTAT	59.993	20	254	2133	2386
GCACAATGCCAAGTAGCAGA	60.019	20	249	901	1149
ATCTGCAAAGTGCTGCTGTG	60.207	20	138	17	154
CGATATTCCTAGCTAGCTTTCC	59.101	23	232	725	956
TAGTCTGTGAGTGCCTGGGA	59.415	20	278	2942	3219
TCACTCATGCATCTTCCACA	58.728	20	249	8745	8993
CCTACTTGCATTGTGCTCCA	59.864	20	112	0	111
AAAGTCGCAATCAGCAACAA	59.469	20	180	1651	1830
TCTTTTACAAGGTGGGTGGC	59.971	20	147	427	573
CCTGTCAAAGGAGCAATGGT	60.111	20	185	351	535
TGTAGCCGACCCCAATTTAT	59.297	20	140	498	637
CCCAAGACCCCAATTTGAT	59.59	19	109	9	117
GATGGACGTCGACGATTTCT	60.081	20	261	158	418
GTAACCAGCAGTCCCCAAAA	59.971	20	146	230	375
CGACGAGAAAGTCGTGTCAA	60.025	20	222	262	483
CAGCCGAGAACATCATCAAA	59.799	20	267	0	266
GTTGGAAATTGCCTGCATTC	60.457	20	246	782	1027
CTTCCCTCTCAAAACCATCG	59.665	20	233	32	264
CCTTTAGAACTTGCTCCACCAT	59.653	22	268	16	283
GAGAAACAGAAGTTGCAGCA	57.743	21	105	2543	2647
TCAAATTATCTGCTTCCCGC	60.175	20	138	1264	1401
ACGTAGGGTTACCGGAGCTT	60.019	20	193	270	462
TGATGCAGACTCGAGGTACG	60.008	20	244	480	723
CCCAAGACCCCAATTTGATT	60.91	20	108	9	116
CACCCTACATGGTCTCTGCC	60.533	20	225	121	345
GGGAAGATTGGTGGTTGATG	60.173	20	204	4	207
ACCTCCTTCCACCACCTTCT	59.968	20	202	0	201
AACGGAAAAGCTTCGTTTGA	59.861	20	187	437	623
CCTTCATACCGAACCCTTGA	59.926	20	235	12	246
TGTTCCAATTACCTCGAACCTT	59.871	22	191	406	596
CCCAAGACCCCAATTTGAT	59.59	19	235	584	818
CCAATTCTTTTATGTGGGTTGC	60.577	22	228	1258	1485
ACACTTCCTTGCATTCGTCA	59.293	20	205	5	209
TTGATGGAGGCCTTATTTGC	60.038	20	259	294	552
GTGAGGACGGCAGAAGGTAG	59.867	20	219	469	687
ACAACCCCTACTCTTTTCTTCC	59.941	24	174	32	205
AAACAGAAAAGGATGCCAGC	59.316	20	154	1941	2094
TGAAGGACCTCCTGATTCGT	59.655	20	231	5609	5839
ACAATGGATGAAATTCCCGA	60.133	20	269	300	568
TTCCAGGTCCTCTGTCGTTT	59.697	20	146	101	246
ATTTCATTCCTTTTTCCTCCTTT	58.618	23	167	335	501
ACCTCATCGCCACCTAAATG	59.955	20	252	19	270
GCACTAGTAGATAGTGGTGCA	59.364	26	200	4	203
TGCCTGATGAACATCCAAAA	60.049	20	268	4	271
GAGGCACGGTCTTTATTGTGA	60.125	21	247	4	250
GACGTGGTTTGCAGGCTATT	60.14	20	103	471	573
TTTCACATTTTCAAGCGGAA	59.277	20	187	2	188
CAATCGATGCGCAAATAAAA	59.677	20	124	229	352
CCCAAGACCCCAATTTGATT	60.91	20	100	23	122

TTTTGCATCTGGGTTCCTTC	60.051	20	133	3068	3200
CCACCATGAAAGTCCCCTAA	59.784	20	200	1140	1339
TTCCCTAATGCTGCCTTTGT	59.708	20	179	37	215
GCTTTGGCAATCAAAACCTC	59.691	20	139	703	841
CAGCGAAGAAATTCACCCAT	60.074	20	240	3402	3641
ACAAGGGCGAGTCTCAAGAA	59.989	20	159	31	189
TCTCCTCTCTGCAGCCATCT	60.246	20	168	20	187
TCGATCGCTTGGATCTTAGAA	59.93	21	227	7	233
CCCTTATCCCGTGTTTTGAA	59.795	20	235	1526	1760
AATTACAGCATGAGCAGTCCG	60.285	21	202	27	228
TATAAGCCTACAAGGGGGCA	59.564	20	143	1586	1728
ATTGACAATGTACGCACGGA	59.995	20	249	3	251
AGATCTATGGCTTCCGCTTG	59.434	20	280	27	306
CCATAAATGCATGCAACGTC	59.96	20	114	264	377
GCAAAAATCGGCACTAACCA	60.999	20	162	7	168
CCGAAGTGCTAGACCCAAAG	59.869	20	130	122	251
GTCCAAACTGCGATTCCTTC	59.676	20	244	33	276
TGGAGTGATTAATATGCAATTT	60.563	26	249	31	279
ATCCTCGAGATGGGAAGAGC	60.703	20	126	31	156
TGCTTTCTTCAGCATGTTGTC	59.065	21	169	7	175
CCCAAGACCCCAATTTGATT	60.91	20	100	17	116
CCCAAGACCCCAATTTGATT	60.91	20	110	7	116
CCCTGAATTTGATCCTGGTG	60.309	20	232	1846	2077
CTGCTTTCTTGTCCTCGTCC	59.989	20	161	253	413
CAACAACAATTAGCAATCGAA	60.048	23	274	69	342
CCATAATTACCGGCGTCATC	60.175	20	193	303	495
TCTGCACATCTGAATTTACAAA	57.528	23	226	162	387
AATTCCGAACCTCGAGTCCT	60.074	20	181	770	950
ATGATCGGTTTCAAGGGTTG	59.79	20	205	1409	1613
CCTCTTCGGTTGGTTTTGAC	59.569	20	225	24	248
CGCAGTATACCTCTCCGTCC	59.717	20	278	358	635
GCTAAGGGGGAGAATGGTTC	59.903	20	142	5633	5774
TGGAGGACTAGATTTGGGGA	59.478	20	105	19	123
AACTTTGTTGAATGAGCCCC	59.031	20	280	500	779
ATCCTTGGCCCTTTTCTGTC	60.443	20	256	2	257
GGAAAGTGATCCTTGGGATG	59.336	20	116	9	124
GCATAGTGCAAGACCCCAAT	59.962	20	160	168	327
AGCAGCTGACTAGTGGTGGG	60.466	20	266	6	271
AATGATGACCTCATCTCCGC	60.042	20	146	935	1080
CCCAAGACCCCAATTTGATT	60.91	20	265	457	721
CCCAAGACCCCAATTTGATT	60.91	20	109	8	116
GCTGCATCAATGGAGCTTCT	60.514	20	276	1497	1772
CCTTGAAATCGAACTCTCGC	59.955	20	213	954	1166
GGTGATGTTGCCAGACCTTT	59.973	20	246	362	607
TTACGCTAGTCCGTGGGTTT	59.632	20	168	1039	1206
TCCAATGAGACACACTCCCA	60.088	20	220	1627	1846
TTCTGTGCATTGCCATTGAT	60.08	20	275	3	277
TAACTGACCTGCAGCGGAAT	60.796	20	279	689	967
CACCAAACTCAACCATGCAA	60.552	20	280	3193	3472
AAATGGTTCGTAACTGCCCA	60.365	20	221	354	574
GGGTTTAGACGTCATGCACA	59.572	20	222	46	267
CCCAAGACCCCAATTTGAT	59.59	19	104	17	120
CACCATTGGATGATGGTGAC	59.611	20	107	0	106
AAAGCTTCGTAATATGGGCG	59.234	20	151	2053	2203
TGGGAGTCAACTGATTGCTTC	60.248	21	212	673	884
GTCGAGACGGGACTGTGAATA	60.126	21	267	2144	2410
GATGGGCACATACTGGTGAA	59.374	20	175	4	178
CGATCGAGCTGAGAAAAAGC	60.235	20	279	4	282

GATTTTCTTGGATCTCATGCCT	59.559	22	262	614	875
CGCACTTGAAATTCCATCC	59.064	19	241	35	275
CCCAAGACCCCAATTTGAT	59.59	19	134	1	134
CAGCAGCCATCTGTTCTTGA	60.136	20	242	292	533
CCCAAGACCCCAATTTGATT	60.91	20	100	23	122
TCGTGTAAATTGGGTGGTCC	60.615	20	223	518	740
TGCAGCGCAAAGTCTACATC	60.165	20	206	6	211
TTTGCCGGTCGATAACTCTC	60.214	20	264	759	1022
TCGTGTATGGCAAGGTTCTG	59.716	20	260	29	288
TGTCTTGTGCTGAAGATGGTTC	60.299	22	263	26	288
ACAAGGTGGTGGCTCAAAAG	60.149	20	250	1527	1776
AAGCAATTGGAAGATGGTGC	60.081	20	213	651	863
GCCCATTTTGATCACCATCT	59.756	20	246	446	691
GGCTTATCCCAAGGTCTCCT	59.536	20	198	4966	5163
AATCCGTTATTTCTCCCGGT	59.666	20	258	723	980
GAGCTGATGGAAACACTTCG	58.443	20	276	1789	2064
TCCCATCTCAATCGTCACAA	60.048	20	274	7	280
AAAATCGCACGACGAATACC	59.967	20	167	751	917
CCTTCAATTGCCCTTCACAT	59.933	20	186	768	953
TTCCGACCCTTCAATAATCA	58.011	20	214	6	219
GGAAGATTCGAATAGGAACGC	60.054	21	214	2644	2857
CTTCCCAGCCACAATGTGTA	59.566	20	250	110	359
AGGCTGGTCTAAAGCGCATA	60.003	20	232	495	726
ATCTGATGTGAAATGTGTGGAT	57.865	24	179	19	197
TGTAGCCGACCCCAATTTAT	59.297	20	253	467	719
GCATTTTTCACTTAGCCGAGA	59.488	21	226	28	253
GGGTGAGGGAGAAAAAGGAA	60.414	20	237	130	366
GAGGATCGACTGCTCTGGTA	57.97	20	247	55	301
AATATAGTTATCACAGGATCAC	58.111	27	212	1406	1617
GGATTTCATCCAAAAACCTGA	58.868	21	274	2145	2418
GAGCAACTTCTTGGCTCGTT	59.621	20	113	160	272
AGTAGATCCATGTGGCCGTT	59.434	20	196	985	1180
CAGCATCTTCATCTGCCAGT	58.987	20	141	18	158
TCGAGTCGAGTGTGATACATTG	58.802	22	132	205	336
GTTCGATCGTTTGTCCTCGT	60.119	20	192	127	318
GTACGAAGGCTCATGAAGGG	59.694	20	172	1837	2008
TGTTCATGTCAGAGTGGGGA	60.088	20	279	2658	2936
GAGCAAAAAGACCAAACCCA	60.088	20	265	340	604
GCTGCACATATTATGCTTTGCT	59.437	22	257	6	262
ATTCGAAGGTGTTGATCCCA	60.317	20	209	174	382
ATGATCTGAAGAAGCGTGGC	60.37	20	260	89	348
ATCCCACCCTTCACCATTTT	60.422	20	117	2	118
CCCAAGACCCCAATTTGATT	60.91	20	183	870	1052
TCACAAAAATATTTCCCGGC	59.773	20	195	38	232
GAACAAAACATTTCGGGGTG	60.206	20	161	3872	4032
GGTAAAGGGCAGGGTGAAGT	60.361	20	207	9	215
TTCCCGTTCTCAGGTCTCTC	59.38	20	209	222	430
AATAAAATGTCGTGAGCCCG	59.96	20	149	11	159
ATTGCAGGGTCTTGCATTCT	59.7	20	230	628	857
GTGGTGGTCGCAGAGTTTTT	60.156	20	127	159	285
GGCGTGTTTGGGATGTTTAC	60.235	20	216	10	225
ATTTGGCATCCATGTACGGT	60.081	20	167	2002	2168
GCTTCTGCCTGAATTTGGAA	60.331	20	207	286	492
TCCAGATGCAAACCATGCTA	60.22	20	128	3311	3438
CAGAGTTGGGATGCCTCAAT	60.073	20	167	74	240
AGCCAAGAAAGCGCAATAAG	59.63	20	224	25	248
GCCAAGTTGACACACACAGG	60.203	20	145	35	179
GGGACCCTGTTTTCCAGAGT	60.349	20	260	16	275

ATGTGTCATTGTTTCGTGGAA	58.888	21	101	3	103
CAAAAGGTTTTTGACTCTTACC	60.077	25	172	409	580
TGGGCTTTTAAGGAAGACGA	59.817	20	230	522	751
ATTGCGTTGCTTAATGGGAG	60.096	20	275	263	537
GCAGCCAAATACACTCAAAAC	60.173	22	254	161	414
ATAGCCGACTCCGCATAGTG	60.257	20	236	4632	4867
TGTTTGAAATTCCTGCCTCA	59.247	20	230	82	311
AATCGAGAATGTGGACGGAG	60.073	20	203	846	1048
GAGCGTGCGGAGCTAGTATC	60.147	20	197	128	324
GGTAGGCTGGTAAGGGCTTC	60.096	20	199	7953	8151
GGTGGTATGCTGTGGAGGAC	60.395	20	131	54	184
CCCAAGACCCCAATTTGATT	60.91	20	248	530	777
TGCTTCCGTGTTTTATCCATC	59.952	21	111	46	156
CTGCAGCCATCTGTTCTTGA	60.136	20	202	5	206
TGGTGCTGGAGGTGACAATA	60.112	20	269	367	635
CAGACGCCAATTACAGGTGA	59.716	20	236	28	263
CAAAAACGAAAGCAAGCTCA	59.226	20	153	4587	4739
TTGTTGTATGCGGTGATGGT	59.847	20	191	8	198
GCTTCAGCGATCAACAAACA	59.995	20	213	1321	1533
CCTCGCCTTCATCGTAAAAA	60.202	20	198	9	206
AACCGTGTGCCCCTAAAAAT	60.593	20	232	6	237
GGAAAGTGATCCTTGGGATG	59.336	20	116	4	119
CCCAAGACCCCAATTTGATT	60.91	20	247	1144	1390
GCCATCGAGCTCCTTTTATG	59.807	20	196	32	227
ATGGGGTGTGAGGAAATGAG	59.779	20	188	571	758
AATTCGAAAGTTTGCCAAAAA	58.773	21	180	213	392
GGCCGATATTTTGGCCTTTA	61.096	20	205	37	241
TAAAGTTTGGTGACGACCGC	61.06	20	270	927	1196
CGTTTGACAAAAAGCGTCAG	59.507	20	225	496	720
TCATCATCAGGGGGAGTAGG	59.879	20	126	920	1045
AATGGAGTAGATTTTCCCATGA	57.552	22	152	205	356
CCCAAGACCCCAATTTGATT	60.91	20	104	16	119
GCATGTAACTCATGTGTCCCT	57.525	21	268	1136	1403
GGATTCGCAAGATCGACAAT	60.043	20	216	1108	1323
AGTAAAGGGTTTGCGCTTGA	59.883	20	265	936	1200
ACGAATTAGCGTTTGATGGC	60.103	20	267	2504	2770
GCTCCTGCACCAGAACTCTC	60.143	20	245	178	422
AAACATCTTGCCACAGGAGG	60.111	20	278	66	343
TCCAAATGTAACTCGACCCA	58.973	20	186	1338	1523
AGCAACTTCTTGGCTCGTTG	60.571	20	280	346	625
TTGGAAAGGCTGAAATGGAC	60.051	20	276	294	569
CCCATCACCCACCACATAAT	60.317	20	194	3170	3363
TGAAAATCCCGCTGCTCTAT	59.807	20	235	691	925
CCACCCCTAGCAAAGTTGAA	60.103	20	222	2615	2836
AGATTCGTCCCAAAAACACG	59.971	20	207	178	384
AGAAACTTGATGCTGGTCGC	60.406	20	181	1780	1960
CTGACTCTTCAGCCATCTTGG	59.997	21	208	466	673
CGGCGACCCTGATACTTTAG	59.724	20	185	918	1102
TAAGCAGCTCTTGCATCCAG	59.322	20	100	2	101
TTCGAGGGGAGTGTTGAAGT	59.697	20	275	43	317
TGAAATGGTAGAAATCGCCG	60.961	20	213	46	258
TGGATTATGTAGCTGACCCCA	60.337	21	150	293	442
TAGAAGGAAACCGAGAGCGA	60.088	20	225	749	973
ACAGAGGTGGAGCAGAGAGC	59.738	20	276	551	826
ATGGAGCAAAAGTGGACGAG	60.255	20	260	4	263
ATAGGGCAGGCCTAAGGTGT	59.983	20	249	400	648
GCCACACGAGGAATAGGAAA	60.074	20	223	735	957
GATCCGACACAGAGCCAAAT	60.081	20	171	996	1166

CAAAAGTTATTTTCGAGGACG	58.432	22	242	34	275
CATCCCAATTTCACCTTTCC	59.22	20	274	2809	3082
GGTCATGCGTTCAAGGTTTT	59.978	20	254	344	597
GATTTGATGCCACAGTTGGA	59.502	20	268	349	616
CATACGATTACGGGACCCAC	60.074	20	275	1214	1488
AGCTCGAAGTGGAAGACGAG	59.745	20	222	8	229
ATGATCCATATAGCCGACGC	59.914	20	245	1949	2193
CCTTCAGCAGCCTTTGTCTC	60.134	20	189	1104	1292
AGGGTTAAAGAAGCCGAAGC	59.856	20	267	45	311
TCGGAAGCTTCAAGTCCAAT	59.813	20	269	260	528
TAGGAACCGGATACAGCCAC	59.955	20	148	249	396
AGAGGCCGGATGATCTACAA	59.653	20	217	1	217
GTTGCCTGAGGACTGATGGT	60.12	20	239	1214	1452
AAGGACAGGACAGCCGTATG	60.134	20	268	820	1087
GGTGAAAAACCCGAGTTCAA	59.948	20	116	2	117
AAAATGCCCCTCTTCTCCAC	60.443	20	206	251	456
AACCCTAAATCTTCATCACAC	58.124	22	276	633	908
TTCATGTAGTCGACCCCAATTT	60.593	22	100	389	488
AAAAGATTTTACGTGTTTCACG	57.937	23	109	61	169
CTCATTATGATGCTCCGCCT	60.199	20	176	142	317
CCTCTTGCATATTGTGGCCT	60.096	20	227	204	430
TTGTTTTTCCCACAGGAAGG	59.942	20	162	2194	2355
TAGGGGAAGTCTCGGTCTGA	59.797	20	229	349	577
CAGCGCTATAGGTTGCTCAAT	59.532	21	139	836	974
CCCAAGACCCCAATTTGATT	60.91	20	178	2189	2366
ATAGTGCATCGTGGTTAGCG	58.824	20	249	375	623
GTCCCCAGAGATGAAAGAGC	58.818	20	205	6	210
GACAGGAGGAAATAATGAGAT	59.867	25	268	412	679
ATGTAGCCGACCCCAATTTA	59.297	20	224	307	530
TGACTACAACGACGATTCGG	59.716	20	252	117	368
TGATACTTCGCATCTCACGG	59.823	20	158	0	157
GGCTACATACATCCGCCACT	59.985	20	155	2	156
TTTGATTGGGAATAATTGGG	57.289	20	231	285	515
GGCCTGAGCAATGGAATAAA	60.038	20	266	165	430
TGCACATAATAGCTGCGTTTG	59.916	21	225	0	224
TCCCGGTACGACGAAATTAG	59.953	20	228	608	835
CTTTGTTGCACTAAGTTCCAAA	57.586	23	260	270	529
TCGATTGTCCACAATTGCAT	59.931	20	168	1520	1687
CGGCTAAAATCGGTCAAAAC	59.586	20	248	0	247
TGATGAGGATTCTGTGGTGC	59.637	20	170	67	236
TGTGGATATTCTTTAATTTGTG	59.318	24	206	565	770
CCAGCCTTCCAAATTACCCT	60.312	20	238	3196	3433
ACAGATTCGAGGCTACCGTG	60.277	20	175	3872	4046
AACCCGGATTGACACTCCTA	59.405	20	231	45	275
CCAGCTCTTTCTGAACCCTG	59.982	20	216	484	699
TGATGTTCCTGAAACGAGTGA	59.278	21	172	37	208
TTGGGACAAAAGAAGCTGAA	58.475	20	279	1931	2209
AGTGAAGGGAATGGAGGGTC	60.314	20	220	502	721
TTTTAAGGAATGTGCAATTTGG	59.022	22	200	26	225
GGTTATGGTTTTTGCACCCA	60.597	20	157	87	243
CCCAAGTTGAATTGTTAGTATC	60.928	24	280	381	660
CTGTAATGCATGGGGGAGAG	60.474	20	227	38	264
GGTCCATGAACCCTGGACTT	61.152	20	102	357	458
TGCCAAATAATTCCGTCTCA	59.112	20	258	158	415
TGCAGATATGGAGCAATTTTT	57.413	21	239	20	258
AGCATTGAACAGCCCAAGTT	59.74	20	207	0	206
CCCAAGACCCCAATTTGATT	60.91	20	132	180	311
ACTCTTCTCCCGTGGACGTA	59.721	20	245	288	532

CGTTACTTGCTGGAGCTAAAA	57.442	21	158	58	215
GAGGTGTTTTCCCACGTCAT	59.827	20	182	768	949
GGAAGAGTGGGGGAGAAGAC	60.05	20	143	595	737
CCAGCAGCAGACCAGAAAAT	60.397	20	231	30	260
TGCTCATTATTTGATTGGCG	59.662	20	216	12	227
ACGATGCACAAGACATGAGG	59.707	20	260	144	403
GCAAGACAAGCACAATTCCA	59.847	20	160	533	692
ACAGGCATAAGCTTCCCCTC	60.599	20	267	491	757
TTATCATCACTTTTGCCGGG	60.827	20	180	413	592
CCCAAGACCCCAATTTGATT	60.91	20	203	2634	2836
GGTCACAACGGAAACAACCT	59.867	20	229	1610	1838
TTTGATGCTCAACTTCCCAA	59.247	20	280	2136	2415
AACCCCTCGTGTTGTTTCAT	59.308	20	246	1235	1480
TCTCCTCTCAGCAGCCATCT	60.246	20	262	228	489
TTTGTTACATGCGGAACCAG	59.585	20	127	523	649
TTTTGGTTTCGGTTATGCAA	59.05	20	228	1080	1307
GAGGGGCTGATTGGTGTAAA	59.933	20	256	417	672
ATTTCCACCGTTCAGACAGG	59.966	20	276	51	326
TAGCAGGCCAAAGAGGAAGA	60.088	20	150	45	194
AATCAGAATGGTTGGTTGGC	59.797	20	193	80	272
GGGCCTGTGCTCATAGAGAG	59.973	20	271	883	1153
AAAAGAGATGCCAGGAAGGG	60.569	20	264	63	326
GCTAGTTGCACCCCTGTCTC	59.874	20	161	968	1128
TGTAGCCGACCCCAATTTAT	59.297	20	102	20	121
GGAAACCCCATCCAGAAGAT	60.133	20	200	655	854
AAAGCTCGAACTTGTGGCAT	59.882	20	270	1560	1829
TCCTTAGCCCAAGTTGTACCC	60.359	21	167	182	348
GACATCACTTGTGAAACCCG	58.984	20	242	2	243
GGACTTTTGATGTCCAATGGT	58.755	21	253	2150	2402
TGGGAATCTTTTCATCGACA	59.049	20	162	8	169
TGGGGAATTCACGGAGATTA	60.266	20	125	98	222
CCTTCGTTTATTGGGGATCA	59.756	20	268	1281	1548
CATCCAGACAACGCACTCAT	59.707	20	274	6892	7165
TCATCCCTGTGCATTAATTTTT	60.194	23	240	50	289
TCTTACCATGCTCACCCTGA	59.241	20	203	23	225
CCAACTTGCTAGCCTCATCA	59.024	20	257	933	1189
GCAAACAGAAAATGAGGGGA	60.051	20	258	414	671
ACCAGCGCTAACACGAAATC	60.278	20	280	76	355
GTCCCACCAATTTGTCCTAAA	58.798	21	133	560	692
ACTCAGAATTCCGATCGTGG	60.073	20	204	72	275
CTCTGGTATGGACTTGGGGA	59.92	20	151	177	327
AATCCCACAAACGGAAACAC	59.694	20	184	1475	1658
GCACCTCTTCTATTGCTGACTT	60.438	23	115	108	222
AGAAGAGGATGTTGGCGATG	60.218	20	186	27	212
TCCTGCATTTGTGTTCCTGA	60.24	20	196	217	412
TGAAGAAGCCCCTACAAGGA	59.807	20	238	8305	8542
GCTTGGGTGGTTGTGTACCT	59.891	20	212	1075	1286
GTCTCCAACGGCATCTCAA	59.778	19	259	453	711
CGGCTACAGGCTACTCGCTA	60.689	20	240	17	256
ACGTCAGCCTGTGGGTTTAC	60.035	20	108	13	120
CGTGCAACGAGAACTTCATT	58.926	20	187	2510	2696
GTAGTGGTATGGTGTGGGGG	59.966	20	276	647	922
CAAAATTCCATGACAACCGA	59.371	20	181	1223	1403
AACCGACACTTGCAAAAACA	59.22	20	274	52	325
TCAAGCTGATAGCTCCGACA	59.697	20	209	181	389
ACCTTCGTCAAGGCAGAAGA	59.989	20	214	4	217
ATGGGGTGATGTCGATTCTT	59.218	20	274	108	381
TGATCCACCCTATTTTGCATT	59.287	21	264	944	1207

TGAATTCTTGCACGTTCTCG	59.988	20	255	450	704
TGTAGCCGACCCCAATTTAT	59.297	20	204	5840	6043
TGTTTTCATTTGAATAAATACG	58.972	26	249	171	419
TTGATTCGTGAACATTAGGCTC	60.143	23	135	55	189
AACTCGAATATCTTGCCGGA	59.668	20	266	15	280
TGATGGCGAAGATGCTTATG	59.792	20	253	2230	2482
GCGATATAATCTCTGACGATTG	60.102	23	112	9	120
TTGCTTCAGCACCTTGAAGA	59.716	20	184	410	593
TCACTGGAATGTCAAGGCAG	59.831	20	102	163	264
CTTGTGAGCTACATTCCCGC	60.796	20	199	8	206
AGCGTTCTTTCCCGAGTCTT	60.382	20	100	10	109
ATGTAGCCGACCCCAATTTA	59.297	20	206	72	277
AACAGAGTTTCGCCAAGGAA	59.853	20	207	627	833
GCCGAGACCAACTCTCTACG	60.012	20	202	1194	1395
CCCAAAGACGAATAACAGCC	59.569	20	260	60	319
TACGCGGCCATCTCTATTTC	60.196	20	213	2051	2263
CCGGCAGTTACATATTCGCT	60.117	20	244	17	260
GCGTATCACCATTGCTGTTG	60.142	20	107	645	751
AGGTTGCGTACATCTGACCC	59.997	20	101	28	128
TGAAACGGCTCCTTAACTGG	60.241	20	274	231	504
ACAAACAATTCATTGGTGTTCT	60.182	24	179	410	588
TCTCTTGCATCACTATGGGAAA	59.708	22	262	98	359
ACGGACATGGCGTATTTCTC	59.962	20	271	678	948
GTTGGGCAGCCAAATATTGA	60.837	20	160	76	235
GATGCCATATGCGATGATGA	60.427	20	270	5	274
TGTAGCCGACCCCAATTTAT	59.297	20	122	1961	2082
ATTGACATCGAAATCCTGGG	59.75	20	232	25	256
TCTCGTTTCAGCACCAAATC	58.85	20	236	1310	1545
AGCTTCAGCTCCTCACCAAA	60.134	20	173	23	195
CAAAATCAACACCATGTCCG	59.816	20	234	6006	6239
CAAGTTGAATCAGAACGGCA	59.84	20	205	535	739
GGTTCAAGTGTTTGGGAGGA	59.943	20	168	345	512
GAGATGACCTACAAGGAAATT	58.694	24	171	608	778
TGGTCTCTGTCCATTGTGCT	59.261	20	161	42	202
CATCCAACATGAGGGAAGAGT	59.003	21	202	2499	2700
AACCGAGGTTTTTGCTTGC	60.242	19	183	21	203
GCAAGCGGAAATCACCAG	60.353	18	121	2255	2375
AGGAAGGACCTAGGCCTGAA	60.204	20	222	884	1105
TTGTTAAAATCTTCAAGCAATA	59.215	26	160	13	172
TCTGATCCCCCAAGACCC	60.835	18	110	19	128
CGAACCAGGCCGACTAATAC	59.592	20	221	1217	1437
ACTTTGAAGCTCGGAAACGA	59.993	20	217	39	255
CCGCATCGGCCTATTTACTA	60.075	20	150	280	429
AGTCACGAGCATGTTTGCAG	60.056	20	235	1792	2026
TTCCCTGTAGAGGCAATGGA	60.594	20	242	41	282
TTGCCAAGATTTTTGCTCCT	59.823	20	276	3	278
TCGTTGATTGTACGAGTCGC	59.871	20	200	91	290
GGTAACGTTTTCCGACCAAA	59.839	20	194	28	221
GCGAAAGGTTTTGGAAATCA	60.053	20	184	1412	1595
TCAGTCTCCGGAGTTCCATT	59.655	20	267	4443	4709
TCTTCCACAGATTTCCCATGA	60.445	21	171	392	562
TGACAATGATCCCCAAATGTT	60.044	21	270	1403	1672
CCCACTTCCCCATTCAATAA	59.617	20	214	170	383
AGGTTGCGTACATCTGACCC	59.997	20	212	3342	3553
TGTACTCAATGAAATAGGGTG	57.629	24	250	576	825
TTTTAGCCGACCCCAATTTAT	59.7	21	100	321	420
TGTCACACGTATTTTTGCAGC	59.79	21	249	69	317
TCGAGGCAGAGAGGAGAGAG	59.962	20	252	55	306

TGTAGCCGACCCCAATTTAT	59.297	20	176	302	477
TACAGTCCGTGTTCCGATGA	60.112	20	129	45	173
ATGTAGCCGACCCCAATTTA	59.297	20	133	91	223
CGCTTGAAGAGCAGTCAGTG	59.922	20	146	628	773
GTGATTTGGGGTGGATTCAG	60.173	20	202	186	387
GAATCCCCAACACATACGGT	59.532	20	197	59	255
CAATGTACCTTGGGTCGCA	60.523	19	187	154	340
GACCCTGGGGGCTATCTAGT	59.42	20	176	3	178
GCTCCCACCACAACCAAT	59.318	18	101	511	611
GTCTCCTTCCATTCCTTGGG	60.822	20	135	549	683
GCTGTGGCAGAAAAGAGAGG	60.134	20	214	607	820
AGCCGACTTCACATAGTGGG	60.134	20	122	577	698
AGGTCAAGGACTCGAAACCA	59.697	20	240	436	675
TGAGGACTGACGATGAGGTG	59.82	20	138	74	211
TTCTTGCCCGACTTCTGAAT	59.813	20	198	2	199
TTTTCGATCTTAGTCGGTCCA	59.693	21	272	881	1152
GACGTTGGTGGGATTTGAAC	60.218	20	204	1308	1511
TCGAAGTTTTGACGGGATTT	59.546	20	183	575	757
AGAATTCCGGTAAGCCCAAT	59.799	20	177	3763	3939
TTCATGTAGCCAACCCCAAT	60.192	20	158	7196	7353
CCCAAGACCCCAATTTGATT	60.91	20	247	54	300
GCAACAACAGCAGCAACAGT	60.104	20	240	674	913
AGAGCAGAGCAAAGCAGCTC	60.187	20	174	974	1147
AGGTTGCGTACATCTGACCC	59.997	20	108	317	424
TTTATTGGGGGAGAATTCTTGA	59.782	22	280	54	333
CATGTGAACATGGTGCATTT	57.804	20	147	2	148
GACATGGAGGAGGGACGG	61.494	18	114	213	326
AATGCTGTTAGGTGCATTGAA	58.307	21	204	222	425
GATGATGATGCCACTCTTGG	59.04	20	156	36	191
GAGCGAAGAACACAAGCACA	60.183	20	237	567	803
TGCTTGAAAATGCCGTTGTA	60.251	20	244	200	443
ACGGTAGGGGGCAAAAATAC	60.075	20	266	50	315
ATGGCTTGATTTAGCCCATTT	59.821	21	211	1	211
TTTCCTCAACCTCGTATTCTTA	60.02	24	258	731	988
TTTGATGTATGCGTCGCTGT	60.288	20	266	341	606
TGAAAAATGTGCGAAGTGCT	59.469	20	259	808	1066
GTTGTTGCTCCTCCTTCAGC	59.997	20	254	45	298
TCGCAACGGAAACAATCTCT	60.776	20	133	56	188
TAACCCAATCGCAGATTTCC	59.901	20	200	0	199
TTGCATACCTTCCGATCAAA	59.112	20	243	12	254
TGCAGATTGCGATGGATAAA	60.179	20	113	242	354
TCCCAGCACTCATCTGTTTTC	60.248	21	240	1054	1293
GTGCCTAATACTGTTTTACGTA	58.872	26	277	121	397
TTTGGTTCATGTAGCCGACC	60.894	20	167	3161	3327
TTGAATGCACAGAGAGATGGA	59.384	21	190	15	204
TGCCATGCTATCCTAGTATTCG	59.257	22	226	465	690
AGGTTGCGTACATCTGACCC	59.997	20	116	2	117
TGTGCGTTTTTGGCATAGTG	60.698	20	262	909	1170
TAATCCCAAACTCCCCAACA	60.162	20	277	2	278
AGGCATGATCAATCAGCTTGT	59.714	21	258	184	441
CAGCAATCGCAACTTCAGTC	59.596	20	268	536	803
TAGGCAAAAAGGAAGCATGG	60.202	20	183	20	202
ATGACGCGGGTGTTCTTATC	59.962	20	191	1093	1283
TTTAAGTTTATTCATTTATGTTG	57.211	27	278	152	429
GGCATCATCAATAGCTTGGG	60.435	20	244	41	284
AGGCTGGGAACCAATAATCC	60.152	20	160	7	166
TTCCCAAATCATCTTCACCC	59.727	20	147	183	329
GCACTCCATGCTACCCTCAT	60.104	20	190	4	193

AGCAAGCACGAGTGGAGTTT	60.058	20	151	364	514
CTTTTGGGCAAAGGATCAAA	60.046	20	265	68	332
CCAAATCCCCTTTTGACATTT	60.041	21	116	568	683
TGAGAGATAAAGCCGGGAGA	59.91	20	276	166	441
TTGTCATATGAATCATGAAATT	57.088	24	186	3	188
AGGCCGAAAAGTACAAGGCT	60.262	20	179	21	199
GTTTGAACCATGGACAGGCT	59.973	20	247	171	417
TCGATGCCAAAATGTAGCAA	60.215	20	253	100	352
GATCCTCATCCTCCTCCTCC	59.973	20	217	299	515
TTTGGATAAAGTTATCAAGCTC	59.326	26	258	1163	1420
CCGGAAAAGGGAAAAGAAGT	59.566	20	233	298	530
AGCAGTTCCCGAACCTGATA	59.694	20	174	3237	3410
TGTGGCAAGGTTTTAGGAGG	60.103	20	172	3859	4030
GGTTTACCACACAATTCAATCA	58.776	23	146	27	172
TTTCCCCAACCTCAACATTC	59.767	20	126	69	194
GGTGACCAAGTGGCATTCTT	59.973	20	205	188	392
TGACATTTTTATGCTAGTTTGA	60.189	25	267	539	805
TTTCGAAAGGCACAAGATCA	59.395	20	266	1085	1350
GGAACCCCGCTACAAAAGAT	60.32	20	258	1176	1433
TTGTTCTTTCAACTTGAGCCA	58.54	21	276	563	838
TGTGCCGTTGAAATGATAAGA	59.172	21	130	17	146
ATACGTCGCACAATGACCAA	59.995	20	195	2456	2650
TTCTTGCATGGGTATTGCTT	58.241	20	276	821	1096
TCCGAAGTCTCAGTTGGGTT	59.697	20	269	436	704
CTACCCTGGGTTTGTTCCTG	59.444	20	126	272	397
TACGGCTGCCTCTTGACTCT	60.156	20	254	1243	1496
AACACGATGGCGATGTATGA	59.955	20	250	180	429
ACTACCAGTCGGAGGAGCAA	59.867	20	161	632	792
CTTCATACGCGAGGGCTTTT	61.599	20	261	486	746
CATCATCGGGAGGAGTAGGA	60.027	20	182	1126	1307
TGTTAATAGGGCAAAATGCCA	60.321	21	200	20	219
CACAATTTCAAGAACCCCCA	60.724	20	256	18	273
AACTCAAACGATAATCTCAAT	59.06	24	173	11	183
AAGAAGCTGGAGCTAAGGGC	60.117	20	255	2374	2628
CCCCTTTGTCTCCTTTGTCA	60.081	20	250	1415	1664
CGCATCCAAATACTTGTTCG	59.182	20	247	256	502
GAGCAACTTCTTGGCTCGTT	59.621	20	227	37	263
CACGGGCACATAATGAACTG	59.988	20	231	1637	1867
GTGCAGTGATCGGTTCTTCA	59.837	20	246	298	543
TTCTCAGAAATGGCCCGTAG	60.206	20	256	1097	1352
GGATTCTTGAGCCAAAAACG	59.685	20	256	50	305
GTTTCAGGGCAGACTTGCTC	59.997	20	131	376	506
AAGAAGAAGCTCCTCCCACC	59.817	20	145	110	254
TGTAGCCGACCCCAATTTAT	59.297	20	269	1270	1538
TCCATGACCTTCGACTTTGA	59.215	20	275	574	848
CCTCTCGACTGGGTTTTCAC	59.697	20	273	2409	2681
GGCGATGGTGTTGTCTGTTA	59.572	20	260	186	445
CCTGAAACGAGTGATGCTCC	60.801	20	220	10	229
TGTTGAAATTGGACCAGCAA	60.088	20	261	2298	2558
GGACGGATCGGATATGAGTG	60.303	20	216	35	250
GGGGCTGCTGATAGTGTGAT	60.104	20	233	1616	1848
AGGCTTAACCAATTTTGGGA	58.556	20	258	64	321
GCGGTGACATTCTTCCAGAT	60.081	20	173	2202	2374
CAAAATAGCCCGAGGTTGAA	60.067	20	127	108	234
GCATGTGAGGGTGGTTGAGT	60.999	20	177	560	736
TTCGTGATTAATTCCGACCG	60.827	20	163	415	577
CTGCAGCCATCTGTTCTTGA	60.136	20	202	6	207
AGACCAGTTTTGCCCTGGTA	59.592	20	173	763	935

TCAACGACGAGCTGCTTAGA	59.888	20	118	12	129
AGTGTGGGTTCTTTTATTAATT	60.101	27	278	309	586
GGAATTGTTGTAATCTCGCAC	60.731	22	254	27	280
TTTTGTACGGGTCGGGTTT	60.213	19	176	51	226
ATTTGCTTACGGAAACAGCAA	59.772	21	203	43	245
CGCAATTTACAACCATTATCTT	58.625	23	163	2280	2442
TGTTCATCCGTGTTACCCAA	59.816	20	263	51	313
CGACTGGTCCGAATCTGAGT	60.261	20	117	876	992
GCGACATTTAAGAGTTGGGG	59.569	20	263	1093	1355
CCAAGTTCAGTCTTCTTCATCC	60.646	23	260	774	1033
TGGAAATTCTCCTCCCTTTC	58.161	20	177	1	177
GGCAAGGTTCGAGAAAATGA	60.192	20	211	178	388
CCACCAATTTCTATTTCCTTGC	59.844	22	220	16	235
TGTAGCCGACCCCAATTTAT	59.297	20	149	762	910
ATTTCGCACTCCAAGACACC	60.119	20	177	298	474
ACACCAAAGCCTTAATCCCA	59.429	20	129	38	166
TGAACACAATCAGTATCGTAA	60.514	27	143	153	295
TTGCCAACCTCATTTGTTTT	58.12	20	276	94	369
TGTAGCCGACCCCAATTTAT	59.297	20	154	257	410
GTACGCAATCATGCATCACC	59.963	20	135	101	235
AGATGATCCGAACGCAAAAC	60.081	20	230	5	234
GCCGCGTACTCTTGTCTCAT	60.428	20	257	161	417
TCATGTAGTCGACCCCAATTT	59.302	21	276	12	287
GAATCTGAAGAAGCCATCCG	59.773	20	159	9	167
GAGCTTCTCGATCGGTTCAG	60.096	20	165	15	179
TGTGTTGATGGAGCAAGAGG	59.831	20	172	54	225
AGGGGGAGAGTTCTCTTGGA	60.186	20	235	110	344
ACTCCCACCAGCACGATTAT	59.434	20	201	26	226
GCTGGAGCAAACTCTTCTGG	60.134	20	154	279	432
CATTGATCGTATTTGGGATCTT	59.693	23	236	99	334
TCAGGATTGAGTAAGCGGAAA	59.831	21	278	65	342
CGTGGCTGCCATCAGTATAG	59.322	20	198	0	197
GATCTCCTTCACCACCTCCA	60.048	20	161	286	446
GGCCATTGCCATCAACTT	59.456	18	262	7	268
GGAGCTAAGGGCTTCCAGAT	59.811	20	166	160	325
CCCTAGGCACGATGGTACTG	60.529	20	255	772	1026
ATCATGTGCAACTGTGTATGC	57.059	21	236	25	260
GATCATCAAAGCCCCTCAAC	59.488	20	100	10	109
TTCCACTTGCTCGACTCTGA	59.701	20	268	16	283
ACAGGAACAAAAATGGTGGC	59.836	20	175	574	748
AAGTCTGCTTGATGTGGCCT	59.874	20	276	554	829
TTGATTTCGCAATATGGTTTGA	60.315	22	275	226	500
TCCCATCTCCTTTGATGAGG	60.003	20	179	30	208
ACAACATGCAACACCAAACAA	59.92	21	182	381	562
TGGTGAAACCGGAGTCTAGC	60.255	20	204	83	286
TCCTGAAACGAGTGATGCTC	58.96	20	173	24	196
GTGGTCTAAACGGTGATCCG	60.375	20	218	6	223
GCGGTGAAGCTGACGTTTAT	60.278	20	159	634	792
TTTTGAGGATTCTGGATGCC	60.014	20	101	70	170
ATCCCCGGACAAGGATCTTA	60.652	20	105	82	186
CACACGCAGTGTTTATGTTGG	60.081	21	107	66	172
ACTTGTCCCATCAAAATCGG	59.79	20	150	10	159
GATGAGGAAGATGAGCCGAA	60.303	20	191	189	379
AGGAGCATCATGAGGAGGAA	59.761	20	159	85	243
AGGACCTCGAGAACGATGAA	59.803	20	100	38	137
CTCTGCACTTCGTCCTCCTC	60.135	20	267	67	333
TGTAGCCGACCCCAATTTAT	59.297	20	115	253	367
GAGGCGGGAAGGGTTGAC	62.969	18	231	188	418

TTTTTCTTATTTTATCCCGATTTTT	57.886	25	268	1591	1858
CATATCTCTCTTTCTCCTTCTCT	59.63	27	155	75	229
ACCCCACATAGTGGGAAAAA	59.146	20	242	3372	3613
GTGGGGAAAATGAGATGGAT	58.641	20	232	16	247
GATTCTGTGGTACGTGCCCT	59.997	20	183	478	660
GTTGGGCAGCCAAATATTGA	60.837	20	265	322	586
CGAGCCTGGATTCTTCTCTG	60.088	20	259	63	321
TTTCGAAATTGGGGGTTTTT	60.5	20	230	32	261
GCCCCTCGTATATAACTAAAGA	59.539	26	125	780	904
TAGTTACCGGCGTCATTGTG	59.609	20	163	734	896
TGGAGAAGTTAACCAAGGGG	59.024	20	107	229	335
GGGATGAGTTCTCTGGAGTTTG	60.11	22	277	417	693
CCCCCAGTGAACGAAAATTA	59.795	20	243	370	612
CCATAATTACCGGCGTCATC	60.175	20	100	20	119
TGCCGATAAGACCTCTATGTGA	59.73	22	237	503	739
GAAGATGAAGTGTCGTTGCG	59.445	20	227	1412	1638
TTGGGATTAAGGCTTTGGTG	59.931	20	216	726	941
TCGCTCGTTCTGATTTTCTG	59.148	20	143	488	630
CATTAGGGCAAAAGCCAAAG	59.715	20	118	54	171
CACGAACGGTTTTGATTCG	60.096	19	238	17	254
GTTGTTTCCATTCCGTGACC	60.218	20	155	405	559
TAATCATTCAGAGCCCAGCC	60.177	20	269	9	277
ACTGTGAGGAAAATGGTGGG	59.82	20	230	608	837
AGAGGTCGTGGACGAGGTAG	59.325	20	138	68	205
TTGTATGCCTTGGAGGAAGC	60.214	20	265	304	568
CATGTAACCGACCCCAATTT	59.546	20	163	4052	4214
CTGGTCGAACAACGAGTGTG	60.348	20	201	56	256
CAGTTTTGTGCGAGTTTGGA	59.881	20	213	20	232
GGGTTTAGACGTCATGCACA	59.572	20	241	92	332
AGGAAATGATCACAGGCCAT	59.366	20	237	244	480
CCCTTTAATTGGTTGGTTGGT	59.967	21	243	2269	2511
CTAGCCGGAGACCCTTTTG	59.815	19	137	47	183
AACAACCGAGCAGAAACCAG	60.291	20	149	338	486
CGGAGATGGAGGATGTGAAG	60.612	20	167	56	222
TAGCAAAAAGGTGTCCTGCC	60.249	20	182	43	224
CCCAAGACCCCAATTTGATT	60.91	20	175	1792	1966
CGTTACTCCCACATGCACAC	60.032	20	267	358	624
TGACAATTTATCATTTCCTGTAA	59.207	27	250	2472	2721
CCCTATCTCCGGGAAGAACT	59.531	20	135	48	182
CTATGGTGGATTGGTGTGGA	59.215	20	134	398	531
AAAACCAAACATGCTTCCACA	60.393	21	240	427	666
GGGGGAATTCATGGAAGGTA	60.881	20	230	862	1091
CCGGTACATGACTTCGAGGA	61.055	20	105	373	477
ACCAAGATTTCCGAAACCAA	59.406	20	214	4	217
CCTGAGAAAACTGATGTTCCTG	58.837	22	107	14	120
TGCACTTCATTTTCAATTTATGC	59.167	23	240	20	259
AGATTTTGTGTGGCGGGTTA	60.365	20	215	19	233
GCCCAATTTGTGAGAGTGGT	59.973	20	203	905	1107
CAAACATGGGAGGGTTTTGT	59.688	20	196	83	278
GCAGCTCCATGTCCTTGTTT	60.263	20	260	197	456
CAGGTTGACCTGTTTATGCAA	58.687	21	236	459	694
GTATTCAGGCTCGGACGACA	61.208	20	110	391	500
CCGTTTGAAGAGTTATGTGCAA	60.166	22	109	261	369
ACCATGAACTTCAAATGGTGA	57.908	21	242	984	1225
TTTTTGCCACATTCCCTCTC	60.051	20	274	67	340
CCGGTTAATGCACATCCCTA	60.712	20	248	530	777
TACGCTGCGCTGCACTAATA	60.706	20	254	10	263
CTGAAATAGGGGGAATGCAC	59.387	20	220	803	1022

GGCGAAAAATATTTCCAGCAA	61.24	21	194	805	998
ATTTGAGAACATTGAGGCGG	60.074	20	229	1141	1369
TCATGATGCATACGAATGATAA	59.373	24	237	1267	1503
ATGATGCCACTCTTGGCG	60.806	18	139	57	195
AGGAATACCGACGGACAGAA	59.55	20	279	3190	3468
TGGAAACCTCTATGCCATCA	59.075	20	244	2108	2351
TAGCAGGCCAAAGAGGAAGA	60.088	20	277	104	380
GGAAATGGACCCACAACATC	60.034	20	233	2044	2276
AAATCCTGTCGTATCGCAGC	60.243	20	256	3	258
ATGGTTTGATGTAACATTCCGA	59.205	22	260	297	556
AATAGAGATTGCACTCGGGC	59.297	20	258	797	1054
TCTAGCTCAATTCCCAACGG	60.206	20	199	181	379
TTTTCCCTAACTCTCATCCTTTT	57.568	23	254	444	697
TCAGCAGCCATCTGTTCTTG	60.136	20	196	101	296
GCATCATCATCATCAAGCATC	59.049	21	271	361	631
TTCTCAAGAATTTGGCACCC	60.051	20	178	3718	3895
AGGTTGCGTACATCTGACCC	59.997	20	232	1001	1232
AGATGACCTCTGTCGTGCAA	59.42	20	235	709	943
CTCGATCCAAACCACGACTT	60.111	20	263	48	310
GGTGAATCAGCAGGGGTTTA	59.933	20	182	248	429
CCTGCTATCGCTTGGAGAAG	60.11	20	211	105	315
ACGCGAGTTCAAAGCTGTTT	60.059	20	166	141	306
AATTTCGAGTTTCGGGCTTT	60.075	20	159	15	173
TCCAACCCTATCTATGGCTCC	60.293	21	229	252	480
GTAGGCGATTAGTGGAAGCG	59.867	20	272	1043	1314
TTTTCTTGAAAGTACGTACACTT	57.088	26	242	768	1009
ATGGCATGTATGGGTTGGAT	59.9	20	194	4	197
GGAGAAGGAGAAGCAGCAAA	59.694	20	161	444	604
AGAGGCAGCTTCTTCGTCAA	60.277	20	149	583	731
GGGTTTTTGTGCCCATTTATT	59.943	21	114	174	287
GAGATGGACGATGATGTGGA	59.431	20	172	172	343
CCTGTAAGCTCTGGAACGGA	60.388	20	259	32	290
CTCGGGATCAATGACATTCC	60.281	20	183	1	183
AGAGTACCCCACACGAAGACA	59.631	21	216	469	684
GAGTGGCCGACATTGAAGAT	60.081	20	260	101	360
GCCGAACCCACTGTGATATT	59.82	20	221	35	255
CACTGATCGTACACGATGGC	60.144	20	127	671	797
AACCCGAATAAAAGAACCCG	60.177	20	162	84	245
AACCAAGGGGATCGTAAAGC	60.32	20	269	0	268
ATATGTGGGGATAGGGGTGG	60.652	20	150	110	259
CAATTCCTTACTGAATTTGGGG	59.711	22	187	276	462
GTGATCCGTCCCCATCTAAG	59.361	20	270	30	299
TGTGGGACGGACCAAAAT	59.737	18	261	142	402
GGGGGCTATCTTGTGAGTTG	59.55	20	234	0	233
GGAATTGGAGTGGTCTGTGG	60.363	20	142	104	245
TTTATGTAGATATGGAGCGATT	57.561	25	238	367	604
TTCATCGACTCTCGCATCAG	60.096	20	238	440	677
ACAGCTCGCAAGATGAGACC	60.564	20	249	621	869
ACAACCTCAGGCTGCAAAAT	59.74	20	214	489	702
AACACGAACTTGCCGATTTTA	59.639	21	279	25	303
AATTGCAGGGGAACACAAAG	59.971	20	144	1742	1885
TTTTGTAACTTGAGCAATTTATC	59.966	26	199	1628	1826
CTCAGTAATCGCCTGATGGC	60.765	20	252	79	330
CGCCCAGTTTTGGTCATACT	59.993	20	141	44	184
TTTGATGAAATCAGTTGTTTGAT	59.355	26	174	3	176
AGCCGGAAAAAGGAAAAGAA	60.177	20	256	202	457
GCGTGCACAAAATGGTAAAC	59.09	20	260	42	301
ATTTAAAACCGATCCCACCC	59.888	20	274	163	436

CGAGAAGATCTTGAGGTCGC	60.096	20	102	72	173
TCGTTCATTCACGTAGAAGTTC	59.799	23	239	664	902
TTCAGCGGATTGAGTGTCA	58.88	19	217	23	239
AGCTGGATTACCAGTGCGTC	60.285	20	209	293	501
AGTTGCTTTTGTTTGGAGCG	60.42	20	159	486	644
GTCTAGGATCTCTTTCGCCG	59.031	20	263	1104	1366
CGAAAGAAACACACGTGAGA	60.318	22	226	224	449
CATCAACTCAACAAAGCCGA	59.84	20	114	1150	1263
AGCCTCCCTCTTTAGCCATC	59.811	20	221	176	396
TTGAATCCCAGATTGCATCA	60.009	20	208	633	840
GCAACGGAAACAACCTCTTT	59.218	20	169	691	859
TCCCATAGCATTTTTCAGCC	60.038	20	205	610	814
TCCACATTGGGTAACTTTCTAG	59.471	24	261	90	350
TGTGTGCATGTATTGACAGGA	58.558	21	171	2436	2606
TCGAACCTTCTGCAAAATAAT	59.253	22	279	712	990
ATGGGCATAGGATTTTGGGT	60.399	20	193	84	276
GGCAAGAATCCTCACCAAGA	60.195	20	186	1011	1196
TTTTCACACGTTTCGCATTC	59.712	20	155	30	184
CTCCTGCACTCCAATGTCCT	60.261	20	272	6	277
CCTGAAACGAGTGATGCTCC	60.801	20	204	103	306
ATGTAGCCGACCCCAATTTA	59.297	20	167	866	1032
GGGTTTAGACCGATGTCGTG	60.375	20	184	2406	2589
ATCTTGGAAGTTGGAATGGC	58.984	20	276	20	295
TGGTGAAACGAGAGCAATGA	60.39	20	198	279	476
AGTACGCCTCGGTGGTTAAA	59.632	20	207	50	256
TCGTAAACGAGTGTTGGAAAA	59.663	22	271	330	600
TATTCGGGCATCCCATAAAG	59.751	20	262	1189	1450
GACAACACTGGAGCTGTGGA	59.872	20	149	4941	5089
GGAGTGCATGCTCCAGACTC	60.989	20	112	93	204
GCAGACGTAGGAACGGAGAG	60.012	20	139	3	141
GGTTTACTCGCTCTTGCTCG	60.154	20	163	0	162
TTGTCATATGAATCATGAAATT	57.088	24	210	289	498
ACTATCATCCTCGGAGGCAA	59.653	20	232	153	384
GGCAGTACTTGAACCTTCGC	59.882	20	155	15	169
ACAGGAAACGTAAAGGCCG	60.118	19	218	39	256
GAGCGCATGTTCCAGACTTT	60.406	20	106	4	109
GCCTTTGGTCTTGTCCGTAA	60.11	20	120	458	577
GAATGTTAGCGACCCAGCAT	60.103	20	142	0	141
ATGTAGCCGACCCCAATTTAT	59.585	21	269	277	545
ACTCACCGGAGAAAACCTCA	59.697	20	205	103	307
CCATAATGTCCGGCTGAATC	60.296	20	101	22	122
AAATGGTGGCAATAACGGAG	59.823	20	265	600	864
CCCGAACACTAGTGGGGTTA	59.846	20	278	199	476
CACTCGTTTAATGTTACACTTT	58.053	26	280	192	471
TTTGTTTATCGTTTCCGTGTTTT	59.809	23	189	393	581
CCCGAACGATGTCAGTACCT	59.989	20	163	168	330
TGGGATGAAATTCAAAAGGG	59.733	20	148	67	214
TGGAATCCGAGAAAATCAGG	60.006	20	196	4	199
AAAAGTTTCCACACTTGCCG	60.147	20	254	100	353
TTCAAATATTCGACTCCGGC	60.038	20	213	40	252
GAGAGTCTTCCGACAAACCG	59.844	20	199	127	325
CGGTGGTCATTTTGGGGATA	62.75	20	181	114	294
TCCGACACATGAGCTATTGG	59.673	20	264	10	273
TTTTGGATCCACACCTTCAA	58.947	20	258	836	1093
CCACCCCAACCAAATAAAAA	59.537	20	204	19	222
TCCCACTAAGCTAGCTCCCC	60.723	20	132	63	194
TATTTGTGCCTCGTTTCGTG	59.729	20	205	20	224
TCGACCTGCTCCTTTTCAAT	59.813	20	224	1137	1360

ATAGCCGATCCCACAGAGTG	60.096	20	202	2387	2588
TTGATGAAGGCGGGAATATG	60.797	20	268	2462	2729
AGCGTAGCTTCAAGGATTCG	59.615	20	114	7	120
TACATAGCTGTGGCCTGTGG	59.74	20	172	5033	5204
CATGCCGAGTTTTTCTCATTT	59.215	21	276	344	619
CTGGGCAGCCAAACATAGAG	60.786	20	146	59	204
AACAGGGATTTTGAAGGTGCT	59.99	21	163	498	660
CCGACTAGGACTAAGGGTCCA	60.493	21	100	390	489
CTTACATCACATGCCCCACA	60.39	20	154	287	440
AAGAGATGGGGGTCAAGGAC	60.314	20	187	234	420
CGTCATCCCCCTAGTTCATC	59.361	20	196	1	196
CCCCTTCAACTCACACCAAG	60.536	20	256	1058	1313
TTTTCTTGCAGGTGTGTTCG	59.881	20	265	1038	1302
ATTCGTCAGTTCCACCGAAA	60.495	20	216	36	251
TACAGCTTGGTTTCGGAGGT	59.734	20	125	6	130
GGAAAAAGTGACTGGGCTTG	59.711	20	251	232	482
TTTGGTGGTTAGGGAGCTTG	60.103	20	165	669	833
ATTGTCAAACCAGCGAGAGC	60.406	20	186	353	538
ATCATGTTGTCCCCTTCTCG	59.927	20	274	3578	3851
CATTTTCACGTGACCCTATTGA	59.861	22	251	653	903
TTTACGTCGGAGGGTTCAAT	59.429	20	260	26	285
GCTGCTGTCCATGAAGTTGA	59.992	20	272	45	316
TTTGGTTCATGTAGCCGACC	60.894	20	140	874	1013
TTGGTTAATGTAGCCGACCC	59.823	20	203	47	249
CAGACCAGCTTCCCCTGTAG	59.861	20	208	3	210
CAGATCGGTTTACCACGACA	59.566	20	134	405	538
GTGTTCCGATAATCGCCAGT	59.962	20	138	22	159
AACAACATTAACAATCATGCC	59.288	23	213	1177	1389
CTCCCAAAACCTCACCTCCT	60.48	20	215	644	858
CCCACTAAGCTAGCTCCCCT	59.864	20	124	7	130
TTTATGTTAACGCACAATATTC	58.556	24	277	438	714
GGTGTGTTTCAAGGCAAATTC	59.467	21	254	1089	1342
TGAGGATTCTGTGGTTCGTG	59.676	20	166	77	242
TCTGATCTCCGGTCGACAAT	60.622	20	216	3081	3296
GCACAACAACCACTAATCCG	59.05	20	177	42	218
CAACTTGGCTACCCCTATCG	59.587	20	198	160	357
TTGAACCCGATTTCTTGTCA	59.097	20	175	321	495
TTAGCAATGTTGGTGGCAAA	60.111	20	210	3672	3881
AATTGCCGTGTGAAACCAAT	60.235	20	238	769	1006
GCATGTTTGTCGTCCCCTAC	60.384	20	262	2885	3146
AATTGCTGCAAAAATCAGGG	60.074	20	203	1548	1750
GCAGAAGCACGATGCTCTTA	59.326	20	154	766	919
CACTATGCAAATCAGTGCCG	60.28	20	160	236	395
CCTGTTTGAAATTCCTGCCT	59.17	20	236	56	291
GCAAATCCAATCATCTCCCA	60.812	20	273	456	728
AGGGCTAAGAGGAAAGACCG	59.842	20	249	22	270
CCATAATTACCGGCGTCATC	60.175	20	124	102	225
TTCCCATAATTACCGGCATC	59.621	20	107	228	334
CGTCAGAATATTTATTCCATGT	57.195	24	270	160	429
GGCGTAAACTAACTGGTGGG	59.494	20	240	47	286
ATGTAGCCGACCCCAATTTAT	59.585	21	118	2398	2515
CCGCTTCCTTTGATACCATT	59.043	20	161	1033	1193
ATCCCGGAAGAAGAACGAGT	60.074	20	263	860	1122
TGTAGCCGACCCCAATTTAT	59.297	20	152	1231	1382
CTCCGCCAGTGACTGTATTG	59.314	20	264	1299	1562
TTCCCCAACTTCTTCCTCCT	60.045	20	278	393	670
TTTCCAAGGCCAATGCTAAC	60.074	20	231	1689	1919
TTTCCTAAATCATGATGGTGAA	59.123	26	210	159	368

GGTTCGAAAACCGTTGTTGT	59.875	20	219	747	965
CTCGGATTGGATTTCCTCAC	59.483	20	107	10	116
TGGGGGAATGTAATATCATTGA	60.261	23	271	345	615
CTTGGCTCATTGCAAGCATA	59.976	20	162	823	984
TTGTGTCCGACCTTGTTCAC	59.571	20	167	5	171
CTCCCCGACTTCTCCAACTT	60.619	20	143	51	193
GTTCGAGTCTCAATGGGGAA	60.05	20	112	1902	2013
CTGTCTAATTTTGGTCGGCA	58.771	20	275	1796	2070
GAAGCGTGGGAGAAGCTAAA	59.592	20	266	28	293
GTAGATTTCGGGCCATTTCC	60.642	20	279	69	347
ACCAATGGTGGTATGGTGTG	58.984	20	149	81	229
GCCATTGCCACGATGAATAC	61.27	20	247	1189	1435
TCTTCGGGATTCTCCATGAC	60.011	20	225	36	260
GCGGGCAAATTTCTTTTTCT	60.547	20	102	348	449
GTCTTCTTGACGCCGCTC	59.663	18	101	25	125
CTAATGTTTCCTCCACCGCT	59.195	20	202	58	259
AGACTAAGGCGGAGTGAGCA	60.156	20	269	215	483
ATGTGAACCAAGTACCCCGA	60.232	20	273	33	305
GACGACGTACAGCTAAAGCG	58.752	20	175	9	183
ATGAGCCATAACCCTCCCTC	60.293	20	178	40	217
AAAACCCAGTTCCCCTTGAT	59.668	20	150	1134	1283
GATGTCGTTTTGACATCCCA	59.348	20	254	1	254
GATCTGGAGTCGTCGGTGAT	60.08	20	265	761	1025
CGATTCCACATATCTCCACAAA	59.823	22	259	387	645
TGTGAAACTTGACGGAATGG	59.541	20	209	583	791
TGGGTACAGGTTGTGGGTTT	60.126	20	196	94	289
TCCTGCATGGCTGTAAACAC	59.722	20	260	499	758
TGGGTTGCAAAATTAATCCG	60.671	20	217	667	883
CCACCGAAATCTTGGGTTTA	59.795	20	238	108	345
TCCTCGCTCTCTCCTCTCAC	59.817	20	133	701	833
CACAAAATTAAGCGCAAGCA	60.017	20	175	73	247
CCCAAGACCCCAATTTGAT	59.59	19	218	48	265
TGTCATGGGAGCTTAACTTAGG	60.136	23	183	58	240
AAACACTAGCAATGACACTTCC	59.265	24	188	24	211
CAGCTCAGGGGAGTTCACAT	60.261	20	191	211	401
CCCACTAACACCCCTCACAT	59.697	20	191	54	244
ATCGGAGGTTGAGTCTGGTG	60.112	20	275	43	317
AGGTGCGAGGGAGATTATGA	59.653	20	238	69	306
CGTTCATCATTAACCCCCAC	60.051	20	138	6	143
ACCAGGTTTGAAGTTGTCGG	60.005	20	163	1	163
CCTCTCTTTCACAGCCTTGC	60.134	20	237	1144	1380
CAACTTGATCCCTATCACGC	58.173	20	222	18	239
CAGGGCGTGACAGTAACTCA	59.897	20	258	773	1030
GGAGTTCACTGTGGGATCGT	59.969	20	273	609	881
AACGCCTTCTCGGTTGAGT	59.859	19	269	1424	1692
CGGGGAGGAATAGAATGCTT	60.411	20	168	35	202
CCTCAGCAAAGTAATTCCCG	59.702	20	248	128	375
CAACAGAAGACCCGAGCCTA	60.388	20	231	701	931
AAAAGCAGGAGATGACAGCC	59.434	20	247	525	771
TCATAACATCGATGAGTGTGGA	59.874	23	100	266	365
AGAAATGGGGCTTTTTAGGG	59.437	20	261	67	327
GGCCAACTGAAATTTGAAAGAA	60.451	22	176	3	178
CAAATCGGCATTATTTAATGGA	60.052	23	175	563	737
TTGGCTTATTGGTCTGGAGG	60.066	20	261	1583	1843
GCACATTTGGATTTACCGAGA	59.952	21	200	829	1028
CCGTCTAGGGCTTCAACTTCT	59.893	21	179	66	244
TCCCAATTTATAACACACTAAT	59.917	26	213	1035	1247
CCATCAAAACCATCACCTCC	60.173	20	160	212	371

TTTTTGTCAATGTGGGATTGAT	59.182	22	263	176	438
ATGGTTGCCTTTGTTTGGAG	59.971	20	141	227	367
ATCAGTCCCGTCTAGGGCTT	60.096	20	181	65	245
CGAGAAAGAGAGAGATGGGG	58.963	20	177	207	383
CTAGTCCGGTCCAAACCAAA	59.964	20	181	2209	2389
CAAGACCCCAATTTGATTGC	60.309	20	186	58	243
GAAGAGCGCCAGTATGGGTA	60.235	20	199	3971	4169
GTTCATGTAGCCGACCCAAT	59.82	20	186	2631	2816
AAGCTCCGCTCCATGAACT	59.965	19	238	905	1142
GAGAACCAGATTGTAGCGGC	59.843	20	115	402	516
TAGTGGATTGGGGAGGATGA	60.272	20	238	1814	2051
CTTTTGAGATAGGCGCTGCT	59.752	20	253	16	268
CATGCGGATCACCACATAGT	59.399	20	154	0	153
TCAAGCCAAATCAAGAAGCC	60.331	20	259	335	593
CCTTGCGCCCTTTAAAACTA	59.381	20	107	6	112
GTTGACGAGAGAAACTGGGC	59.851	20	260	564	823
GTCAGAAACCGGTGTTCCAT	59.827	20	268	407	674
CAATCAACCATCACATCCCA	60.177	20	218	10	227
TCAGAAATCCGATCCTGGAC	60.011	20	276	65	340
ACCCCAATTTACTGGGATCA	59.101	20	198	529	726
GCTGGGAACCAATCATCCTA	59.894	20	208	26	233
ACTCACCTCTCCCTCGACCT	60.258	20	234	14	247
TGATGCTTGGGATCTTAGGG	60.029	20	190	4	193
AGGTGAATTTGGTCCTTCAAA	58.54	21	279	671	949
AGATGTGGCACCTCCTGATT	59.535	20	108	0	107
AGATTACACGTTGGGCCTTC	59.056	20	182	2059	2240
TGAAAATAGTTGTGCCTGGGT	59.485	21	208	246	453
TTCCAATTCTCTGGGTCAGG	60.042	20	154	1112	1265
AGGGATATGTGGGTGGTGAG	59.655	20	139	853	991
TCTTCGGGATCACAATTTGG	60.832	20	275	413	687
TTCCACGATGACGAGAGATG	59.787	20	159	572	730
GGGTTATCACCTGATTACTACC	60.567	25	242	241	482
AACTTTGGTTCATGTAGCCG	57.757	20	107	280	386
GTGACACAAACCAAAGGTGC	59.037	20	222	16	237
ACCAATGGTGGTATGGTGTG	58.984	20	203	2	204
ATCTCAGCTTCACCTCCGAA	59.95	20	250	276	525
CGTTGTGTGCACCTTCCATA	60.574	20	250	2714	2963
TCATCAACGTTCTTGGGTTC	58.543	20	160	57	216
AGCCTTATTTCCCACCCACT	59.827	20	134	4114	4247
TGGCCACATCGTACTTCTGA	60.263	20	194	38	231
ATTGGCTGGATGTATTAGGATA	57.193	24	148	102	249
TGCGTCCTCATTGTTTATGC	59.694	20	268	974	1241
GAAATGGTGGTTCATTTGGG	60.029	20	175	2300	2474
ATGTAGCCGACCCCAATTTA	59.297	20	280	38	317
AGTCTGTTGAGCAGCAGCAA	59.929	20	266	822	1087
AACACTGGTAATGACGCTTCG	60.183	21	237	7	243
TTTGTATGCTTGTAGTGGTTCCT	59.162	24	215	274	488
ATCCGTTTAGGCAAAGGCTC	60.582	20	216	2140	2355
GAGGTGGAGCTGAAATTTGG	59.67	20	242	1802	2043
ATTCCTTCCCCGTCATCTCT	59.896	20	218	1703	1920
CTCCTCGCCTCCTACATCTG	59.966	20	263	145	407
ATGGTAGAAATCGCCGCC	60.973	18	196	6	201
TCCACCAATTTCTCCTCTGG	60.042	20	200	325	524
CCACAAGTTATCACACCCCC	60.088	20	210	243	452
GATGAGTTTTGGGTGATGGG	60.173	20	264	328	591
GGAAATTGAATAGGGGGACC	59.47	20	225	656	880
GTGTAGCCGACCCCAATTTA	59.823	20	100	256	355
GTTTACGGAAGCATGATGGG	60.331	20	157	3134	3290

GCCGGATTCTCTTTCGGTAT	60.419	20	233	15	247
GTCTGTGAAGTCTTCCGCGT	60.453	20	269	40	308
CGCAATGGAAACAACCTCTT	60.11	20	270	2177	2446
TGGAGACGGCGATAGAGTTT	59.836	20	270	1437	1706
GAAATGGAATGGTACGAGGG	59.244	20	146	617	762
GTTTCCGGAGATCACACAGG	60.51	20	141	187	327
TTTTGTCCACCCCTCAATTC	59.767	20	265	18	282
ATAATAGTGCCCCGAAAGGG	60.164	20	207	144	350
GCCGAATCTTGACTGTCCTC	59.81	20	209	41	249
GATTTTGTATTGCCCGTTGG	60.188	20	181	47	227
TGGAGTTGCAGATTTTTGGA	59.247	20	145	4726	4870
TTCAATGTTCTGTGGAACGC	59.697	20	150	10	159
TCTGCAGCCATTTGTTCTTG	59.988	20	263	250	512
TTGATGAGCCATAACCCTCC	59.894	20	239	87	325
ATGTAGGCAAAGGCTGCTGT	59.904	20	119	3	121
TCCCAGAAAATTCTTTTCCTTT	59.943	23	224	350	573
ATGGGAGGATTCCGTCTTTT	59.766	20	243	5379	5621
TTGCTCCTTAAAGCTCCTGC	59.73	20	209	2123	2331
AGCTTCAGCTCCAGGGTTTT	60.382	20	253	414	666
CACTTTGTGTTAATTTAAAGGT	57.158	24	226	53	278
AGTGGTGAGCGAAGGTGGT	60.729	19	224	275	498
GCGTCTCCAAGATCCCATAG	59.653	20	189	82	270
ATGTAGCCGACCCCAATTTA	59.297	20	176	1684	1859
TGAAGGTTTTGAATTCCATTGA	60.21	23	280	656	935
TGACAATTCCTATGCTTAAACT	58.032	24	188	132	319
CCTTTTCAAAGTGGACTATCAA	59.472	25	170	185	354
AGAATTGTGCACCACGTTTG	59.615	20	253	927	1179
TCCGAATCCGTAATGATCAAC	59.776	21	240	22	261
CGTCCTAGTTCTTGTATCAAGT	58.941	25	195	11	205
CGCCTAAAAAGTTGTTCCCA	60.103	20	197	3	199
TGGGGGATAAAGATGCAAAG	59.894	20	213	956	1168
ATTTCGCTAATGCGAGTGGT	59.736	20	215	2	216
ATGCGTGCAATGAACAAGAA	60.265	20	224	0	223
ATCTTGAATGGGCTTCTGGA	59.629	20	227	512	738
CAACGGCTGGTCCTTGTATT	59.993	20	267	31	297
CACGGGAATAAATTGTTGGAC	59.192	21	169	535	703
CAATCATGTACACCCGCTTC	59.002	20	197	147	343
TCTGGAGCTGGATGATGATG	59.743	20	228	733	960
TGAATGTACTTTAACCACTGCA	60.327	24	233	535	767
GTAGCCGACCCCAATTTGTT	61.099	20	247	766	1012
TTCTGGGAGGTATCTGCTGG	60.21	20	140	882	1021
GTGGATCATCAAGGTGAGGG	60.326	20	204	469	672
TAGTTGACCCCGCATAGTGG	60.904	20	159	229	387
TGCAATGGCTTTTCATTGTTT	60.482	21	227	186	412
TGTGTGTCCCATATTCGCTT	59.002	20	227	4603	4829
TCTCCCCCAATTTGTACAGG	59.784	20	168	4	171
CGCAATGTACCTTGGCTATG	59.206	20	147	704	850
GGGGCTCAATTCTAAAAGCC	60.041	20	170	1591	1760
CGTTACTTGCTGGAGCTAAAAA	59.64	23	177	83	259
CCCGTGATTTTTACCCATTG	60.046	20	248	15	262
ACACCATTATCTCCAGCTCCA	59.565	21	256	253	508
CATCAAACCCAAACCAACCT	59.688	20	160	281	440
TGTAGCCGACCCCAATTTAT	59.297	20	209	809	1017
TCCAAACAAATCAGCTGCAA	60.379	20	173	631	803
GCACTCGAAGAGTAGCGGTT	59.644	20	200	17	216
CAAGAAGGCGTTGGTGAGAT	60.255	20	278	550	827
TTTTTGGAACGGGATTCGAT	61.524	20	212	498	709
AGCCCCTTCGGTAAAAATGT	59.835	20	216	867	1082

CGAAATCTCACGACGCATTA	59.833	20	110	1673	1782
CCGTGTACACCCCTACCACT	59.762	20	260	814	1073
CCCAAGACCCCAATTTGATT	60.91	20	188	2452	2639
CCTTGCTCGAGATCCCAATA	60.17	20	233	265	497
TCAGATTGAAGAAAAGCCGC	60.469	20	141	1167	1307
TGTCGGTCAGCGATTCTTTT	60.776	20	267	980	1246
AATTCAATTACCTGCCGGA	58.024	19	202	31	232
TGGAGGGAAGGAAGTTGTTG	60.081	20	186	1826	2011
GTGGAGATTGACGATGCCTT	60.081	20	227	2	228
AACAAAGGATGGATTTGCCA	60.309	20	247	823	1069
AAGCAGAAGAGTGCATTAATC	59.471	23	237	273	509
CTCTGAACTCAACCCCAACC	59.549	20	136	4887	5022
CCCCCATACTTATTGATAAACG	59.88	24	245	65	309
CAGACAAATCTCAACGGGCT	60.255	20	262	3826	4087
CAGCTACCCATCTGCCAAGT	60.277	20	228	421	648
CATGCAACAGAAAATGCCAC	60.119	20	267	1	267
TGCAAAGCATACTTACAGAAA	61.017	24	223	4	226
TCCGCTGAGATAATGCTCGT	60.905	20	269	4226	4494
ATCAATGCACCAAGTGCAAA	60.119	20	171	792	962
TTTAATTAGTTCCACGCGCC	60.095	20	247	2216	2462
CAATTTCGAACGTATTTTTACA	58.246	24	198	1074	1271
TCGAGCTGTCCTTCAACAGA	59.701	20	166	152	317
CTCTCACCCCAATCCCCTAT	60.147	20	205	502	706
TGAATTGTGTCTGCTTCGGA	60.39	20	250	977	1226
ACAGCTACAACGAGCCCACT	59.937	20	255	728	982
AGATCATTCGCCAACACCTC	60.081	20	151	789	939
ATGGTGACAATCGTGCTGTC	59.557	20	161	1100	1260
TGCTCGTCAATGATTTTTGC	59.816	20	260	2218	2477
TGAGAGGACACCCAAGTGGT	60.563	20	170	5	174
TGAGAATTAGCAATTGAAGTTG	57.791	24	263	537	799
TTGCTGGCAGTGAAGCTCTA	59.888	20	215	619	833
GGAGGCCCTACAGAGGAAAC	60.074	20	225	16	240
CCCTAATCTCCCTGACCTCC	59.89	20	271	527	797
TGCTTGTGGACCAAAGATTG	59.691	20	142	1462	1603
CCCCATCCCTAAGAACATCA	59.744	20	228	193	420
TGTTGGTGTTGCTATTCCCA	59.964	20	184	364	547
GTGACAACGATGGATACCCC	60.057	20	230	65	294
AGGCCACGTAAATACGAACG	60.018	20	258	804	1061
TGCTTTCTCTCTCCTCCCAA	60.065	20	223	1616	1838
GGAGGTGGGCTCTCATGTAA	60.073	20	243	272	514
GTGTTCGGGCTAAATGTGGT	59.859	20	129	29	157
TGGGCCGATCCTATCAATAA	60.247	20	158	1006	1163
GACCACCTGCATTCACAGAA	59.682	20	256	622	877
ATTTGGAACCTTGTGCGTGT	60.419	20	186	195	380
TTCCCTCAACCTAGACCTCG	59.28	20	143	26	168
CGTAGTGCATGTCTGATTCTGA	59.95	23	255	967	1221
ATGCCACATAACGCATTCAA	59.96	20	267	569	835
ACCAGCATTTTCAGAGCCAC	60.263	20	188	240	427
CAGCAACCACGTACCATGAC	60.032	20	203	5712	5914
CCCAAGACCCCAATTTGATT	60.91	20	176	2377	2552
GGAAACATCAACACACGCAT	59.425	20	247	523	769
TGAGTGCGTTTGTACTCAACC	58.84	21	181	99	279
TCTGGATAAACCCACGGACT	59.405	20	234	12	245
AAACGCATTTTGGAGTTTGT	57.275	20	186	43	228
GCTCTCACTGCCATGAATGA	59.95	20	184	835	1018
AGGCGGGACTGTGAATAATG	59.955	20	151	464	614
CAATGAAGACTGAATCTCGGA	59.312	22	182	1061	1242
TGAAAAATCTCGAAGCAGGG	60.323	20	256	44	299

GCACCAAGACCTACTGAGCC	59.874	20	244	332	575
GATATCCGGTTTTGCTCACC	59.391	20	189	324	512
TCATCAACTCCCCTCCATTC	59.862	20	249	944	1192
CGTGTTAAGTTGTTAACCAATA	59.456	25	171	93	263
TGCACCAAAGGAGGTTCTCT	59.844	20	238	251	488
ACACGTGTGGAGTGGTGAAG	59.623	20	227	31	257
GTGCACAATCACCAAGATCG	60.12	20	233	876	1108
GATTTTGTAAACTGCCCGGA	59.938	20	114	508	621
GCATATCTTGGGGGCATAAA	59.757	20	275	1	275
ATACTTGCCGTCGCCTATGT	59.62	20	278	31	308
CTGACTGACGTGGTTTGCAG	60.5	20	241	62	302
AGGTTGCGTACATCTGACCC	59.997	20	250	1220	1469
TTTCTGTTGTCAGCCCACTG	59.873	20	233	672	904
TTTTGTGGATATTTGTTTATTGT	60.054	27	175	661	835
TATGCGATGATTGCAAGGTT	59.14	20	264	477	740
TAGGCATGGATTGCATTTGA	60.035	20	114	334	447
CAACATTGGATTCGAAAGGG	60.301	20	219	171	389
TGAATGGAGCTACGGTGAAA	59.272	20	118	17	134
TCCAATTTTCTCGCCTAAAA	57.52	20	185	962	1146
CGGTGATATAGCCGAAATTTTT	59.428	23	276	9	284
CCGTGTGATAGGAACCATCC	60.195	20	199	593	791
GATCTTGATGTTGTCGCTCG	59.399	20	187	169	355
AGATGCACCGGTTAGGAAGA	59.694	20	176	80	255
CCAATATGGTTTAAAATTCTTC	59.976	24	253	47	299
ATCTCACATACATATAATTGAG	57.101	27	241	217	457
TGGAAGTAGCAGATTGCGAA	59.566	20	232	385	616
TCAAATCAGCTTCTTGGTTGC	60.38	21	252	478	729
CAGGATACTGGCAAACAGCA	59.864	20	260	2585	2844
CCCAAGACCCCAATTTGATT	60.91	20	125	3	127
GACGATCACCGGTTCTTGAT	59.934	20	164	264	427
CCTGAGGATGAAGTGGAGGA	60.191	20	190	86	275
CCTTCGCACCACTTCACTTT	60.291	20	237	293	529
CCTCAGCGTCTTGAAAATCC	59.813	20	251	587	837
GTCGCCTCACCTTCATCTTC	59.81	20	264	46	309
GATGATCCACGCAACTCAAA	59.654	20	102	232	333
TGGCATATTTATCGGGCATT	60.137	20	233	17	249
CCATAGGTGGGGATCTGCTA	59.91	20	167	6	172
GCCCAATACGTCCATTTGAA	60.701	20	134	2577	2710
GAGCTTTCCCACTGTATCCG	59.694	20	254	388	641
GTTCCATGCTTGTCTGCTCC	60.812	20	109	438	546
GCGGATTTACAATTCGTGCT	60.103	20	230	903	1132
AAATCGGCTGAAGTCTGCAC	60.406	20	272	2084	2355
TGTAGCCGACCCCAATTTAT	59.297	20	103	341	443
CCTCCCTCTGCATTCTCAAC	59.803	20	276	374	649
GGGAATAGCCCACCAAACTT	60.187	20	185	1080	1264
AAAGGTCAGATATTGAACATC	59.647	25	175	4388	4562
TGTAAATCCGGAACTGGAGC	60.074	20	229	938	1166
AAATTTTCACCCGCAAAGAA	59.564	20	224	2525	2748
TACCGACAATTTTTGCTCCG	60.989	20	179	283	461
TAACCCAGGCCATATACCGA	60.167	20	201	23	223
GACACACACCATTCCCAACA	60.27	20	196	1289	1484
CATTAGGCTTGGGAGACGAA	60.206	20	196	670	865
GGTGACAAGTGTTTGAGGGAG	59.607	21	108	916	1023
GAGCTTCTTGATTCCATGTCA	57.878	21	252	973	1224
GGTCGTACTGGTGCCTGAAG	60.711	20	226	704	929
CCCCAGGATCAAATAAACCA	59.617	20	182	7	188
TGGTGGTAATGCCAAGAGAG	58.722	20	239	246	484
TCGAACTTGTTCAGGCACAC	59.88	20	249	1444	1692

GACACAGAGGCTGACGATGA	59.988	20	115	15	129
CCGCCTCTATTTCCGTAACC	60.811	20	265	163	427
CATCTCCGGAATCTCGACTG	60.758	20	221	287	507
GGAAATAAATGGATTTTCGTG	57.992	22	271	442	712
TGTTCCTTTACCAGAGGCGT	59.734	20	170	92	261
GATCCGTAAAACACCGTTGG	60.227	20	238	24	261
TGAGCTGGTAATTGCCACAG	59.864	20	243	2591	2833
CCATTGGTACAAAAGTTTGCC	59.37	21	110	6	115
GATGTACGCAACCGTACCCT	59.882	20	171	2095	2265
GGCACTGTCACCGGATTATT	59.82	20	273	243	515
TGTAGCCGACCCCAATTTAT	59.297	20	127	6	132
AGAAATGGATCCGAATGAGAA	59.909	22	231	278	508
TTTGATTGGGAATAATTGGGT	58.163	21	280	1731	2010
GAAGAATTAGTGGAGGGGCA	59.126	20	163	195	357
ATCGTGTGGTTCGAATATGAA	59.343	22	151	38	188
CAAATGGGACAATCCATTCC	59.991	20	175	37	211
TGACCTTATGGGGTACTGGG	59.665	20	232	55	286
TGTAGCCGACCCCAATTTAT	59.297	20	156	274	429
AGGAAGTGGGTTCTGTCCAA	59.549	20	275	3874	4148
GCCAACTAAGCGATCCATGT	60.103	20	158	935	1092
GATGATGTTTGGTGGAGAGGA	59.918	21	187	47	233
ACCCTGGCCATCTTCTTTCT	60.074	20	133	9	141
GCCAGAGCTCTTTCACAAGG	60.134	20	177	1307	1483
ATAGTGGTATGGTGTGGGGG	59.405	20	190	361	550
GCCTGCATGATTTTTATGGG	60.289	20	273	3320	3592
CTTTCACACTGTTGCACCTCA	59.93	21	129	0	128
GCCATAGCTGATATAGCGGG	59.688	20	234	282	515
CTCCACTTTTCGAATGTCCC	59.526	20	266	6096	6361
CACAAGAAAATCCATCGCCT	60.074	20	101	3	103
AAAGCCATATGCGGTAGGTG	59.982	20	277	0	276
AGAATACCAACAACTAAATAC	58.064	26	267	196	462
TGCACCGTGTGCAGTTATTT	60.18	20	219	127	345
ACCAGCTCACCACCACTTTC	60.159	20	264	2104	2367
TTTAGTTAGCCCTTTGAGCCTT	58.653	22	232	1	232
CCTTTTGACACAAGAAAACCC	58.589	21	224	169	392
CGACCTCCACCTCCTGTTAG	59.715	20	187	286	472
AAACGAGAACTATGAAGCACC	58.906	22	227	4	230
GAACGTTTCTGGCAATCTCC	59.676	20	211	574	784
TTCTTCTTCCCTTGCTTCCA	59.926	20	197	794	990
GGGTCAGATGTACGCAACCT	59.997	20	262	972	1233
AATCCACATTATTTCTCACTCA	58.455	24	220	34	253
TCATCCTCGGAAGCAATCTC	60.303	20	264	37	300
TTTAGATAAGCATACACCATC	59.08	26	187	545	731
ACGTCAAGCTGGCATATCCT	59.723	20	168	201	368
GGGTAAACCCACGGACTAGC	60.743	20	111	8	118
ATCTCCACCCCTTACAAGCA	59.55	20	232	304	535
ACAGGCACCAACCAAGAGAT	59.579	20	195	231	425
TTCCGGTCTCACAGTTTTCC	60.088	20	259	147	405
CACACGTTCTTGAGGGAATC	58.129	20	238	509	746
AGGAGGTGGTGGTGAGGAAT	60.77	20	126	2	127
ATTTTACGTCACACAACTCGA	57.364	22	139	2785	2923
TCAATGGTTAAATTGGTATTTG	57.935	25	199	108	306
ACTGCACCTGAATTGCATTG	59.722	20	197	3	199
AATCCCATTTTGATCCGTCA	60.133	20	234	720	953
ACTCGCTCGATCGTTGTTCT	60.02	20	205	476	680
CCGAGACCCCAATTTGATT	59.735	19	119	20	138
GAATGCAGCATCATCACACA	59.202	20	261	1794	2054
GAATGCAGGTGGAAATGAGG	60.461	20	110	351	460

TCATTGAAGTGACCCAACCA	59.935	20	235	2475	2709
ACTGCAACCCGTAAATGGAA	60.365	20	218	3138	3355
CATCCCAACCACGTTAGCTT	59.993	20	185	1619	1803
CTCATGTGTCAAATTGGCGT	59.572	20	125	163	287
TCCAATCAAGTCGACAAACG	59.691	20	133	163	295
TGTAGCCGACCCCAATTTAT	59.297	20	170	460	629
CTTCATCATCCTCATCCCCC	61.604	20	248	3159	3406
AGGTCATTGCAAGGAATGCT	59.7	20	273	3509	3781
CGGTTGTTTCAGACTTCGTG	59.335	20	276	301	576
ACCAGAGAAGAGTGAGGCGA	60.135	20	231	264	494
CCTGTGTCAGGGCTAGCTTC	60.012	20	201	514	714
CAGCGACTGGAAATCAAGG	59.379	19	122	7	128
GCGGTGTATGTCCCTCAACT	59.997	20	249	5	253
TGCAGAGATGGACGTGTTGT	60.319	20	149	1551	1699
ATAATCCGGTCCCTTCCAAA	60.502	20	245	155	399
CTTGCTCGAATTCTTAGCCG	60.11	20	167	255	421
CCAACCCGCCTTATCTAAAAA	60.304	21	230	448	677
GGAACTTGCGAAAATGGAAG	59.685	20	152	65	216
AATAGCGCTTGATGGGAGG	60.185	19	199	121	319
TCACTTCATAAAGTCCGCCC	60.074	20	153	123	275
TTCCGTCGTCTTTCTTTGCT	59.993	20	151	4033	4183
TCCTCTCGATCCTCGTTACA	58.387	20	103	8	110
TGTTGCTCATGACAAATTCAAT	59.996	23	135	1354	1488
GGATCGACACGGTAAGGACA	60.924	20	270	158	427
GGGTCACACGAAAGTTTACAA	58.675	22	190	465	654
CTAGGCTCCCATAGTGACCG	59.711	20	111	48	158
CGTTCAAATCACCAACATCG	59.964	20	276	364	639
GCAAGTTGGAAGCCTTGACA	61.355	20	224	18	241
GGGGAGAAATGAAAAAGGGA	60.237	20	173	21	193
AAGGTTTTAACAGTCCTCCGAT	59.453	23	227	4096	4322
AACTGAGACTTCTGGCGAGG	59.598	20	273	72	344
AATGCCAAGAGCAAGACGAC	60.406	20	160	3643	3802
CCAAATGAGCTCGGTTGATA	58.721	20	277	585	861
GAGCAAAGACTCACGAGCAA	59.318	20	280	326	605
ATTCCCACACGTTCCCATTA	60.051	20	201	223	423
CAGCCATGAATATCAGTCGAA	60.096	22	235	489	723
CACATTAGAGCACATGGAGGA	58.736	21	217	331	547
CATGCTTTTCGTCTCGCATA	59.976	20	135	188	322
GCTAAAGTGCCTCGTGCTTC	60.162	20	169	4279	4447
TACATGGATTTCCAGCAGCA	60.22	20	149	10407	10555
CGAAAGGGAGATTTGAGCCT	60.703	20	268	495	762
TGCACTGCATTTCCTTCGTA	60.401	20	196	126	321
CCACCATCATCTTCCCATTC	60.135	20	279	479	757
TTTCAGGTTGGGATGAAAGG	59.903	20	215	0	214
TGCATGCGATTAAGTAGCCA	60.378	20	274	4272	4545
GCCAATTCGTCTCGTGATTT	60.081	20	193	273	465
ATTCTCTCTTCTTCGCCACG	59.574	20	262	67	328
TGGTCCCAAAATCGACGTA	59.909	19	253	120	372
CAAATCCACCGTCCAAAAGT	59.83	20	239	11	249
TGATCAAAATCGAGAAAGCG	58.991	20	260	438	697
TGAAAATGAATTGGGGTGGT	60.029	20	276	1880	2155
CAGCCCTTAACTGCCAAAGA	60.378	20	258	3	260
TTCCATCTAAGGCTCCCAAG	59.264	20	251	1	251
CTTTGCACATGAACAATCACA	58.172	21	278	682	959
GCCATTGAAATTACCTGCAAA	59.957	21	121	22	142
AAACTGCTGAGACGGAGGTG	60.444	20	100	338	437
TTCTCGCCCTCTAAGGTTTTC	59.843	21	274	566	839
GATTCTTTCGTGGAGTCCGA	60.195	20	134	398	531

CAATCCAACCCAAGGTGAGT	59.82	20	153	107	259
TGAGGGGGAAAAGAGAGGAT	60.008	20	279	1119	1397
CCCCAATAAACCAAAAACCC	60.265	20	271	2585	2855
TTTTCCATTGGCATAGTTGAA	58.148	21	262	957	1218
ATGAGCTTTGGCTTCTTGGA	59.955	20	183	940	1122
AACTCAACCCAACGCAAATC	59.978	20	144	49	192
TATTTGCATACTGCATGGGC	59.549	20	191	199	389
CAGAGCGCACTCGAAGAGTA	59.49	20	153	181	333
CAACATACCCAATTATTCCCA	58.606	22	132	11	142
TCCTCCATAACTTTTTCCTCAC	59.987	23	236	62	297
AAGAACTCGCAGGTTCCTTG	59.473	20	102	164	265
CGGTTTGGTGAGAAGTACGC	60.689	20	175	530	704
GCAAGAGAATTGAAGAGCGG	60.096	20	274	12	285
TCTTCCCCAAAAGTCACCTG	60.081	20	260	625	884
TCGTTGCCGGAAAATGAATA	61.319	20	261	258	518
ATGTAGCCGACCCCAATTTA	59.297	20	103	41	143
TGAGGAGGAGGAGAGTGGAG	59.503	20	179	435	613
ATCCGTGTGCATTTGTGTCA	61.013	20	107	1	107
TCCACATCTTCCCAATCCAT	60.135	20	170	246	415
AGCCCATGTTTTGAGAAATTG	59.077	21	214	98	311
TTGGGAGAAGGGTTTGTGTC	59.943	20	154	412	565
CGGCTTCTCTGTCTCCACTT	59.598	20	213	200	412
GGAGAAGCACCTCCTCTGTG	59.986	20	244	238	481
CCCAGTGCCACTCAAATCTT	60.111	20	158	22	179
CAGCCTCCCAGCAAGTTATC	59.836	20	108	893	1000
TAAAAATGAAACCGGCCAAA	60.287	20	219	1783	2001
AGGTTGCGTACATCTGACCC	59.997	20	227	3047	3273
CTGTGGTGGAGGAGGAAGAG	59.828	20	237	38	274
GGCTTGTATGGTTTGGGAAA	59.801	20	211	76	286
TTTCAACATTCAAAATTGGTAT	59.665	25	273	18	290
TTTTTATTAGCATTTTAAACCA	57.364	26	220	601	820
TCTGGCCTGATCTACAGCCT	59.973	20	244	78	321
CATGCAGACCACTTTTGGTG	60.152	20	273	26	298
GCCTCGATCCTAACGTGTGT	60.142	20	241	1545	1785
TCACCCCTCATTCACATCAA	59.893	20	217	560	776
CAACACCTAATCAAGAACAAA	59.577	24	159	75	233
GAAGGGGTGGAGATACAGCA	60.073	20	110	308	417
CGGTTGTCATAAGACCACTTC	60.03	22	110	16	125
AATTCGCTCACGAGTTTGGT	59.74	20	170	5069	5238
AGGGGTAGGGGGTAGACCTT	60.068	20	120	103	222
AGGACTGCCGACCTCTTTCT	60.393	20	134	483	616
AAAAACATTAAATCAAACTGT	57.811	26	228	242	469
AAGGGAGCTACAACCTTTCAT	58.783	22	225	200	424
GAATATATCCCGGCACGATG	60.139	20	153	0	152
AGAGTCATTAAGTGTGGTCTC	59.69	23	140	967	1106
TAGACAAAGGCTCTGCCCAT	59.836	20	250	20	269
CCCAAGACCCCAATTTGATT	60.91	20	175	2647	2821
TTCTTGAATCTCGGCGAACT	59.955	20	150	231	380
GAAGCACGAGTGCTGTGATG	60.627	20	230	2019	2248
TGCTGTTTTGTTATAACCCCG	59.876	21	125	184	308
TGCTTCTGGTAGCAATGGTG	59.864	20	262	382	643
GAATGAATTCGAAGTTTGGGA	59.945	22	149	408	556
TGTAGCCGACCCCAATTTAT	59.297	20	125	1057	1181
TTGAACAATGGTACCTCCTCCT	59.864	22	134	11	144
TTATAACGTGGGAACCAGCA	59.037	20	241	688	928
AGAATCAAGCAATGGATGCC	60.043	20	199	595	793
TAACAAAGGGGCCAAAAGG	59.917	19	280	11	290
AGGAAATGCGAGAGGGATTT	60.039	20	240	253	492

TGAAGGCGGAGGTTTCATAG	60.206	20	270	132	401
CACAGACATCTCTGCATCGG	60.426	20	273	262	534
AGTGCGGGGTAAAAATGTTG	59.861	20	202	237	438
CTTTGTTTGGAGCGCGTG	61.555	18	256	48	303
TCTAAGGCAAAATAATGATGG	58.634	24	210	211	420
AGACTCGTTCAAATCCTGCC	59.288	20	219	5781	5999
CGTTTGGTAGGCTCGAAAAT	59.225	20	218	59	276
TGGGATTATGTTTGGATTTCA	57.804	21	131	1	131
AATGCCGCAATTTCAAGTTT	59.592	20	245	685	929
AAGTCATTCCCTCGTCTCCA	59.655	20	193	124	316
CTCCTGCTTCACCTCGAGTC	60.135	20	271	15	285
CTGAGAGCAATACCGATGGC	60.765	20	276	1784	2059
GTGGGAAGAATGCGAAGTGT	60.119	20	245	788	1032
CCGGCTCAAAGGACAGATAG	59.83	20	263	277	539
GGATACGACCTTGCTCCAAA	60.074	20	242	228	469
TCCACAACCTCTCATCTCCC	60.048	20	110	378	487
TCCTCACTGAGTCTTGATATTG	57.06	24	272	509	780
GAGAACAATCAGCACCGTCA	59.837	20	169	1566	1734
GCGATATCACGTTTAACGGC	60.485	20	173	88	260
ACCTTCCAATCAGCCTGCTA	59.836	20	168	47	214
ACACAATAACCATTCGTTCTCA	57.154	22	241	157	397
GAGAGGGAGAGAGATCGGAA	59.904	21	129	206	334
TGTGCAATGCAACAAGATGA	59.833	20	176	52	227
TTGGAATTGAGCAGCCTTTT	59.823	20	242	346	587
AACAATGGCTGCTGTTAGCC	60.278	20	211	375	585
GAATAGCCCAAGGGAGGAAG	60.032	20	211	1616	1826
TGAGACTCGAACCTGTGAGC	59.129	20	231	18	248
CCTGAAATTTGGTAGGCGTG	60.493	20	220	1274	1493
TACCTGCCGGAATGTTGC	60.631	18	108	33	140
TCGCTAGAATCTCATCCAGTTG	60.276	23	280	211	490
GATGTACGCACTTGGTGGTG	60.032	20	157	579	735
CCACAAAATAATAAGGCGGC	59.455	20	209	4	212
AACATCCACAAATCATGCGA	59.931	20	215	23	237
CCAGCTCCGAGCAAGTTATC	59.978	20	247	41	287
TTGTTTAGCCGGATCCTGAG	60.206	20	248	1846	2093
CCGATCTCACAAGCCAGAGT	60.408	20	181	2369	2549
TTTCCCATCATTCACGACAA	59.9	20	245	132	376
CTGAGCCATCGAGGTATGGT	60.096	20	279	231	509
TACCAAACAGCCCACTCCA	60.096	19	277	676	952
CTTGGGCCTGCACTACTCTT	59.496	20	254	3048	3301
TCCCTCCAATTTCCACTTGA	60.43	20	229	6	234
AGCTTGATGGTGGATGTTTG	58.57	20	238	207	444
ACCGTACTCCGAATGAATGC	59.962	20	175	2361	2535
CGGGACCGTGAATAATGACT	59.813	20	158	1041	1198
GAGATGATGGCGGATGGTAT	59.739	20	243	1430	1672
GCATGAAGCAGAATTGTCCA	59.805	20	217	40	256
ATTGTTTGTGAGCTTCCGCT	59.882	20	259	3647	3905
ATTGTGCTATTATCTGCGCC	57.897	20	141	244	384
TGTAGCCGACCCCAATTTAT	59.297	20	167	93	259
TGCATGCATCTTTTTCTCTTTT	59.013	22	273	35	307
TTCAATGAGGACAATCTGCG	59.799	20	149	868	1016
AACCCACGACCACAAGGTTA	60.269	20	231	287	517
GACAGGCCTGAGTTCGGTAG	59.867	20	248	3254	3501
CTTGGCATCCTCATGGAAGT	60.073	20	268	3951	4218
TGTAAGAATGCATTGAGTCAA	57.003	23	195	612	806
TTTCTTTTGGCCAATGTTGA	59.133	20	263	193	455
CAAGAATGTTGACCAAGAGCA	60.284	22	215	242	456
GCTCTTACACCCATCCGAAA	60.074	20	245	303	547

TGTGTCAACAAACCGGGATA	59.816	20	216	12	227
GGGTGTCCTCGACATTTTTC	59.386	20	268	90	357
GGGAGGGGATGATTTGAACT	60.133	20	210	235	444
CTGCAACTTTCCATACGGCT	60.27	20	275	123	397
AATTACCTTCACTCACCAGAA	57.008	23	266	89	354
AATTACAAACCCGCATCCAT	59.162	20	209	417	625
CGAGGAGTTATGGGAGCAGA	60.353	20	149	14	162
TGCAGATGGAAGATGAGCAG	60.096	20	186	892	1077
ACTTGATATGGATCCGAGGCT	59.939	21	203	550	752
GGGGATGAGTTTGTGAGGTT	58.842	20	216	58	273
AAAGTGACCTCTGAAGCGGA	59.989	20	168	980	1147
GAAAATTGGGGATCACATCG	60.133	20	226	96	321
CCGTTTGATTCATCGGAAAC	60.309	20	149	798	946
GGACTTGATTTGCACTCCGT	60.119	20	183	336	518
CCCGACCACAAAGGAATTAT	58.762	20	261	363	623
GATTCAAGCCCCAAAGTCAA	60.051	20	142	1101	1242
TGTAGCCGACCCCAATTTAT	59.297	20	148	212	359
ATTGATTATCATGTCGCTCGC	60.081	21	112	983	1094
CTGATTGTACACGATGGCGA	60.687	20	236	241	476
GCGGATAAGCTCGAACAGTC	59.985	20	169	17	185
CCACATTTACTTGATGCATTCT	59.457	24	110	11	120
TGTCAGGATATTGACAAGGTG	60	22	165	2057	2221
TGAATATCGGTTTCATCGCA	60.035	20	100	40	139
ACCCAACACCAAATTATGCC	59.551	20	246	1	246
GGGTCTGTGGATCGGAATAC	59.218	20	275	4003	4277
ATTTAATCCCGTGCAACGC	60.852	19	230	47	276
ACTTCAGGGCCAAATGTGAG	60.111	20	271	4724	4994
TTCAATTTTCACAAAATAACGC	59.542	23	272	117	388
TAAGGCTGTTGGGGTATTGC	59.96	20	214	1333	1546
CAGGCAGATTCTGGTTCACA	59.831	20	279	3478	3756
GTTCGGTTGTGAAATTGGCT	59.978	20	204	400	603
TAGCATGTCCGATTGACACC	59.527	20	115	194	308
TCTATCGCCCTTGCTTGACT	59.978	20	195	123	317
TGAAGATCGGGAACTGAAGG	60.187	20	116	941	1056
GTCAAGACCTTTTGGCGAAC	59.717	20	246	3	248
TTGAAAAGGATGGTGAAGGG	59.903	20	158	19	176
CCCAGTTTTGGTCGTACTGG	60.401	20	225	19	243
CTAGGGTTGACCCACCTCAC	59.425	20	174	1689	1862
TTTGGTTCGATCACGCCTA	60.204	19	262	110	371
GCTCAAGGTTTGAACTCGAAA	60.75	22	278	1261	1538
TAGTCTCTGCCAAGTGGGCT	60.012	20	186	274	459
TTTTCCAAGACCGGAAACAA	60.452	20	262	310	571
AGAAGGCTTTCGCCTTTTTC	59.966	20	249	85	333
ATCAATGGCGAAGGCAGTAT	59.556	20	113	577	689
AATGTTGTTTAGGTTCTCAATT	57.821	27	264	84	347
TGGGCGTAAAATAGAGGTGC	60.096	20	224	5711	5934
CATTCCAATGCTTGAAGCTG	59.42	20	261	50	310
GCTAGATCGCTCCTCCAAGA	59.676	20	116	66	181
TCAACCCTTCGGATGAAGAA	60.572	20	204	2430	2633
TGCAGATCATTCACATGTTTCA	60.119	22	184	55	238
CTTCGATGTATTGTTGGATAAT	59.692	25	217	404	620
ATGCAATCACAGACTGCCCT	60.688	20	230	352	581
GCTCGGCGATACTTGTCTTC	59.985	20	225	35	259
GCCCTCTGCTTTCAAATTCA	60.331	20	105	1007	1111
CCATCACCATCACCATCATC	59.565	20	256	744	999
AACACTAACCTGAAGCCATGA	60.178	23	241	14	254
GGGCTCGGAGGATAACTCAT	60.431	20	271	354	624
CCCAAATGGATTGGGTTCTA	59.617	20	114	90	203

CCGATTTGCCGTTCTATCAT	59.923	20	179	439	617
CCCCTTTCGGTGTAGACAAA	59.964	20	274	973	1246
CCCGAGGGAGTCACAATTTA	59.926	20	247	44	290
CGCACGTTTGTATTTTTATTTTT	57.532	23	110	261	370
ATTACGCATCAGCACAATCG	59.718	20	278	91	368
GTTACATCCCACCGGATTTG	60.051	20	229	257	485
ACACGTCTAGATGGCAAGCA	59.47	20	210	2031	2240
CTTCAATCAATCCCCCTGAA	59.864	20	249	4172	4420
AAATGCACTGGTTAGGAGGGT	59.878	21	195	1090	1284
TGAGCAAACTAAATTACAACG	58.142	24	252	3716	3967
CCATGGCTTTTCAACCAGAT	59.933	20	191	771	961
TAGCAGGCCAAAGAGGAAGA	60.088	20	270	62	331
TGTGAGGTTGAGGATTGCAG	59.831	20	111	876	986
CTCTCCCTCTCTCGTGCTTG	60.275	20	136	140	275
ATTTTCGTCGCCCCTCTTAT	59.93	20	228	71	298
GGTGGTATGGTGTGCAGAAA	59.42	20	247	326	572
AAGTAGGGTCAAACACGTGAA	57.253	21	262	37	298
GCCCATCTGACGATAGAAGA	57.834	20	174	592	765
ACTCCTTTCGTTGCCAAATG	60.11	20	256	180	435
CTAGATCATCAAATGCGCCA	59.792	20	262	597	858
TTTGGTTCATGTAGTCGACCC	59.845	21	160	1023	1182
AATGTTTCGATAAACGGGGA	59.273	20	180	24	203
GCGACGATTGAATGGTATCAA	60.852	21	226	235	460
TCTGCAGCCATCTGTTCTTG	60.136	20	186	11	196
TCGAAATCATGGTTCGTCAA	60.049	20	254	968	1221
GGCCAGTGATGACACAGAAA	59.682	20	141	3962	4102
TTATCCAACCCAGCCAACAT	60.192	20	239	492	730
CTGTCTAATGTTTCCGCCG	59.282	19	237	773	1009
GGTAGCTACTTCAGTGGCGG	59.898	20	195	51	245
GCATCGGCTGGTGAATTATC	60.444	20	272	104	375
ACTTTGATGCTTCGTCCAGC	60.406	20	233	15	247
TCCCAAAGAGCAAACAGCTT	59.993	20	187	879	1065
TCGGCCTCCGTCATTATTAG	60.053	20	271	250	520
GGCTGTGCTCATCCGTAGTT	60.285	20	217	399	615
ATGTAGCCGACCCCAATTTA	59.297	20	194	302	495
ATCTTCTTCTCCGCCGTCTT	60.349	20	169	395	563
ACTGTTGTTGCTGCTGTTGC	60.104	20	244	2	245
CAGCTTCCCCCAATACTCAA	60.066	20	141	452	592
TTCCCCGTACACAGTGATTTT	59.345	21	225	959	1183
GGCCAAAGAGGAAGAGTACG	58.934	20	241	243	483
TGTTCCAAGCTTTTCTCCTCA	59.978	21	217	178	394
TCACATTGCTCTGCAAGTCC	59.992	20	156	173	328
GCCCTGCCACGTTCTATTAC	59.597	20	209	996	1204
GGCAGCAGCCTCTTAATCAC	59.985	20	152	326	477
GATACCACAACTGGGCAACC	60.24	20	270	10	279
TTTGGGAAATATGGATCGAACT	59.68	22	221	417	637
CCTGCGAACTTTCCTAGCAC	60.015	20	146	230	375
AGCAGAGGAGGACGATGAAG	59.555	20	209	246	454
CCGCACTTGACTACTCAGCA	60.199	20	271	547	817
TCGGGATCTTGATGGTTCTT	59.483	20	275	187	461
CCAAGAAAGTGGAGAAGCGA	60.508	20	279	245	523
AGAACTGTGGAACTGCAGGG	60.298	20	274	453	726
CTCGCCCAAGTGACTGAGAT	60.408	20	121	11	131
TACCTTGTCGGTAAATCGCC	59.96	20	180	367	546
GGGCTAATAATGCCCAAGGT	60.171	20	142	253	394
ATCATCGGGCTTTGATGAGT	59.513	20	210	9	218
CACCATACACGGTCACGTCT	59.467	20	160	336	495
TAAAAGTGCCCGACTGGATT	59.569	20	246	27	272

GGCCAAAGTGGTGAATCAAG	60.495	20	278	3	280
ATGTAGCCGACCCCAATTTA	59.297	20	233	267	499
AACACAAATATGCCATGCAAG	59.411	22	269	223	491
TTCGATAGCAAACCTTTCCG	60.202	20	220	1163	1382
GGAAGCTGTTGGAGCTGAAG	60.134	20	192	62	253
GTCAATCCCAATGACCATCC	59.995	20	213	202	414
TCCCATGCAAACTGAATCCT	60.461	20	220	1309	1528
ACGAGGGAACCTACCACCTT	59.856	20	164	3227	3390
TGAATTAGAACCGATGAGCAA	59.72	22	280	40	319
AGTGAAGCTAGTTGCTCGGC	59.786	20	252	483	734
GAAGTTAGAGGAGGTGGGGC	60.074	20	273	569	841
TCCAATTAGGACAATCAAACC	60.055	22	194	222	415
TTCTTGGCTCGTTCCTTCAC	60.375	20	202	180	381
CATGTGTGGGTGGTTCATGT	60.138	20	206	990	1195
TCGTCGCAGAGCTAGTGAAG	59.49	20	250	821	1070
AAACAGCAATTGGAACTCACT	59.286	22	232	332	563
TGGACAAGATTTTCCACCTCA	60.48	21	259	1623	1881
AAAACAAACATATGCTTTCCC	59.775	23	143	5	147
TAGCCAAGACCCCAATTTGA	60.439	20	210	2152	2361
AACACGCGAGTTTAAGGGAG	59.378	20	218	127	344
CCAGTTCAACCCATGAAACC	60.21	20	195	326	520
AGAGCCGTTGAATATCGGTG	60.096	20	196	427	622
TGCTAGCACCTCCTCTATTGC	59.629	21	206	81	286
AAGGCCCCCTTGTCAAATAC	60.187	20	162	51	212
AACACAATAACGGTACCCGC	59.752	20	270	1453	1722
TTTCCCTTAGCCATGAATCG	60.031	20	265	484	748
GGATCAGCAGTGGCTTTCTC	59.957	20	225	991	1215
GCCCTGAGTATGGAAAGCAA	60.214	20	277	1947	2223
CTCTTCCACCTGTCTCACCG	60.85	20	210	5843	6052
AGGTTGCGTACATCTGACCC	59.997	20	102	38	139
CTGAGTCTGATGCTTTTGCG	59.74	20	266	1505	1770
GATTGTTAACCCATTCCCACA	59.537	21	187	121	307
AAAAGAGTTGACAGGGGCAA	59.711	20	276	233	508
TGGCTGTTGTTGAAGTCGAG	60.025	20	248	2173	2420
TCTCCCTCGATCCTTATCCC	60.367	20	125	1201	1325
TCTTGATATCTTGGGCAATTGT	59.541	24	195	32	226
CCTCTCATTCACCCTCATCC	59.46	20	195	28	222
CTCTCTCTTCTCCCTCGGCT	60.23	20	120	245	364
CCTTTCTGGACATGGATCGT	59.927	20	255	1191	1445
GTATTCAGGCTCGGACGACA	61.208	20	105	41	145
AACCCACATACTCGAGGCAC	59.997	20	147	225	371
ATACGTAAGGCCGAGAGCAA	59.867	20	136	212	347
GTAATGTGGAGGCCTTCGAG	59.694	20	160	34	193
CGTGTTCGTTCCTAGCTTCC	59.875	20	159	317	475
ATCGGAGATGGTGACGATG	59.441	19	209	1310	1518
TACACTTTGAGTGGCGATGG	59.716	20	252	31	282
TAAAGACCGACGCTCCTCTC	59.574	20	207	43	249
CTCGGGATCAATGACATTCC	60.281	20	273	162	434
TGACCTGAAATCAGCAAACG	59.84	20	203	259	461
AACAAATCATATGGCCCGTC	59.651	20	245	13	257
ATGCGCTCTAACTTTCGCAT	60.01	20	241	928	1168
GCAGGACACAAACGAATCAC	59.143	20	189	675	863
CGTGCACATTTGTTATGGACA	60.43	21	103	4	106
AGTGTGCAGTGTGCTTGGAG	60.096	20	276	277	552
TCATGATGGTCCTGATGGAG	59.425	20	123	226	348
ACCAATGGTGGTATGGTGTG	58.984	20	230	38	267
TTTCTTTTTCCCCGTCCTCT	60.046	20	195	500	694
CAGGACTTGGAAATGGGAGA	60.042	20	178	2293	2470

TGTGGACAAAATTTCAAAGTG	59.876	22	271	4	274
TTTGAAGTCATGTGTCCTCCAT	59.454	22	230	746	975
AATTTGATTGGGAATAATTGG	58.965	22	129	24	152
ACATTCGGGGGAGAAGGTAT	59.651	20	197	12	208
ACGATGTTGGGTTTGTGGAT	60.096	20	194	402	595
AAGCCACCTACAAGAATGCC	59.198	20	278	6	283
AGCAACATCCATCGAATTGT	58.019	20	270	1114	1383
AATTTGATTGGGAATAATTGG	58.965	22	175	730	904
AGTTGCTTCGGATGCTTCAT	59.843	20	114	17	130
GCAACCGAGCTCTAACAAGC	60.162	20	251	78	328
TTCCCGAGACTGAGATGGAC	60.199	20	148	8	155
TGCTTCAAGCTACTCGGAAAA	60.138	21	184	2615	2798
GTTTTTGAATGGCAGTGGGT	59.836	20	198	2465	2662
CTGGCTCTGAATCACCCACT	60.261	20	276	59	334
AAGGTGTAGATCTGGCGGG	60.081	19	161	1113	1273
CTCGTGCATTTTCCTTGACA	59.84	20	217	939	1155
GATCTTCATTGCGGGGATTA	59.862	20	130	1826	1955
TGAGGTGGAAGCACTTGTGT	59.31	20	156	323	478
TGTGACTTTCATTTGTTAGCCC	59.134	22	219	483	701
CAGCCCCGATAATGAGAAAA	60.031	20	212	358	569
TGCACAAAACCTTTTCCCAT	60.344	20	270	1034	1303
GCAAATCCATTTCTCTCCGA	60.155	20	139	57	195
TTTCGTAATCCTGGATCGCT	59.668	20	257	328	584
CTACCTCCATGTGTGCGCTA	59.888	20	156	11	166
TGCGCCATAGGAACTATTTG	58.794	20	249	1435	1683
TAGTTATTCCGCAACGGAGG	60.089	20	235	2910	3144
CTCAAAACCGAATGGAGGAA	60.044	20	161	569	729
AATGGACATGATTTGGAGGG	59.605	20	206	6	211
TTTGTTGTTGACTGGAGGCTT	59.766	21	260	17	276
AGCTGCAATCCTTGCTGTTT	60.022	20	270	269	538
AGCGACTAGTGCTGTAGAAGG	60.233	22	183	131	313
ATGGTGTCAACACATTGGGA	59.656	20	279	14	292
AGGCCGAACCACCTATTTCT	59.962	20	219	0	218
CAACTCCCTCCCACATTCAC	60.363	20	138	4	141
TCTATTGTGCCGATTCCCTT	59.528	20	248	4050	4297
GCTGATGGATGTGGATGATG	59.882	20	159	592	750
GGACGATTGCGTCACTGTTA	59.722	20	275	7	281
TTCATGTAGCCGATCCCAAT	60.296	20	118	234	351
TACAACCAGTCTAAGCGGCA	59.488	20	273	2481	2753
ACCCTGCATGTCAAATTGCT	60.526	20	171	21	191
CAATGTCGCATATATTACTTTC	58.176	24	208	245	452
AATTCACAAGCCCAAACGAC	59.978	20	220	1767	1986
AACATGCGCTTCTTATATTTG	59.695	23	230	30	259
TCCTCATGTCTTTGGCCTCT	59.803	20	240	5	244
TGAAGGATGCATCTTGCTGA	60.504	20	133	6	138
TTATCGATTGTTGCCCTCAA	59.112	20	260	43	302
TCAACTGGGAAAACCTGGTC	59.943	20	100	1899	1998
TGGTCGTGTCGAAGTTTGAA	60.278	20	188	722	909
CCGACGACCAAATGGATAAC	60.192	20	200	417	616
CCTGTGCTGCCATCATATTTT	59.974	21	268	3	270
TCAATTCATGATGGTCATTTCA	58.82	22	240	982	1221
TAGTCGTGGCACACAGGAAC	59.751	20	164	704	867
AGGGACGCTATCGATTTGTG	60.096	20	255	1	255
CACAAAACATGCATCAGCCT	59.722	20	274	3	276
ATAGCAGGCTCGACCAAGAA	59.978	20	207	359	565
CAGGGCTGCTGAATGATATG	59.251	20	275	808	1082
ATGGCCAAGTCAAAGTCACC	59.973	20	163	330	492
AAATGCAACATGTGATCTCAA	59.94	24	221	475	695

TAGAGGCTGCGAATTTCCAT	59.807	20	276	365	640
AGCCATCTCAAGAGTCGTGG	60.408	20	274	347	620
TGTTTGGAGCGGGAATATCT	59.528	20	146	3246	3391
CCAAGAATCTCGATTCCCAA	60.006	20	207	1133	1339
CATCATGTTTAACTGGATTGTG	59.397	23	268	124	391
CAATAAATTGGGGTCGGCTA	59.789	20	134	6	139
GGAAGTGGGGGTCGGTATAA	60.929	20	207	314	520
GGAGAAGGGCAATTGGGTAT	60.152	20	210	366	575
GATTGCTGGAAGTGGTGTCA	59.682	20	118	8	125
CCTTGGTTTTTGGCCTTTTT	60.317	20	198	263	460
TCCTTCCAAAGCCTGACTGT	59.844	20	260	4551	4810
ATCAAGCAAGCATCTCAGCA	59.704	20	170	801	970
TAAACTGGAGCACAAACCGA	59.317	20	259	815	1073
AATTTGAAGACGTGGCTGCT	59.882	20	136	1000	1135
GGTCGTTGGTAATTGGACGA	60.755	20	173	723	895
AATTCTCGCTGAAAAATGCC	59.301	20	245	15	259
TGGCTTGCAGAATCAAGAAA	59.542	20	252	956	1207
GTGGTCATTTTAGGGGATGC	59.249	20	168	211	378
CCTACCCACCCAGGTCATC	60.183	19	272	8	279
TGTGAGCCATCTGCAACATT	60.272	20	206	49	254
TCCGTTTTTGTTGTCCAATG	59.415	20	263	544	806
TGTCATACCGGCACAAGTTT	59.05	20	206	928	1133
AACCCAATACCCAAACCCAT	60.166	20	143	13	155
TGCAATGGCTTTTCATTGTT	59.161	20	164	191	354
GACCAATTTGAACGGTTTGG	60.206	20	214	180	393
GCGGAGGCGACTTATACTTG	59.867	20	156	37	192
TCCAAGAATCCCTTCCAAAA	59.476	20	230	277	506
CGAAGACGTCAATTTGGTCA	59.691	20	245	1214	1458
TTTTTAAGGTGGGGAGAATGT	57.596	21	252	41	292
TGTAGGCATAACTATGATTGG	59.768	24	115	4	118
TCCAACTTATTGCATGTTGAAC	58.688	23	259	711	969
GATCCGTTCTCGCATAGGAA	60.177	20	273	18	290
TGATGTTGGTGGGATTTGAA	59.75	20	223	473	695
TTTTGCGTCCTTCTGCTATG	59.062	20	261	105	365
CCTCCCTTCACCTTCAAACA	60.081	20	196	3240	3435
TCCGCGTGTGCAATAAATAA	60.096	20	111	2997	3107
ATTTAACGTGTGACCATGCG	59.469	20	194	719	912
ACCTCAGGTTGCTCCGAACT	61.219	20	270	197	466
TTACATATTTCTTGCGGCCA	59.169	20	217	374	590
CAGGGCCCTAGAAATTAGCA	59.315	20	254	448	701
ACGGGCTGATGTAGAGGAGA	59.827	20	203	55	257
GGCATATGCGAGTTCCTGAT	60.066	20	222	60	281
TTTATCAAGGGCTGGGGTTA	59.406	20	272	959	1230
AAGGAGATCCACTCTCGCAA	59.95	20	128	232	359
GGATGAGCTACTGGAGCGAG	60.119	20	273	388	660
GACGTTCGACTTCTTTCCGA	60.375	20	256	1242	1497
TCAACGCTCACCTTCACATC	59.837	20	205	80	284
TGCGGTTGCTACTTCAATCA	60.401	20	193	7	199
CTGGCCAACTCTCCCTTCT	59.39	19	204	386	589
TCCTGTGAAATGTCCTCAACC	59.958	21	268	2	269
ATGTAGCCGACCCCAATTTA	59.297	20	140	1001	1140
TTGGTTGGTGATTTGGGTTT	60.066	20	279	88	366
CAGCATTCTATCTGGGCCAT	60.059	20	256	4424	4679
ACATTCAGGCAGAAAATGGG	59.933	20	280	903	1182
AAGTCAGACACAGCATCCCC	60.12	20	190	61	250
TACTTCTGACCCCGCAAGAC	60.255	20	254	30	283
CCCAAATCAGAAACGCCTTA	60.067	20	246	58	303
CAATTCGAAGCCCAAATCAT	59.901	20	143	23	165

ATTTGAACGTGGGAGGTGAA	60.353	20	276	35	310
GGGATAGCACGTCAATAATGC	59.452	21	280	814	1093
TTTTTCTTGCACCAAATAGGTT	57.875	22	124	436	559
CCGCTTACCTAGATGGGAGC	61.099	20	217	0	216
AAAAGTCGCCGTTACTGGTG	60.168	20	253	375	627
CCCGAGAAATTGGTCTCAAA	60.044	20	223	540	762
TGCAAGGTCTTCTCCAACCT	59.844	20	208	49	256
GGACCCTCAAGCCACTTAAA	59.17	20	202	295	496
GTGTGTTGTCACGGAGAGCC	61.77	20	137	939	1075
ATTGTCCGAGTCCGAAGACA	60.656	20	215	451	665
TCATCGAACAAGTCCTCCAA	59.215	20	259	449	707
GGGGAAATGTGCCAGTTAGA	59.933	20	252	291	542
AATTTGGATTGAAAATGAGAG	57.344	24	186	806	991
TGAATGCCAACTTGCAGAAC	59.847	20	236	860	1095
TCAGGGTTTCAACATTTCAGC	60.103	21	279	271	549
CCCTCAGTTGGCATTCAGTT	60.111	20	194	506	699
GGGGAATTGATGGACATGAT	59.42	20	270	135	404
TGATGCTCTACCACTGCACC	59.862	20	217	172	388
CCGATGAAAGAAGAGCCAAA	60.323	20	254	892	1145
TCCCTTTCCCTGAATGTCTG	60.042	20	191	2824	3014
GCCCCTGTTTGCAATGTAAT	59.829	20	240	464	703
TGGTTGGTCTGATGATTGTGA	59.951	21	198	3	200
TCCTCACCCCCTCTCTTTTT	60.045	20	248	13	260
AACTTTGACTGCTATGCCGC	60.416	20	158	41	198
GAAGAGCAAGAAAGCATGGG	59.955	20	187	2721	2907
TCAGTCCCACCAATCACAAA	59.935	20	200	647	846
AGAGAGGGCTTAGAGACGGG	59.972	20	252	11	262
GGAGACCGGGTAGAGGTGAT	60.336	20	228	371	598
GGATCAGCAGTGGCTTTCTC	59.957	20	207	788	994
ATTCTTCGCATCAATCCCAC	59.9	20	265	256	520
TGCTCTCGTTTGCCTTGTTT	60.944	20	253	8	260
CGACTCAAGTGAAGCAGCAA	60.324	20	271	1171	1441
GCTTCTCATGCCTCTAGGGT	58.5	20	232	90	321
GGTTTTGGTGATGTATGTGGC	60.111	21	104	37	140
TTGAACTGAAAAAGTGGGCA	59.293	20	148	5185	5332
AGGGTTCGACTTCTTATGGC	58.267	20	266	71	336
AAACTTATTTTGCATGTGATAT	60.036	26	256	2	257
TTGTATGGGTCGGTTTCAGC	60.894	20	182	41	222
GAACCCGATGAGGAAGATGA	60.011	20	206	148	353
AGCAACACCACAAACCCAAT	60.277	20	210	797	1006
GTCTATGCTGGGATCACCGT	59.957	20	241	2283	2523
AGGGAGAATTAGTGGAGGGG	59.392	20	137	33	169
TCATTTCCCGAAATAGCCAG	60.031	20	274	123	396
TTCGGAAACACCTAGAACGG	60.103	20	118	158	275
TGCAAAGTTCACATTCAGTCA	57.882	21	183	1599	1781
GGGCGAAATGACAAAAATTG	60.302	20	174	1928	2101
GGAATCGTGTTTGCTCAGGT	60.119	20	146	1363	1508
TTTTTAGGAGTCCCGAACCA	59.541	20	257	724	980
AAAGTGCACCTGAGCCATTC	60.263	20	234	2126	2359
ACGGAGGTCTCTTGGGTTTT	59.972	20	235	395	629
TGTGTGATTGTTGTGGCAAA	59.563	20	255	282	536
TTCTTCTTTCCATTCACCCG	60.044	20	233	30	262
GCGCAGTTCGATCAGTTTTT	60.395	20	207	140	346
CCGGTACATGACTTCGAGGA	61.055	20	224	107	330
GGAACCATTTCGTTAAAATTAT	59.929	26	269	192	460
GGTCCAATAAATGTGGGCCT	60.94	20	271	1618	1888
TTCGGAAACACCTAGAACGG	60.103	20	118	117	234
TGGTCTGGGAGAACTCCACT	59.682	20	222	967	1188

TCACATTTAACCTATGAGTCTG	59.565	24	117	684	800
CTGCTCGTGAAGGAGCAAAT	60.538	20	239	459	697
AATTTGATTGGGAATAATTGGG	58.965	22	155	128	282
TTGTTTTGCGCAGTTATGGA	60.251	20	249	41	289
TGGTACCACGAGGAGGAAAA	60.486	20	223	657	879
TCACCCAAGTCCAATCTATTCA	59.429	22	268	80	347
AACGGGGAAAAACAAATTCA	59.292	20	277	53	329
TTGTCTACCATCTCGGGTGC	61.067	20	252	455	706
GGTTGAGCCACCCATTTTTA	59.801	20	236	83	318
CCAGCACCTCCTCTATTGCT	59.454	20	265	18	282
GCATTTTCAGAGGTTGCGTT	60.257	20	121	661	781
CCTTGAGGAGCAATGGAGAC	59.803	20	268	3783	4050
GGTCTCTGGATCAGGTTGAGA	59.243	21	187	312	498
ATCACAATGCCATCACCTCA	59.925	20	242	304	545
CCCAAGACCCCAATTTGAT	59.59	19	276	1730	2005
ACGTTAGAGGGAGTCAGGCA	59.867	20	195	1644	1838
CCGCCAAATGTGGATAGATT	59.784	20	215	28	242
GAGGTGATCGGTTCATTGGT	59.786	20	218	5524	5741
ACGTGTCTATTGAAACGATGA	59.939	24	275	270	544
TGATTGTGCCTCTCTCCCTT	59.803	20	235	3121	3355
ATTGTTGAAATCGCTTGGCT	59.713	20	136	728	863
CGAGGGTGATGAAGGAGCTA	60.353	20	279	919	1197
TTCTAAAGTGCAGGATGGCA	59.42	20	184	83	266
TGTAGCCGACCCCAATTTAT	59.297	20	231	2427	2657
CACCTCGAACCTTCTGCAA	59.968	19	272	3240	3511
GGTATATTTAAGCACCGCCG	59.477	20	194	101	294
CAATGATCCTCACATTGCCA	60.481	20	168	36	203
AAGAGAAGCTCGAAGGGGTC	59.957	20	144	236	379
AGCTTATGCAGGACAAACCC	59.198	20	231	1	231
TGCAGGTGAGACTTGCCATA	60.413	20	190	5	194
TCCGGTTGGTCTCTTAATGG	59.926	20	233	1554	1786
AAGGTCTCCTGTTCACGCTG	60.444	20	170	330	499
TCCAATCCAATCTTCGAGGT	59.483	20	123	2	124
AAACGTGAGGTTTTGACGAGA	59.766	21	226	130	355
AAGAAAGCCCACCTGATCACT	60.125	21	167	55	221
TCATCTGTATTCGACTTCTCCA	57.422	22	279	69	347
AAAAAGTGCCTCCCTCGATT	60.074	20	233	1554	1786
ACGTTCCAGTGGTTCAAGTCT	58.709	21	280	187	466
AGCGAAACACGCATCTTTATG	60.278	21	249	21	269
ACCAACAGCACAAGAAACGC	61.275	20	173	89	261
CTACCCACCACCAACATCAA	59.262	20	175	36	210
CTCATGGATCTTCATCGGCT	60.181	20	275	377	651
CGCCATGGAAAGGTAAAATG	60.315	20	212	247	458
TGCATCATGCTTTCCATACTC	58.738	21	141	934	1074
TGCCAACCAACAAGCATAAT	59.041	20	252	3200	3451
ATAATTGCAACCAAACCCCA	60.053	20	139	325	463
GTGCAAAGTGTCCTGAGCCT	60.453	20	175	295	469
TGTAGCCGACCCCAATTTAT	59.297	20	210	508	717
ACATGGGGGTCTGCTATCAT	59.243	20	255	304	558
TTCTTGATACATGGGCGTCA	60.073	20	168	513	680
TCCTATCGAATACCCCGACA	60.288	20	186	95	280
ACCGGGATCCTTTTCAACTT	59.805	20	186	312	497
ACACCTCCATGGCAGACTTC	60.12	20	258	2149	2406
ATTGATGACGATGACGTGGA	59.925	20	120	887	1006
AAACTTCAAATGAATCTTCAAC	57.089	24	106	429	534
TCCTAGAATTCCAATACGTGGT	58.941	23	248	236	483
CCAAGCAAGAGATTATCACTC	57.956	22	207	85	291
GTGCTGACTGTCGAAGACCA	60.03	20	270	880	1149

TCAGGATTCCGGAAAAGTTTA	58.681	21	206	768	973
TGGATTGTTGATTTTTGCCA	59.907	20	269	9	277
AAAAAGCCCGAACCTGACTT	60.11	20	185	56	240
AGCTGTCTTGATTTACCTTCAC	59.833	23	207	1188	1394
GGCTTCCTGTCTCTGTCAGC	60.143	20	169	2413	2581
AATGGTCACACCCTACAACAA	57.841	21	164	490	653
TGTAGTCCTTCCTCACAAAGAC	59.72	24	260	134	393
GGCACGTAGGCTACAGCTTC	60.044	20	280	9	288
CAAAAGGTGGAAAGTCACCAA	59.994	21	243	3108	3350
TCAGGGAACATACATCGTCG	59.522	20	277	261	537
CGTGTTTGTCACCCAGAGAA	59.72	20	277	537	813
CCCAAGACCCCAATTTGATT	60.91	20	251	2173	2423
TTCAGAACAAGGAAGCCACA	59.415	20	200	1236	1435
GCTGCACCATCTAGGAGAGG	59.973	20	151	310	460
TAGGAGAGTGGGAGTGGTGG	60.104	20	187	455	641
TCGGAAATCTGGTCATTGAA	59.049	20	228	534	761
TTCTGTGGTTTGGGTTTTGA	58.995	20	255	541	795
TGATTTAAATAAAAATATGTTG	57.023	25	100	1622	1721
AGCATCAAGCCTGCTCAACT	60.164	20	105	1237	1341
CCACTGAACAACTGCAAGGA	59.873	20	112	996	1107
TAAACTGGAACCGAAGGCAA	60.608	20	146	358	503
GGATGGCCTAAGATCAGCAA	60.177	20	207	337	543
TTTGGAAACCGTTGATGACA	59.941	20	254	19	272
TCGAATCAAGATTTCTCACGC	60.346	21	137	318	454
CACACATCCTTCTCTCCGTG	59.257	20	244	6	249
AGGCAAGACTGGTTCCAAAA	59.711	20	200	9	208
CGAACTAGCTCACGAGTCGAA	60.715	21	261	3007	3267
TCATGTATACCCCGTGAGCA	59.948	20	276	459	734
AAGCCTCCTCCGTTTTCAGT	60.247	20	261	100	360
CAGTGGGCAAACCAGATTTT	59.971	20	222	2045	2266
GACACCTCCGTCAACACCTT	60.009	20	167	385	551
CCCATACGATATCACCGACC	60.036	20	263	535	797
TTCTTGGCTGTGGAATCCTT	59.67	20	212	472	683
CCAATGATTGTGGAATGAATG	60.564	22	181	1183	1363
CTTGAACATCCGAAAGAGGC	59.813	20	112	1972	2083
GAATCTGAGCTGGAGTTGGG	59.803	20	161	728	888
CCGCACAAAGAAAATGATGA	59.664	20	110	1184	1293
GTGGTGGTTATGGAGGAGGA	59.779	20	207	142	348
ATGCCCTCGATGATGATGTT	60.312	20	268	98	365
TCTCCGCAATTCGAAAAATC	60.153	20	263	70	332
CTCTCCGACGATGAGGAAAT	59.239	20	106	905	1010
ACAAGGGAACCACAATGTCA	58.827	20	252	65	316
CACAGATGCCCTGAGTCAAA	59.831	20	238	0	237
GGCTAGTAGTAGTGGGAGGAG	59.049	24	277	130	406
AGTCGGTTAGCGTTGCTTGT	59.943	20	140	55	194
AAACCTTGAAGGAACCCAGG	60.332	20	241	150	390
CTTGAAAAATCTCGAAGCGG	59.953	20	188	26	213
AGCAATTTCTTGGCTCGTTG	60.386	20	229	559	787
GTCTCCACCACCTCCACCTA	59.962	20	161	253	413
TTTCCAATCCAATTCCTTGAA	59.374	21	117	146	262
ACGCGATATCCGTGTAGCAT	60.52	20	244	453	696
AACTTCTGCTTATCGCCTGC	59.62	20	192	133	324
TCATGAAAATGAAAAACGCAA	59.179	21	139	818	956
GCCGGTCCCATAACAAGTAA	59.823	20	161	1949	2109
CCATATTGCACCCAGAGCTT	60.096	20	227	838	1064
CCCAAGGCTGATGATCTTTT	59.126	20	212	1732	1943
ATTGCTGGATCTGATCTGTGG	60.088	21	224	173	396
TCGTTCTTAAAAGTTATGGCAC	59.569	23	104	2964	3067

TGCCGGATTTGGATAGATTC	59.862	20	132	521	652
CCCAAGACCCCAATTTGATT	60.91	20	183	1432	1614
GGAGGTGGAGGATTAGGAGG	59.89	20	177	721	897
TGTAGCCGACCCCAATTTAT	59.297	20	227	250	476
ACACATTTACAACCCGGCAT	60.118	20	210	3154	3363
TCCCGACCCAATAAAAACAA	60.16	20	252	1144	1395
CTCAAGATGCGAAGCAAACA	60.134	20	238	115	352
ATGACTTCTGGTACACCCCG	59.844	20	208	125	332
TAGCATGGAGTTGTGCATGG	60.687	20	236	217	452
GGGGATTCCTACAAGAAGCA	59.126	20	280	740	1019
GGATTGGATACCAAAAGGGG	60.37	20	267	879	1145
GCATTACAATGAACCACCGA	59.4	20	246	1931	2176
CTCAAACACCAGAATTGCCC	60.495	20	152	76	227
CGAGGAATAGCTTGAGTGGG	59.83	20	213	2401	2613
GTCGTTTTGTGTCATCCCAA	59.394	20	112	49	160
GCATGTCAATTGTCGAGCTTT	60.272	21	273	25	297
GTGCTTGGATGTTGGGATTT	59.797	20	131	3	133
CAATCTTGGAGCTCTCAGCC	60.096	20	260	2185	2444
TGTAGCCGACCCCAATTTAT	59.297	20	279	1438	1716
AGTCCGCATAGGTTCGATGT	59.579	20	225	191	415
GGCCATGGAACCAGAATAAA	59.762	20	153	446	598
GCATGATTAATCCGTTGCATT	59.815	21	237	6	242
GAATCAATTCCCCAATCCCT	59.959	20	118	403	520
CAAATTCGAATCCCACCAAC	60.17	20	120	7	126
GACCGGGAAAATTACATAAAC	60.01	24	280	26	305
TGTAGCCGACCCCAATTTAT	59.297	20	279	1885	2163
ATTGAACAACACCTCCTCCC	58.842	20	266	1078	1343
AAACTCGAAAACCCAATCCC	60.166	20	180	9	188
GTGGGATTGGATTTGATTGG	59.991	20	143	93	235
GTTCATATAGCCGACCCCAA	59.784	20	164	1302	1465
AAACGCATTCCCATCCATAA	60.153	20	112	51	162
CAGCCATTCCCCTAAAGTCA	60.066	20	280	1229	1508
GCAAGGTTTGTTCGTGCTCT	60.44	20	183	1107	1289
TTTGATGATGTTGCCTGGAG	59.648	20	252	126	377
ACTTGCCGGAAAATCAAGAA	59.685	20	272	235	506
GCGGAGAAGAACATCCTCAG	59.95	20	149	859	1007
GAGTTGGTCCATTTGCCATT	59.797	20	277	15	291
ACTCGAGCTTGACACAACGA	59.622	20	203	1000	1202
TTTTGCTCATCTTGTCTGGG	58.847	20	273	71	343
AAAAACCTGGTCTTGCCAGT	58.695	20	162	494	655
TTGCCATCATCTTCAATGGT	58.926	20	224	112	335
TTGCCATCATCTTCAATGGT	58.926	20	226	100	325
ACATACCGTATCCCGCAATC	59.674	20	102	107	208
TTGCATATTGAATACAATGTCG	59.675	25	278	243	520
GGCCAGTCTCAAGCTGCTAA	60.678	20	164	1091	1254
GCCCTCAATTTTATACTCGAAA	58.292	23	265	126	390
GTGGTGGATCTTGTTGAGCA	59.682	20	262	2629	2890
ATCGTTATTGCCGGATCCAT	61.42	20	133	43	175
TGGCTAAGCCCATGAAAAAG	60.202	20	168	1182	1349
TCTGTGCACCATCAAACTCAA	60.294	21	202	914	1115
CAAGAGAGGGCCAAGTCAAT	59.284	20	219	148	366
GCAAGGGTGGTGCTCTTATT	59.198	20	256	5	260
CAAGGAGCATGTGGGTCAG	60.253	19	261	109	369
CTTCCTCATTCTCCGCAGTT	59.43	20	190	2461	2650
CCATTGAAGCTGCACTGTTT	58.926	20	241	2133	2373
CATCATCATCCTGTTGTCGG	59.918	20	172	219	390
TATCGATGCACAAGATTCGC	59.799	20	232	510	741
TTTTCTATGACGCGGAAACC	60.074	20	231	83	313

TTGCTTGCCTCGTTTAATTTG	60.245	21	147	647	793
CTTTTCCCCTAAGCACAGCA	60.378	20	180	113	292
GCAACCGAGAGGTTATCGAC	59.7	20	271	2601	2871
TCAAGCACAAATCTCGATTAC	59.229	22	188	269	456
CAAATTCCATGTGTCGCCTAT	59.837	21	262	610	871
CGTGGGTGTGAAGCTTGTAA	59.758	20	257	1669	1925
TGCATTCCTATGCCAGTCCT	60.624	20	186	993	1178
TGTAGCCGACCCCAATTTAT	59.297	20	213	1654	1866
TCCCAAAACATCACCTCCTC	59.903	20	111	28	138
TTCCTATAATGCCCCTCGC	60.009	19	120	28	147
CAAAGAAATCATTCACATTCG	59.451	22	114	160	273
GGAGGTGTTGGACAGCCTAA	60.111	20	255	134	388
CCAATGACCAATACCCATGA	59.049	20	237	67	303
TATGGCGGGTGACCTAATTC	59.784	20	261	6	266
TGATTCTGTTGATGCCAAATCT	59.574	22	203	4164	4366
TGTAGCCGACCCCAATTTAT	59.297	20	249	80	328
AAATGGTTTCCATTCCTTCCT	58.813	21	200	45	244
TTTTTCGTTGTTCCCTTGGA	60.452	20	262	474	735
GCACTGATAACTTCTCCCGC	59.843	20	165	138	302
TGCACGTAGATGTCAGAGGG	59.855	20	247	66	312
CGATTCGGTGATTCCAAAAT	59.762	20	212	1316	1527
CCTAAATCCCAATTACGGGA	58.759	20	229	4796	5024
GGGACCTTTCAGTCACCAGA	60.088	20	136	1569	1704
AGTCGGCATACTAATGATAAT	59.022	25	273	2829	3101
TGGTGCCATCTTCTTCACAA	60.24	20	145	881	1025
GGTTGCACAAAGTAGCTTCAC	60.347	22	216	77	292
ATGGGCTTTTCTCACCCTTT	59.94	20	220	1207	1426
CGTAATCCGAAGTTCCATTCA	59.946	21	266	895	1160
CGCGGATAGGATCTCTGTGT	60.24	20	258	128	385
TCTCGAGCATGTGGTGGTT	60.263	19	279	487	765
TGTGGAGCTTGATACGACGA	60.413	20	233	2169	2401
TGAATCCCTATTGTCGAGAGC	59.283	21	191	876	1066
GTGAAACTGCGAGTTCAATCA	58.914	21	156	218	373
GTGAAACTGCGAGTTCAATCA	58.914	21	156	217	372
TTGAAAAACCCTGGTCCTTG	59.942	20	112	12	123
AAAACCGTAATTTCACCCCC	59.924	20	247	1300	1546
TGAAATCGATCCCGATTATTCT	59.772	22	175	949	1123
CTTTCCGATGCGAACAAAAG	60.742	20	242	1878	2119
TTAATGGCTTGTGAATACGGC	59.978	21	272	5	276
ATATCATTCCCCGAGAGGCT	59.888	20	171	125	295
CAAACTCCACCCAACCACTT	59.861	20	155	2323	2477
CAAGGGTAAGGTTGCGTACA	58.699	20	191	139	329
AATTTCGGCCACCATTGTTA	60.188	20	279	469	747
TGACCCCCAGACTCGATAAC	59.927	20	151	2664	2814
TTAAAGGTCCATCAATGCCC	59.762	20	200	127	326
AGTGCGTGAAGCAAGTACGA	59.664	20	261	121	381
TCGTGGGTAAACACACCAAA	59.857	20	233	388	620
AGGTGGTGTGGTTTCAGGAG	60.002	20	224	416	639
GCAAATCGAAACCCTTTTCA	60.053	20	260	879	1138
TTGTTTAGGGTTTTGGGCTG	59.968	20	191	1205	1395
CACAACAAGGACTTGCATGG	60.152	20	107	49	155
GATTTCCAAAACACATTGTTTC	60.128	24	188	207	394
ATGTGCTAACCCCTGGCTTT	60.875	20	181	450	630
GTTGGGAGTTCCGACCTGT	59.953	19	247	3	249
AAATATGGCCAAGTTCACCG	59.823	20	278	1725	2002
TCACGAAACAGGCAACAAAA	60.271	20	161	125	285
ATACGGCGAGGATTAGGAGG	60.431	20	218	812	1029
GCATTTGATACCGTAGCAGTT	59.706	23	191	334	524

ACTCGCAATCTTGAACAGGG	60.255	20	268	2158	2425
CTTACGTAGCGGAAAAACGG	59.774	20	200	563	762
GCGAATTTCATCCGTTTTTG	60.436	20	181	937	1117
TCTGCATGCATGGCAATAAT	60.066	20	157	1492	1648
GAGGCTACTACATTTTGCCCC	59.979	21	191	26	216
CCCAAGTCGGTTTCAACTTTT	60.371	21	213	306	518
TCATCATTGGCTCCCATTTT	60.274	20	177	97	273
TCAGTATGTGATCCGCCTTTT	59.583	21	216	0	215
CACGGATTCGAATTGTCTTCT	59.184	21	252	751	1002
AACGGAAACAACCTCTTTGC	59.218	20	267	42	308
CGATGTTCGCTTCCACTACA	59.864	20	280	50	329
TAGCGAATGATCGACCTGAA	59.375	20	137	456	592
AACCCCAAAGACCTTAATTTG	58.907	22	102	706	807
ACTACCCGAGCTTCTCCCAT	60.096	20	241	414	654
AGATACGACCTTGCTCGCTC	59.603	20	154	320	473
TGTGCTCTGAATAGGACCGA	59.394	20	243	3508	3750
CACAGACACAAGCCTTCCAA	59.873	20	137	491	627
TTTTACGCTTAAACTGGCCG	60.251	20	249	361	609
ATTCTCCCATGCCCATCAC	60.708	19	195	206	400
GCAAGAGATTCTTTGTCGCC	59.962	20	172	1347	1518
ACCTTCATAATTCTCGAAAGGT	59.104	24	216	24	239
GGAGGAGGAGGTGGTGATTC	60.86	20	190	478	667
TCAAACTCGTGTGAACCCAA	60.128	20	147	342	488
CTGTCTTCACTGTCGCCAAG	59.616	20	155	474	628
CTGAACCAGAAGAGCCGAAG	60.126	20	248	1637	1884
TTGGTGTGAGTGGAGTTGGA	60.129	20	203	704	906
TCTTCTTTAACCGACCACCA	58.201	20	152	3	154
AAAAACAGATTCCATGGGCA	60.309	20	198	420	617
CCGCTATCCCCTCCTTTTTA	60.393	20	252	55	306
ACGAGGGATCGCATATGATT	59.372	20	195	254	448
GTCTCAGGGAAGAGGCAGTG	59.986	20	231	130	360
ACCCAATTGTTGTGGATGCT	60.24	20	163	883	1045
CACCAAACCTTAGGGCTCAA	60.103	20	278	1889	2166
AGTCCAAATTCGTGTAAGAAAT	59.101	24	111	266	376
GACGTGGATCGATGTGATTG	59.925	20	276	1295	1570
TGATTCGTACCGGGTCTCTC	60.073	20	135	791	925
TTTGGTCACTTTGCACCTAAAA	59.663	22	172	496	667
CCACCACCCACTCCAATACT	59.697	20	219	169	387
CTGGATGGAGAAGGTCTGGA	60.191	20	194	733	926
TGGGGAACCACCATGTTTAC	60.474	20	171	11	181
ATTGAAGAGCGATTCCGAGA	59.917	20	117	73	189
AATTTTCGCCATTTGCTTGT	59.592	20	234	392	625
GCATGGACAAGACGGGTAGT	59.997	20	163	1831	1993
ATCGACATTGAGGTCAACCC	59.786	20	137	901	1037
TCGATTGCCTCTGCAACATA	60.366	20	277	1328	1604
TGCCATAACGGCTAGTCTCA	59.444	20	252	100	351
TGGCCGTGACATGAAATACA	60.936	20	158	396	553
GGCTATTGAGGAAGATGCGA	60.318	20	274	2169	2442
GAGGAGTCAGACGCGAGAAG	60.284	20	145	5	149
GAAGCGAGTCACCCAAGATG	60.801	20	183	560	742
CGGGAAGACCAAAAAGTCAA	60.081	20	252	27	278
TGGCCCATTTTTGAATTTGT	60.167	20	155	738	892
TTTGCACTTTTTATGGGGGA	60.294	20	269	47	315
TTAGCTACAGGTGGGGTTGG	59.986	20	254	102	355
GAAAGTGGAAGCGAAGGACA	60.375	20	259	822	1080
TTTTACGCAAATCCGAAGGA	60.56	20	245	477	721
TGTTCGTGGAAGCAAAAGAA	59.439	20	173	146	318
CACCTCGTGAGAAAAAGGGA	60.224	20	210	3480	3689

CTTGGACACGTACACTTGCG	60.361	20	121	1846	1966
AGAGGAGGTGGAGGTGGATT	59.929	20	268	564	831
AGAAGGGCCTTGTCTTCCTC	59.817	20	270	24	293
AATTCTTCCTTGGTGGGCTT	59.94	20	260	416	675
AGAAAATGCTGGAAATGAGGA	60.075	22	161	269	429
GATTTAGCCTTCCGGCTCTT	59.82	20	208	118	325
GGATGTATCAGGTGGTGGGT	59.511	20	255	787	1041
ACTGGAAGCGATCAATCCAC	60.081	20	256	1522	1777
AGGGATCAAAAGCCAACCTT	59.94	20	150	339	488
ACATTTCATTGCCATTTCCA	58.82	20	196	629	824
GAAGGTTTTGATAAATACGATT	59.382	25	130	1220	1349
GTCGCAGATGAATCCCTTGT	60.081	20	277	2294	2570
CGGGGATCAAATGAAATCAA	60.64	20	227	576	802
TGTGGGAGAATCAAAGAGGC	60.195	20	248	422	669
CTGATTGTACATGGTGGCGA	60.539	20	274	9812	10085
ATGTAGCCGACCCCAATTTA	59.297	20	214	309	522
ATGAGAGGGGAGAATGGGTT	59.755	20	215	783	997
GCAACGGAAACAACCTCTTT	59.218	20	150	12	161
AGTTCATGTGGTTGTTGGCA	60.008	20	103	11	113
TGCCAAAGTCTCCCATTTTC	60.051	20	203	3828	4030
TGGCGGCTAAAACCCTAATA	59.581	20	264	261	524
CGTGTCCCCGTCATGTAAAG	61.343	20	193	93	285
CAGAGCGCACTCGAAGAGTA	59.49	20	117	379	495
CCTCTTCATTGACTGGTGCC	60.656	20	153	11	163
CGCCTCCGATGTTTAAGTTC	59.708	20	231	129	359
CCTTAGTGCCTCTTGGCATC	59.836	20	276	1884	2159
AGCATGCACAACTAAAAAGCA	59.952	22	208	444	651
AGGTTGCGTACATCTGACCC	59.997	20	171	10	180
ATATCACCACCTCCACCACC	59.511	20	272	124	395
ACATGCAATGTTGGGCACTA	59.995	20	273	767	1039
CCCCGAACAATTTTTCCTTT	60.157	20	233	153	385
CGCCTTATGAGGTTCACCC	60.467	19	274	1143	1416
TGGGTTGGTGGTTTGGATAC	60.474	20	180	118	297
AGGTTGCGTACATCTGACCC	59.997	20	117	40	156
TTTGTTTTGTCCCCATCAAAG	59.825	21	170	132	301
TTAGTTCCAAATTGTGCCCT	57.217	20	245	2476	2720
GGAGGGTGTTGAGTTTGAGG	59.549	20	271	605	875
AAAAGCGTTGGAAAGCTGAA	59.996	20	159	108	266
ACCATGGAAAGTGCTTGTCG	61.096	20	270	74	343
GCTCTCCTTCAACCTCCTCC	60.336	20	243	249	491
TGGATATCATTGTCGCTGCT	59.256	20	210	129	338
TGGATATCATTGTCGCTGCT	59.256	20	210	132	341
GTCCTTTTCTTCATCCTCATCC	59.037	22	100	150	249
AGTCGACGGTCAATTTCCAG	60.111	20	108	8	115
TCGCCGCTTCCAGATATTAC	60.196	20	155	625	779
ACACGACAACCCAACACAAA	59.897	20	213	9	221
TGTTTCATCTGCTTGTTCGG	59.84	20	121	173	293
CAACAATTATTGCGCTCGAA	59.842	20	238	301	538
CGGTTGACCTCACCACGTAT	60.833	20	221	285	505
GAATTCGAGCTCCGGTAGTG	59.836	20	143	1313	1455
ATTACCTTCTCTCGCCGGAA	61.08	20	227	87	313
TACATTAGCCGTAAACCGGG	59.847	20	269	54	322
TGAAAAGTTTGGATAATTCAC	58.664	23	267	26	292
TCATTCCACAATCACAACCC	59.193	20	202	1042	1243
TCATTCTCGGAGTTGAGCG	60.08	19	208	1055	1262
TCGAAGCATAGATGCCCATA	59.236	20	217	636	852
CAAGTTTGGGAGGTTGGATG	60.345	20	164	0	163
GGAGTCTTCTGCATTTGGTTG	59.726	21	166	885	1050

AGCCACACAACCCACAAAAT	60.277	20	150	2	151
CCCAAGACCCCAATTTGATT	60.91	20	193	2817	3009
TGGATTCCTTGTTCGATTCC	59.871	20	186	307	492
CCAGTTTTCTTGTCGAGGGA	60.224	20	162	927	1088
TATACACCATCATGACCGCC	59.23	20	152	860	1011
GCAACTTCAGCAGCAACAGT	59.243	20	145	1	145
TACAGAGTCGGACGATGACA	57.745	20	280	257	536
ATTGCGTAAACCTGACCCC	59.805	19	187	722	908
CCCAAGACCCCAATTTGATT	60.91	20	111	1205	1315
TTGGATAGTAGGATATGATAA	57.698	26	246	175	420
TGGCCAAAACGATTCTCTAA	58.361	20	270	62	331
CTCCTAGCTGGAGACCCCTT	59.834	20	174	115	288
TAAGGTTAGCAGTTTGGCCG	60.257	20	264	197	460
TCCAATCACGAGAACACGAG	59.831	20	248	73	320
CGCCACATTGCTTACAGAAC	59.347	20	129	127	255
TGTAGAACCTTCCAATCCGC	60.074	20	267	185	451
GCTTACCGGCGACTATCTCA	60.374	20	225	482	706
GCCATGAAATTCCCATCACT	59.756	20	248	8	255
ATGTGCACCGACAGTTTTTG	59.615	20	272	642	913
CCAATTCGAAGCCCAAATTA	59.901	20	198	258	455
ACCCAGAAAAACGAAACACG	60.008	20	275	30	304
CAAGCCACAGCTGTTCAGAG	59.77	20	207	306	512
TGACAATTGGTTTCAGGCAA	60.088	20	240	30	269
TCACTTTCCTTTTTCGGACG	60.22	20	242	7	248
TTTGGAAGGTGGAACCTCAT	59.381	20	280	295	574
CGAGGTGATTTGGACCAGTT	59.966	20	111	1798	1908
TCATAACAGTCTTCGACTAGCT	58.036	25	262	98	359
GATGATGTATGCCTGTGGGA	59.327	20	165	7	171
TGTGTGGAAAAGGGGAAAGA	60.465	20	279	59	337
GGTGACCAAAGAGGTGGGTA	59.82	20	249	223	471
GCATGGTCTTATTGACGTGC	59.156	20	240	584	823
AGTTTAAACCCTCCCAACCC	59.191	20	216	89	304
TCAAAAGATGAGCTACGAGCA	60.152	22	242	375	616
AGGATCACCAAAGGGACACA	60.363	20	247	72	318
CCTAACCTGCGTTGGAACAT	59.993	20	189	126	314
TTTGAGCAGGAATGTTCTTCA	58.488	21	251	70	320
TCCTCAATAATCAAACCTCGG	59.03	21	176	985	1160
TGAATTTGCGACATTATTCATT	59.854	23	255	13	267
AAGTTCACATTGAAATCGACA	60.042	24	269	231	499
TTACAGTTGCCGAAAAATGC	58.819	20	125	16	140
TTCAAACTCCATCGCTGAAA	59.395	20	171	298	468
TTGTGTTAATTATGTTTCAGTTT	57.115	26	249	1744	1992
AGGGAAGAGAGAGAGTCGCC	60.096	20	219	461	679
TCCCACAAAACCAAACACAA	59.834	20	263	1075	1337
TTTCATCAAAGCCTGAAGCA	59.542	20	196	222	417
CTCGGGATCAATGACATTCC	60.281	20	271	708	978
GTCGGAGTTGGAGTTCTTGC	59.851	20	175	1406	1580
TGGGTTCATTATCAAGAATTGC	58.946	22	241	15	255
GGGTTTTAGAGGGGAGTTGG	59.799	20	156	760	915
TGGCAGAACCAACCCTAAGA	60.626	20	245	366	610
AGCATGTGACATTTCCCGTT	60.384	20	271	1115	1385
GAAAATGAGGTGGGATGTCG	60.317	20	169	291	459
TCTCTGAATCCGGCCTAGAA	59.91	20	220	2442	2661
CTTCATATTGGGGCCCATC	60.103	19	253	468	720
TGCCCTAATCACACATTTCCT	59.443	21	191	218	408
AACAACATAAGGGAAGGGGG	60.046	20	231	1453	1683
AAGACCGTGGCGAAAATATG	59.96	20	147	1359	1505
GTGGGACCTTGCTACTGAGC	59.874	20	260	1583	1842

GTGACAACGATGGATACCCC	60.057	20	140	48	187
ACCTCCATCACCAGGCATAC	59.81	20	215	3494	3708
ATTAAAATGGTGCGAATGGG	59.66	20	260	4	263
GGGATGGAGAGGATTGGTTT	60.133	20	185	290	474
GAGAGAGGGGAAGCAGAAGG	60.468	20	117	3656	3772
ATCAGCCTTCGCCACTACTC	59.459	20	267	6780	7046
ACAATTGCACGATGTTTGGA	59.972	20	263	503	765
TTTTCAACCCTCATACCATATT	58.384	24	237	1439	1675
GCAGTTGTTGCGGATAGTGA	59.871	20	252	105	356
GTGCGTGTGTAACCGAGAGA	59.905	20	279	406	684
CCAAGGAACTTTTCTCCCAA	59.143	20	270	2615	2884
CCCTAGCCCTACCGGAACTA	60.455	20	247	553	799
CTCTCCCACTATTCCCACCA	59.92	20	137	212	348
TTTGCCAAGAGACACGACAC	59.88	20	204	1927	2130
TCACGTAAAGCACAACGCAT	60.324	20	241	802	1042
CGAATTGAATTAATTTTATGAA	59.807	26	213	98	310
CCCCACCAGAAAAAGGATAG	58.502	20	103	20	122
GGATTAAGGGGTTGAGGAGG	59.761	20	181	898	1078
ACATGAAGCTGAACTCGCTG	59.191	20	207	538	744
CGTGTCCTTATCGGATCGAC	60.483	20	173	24	196
ACAGAAACACAGCGGGAATC	60.119	20	269	1427	1695
TCGTTGATGATGCAAAGAATG	59.679	21	252	180	431
GAACCAAAACTTGCTGACCC	59.574	20	101	49	149
TCCAAGTCCCCCTCATACAA	60.309	20	167	0	166
GACATCTGGCCCATTTTCAC	60.326	20	251	169	419
ATGAGACTAGATGGCGGGTG	60.096	20	266	94	359
AGGTTGCGTACATCTGACCC	59.997	20	119	42	160
GGGCTTCGTTTGATGACTGTA	60.125	21	214	62	275
ACACGGGTGGAAGTGAGAGT	59.604	20	190	439	628
CATCCACAGTGAAGACCACG	60.154	20	232	45	276
CCTCTCCATCAGCTCCTCAC	59.945	20	240	1219	1458
TGAGAGGAAGATCCTCGGAA	59.879	20	247	72	318
TCATTGACTATTCTTTTAACTTT	59.262	27	204	1556	1759
CTTGGGAGTTGCTTCGTAGG	59.869	20	271	141	411
TGGGTCCTATCCAGTTTGGT	59.259	20	150	3843	3992
GGAGAGGCGTGGCAATAGTA	60.235	20	121	278	398
TGCCATACAACACCACTTGC	60.584	20	143	349	491
TTGGGCACTGAGATTCTTGA	59.369	20	241	154	394
AGCACGTCCAGAGGAGACAT	59.866	20	168	112	279
GACCGTACAAGATTGCGACA	59.722	20	217	1016	1232
TTGGTCTCAGGAATGGTGCT	60.656	20	279	102	380
GGAACACTGCAAAATGAGCA	59.847	20	263	31	293
TCCGGTCAAAAACAGAAACC	59.948	20	161	365	525
CCTTCTTTAGAGGTTGGGGTG	59.977	21	193	207	399
TTGGTATCTTCCTTGCCGTC	60.074	20	125	48	172
TGCGACCACTAAGCAACAAC	59.911	20	179	2541	2719
CGATCCTTTATGGATTGGATCA	61.002	22	276	872	1147
CAACTTGACATAGCATTCCCA	58.637	21	113	1	113
CTCTCTGCTCACGCTCTTCC	60.431	20	190	320	509
CCCAAGACCCCAATTTGATT	60.91	20	195	1	195
AAAACCAATTGACAATGAGAG	59.864	23	253	95	347
AAGAGTGCAGCCATCGTACA	59.47	20	145	224	368
TGCCCTAGATCTCACACACG	59.855	20	195	466	660
TGGTGATATTATTGTGATTCCC	59.801	23	271	363	633
CCATTTAGCAAACCCCACAT	59.685	20	136	23	158
AAATTTTCATTTTTACTTACGC	59.89	26	217	166	382
GACACTTTGGCGCTCGTAAT	60.278	20	151	306	456
TTATGATTCGGGTGTGTGGA	59.774	20	165	89	253

ACCTTTTCTCCATTTTCCCG	60.291	20	171	1320	1490
AGAGACGGTGACGTATTGCC	60.142	20	237	488	724
TCTGGGTTTTATTTTTGCCG	59.937	20	279	1958	2236
TCTCCAAAATCGCAAACCTC	60.192	20	147	399	545
CAAAAGGACAAGGGTTCGAG	59.705	20	118	15	132
ATCCCTAGAAGCGCACGAGT	61.306	20	170	277	446
CAGCAGTCTGGATCTCCCTC	59.945	20	241	15	255
TAAAAATGAACGAGTCGCCC	60.074	20	213	1190	1402
GACCACCTTTCTTTCCACCA	59.943	20	141	13	153
TTCCTATTTTTCAGAGTTGAAC	59.203	24	250	185	434
TTGGGTTTGGAGTGAAAACAA	60.363	21	273	1781	2053
CACCTTGAATTGACTGCCATT	59.985	21	206	439	644
CTTTCTCATACCCTCGTGGC	59.694	20	277	23	299
CGGTTCATGTGTGTACTGGG	59.873	20	247	420	666
TGCCAGAACACATAAATTTTGA	59.524	23	219	213	431
TCAGCAGCCATCTGTTCTTG	60.136	20	245	335	579
AACAAACCCATCACTCCGAC	59.827	20	125	1566	1690
TCTCATTCTTACGAGTGCCGT	59.89	21	217	186	402
GGATGAAGAGGGAGGGTTTG	60.822	20	144	0	143
TGGTGATGGGATGACTTCAA	59.893	20	231	730	960
GCTTGAAGTAGTGGGGATCG	59.694	20	136	131	266
CCTTTGAACAAAGAGTGGGG	59.563	20	260	65	324
TGTAGCCGACCCCAATTTAT	59.297	20	172	243	414
GGAGGCATAAAAACCCCAAT	60.02	20	244	77	320
TATATGCAGGTGTGCCTTGC	59.718	20	252	1882	2133
GGTGCAAGAATTTCCCAAAA	59.916	20	235	17	251
CACAGGGCTTAGGAATGGAA	60.066	20	239	379	617
TTGACCCCTTCACTATCTCCA	59.536	21	274	346	619
GGGTCCTTGCTAAATTGCAC	59.574	20	169	5	173
ATGTTTGGTTTTGAGGGCAA	60.344	20	227	350	576
TGCCACCACTCTTCTTACCC	60.111	20	170	698	867
AGCAGAGTTTGTTCGTCGGT	59.914	20	258	437	694
TGTAGCCGACCCCAATTTAT	59.297	20	180	2356	2535
TTCACGCCTAATTAAACCATTG	59.044	22	270	314	583
ATAAAGGTGGCATGAGCAGG	60.096	20	173	764	936
AGCTCAGGTTGTGCACGATAA	60.842	21	106	12	117
CATTATCTAATGATTAACAGTT	57.748	26	159	296	454
TCAATGATCCAATCCCCACT	60.135	20	278	943	1220
TCTGTGTTGTGGGTTGCAGT	60.203	20	136	1665	1800
AGGGTCCCTCCTTATTGACA	58.446	20	201	156	356
TATTCCCTTGCCAACGTTTT	59.451	20	170	211	380
GGTCGAGTAGAAGAACCCCC	59.935	20	145	358	502
GCGCAAAACAAAACACATTG	60.155	20	224	3431	3654
TTTGGTTCATGTAGCCGACC	60.894	20	228	729	956
TCAATGAAACACGCTTTGGA	60.234	20	196	1446	1641
CGACATCGCATCTGGAAAT	59.62	19	274	407	680
TTGGGGATTGAACCCAGATA	60.126	20	130	602	731
CGGTGGCTGTTATCGAAGG	61.577	19	246	344	589
CGATGCCGTTTGAAGGTACT	60.132	20	264	227	490
GAGTTGGCTCACGATACGGT	60.142	20	242	70	311
TGAAGGAACAGAAGAAGCGG	60.508	20	262	417	678
GTGCAGCTCCTCAAAAAGGT	59.478	20	228	6	233
TGGGGGTGCATTTAATGTTT	60.053	20	178	1687	1864
CAGAGCGCACTCGAAGAGTA	59.49	20	258	783	1040
AACGTGGGGTGTACGTTGTA	58.825	20	265	704	968
TGTGTGAGTTTGGTTAGCCG	59.758	20	123	34	156
GCAATAAATTTCTATGTTGCTC	59.562	24	274	628	901
AGTTTAAACCCTCCCAACCC	59.191	20	237	101	337

TGGGACAGAGAAAGAATGCC	60.195	20	163	111	273
TGTAGCCGACCCCAATTTAT	59.297	20	261	151	411
ACACGTGACAATGAAAAGGG	58.469	20	187	14	200
GGAGCTTGCGTCTTGTCTTC	60.142	20	280	152	431
TGTGTAGGAAGATGTTGGCG	59.716	20	181	660	840
ACACCAAAAGCAAAAGGCTG	60.284	20	272	2	273
TTGCTCAAATATTTCAAAAAGC	60.126	24	277	2	278
ACCTCCCGAAAGAGGAGACT	59.295	20	264	483	746
AGCGATTCTCTTCGAGCAAG	59.859	20	157	131	287
ACAAATATGCCCTTCTCCCC	60.152	20	113	31	143
ATTTGGAGGGCAGCAAGTAA	59.708	20	202	164	365
AAAAAGCCACGACCTCTTCA	59.853	20	267	873	1139
TCATCCCTTCCAACTTCTGC	60.195	20	222	940	1161
GGAGATTTCGCCATTCAGTG	60.603	20	162	31	192
CGTAAAAACCCGAGAAATCG	59.581	20	177	81	257
TCGCATTCTACTCCATTTTCCT	60.095	22	267	113	379
AATGAAGACTTTGGGGAAGGA	59.926	21	227	245	471
GCCGATTTGTAAATTTGAGG	57.255	20	275	345	619
CAATGGTCCAATTTCCACCT	59.647	20	251	4	254
TAAGGCTTACGTATTGGCGG	60.109	20	127	432	558
CTCGAATTCAAACCCTCCAC	59.526	20	101	32	132
AATTTGATTGGGAATAATTGG	58.965	22	138	1686	1823
AAACAGACCCACCAAGAACA	58.03	20	275	6	280
TGTAGCCGACCCCAATTTAT	59.297	20	119	618	736
TTCCATTATTGCTTCCACCC	59.762	20	170	1538	1707
GATTGTTGAAGGCCGACAGT	60.119	20	247	9	255
GCAAAGGTTTTCCGATCAAA	60.053	20	222	74	295
ATCGGGAAAACGAGGAAGTT	59.94	20	140	867	1006
GTAGAGGTGTCAAAACGGGC	59.598	20	279	91	369
ACCGAATCGGATTGTTTCAA	60.309	20	172	352	523
GACGTGCATGAAAGTTGCTC	59.45	20	261	298	558
GGCAAACCACCCTTTTCTTTA	60.33	21	205	299	503
AATAAGCAGCAGGGCATGAA	60.742	20	216	376	591
GCACATGCATTGAATTTGGT	59.405	20	176	503	678
CTTAAGCGAGAAAAGCGGC	60.237	19	135	31	165
CAGAACACGTTTTAAATGTTG	59.085	23	154	0	153
TTTTACTGGCGTGTGGATGA	60.111	20	275	840	1114
TCGAGTCCACTGTGCAAGAT	59.42	20	175	1105	1279
TTGAAGGGACCCGTGAGTAA	60.486	20	248	1248	1495
TGGCCTCTTCAGAAGGAGAA	60.065	20	151	103	253
ACCTCAAACACAAAAAACCCG	59.869	20	273	13	285
AGGTCATCTCTCCCAAGTCAA	60.11	22	258	160	417
CTCTTTTCTCTCCCCCGTTT	59.685	20	127	85	211
TCCACGTGGCTTATGGAGAT	60.483	20	269	18	286
TTCTCAGCCTCAGCTTCTGG	60.812	20	199	804	1002
GCTCAAATCGGAATTCAAACA	60.067	21	169	6	174
CGACTGGGCCTATCCTATCA	60.051	20	272	571	842
ATGGGCCCAACACCAGATA	61.143	19	210	662	871
AAAATCCTGTGTAGCAGGGCT	60.144	21	257	511	767
TTCCAAGGTTTGGGTTTCAT	59.264	20	234	428	661
TTTGATGCGCTCTAGTTGGA	59.566	20	266	60	325
CCCAAGACCCCAATTTGAT	59.59	19	204	1	204
AATCAACGAAATGAAACCGC	59.945	20	166	269	434
ATCCGAGCAGCCTAATGAGA	59.939	20	245	553	797
GTTCGAAGGGTTGAGGATGA	60.05	20	265	119	383
TCTCCACTCTCCTCAATGGC	60.349	20	105	243	347
TTTCATTTGATATTTCCAGAGA	58.566	24	265	297	561
GGGAGGCTATTTTGGAGAGG	60.032	20	219	777	995

CGTATCGGATTAATGACTCGC	59.583	21	269	345	613
AAATTGGGCACCAGAATCAG	59.933	20	159	233	391
CTGGACAGACAACTGGCAAA	59.873	20	103	2437	2539
ATGTAGCCGACCCCAATTTA	59.297	20	212	2320	2531
CCCAAGACCCCAATTTGATT	60.91	20	165	1076	1240
GAAAAATACAGCTAATCGGTC	59.786	24	239	283	521
AGTGCAGCAATACCAAACCC	60	20	184	172	355
TCATCAATGGGATCTGTTGC	59.456	20	157	803	959
ACGTGAGTTGGAGGAGTTGG	60.151	20	268	2145	2412
TGAGGCAAGACATCCTCCTT	59.803	20	273	508	780
TTGCATGCCTAAAGGGAGAC	60.214	20	268	61	328
GCTTTAGTGGGACATCCGAG	59.694	20	262	1874	2135
TACAATGGCCTGAGCAAGTG	59.864	20	233	507	739
CTCTTCGAGCGAGTTCAAGC	60.419	20	153	256	408
CTTTTTGCCCTATTTTCCCC	59.782	20	253	534	786
AGCTTTGCCGGTGTCATAAT	59.597	20	270	2228	2497
ATTCATTGGTTCTCCATCGG	59.75	20	267	579	845
TTTGGGATACGACCTTGCTC	60.074	20	217	365	581
GCCGTTATCACTCAGTTTTCG	59.761	21	257	460	716
AGTTTTAGGCGGGAAAGCTG	60.731	20	256	29	284
CACCGCAAATATACGAAGCA	59.725	20	167	854	1020
CATCTGATCCACCGCTCTCT	60.372	20	263	525	787
ATGCTGCATGCACTATTTGG	59.718	20	113	779	891
CGACTGACCCTTGTTGTGTG	60.194	20	171	90	260
TCGAGCAGGAAATGTGGATA	59.226	20	273	1396	1668
ACTGGGACAGGCTCTTGTGT	59.756	20	158	21	178
GATCGGCAGTGGCATTTT	59.61	18	113	502	614
ATGGAAGAACCCAAAAAGCC	60.299	20	116	1283	1398
GGATTTTCATGGGTCGTGTC	60.181	20	280	3691	3970
CGGAACAACCTATCAGGCAT	59.955	20	174	3429	3602
TCTTGCAGCACTATGGGAAA	59.42	20	146	12	157
TGAAAACGGTTGATTGCAGA	60.234	20	264	42	305
TTCATATTCCTGGCGAATCC	59.862	20	119	2214	2332
GTTTTAATGCATCGGCTGG	59.126	19	280	947	1226
GGTGGTGCTCCAAATCCTAA	59.933	20	103	1843	1945
TTGGGGACAAAGCAAAATTC	59.916	20	146	7	152
TTCCCGAGACTGAGATGGAC	60.199	20	226	192	417
CAGAAAGGGGCAGATTCTTG	59.807	20	203	3242	3444
ATGTCCCACCAATTTGTCCT	59.116	20	191	12	202
TCCCTCATTTGAACAAAACG	58.597	20	255	1106	1360
CAAAATGAAGCAGACTGCCA	59.988	20	138	321	458
ACATCAGATCTCCGTCAGCA	59.372	20	193	14	206
TGATCTTGAAACCGTGATGG	59.496	20	264	3413	3676
TAGGGGCTCGGGATTCTTAC	60.411	20	242	477	718
TTTATGCATGCGTTCACTCC	59.694	20	276	400	675
TTGCTGTGCATTTAACCACG	60.698	20	223	81	303
TTACATGCAACCTCCTGCTTC	60.264	21	243	1433	1675
TGAGACGAGAGAGGGGGTAA	59.797	20	266	280	545
TGGTTTTGGCAAACTGTGAG	59.734	20	129	431	559
TTGCAAGAAAACTGTCCCGT	60.668	20	233	71	303
TGCAGGAACACCTGAATCAA	60.24	20	255	79	333
CCGCAGAGGCGATCTCTA	60.201	18	166	217	382
AATGGGGTAGCCTGGAATTT	59.666	20	252	347	598
CCGGTTTCTGAATTTGATGG	60.301	20	273	107	379
CCAACCGAACTAGCAGAAAA	58.027	20	280	12	291
CCATTGCTTAAGCTCCCTTG	59.839	20	207	256	462
AAATTAAAATTGGGAGCGGG	60.142	20	274	46	319
CACAACCATGTCAGCCGTTA	60.574	20	120	178	297

CATCGCATTCAATTACCCAA	59.377	20	189	408	596
CCAATTTATTGGGATTAAGGC	57.539	21	279	791	1069
CATATCCATGGGTACGGAGG	60.029	20	223	908	1130
CTCGACGTTGCAGAAGTTTG	59.634	20	108	111	218
GGTGGTATGGTGTGGAGGAC	60.096	20	103	74	176
AAGTGGTAGGCGGATTCCTT	59.962	20	240	691	930
TGATTGGTTAGAGAGTATGTGA	59.971	27	279	557	835
TAATGGGGGTTTGAAGTTGG	59.657	20	274	42	315
TCGGGTTCATTCTGGTTCAT	60.317	20	149	324	472
TCACAACCAGTAAATATTGTAG	58.64	26	203	640	842
CCAAACCCACAGAACGAGAT	59.966	20	173	972	1144
TTCTTGCTTTTTGCCATGTG	59.849	20	170	796	965
GAGATGCGCTGGATAAGGAG	59.939	20	166	84	249
CGAAAGAGCAAATGGGAGTT	59.312	20	268	69	336
TATGCATGGATGGTGTACCG	60.22	20	252	1068	1319
GAAACGATCGCCTACGAGAA	60.352	20	214	46	259
CAATTGCAAGGAATTTCCCA	60.807	20	237	247	483
TGTTTAAAAGTTTCCTGCACAA	57.571	22	240	888	1127
GCATCTTCTTTTGGGGATCA	60.014	20	117	1119	1235
TGTCCTGGGGTTTTGAAAGT	59.425	20	277	10	286
GGGCATGTTTGGGAGTAGAA	59.933	20	254	413	666
CGCCGATCCCTACTTTTCTC	61.08	20	196	708	903
CTGCTCCAAGACCAAGAACC	59.844	20	230	837	1066
AAAAGTACGTGGGTCGTTGC	60.037	20	248	344	591
TTCAAATTAGCAACAAAAATGA	58.007	24	244	305	548
ATCGAGCATAGAAAGGTGGC	59.297	20	203	743	945
GGTAGTTCTGGTCTCTGGCG	59.867	20	140	1376	1515
GAAGGATGCCAATGCCATAA	60.807	20	245	126	370
TCCTCTTCTGCCATTTCAGC	60.483	20	160	1457	1616
TGGCAGATGATCAAAGGATG	59.604	20	200	3752	3951
CTCAGGGAGTTCCATGACTCT	58.327	21	101	595	695
AAAAAGCGACGAAGAACGAA	59.996	20	270	228	497
AAAATTTTCATCAGTTATTTGCT	58.388	25	178	27	204
CATAAGGGCGGGAATAAACC	60.508	20	261	178	438
CATTCGTTGTTGGAGCCTCT	60.255	20	109	11	119
CTTCTCCCCGTAGAAGCCAC	61.142	20	268	91	358
AAACACCTCCTCCCCATACC	60.052	20	235	572	806
TTGTTGCTTGGGAGCTTGAT	60.776	20	210	307	516
TCCATCTCCTCAAAGCACCT	59.803	20	253	1158	1410
TGCATGCTCATAATGCCATA	58.679	20	214	733	946
GTGTCAAGGATGGGGACACT	59.817	20	220	373	592
ACACCCTTGCGAATCTGAAA	60.636	20	224	242	465
CCCAAGACCCCAATTTGATT	60.91	20	153	64	216
TTACTGGCTCGTTCATGCAG	60.011	20	200	614	813
GCAACGGAAACGTCTTTGTA	58.822	20	153	347	499
ATGAGACAGGTTCTCGTCGAA	59.859	21	177	6	182
AGTTGCCTACAAGGTTCGCT	59.008	20	267	418	684
TGAGGGATGCATTAAAATAGGA	59.824	23	133	9	141
AGGTCAGAGGTGACGGTTTG	60.151	20	245	797	1041
AAAAATTTAGGGCGTTACGAA	57.906	21	270	1009	1278
TCAAACATTCTCCTTCCAAAA	57.325	21	121	24	144
AAACGGAAACAGATTCACCG	59.971	20	187	270	456
AAGTCCCAACATTTAGGCCC	60.187	20	227	2683	2909
GACAAAAATTTGGCGATGCT	60.081	20	270	61	330
TGATCGATGATCACCCACAT	59.724	20	240	490	729
GGGTCGTTCAGCCAATCTAA	60.074	20	278	2072	2349
ATGTAGCCGACCCCAATTTA	59.297	20	251	344	594
TTCTCTTTGGCTTTTGCAGG	60.493	20	279	358	636

TTCCTGACGCTGAGGAAGTT	59.989	20	241	297	537
TTGGAGGTTTGTGGTGTTTTT	59.364	21	219	1	219
TCCGAATATTCATTGCCCTC	59.862	20	276	175	450
ACATCGAATTCTTTGGCGAG	60.214	20	261	1218	1478
CCCACTATTTCCCCTGAACA	59.784	20	245	442	686
CCCAAGACCCCAATTTGATT	60.91	20	126	5014	5139
TCGCTAACATGGTTCGTTTTT	59.639	21	272	1227	1498
TTACGACCACTTGCTCCCTT	59.734	20	179	858	1036
ATGTAGCCGACCCCAATTTA	59.297	20	192	267	458
TTCCTTTCTTAAGCTTGTGAAC	57.936	24	193	510	702
CCGAAGACCTAAGCCACAAG	59.869	20	171	258	428
CAAAGGTTTCGCCTTCAATC	59.685	20	218	144	361
TTGTCAACCCAACGCTACAC	59.615	20	246	4795	5040
TTGAGCTTCTTCATCCACCC	60.195	20	160	398	557
ACACAAACCCAATTTCCGAG	59.83	20	237	351	587
TCATGAAGCTTCTGTCGCC	60.088	19	255	923	1177
TCATCCAAGTTCGTGTGAAATC	59.978	22	223	15	237
CCAAAATCTCGGCTTCAATC	59.645	20	207	893	1099
AGATTTTTCATGGCCCTTTG	59.019	20	271	175	445
ACCATAGCTCGGAACACCAT	59.434	20	219	5	223
TCTGATCCTTTGCATTTAGCA	58.52	21	280	477	756
GGTTGCCTGCACCAAGTAAT	60	20	117	46	162
ATGTCCTTTATCTGTTATGTTTT	57.249	27	280	1370	1649
TGGTGATCTACATCTCTTCCCA	59.55	22	197	240	436
TTTTGGAGGATTTGGAATGC	59.878	20	211	1208	1418
AGCAAGGTGATTCCTTGTTGTT	60.04	22	208	54	261
TCCTAAACAGATCGGACAACA	59.609	22	215	450	664
ACCACGTCAGCCAGGTAAAC	60.035	20	201	9	209
CCCAAGACCCCAATTTGATT	60.91	20	138	1233	1370
GGAAGAGAGAGAGGCGTTCA	59.679	20	200	385	584
CCGTCTGCGCCTTAAGTTAG	60.032	20	209	3	211
TCACGGAAAACCTAAGTGGC	60.11	20	225	582	806
ACGCTTCATTTCATCCCATC	59.9	20	228	843	1070
TATCGATGGAGCAGCAATCA	60.329	20	189	2337	2525
CTCGTCTTCCGTGGATAAGC	59.836	20	143	249	391
AAAGGAAATCCCCTCACCTG	60.298	20	204	204	407
TTCAGGTTGAAGTCTTGGGC	60.232	20	280	468	747
TCGACCGGCTTCATTTATTT	59.547	20	221	1272	1492
CGACTTTGGGGCAATAATGA	60.827	20	206	1293	1498
GAATTCAAGCCGGTTTCTGA	60.192	20	207	705	911
AGTAAAAACAGGCGAGGCAA	59.883	20	248	863	1110
ATGAGAACCCAAATCACGGA	60.317	20	212	836	1047
AAAAGGATGTTCCAAAGGGC	60.299	20	116	0	115
CCCCAATACCCCAATTTGA	60.369	19	223	968	1190
TGGTGGAGCGAGATAAGAGG	60.353	20	259	2385	2643
AAACCAGCTCATTTGTTGGC	60.118	20	164	2376	2539
ACGCGGATTTGAAAATGAAA	60.436	20	210	825	1034
CGTATTCTTGGGTGAGCAAAA	60.117	21	268	2304	2571
TGATCGCATGCCTTAACAAA	60.215	20	104	14	117
ATTCTATTGGGGCGGGATTA	60.478	20	279	523	801
AGGATTTTGAGGATGCGTTG	60.074	20	107	454	560
CTGATCGGCCAAAAACTAGC	59.845	20	271	1862	2132
TGATAAATTAAACGTAAGTGA	58.343	26	152	331	482
CACCAGCTTCGACACACAGT	59.94	20	180	1839	2018
TTGAGTATGGATCCACCGAA	58.923	20	259	1042	1300
GGGAGTGGCTGAGCTTGTAG	60.012	20	113	448	560
CAATCAAACCCCAAGACACA	59.389	20	199	588	786
TTGTCTGGATCCTTTTGCCT	59.67	20	262	1685	1946

CCTCCGCCTAGACTCCTTCT	59.972	20	279	345	623
GTTGGGAAACTCACGATGCT	60.119	20	142	1547	1688
CTCCGAATCAGAGCCTTGTC	59.95	20	238	1235	1472
GTTTGTCTGAAAAATCGGCG	60.617	20	269	671	939
AGCAAAAAGTTGGCGATCAT	59.713	20	248	155	402
GGTGCCGACCAGTAATACGA	60.914	20	249	2897	3145
TGCTAACAAATATGCATTCCAA	58.25	22	267	197	463
TTCACGTTCAATCCCTCACA	60.088	20	115	185	299
TGATATTCTTCGCGAGCTGA	59.67	20	193	2969	3161
ACCCTTGTGAACAAACTCGG	60.005	20	227	48	274
AATACGCACGAACATGAGCA	60.288	20	209	918	1126
CGGATTCCTTGGTTTTCAGA	60.044	20	261	411	671
GTCGGGACTCTGGTGGTAGA	60.112	20	121	1361	1481
GTGAAGCGAAAACTGAACGTC	59.912	21	280	58	337
ATCCCCTCCAAATTCCAAAC	59.996	20	229	418	646
TGCTTTCATCACTGGCAGAC	59.992	20	161	850	1010
CCAAATGTCTCCCGAGTTTG	60.486	20	113	307	419
CAACCTCAATTACCTCCCCA	59.784	20	278	4410	4687
CCAAGGTTCTGGGCTGTAAC	59.592	20	269	1070	1338
CATGAGCTCCGTGTTGAAAG	59.44	20	233	131	363
CCCATACCCACATTTCCAAG	60.044	20	129	1823	1951
GGCTAGTCGTCTCGGCATAC	59.866	20	228	1186	1413
TGTAGCCGACCCCAATTTAT	59.297	20	152	1283	1434
TTCCCAAGCCATCAATTTTC	59.878	20	267	114	380
AAAATCCTAATTGCTTTGCACC	59.525	22	236	504	739
ATAATTTATCCCGCAAGGGG	60.002	20	266	36	301
AGACTCGTTGCCAAGGGATA	59.694	20	250	1015	1264
AAATGGAGGAACATGCCAAC	59.797	20	276	1940	2215
TGTGTGGGAAAGGACAGTGA	60.129	20	224	186	409
AACCGACTTGAAACCTAGCG	59.378	20	274	50	323
AAGTCACCGGAAGCCATTTA	59.569	20	200	2658	2857
GATTGTTGAAGGCCGACAGT	60.119	20	280	265	544
AGGCAGAAATCAACCACGTC	60.119	20	131	18	148
TCCAGATGAGAAAGATGGGG	60.003	20	195	2356	2550
TGAGGAGTGGGTGTCGATTT	60.51	20	264	1095	1358
AAACACCCAACAGAAATGCC	59.836	20	245	1810	2054
GATTGGTGGGAAGATGATGG	60.135	20	261	544	804
TGACACAATACCCCTGGTCA	59.806	20	256	1059	1314
AAGCTACACGCCAATGGTTT	59.637	20	209	306	514
ATGCTAACTCCCCTTCCCAT	59.789	20	262	28	289
TGTTTGGGTGAACTTGGGAG	60.923	20	185	3	187
TGGAGAAAAATCAAAATCCCA	59.374	21	216	1383	1598
CGAGTTGCAAGAACCCTCAT	60.255	20	262	160	421
ACGCTTATTTTTGTAATGGAAT	59.73	25	267	12	278
CGACCTCACATAGTGGGAAAA	59.978	21	253	253	505
CAGCATCTCGATACCACAGG	59.267	20	239	232	470
TTGCTTCAACACAAATTTCACA	59.25	22	194	442	635
AGCCAAAATTTCCTCCAAGG	60.423	20	247	1411	1657
TCCGACATCAATGGCAGTAA	60.073	20	229	1035	1263
CACTGGGACTAAGCGAGAGG	60.005	20	254	3193	3446
GCGTGGTAGAGCGTCTTCAT	60.428	20	209	1010	1218
TTATTTCGCGGATCCAAGTC	60.038	20	162	282	443
CTTCGTTGAATTTGGAACCC	59.406	20	164	9	172
TCGCCCCTTAGAAGAGGTTT	60.2	20	194	91	284
GCTTCAACCCTTGTTTGCAT	60.118	20	235	89	323
TAAGGCAAGGAAAGCTCGAA	60.089	20	121	32	152
CCCAAGACCCCAATTTGATT	60.91	20	277	2250	2526
ACCCCCTCCACACTCTCTCT	60.112	20	266	1446	1711

TCGTATTCCTCATTAAGCCCC	60.286	21	256	7	262
TGCTTTGAACTTTTCCCTGG	60.22	20	217	339	555
CCCGAGATGGTAGCACATTT	59.955	20	121	1269	1389
TCGACTACCAAGTCCGGAAG	60.246	20	235	404	638
ACTAGGGAAGTTGGGAGGGA	59.928	20	236	174	409
TTCCGCTCCCCTAAATATCC	60.24	20	126	577	702
GAGGCATGGTTAGGTTTGGA	59.933	20	219	727	945
CCAAAATCTCGGCTTCAATC	59.645	20	278	687	964
TGCCAATTCAAATCTCCACC	60.843	20	149	9	157
TTTGGGATGATGGTTTGGTT	60.029	20	131	8598	8728
CCCAAGACCCCAATTTGATT	60.91	20	130	1765	1894
AGGAACAAAAGGGAATCGGT	59.805	20	233	938	1170
CTCCAAATGTGATGTCACCG	59.96	20	154	41	194
CATGTAGCCGATCCCAATTT	59.784	20	243	1992	2234
GGGATACGTATTCGTGGTCG	60.214	20	204	3851	4054
GGCTTACGCTTCACGACTTC	60.022	20	264	835	1098
CAAAGAGTTGTTTTACAGACC	59.626	25	269	413	681
CATGCGTTGTCCATCATCTC	60.08	20	156	1421	1576
AGAAGCCAAAGGAGGAGGAG	59.95	20	185	555	739
GTGCTGCACAAGAATGGAGA	59.992	20	280	322	601
CCATTTTTCCACTCCTCCCT	60.298	20	176	277	452
ACAGGCCAACTGAAATCTGAA	59.726	21	224	0	223
TGAGCACTCAGAGTTGCGAT	59.733	20	227	185	411
TGCAGCTAGTCCCTGCTTTT	60.154	20	279	145	423
TGCTCAGCTTCTCCATCTCA	59.812	20	160	1077	1236
GCATAGTTCGAAGGACAATAT	58.287	23	280	1489	1768
ACCCAGAGTCCATTCCACTG	59.962	20	170	83	252
TGATGTCAAAAGCGTTCTCG	59.988	20	199	152	350
CAATCGACCACCCGATATGT	60.603	20	260	131	390
ATTCTATGCCTTCAGCAAATG	57.031	21	165	4	168
CCGTCTTTGGAGCATGAAAT	60.074	20	123	193	315
CCAATTGACAATGAGAGGAGA	57.723	21	256	125	380
CCGTGTATAAAGCTGCACGA	59.895	20	214	88	301
CCATCGTTTTCAGGGAGAAG	59.665	20	270	888	1157
GAGGGAGGAAACTTGACCCT	59.534	20	201	1	201
TGTGGTCACACACTCCATGA	59.518	20	264	381	644
GTGGTGCAGTTGGATGACTG	60.162	20	191	816	1006
GGAAATTGTCGTGTAGTGGTG	57.994	21	259	457	715
ATCCAAACCAGAAATGGCAG	59.933	20	102	1557	1658
GGTCATAGGAATTCGAGGCA	60.036	20	219	415	633
GTTGCAACTTCCCACCTGAT	59.973	20	264	602	865
TGATTCATTCATTTGTCAACAC	60.777	23	238	90	327
TGCAGTATGTTACCGCGTTC	59.759	20	230	383	612
GTCCTGCAGCCCACTTTTTA	60.249	20	201	347	547
TTCCTCTCTGATGAGGCGAT	59.91	20	225	386	610
TTGTTGCAGAAAAGGGGAAG	60.22	20	214	57	270
TTCCTCGCGAAATTAGCATT	59.816	20	280	165	444
AGCCTTTCACTGGTAGTGGC	59.357	20	185	1920	2104
CGATCCTTCGATCTTTGAGG	59.767	20	236	3099	3334
TCATGTAGCCGACCCAATTT	60.331	20	127	810	936
TAAACCCCGTCACCTTATGC	59.823	20	160	628	787
TGATATTCACTTGCCCCTTCTT	59.966	22	263	206	468
CAATAACGGGTCTCTCTCGC	59.836	20	266	134	399
CCCTCGAAATATCCTCCTCC	59.859	20	277	988	1264
TCAATCATCACACACATACCC	59.697	22	277	2584	2860
GGTGTGAAAAAGAGGGTGGA	59.943	20	195	4	198
AACCTCGTGCAAAAATTCCA	60.481	20	261	351	611
TCCTCGATTCCGATTTTCTG	60.148	20	276	162	437

TTTTCTCATGAACCATCCCC	59.727	20	251	3607	3857
CTTGAGGACATACATAGTGAA	57.462	24	248	457	704
GTCACTCCACCTCAGTGGCT	60.315	20	210	541	750
AACTGCTCCGTCTGCATCAT	60.833	20	139	1501	1639
GCAGGGTTTTCGACAAAAGA	60.227	20	214	659	872
TTGCTTAATTCCTCATCCGA	58.308	20	217	325	541
GGAAGGAAGGAGGGTGAGAG	60.186	20	197	5886	6082
CTCGTCCTTTTTCTCGAACG	59.986	20	206	276	481
CCCAAGACCCCAATTTGATT	60.91	20	215	24	238
GCTCTTCGACGACCTCAATC	59.957	20	116	757	872
TGAGAAACCCATTTTGGCTG	61.001	20	254	60	313
CCATTTCTCCTTGCATCGTT	60.074	20	278	70	347
TCAATTACGATCGAACCACG	59.542	20	271	1575	1845
CAGAGCCATGGTTCAGGAAT	60.073	20	267	1290	1556
AGGTTGGTAGTGGAGCTGGA	59.721	20	129	828	956
GAAAACCCTGTGTAGCAGGC	59.74	20	180	0	179
TCGAATGCTCACGTTGAAAA	60.379	20	148	38	185
GATGGGGTGTTTTGAGAGGA	59.903	20	154	1959	2112
AATTCGACAGCCATTCAACC	59.939	20	226	873	1098
ATTCTCGTTTTCCACATGCC	59.939	20	198	257	454
GTCATCGAGTGCTGCAAAAA	59.995	20	107	1176	1282
TCACCATGTTGATGAAGCGT	60.12	20	135	160	294
TGGAGTTCACGTAGCAAAACA	59.376	21	274	632	905
TTTGGTTCATGTAGCCGACC	60.894	20	249	1166	1414
CACCTCTTGCGGGGTATTAT	58.928	20	212	901	1112
GGGCACGTACAAAAGAGACC	59.598	20	253	3022	3274
AGCCCTTGCTTTCACCAGTA	59.875	20	253	741	993
CAACATCATTCCCATCACCA	60.177	20	256	402	657
CCATCCACGTATTTTGCTCC	60.331	20	201	411	611
TGACCAATGAGTCGACTTGC	59.837	20	181	362	542
TTGCCGTATTTCTATGCCAC	58.653	20	265	190	454
TATTGTGGTTGGATGGTTGG	59.097	20	262	22	283
ATTCGTCGATGGATGACTCC	59.893	20	228	317	544
ATTGGCATTTGATGTATATTGG	58.273	23	185	602	786
CCCGAGATCTATCATGGTGC	60.448	20	124	371	494
CTCAGTCTTCTCCGCCTCAG	60.275	20	227	135	361
TCCTCGCTCTCTCCTCTCAC	59.817	20	130	755	884
CCATCCTTTAAGTACTTTGACT	59.504	27	217	66	282
CCCCAAATTCGACAAACAAT	59.662	20	214	201	414
ATTCGGCTCTTCTTCTGCAA	60.096	20	270	14	283
ACCACAAATTAATCGGGCAC	59.691	20	207	356	562
TGGAATAAGGCAAAAAGGAAA	58.726	21	276	2999	3274
TGCCAGAAAATGTTGCTTCA	60.379	20	209	1178	1386
CCTCGTTCCAAAAGCATTGT	60.11	20	137	221	357
TGCGTGTTTGCATCCATTAT	59.96	20	220	4453	4672
TTCTTGGCCTGATTTTCCTG	60.184	20	141	463	603
TTTCCGTGAACATAGCTTGAA	58.426	21	193	332	524
TGCATTTGACAATCGCATTT	60.081	20	176	429	604
ACCTCCCTCTCCTCGAAAAC	59.676	20	234	437	670
GGAGCAGATCCAATCTCCAA	60.158	20	268	92	359
ACGTTATACTCACGCCCTGC	60.162	20	275	1681	1955
CGATGGGCAACAATAACCTT	59.823	20	158	354	511
AATGTTGAGCCCAACCCAAT	61.497	20	215	1452	1666
CAGCTGTCTCGCACAAGTTC	59.776	20	186	1024	1209
TCGAACCACAGCAAAAATCA	60.234	20	137	7	143
AGGACTACCCGGACTTGGAT	59.817	20	198	120	317
ATTGGCCAAGGACATAACCA	60.192	20	247	217	463
GGCAAAGGCTTGTGTTTCTC	59.859	20	135	20	154

TGTGGAGTGGACCTCATTCA	60.088	20	192	104	295
CTTCGCACAAGTTCTCAGCA	60.324	20	240	594	833
GGTTCAAGTGTTTGGGAGGA	59.943	20	270	750	1019
TCACATCAATGCGATGAAGAA	60.213	21	230	574	803
GGTATGTGGGATGGCACTTC	60.203	20	242	4170	4411
TGACCCCAAATCAGCCTTTA	60.439	20	245	420	664
ATGAGCACCTTGACAATCCC	59.934	20	250	1835	2084
TAATTGAAGAAAGCCGCACA	59.443	20	142	8	149
ACACTCCCCACAACTCCTTG	60.002	20	280	654	933
TTTGGTCGAGGACCAGAATC	60.05	20	278	75	352
TTCTTCCAATGCAGAGTCCC	60.195	20	137	1003	1139
CCAATCAAGGTCAATGCAGA	59.648	20	270	115	384
TCCATCATTCCCTTTCTTGG	59.864	20	252	1103	1354
TGGGCATTCAGTGGGATTAT	60.155	20	245	997	1241
TTTCTGCATTAGGGTTTAGGG	58.262	21	114	3	116
CCAGTTGCTTTCTTTCCAGC	59.993	20	269	487	755
TGATGTTCCAATGGAGGAGA	59.009	20	241	1820	2060
GCCCATTTACATCATTTGGG	60.016	20	156	455	610
GGAGTGGACAACGTAGGGAA	59.966	20	257	539	795
ACAAAAAGGAAATAGGCGGG	60.305	20	122	713	834
CACAGCCGATCACACATTTC	60.12	20	176	41	216
AAAAGGAAACAAAGCAGCCA	59.861	20	236	1483	1718
TGAATTGTGGAAACACCTCG	59.541	20	120	5	124
TGCAAACAAACCCGTACAAG	59.627	20	231	338	568
CAGAAAAATAAAAGACATACG	57.384	26	221	209	429
CGCTTTCATGTCAGACGTTC	59.445	20	162	399	560
ACCCCATATAGCGGGAAAAA	60.508	20	146	1415	1560
TTCCAGCTGAAACTGTGAGATT	58.983	22	191	405	595
TTCAAAGCATCCCTTCTCTTAC	60.243	23	216	675	890
GCGCATTGCAGAGATTGATA	59.944	20	236	2286	2521
CACCATGGGGGATCTTCTAA	59.744	20	154	1037	1190
TTGCAAGTACACTCCATTTTGT	57.364	22	258	8	265
TTTGAGCAGGAATGTTCTTCA	58.488	21	233	131	363
ATACAATGACGAAAACGCCC	59.829	20	147	453	599
ATAGCCGCCTCTTTTCCATT	60.061	20	201	3	203
CATCGAGTGATCCATTGTGG	59.918	20	219	203	421
ACATCGGATTCCAACTCTCG	60.073	20	279	506	784
CCCAAGACCCCAATTTGATT	60.91	20	118	1197	1314
GCCCTGTCATTTTTGAGCAT	60.081	20	223	1115	1337
CCACTTCTTAACCTCCGTGC	59.734	20	208	546	753
GCTGCAGCGTTTGTACTCAA	60.203	20	165	173	337
TGGTTGGCAGGGTATCATTT	60.192	20	158	8	165
TTCAAATCTCGCCTACACCC	60.074	20	197	1107	1303
TTTCACTGCTGGCTCCTCTT	60.134	20	247	571	817
AACAGCTTTCTCGGATGGAA	59.813	20	163	1461	1623
GTTCCCCAGAACGTCACACT	60.009	20	196	514	709
TTTCTGTGATCTCTCCGCCT	59.95	20	274	373	646
CGTAAGCCAATGCAGTGAGA	60.011	20	273	2521	2793
ACCCACATATTCTTCAAGCGA	59.583	21	253	42	294
CACTCAATTTTCTCGGCCTC	59.813	20	189	1009	1197
TAGGCCAAAGGCCTTCTACA	59.839	20	178	190	367
TTTCTCCATTCGTTACTGCAT	57.379	21	266	520	785
TGGGTGCCTTTGTTCTTTTC	60.088	20	124	120	243
GTTGAACGGGAACGGAACTA	59.971	20	258	242	499
GAGGCGTATGAGATGGAGGA	60.181	20	138	453	590
TCGATGAAGGGAAGAAGGAA	59.744	20	210	997	1206
AGAACATCGAAGCTTTTGGC	59.457	20	265	679	943
CCCAAGACCCCAATTTGATT	60.91	20	275	1076	1350

AATCCCTCTTCTCCTCCACC	59.492	20	239	1619	1857
AAGCACAAGAAAGAACCCTG	60.275	22	237	48	284
ACATGCCCAGCAGGTTAGAT	59.579	20	269	1727	1995
GCGCACTCGAAGAGTAGCTG	61.413	20	278	902	1179
ATTTCCCAAATCCCGTCTTT	59.644	20	231	2808	3038
GCAATCTCTCAAAAGCAGCC	60.103	20	179	155	333
AAGCTAGCAAGGCAGCATGT	60.183	20	222	1427	1648
AGTTGGGCCTCTTCCAACTT	60.11	20	242	742	983
GCGGCGGAGATAGTCTACTG	60	20	136	228	363
ATTCCACTCCACCACCTACG	59.844	20	120	2114	2233
GAGTAGACTCCACCGCCTTG	59.867	20	274	501	774
ATTTGGTGCTTGCCTGCTAA	60.772	20	179	3	181
TTCGGTATATAAGTCATGTGTT	59.262	25	260	218	477
CCTTGGTCGATCTCATCACA	59.631	20	264	1308	1571
TCGAGTTGATCTTGCCTTTG	58.999	20	253	67	319
GGAAGAAAAGTGCGATGACG	60.776	20	272	371	642
TGGCCGTTGATAAAGAATCC	59.901	20	264	335	598
GATGAGGGAGGCACTAGACG	59.827	20	110	353	462
ACACGTGTCGCATTTTGTGT	60.08	20	215	14	228
AAAATGACTAATCTTGAACATG	59.582	24	256	106	361
CTACTCGCTACGAGCCACG	59.773	19	249	192	440
TGCACTCATTAATTGTTTCGG	58.688	21	200	349	548
CCAGCTTAAGCCTGCATTTC	59.982	20	233	113	345
TCGGGTGGTGTGTAGTTGAT	58.854	20	221	64	284
TGTAGCCGACCCCAATTTAT	59.297	20	246	1012	1257
ATACAGTCGCCGTGGAAAAC	60	20	153	23	175
GGCGACAAAACTTGGTAACG	60.534	20	121	38	158
ATGTAGCCGACCCCAATTTA	59.297	20	191	557	747
AAAATCATCCCAATTCCCAAC	59.881	21	147	15	161
TAATGGTTCGAGGGATACCG	59.778	20	241	490	730
GTGGAAGGCGGAAAGATACA	60.074	20	217	4	220
CTGCTCCAGCGCTTTTCTAT	59.752	20	256	182	437
GAAGAGTTGAGAAGGCGGTG	59.989	20	220	740	959
TCATTGGGAAAATGATTTGG	58.255	20	225	1900	2124
GAAGGAAGATGGATCGTGGA	60.011	20	221	508	728
ACTTCTGAAACCAGCGAACG	60.431	20	111	81	191
TCCTTTTGAGCCTGGACAAT	59.67	20	217	23	239
TCGTTTCGAATAGCGGTAGG	60.223	20	239	340	578
TGACAACTTGTTCTGGGTGC	59.726	20	191	2	192
TTGAACAGGGAAAGCAGGAG	60.366	20	239	5	243
CCCTCATTCCCTCCTTCATT	60.264	20	254	1971	2224
GTGAAAGCGCCATTCTTCTT	59.457	20	209	1847	2055
TGGTTGAGGAAGGAGAGCAT	59.803	20	198	317	514
GAAAGGGGCAGTTAAAAATCG	59.957	21	104	0	103
ACAGGCAATCTGCTTAGCCA	60.934	20	223	2147	2369
ATGTAGCCGACCCCAATTTA	59.297	20	168	773	940
AGATGGAGGAGAGGTCGTGA	59.792	20	166	555	720
TGCAACACCTCCATCATCTC	59.637	20	257	569	825
TTTTAGGAGTCGTGGGTGGT	59.449	20	108	418	525
GAACCAGCCCATCCCTTTAT	60.152	20	253	90	342
AGCTGAACCCCAACCAAAAT	60.723	20	210	341	550
CAATTTAGCTGAAATCTCAACC	58.119	24	243	429	671
GTTTATGCAGCCGAGGATGT	60.103	20	237	223	459
TGTCCATGTGGCATGAAAAG	60.517	20	271	1017	1287
TCCCCTCACCTTTCTCTCCT	60.186	20	199	0	198
TCGGGAATCGACATTCTCTC	60.158	20	141	37	177
GGGAATCAACCCCAAGTTTT	60.032	20	273	219	491
CACACTTCCCCCTCTTTGAA	60.081	20	110	8	117

TCAACACATTCAGCAGGCTC	59.992	20	277	65	341
TCAATCGCAACTGCAAAAAC	59.856	20	278	44	321
AACGTTCGCTCCAAACAATC	60.118	20	278	124	401
AGGCATGTGGGAGCATAGTT	59.579	20	182	158	339
TAGCAATGGACCTCGCATAA	59.281	20	186	342	527
CTCTCTCCTAGGTCCGTCCC	60.208	20	186	972	1157
ACGATGAGGAGGATGACGAC	60.08	20	202	311	512
CAGGTTTGGAGGAAAGCAAG	59.846	20	236	582	817
GCTATCGGTGGGGTCTGATA	59.917	20	116	315	430
CCGGAAGATGGACAGGTAGA	60.065	20	172	1	172
AATCACGTGTCTACATTTTTAA	58.63	25	229	426	654
TTGGGATTAAGGCTTTGGTG	59.931	20	129	952	1080
GTCTTCCGCGTGCGTATAAT	60.124	20	226	38	263
GCCGATAAATGAATTCGAGC	59.649	20	247	379	625
CCCTGACTTGTTGATGGCTT	60.111	20	143	0	142
CAATAAATTGGGGTCGGCTA	59.789	20	127	26	152
TCGAATTCAAAAACTCCCAA	58.187	20	225	355	579
CAGCAGATTGATGGCTCAAA	59.948	20	175	702	876
GCTCCATTGTACGTTTCCCT	59.056	20	136	124	259
GTTCAACAGGAGGTGAAGCC	59.703	20	125	2348	2472
TTGAGTGGCGCACATTAGAC	59.871	20	157	16	172
AGGCTTTACTCGGTTTGGGT	59.998	20	278	180	457
CCAATGTCTCGTACCCACCT	59.844	20	232	561	792
CACCATAAGATCCCGAACCA	60.713	20	252	115	366
TCAGAAACAATACACACCTAC	60.341	25	121	0	120
CTGTCATGCAAGCAGCAACT	60.207	20	249	349	597
AACCGGAACATAAGTGCCAA	60.365	20	268	335	602
TCCAAGCTCGACAACTCTGA	59.701	20	179	5	183
CAGAGCAAGAAAACATGCCA	59.988	20	190	529	718
AGGCCATTGTTGTTGAGCTT	59.74	20	240	1449	1688
TGCGAACCAGATGCATTATC	59.652	20	143	111	253
GTTTTCTGTTTTTGTTCTCCTGC	59.338	23	264	5	268
ACGTCGATCACTTCAACCTTT	58.709	21	228	604	831
CGAGATTGAGGAGAAGCAGG	60.088	20	245	576	820
GGTGGCATCATCAACAACAA	60.376	20	251	756	1006
TCTTCCAAGATCACACAGCCT	59.859	21	263	1156	1418
AGTCCTTTCCCTCTGCAACA	59.844	20	221	1198	1418
CGTGATAGCAGAGAAAGGGC	59.978	20	126	736	861
TCCGTGGTGAACAAGTTGAA	60.128	20	239	366	604
GCGTGGTGGGGATTTAAGTA	59.823	20	141	869	1009
CAGTGAGAGCCACCACATTG	60.309	20	172	6	177
TTCCTTTCTTAAGCTTGTGAAC	57.936	24	150	939	1088
TGTTCTCGCTTAGATGCACG	60.157	20	179	213	391
AAAAGTGTCGTGGATGAGGC	60.119	20	235	211	445
CACAAAAGGGCCTCTGAATC	59.67	20	234	133	366
CGGAAGAGGTATCGCTCAGA	60.495	20	233	3659	3891
TCTGTAGCTGATCACCGTTTG	58.937	21	280	108	387
CTCCCTCTTCCCCTTCAAAC	60.045	20	243	968	1210
GGGGTGTTCGAGACTTGAGA	60.238	20	237	201	437
TATGCCACAGACCACAGTGC	60.756	20	207	300	506
CAAACCGCCAAATTCAGATT	59.938	20	273	80	352
AATGGTGCTAGCGTGATGAA	59.301	20	221	384	604
AATTAAACAAGCCCCTGCCT	59.966	20	247	330	576
TTTCCATGCACATGTAAGTTTT	58.601	23	105	119	223
GTACCTTTGCGGGTAAATCG	59.474	20	122	529	650
GGAGGAGAGGGGTAGAATGG	59.89	20	144	409	552
ATGTAGCCGACCCCAATTTA	59.297	20	171	1325	1495
TTCTTACAGTTGGCTGCGAG	59.22	20	231	49	279

ACTGTCCAACCAATGCACCT	60.431	20	176	454	629
ACCTGATCGGTGCGATTAAC	59.962	20	269	423	691
CCATCCCATCATTCCATCTC	60.096	20	153	912	1064
GCTTCGGTGGTTAAATTCCA	59.938	20	164	467	630
CACCCTTGCCTTCATAGGAG	59.688	20	137	2145	2281
GCTCCTCATCCTCCTCATCA	60.312	20	269	287	555
CATACCTCATCCCGCAGATT	59.917	20	271	1801	2071
CGTGGAAGGGTGACTTGAAT	59.966	20	157	194	350
GCTGACCTCACATATTGGGAA	59.947	21	252	10861	11112
AGGGAGAATTAGTGGAGGGG	59.392	20	150	347	496
TCGGGGAGAGTCAAGAGTTG	60.377	20	225	499	723
TTCGTCTCCAAGGAAAAAGC	59.429	20	100	68	167
CTGTTTGTTGCTGCAGTTGG	60.485	20	275	149	423
GTGGGCCAATTGAGTTTTTC	59.41	20	201	534	734
CCCAAGACCCCAATTTGATT	60.91	20	102	5825	5926
TGCAAATACATCGAGCGTAGA	59.481	21	173	204	376
CATGAACCTTTGGAACAGGG	60.345	20	154	693	846
AAGTGATCAGCCGAGGATTG	60.218	20	246	1050	1295
TCCGCCGGAAATTTTGTA	60.005	18	213	370	582
AAAGGATATATTCACTGGGTTG	58.472	23	271	120	390
ACCGAGAGAGAGGGGCATAG	60.746	20	219	904	1122
AATTGGAAGGCAACTGCTCA	60.776	20	187	22	208
CCCAAGACCCCAATTTGATT	60.91	20	199	2335	2533
ATTGTAGAAAGGGCGCAGAA	59.845	20	112	2384	2495
TGGATCTGGAACATCAGCAA	60.201	20	195	736	930
ATCTAGCTGTGAGATGTCTCTT	59.219	24	272	557	828
TGCATCCACTTGGTGAGAAA	60.24	20	178	1029	1206
CCTTCCTTCGTCGATGTTGT	60.111	20	165	795	959
GCAAAGGAAATTCACGAGGA	60.192	20	186	162	347
GGTTCATGTAGCCGAAACCA	60.894	20	114	2210	2323
TGTCGTTTGCTCCTCTTTCC	60.375	20	225	4	228
ATTGGGTACCATGTGGCAGT	60.119	20	265	246	510
TTCTATCGAAGACCGCATCC	60.177	20	235	2016	2250
CGGAAGTGATCACAAGGGTT	59.966	20	171	17	187
GTCCTGATTAGGGATGCCAG	59.508	20	269	4339	4607
AGGGAAATTTGAGTGGATGCT	59.954	21	256	516	771
CGTCGTCGTCGTCATCTTC	60.419	19	200	152	351
TGTTTGAACGACTGCCTTTG	59.881	20	242	372	613
GCCGACCCATTACTAATCCA	59.784	20	266	629	894
CGGTATTCTCAAATGCACGA	59.688	20	203	1072	1274
TGGTGTTGATTGTGGTGGTT	59.701	20	242	593	834
TTTTCCCAATGGGGTTTGT	60.014	19	274	410	683
TTAGGTGAAGCCAACATCCC	59.933	20	163	1721	1883
TTCCTGGAGGAGTTGTGACC	60.088	20	218	69	286
GGAAGGAAACCCTTGCACTA	59.17	20	140	7	146
GGAGGAGGAGCATCATAACG	59.653	20	187	1250	1436
GATGGACTCCGATGACGATT	59.893	20	267	7	273
CCTCTCTCTTCGTTCATCCG	59.943	20	222	235	456
AAAATTCAAAGATTTGGGGGA	59.645	21	148	1	148
GAGGATTCCCTCCAAGATCC	59.835	20	265	43	307
GCACATGCGGTCTGTATCAC	60.152	20	131	388	518
TTGAGAAGACGCGAAGTGTG	60.175	20	261	5	265
TGGCTGAGTTAGATGCCCTT	59.836	20	258	2019	2276
TTTGCAGCCGAACTACTGAA	59.609	20	263	559	821
TTTGGTTCATGTAGCCGACC	60.894	20	191	854	1044
ACGACAAAGCTGAGGCTGTT	60.058	20	222	1907	2128
GATGCTAGCCGGAGATGTTC	59.803	20	155	350	504
CTTCTGGGGGTTTGGATCTT	60.298	20	259	2970	3228

ATAATGGAACGAGGGTGACG	59.813	20	238	0	237
CAAGGGTAAGGTTGCGTACA	58.699	20	234	29	262
TGGCATAACACTGAAGTGACA	59.245	22	270	19	288
AGCCACAAAAACACTTAGGCA	59.799	21	268	32	299
TCCAGTTAAACCAACCTCGC	60.11	20	203	1651	1853
GAAAGAGAGAGAAAGGGGCG	60.455	20	144	1234	1377
TTCCATGCAACTTTCTACCAA	58.28	21	267	77	343
GAATGGAAGATCCTTGCACC	59.488	20	167	27	193
TGTGATGCAATGCGGTATTC	60.498	20	231	310	540
CCCGGGATTTCTAAATGGAT	59.978	20	238	967	1204
GAAGAAGAATCTGAGCCAGCA	59.708	21	192	1060	1251
GAGGAAACAGAAGCACTGCC	59.997	20	121	949	1069
GGAAGTGAAGTCGGACGAAA	60.232	20	109	7	115
GGCGACTCACTTAAGGTTGTG	59.788	21	136	161	296
TGTAGCACAATTGCCTCTGC	60.019	20	200	80	279
CAATCATTTGAAAATTGACTCG	59.428	25	255	662	916
GCAAAACATTTCACCTAGCCA	60.124	21	279	694	972
ACACGATTAACTGCCTCGCT	59.904	20	141	2266	2406
CCCCAATTAGTCGTAGCCCT	60.332	20	169	1453	1621
TGCTGAAACTGGTGGAGTTG	59.873	20	202	1892	2093
TGCCACCAATTTCTCATCCT	60.461	20	245	935	1179
AAAAAGTTTAGGGGCTCCAC	57.352	20	278	24	301
GTGGAGTGGTCAAGAAAGCA	58.854	20	100	12	111
ACGTCTCTCGCACTCCTCAT	60.017	20	122	1	122
CCTGCCTCACAAAATGGAAT	59.933	20	182	2254	2435
TTCCGGACCAAACTTTAATGTA	59.441	23	270	856	1125
GGAAGAAATCACGAAATGCC	59.51	20	267	2191	2457
TTTTCAAGCAAAATTTCAATTA	59.911	25	275	298	572
GATAATGTGGCGGAGTTTGG	60.331	20	125	40	164
TCTGGTTCTTTTGCTCCTGC	60.517	20	231	2828	3058
TGTAGCCGACCCCAATTTAT	59.297	20	168	2486	2653
GTTAGGGGAGCTGCAACAAG	59.875	20	246	1422	1667
AAATAGCGCATTTTCGTGTT	57.483	20	103	3	105
GATCGTCCAAATCGTCATCC	60.289	20	221	378	598
TGAGGGAGCACTAAAAGGGA	59.807	20	254	240	493
TGCCCCAACTGTGACAAGTA	60.152	20	206	998	1203
AAACCCATGCATTTGATTCC	59.628	20	269	471	739
GCCACATGGGAAAAAGAAGA	60.051	20	253	36	288
GGATCTAGTGCGGGTTACCA	59.955	20	179	33	211
GACGAGGATGAGAGGAATCG	59.761	20	237	3263	3499
TGAGTTTTGGGAGCAAATTACA	59.625	22	250	398	647
CGCCTTCACTGCCAAAATA	59.818	19	108	17	124
TCCAATGCTGGCATGTGTAT	59.955	20	171	253	423
CAGCCCAAGAAAAGATCTGC	59.955	20	221	141	361
AAGGGGAATGAAATGGAACC	59.996	20	230	54	283
AATGTAGCCAAACGCCTCC	60.088	19	198	646	843
CTGAAATCCGGTTCAGTGGT	59.966	20	148	25	172
TTGCTTGGGGTTAGGTTTTG	59.968	20	134	794	927
CTGAGCAGGTGGAAAAGTGC	60.975	20	224	1202	1425
ACTCTGGACTACTGCCCCCT	60.133	20	214	182	395
AGCCCCAAATGAAGAATCAA	59.505	20	275	262	536
AGTGGTCTTCCTAGGTGGCA	59.721	20	131	1013	1143
ATGGTTTGTGCCTGCAAACT	60.559	20	230	973	1202
GGCATGGGCCTTTAATTTTT	60.148	20	154	68	221
AAATGTTCCTCATCATCCCG	59.75	20	100	724	823
GTTGATTTGGATCAAGGCGT	59.939	20	269	671	939
AGTTTTTGGAGTCCACCCCT	59.834	20	177	835	1011
GTCATCAGAGCCATCCCATT	59.893	20	146	53	198

TGATGCTGCGGAGTCAATAG	59.972	20	168	264	431
TGATGAAGTAAAATAGTGAGT	57.311	27	151	265	415
CGTGGAGAGTGGTGGATTCT	60.112	20	197	259	455
TTATGGATCGAACATTCACGA	58.98	21	196	257	452
CATCGCTTGCTTTCCATTTT	60.209	20	188	747	934
CCAAATCCGGTCATTCTCAT	59.75	20	190	227	416
AGACTGGTGTTGCTGCTGTG	60.096	20	275	75	349
AATGGGCGGTGTAAAAGAAA	59.451	20	163	712	874
GGATACGCTGGAAATGTTGC	60.478	20	278	705	982
ACTTGTTGGGTTGGGTTTTG	59.728	20	264	680	943
AAAAACGTGGTCAAATTCAAG	60.249	22	225	57	281
TTCATGATTTCTGTTCGGGA	59.049	20	253	492	744
TGATGGATCAACAACACATCG	60.383	21	172	72	243
GGGTGACCCAGAAGTTTTGA	59.943	20	240	1644	1883
GGAATTCAATCGAGCAATGG	60.414	20	257	1863	2119
ATGGCCCTAAACACAGCAAG	60.132	20	272	419	690
GCGTGATGCTGGATGTAGTTT	60.154	21	210	4	213
TCTTCTTTATCCCTGGTGTCG	59.181	21	270	17	286
GGCGGTGGTGATTTGTAAAC	60.235	20	242	1586	1827
AAATCCAATTCATGCATCCC	59.587	20	240	216	455
TCATGTATTTGAATCGGCCA	59.891	20	260	29	288
CGGGTTTGAAGGGGATTTAT	60.013	20	223	1216	1438
TGTCTCCCTCTTACCATCTCAA	58.789	22	259	1317	1575
GTAAACCCTCCCGGTAAAGC	59.835	20	220	473	692
CCAGTCAGGCACTCCAAAAT	60.111	20	263	1021	1283
GAGGTCAACGATTTTGGCAT	59.939	20	245	422	666
TAACCCAGCCCATTAGCATT	59.433	20	134	238	371
TTGGAAAGCAAACCCTGGTA	60.472	20	211	400	610
GAGTGTGTCTGGCAACATGG	60.162	20	191	2	192
CAACCTCCTTGCTCGGAATA	60.206	20	247	1235	1481
CCCTTCTTTTCAAGCACTGG	59.846	20	202	415	616
GACACATGCTCGAAAGGGAT	60.081	20	180	7	186
ATGGGTAGGGAGTTTCACCA	59.259	20	244	395	638
AAGGGGAGCAAGAGGAAGAA	60.319	20	111	9	119
ACTCCTTGATTCTTGCACCG	60.255	20	200	396	595
GTCAGGTTTCTGATCCGAGC	59.81	20	271	26	296
TGCTCATCAACACTGCCTTC	59.992	20	239	1095	1333
TGGAATAGGTTTCTTTGGAGAC	59.987	23	116	46	161
AACCAACATGATGAGTGACCC	59.694	21	184	66	249
GTCTTCGTCACTGCCGTCTC	61.021	20	113	486	598
ACAACTATTGCGCGACTCAT	58.407	20	166	247	412
ACTTGGTCATTTAATGGATCA	58.303	22	270	511	780
CCCAAGACCCCAATTTGATT	60.91	20	177	144	320
TTCCGGTAAGCATACAACCC	59.823	20	280	548	827
CGCTTTAGCGGATTGATGTT	60.23	20	261	372	632
GTTTATGTAGCCGACCCCAA	59.823	20	185	491	675
GGGTTATCTATGGATCACTACC	58.734	24	212	542	753
GAGGAGGGGTGGTTTGAGAT	60.314	20	215	13	227
ATGTAGCCGACCCCAATTTAT	59.585	21	175	3607	3781
GCAAGTAGGTGGATTCCCAA	59.933	20	245	1513	1757
AATAATGAGCATTCCCCGTG	59.784	20	279	760	1038
AGAGGATTCACCACCACCAA	60.363	20	116	4	119
TCGAATCAGTTACCATCACCA	58.987	21	256	56	311
CTTGAGCACAGAAAATCCGC	60.914	20	249	49	297
TCGATCCAGTTCTTGGCTCT	59.95	20	259	228	486
TTCCAGAAGTGATGCAGGTG	59.831	20	249	537	785
AAATGATTGCTTGGCTTGAA	58.361	20	252	589	840
TTTTTCTTTTTCCTCTTGTCATC	59.307	24	240	576	815

CACCCAAAAATCCTCTTCCA	59.903	20	169	82	250
TGAAATTGGGGTGACTGGAT	60.173	20	206	175	380
ACCCCACATAGTGGGAAAAA	59.146	20	163	790	952
TCTCTCATTCTCCATTGCCA	59.322	20	274	136	409
GACGGCGTCGTTTTCTTG	60.39	18	256	146	401
GACGGTGAAGCGTTTAGCAT	60.278	20	258	3025	3282
GGTAGCCGACCCCAATTTAT	60.041	20	217	393	609
ACCACGATTTTGACTGGGAT	59.263	20	241	429	669
GATCGTTCTCGGATGCATAAA	60.052	21	240	677	916
GCCACTGCAGGTGTACTCAA	59.905	20	103	614	716
GTAATTTCAGCGGGGAACAA	59.938	20	234	4886	5119
GACACCTCATGCGAGTCAAT	58.673	20	199	125	323
CAAGGAGTAATCGGGGAGTG	59.545	20	263	1083	1345
TTGAAATGGCGGAGAGATTC	60.155	20	212	429	640
AGCTTTTGACCAAGGAAGCA	59.993	20	211	141	351
ATCCAAGTCCATCTCCTCCC	60.278	20	225	286	510
ATCCATCCTCAAGGGGTTCT	59.755	20	207	12	218
AAAACTTCGACCCCTGGAAC	60.34	20	257	9	265
AGGTTGCGTACATCTGACCC	59.997	20	254	3711	3964
ATGTAGCCGACCCCACATAG	59.836	20	127	688	814
CACCGAGCTCAGATTGGTTC	60.801	20	234	3070	3303
CCCATGTGACACTTCAGCAG	60.309	20	143	599	741
TGACGGTGAAAAATAGCGAA	59.301	20	255	194	448
CCCAAGACCCCAATTTGATT	60.91	20	154	180	333
GGTTTTTGGCTGGTTTTGAG	59.587	20	137	1594	1730
CGCACCAAAAGTTGTTTGTC	59.22	20	239	1281	1519
TTTCATTTCCTTTGACTTGCG	60.229	21	110	427	536
TTTCAATATTTAACTGAATTAA	57.55	26	162	563	724
AAGAGGGCCACAAACCCTAT	59.827	20	220	17	236
TCGAGAGTTCGGATTTTTGAA	59.809	21	116	344	459
CCCAAGACCCCAATTTGAT	59.59	19	130	3022	3151
CTACCGTATGAAAGGGGCAC	59.452	20	190	41	230
CCCAAGACCCCAATTTGATT	60.91	20	253	4794	5046
AAGTCATGGGTATGCAGGGA	60.34	20	189	6	194
TTGTGTTTTGAGCACTTCGC	60.035	20	251	485	735
CCCAAGACCCCAATTTGATT	60.91	20	180	1962	2141
ATGGTGTCCACTTTCCACCT	59.279	20	192	628	819
TTTTGAGAAGGTTCCTTAATTC	59.227	26	255	256	510
ATTAGCAAATTTCGGGACGA	59.547	20	269	385	653
TCACAACAAGAGCGTGCTTC	60.183	20	130	915	1044
CCTCAAAAACCAATAAATGAA	60.871	24	271	7	277
TGCTGACAATGATATGTGTTCA	58.039	23	223	556	778
TGGCATCCAATCAACAAGAA	60.049	20	273	140	412
TTGAAATTTCGAGTTGGACG	58.745	20	257	626	882
TGGCCAAATACCCGAATTTAT	60.385	21	206	5	210
ATGTAGCCGACCCCAATTTT	60.562	20	165	976	1140
TGGAAGTTTTACGAGAGCCG	60.378	20	213	275	487
AACCCAGCGTAGAGGAGGTT	60.132	20	263	4741	5003
TTTTTCGCGACAGTCAAAGA	59.585	20	173	0	172
GCCGACCTCACATAGTTGAA	58.724	20	223	320	542
GTTTCTGCCCGTGGACATAG	60.517	20	280	86	365
TCCTAATCCCCCGAAATACC	59.978	20	165	651	815
TAGGTCAGTGGGGTGGTCAT	60.238	20	134	529	662
TGGGGTGATTATGGTGGTTT	59.91	20	201	239	439
ACACTTTCGAGATATAAATTCA	57.327	27	251	475	725
TGTTTATGTTTGATGTTATGTAT	58.499	27	278	0	277
TGGTTGCAAGTCTTTGGTTG	59.734	20	273	2	274
CATGAAGATGAAGCTGCCCT	60.362	20	159	68	226

TTGTGGCTCTGTGCCTCTTA	59.591	20	161	1173	1333
CTCCTCGCTCTCTCCTCTCA	59.962	20	131	577	707
GCACGTGCGTAGAGGGTAGT	60.343	20	222	472	693
AAAATGACATGCAAGGAAAAA	57.299	21	226	952	1177
TCTCCTTGTTTGGGAAGTGG	60.081	20	153	8	160
TGAAAAGTGCCTCCACACTG	59.873	20	248	75	322
CCCAAGACCCCAATTTGATT	60.91	20	211	3393	3603
ACTAACTGAGCTTGAGCGCC	59.786	20	189	210	398
TTTCACCTATGCATTTGCCA	60.073	20	275	3265	3539
ATTCATTCCCATCCGTCAAA	60.133	20	196	1783	1978
ACATCAGTGTGTTCGGTGGA	60.005	20	253	3474	3726
GAACGTGCAGCTCAACAGAA	60.183	20	188	2	189
TCGATTAACGAAGTCTCTCCCT	59.371	22	274	695	968
ACCATCAGAGCACGACAAAA	59.293	20	269	1543	1811
ATTCACGACGTGCAAACTGT	59.217	20	264	430	693
AACTCCGCAATCACTTTGCT	59.882	20	209	629	837
TTACTTACCACCCAACCCCC	60.826	20	235	8278	8512
GCCTCAGTTTTCAGCTTTGG	59.993	20	260	710	969
ACCTACTAAGGCCTTCCCCA	59.955	20	277	170	446
CCACTACCATACTGGGCGTT	59.875	20	213	540	752
CAAAGACCTAAGGCACCAGG	59.728	20	258	6185	6442
ATGTAGCCGACCCCAATTTA	59.297	20	262	431	692
GCTCCCCTTCACAATAACCA	59.933	20	268	2	269
ATGTAGCCGACCCCAATTTAT	59.585	21	267	2321	2587
ACCACAGGTCGTTTGAAAGC	60.156	20	216	731	946
TTCCAATCTCAAGGGGATGA	60.395	20	263	205	467
TGCATGTTGATGTGTCTGCTT	60.326	21	271	948	1218
TCTCCGACCCATCTACCAAG	60.065	20	255	253	507
TGGAGGAGGACCGAGATATG	60.027	20	273	247	519
TCTACTGGGATAGTTGCGGC	60.235	20	198	657	854
TGTTGGCGAAACCCTATGAT	60.331	20	241	778	1018
AATGCTCCACCCAATGACTC	59.934	20	140	1409	1548
CTGCATGCATTTATTGGACG	60.096	20	259	1656	1914
CCAAGTTAGGGTTTCTGACACA	59.142	22	149	502	650
GAGCCTGCTTTTTAGTGGCA	60.523	20	280	3520	3799
AATTGGTTTGAAATTACGCGA	59.485	21	265	2659	2923
TCCACCTTTTCCCTCACAAG	60.081	20	167	220	386
TTAACTGGCAGAGCAGCCTT	60.154	20	220	63	282
TGATCGACAAATGAATCCCC	60.67	20	111	6	116
ACGACCAATTGCTTCGTTTC	60.118	20	212	603	814
CAGCAAGATGAGATCACCGA	59.942	20	216	4405	4620
AGTGGCTGGTACGGAATACG	60.015	20	159	689	847
GAGAGGAATCAAGCCTGGTG	59.803	20	221	509	729
ACATCCCAGAACAAGGACCA	60.363	20	104	281	384
TGTCCTTAAAACCACCGGAC	59.83	20	119	462	580
TCACCTCCATTGCTTTTTCC	60.051	20	199	948	1146
AGGAAGGCCTTAGTTGGGAA	60.068	20	278	1259	1536
CTGAGAGAAGTCTGGGAGCG	60.275	20	196	944	1139
GTGCCTAGCTTGTGTTAAATTG	60.199	23	197	107	303
CTTTCACCGTCTCATCGACA	59.831	20	229	412	640
GCACATTTGGGGTTGTGAAT	60.624	20	270	287	556
TGACAATTAGCAACCCACCA	59.964	20	179	1299	1477
CGAACTTCGTGACGTGAACA	60.906	20	151	157	307
TGTTCCATGTAGTTGAGGCG	59.716	20	273	237	509
GCACAACAATGATTTTTCAGTC	60.032	23	272	1074	1345
TGAATATTTAAAGGGATTGTTTA	60.006	26	263	887	1149
TCAATGACAAAGGAAAACGAT	59.975	22	201	10	210
ACCGTAAGGTTGCGAACATC	60	20	184	1206	1389

CCCACTTGCATTCTCCACTAA	60.118	21	158	2191	2348
GATGAAGGAAAGTGCGAAGG	59.813	20	111	312	422
TAAAAGCAAAAAGGGCATGG	60.068	20	251	94	344
CAAGATTGGTTTTGTGCATACT	59.602	24	233	1269	1501
CCCAAGACCCCAATTTGATT	60.91	20	275	1738	2012
TCTTCTAGGGGTGCTTCTGC	59.574	20	161	719	879
CAGTTCTTTGCCTTCCCTTG	59.846	20	175	17	191
CGGAGACTGGAGGTGGACTA	60.252	20	166	629	794
TCAGCACCCACTGTGAAAAC	59.726	20	265	424	688
GAAGGACCGAGTTGCAAGAA	60.375	20	184	59	242
ACATGTTAAACAACCCCACCTT	59.543	22	257	442	698
CATTTCATGATCACCAATTTGC	60.196	22	237	186	422
CTGGATTCAAACCCTCTCCA	60.042	20	246	228	473
TCTGGAATGTTTTGAGTTAATG	58.311	23	237	511	747
TACGCATTGGTTCGTAATGG	59.443	20	268	5	272
AGAGATACCACCGTTGCCTG	60.134	20	251	71	321
TTTCACGTGTGCTATTTCGG	59.729	20	181	3299	3479
TGTAGTGTCAGCAGCAGCCT	59.801	20	121	694	814
ACCTCTAGCCCGGTGAACTT	60.132	20	210	3	212
GGAGACCGAATTGGTAGCCT	60.464	20	229	12	240
AAAAGCGAAGAGAGCGAATG	59.73	20	260	189	448
ATCGAATTACCCGTTTGTGC	59.829	20	248	689	936
CAATCGGCCAAAATGTATCC	60.153	20	235	2	236
CGAGGGCGCATGTACTATCT	60.257	20	181	3733	3913
GAATCCACGACAAGGTGGTT	59.827	20	149	12	160
ATGGAACAGTGCGACAAATG	59.572	20	258	1944	2201
TGGAGGATGTAGAAGGTGGC	60.073	20	214	939	1152
GAGCTCCTTGTCGTGAGCTT	59.751	20	135	3641	3775
TCATACGCATGAGGGATAAAA	58.122	21	230	134	363
AGGTTCTTCGTCAAAAGGCA	59.853	20	153	3	155
TGGTGTAGATTAACACAACTTG	57.939	27	254	536	789
TTTGGTTCATGTAGCCGACC	60.894	20	223	307	529
AAACGGCACCGAATACAAAC	59.867	20	187	122	308
TGTTTTAAGACAAGGGGCGT	59.609	20	232	2425	2656
TCTTCCTCTTCTTGCCTTGC	59.694	20	256	2145	2400
CCACGGTCATTTCTAGGGAA	59.926	20	262	695	956
GCCCCTTGATTAACATCCAT	58.717	20	279	150	428
TCAAATCCTCCCTACCCTGA	59.478	20	274	26	299
GTGATGAAGCGTGTGAGGTG	60.319	20	126	1403	1528
ATCAAAACAGGGGATTTGAAG	59.814	22	268	241	508
GAAGGGCCTTGTCTTCCTCT	59.817	20	257	281	537
GGTTTTCTTCTGGTTCTGCG	59.853	20	156	745	900
AATGAACGGGAATAGCTGGA	59.528	20	149	1236	1384
GAGCTGCAACTAAGGCCAAC	60.022	20	222	127	348
TTTTAATCACTATACCCGATTTC	58.455	24	252	1174	1425
TGTTAGCCCACATTGGATGA	59.924	20	269	392	660
TGGGACCAGAAAGATGAAGG	60.042	20	225	508	732
AGAGAACAAGTGGGTGCTCG	60.444	20	200	39	238
AAAAGGAGGAAAAGGGACGA	60.046	20	168	1749	1916
CAATCTTGCACCACATTTGC	60.119	20	142	5005	5146
ATATTGGGACATAGCCCGGT	60.419	20	245	226	470
CGAGTTTATGACCATCCGGT	59.813	20	118	5	122
GGGTGAACCTTCCATCATTC	59.192	20	126	1	126
GGCACAGATTTCGAGGTAGC	59.843	20	166	364	529
GGAAAACGCGTTGCTATGTAA	60.143	21	201	417	617
GAAACCGTCGGAATTACTGG	59.429	20	174	30	203
AAGTTCACACCCGAATCCAA	60.353	20	174	254	427
ATTCCACATCATGCAAGGCT	60.492	20	269	790	1058

TGACATGATGGGGGAAGAAT	60.135	20	232	243	474
ATAGAAGGGGGATCGGTTTG	60.145	20	228	875	1102
AAAGCGAATGCCCTTTGTAA	59.72	20	246	2651	2896
CGCCTTTGCTGGTGTTTATT	60.131	20	234	447	680
ACGGAGAATGGAGATTCACG	60.073	20	260	5	264
TCTGCTGCTTCATCTGCATT	59.704	20	218	1001	1218
TGTCGGTGTTACCCCAATCT	60.232	20	169	1363	1531
CAAAACATCATTCACGACGC	60.119	20	268	313	580
TGGGTTTATTGATGCACCTG	59.395	20	206	556	761
TTCATCAAGAGATTACGTTTTA	58.427	27	146	114	259
TGATATCGGGCTTTGAGCTT	59.807	20	197	587	783
GTTGTCGTCGGAGGAAGAAG	59.844	20	208	462	669
CAAGAAAACAGTGGGGGAGA	60.081	20	170	1203	1372
CGCATGTCATCACTCGCTAT	59.854	20	126	998	1123
ACGAAACCCCTTCCACTGTT	60.776	20	129	122	250
CTGGGTAAACCCACGGACT	59.829	19	276	809	1084
CTCTCCAAATCCCACCAAGA	60.042	20	210	2014	2223
ACGGGGGTGTTAGTTCAGAAT	59.743	21	273	49	321
TCCCTCGAAGGTAAGAGCAA	59.948	20	187	108	294
AACCTTGACGAGGAGCTTGA	59.989	20	252	474	725
TAGCAAGGAGGAAGGAAGCA	60.088	20	270	1638	1907
AAAAATAAGCGCCACGTCAC	60.138	20	279	1044	1322
GCTTGGAGAGAAGGAAGCAA	59.694	20	243	105	347
AATGCAGCTTGGTCGAGTTT	59.882	20	165	2501	2665
GGAATCCTCTGTTTCCGCTT	60.578	20	262	1911	2172
TCGTGCCTGTCCTAACAATG	59.716	20	130	486	615
CCAACACTTGTGCAAACTTCA	59.79	21	280	908	1187
ATTCGATCGTAAAACAGCGG	60.096	20	252	103	354
GCCCTGTTACATATTTTCCCAC	59.614	22	213	543	755
GGACTCCGTCATCCTCTTGA	60.199	20	243	2331	2573
ACACCCACTCCTCCCTCTCT	60.112	20	244	53	296
TGCTAAAAATATGATGAATGC	57.474	23	203	7	209
AATACGACGAGGCGGTTTTA	59.609	20	259	1471	1729
CGAACAATTTTCAAACGGCT	60.11	20	245	1323	1567
GTAAATGGCCGAATCAGGAA	59.901	20	149	1650	1798
GCAGTGCGACAAGCATTAAA	60.021	20	180	781	960
GTGATGATGGTGCAGCAAAG	60.272	20	174	943	1116
AATAGTACAGTGGGTTTTGCTA	57.832	24	215	1119	1333
CCACTCCGTCTTCTTTTGGA	60.224	20	242	22	263
TTTGATTGGGAATAATTGGG	57.289	20	170	1010	1179
CTTCAACTTGGCGCACTGTA	60.05	20	262	632	893
GAAACGCGTCCTGATAGGAAT	60.465	21	218	282	499
TAATGCAGGTCACCAGTCGT	59.165	20	276	2	277
CCAATTCAAGTCAGTGTTCCTT	58.227	22	257	262	518
GGGTCAGATGTACGCAACATT	59.874	21	269	280	548
AATGGGCCAACTACAGTGAAT	58.45	21	250	2160	2409
TTCGATTTTGGGAGTTAGGG	59.016	20	145	0	144
ACATTCGTGGCATTTGGTTT	60.235	20	160	4	163
GGTGATAAAAATGCCCAATCA	59.652	21	274	375	648
AGCACATGCTGCTCACAAAC	60.064	20	236	134	369
CATCCTCCATCTCCATCCAC	60.288	20	218	1847	2064
AAAAGTCCATCCCAAGAAAAA	57.71	21	253	325	577
TACCCACTGGAGGTGAAAGG	59.959	20	268	1885	2152
ACCCTACGAAGGGGAGACAT	59.817	20	279	348	626
GGGCTTCATTTCTTGTCTGC	59.82	20	204	345	548
CTAATTTTACAAATTTAACGAG	57.347	27	187	296	482
GCCTGTCTTTGGAACACCAT	59.973	20	118	5697	5814
AAGCCATCTTCCTCTCCTCC	59.778	20	205	557	761

TTCCTATGGTTGTTGGCGTT	60.365	20	226	1145	1370
TGGAGGAAAAGTTCTTTCAATT	59.988	24	276	526	801
ACACCTACCATAACGGCGTG	60.827	20	110	4	113
ACATCAAAAGTTTTCCAACATC	59.793	24	264	364	627
CTCGAGCGATTCAACTTGC	59.688	19	255	567	821
GCCTTCATCATCTTCTTCGC	59.923	20	231	172	402
AAAAGAGCGGAAACAGAGCA	60.132	20	236	342	577
GATTCTCCACTCTCCCCTTTTT	59.947	22	173	949	1121
GGACAGTTCACATGCAACAAT	58.485	21	240	5924	6163
TTGTGCACGATTTACGCATT	60.14	20	155	1810	1964
AATCAGCCAAGTCGAAGGAA	59.813	20	150	61	210
TCCAATCATTACCCTTGGCT	59.387	20	230	16	245
GCAAGTTATCAAACCGCCTC	59.713	20	134	1900	2033
ATGTAGCCGACCCCAATTTAT	59.585	21	242	572	813
CGAAACCCTCGTTACACCAC	60.41	20	188	622	809
GTTCAAGTTTTGACAATGGGC	59.467	21	257	23	279
AAAAGCAAAGCGAAAAAGCA	60.13	20	271	908	1178
CTAAATGTAGGGGCACCGTC	59.452	20	218	2837	3054
AACGGCGTTTTGAATACTGG	59.996	20	111	590	700
AGGTCAAGTTCACACCAAACA	58.102	21	124	52	175
TCTTGGGCTTTCAAAAATGG	60.046	20	156	533	688
TGTGGATGAATGCAAGGAAA	60.049	20	200	317	516
TTCGCGATGAAGGTTCTTTT	59.823	20	180	566	745
ACACAATCAGCACAGTGCAA	58.871	20	128	3	130
TCGTTCATCTGTCTTCTGCG	60.136	20	116	248	363
AGCATGCACAAAACGAGTTC	58.929	20	142	56	197
GGTGGAAAAGAGGGAAGCTC	60.19	20	161	506	666
CAATGCTTATGTTCCCTCCCT	60.326	21	235	851	1085
TGGTTCCTATGTTGTCCCAAA	60.213	21	224	961	1184
GGCTTTCAAGCTATTGCAGC	60.124	20	252	3325	3576
TAGGGAGATGATGAGGTGCC	60.034	20	274	1513	1786
GAGACGAGCCATTGTTGGAT	60.081	20	149	498	646
TTTGCAAATTCAATTGGACG	59.538	20	190	22	211
TTACGTTTACAAATCGCCCC	59.832	20	219	235	453
TGCTTTTCCATTTTGCCATT	60.436	20	237	969	1205
AGAGAAGGTGCCCTGTTGAA	59.844	20	221	2522	2742
TGCTTCTGAAGGTTCTGCCT	60.134	20	182	30	211
TGGAGGCATCAATCTTGTGT	59.09	20	236	792	1027
GGAGGCGTCAGCTTACATTG	60.796	20	267	848	1114
GGAGCCATGAGACTAGACGG	59.827	20	209	280	488
TTTTGCAATTTTCATTGGCTT	59.595	21	110	307	416
TGAGTTCAAAATGTCAAAAGTA	60.614	26	245	460	704
CCTGAACCACCACCTAAACC	59.304	20	178	11	188
GTAGGTACAACACCATGCCG	58.926	20	199	1	199
CACCAGCTTCTGAACCCATC	60.656	20	113	1948	2060
GGCCGCCTCATACTTTGTAA	60.096	20	172	188	359
TAGATCCCCCTGTCCCTTTT	59.761	20	195	333	527
AAGCGCAAATATATCCCGTG	59.95	20	232	5161	5392
ATTGTTTTCCGCCATTCTTG	59.938	20	241	492	732
CTCCCTCCTCATTCTCACCA	60.191	20	119	832	950
CGTCTACGAGGACGTGCTAA	59.097	20	228	1097	1324
TTCCTTTGTCAGGTTTGGCT	59.711	20	227	1397	1623
CAAATGTCGTGTTGAGTGGC	60.16	20	227	893	1119
AACTCGAAGCCTTGACCTGA	59.989	20	226	1532	1757
TATCGGAGGAGGATGTGGAG	60.027	20	199	596	794
TTTTCCTTGGGTAAATTGCG	59.937	20	266	743	1008
TTGCCGGTACATACATGGAG	59.42	20	225	54	278
GTTCTTGGTTGGGAGGTGAA	59.943	20	249	2929	3177

TTCAAGCAATTTCTGCCAAA	59.42	20	255	767	1021
ACATCTTTACTGCACCACCAGA	59.662	22	262	1370	1631
CCATCTTTCTTTCTCGACGG	59.807	20	177	1389	1565
TCCATGGACGGAAGAAGAAC	60.05	20	196	156	351
AGGAAGGGAATGGTTTCACA	59.381	20	192	11	202
CACGCGCATTTAATTTTGTG	60.131	20	267	1277	1543
GAATTGGCCTTGCTTGCTTA	60.343	20	231	278	508
CAGCATACCTAAACCTCCCTG	58.73	21	260	16	275
CCAATTTGGACCAAGTCACA	59.389	20	135	608	742
ATTTTACGGTGGCAACTTGG	59.861	20	118	513	630
AAATCTGGATCCATCAAGCG	60.036	20	195	1224	1418
TCCTTTGTTCTTTCTGTAGCCTC	59.078	23	268	817	1084
TTGATTTCCAGTCCCCATTC	59.727	20	229	1353	1581
GGTTCATGTAGCTGACCCCA	60.924	20	175	815	989
AATTGCCAATACCCAATCCA	60.016	20	273	31	303
AAAATGACGTGAAGTATGAAG	59.557	23	251	991	1241
GGAACAAGAGATTTCGCAGC	59.962	20	166	334	499
GCACGGGTTGAGTTCTTGTT	60.156	20	205	511	715
ATAGCAACATGTGCAAGCCA	60.288	20	171	288	458
GTTAATTTGAGCGCTGGAGG	59.845	20	185	97	281
AATGGCGATGAAGGAGAAGA	59.773	20	254	926	1179
AAAGGAGAACGTGGGTTGGT	60.776	20	161	711	871
TTCCGCTGTTACTGTTGCTG	60.05	20	244	414	657
TTTGGTCGAAAAGTACGCAA	59.344	20	172	9	180
AGGAATCCCTCTTTCTCCCA	60.008	20	277	682	958
TGCTGAGCTTAGGCTTAGTGG	59.799	21	243	1666	1908
AAAATGTTTGTCCTCGGCTG	60.11	20	264	64	327
CCTTCTCCCTCTCTCCCACT	59.801	20	192	614	805
CAGGGACTGCTAAAGGCAAA	60.378	20	196	1186	1381
GAGAACATGTGCAGTGTCGG	60.319	20	277	727	1003
GGAAATGGAGGCACTGATCT	59.094	20	274	691	964
CCACATAGCAACGAAGCAGA	60.011	20	252	2313	2564
GACCCCACATAGTGGGAAAA	59.647	20	154	1066	1219
TTCGGGTTTCACAATTCACA	59.941	20	123	1045	1167
TTCGAAATCGTGCACCTAAA	59.301	20	238	767	1004
AGGCTTGTTGACCGCTTAGA	60.015	20	251	134	384
AACGTAGGTGACGATGAGGG	59.989	20	138	258	395
TTCGTCTTCTGCCTCTTCGT	60.134	20	246	118	363
CAGCTCCTCCTCCTCTCCTT	60.088	20	230	730	959
AGGCAAAGCAGGATGAAGAA	59.955	20	121	803	923
AACAGGGTCCCTTCGTTTTT	59.842	20	210	563	772
TCATTTCAGTTTGCACTAAGCCT	60.302	23	224	6	229
TGTTGGTTCAAAACTAATCCAA	57.617	23	116	2517	2632
CCTAGGCTCTCAGACACACG	58.621	20	241	284	524
ATGAATGCCAAAGAAGTGGC	60.081	20	216	919	1134
ATTGCCTTTTGGATGAAGCA	60.585	20	235	359	593
GCACTCGGGATTACTTGAGC	59.843	20	245	1903	2147
GGTACGTCGATGGCTAGAGG	59.717	20	110	3440	3549
TGGGGAAAGACCACTCTAGC	59.284	20	271	0	270
CACGATTCATATGTGCTTCCA	59.557	21	264	31	294
AGGATCAAGTGGGCAAAGAA	59.67	20	279	4497	4775
CCCACGTACGATCTCAGGTT	59.989	20	221	183	403
TCGATCCCATGGAAGAAGAC	60.011	20	215	1681	1895
GGAGAAGCTGATTGTGACCC	59.661	20	149	9	157
GGGTAAGCAAAATGGTCAGC	59.574	20	216	1759	1974
GAGCTGGCCGTAGTTTCCTA	59.476	20	198	485	682
TTTGCATGTGAAAAATGGTTT	58.057	21	206	968	1173
TGAGGAAAATGGGTGGAAAG	59.903	20	260	685	944

AGCAATCTCTACAAGCGGGA	59.978	20	210	67	276
GCTGTGCATTATCACCTACCTC	58.747	22	275	666	940
GCAAGCATTTTCACCACCTT	60.118	20	260	390	649
GCCTGAATAACGAATGTTGGA	59.952	21	139	351	489
AAAAACAACAAACAACCACTT	58.621	23	168	207	374
GTCCATCGACTTCACCACCT	59.969	20	101	1359	1459
TCACTTGCCTTGTTTTTGCTT	59.912	21	225	407	631
TTGGAGAAACAGTGCTGCTG	60.175	20	195	988	1182
AGGGCTCTGCTAAAACGACA	60.015	20	266	142	407
TTTTAAATTAAGAGCCACCCAT	58.286	24	178	400	577
CATGTTCCTCGGAATCACCT	59.927	20	228	647	874
CGAAGCCCGAGCCTAATAAT	60.547	20	199	370	568
AAACCAACATTCACCACCTTT	58.331	21	231	487	717
AATTTATTGGGATTAAGGCTTT	57.79	23	192	754	945
TCAAACCAGATGACCCAACA	59.935	20	133	947	1079
ATGTAGCCGACCCCAATTTAT	59.585	21	112	2141	2252
GCTGCTGTCCACATAGCTGA	60.168	20	186	63	248
CGTCTCTCCGTTGTGTTTGA	59.873	20	280	2487	2766
GATTTCAGCCATGGTTGCTT	60.081	20	272	383	654
GCACCCTAAGATGGCAGAGA	60.362	20	229	496	724
AGGCAGCATTGAGGATTGAT	59.658	20	174	104	277
GCTAAGGCTGAAAGCAATGG	59.982	20	180	693	872
AAATCCCTCCCTTTCCTTCA	59.875	20	266	4843	5108
TTACGCTAGTCCGTGGGTTT	59.632	20	207	182	388
AGCCGATGTTCGTGAGAAAG	60.397	20	261	436	696
GATCTCAACTTGGGCTTTGC	59.82	20	219	1336	1554
CAGGCATAACCATTGCCTCT	60.096	20	260	17	276
TGCAATTCCTGGAACCTTCT	59.67	20	261	1768	2028
AGGATGAAAGGGAGGTTCGT	59.935	20	135	534	668
TGTAGCCGACCCCAATTTAT	59.297	20	231	1329	1559
CCCAAGACCCCAATTTGATT	60.91	20	250	1864	2113
TTGCCTCCTTACACTTATTTATC	59.631	26	203	2437	2639
TTTCACCGGTTATCTGCCTC	60.074	20	138	241	378
CCGCCTCTCCTCCTCTCTAT	59.935	20	255	1182	1436
ATCCATATAGCCGACCCCA	60.126	19	176	0	175
AGGCAACACGCTTCATTACC	60.14	20	161	3	163
TTGCAAGCTGATAGGTGTTCA	59.478	21	278	2180	2457
GCTCTCATGCGTACAAGCCT	60.569	20	277	613	889
GCTCCGTCACTGCTACATAGTG	59.965	22	261	837	1097
TCAATATGACGACGGCTCTG	59.823	20	263	192	454
TGTGAACGGCACGACATATAA	60.006	21	265	196	460
GGGCATTTTCACAGACGATT	59.939	20	235	2520	2754
AGCGGAAGTACAAATGGACG	60.132	20	200	1532	1731
GCAACATCATCCAGATTGGT	58.36	20	236	661	896
TACACGTGAAAAGGTTGCCA	60.149	20	266	596	861
TTATCCGATCGTAAGTGGGG	59.778	20	277	530	806
AGTACAGGCTGGCATCCCTA	59.717	20	192	2276	2467
TGGCCTACGTTACTCAACCC	59.993	20	198	1020	1217
TGCTATGCTTGGAAGTTATGTG	59.793	23	110	2596	2705
ATTACCAGTCAAGGCATGGG	59.813	20	277	66	342
TTCCCTTGATTTTTCCTGTG	57.643	20	150	59	208
CCCAAGACCCCAATTTGATT	60.91	20	210	2098	2307
CCAGCACAAAACAAAATGCT	58.822	20	280	654	933
CTAGCCTTAATTTGCGACGG	59.868	20	251	166	416
CCCAAGACCCCAATTTGATT	60.91	20	109	1105	1213
TTCAATTCTTTGGTCGGGTT	59.406	20	110	2377	2486
CTGCCCAGAGAACTTGAAGC	60.134	20	100	1884	1983
AAAAAGCAGCACCAGCAACT	60.059	20	152	996	1147

TGTGATTTCGTTAGGTCTCCAA	59.609	22	244	1080	1323
TTTCCAAGTACGGGTTCGAG	60.103	20	248	152	399
CACAGCACCCATTCTTCTCA	59.831	20	146	1505	1650
TGCTAAGGTGACGCAAATGT	59.347	20	264	7536	7799
GGAACCGTGCGATTTTCTTA	60.074	20	172	245	416
CATTGGCATGTAGTGATGGC	59.955	20	144	464	607
GCATTTTATTAACGTGGGCG	60.335	20	174	13	186
TGAGCTTCCACCTCTTTGGT	59.844	20	215	104	318
ATGGACTGTGGTGCTGCATA	60.144	20	275	62	336
TGGGCTAATAATGGAGCTGG	60.053	20	272	6117	6388
TTTTCGACGACGACAGTTTG	59.881	20	139	0	138
CCGTTACGATTGCCCTAAAA	59.958	20	109	44	152
CCCAAGACCCCAATTTGATT	60.91	20	186	941	1126
AAACACAACTGGCATCCCTC	59.973	20	181	16	196
TGAGAGTACGCACAGCAAGG	60.199	20	170	59	228
AAAAATAAAATATATATGGGG	58.563	27	174	95	268
TTTTTGGATGGAAAAATGGC	59.751	20	156	1518	1673
TGTAGCCGACCCCAATTTAT	59.297	20	166	1291	1456
CCTCCACCGTTACCTCCATA	59.807	20	218	632	849
GTCACTGCACCACAAGATGG	60.162	20	194	7	200
TTTTGAGGTTAGTTTGGCCG	60.103	20	128	585	712
ACCGTCTCATAGCCCATGTC	59.957	20	214	54	267
TCTTGTCGTTTCCCTTTTGC	60.227	20	176	164	339
GTGTTCGGAAAAGAGGCAAA	60.227	20	253	460	712
AGGATCACCACAAACTCCCA	60.363	20	277	2875	3151
GAAGGAACCGTCAGCAATGT	60.119	20	272	2131	2402
CAAATTAATCAATCTCCTCCTC	58.164	23	110	2038	2147
TTGTTCAAGCAATTCCTCCC	60.051	20	270	382	651
CTGAATTACGGCGTGGATTT	59.96	20	256	0	255
GAGTTCCTCCGAGCTGTTGA	60.533	20	248	1669	1916
CGTGTGGAAGGAGGGTCTAA	60.103	20	146	408	553
ATGGATGCGTTGCAAATCTA	59.14	20	267	2494	2760
CCTCAAGGTTCAATTGACTGC	59.726	21	245	2771	3015
GAGAGGTGAAGAGGTGGACG	59.835	20	249	149	397
TTCAGACAATGAGGGCTGTG	59.831	20	161	867	1027
ACGCAACCAAAGAAGGTTGT	59.639	20	107	3	109
ACAGCGAATCACCAGAGGTC	60.269	20	111	144	254
GGGAGAAGAATTCACGAGCA	60.34	20	228	25	252
ATGTTGCATGTGAGGTGCAT	59.999	20	265	326	590
GCATGCATGTGATGTCTGAA	59.202	20	110	1533	1642
CATGTGGAAGTGTGGAATGG	59.806	20	267	340	606
TTTGCAAAATGACACACGAA	58.728	20	268	1468	1735
TGCCACCAAGGAGAGTACAA	59.288	20	133	414	546
GTGCCATGAATATCGTTCCC	60.163	20	150	835	984
CTTCTTGCATGTCTGGAGCA	60.136	20	188	496	683
TCGTCACAATTTGCTTCCAA	60.234	20	260	662	921
CCCAAGACCCCAATTTGAT	59.59	19	201	1394	1594
CCTCAAGACCCCAATTTGATT	60.173	21	167	375	541
ATCAGAAGATCCAGCATGGG	60.034	20	186	494	679
TGATTAATTGAAGGTTGAGATG	59.891	25	210	20	229
AGGTTGCGTACATTTGACCC	59.859	20	246	3222	3467
CTCGGAAAATTCCAACGAAA	60.046	20	227	941	1167
AATGATTGATGAGAACCGCC	59.9	20	248	958	1205
ATTCTTGCGTGCTCACCTTT	59.882	20	191	2090	2280
ACGGGTAACACGGACATGAT	60.119	20	205	87	291
CTCAGCCCTATTGTAGGCCA	60.227	20	253	1385	1637
ATCTTCATCCTCCCACCTCC	60.278	20	155	626	780
ACCACAAGCTTCCACCAATC	59.973	20	217	269	485

AGTGGAATGTGGGGAGAGTG	59.962	20	125	834	958
ATGCAGTCGGCTCTCTCAAG	60.7	20	258	525	782
TTGATTCGTGAACATTAGGCTC	59.229	22	251	101	351
TCCCCCAATTGACAATGACT	60.173	20	196	5	200
GCATTAAATCTATGTTCCATTC	57.748	23	240	1256	1495
ACGGGCGGTTTTTAATGTTT	60.577	20	237	86	322
GAATAAGGAATTCGCACCGA	60.038	20	171	35	205
CCTCCAATCCATCCTTACCA	59.744	20	248	640	887
TGCATTAAGGGTTGGAGACA	59.123	20	205	445	649
TTCGAAACCACTCAACCCAT	60.353	20	213	86	298
ACGTTCTTCATCGCCTTCAT	59.7	20	118	863	980
GACGACGTTCTGAGGGAGTC	59.841	20	176	812	987
CAGATTCAAGGCGGAATGTT	60.074	20	212	272	483
TTGGGAGTGCATTTTCCTTT	59.546	20	262	8	269
GGAGGCTACTCTTTCCAGCA	59.574	20	228	17	244
AGATTCAGTCGGTTTGTCCG	60.111	20	243	715	957
TACTACCCCATCTTCGCACC	59.955	20	193	422	614
GGTTTCGCCTTGTCCTTGTA	60.11	20	254	942	1195
CAAGAGCATCCCACTTCACA	59.831	20	272	873	1144
TGCCGATCGCAGTTATGTTA	60.237	20	190	200	389
CGAGAAGATCTTGAGGTCGC	60.096	20	263	884	1146
TGAGCACATCGGAGAAAGTG	59.984	20	278	113	390
TGTTGTAGCACTCCGTCAGG	59.897	20	266	1134	1399
ATAGAGGAGGTGCCGTCGTA	59.717	20	199	5	203
ACCGTGTAGTTGGCTATGGG	59.875	20	215	462	676
AATAATGGCTGCTGCAAAGG	60.23	20	210	827	1036
GGTCTCGTGGTGGCTAGAAG	59.867	20	180	558	737
TCCATGAAACATAAATCTTGCC	58.946	22	159	11	169
AGCTGCATGAGCAGGAATTT	59.985	20	185	1098	1282
CGGTGATGGTGAACTTGTTG	60.001	20	262	739	1000
CAGGTTATGTTCCACGGTGA	59.415	20	203	1	203
GGGAAGCTTGTGGAGTTGTG	60.69	20	218	1205	1422
TCACCATATGTTCAACCTGTCA	59.772	23	245	9	253
AACGTAAATAGTTGCGCCTCA	59.793	21	249	4348	4596
TTTGTGGTCTGCTGATACCG	59.716	20	167	601	767
CCCTGTACTCATGAACGGGT	59.844	20	202	87	288
ACCGTTCCATCAAAGACCTG	59.966	20	203	1200	1402
AAGCTTCAATTCCCCTGACA	59.67	20	254	863	1116
CCTCCAGCATCCGAATATGT	59.917	20	161	475	635
GGTGGTGGGGAAGAGTAGTG	59.425	20	238	3691	3928
TCCTTGCAACTCATTCACCA	60.24	20	149	1930	2078
TGCTTCAAAAATTCAGCCAA	59.42	20	139	573	711
AGAAACATCATCATGCCGTG	59.527	20	144	53	196
ATGGGCCTCCTCCTTAAGAC	59.536	20	277	502	778
GTTGCTTATCTGGTTGCCGT	60.14	20	278	155	432
ATTCGACACCAATTTCTCCG	59.933	20	212	501	712
CTCCTTCCCAGCACCTATGA	60.21	20	280	235	514
TAACCCCTGCATCCTGAGAC	60.073	20	113	1071	1183
ACGACAATCACAAAGTCCCC	59.827	20	216	1000	1215
TCCACACCTCCACCTCCTAC	59.962	20	155	331	485
CCCAAGACCCCAATTTGATT	60.91	20	149	2979	3127
CACCTTAGTTGTCAGGGGGA	59.959	20	180	1942	2121
TGGCATAGTGAACGGAAACA	60.111	20	256	2365	2620
CCCGATATGGTAGACGGTTT	58.787	20	243	847	1089
GTTTTGGGACACTGCTCCTC	59.703	20	136	2977	3112
TCCATGGCCTAATTGGTCTC	59.894	20	264	409	672
GTAACATTCCGCGTTTTCGT	60.003	20	217	767	983
ATCTGGTGGATCTTCGGTGA	60.475	20	232	557	788

CAGAGGACGAGTTGGATCGT	60.261	20	267	2066	2332
TTCAACTAATGAAAACGGCAG	59.758	22	145	7	151
CATGCAATAAGTTGAGAAAAA	59.585	25	111	4	114
GGTTTTGGAGAATTCAGGCA	60.051	20	255	6	260
TCAAATTTCCCAGCAGGACT	59.67	20	234	2214	2447
CAGAGAAGTGGAAAATCCCG	59.665	20	124	469	592
CCATGGTCGACGAGTTGTAA	59.566	20	266	658	923
TTGTGCCCTTACCCAGTAGG	59.986	20	222	751	972
AGATGTACTGACGGATCGGG	59.95	20	215	288	502
GCTGTTGATCAATGGGTGTG	59.967	20	177	3634	3810
GCACTCCCTCAAAATTGACC	59.532	20	108	650	757
ATGGCAATGCTCATCAGGTT	60.492	20	270	226	495
TTGATTCATGTAGCCGACCC	60.864	20	206	2200	2405
GCCTTAATTTCCCACCCACT	60.187	20	270	3	272
TGGGATATGATGTTTGTGGG	59.049	20	226	5	230
TGGTGGCTCTTTCAATTGCT	60.776	20	255	1516	1770
GGGAAATTCTGACAATGACAA	58.554	22	187	5765	5951
TGTTGGACGGAATCCAAGAT	60.317	20	209	1107	1315
CTGGTGGAAGGTTTGCAAGT	60.149	20	155	1181	1335
AGCTTGTTCGCTTCGACAGT	60.201	20	217	462	678
CCAAGGCTTGCACCCTACTA	60.262	20	277	1074	1350
CCCAAGACCCCAATTTGAT	59.59	19	122	3834	3955
TTGTCAATTTTGAGTCCCAGG	59.956	21	252	526	777
TGGGAAAGAGATATCGTGGG	59.887	20	141	3209	3349
AGTTGGCATCCCAAAGTCAT	59.41	20	196	4	199
TTTGGTTCATGTAGCCGACC	60.894	20	254	392	645
TGTCGTGATAGCCAAGTCCA	60.263	20	224	624	847
GTTTGGTGAAATCGTCATCG	58.976	20	257	227	483
GCAGCGGACTGTAAGTTTCC	59.882	20	217	385	601
CAATTTGGCACCATGAGAGA	59.648	20	270	586	855
GTTCATGTAGCCAACCCCAA	60.755	20	200	3346	3545
GGAGCTCTTCGTCGAGATTG	60.096	20	261	679	939
TCCATTCGTGTAACAACCCA	59.816	20	117	660	776
ACAAAAATGGATTATGGGCAA	59.18	21	227	287	513
TTCGTTGGCTTTGCATATTG	59.702	20	267	1339	1605
TGATGAGTTTGAAAGGCGTG	59.84	20	230	1805	2034
TTGAGGTGGATGTGGAGTTG	59.52	20	268	728	995
ACTGCTAGGCATCAAGGCAT	59.866	20	166	758	923
TTCCTCCAACAGGAGTTTGG	60.081	20	267	471	737
CAGAAATCCGAAGCACGATA	58.869	20	179	309	487
CACGATGGTGATGAAGATGG	59.918	20	257	563	819
CTCCCCTATCTCCGCATACA	60.051	20	109	347	455
CCATCATGCATTTTTCTTTCA	58.613	21	276	3221	3496
AAGGGCCATAAATTGTGGAA	59.273	20	245	1084	1328
TTTCTCTTTCAACGCACACG	60.027	20	205	284	488
TCCACAGTCTCAAAGTGCAAA	59.475	21	223	3265	3487
GTTGTACGTCGAGGCCGTAT	60.022	20	160	2011	2170
AACAATTCCGTCATCCCAAC	59.653	20	135	1398	1532
CACCATGGCTGTGAGAGAGA	59.98	20	153	164	316
ATGTAGCCGACCCCAATTTA	59.297	20	265	2979	3243
GACTCTACCAGGAACGGGGT	60.371	20	276	102	377
AAAATGGGAGTGGAGTGGTG	59.82	20	207	710	916
TACTTTACCGCGGTTTCTGC	60.264	20	105	642	746
TACTACTTCCGTCCAACCCG	59.986	20	193	108	300
ATCAACTTCCGAAGAAGCCA	59.813	20	188	1012	1199
AACCAAGACCCCAATTTGATT	59.563	21	223	3259	3481
CATGGCCTTGCTGGAGATAC	60.624	20	273	1288	1560
CAAAACCAGCAACCTGGAAT	59.971	20	213	1243	1455

CGATGTTCATTTGCACTGGA	60.665	20	155	3	157
ATCAAGCAGCCCTTTGTCAT	59.7	20	184	2318	2501
TTGTATCACCTCCGCCGTAT	60.352	20	237	241	477
TTTCCTGTGCGTGAATTTTG	59.706	20	220	933	1152
TTTCCTTCTTCCATGGTTGC	60.051	20	254	582	835
TTGACATTCTTGGCAGTTGG	59.691	20	232	5720	5951
ATGTAGCCGACCCCAATTTA	59.297	20	217	5359	5575
AGACCATGCAAGTGGTTTGT	58.058	20	116	319	434
GAAGATGGTGGCGGAGAG	59.291	18	163	1060	1222
CCCAAGACCCCAATTTGATT	60.91	20	234	470	703
CGCGTGGGCTGTTAGTTTTA	61.166	20	276	1824	2099
TCTTGAGGAAAACCAGGAGC	59.405	20	254	44	297
TGCAGCTCCTGTGAATTCTG	60.136	20	107	1153	1259
CCATCTGGGTTTTGGTGACT	59.82	20	142	30	171
CACTTGTGGCTTTTGGAGGT	60.149	20	278	1302	1579
TGAACAAGTGTACCTCTGGTG	60.066	22	243	635	877
GAAGAGTAGCAACTGCGGGT	59.501	20	263	1238	1500
TAACCCGTTTACGTTAAATTTA	58.178	25	244	2986	3229
TGCATGAGCCTCGTACAAAA	60.401	20	232	6	237
CCAATGCTGTTGTTGAAACG	60.149	20	188	372	559
GGTTCATTTAGTCGACCCCA	59.79	20	101	2017	2117
CAGGTTTACGGGGCAGAATA	59.953	20	227	1172	1398
GCAGCATTTGATCACGAAGA	59.955	20	157	900	1056
ATGGAACTCCAAAAGGGGAC	60.169	20	249	2161	2409
TGCAATGTAGCCCTTAAAACTT	60.511	23	277	1	277
ATATTTTGGGGAAAGGGGTG	59.882	20	171	1123	1293
AGAAAACAGTTGCAGCACCC	60.299	20	227	1193	1419
CACGAGCCTCAAAATCATCA	59.799	20	274	957	1230
AGTCGATTGCTTGGGAACAG	60.255	20	187	1193	1379
ACTGATTGAGAGGGCACACA	59.261	20	273	507	779
GCTGGGGATATTTCCAATGA	59.722	20	270	126	395
TGGAGAGTGCAGAGATGTCG	60.138	20	107	82	188
CACAAACGACACAAGTCCGT	59.641	20	227	2279	2505
GCTCATTCCCTGGATTGCTA	60.177	20	255	1071	1325
GCACTTATCGGAAATCGAGC	59.813	20	234	1132	1365
CAGGCTTGCCTTCACATCTC	60.945	20	250	1979	2228
GAGCTTGGCAGGAACTATGC	59.985	20	188	668	855
CCCAAGACCCCAATTTGATT	60.91	20	215	1748	1962
CGTAATCTTTCCTTGCCTGC	59.845	20	208	521	728
CGAGGTTGCGTCCAAAATA	59.673	19	267	415	681
CCTCAAAATTCGCCAAGAAA	60.181	20	124	2567	2690
TGTCCTTTGGGTTCGTAAGG	59.964	20	235	2771	3005
TCTGCAGAAGTCGTGAAACAA	59.624	21	145	2278	2422
CCCAAGACCCCAATTTGATT	60.91	20	179	575	753
CGAAGCGAGATAGCCAAAAG	60.11	20	119	7	125
CCAGGTAACCCCCAAGTTCT	60.218	20	227	293	519
CCATTTGCTTGAAACGTCCA	61.968	20	280	981	1260
CTAAATCTGCCACCCGAGAG	59.83	20	212	2487	2698
TCGCTGTGTATGCATGAGTG	59.436	20	131	570	700
CAGGTCATGACATAGTGGCG	60.136	20	220	267	486
GCCAAAAACCCACAACCTTA	59.839	20	267	429	695
AGGCATGTGCCATAATCACA	59.955	20	182	2003	2184
TCGAGAGCAAACTTTTTGGAA	59.982	21	279	140	418
TTGATTCAATATTAGCCGTCCC	60.168	22	273	828	1100
TTGAAAACTTTGGGATGGGA	60.28	20	249	213	461
AAATGACAGCCCCTATGCAG	60.096	20	152	0	151
TGCAACCCTTCTCTCTCCAG	60.523	20	189	53	241
TTGCGGAACCGTCCTAGTTA	60.628	20	259	1	259

GTCTTCCCGCTCATCATCA	59.734	19	250	967	1216
AGGAGGCTTGTACGGACCTT	60.132	20	260	13	272
AACAAGGGTAGGGGAAGACC	59.299	20	260	4977	5236
GATCTCCTTCACGGGATCAA	60.011	20	248	123	370
GAGGTTGAGGTGTGCAAGGT	60.159	20	269	81	349
CCGTGGTACAATATTCGCCT	59.845	20	177	11	187
AAGGCTTTGCAGGACAAGAA	59.993	20	203	1801	2003
GGTCCATCCATTCAAGGTGT	59.636	20	124	36	159
TTATGTCCCGGAAAAGCCTA	59.542	20	218	506	723
CCCAAGACCCCAATTTGATT	60.91	20	145	653	797
ACGATGATGATGAAGGAGGC	60.042	20	197	542	738
GCTGAGGAGAGTGATGGTGG	60.829	20	228	2176	2403
GTGGGTAGTATGCCGTGCTT	60.022	20	197	1592	1788
TCTGTGGCCAGGATTCTTCT	59.803	20	279	7	285
ACCGTTCTCAAAAACCCCTC	60.34	20	269	338	606
GCCTTTTAGTGGTCCGAGG	59.679	19	280	347	626
CCAGATCCATCTTTCCTCCA	60.003	20	167	1345	1511
CTCATTTCGAAGGAATGCGT	60.214	20	236	1615	1850
AGCAATAAGGCAGCAGCAAT	60.01	20	166	644	809
TCCACGACTGCTTTGTTGAC	59.88	20	156	359	514
GTAATGTCAGGGTGGCTGCT	60.142	20	211	1748	1958
CCCAAGACCCCAATTTGATT	60.91	20	234	1743	1976
ATTTGCATCTTGAATGGGCT	59.533	20	230	4775	5004
AGAAACAGATTGGGTGGGTG	59.82	20	144	1457	1600
CCATGGATGCAACAATGACT	59.374	20	242	971	1212
AAACCGGATGCCCTATTCTC	60.286	20	254	4460	4713
GAAAAACAAACGGCCAAGAA	60.089	20	227	433	659
TGATGTTTGCATTTTAAGATGA	59.143	25	277	4620	4896
ATTTGTCGGGTCAAATTCCA	60.17	20	268	1579	1846
CCATTTTTGTTGAAGCCCAT	59.801	20	256	617	872
TTCTTTATGGGGAGCTGGGT	60.817	20	236	5869	6104
TAAGCATAAAAGGCATCGCTC	59.49	21	127	4	130
AAATGAAAGGTGACCATGCC	59.797	20	238	3768	4005
GACCGCCGGTATAACTCTCA	60.096	20	161	1711	1871
GCCTTGGACTTGTTGTCGAT	60.119	20	130	459	588
AACCACGACTTATTCATTGCG	60.011	21	261	1596	1856
ATCCAGGATGGTGGAAATCA	60.135	20	205	4616	4820
GAAGCGAAAAGCATTTGACC	59.829	20	278	494	771
GCCAAGATCAGCAGATCACA	59.95	20	242	745	986
TGCAACATGGTCAAACTTGG	60.552	20	209	301	509
GCAATCGACACTCCCACTTT	60.119	20	186	356	541
AATGTGGCCAATCTTTTGTTTT	59.758	22	260	5	264
GCCCATCTGCATATTCTTCAA	60.052	21	188	1818	2005
GCAATACGCTGAATGCAAAG	59.472	20	256	397	652
GATGGTGCTTTTGCTCTGGT	60.263	20	161	9	169
TGTGTGGACGGAAAACAGAG	59.72	20	267	1389	1655
TGAGAGAGGTGGTGCAGATG	59.98	20	204	1202	1405
GCTGGAAGAGTGCGGATAAT	59.297	20	197	9	205
GAGACATCTGGTGAGGGGAG	59.638	20	208	1675	1882
CGGCATCCATCTCAATCTTT	60.036	20	223	96	318
TCACTCCTCTCACTCGCAGA	59.846	20	167	904	1070
TGACAGCTGAATCAGTCGGA	60.557	20	279	1887	2165
AAGCCCGTGAAAAAGGAAAT	59.945	20	256	1771	2026
CTTCGCTTTTGGCTATCTCG	60.11	20	229	1823	2051
AACTGCCACATGGACCGTAT	60.263	20	191	876	1066
CTTTGGTTCAGGTAGCCGAC	59.734	20	248	1952	2199
CCCAAGACCCCAATTTGATT	60.91	20	188	2577	2764
TTCACGAATTTTTCATTCAGGT	59.871	23	208	906	1113

ATGCTTTAGCAACACCAGCC	60.278	20	229	1	229
TTTCATTCGCTTCCATTCATC	60.031	21	279	4928	5206
CCTACCCACCGAATTGAACA	60.745	20	171	312	482
TGTAGCCGACCCCAATTTAT	59.297	20	243	2927	3169
TTGACACACTCCCTCTGCTG	60.022	20	143	5315	5457
TTTTCAAGTGAAAGGTGCAATC	59.248	22	155	6	160
GTCCAAATCCGACAGATGCT	60.081	20	113	1520	1632
CACCGAGAATGACACGACAC	60.162	20	278	1672	1949
CATGCAAGGAGCAGCAGTAA	60.157	20	144	0	143
TTTCTGGATCCCATCTGAGG	60.003	20	152	836	987
TAGGGATCGCTGCTGAGAGT	60.119	20	243	624	866
TCAAATGGCAGACAAAAACG	59.706	20	239	6	244
TTGATGGGTCTTCCCTGATT	59.336	20	264	7	270
ACGACGACCAAAGGAATGAG	60.111	20	258	30	287
TCAATGCAGCATCCTGAAAC	59.805	20	134	3	136
AGTTGAAGCAACCAACCTGC	60.299	20	265	3	267
CCCAAGACCCCAATTTGAT	59.59	19	120	2993	3112
AACCAACAGGAGGCAGACAG	60.298	20	194	3248	3441
TGCATACCCAAGATTGTCTCC	59.947	21	269	524	792
TGGCCACGAAGAATTAACTTG	60.117	21	269	63	331
TATGCTTTCCGAGTGCTTGA	59.566	20	239	794	1032
ATGTGATTGCACCGACAAAA	59.972	20	239	3650	3888
CCGGAGAGGGCATCATAGTA	60.051	20	169	1899	2067
CCCAAGACCCCAATTTGATT	60.91	20	159	5799	5957
ATTCCATCACCATGATCCGT	60.018	20	152	561	712
AACCTGCCTCGACATAGCAG	60.419	20	188	2121	2308
ACGTTGCCTTGTATTTTGCC	60.003	20	258	1192	1449
CCTGGCTACTCACCCTTCTG	59.861	20	154	904	1057
TGAGCACAATCTTCAGGTGG	59.831	20	261	9	269
TTTTGGGCAAAGGATCAAAT	59.388	20	190	30	219
TTTGTCTCCTGGTGTTTGGAC	59.997	21	180	2231	2410
AAAAGTGGTGGAATTGACGG	59.83	20	128	1570	1697
AAGTTGGGTGGAAGATGCAG	60.111	20	263	697	959
CCGTACCCTCCTCCTAGACC	59.95	20	179	673	851
TCGTTTCCTTTTGGAGGTGT	59.569	20	248	23	270
TGTGAAAAACACGTGACATCAA	60.05	22	117	2239	2355
GCAGAAGGAGCCAAAGAAGA	59.694	20	195	985	1179
GGTTAAATTAGGCGGGTCGT	60.204	20	237	2835	3071
AGTTAGGAACGAACACGGCA	60.689	20	243	250	492
CCCAGAACAAAACCATTGCT	59.971	20	156	3770	3925
GAACTTTGATCCGAAAACGC	59.691	20	268	118	385
TGTAGGCCCATAGCCACATA	59.016	20	219	138	356
GTCAGCTCAAATGGCAGGAT	60.226	20	209	6	214
TGGAACAGCACAGACTGGAG	60.022	20	153	214	366
CATAGGGGCTCTTTGGTTCA	60.066	20	249	226	474
CCTTCACACCAAACTGCAAA	59.734	20	249	3462	3710
ACGCGGTGATAAAATCTTGG	59.96	20	188	1747	1934
CCTCCGTCCCTCTCTCTCTT	59.945	20	223	3104	3326
GCTAGATGCTCACCTCTGCC	60.127	20	278	3803	4080
CCTCAGAGGAATCCACCTCA	60.191	20	252	2626	2877
CAAGCAAACTGGTAGCCTCC	59.875	20	256	1770	2025
TCAGTTGCCTCTTTCAGCCT	60.134	20	260	501	760
CAATACCCGAATCCATCACA	59.2	20	117	3717	3833
ATTAACACCGGCATTGCTCT	59.597	20	217	2724	2940
AATCCCAATCCCAATCACAA	59.991	20	111	702	812
CCAATTTATTGGGATTAAGGC	57.539	21	268	3814	4081
TCATATGACGCAATGCACCT	60.104	20	250	503	752
GGAATGCAACTCAAACCACA	59.547	20	159	20	178

AAAAACGAGCATTGGCTGTC	60.257	20	170	1229	1398
TCCTAATACGACTGCCCACC	59.955	20	219	163	381
AGAAGGCGAAGAGGAGCAAT	60.484	20	199	781	979
CTGCACATTTACAACCAACAA	59.953	23	141	3	143
CCGATTCCTTGAATTTCCCT	60.258	20	280	2779	3058
ATGTAGCCGACCCCAATTTAT	59.585	21	157	3318	3474
AAATCATAGCTCCGCCATTG	60.06	20	224	648	871
CGGATATTCGCCCCTTATCT	60.26	20	177	487	663
TGGTCACTAGAAACCCCAGC	60.111	20	101	134	234
GTCCGTTGTTGCTGATCCTT	60.119	20	159	1573	1731
TCCAAAGAAAAAGCAAAGGA	57.609	20	274	1276	1549
CGGAAGTAGGAAAACACCCA	59.964	20	241	742	982
GCTATACCACGCCCTCAATC	59.556	20	255	2897	3151
AACCATGCTCTTTCCACCAG	60.111	20	255	563	817
CCACTTCCATTCTCTTCCCA	60.042	20	149	2343	2491
GCCCAAGTGTAAGAGTCGGT	59.212	20	176	220	395
ACCCTCCAAGATGACACCAC	59.817	20	209	1781	1989
GAGGGAAGTGGAGGTGATGA	60.048	20	190	496	685
TTGCTTGATCATTGCTGCTT	59.572	20	193	1310	1502
GCAGCAACAACCATTGAAGA	59.847	20	193	232	424
CCGACCCCAATTTATTTGAA	59.633	20	200	1921	2120
TGCGTACATCTGACCCTCAA	60.263	20	260	1012	1271
TCAGTCAAACCACTCGGTCA	60.285	20	200	1753	1952
CTCCCAAAGTCACCTGCATT	60.111	20	228	536	763
GCTGCGTTTGATTTTCTTCC	59.829	20	124	148	271
CCCATGTGCTGTGATGAACT	59.551	20	222	4	225
AACGAGATGCTCTCGAATGAA	59.97	21	242	10	251
TGGAGTAGGGGTCATTCCAA	60.309	20	166	7	172
AATGATAAGATCAAGGCCGA	57.244	20	277	117	393
GTTCTGCAAAAGAAAAGGCG	59.996	20	195	597	791
TTCCATGTCGAGTTTGTTCG	59.691	20	256	915	1170
CAAAATCAACCATATTTTCGCC	60.533	22	232	391	622
CATTCTAAACAATTGGCTGCTG	59.779	22	237	5622	5858
CGTAACATGCCACCAGTGAG	60.175	20	200	2362	2561
GAGGAGAATGCGAAGGAGAA	59.508	20	261	3070	3330
TGACGACTGTCACGGACTTT	59.31	20	241	41	281
CTCTTCGAACCCCTTGTTCA	60.224	20	259	2601	2859
TGGAAATGGAATGTGAACGA	59.9	20	198	13	210
ACTTCCCGTGTCCAGTCTTG	60.151	20	234	905	1138
AACTGCAAGATTCAGCGACA	59.596	20	229	1672	1900
TGTAGCCGACCCCAATTTAT	59.297	20	206	2930	3135
AGCCTCAAGATTGCAACCAC	60.263	20	158	2	159
CCATTCAACTCCACAACCAA	59.389	20	227	731	957
TGCTGCGGACAAATAACTGA	60.401	20	252	20	271
TTGAGTTGAGGTATGAGAAAA	59.658	26	280	311	590
CTTGAAGCATGCACGATGAC	60.423	20	105	5	109
TCAATGCAGGATGATTGCATA	60.05	21	177	25	201
ACTGTTGCGTTATCCAAGCC	60.14	20	238	5	242
GCGTCGCTAACTTCTGCTTC	60.3	20	131	156	286
CTGGCTCCCCAAGAATTACA	60.066	20	187	513	699
CTCTGTCCCCCTCGTTCTTA	59.28	20	211	595	805
GGAAAGTTCTTCGTTGCTGC	60	20	262	2397	2658
TTCGCCACCTCCATTTCTAC	60.074	20	228	410	637
CTCCCGAATACTTCTCCGAA	59.264	20	236	706	941
TCTTTCCACCCGAAATTGAC	59.91	20	256	2621	2876
AGACCAACAATTCCAGGTGC	59.973	20	275	1264	1538
GTGGCAGTTATAGCGGTGGT	60.022	20	173	1703	1875
CTGCTAGCACTGCCCTTTTT	59.654	20	148	3199	3346

CGACTAGCCACGTTCAATCA	59.864	20	274	1163	1436
CTTTTACCTTAATCTTCACCCTT	57.662	25	257	1648	1904
AAAGAGGTTGTTTCCGTTGC	59.218	20	232	1189	1420
AATCATCGCCACATCGTGTA	59.955	20	131	426	556
TGATCGTATCTGGTTGAAAGTT	59.144	23	261	1364	1624
TGCTTGATGTGCTCAGCTCT	59.887	20	203	2088	2290
TTGATTCCACCTCTTCACCC	59.903	20	215	1296	1510
CCCTACATAGGGGGAAAAGG	59.655	20	130	1951	2080
GAGGGGTAGTGGGAAAAAGG	59.799	20	138	2138	2275
CCGACCATTCAAATTTCCAC	60.17	20	129	14	142
TTGGCAGGAAATCACACAAA	60.088	20	256	3323	3578
CCAATAAAATTTTGCCCCAA	59.648	20	218	216	433
TAATCACCATGGACTTCCCC	59.605	20	191	2698	2888
CTGGGGGTGAATTTTGGTTA	59.657	20	144	1497	1640
GATTGGCCATGAAAATGGAG	60.274	20	194	293	486
CACCTTTGACTCGCATTTCA	59.84	20	270	3710	3979
TCGAGAGCTCTGGTGTTTTG	59.161	20	221	2431	2651
AACGCGAGGAGAAAAATGAA	59.823	20	250	371	620
CCTACAAAATGGGTCTCTTTGA	58.238	22	167	2658	2824
TCTTCAGAAGCTTGCTGTGC	59.47	20	258	2774	3031
TACCTCCATGAGCAATCCGT	60.483	20	267	9	275
TCATGCAGATTTAACCGACAA	59.172	21	128	24	151
TGTGAGGCGTGTTGTTTCTC	59.88	20	240	217	456
TATGTTCGGTATAAGGCCGC	59.95	20	142	1361	1502
TGGTTCATGTAGCACATCCC	59.374	20	156	4490	4645
TGCATCCTTCCATCTTGGTT	60.461	20	199	3171	3369
CACTCACACAGCCAGACACA	59.454	20	242	1110	1351
GGGATACAAATGAGTGTTTAG	58.944	23	270	2588	2857
TAAATGTGGAAATCGCATGG	59.377	20	273	1173	1445
TTGAAGAGTCGTGCAGTTCG	60.175	20	269	446	714
CCACCCCAAATTCTCATCAC	60.173	20	180	6	185
AAAATGAAAGGAGGGGTGCT	59.94	20	124	1079	1202
TTGGTTCATGTAGCCGACCT	60.517	20	115	3429	3543
CCACGGTCTCCCAATTCTTA	59.926	20	275	2777	3051
CTGCCAAATCTGGGACTGTT	60.111	20	169	146	314
GGGTGAGGGGATGTCTATCA	59.737	20	101	331	431
ATATCTACCGTTTCGGGTCG	58.928	20	227	837	1063
CGGTCTCTCAGTTAAGTCTATC	59.98	25	143	644	786
AATAATGCTACACGCCTCCCT	60	21	209	8	216
CATTATGCAGGAACTCGCAA	59.833	20	136	5247	5382
AGGTCATACGGGATGTGGAA	60.195	20	225	125	349
TTTTCGATTTCATCCTCATAGC	58.337	22	255	2687	2941
AGGCTCGCAGACAACAGAAT	60.02	20	220	2575	2794
GATCCATATAGCCGATCCCA	59.705	20	143	1623	1765
CAGGTTGAACACCCGTTGTA	59.46	20	226	122	347
AGGATACGTGGATGGAGACA	57.94	20	154	692	845
TGTTTGGTATGTGACCCCAA	59.667	20	254	870	1123
TTGCACAAAGTTTTGTTTCCAT	59.536	22	230	1848	2077
TAGGGCTACCGGACACTACG	60.147	20	259	3720	3978
CCAAGGCAGAGAAGTTGAGG	59.982	20	207	6027	6233
CGACCATCCTTCCCTGATAA	59.887	20	150	5	154
GGGGGAGAGAGATGAGGAAG	60.149	20	235	1796	2030
CCCAAGACCCCAATTTGATT	60.91	20	168	1893	2060
CACTCATCCACATGCTCGTT	59.707	20	197	1974	2170
GTCCTACACACCAAGTTCATCA	57.574	22	214	1513	1726
TTCACAAGATTTGGTTGGCA	60.088	20	131	1060	1190
AGGATGGTACAGTTGGCTGG	59.989	20	252	3823	4074
TGCCTCGAGAGTAAGAACCC	59.43	20	168	6	173

CGCACGAATTGCTACCCTAC	60.658	20	225	466	690
TGCTCATTTGTCAACCAGTCA	60.294	21	218	148	365
CCCAAGACCCCAATTTGAT	59.59	19	152	2071	2222
TCCTGCAGCAAGAAGAAAAA	58.771	20	200	0	199
CACTCTCCGCCCTCTCTACA	60.545	20	182	4354	4535
TGGTGTAGATTGTGAATAAAA	59.016	25	108	4	111
CAAAGAAATCAAAGGACCCA	59.05	21	262	3314	3575
TTGATCATTTGGGAACACCA	59.75	20	258	5354	5611
CCATTTGCAATGGACAAAAA	59.396	20	146	1585	1730
CGGGTAACTTCATCATGGGT	59.67	20	269	8588	8856
TAACAGTTTCCGCCCATCTC	60.074	20	184	7	190
AGAAGGTGGGCAGTAAGGCT	60.268	20	192	1965	2156
TCATTGAAACCTCCTCCTCG	60.187	20	213	2777	2989
GTTTGAATACGTTTGGCGGT	59.867	20	144	2146	2289
CAAAGCTAAAACCGCACAAA	59.003	20	255	23	277
GACGACGAGGTTTAGGACGA	60.255	20	230	1028	1257
GAGTTTTGTGGCGGATTGTT	59.978	20	224	120	343
GTATTCACGGGCAGTGGAGT	59.997	20	250	953	1202
TCTCCCGGGATGTTAAAGC	60.021	19	166	2567	2732
CGTTTCCTCTCATTTGCAGG	60.766	20	233	0	232
GCTTGTTAGTTTGGTTATGTCG	60.076	23	228	3094	3321
TGCAGTCAGCAGCAAAAGTT	59.788	20	267	2874	3140
ACAGATGGTTCACCAGTCCC	59.817	20	164	4387	4550
TCAATGACATCTACACCGCC	59.527	20	258	1	258
TCTATGGTTCACATGGTGCC	59.374	20	173	35	207
CAACTAAATTGCCCCATGCT	59.96	20	266	3230	3495
CCAGTCTTCTAGGGCTGCTG	60.149	20	191	112	302
ACACACCCAATTCTTCAGCC	59.973	20	130	410	539
ACGCTTTCACTGTTGTCGTG	59.946	20	235	561	795
TCATTTCAATTCGAACGCAG	59.809	20	250	820	1069
GCATGCCCTTACAACGAAGT	60.14	20	161	617	777
GTATGCCACCCTTACAAGCC	59.457	20	157	1264	1420
CTAGAAACACCTTTGCGGCT	59.517	20	224	1511	1734
CAAGATAGGCCCGAAATCTG	59.662	20	163	754	916
GGCCTTCAAAAGCATAACCA	60.074	20	232	971	1202
CACAGCACAAACTGATCGCT	60.056	20	232	265	496
AAATCTCCAAGTCCCGTTCA	59.526	20	184	10	193
GAACGAATTGAAAGTTCCGC	59.691	20	263	1129	1391
ACGGCAAATTAAAATGCGTC	59.971	20	266	1181	1446
ACAAATTTGCCCTCTCCCTC	60.443	20	156	0	155
GAGACTGTGGATGGGGAAGA	60.048	20	218	594	811
GATGAAGACTTGAAGTTGGTG	58.695	22	247	382	628
TGTTTTCGGATCAAAAGTTGG	59.961	21	250	2724	2973
AATGCCTTTTTCTGCCATGA	60.585	20	269	2283	2551
CAATATTGCTGAATCGAGCG	59.425	20	194	1458	1651
GTTGGTCGGAGATGATGGTC	60.335	20	169	1201	1369
GGTCCGAATACCAACACCAC	60.096	20	258	996	1253
TCCAGAGAGAGAGAATGCCC	59.486	20	273	261	533
TGCTTCTTGATCAAATTCCG	58.843	20	275	926	1200
GATATGACAACCATCCGCGT	60.754	20	266	798	1063
ACACAAGAGGGAACACCCAC	59.859	20	109	739	847
GGGAGGGAGTTTTTGTTTCC	59.783	20	276	3818	4093
GCTGTTTGGTTTGGCAACTA	58.822	20	253	324	576
ATTTCACCGCAGCAAAACTT	59.752	20	263	128	390
CCGAGGAGAATCAAATCGAA	60.148	20	240	329	568
AATGTGGAAATACCCTAAATT	58.269	23	215	1337	1551
TTCCTACCTTCACTAGTTTTCAT	59.946	25	129	380	508
TCATACGTGGCTTCTCTCCC	60.218	20	210	801	1010

CGAAGGCCTTTTCGAAGTC	59.94	19	146	576	721
TGAATCTGCAATTTTCTTGTTG	59.75	23	145	327	471
AGGAGGTAGAAACATGGCCC	60.328	20	149	505	653
CACACAAAATTGTGCCTTGC	60.157	20	262	18	279
CGGTTGATTTTGAAGTGGCT	60.11	20	231	103	333
TTAACAATTATTTGAGGCGCA	58.375	21	186	737	922
GGGATGGTGGAAGAGCAGTA	60.073	20	200	1365	1564
TGCTCTACATTCGGTGGAAA	59.272	20	255	460	714
CGGTAACCAAGAAGGCACAG	60.679	20	279	813	1091
ACCCCGTATTTTCACAAATAAA	57.523	22	238	89	326
TTGTTAATGGGGTGGGGATA	59.872	20	267	712	978
CATTATGGACGGTTCGGTCT	59.813	20	274	1985	2258
CCCGTATTTTCTTCGGGTTT	60.177	20	183	67	249
TCTCCTGTTTATTTCCCCCA	59.359	20	270	544	813
TGGTGTTTGTGGGTGATGAA	60.829	20	254	208	461
ACATGGGGTTCGAGAATGAA	60.317	20	173	800	972
AAGGGAAATTCAAGACGTGG	59.028	20	100	29	128
TGCAGTACAAATTTAGCTGGA	60.082	24	130	257	386
GAATCAAACGCTGGATTTGG	60.448	20	262	8	269
CCCCCTGCCTTTCTTTCTAC	60.068	20	148	465	612
GACGATCGACGGAATTTAGG	59.528	20	182	256	437
CGCAGTCTCCTTTTTCTTGG	59.986	20	195	340	534
GGGCGTTGTTCTGTACTTGG	60.55	20	243	8	250
AGAAACGATCTCGTGCCAAC	60.263	20	265	1611	1875
TCGGAGAGCTAACAGAGGGA	60.088	20	231	26	256
TGCGCGTATGCATAAGGTAG	59.886	20	170	4415	4584
CAGAGCGCACTCGAAGAGTA	59.49	20	242	336	577
AAAACACCTGGGACCACAAT	59.162	20	275	162	436
GTGGGCAGATAATGGGTGTT	59.676	20	198	865	1062
GGATTCAGCTGGAAAAACCA	60.051	20	183	132	314
TGATCATCCTCAGTTGTTGATT	59.985	23	279	382	660
TAGTTCCGAAATGATTGCCC	59.901	20	254	2204	2457
CCGCCCTCAAGCCTAGTTAT	60.593	20	237	5815	6051
AATATGTTTGAGGCTGCGCTA	59.888	21	261	1260	1520
GCCTTTCTCCTTTTCTTTAACCA	60.114	23	164	971	1134
TCTTCCGTAAAGCGAAGGAA	59.953	20	252	759	1010
ATCATTCACCAACACGCAAA	59.972	20	113	3050	3162
TCGTCTCCCGTTGAAAAAGT	59.711	20	201	6515	6715
TGTTGCAGATGTTTCTTCGG	59.84	20	272	671	942
AGCCCTTTGGAGGTAGGTTG	60.488	20	121	1506	1626
AGGGGTAAGCGAGGGTATGT	59.848	20	193	12	204
CGGTCAACCGATTCCCTAT	59.759	19	246	637	882
TTTGTGGACCTAACGCATGA	60.111	20	141	395	535
GTTGGATGAAATAGTGCCGC	60.478	20	159	11	169
CAGGGACGGTGCTATTTAGG	59.587	20	148	196	343
TCCGAGCCTGAGTCAATTCT	59.95	20	217	198	414
CAATTTGGTTGGGTGCTTCT	59.971	20	215	20	234
ACGGATGAGATGCAAGAAAA	59.699	21	279	1930	2208
GAACCACTGAACCACGGAGT	60.009	20	101	708	808
TTCAGCAGGCGTAGACATTG	60.011	20	166	352	517
TTTTTATTGCGGACGTCAAA	59.189	20	176	2172	2347
AATGGGTTGTCCCCTTTTTC	60.032	20	210	104	313
TGCACCCTGAGCAATAACAT	59.152	20	274	533	806
TTGAAGACTGCGTTGTCGAG	60.175	20	263	613	875
GGGGGCAATGGATTATTAGG	60.349	20	189	2031	2219
CATGTTGTTAGAGTGGCCGA	59.716	20	211	166	376
TTTGGGTCAATCATTTTGGTT	59.168	21	251	509	759
CACGACCCAAATCAACTATTC	59.861	22	279	1781	2059

ACGTTGTCCTTTACAAGGCG	60.168	20	251	101	351
AATTTGAGCAGGGAGCAAGA	59.955	20	183	25	207
TCACCCCTTTCTCTTTCTCG	59.401	20	146	898	1043
CTTTCGTTTCCAATGTCGGT	59.971	20	272	2499	2770
TCCGTGTGGCTAACAATTCA	60.111	20	275	64	338
TTTGGCATTCCTTTTTCAGC	60.188	20	109	38	146
CATGATTTTGGCCTTTCAGC	60.585	20	263	2650	2912
TCTGGCACGAATGGTGAATA	60.073	20	236	608	843
ACATCATGCGGGTAAGGAAA	60.331	20	136	1732	1867
TGCAATCTGCTCCATTTAACA	59.315	21	232	364	595
TCTCGTCTCTCAAGTTCGCC	60.678	20	267	1074	1340
GCTTCCAAATAATGGCTTCAA	59.202	21	227	118	344
CATACATTTTATCATCCATTCG	58.405	23	249	13	261
TGTGAGCGTGTGTGAGTGAA	60.07	20	238	257	494
TTGGCATAATCTGGACTAAAC	59.42	24	236	177	412
AAAATACCATTAACACGCAGG	58.567	22	245	533	777
TAACTACCAACCAGCCGCTC	60.27	20	242	48	289
AAGAAAGGAAGAAACCGGCA	61.088	20	254	109	362
TTGACAACAACTTTGCCAGC	59.888	20	109	459	567
CGTGCAGAGGCACATGATTA	60.834	20	181	2685	2865
TGGGGAGAATGTAATAGCCG	59.916	20	280	1424	1703
TGATGACCTGGAGTTGTGGA	60.088	20	190	6834	7023
CAAATCGCACACATACCAGC	60.142	20	116	450	565
CCATATTTGTGTTTCTCATTCG	59.293	24	207	127	333
GGCTGGTCCAACGGTATTTA	59.823	20	248	528	775
TCTATCTCGGATCCAATGGC	59.998	20	223	1068	1290
GGATCGCCCATCAGATGTAT	59.739	20	233	786	1018
TCTTGATGTTTAGCAGCAGCA	59.767	21	212	965	1176
CCAGTTCCCTCCCTACTCAC	58.591	20	120	227	346
TAGTATTGTCCCTCCACCCG	59.807	20	280	1628	1907
TCATAAGGATTCGGCCAGAC	60.036	20	246	6	251
ATTTTCAATGCCAAGCGAAT	59.552	20	216	226	441
ACAAGTGCTTGAGTCCGCTC	60.599	20	252	1579	1830
TCGTACCAAAATGTGCAACAA	60.022	21	123	3	125
TTTCCCCTTCATGTCCTACG	59.926	20	147	284	430
TGACGGTGAGGATTTGTGAA	60.088	20	258	82	339
TTCTCAGCAGAAGGTGTTGA	57.071	20	223	563	785
TGGAATTTTCCAAATCTGGCT	60.788	21	193	332	524
TCCCATGTATGTAGATTGCTTC	60.218	23	273	131	403
TCTCGTCCTGACAAACTTCAAC	59.377	22	214	82	295
CTCCTCTTGCGAGAAGTTGG	60.126	20	241	49	289
CGCCTTCAAGATCCACATTT	60.074	20	149	391	539
TGGTGAGTTTTTAAGCAACCAT	58.676	22	239	1349	1587
TCACCTTATTTCGCAATTTTCA	59.603	22	155	653	807
CGCTAGGCTTCAGGTCGTAG	60.168	20	231	1416	1646
GGACCCAAAATGCCTATTCA	59.762	20	184	697	880
GGTAGCCAGTTCCCAAATCA	59.933	20	166	13	178
CCCATTTGAATCAACCCCTA	59.617	20	230	517	746
GGTTGTTCTCTGGAAACTGTTG	60.554	23	273	312	584
CAATGTCACATCCCAAGCAC	59.967	20	108	109	216
CGGTTCATGATATTGGGGAC	60.014	20	260	877	1136
CCCCAAAATTTCCCATTTCT	59.992	20	277	1364	1640
GGGGGAATTTATCCCGACTA	59.978	20	122	445	566
CTATCTGCCGGAGACACCAC	60.678	20	222	1348	1569
CGCTGAGGAAGAAGCTGAAT	59.717	20	274	180	453
TTAAAAATAAAACCGGCGGA	59.45	20	141	11	151
ATGACCAAATCAAGGGGCTA	59.387	20	236	1721	1956
TGTCCCACATTGGAAAAACA	59.792	20	248	336	583

GGAACATTACAGTTGGCAAGC	59.629	21	276	2482	2757
CAACACCGTTGTCTTTCACC	59.034	20	182	1355	1536
AGGTTTGAGGGCCATGACTA	59.55	20	205	787	991
GCTTGTTACACCACACTGGG	59.06	20	241	954	1194
GACGCCCACGTGTAAAGACT	60.179	20	129	4	132
TGAGGTGTCCCATACGGACT	60.386	20	156	0	155
TGTAGGCAATTCAAGAAGCA	57.1	20	177	729	905
GGTGAATTTCTTTTTGGCACA	59.967	21	272	0	271
ACCTCGAATGATGTCCGTTC	59.934	20	247	323	569
GCAAATATTGCAGTCAGCCA	59.839	20	280	394	673
GTTTTGTCAGAGGCCACCAT	59.973	20	186	1177	1362
TTCGAGTTTAGTTCTTCTGTAAT	57.073	26	224	397	620
CAACTAGGGGTGTTCACGGT	59.884	20	206	710	915
CGGGACGAAATTTTTCAAAG	59.559	20	250	160	409
GGCGAATTAAAATACACCACG	59.376	21	204	620	823
TGCATTCTAAACTGCCAACG	59.872	20	100	798	897
TTTTTGGGAAATCCTTGCAC	59.916	20	159	496	654
GCTTCCATGTATGAAGATCGC	59.688	21	175	23	197
GGATCGAAAGGTTGTGGAAA	59.91	20	179	189	367
TGGTGATTTTTGCCGTGATA	59.93	20	237	574	810
TGCGGCCCATATAGTTGTAA	59.053	20	243	130	372
AATTCCTCCTCCCCATTCTG	60.264	20	224	224	447
CCATTTGATCTTGGCATGACT	59.947	21	277	1729	2005
AAATAGCAAGTTGATGGCGG	60.096	20	121	271	391
CCATGTGCTTACAAGTTTTGGA	60.032	22	211	1189	1399
GCAGGAGGGTTTCTAATCCG	60.949	20	139	2	140
GAGCCATGATTCACCATCAA	59.456	20	149	0	148
GCATTGTTCACCACCACATC	59.819	20	277	232	508
CCCATGTCTTAAATACTCTGCC	60.369	23	270	1597	1866
GGTTTGGGAGAAAAGCATCA	60.051	20	264	445	708
CCCACTGACTCCTTCCATATCT	59.461	22	238	359	596
AGGAAGGGGGAAAAGGAAAT	60.122	20	199	595	793
TGGCACTTCCAATCTGACAA	60.24	20	229	38	266
AGAATCGACAGTTTGGACGG	60.111	20	228	584	811
GCAATTTTGTTGTTTTGTAAACT	59.539	25	227	639	865
CTCAAACTCCTCCTCATGGC	59.803	20	238	1385	1622
GCAGTTGATTGTTGATTACAAA	58.614	24	279	213	491
GGATTCCTCCAATGACGATG	60.281	20	267	865	1131
TTCCAGAAATTGTGTTGGCA	60.088	20	174	2105	2278
ACCTGAGACGTCACCAGACC	60.161	20	219	2446	2664
ACATGGCTAATGGACTTCACA	59.499	22	263	1089	1351
ATAACCGCCGATTTTGGAAT	60.517	20	236	817	1052
AAAAGTCGCGTATTTTTCGTG	59.307	21	258	345	602
ATTGATGTGCTGTGTTGGCT	59.169	20	137	2440	2576
AGGTTTCGTGTCATGCCAAT	60.384	20	236	6	241
TCCAATTAATCCTAAACCACAT	57.985	24	233	324	556
GTTGGGGTCTTGGCGTACTA	59.993	20	251	142	392
TCTTTTTGACTTTTGAGCAGAT	58.687	23	266	547	812
CTGCTTTACACCCCTCCAAA	60.103	20	163	1795	1957
TCGATTTTTCACAGTAGCAGC	58.187	21	280	835	1114
CAGTGTTTGAATCACCTAATG	59.007	23	182	692	873
CGACAATCAACTGGGTTTCC	60.353	20	178	121	298
TTTTTGTTCCATGTTATTGCCA	60.218	22	213	4585	4797
AGGGTTCAGGGCGATTAACT	59.962	20	197	222	418
GAAGTTTTGGAGATCCGACG	59.67	20	126	291	416
AGGGGCAATTTGTAGACACG	59.993	20	280	813	1092
CGACTTGCCACTGGAATTTT	60.11	20	234	115	348
CCATTGTTAACCCAAAACGC	60.223	20	133	37	169

ATTAACGCGCGCCATATATTA	59.511	21	226	2883	3108
AGTGAGACACTGAATGATATG	58.279	24	239	215	453
TTGTGAATTCAATCGAGCCA	60.197	20	158	254	411
TCGACCAGCACAGTGAAGAC	60.03	20	272	3272	3543
CCTTTATGGGAAGTGGCAGA	60.066	20	154	1107	1260
TTGTTATTTTCATTAAGTTATTA	57.628	27	133	3152	3284
ATCGTGAATGGAAGGACTCG	60.073	20	112	507	618
CACAGCCACAACCTACGAAA	59.758	20	129	1086	1214
GCAGCTTTAGCAGAGGGAAA	59.73	20	278	233	510
TCTGCCATCATCCACCATTA	59.883	20	183	165	347
TTTCGGATGTAACACAGGCA	60.111	20	135	1686	1820
AATTAAGGTTTGCCCTTGCC	60.312	20	185	62	246
ATTCCTTCCCTCTGGATGGT	59.755	20	243	149	391
TAATAGAAGCGGAGGAAGCG	59.586	20	226	826	1051
TTGGAATTAAAACCGAGCCA	60.427	20	213	716	928
CAATCCAATTCCTGTATGGAAA	60.062	23	229	621	849
ACTAGCAACTCGCTCTCCCA	60.156	20	200	103	302
ACGACACTCGAAATGGAAGC	60.263	20	195	1443	1637
AGCAAACACCCCAAGATTTC	59.031	20	129	49	177
TGTGGGATGCAATGAATCTG	60.481	20	279	5246	5524
AAGGATGAGGGAGGGAAGTC	59.492	20	253	825	1077
TTGATGGAATTAAGCTGCGA	59.401	20	245	206	450
CTCCAATCTTCTCCACCTGC	59.803	20	209	2175	2383
GATTTCAACTCGGGCTTGTT	59.174	20	235	1141	1375
GCAGGCATACACTCCCACTT	60.142	20	152	405	556
GTTGGCCCCCTTAGATCATT	60.152	20	199	610	808
GGAGATCAAGTTCGCTCTAGC	61.025	22	257	1674	1930
CAGCCAATCAGAAAAGTCGG	60.766	20	177	2970	3146
TGCTTAATTACCATAAATGCTG	57.673	24	239	1405	1643
TGGAAATAATGGAAGGAGCG	60.031	20	229	996	1224
TCAGGTTCCAGTGGTCAGAA	59.23	20	238	1124	1361
AAAAATGTCAAATAAATTCTCC	59.359	25	200	6454	6653
TATCATTAACGCCCGTAGGC	59.95	20	275	3240	3514
CTTTCCAAATCCCTATGCGA	60.031	20	131	1127	1257
CACAACAATTCACCTCGCAA	60.699	20	193	2130	2322
TGCCCACCCCTAACAATAAT	59.158	20	233	3	235
AATTGCAGTTAATCCCGACG	59.96	20	149	211	359
TCGTGATTCGTTTCGTGTTT	59.174	20	267	13	279
TTCCACCCTCTCCTTTTCTGT	60.096	21	219	402	620
GCAAATCTGGTTTCGCTGAT	60.221	20	264	638	901
CCAATGGTGGTATGGTGTGA	60.088	20	215	172	386
GGTCCATATCACCAACACCC	59.91	20	198	5	202
TCAATACCCGAGAATTGCATA	58.122	21	253	41	293
AACTCCCACCGACAGTTTCA	60.545	20	267	346	612
ATGCAAAAATACGGAAACGC	59.971	20	263	11	273
TGGGTCAGTTTGTTTCCACC	60.791	20	193	0	192
ACCTTTAATGCCTATCGGGG	60.164	20	206	41	246
CGAAATTGGAGCAAGGAAAA	60.181	20	165	142	306
GCAGCCCGAGAATTGTCTAC	59.843	20	228	1903	2130
CCGAAAGAAACGGTGGTAAA	59.968	20	247	1341	1587
GATTTGAACCCACGCCATAA	60.701	20	175	0	174
TCACATATGGTTTCCTTCATGC	59.829	22	242	360	601
TAAGCCAAAATGATCGGCAT	60.424	20	170	0	169
GGAGTGCAATCGAACAAAGA	58.85	20	204	161	364
TATCCGAGGCTTGGAAACAT	59.528	20	232	1201	1432
CCTTAGTGGATTTCATGGGCT	60.326	21	280	1868	2147
TCCGTGGAATGAAATTGAGT	57.991	20	258	960	1217
TGTCCAATCAAGAGGCAACA	60.24	20	107	115	221

TCGTTTCGACATCCGTTACA	60.111	20	164	150	313
GAGTTCGGTGGGTATGGATG	60.195	20	241	40	280
CCCTCCAGCATACCTGCTTA	60.227	20	227	1240	1466
CGCATGTTACGTAAATCGTTAA	59.149	23	249	202	450
ACCCGGTCTACACCACAAAG	59.884	20	204	308	511
CCTTTCTTTTGACTGATGTGGA	59.215	22	243	154	396
TGGAGTGGCATTGCAAGA	59.908	18	168	878	1045
ATGAAAGAAAGTCAGCCCCA	59.67	20	216	127	342
TCGCTATTGTATTTAGGCAGG	57.163	21	107	325	431
CACCCTTGAGGTGTTCATCA	59.52	20	180	155	334
CATTGGCGGTTGATGATAGTC	60.346	21	270	818	1087
TCTCCATCTCCAACTCCACC	60.048	20	156	48	203
TAAAATGGGCGAGAGTGAGG	60.206	20	118	1118	1235
AAGTTCACCTTCGGAGATCG	59.284	20	270	337	606
ACTACAGGAGGGGGTAGGGA	59.811	20	194	1305	1498

Supplementary Table 3. Details of primers used for SSR marker verification

No.	ID	SSR nr.	SSR type	SSR	size	start	end
McSSR_1	scaffold493143_16.2	1	p2	(TC)7	14	4550	4563
McSSR_2	scaffold493642_17.4	1	p2	(AT)7	14	585	598
McSSR_3	scaffold686296_14.2	1	p3	(ATT)5	15	744	758
McSSR_4	scaffold739713_15.6	1	p3	(CAA)5	15	872	886
McSSR_5	scaffold739704_16.3	1	p3	(ATA)5	15	146	160
McSSR_6	scaffold99474_16.4	1	p2	(GA)8	16	176	191
McSSR_7	scaffold714629_18.4	1	p3	(CCG)6	18	592	609
McSSR_8	scaffold254351_14.4	1	p2	(CT)10	20	604	623
McSSR_9	scaffold279605_16.0	1	p2	(AG)10	20	515	534
McSSR_10	scaffold280650_16.7	1	p4	(AAAT)5	20	91	110
McSSR_11	scaffold362989_10.1	1	p4	(CTCC)5	20	948	967
McSSR_12	scaffold50981_15.0	1	p3	(TGA)8	24	2952	2975
McSSR_13	scaffold639648_15.0	1	p2	(CT)13	26	2166	2191
McSSR_14	scaffold675038_10.1	1	p2	(AT)13	26	542	567
McSSR_15	scaffold171052_12.6	1	p4	(ATAA)7	28	1459	1486
McSSR_16	scaffold278700_12.7	1	p2	(AG)14	28	326	353
McSSR_17	scaffold507988_16.9	1	p3	(TCA)10	30	1005	1034
McSSR_18	scaffold124671_15.1	1	p4	(TACA)5	20	276	295
McSSR_19	scaffold708632_12.3	1	p4	(TACA)5	20	175	194
McSSR_20	scaffold734892_16.5	1	p4	(TATG)5	20	1168	1187
McSSR_21	scaffold552987_14.6	1	p4	(TATT)5	20	1778	1797
McSSR_22	scaffold742712_16.0	1	p4	(TATT)5	20	1039	1058
McSSR_23	scaffold1551_14.8	1	p4	(TCAA)5	20	1304	1323
McSSR_24	scaffold559721_10.4	1	p4	(TCAA)5	20	242	261
McSSR_25	scaffold37946_16.9	1	p4	(TCAT)5	20	728	747
McSSR_26	scaffold716555_15.0	1	p4	(TCAT)5	20	2539	2558
McSSR_27	scaffold534298_14.9	1	p4	(TCGA)5	20	954	973
McSSR_28	scaffold434282_14.6	1	p4	(TCTT)5	20	6551	6570
McSSR_29	scaffold600130_20.2	1	p4	(TGTA)5	20	298	317
McSSR_30	scaffold662814_16.2	1	p4	(TTAA)5	20	1866	1885
McSSR_31	scaffold730642_15.6	1	p4	(TTAA)5	20	849	868
McSSR_32	scaffold180742_17.8	1	p4	(TTGG)5	20	1030	1049
McSSR_33	scaffold424746_14.9	1	p4	(TTTA)5	20	1082	1101
McSSR_34	scaffold633212_11.7	1	p4	(TTTA)5	20	423	442
McSSR_35	scaffold661552_12.7	1	p4	(TTTA)5	20	202	221
McSSR_36	scaffold684812_15.2	1	p4	(TTTA)5	20	296	315
McSSR_37	scaffold666666_15.3	1	p4	(TTTC)5	20	2541	2560
McSSR_38	scaffold659643_17.5	1	p4	(AAAT)6	24	1425	1448
McSSR_39	scaffold717962_15.3	1	p4	(AAAT)6	24	460	483
McSSR_40	scaffold743044_16.1	1	p4	(ATAA)6	24	6543	6566
McSSR_41	scaffold529630_12.6	1	p4	(ATAG)6	24	545	568
McSSR_42	scaffold736148_16.3	1	p4	(ATTT)6	24	1740	1763
McSSR_43	scaffold60885_12.5	1	p4	(CATC)6	24	1265	1288
McSSR_44	scaffold65330_12.7	1	p4	(TAAT)6	24	317	340
McSSR_45	scaffold448298_14.4	1	p4	(TGTA)6	24	800	823
McSSR_46	scaffold670842_10.7	1	p4	(TTCT)6	24	925	948
McSSR_47	scaffold732762_14.6	1	p4	(TTCT)6	24	2925	2948
McSSR_48	scaffold437080_10.1	1	p5	(ACACG)5	25	85	109
McSSR_49	scaffold574523_12.8	1	p5	(CCTAA)5	25	186	210
McSSR_50	scaffold78862_14.0	1	p5	(GCGGG)5	25	1209	1233
McSSR_51	scaffold733662_13.5	1	p5	(TGCTT)5	25	144	168
McSSR_52	scaffold171052_12.6	1	p4	(ATAA)7	28	1459	1486
McSSR_53	scaffold554235_20.7	1	p6	(ATCGGG	30	204	233
McSSR_54	scaffold576716_13.1	1	p6	(GATTTT)	30	908	937

McSSR_55	scaffold652042_14.8	1	p6	(TTCTGG)	30	72	101
McSSR_56	scaffold722193_18.0	1	p6	(GATTGG	30	1163	1192
McSSR_57	scaffold708599_14.5	1	p5	(AAAAT)5	25	254	278
McSSR_58	scaffold419361_15.9	1	p5	(AATAA)5	25	767	791
McSSR_59	scaffold404725_15.9	1	p5	(AATAC)5	25	527	551
McSSR_60	scaffold567385_10.3	1	p5	(ACAAA)5	25	64	88
McSSR_61	scaffold437080_10.1	1	p5	(ACACG)5	25	85	109
McSSR_62	scaffold720454_13.9	1	p5	(ACCTA)5	25	1226	1250
McSSR_63	scaffold588661_14.1	1	p5	(AGATA)5	25	2021	2045
McSSR_64	scaffold129996_14.2	1	p5	(ATAAA)5	25	2190	2214
McSSR_65	scaffold652062_16.1	1	p5	(ATAAT)5	25	407	431
McSSR_66	scaffold741994_15.2	1	p5	(ATATT)5	25	227	251
McSSR_67	scaffold737970_18.1	1	p5	(ATCTA)5	25	227	251
McSSR_68	scaffold209057_14.9	1	p5	(ATTTT)5	25	28	52
McSSR_69	scaffold281552_10.3	1	p5	(CAGGC)5	25	240	264
McSSR_70	scaffold436901_11.6	1	p5	(CCAAG)5	25	228	252
McSSR_71	scaffold574523_12.8	1	p5	(CCTAA)5	25	186	210
McSSR_72	scaffold346597_11.5	1	p5	(CTTTT)5	25	41	65
McSSR_73	scaffold740060_14.4	1	p5	(CTTTT)5	25	123	147
McSSR_74	scaffold549972_10.6	1	p5	(GATGG)5	25	81	105
McSSR_75	scaffold502759_17.3	1	p5	(TAAAA)5	25	49	73
McSSR_76	scaffold450612_11.1	1	p5	(TTAGG)5	25	74	98
McSSR_77	scaffold732293_13.2	1	p5	(TTTTG)5	25	1908	1932
McSSR_78	scaffold740879_14.0	1	p4	(AAAT)7	28	1280	1307
McSSR_79	scaffold722963_14.3	1	p4	(ATTT)7	28	368	395
McSSR_80	scaffold314358_14.9	1	p4	(TTGC)7	28	1703	1730
McSSR_81	scaffold498369_13.7	1	p5	(AATCT)6	30	470	499
McSSR_82	scaffold733459_14.0	1	p5	(TATCT)6	30	1080	1109
McSSR_83	scaffold741982_15.1	1	p5	(TTTAT)6	30	1285	1314
McSSR_84	scaffold736788_12.7	1	p6	(CAAAAT	30	540	569
McSSR_85	scaffold156626_11.2	1	p6	(CCAACA	30	252	281
McSSR_86	scaffold502162_13.7	1	p6	(TAGTAT)	30	215	244
McSSR_87	scaffold339935_15.1	1	p6	(TCCACA	30	903	932
McSSR_88	scaffold740076_14.2	1	p6	(TGTGGT	30	1359	1388
McSSR_89	scaffold97925_17.0	1	p6	(TTGGAC	30	420	449
McSSR_90	scaffold634405_15.1	1	p5	(TCGGG)	35	1527	1561

FORWARD PRIMER1 (5'-3')	Tm(C°)	size	REVERSE PRIMER1 (5'-3')	Tm(C°)	size
AACTGACGGGTGATCAAAGG	59.966	20	GGCTGCAGAAGTGTTGATGA	59.992	20
TGCGTTCGAGTTCAGAGTTG	60.175	20	ATACGAACACTGCACCACCA	60.032	20
GTCCATGTCCTCGTCCTCAT	59.928	20	AACATCGAAGCTTTTGGCTG	60.386	20
CAGTTTCAAGGGGAATCGAA	60.044	20	TATGCTTTCCGAGTGCTTGA	59.566	20
CCCACATCCAGCTTTCGTAT	59.955	20	GGATTAATGGCCACGAAGAA	59.901	20
GGCCTGATTTGCAATACTGTG	60.517	21	TTCTTGTTGGTGTGTGGCAT	60.008	20
GATCCTCTGGGCCAAATGTA	59.894	20	GAGAGGAATCAAGCCTGGTG	59.803	20
TACTGCTCTTGAACTCGCCA	59.74	20	CAAGGAACATGGACTTGCTG	59.288	20
TGGAAGGATGTGAGATGGTG	59.473	20	CCGAATTCCTCTACCGTCAA	60.066	20
CAAATTAAAATGCGCCACG	60.081	19	ATTTGACGAAGAACGGCTTG	60.249	20
TCTTGTTTTCTCCCCAAACC	59.003	20	GTGGGCAGATAATGGGTGTT	59.676	20
AGACCCCAATTTGATTGGAA	59.22	20	ATGGAAAAATTTGCAGAGCG	60.209	20
ATGCTTTCCAGCCAAGAGAA	59.955	20	TTTCCCAAGGATCAGACGAC	60.05	20
GTTGCTATTGCGGGCTTTAC	59.748	20	ACGGATTCATGGAGTGGAAG	59.927	20
TGACAAAAAATTGAGGCGTTG	59.706	20	GGGATGGTGGAAGAGCAGTA	60.073	20
CGAGCGAGAGGAGAGAGAA	59.966	20	AGACGAGGAAGAACAACGGA	59.844	20
AATTGTGCTCCATTTCCCAG	59.933	20	TCCCCGTACACAGTGATTTTT	59.345	21
CCTATCGTTCCACATGCCTT	59.955	20	ATTTCACCGCAGCAAAACTT	59.752	20
GACTATAATGGCCAGCACCG	60.49	20	CCCTATCAAACCCAGCAAGA	60.066	20
CAATTTCCAGATGGAACGGT	59.79	20	TCGTACACGAGGAGATGCTG	60.008	20
GCCATTCACCATCTCTCGTT	60.081	20	ACATCATGCGGGTAAGGAAA	60.331	20
AATCATGCAACCACAACAATT	57.953	22	TCCACTCCATTGGTTCTTTTT	58.54	21
TCACATACCTGCAACCATGAA	59.98	21	GCTGTGAAAGTATGCCACCC	60.526	20
CCCCCATGAAAAGTCAAAAA	59.772	20	TTGCTTCCAAATAATGGCTTC	59.202	21
GCACTTTCACGGGAGTTGAT	60.119	20	GAGACTGTGGATGGGGAAGA	60.048	20
CGTCATGTCGTTCTTCCTCA	59.831	20	ATTGTCTCCCACCTGAGACG	60.112	20
GGACGAAATTGATCGAAGGA	60.014	20	CCTTGAATCTCAGCACCACA	59.831	20
GAAGCAAGAGAGACGTTGGG	59.989	20	TCGTCTCCCGTTGAAAAAGT	59.711	20
CCGGAATCTGAGAGAGATCG	59.903	20	CCCCAGTTCCCTCCCTACT	60.312	19
CCTGATTAGCCACAAGGGAA	60.066	20	TGACCAAATCAAGGGGCTAA	60.439	20
GACTTCGTGGGCTTGGACT	60.253	19	AGGGGCAATTTGTAGACACG	59.993	20
CCTAGCAAAAACCTTCCAGC	58.973	20	CGGTAACCAAGAAGGCACAG	60.679	20
GTCTTGGTTGCCATCTCCAT	59.934	20	GCCTTTCTCCTTTTCTTTAACCA	60.114	23
CTCTCCATGGACGTAGGTGT	57.578	20	TGGAATTTTCCAAATCTGGCT	60.788	21
GAAGTTTTGGGGATCCGAC	59.326	19	CGCTGAGGAAGAAGCTGAAT	59.717	20
GTCATTTCTCGTTTCGCGTT	60.257	20	TTCGGGACGAAATTTTTCAA	60.407	20
TGTGGATGCTTGTATTTTGGA	59.027	21	GGAACATTACAGTTGGCAAGC	59.629	21
TCTGTTTATAGTCCCCCGGA	59.382	20	CTATCTGCCGGAGACACCAC	60.678	20
AATCAAGAAGCCTCTGCACG	60.538	20	AAAGTCGCGTATTTTTCGTGA	59.772	21
GCATCGACCTTGGACAAAAT	59.939	20	AAAATGTCAAATAAATTCTCCG	59.359	25
TTTGGGAGGGAAAACGACTA	59.541	20	TTTGGGTCAATCATTTTGGTT	59.168	21
TAACCATAGCAAAACCCCCA	60.181	20	TTTCGGATGTAACACAGGCA	60.111	20
TCAGCATTATGTGCTCTGCC	59.979	20	GGTCGGAGATGATGGTCCTA	59.886	20
AGAAGCACAACCAACCAACC	60.012	20	CAGAGAGAGAGAATGCCCCA	60.488	20
GCCTTATCCAACACCACACC	60.24	20	TGTTGCAGATGTTTCTTCGG	59.84	20
AGGGGTAGCGGTGTGTGTAG	60.051	20	AGGTTTGAGGGCCATGACTA	59.55	20
TGGGTTTGAACTGAAACTGC	58.749	20	TTAACGCGCGCCATATATTA	59.233	20
ATTTGGTTCGGTTCGGTTTT	60.573	20	GGTCCATATCACCAACACCC	59.91	20
TCAAACCAGGTTCTTCAATGG	59.956	21	ATCAAGTCAATCCGAGTCCG	60.073	20
TCAAGCAAAAATATTCCGCC	60.04	20	CTTTCCAAATCCCTATGCGA	60.031	20
ACCAAGAGAGAGAAAGGGGC	59.817	20	TGTCCAATCAAGAGGCAACA	60.24	20
TGACAAAAAATTGAGGCGTTG	59.706	20	GGGATGGTGGAAGAGCAGTA	60.073	20
GAGAGTTCAACTTGGCGGAT	59.288	20	CACCCTTGAGGTGTTCATCA	59.52	20
GGTCAGATCAAACCGAATCA	58.489	20	ATTAGCATTGGCGGTTGATG	60.857	20

AGACAATCCATCTCCATCTGG	59.824	22	TCTCCATCTCCAACTCCACC	60.048	20
TCTGGTTTTGGGTTTTCTGC	60.088	20	TTGTGCCCCCAAGATTACAT	60.192	20
TGCAAAAGCACTCTTCCTGA	59.716	20	CAGACCGAATAGGAGTGCAA	58.874	20
GGCAACAAACAGAATCCCAA	60.874	20	GGTTTCGCTGATTTTGTGGT	59.978	20
TGCGAATTGAATAAGGCAAA	59.286	20	TTCCACCCTCTCCTTTTCTG	59.255	20
AAAGAGCAATGTGGCATCAA	59.276	20	CCACTTTTGTGGGTTCTCGT	60.005	20
ATTTGGTTCGGTTCGGTTTT	60.573	20	GGTCCATATCACCAACACCC	59.91	20
TGGCATGCGAGTGCTATTAC	59.862	20	GGGAGAGTGGATGTGTAGGC	59.535	20
CAATGACAACCAAACATGCC	59.823	20	GCAGCCCGAGAATTGTCTAC	59.843	20
TTGCATCTTCATGTGCAATTC	59.685	21	CACAACAATTCACCTCGCAA	60.699	20
AACGATAACGGTAACGATAA	57.743	23	TGGTTTCCTTCATGCTTTTTC	59.192	21
TTATTGCACAGCTTCATGCC	59.839	20	CGCATGTTACGTAAATCGTTAAA	60.289	24
TTCTCTTGGAATGGGATTGG	59.864	20	TCGTTTCGACATCCGTTACA	60.111	20
TGCTCCCTCCAATTAAGACG	60.206	20	TTGCCCACCCCTAACAATAA	60.181	20
GCGCCCATAAAAATGAAATG	60.282	20	TGGTTAGGGGTGTCAAGAGG	59.959	20
GCCGGGTCTAGTGAATGAAA	60.074	20	CCAATGGTGGTATGGTGTGA	60.088	20
TCAAACCAGGTTCTTCAATGG	59.956	21	ATCAAGTCAATCCGAGTCCG	60.073	20
CCGACTTTTATGGCTGCTGT	60.27	20	TTTCGTGTTTAGCCTTTCGC	60.376	20
GTTCGAACCGAACCATGAAC	60.362	20	GAGTTCGGTGGGTATGGATG	60.195	20
TTTGAGGAGCTTTGCGTTTT	59.996	20	ACTCGACTTGATTGCGAACC	60.263	20
TCTAAAAACATGGGTAAAAAT	57.432	26	ATGCAAAAATACGGAAACGC	59.971	20
GAGTATTCATTGTACACAATA	57.132	27	TCAATACCCGAGAATTGCAT	58.038	20
GCAGACCATAATGCTTTTGTG	60.138	22	CCTTAGTGGATTTCATGGGC	59.387	20
TTGAACGAAAATTGATGGTCC	59.793	21	CTGTTGGATTTCAACTCGGG	60.486	20
TCCGTCCACCTCTCAATCTC	60.199	20	TCCAATTAATCCTAAACCACATT	57.985	24
TGCAGAGCAAATTCATGTCC	59.805	20	TTTGATGGATTGTCCGCATA	59.891	20
TTTGTCATGACTTCGGCTTG	59.84	20	AACTCCCACCGACAGTTTCA	60.545	20
GAAGAAGATGTCAAGCCGGA	60.34	20	CCGTGGAATGAAATTGAGTCT	59.042	21
TGCAACAATTTTTGGTATATAT	58.929	27	CCCTCCAGCATACCTGCTTA	60.227	20
TCCGATCGAATGGACCTTAC	59.894	20	AAGTTCACCTTCGGAGATCG	59.284	20
CACTGCTGCTGAGGAGTTTG	59.77	20	CCTTTCTTTTGACTGATGTGGA	59.215	22
GAGAAACTGCAGCAAAAGGC	60.14	20	ATGAAAGAAAGTCAGCCCCA	59.67	20
AAACATACCAACTCACCACTC	57.963	22	AAAGATGGGTGGAGTGAGAAA	59.976	22
CGCCTCGATTGAATCTTCTC	59.917	20	TATATTTCGAGGCGGAGGAA	59.638	20
AAAGCTTTGTCCCACATAGGA	60.001	22	AAACTGCCATGCACACCATA	59.995	20
TTGGCGGAAGCCATAATATC	59.892	20	CCGAAAGAAACGGTGGTAAA	59.968	20

PRODUCT1 size (bp)	start (bp)	end (bp)
201	4485	4685
218	430	647
263	679	941
239	794	1032
276	63	338
266	82	347
221	509	729
265	484	748
199	386	584
237	8	244
198	865	1062
230	2918	3146
258	1970	2227
225	437	661
223	1342	1564
271	202	472
224	959	1182
263	128	390
280	38	317
274	1087	1360
136	1732	1867
280	844	1123
166	1264	1429
229	118	346
278	534	811
237	2438	2674
230	898	1127
201	6515	6715
122	227	348
235	1721	1955
280	813	1092
279	813	1091
278	857	1134
192	333	524
274	180	453
252	160	411
276	2482	2757
222	1348	1569
249	353	601
255	6398	6652
250	510	759
139	1682	1820
166	1201	1366
272	260	531
272	671	942
274	718	991
225	2883	3107
198	5	202
243	142	384
179	1079	1257
150	72	221
223	1342	1564
264	71	334
273	820	1092

157	47	203
280	1118	1397
215	161	375
256	638	893
219	402	620
263	41	303
198	5	202
260	1201	1460
229	1902	2130
193	2130	2322
235	360	594
250	201	450
279	35	313
234	3	236
251	74	324
214	173	386
243	142	384
257	13	269
204	77	280
249	0	248
271	3	273
253	41	293
280	1868	2147
241	1141	1381
234	323	556
208	1611	1818
268	345	612
257	960	1216
226	1241	1466
271	336	606
223	174	396
216	127	342
275	878	1152
268	1211	1478
278	308	585
219	1369	1587

Supplementary Table 4. Identification of allelic fragments in the same horizontal position for genetic similarity

				M. chinensis Benth MX	*M. chinensis Benth TW*	*M. chinensis Benth ZC*	*M. chinensis Benth ZC*	*M. chinensis Benth XU*
	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_1	1			1	0	1	1	1
	2			1	0	1	1	1
	3			1	1	1	1	1
	4			1	0	1	0	0
	5			1	1	0	1	1
	6			1	1	1	1	1
	7			1	1	1	1	1
	8			1	1	1	1	1
	9			0	0	1	1	1
	10			0	1	0	0	0
	11			0	1	0	0	0
	12			0	0	0	0	0
	13			0	1	0	0	0
	14			0	0	0	0	0
	15			0	0	0	0	0
	16			0	0	0	0	0
	17			0	0	0	0	0
	18			0	0	0	0	0
	19			0	0	0	0	0
	20			0	0	0	0	0
	21			0	0	0	0	0
	22			0	0	0	0	0
	23			0	0	0	0	0
	24			0	0	0	0	0
	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_5	1			1	0	1	1	1
	2			1	1	1	1	1
	3			1	1	1	1	1
	4			1	1	1	1	1
	5			1	1	1	1	1
	6			1	1	1	0	0
	7			1	1	1	1	1
	8			0	1	0	1	1
	9			0	0	0	1	1
	10			0	1	0	1	1
	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_11	1			0	0	0	1	1
	2			0	0	1	1	0
	3			0	0	0	1	1
	4			0	0	1	0	1
	5			0	0	1	0	1
	6			0	0	0	0	1
	7			0	0	0	0	0
	8			0	0	0	0	0
	9			1	0	0	0	0
	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
	1			0	0	0	0	1
	2			0	0	1	1	0
	3			1	0	1	1	1
	4			1	0	1	1	1

McSSR_15	5			1	0	1	1	1
	6			1	0	0	6	0
	7			1	0	0	0	0
	8			1	0	0	8	0
	9			1	0	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
	1			0	0	0	1	0
	2			1	0	0	0	0
	3			0	0	0	0	1
	4			0	0	0	1	0
	5			1	0	0	0	1
	6			0	0	0	0	0
	7			0	0	1	1	0
	8			0	0	0	0	0
	9			0	0	0	1	1
	10			0	0	0	1	1
	11			0	0	0	1	1
	12			0	0	1	0	0
	13			1	0	0	1	0
	14			1	0	0	1	0
	15			1	0	1	0	0
	16			1	0	0	0	1
	17			0	0	1	0	0
	18			0	0	0	0	0
	19			0	0	0	0	1
	20			0	0	0	0	0
	21			0	0	0	1	0
	22			0	0	0	0	1
	23			1	0	0	0	1
	24			1	0	0	1	1
	25			0	0	0	0	1
	26			0	0	0	0	1
	27			0	0	0	1	1
	28			0	0	0	1	0
	29			1	1	0	0	0
McSSR_16	30			0	0	1	0	0
	31			0	0	0	0	1
	32			1	0	0	1	0
	33			0	0	0	1	0
	34			0	0	0	0	0
	35			1	0	0	0	0
	36			0	0	1	0	0
	37			1	0	0	0	0
	38			1	0	1	0	0
	39			0	0	1	0	0
	40			1	0	1	1	0
	41			0	0	0	0	0
	42			0	0	0	0	0
	43			0	0	0	0	1
	44			0	0	0	0	0
	45			0	0	0	0	0
	46			0	0	0	0	0
	47			0	0	0	0	0
	48			0	0	0	0	0
	49			0	0	0	1	0
	50			0	0	1	1	0
	51			0	1	1	0	0

	52			1	0	0	0	0
	53			0	0	1	0	0
	54			0	0	1	0	0
	55			0	0	0	0	0
	56			0	0	0	0	0
	57			0	0	0	0	0
	58			0	0	0	0	0
	59			0	0	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_17	1			0	0	1	1	1
	2			0	0	0	1	1
	3			1	1	1	1	1
	4			0	0	1	0	0
	5			1	1	0	1	1
	6			0	0	0	0	0
	7			0	0	0	0	0
	8			0	0	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_18	1			0	1	1	1	1
	2			0	1	1	0	0
	3			0	0	0	3	0
	4			0	1	0	0	0
	5			0	0	1	0	1
	6			0	0	0	0	1
	7			0	0	0	1	1
	8			0	0	1	0	0
	9			1	0	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_23	1			1	1	1	1	1
	2			1	1	1	1	1
	3			1	1	1	1	1
	4			0	1	1	0	1
	5			0	0	0	0	0
	6			0	1	0	0	0
	7			0	1	0	0	0
	8			0	1	0	0	0
	9			0	1	0	0	0
	10			0	1	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_24	1			1	0	1	1	0
	2			0	0	1	1	1
	3			1	0	1	0	1
	4			0	0	1	0	0
	5			0	0	1	0	0
	6			0	0	1	1	0
	7			0	0	1	1	1
	8			0	0	1	0	0
	9			0	1	1	0	0
	10			0	1	1	0	0
	11			0	0	1	0	0
	12			0	0	0	0	0
	13			0	0	0	0	0
	14			0	0	0	0	0
	15			0	0	0	0	0

	16			0	0	0	0	1
	17			0	0	0	0	1
	18			0	0	0	0	0
	19			0	0	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_25	1			1	1	0	0	1
	2			0	0	1	1	1
	3			1	1	1	1	0
	4			0	0	1	0	1
	5			1	0	0	1	0
	6			0	0	0	0	0
	7			0	0	0	0	0
	8			0	0	0	0	0
	9			0	0	0	0	0
	10			0	0	0	0	0
	11			0	0	0	0	0
	12			0	0	0	0	0
	13			0	0	0	0	0
	14			0	0	0	0	0
	15			0	0	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_29	1			0	0	1	0	0
	2			1	0	1	0	0
	3			1	1	1	1	1
	4			1	1	1	1	1
	5			1	1	1	0	0
	6			1	1	1	0	0
	7			1	0	1	0	0
	8			1	0	0	0	0
	9			1	0	0	0	0
	10			1	0	1	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_52	1			0	1	1	0	1
	2			0	1	1	0	1
	3			1	1	1	0	1
	4			1	1	1	0	1
	5			1	1	1	0	1
	6			1	1	1	1	1
	7			1	1	1	0	1
	8			1	1	1	0	1
	9			1	1	1	0	1
	10			1	1	1	0	1
	11			1	1	1	0	1
	12			1	1	1	0	1
	13			0	0	0	0	1
	14			0	0	0	0	1
	15			0	0	0	0	1

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_56	1			1	0	0	0	0
	2			1	0	1	1	1
	3			0	0	0	0	0
	4			1	0	0	0	1
	5			1	0	0	0	1
	6			0	0	0	0	1

	7			0	0	0	0	0
	8			0	0	0	0	0
	9			0	0	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
	1			1	0	0	1	0
	2			1	1	0	0	1
	3			1	1	1	1	0
	4			1	1	1	0	1
	5			0	0	1	1	0
McSSR_59	6			0	1	0	0	1
	7			0	0	0	1	0
	8			0	1	1	1	1
	9			0	0	1	1	1
	10			0	0	0	1	0
	11			0	0	0	1	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
	1			0	0	1	1	1
McSSR_60	2			1	0	1	1	1
	3			1	0	0	0	0
	4			1	0	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
	1			0	0	0	1	1
	2			1	0	1	1	1
	3			1	0	1	1	0
	4			1	0	1	1	0
	5			0	0	1	1	0
	6			0	0	0	0	1
	7			0	0	1	0	0
	8			0	0	1	0	0
	9			0	0	1	1	0
	10			1	0	0	1	0
	11			1	0	1	1	1
	12			1	0	1	1	1
	13			1	0	1	0	1
	14			1	0	1	1	0
	15			1	0	1	1	1
	16			1	0	0	1	1
	17			1	0	1	1	1
	18			1	0	0	1	1
	19			1	0	0	1	1
	20			1	0	0	1	1
	21			0	0	0	1	1
	22			0	1	0	1	1
	23			1	1	1	1	1
	24			0	1	1	1	1
	25			0	0	1	1	0
	26			0	0	1	0	0
	27			0	0	0	1	0
	28			1	0	0	0	0
	29			1	0	0	1	1
McSSR_61	30			1	0	1	1	0
	31			1	0	1	0	0
	32			1	0	1	1	1
	33			1	0	1	1	1
	34			1	1	1	1	0

35			1	1	1	1	1
36			1	0	0	1	1
37			1	1	1	0	0
38			0	0	1	0	0
39			0	0	0	1	0
40			0	0	0	0	0
41			1	0	0	1	0
42			0	0	1	0	1
43			1	0	0	0	0
44			1	0	0	1	1
45			0	0	0	1	1
46			0	0	0	1	1
47			0	0	0	1	1
48			0	0	0	1	1
49			0	0	0	0	1
50			0	0	0	0	1
51			0	0	0	0	1
52			0	0	0	0	1
53			0	0	0	0	0
54			0	0	0	1	0
55			0	0	0	1	0
56			0	0	0	1	1
57			0	0	0	0	1
58			0	0	0	0	1
59			0	0	0	0	1
60			0	0	0	0	1

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
	1			0	1	0	1	0
	2			0	0	0	0	0
	3			1	0	1	1	1
	4			1	0	1	1	1
	5			0	1	0	1	1
	6			1	0	0	1	1
	7			0	0	1	1	1
McSSR_62	8			0	0	1	1	1
	9			0	0	0	1	1
	10			0	0	0	1	1
	11			0	0	0	0	1
	12			0	0	0	1	0
	13			0	0	1	1	1
	14			0	0	1	1	1
	15			0	0	1	0	1

loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
1			1	1	1	1	1
2			0	0	0	3	0
3			0	0	0	0	1
4			0	0	0	1	1
5			0	0	0	1	1
6			0	0	0	1	1
7			0	0	1	1	1
8			0	0	1	1	1
9			0	1	1	1	1
10			1	0	0	0	1
11			1	1	0	1	0
12			1	0	0	1	1
13			1	1	0	0	0

McSSR_74	14			1	0	0	1	0
	15			1	0	0	0	1
	16			1	0	0	0	1
	17			1	0	0	0	0
	18			1	0	0	0	1
	19			0	0	0	0	0
	20			0	0	1	0	0
	21			0	0	1	1	0
	22			0	0	1	1	0
	23			1	0	1	1	0
	24			1	1	1	1	0
	25			1	0	1	1	0
	26			0	0	0	1	0
	27			0	0	0	1	1
	28			1	0	0	0	1
	29			1	1	0	0	1
	30			0	1	0	0	1
	31			0	0	0	0	1
	32			0	0	0	0	1
	33			0	0	0	0	1
	34			0	0	0	0	0
	35			0	0	0	0	0
	36			0	0	0	0	0
	37			0	0	1	0	0
	38			0	0	1	0	0
	39			0	0	0	1	0
	40			0	0	0	0	1

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_64	1			0	0	0	0	0
	2			0	0	0	0	0
	3			0	0	0	0	0
	4			0	0	0	0	0
	5			1	0	1	0	0
	6			1	0	0	0	1
	7			0	0	0	1	0
	8			1	1	0	0	1
	9			0	1	1	0	1
	10			0	0	0	1	0
	11			0	1	0	1	1
	12			0	0	1	1	0
	13			0	1	1	0	0
	14			0	1	0	0	0
	15			1	0	0	0	0
	16			1	0	0	0	0
	17			0	1	0	0	0
	18			0	1	1	0	0
	19			0	0	0	0	0
	20			0	0	1	0	1
	21			1	0	0	0	1
	22			1	0	0	0	1
	23			0	0	0	0	0
	24			0	0	0	1	0
	25			0	0	0	1	0
	26			0	0	0	1	0

loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
1			0	0	0	0	0

McSSR_67	2			0	0	0	0	0
	3			0	0	1	1	0
	4			0	0	0	1	1
	5			0	1	1	1	1
	6			0	0	0	0	1
	7			1	0	0	1	1
	8			0	0	0	1	1
	9			1	1	1	1	1
	10			0	1	1	1	0
	11			0	0	1	1	0
	12			0	0	0	0	0
	13			0	0	1	1	0
	14			1	0	1	1	1
	15			0	1	1	0	1
	16			0	1	1	1	0
	17			0	0	1	1	1
	18			1	1	0	0	1
	19			0	1	0	1	1
	20			0	1	1	1	1
	21			0	1	1	1	0
	22			1	0	0	1	1
	23			0	1	1	1	1
	24			1	1	1	1	0
	25			1	1	1	1	0
	26			1	1	1	1	1
	27			1	1	1	1	1
	28			1	1	1	0	1
	29			0	0	1	1	0
	30			1	0	0	1	1
	31			1	0	0	0	1
	32			0	0	0	1	0
	33			0	0	0	1	0
	34			0	0	0	1	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_68	1			0	0	0	0	0
	2			0	0	1	0	0
	3			1	1	0	0	0
	4			1	0	0	0	0
	5			1	0	1	1	0
	6			0	0	1	0	1
	7			0	0	0	0	0
	8			0	0	0	0	0
	9			0	0	0	1	1
	10			0	0	0	1	0
	11			0	0	0	0	1

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_69	1			0	0	0	0	0
	2			0	0	0	0	0
	3			1	0	0	0	0
	4			1	0	0	0	0
	5			0	0	0	0	0
	6			1	0	1	0	1
	7			1	0	1	0	1
	8			1	0	0	1	0
	9			0	1	0	0	0
	10			0	0	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_70	1			1	0	0	1	0
	2			1	0	0	0	1
	3			1	0	1	0	1
	4			0	0	0	1	1
	5			0	0	0	0	1
	6			0	0	0	0	1
	7			0	0	0	1	0
	8			0	0	0	0	0
	9			0	0	0	0	0
	10			0	0	0	0	0
	11			0	0	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_72	1			1	0	1	1	1
	2			1	0	1	1	1
	3			0	0	1	1	1
	4			0	0	1	1	1
	5			0	0	1	0	1
	6			0	0	0	1	1
	7			0	0	0	0	1
	8			0	0	0	0	1

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_73	1			0	0	1	1	1
	2			1	0	0	0	1
	3			0	0	0	0	1
	4			1	0	0	1	0
	5			1	0	0	1	1
	6			0	0	1	1	1
	7			0	0	0	0	1
	8			0	0	0	0	1
	9			0	0	0	0	1
	10			1	0	0	0	0
	11			0	0	1	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_74	1			1	1	0	1	1
	2			1	0	0	1	1
	3			0	0	0	1	0
	4			1	0	1	0	0
	5			1	0	1	0	0
	6			1	0	1	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_75	1			1	0	0	0	0
	2			1	0	0	0	0
	3			0	0	0	1	1
	4			1	0	0	1	1
	5			1	0	0	0	0
	6			1	0	1	0	1
	7			0	0	0	1	1
	8			0	0	1	1	1
	9			0	0	1	0	0
	10			0	0	1	0	1
	11			0	0	0	1	1

	12			1	0	0	0	1
	13			0	0	0	0	0
	14			0	0	1	0	0
	15			0	0	0	0	0
	16			0	0	0	1	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_76	1			0	0	0	0	0
	2			0	0	0	0	0
	3			0	0	1	0	1
	4			0	0	1	1	1
	5			0	0	1	1	1
	6			0	0	1	1	1
	7			1	0	0	0	0
	8			1	0	0	0	0
	9			1	0	0	0	0
	10			0	0	0	0	0
	11			0	0	0	0	1

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_77	1			0	0	1	0	1
	2			0	0	1	1	1
	3			0	0	1	0	1
	4			1	0	1	1	0
	5			1	1	1	1	0
	6			1	0	1	1	1
	7			1	0	1	1	1
	8			1	0	1	0	1
	9			1	0	1	1	1
	10			1	1	1	1	1
	11			1	1	1	0	1
	12			1	0	1	1	0
	13			1	0	0	1	0
	14			1	0	0	1	0
	15			1	0	0	0	0
	16			1	0	1	0	0
	17			1	0	1	0	0
	18			1	0	0	0	0
	19			1	0	1	0	0
	20			1	1	1	0	0
	21			0	1	1	0	0
	22			0	1	1	0	0
	23			0	1	1	0	0
	24			0	1	0	0	0
	25			0	1	0	0	0
	26			0	0	0	0	0
	27			0	1	0	0	0
	28			0	1	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
	1			0	0	0	1	0
	2			0	0	1	0	1
	3			1	0	1	1	1
	4			1	1	1	1	1
	5			0	1	1	1	1
	6			0	1	0	0	1
	7			0	1	1	0	0
	8			0	1	1	1	0

McSSR_78	9			0	1	0	0	1
	10			0	0	1	0	0
	11			0	1	0	0	1
	12			0	1	0	0	1
	13			0	1	0	0	0
	14			0	1	1	1	0
	15			1	1	1	1	1
	16			0	1	0	0	1
	17			0	0	0	0	0
	18			0	1	0	1	0
	19			0	0	1	1	1
	20			0	1	1	1	1
	21			0	1	0	0	1
	22			1	0	0	0	0
	23			0	0	1	0	0
	24			1	1	1	0	0
	25			1	1	1	0	0
	26			1	0	0	0	0
	27			1	0	0	0	0
	28			1	0	0	0	0
	29			0	0	0	1	0
	30			1	0	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_80	1			0	0	0	0	0
	2			1	0	0	0	1
	3			1	0	0	0	1
	4			0	0	0	0	1
	5			0	0	0	0	1
	6			0	0	0	0	0
	7			1	0	0	0	0
	8			0	0	0	0	1
	9			0	0	0	0	1
	10			0	0	1	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_82	1			1	0	1	0	1
	2			1	1	1	0	1
	3			0	0	0	0	1
	4			0	0	0	1	1
	5			0	0	0	1	0
	6			1	0	1	0	0
	7			0	0	1	0	1
	8			1	0	1	0	1
	9			0	0	0	0	1
	10			1	0	0	0	1
	11			0	0	0	0	1
	12			1	0	0	0	0
	13			1	0	0	0	1
	14			1	0	0	0	0
	15			0	0	0	0	1
	16			0	0	0	0	1
	17			0	0	0	0	1
	18			0	0	0	0	1

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
	1			0	0	0	0	1
	2			0	0	0	1	1

McSSR_83	3			0	0	0	1	0
	4			0	0	0	1	0
	5			0	0	1	0	1
	6			0	0	0	0	1
	7			0	0	0	0	1
	8			0	0	0	0	1
	9			0	1	0	1	1
	10			0	0	0	1	1
	11			1	1	0	0	1
	12			1	1	0	1	1
	13			1	1	0	1	1
	14			1	1	1	1	0
	15			1	1	1	1	1
	16			1	1	1	1	1
	17			1	1	1	1	1
	18			1	1	1	1	1
	19			1	1	1	1	1
	20			1	1	1	1	1
	21			1	1	1	1	1
	22			1	1	1	1	1
	23			1	1	1	1	1
	24			1	1	1	1	0
	25			1	1	1	1	0
	26			1	1	1	0	0
	27			1	1	1	0	0
	28			1	1	1	0	0
	29			1	1	1	0	0
	30			1	1	1	0	0
	31			1	1	1	0	0
	32			1	1	1	0	0
	33			1	1	1	0	0
	34			0	1	1	0	0
	35			0	1	1	0	0
	36			0	1	0	0	0
	37			0	0	0	0	0
	38			0	0	0	0	0
	39			0	0	0	0	0
	40			0	0	0	1	0
	41			0	0	0	1	0
	42			0	0	0	1	1
	43			0	0	0	0	1
	44			0	0	0	0	0
	45			0	1	0	0	0
	46			0	0	0	0	0
	47			1	0	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_84	1			1	0	0	0	1
	2			1	0	0	0	1
	3			0	0	1	1	0
	4			0	1	1	0	0
	5			1	0	0	0	0
	6			0	0	0	0	1
	7			1	1	0	0	1
	8			0	1	1	1	1
	9			0	0	0	1	0
	10			1	0	0	0	0
	11			0	1	0	0	0

	12			0	0	1	0	0
	13			1	0	0	0	0
	14			0	0	0	1	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_85	1			1	0	1	1	0
	2			1	0	1	1	1
	3			1	0	1	0	1
	4			0	0	1	1	1
	5			0	0	0	1	1
	6			0	0	1	0	1
	7			1	0	0	0	0
	8			0	0	0	0	1
	9			0	0	0	0	1
	10			0	0	0	0	0
	11			0	0	0	0	0
	12			0	0	0	0	0
	13			0	0	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_86	1			1	0	1	1	1
	2			1	0	0	0	1
	3			1	0	1	1	1
	4			1	0	1	1	1
	5			1	0	1	1	1
	6			0	0	1	1	1
	7			1	0	1	1	1
	8			1	0	1	1	1
	9			1	0	1	0	1
	10			1	1	1	0	1
	11			0	0	1	0	1
	12			1	0	1	0	1
	13			0	0	0	0	1
	14			0	0	0	0	1
	15			0	0	1	0	0
	16			1	0	0	0	0
	17			1	0	0	0	0
	18			0	0	0	0	1
	19			0	1	0	0	1
	20			0	0	0	0	0
	21			1	0	0	0	0
	22			1	0	0	0	0

	loci.	Marker	Control	lane 1	lane 2	lane 3	lane 4	lane 5
McSSR_87	1			0	0	0	0	0
	2			0	0	0	1	0
	3			0	0	0	1	0
	4			0	0	0	1	0
	5			0	0	0	1	0
	6			1	0	1	0	0
	7			1	0	1	0	0
	8			1	0	0	1	0
	9			1	1	0	1	1
	10			0	1	1	0	1
	11			0	0	0	0	1
	12			0	0	0	0	1
	13			0	0	0	0	0
	14			1	1	0	0	0

15	1	1	1	0	0
16	1	0	1	0	0
17	0	0	1	0	0
18	0	0	0	0	1
19	0	0	0	0	1
20	0	0	0	0	0
21	0	0	0	0	0
22	0	0	1	0	0
23	0	0	1	0	0

y analysis

M. chinensis Benth XU	*Mentha haplocalyx*	*M spicata;*	*Prunella vulgaris*	*Salvia miltiorrhiza*	*Scutellaria indica*	*S. barbata.*
lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	1	1	1	1	1	1
	1	1	0	1	1	1
1	1	1	1	1	0	1
1	1	0	0	1	0	1
1	1	1	1	1	1	1
1	1	0	1	1	1	1
1	1	0	1	1	1	1
1	0	1	1	1	1	0
1	0	1	0	1	1	1
1	1	1	1	1	1	1
0	1	1	1	0	1	1
1	1	0	1	0	0	1
1	1	0	0	1	1	1
1	1	0	0	1	0	0
0	1	1	0	0	1	1
0	1	1	0	0	0	1
0	1	1	0	1	1	0
0	0	0	0	0	1	1
0	1	1	0	0	0	1
0	1	0	0	0	0	1
0	1	0	0	1	0	0
0	1	0	0	1	0	1
0	1	0	0	1	0	1
0	0	0	0	1	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	0	0	1	0	0	0
1	0	0	2	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
0	0	1	0	1	1	0
0	0	1	0	0	0	0
0	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	1	0	0	0
0	0	0	1	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	0	1	1	1	0	0
1	0	1	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0

1	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
9	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	0	0	0	0	0	0
1	0	0	0	1	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
1	0	1	0	0	1	0
0	0	1	0	0	0	1
0	1	1	0	0	0	0
0	1	1	0	0	0	0
0	0	0	0	1	0	0
1	0	0	0	1	0	0
0	0	0	0	1	0	0
0	1	0	0	1	0	0
0	1	0	0	1	0	0
1	0	1	0	1	1	1
1	0	1	0	1	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	1	0	0	0	0
0	0	1	0	0	0	0
1	1	0	0	0	0	0
1	1	1	1	0	0	0
1	1	1	0	0	0	0
0	1	1	0	0	0	1
0	1	1	1	0	0	1
1	0	0	0	0	0	1
0	0	0	0	1	0	1
0	1	0	0	1	1	1
1	1	1	0	0	1	0
0	1	0	1	1	1	0
0	0	1	0	1	0	0
1	0	0	0	1	0	1
1	1	0	1	1	1	1
1	1	0	0	0	0	0
0	1	0	0	0	1	0
0	1	1	0	0	0	0
0	0	0	0	0	1	1
1	1	0	0	0	0	1
1	0	0	0	0	0	1
1	0	0	0	0	0	0
1	1	0	1	0	0	1
1	1	0	0	0	0	1
1	0	0	0	1	0	0
1	0	0	0	1	1	0
0	0	0	0	1	1	0
0	0	0	0	1	0	0
1	0	0	0	1	1	0
1	1	0	0	0	1	0
1	0	0	0	0	1	0
0	0	0	0	0	1	0
0	0	0	0	0	0	0
0	1	0	0	0	0	0

0	0	1	0	0	0	1
0	0	0	0	1	0	1
1	1	0	0	1	0	1
0	0	0	0	1	0	0
1	0	0	0	0	0	0
0	1	0	0	0	0	0
0	1	0	0	1	0	0
0	0	0	0	1	1	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	1	0	0	0	0	0
1	0	1	0	0	0	1
1	0	0	1	1	1	0
1	0	1	0	0	0	0
1	0	0	0	1	0	0
1	0	0	0	0	1	0
1	0	0	0	0	1	0
1	0	0	0	0	1	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	1	0	0	0	0	0
2	0	0	0	0	1	1
0	0	0	0	0	0	0
1	1	0	0	0	0	1
1	0	0	0	0	1	0
0	0	0	0	0	0	0
0	0	0	0	0	0	1
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	1	1	1	1	1	1
1	1	0	0	1	1	1
1	0	1	0	1	1	1
1	1	1	0	0	0	1
0	0	0	0	1	1	0
0	0	1	0	1	1	1
0	0	0	0	1	1	1
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
0	1	0	0	0	0	0
0	1	0	0	0	0	0
0	1	0	0	0	0	0
1	1	1	0	0	0	0
0	0	0	0	1	0	0
0	1	1	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	1
1	0	1	0	1	0	0
1	1	0	0	1	0	0
0	0	0	0	1	0	1
0	1	0	0	0	0	0
0	1	1	0	0	0	0
0	0	1	0	0	0	0
1	0	0	0	0	0	0

0	1	0	0	0	0	0
0	0	0	1	0	0	0
0	0	1	0	0	0	0
0	0	1	0	0	0	1

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
0	0	1	1	1	1	0
1	1	1	1	1	1	0
1	1	1	0	1	1	1
1	1	0	1	1	1	1
0	1	1	1	1	1	1
1	0	1	1	1	0	0
0	1	0	1	1	1	0
0	1	0	1	1	1	0
0	1	0	1	1	1	9
0	1	0	0	1	1	0
0	0	0	0	1	0	0
0	0	0	0	1	0	0
0	0	0	0	1	0	0
0	0	0	0	1	0	0
0	0	0	0	1	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	0	0	0	0	0	0
0	0	0	0	0	0	1
1	1	1	0	0	1	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
0	0	0	0	0	0	0
0	0	0	0	1	0	0
0	1	0	0	1	0	0
0	0	1	0	0	1	0
0	0	0	0	0	1	0
0	0	0	0	0	0	0

0	0	0	0	0	1	1
1	0	0	0	0	0	0
1	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	0	1	0	0	0	1
1	0	0	0	1	0	0
1	0	0	0	0	0	1
0	0	0	1	1	0	0
1	0	1	0	0	0	0
1	0	1	0	1	0	0
1	0	0	0	0	0	0
0	0	0	0	1	0	0
0	0	0	0	0	0	1
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	0	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	1	0
1	1	1	1	1	0	0
0	1	1	0	1	0	0
0	1	1	1	1	0	0
0	1	1	0	0	1	1
0	1	0	1	1	1	0
1	1	0	1	1	0	1
0	1	1	0	1	1	0
0	1	1	0	1	1	1
0	1	0	0	0	1	1
0	1	1	0	0	1	0
0	1	1	1	0	1	0
0	0	0	1	0	0	0
0	0	0	0	0	0	0
1	0	0	1	1	0	0
1	1	0	1	1	0	1
1	1	1	0	0	0	0
0	1	0	1	0	0	0
0	1	0	0	1	0	1
0	1	1	0	0	0	1
0	1	1	1	1	1	1
0	0	1	1	1	1	1
0	1	1	1	1	0	0
1	1	0	0	0	1	0
1	1	1	0	0	1	0
0	1	1	0	0	0	0
0	0	0	1	0	1	0
1	1	0	1	1	1	0
1	1	0	0	0	1	1
1	0	1	1	0	0	0

1	0	1	0	0	1	1
1	1	1	0	0	0	0
0	1	0	0	1	0	0
0	0	0	0	1	0	1
0	0	1	0	1	0	1
1	0	0	0	0	0	1
0	0	0	1	1	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	1
0	1	0	0	0	0	1
0	0	0	0	0	0	0
0	1	0	0	1	0	0
0	0	0	0	0	0	0
0	1	0	0	1	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	1	0	0
0	0	0	0	0	0	0
0	0	0	0	1	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	0	0	0	0	0	0
1	1	0	0	1	0	1
1	0	0	0	0	0	0
1	0	0	0	1	0	0
0	0	0	0	0	0	1
0	0	0	0	0	1	0
0	1	0	0	0	0	1
0	0	0	1	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	0	0	0	0	0	0
0	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	1
1	1	0	0	0	1	0
0	1	0	0	0	0	0
1	0	1	0	0	0	0
0	0	0	0	0	0	0
1	1	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	1	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
1	0	0	0	0	1	0
1	0	0	0	0	0	0
0	1	0	0	0	0	0
0	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	1
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0	1	1	0	0	0	0
0	0	1	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
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0	0	0	0	0	0	0
1	0	1	0	0	0	0
1	0	1	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
0	0	0	1	0	0	0

0	0	0	0	0	0	0
1	0	1	1	0	1	0
1	1	1	1	0	0	0
1	1	0	0	1	0	0
1	1	1	1	0	0	0
1	1	1	1	0	0	0
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1	1	1	0	0	0	1
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0	0	1	0	0	0	0
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0	0	0	0	1	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
0	0	0	1	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
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1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
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1	0	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	1	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	1

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
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1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
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1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
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1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
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0	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
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1	0	0	0	0	0	0
0	0	0	0	0	0	0
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0	0	0	0	0	0	0
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lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
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1	0	0	0	0	0	0
1	0	0	0	0	0	0
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
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0	0	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
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1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
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0	0	0	0	1	1	1
1	0	0	1	1	1	0
0	0	0	0	1	0	0
1	0	0	0	1	0	0
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
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0	0	1	0	0	0	1
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	1	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
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1	0	0	0	0	0	0

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0	0	0	0	0	0	0
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
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1	0	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
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1	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
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1	0	0	0	0	0	0

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0	0	0	0	0	0	0
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0	0	0	0	0	0	0
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
0	1	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
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0	0	0	0	0	0	0
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0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0
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0	0	0	0	0	0	0
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1	0	0	0	0	0	0
1	0	0	0	0	0	0
1	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
1	0	0	0	1	0	1
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1	0	0	0	1	0	1
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1	0	0	0	1	0	1
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0	0	0	0	0	0	0
0	0	0	0	0	1	0
1	1	0	0	0	1	0
0	0	0	0	1	1	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

lane 6	lane 7	lane 8	lane 9	lane 10	lane 11	lane 12
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0	0	0	0	0	0	0
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1	0	0	0	0	0	0

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0	0	0	0	0	0	0
0	0	0	0	0	0	1
0	0	0	0	1	0	0
0	0	0	0	0	0	0
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Supplementary Figure 1