Table S1. Summary of miRNAs identified in this research.

miRNA	**Control_7d**	**AR156_7d**	**Control/ DC3000_14h**	**AR156/ DC3000_14h**
ath-miR1888b	15.49	0.00	188.71	0.00
ath-miR5020a	0.00	0.00	53.78	0.00
ath-miR841b*	27.54	0.00	56.71	0.00
ath-miR5639	6.02	0.00	40.09	0.00
ath-miR169g	119.62	0.00	34.22	0.00
ath-miR852	34.42	24.36	62.58	0.00
ath-miR167c	299.47	138.86	0.98	0.00
ath-miR3932b	95.52	21.11	7.82	0.00
ath-miR864-3p	76.59	63.34	95.82	0.00
ath-miR169c	316.68	194.90	44.00	0.00
ath-miR5663	69.70	0.81	173.06	0.00
ath-miR5644	0.00	0.00	11.73	0.00
ath-miR853	88.64	116.13	64.53	0.00
ath-miR5652	439.74	142.92	95.82	0.00
ath-miR399f	38.72	0.00	4.89	0.00
ath-miR169d	119.62	0.00	34.22	0.00
ath-miR2934-5p	12.05	0.00	57.69	0.00
ath-miR3932a	95.52	21.11	7.82	0.00
ath-miR169b	316.68	194.90	44.00	0.00
ath-miR861-3p	834.72	43.85	62.58	0.00
ath-miR5659	35.28	0.00	60.62	0.00
ath-miR169e	119.62	0.00	34.22	0.00
ath-miR5640	24.10	0.00	146.66	0.00
ath-miR169f	119.62	0.00	34.22	0.00
ath-miR848	120.48	165.66	374.48	1.03
ath-miR773	83.47	0.81	67.46	1.03
ath-miR5629	72.29	123.43	44.98	1.03
ath-miR864-5p	96.38	114.50	132.97	3.10
ath-miR3440b-3p	11.19	0.00	31.29	1.03
ath-miR5024-5p	0.00	0.00	28.35	1.03
ath-miR156h	55.94	0.00	24.44	1.03
ath-miR863-3p	440.60	166.47	796.86	79.52
ath-miR825-5p	137.52	136.83	341.23	76.43
ath-miR847	525.79	36.54	1282.80	300.54
ath-miR395a	132.52	142.11	736.24	179.70
ath-miR5653	462.11	461.25	140.80	53.70
ath-miR395b	413.92	182.71	813.49	312.93
ath-miR860	74.01	38.17	179.91	96.05
ath-miR399b	83.47	0.00	162.31	86.75
ath-miR5020b	161.78	33.29	1075.52	622.77
ath-miR447	2434.47	3839.44	3298.92	1961.25
ath-miR841b	12.91	0.00	207.28	126.00
ath-miR841	191.04	48.72	1696.39	1084.42
ath-miR167d	160993.23	98887.53	133588.69	90855.74
ath-miR164c	3040.29	394.66	602.29	438.93
ath-miR163	9359.23	12958.11	17083.21	12729.02

ath-miR447a.2	11536.40	7238.74	9473.40	7967.90
ath-miR396a	133571.27	37361.46	107132.79	90866.07
ath-miR781	201.37	160.79	437.05	398.65
ath-miR822	53582.37	9563.68	2585.16	2398.12
ath-miR846	734.04	278.54	2329.97	2161.61
ath-miR173	4180.50	1829.58	5966.22	5632.78
ath-miR161.1	202453.18	409385.26	193664.44	183321.58
ath-miR159a	598898.72	362054.89	685703.24	669840.57
ath-miR840	3413.76	1433.29	1391.33	1415.94
ath-miR390	17919.88	7507.54	9537.93	9765.97
ath-miR157	119227.79	59429.32	483871.68	498682.04
ath-miR5026	34388.03	9858.46	3894.37	4093.94
ath-miR396b	169956.62	32263.32	84941.83	92298.53
ath-miR171a	2696.07	736.54	2012.20	2228.74
ath-miR823	1853.60	1827.15	6568.51	7406.07
ath-miR167	1744874.46	823936.88	151563.60	171346.50
ath-miR164	33690.13	11899.99	19748.55	22660.23
ath-miR172	4458.46	1851.51	5677.78	6701.71
ath-miR169	322.70	176.22	211.19	252.00
ath-miR850	523.21	764.96	143.73	173.51
ath-miR159b	491585.96	321583.22	769013.21	973741.31
ath-miR777	561.07	590.37	90.93	116.70
ath-miR5642	18.93	0.00	80.18	103.28
ath-miR472	3214.12	2803.25	4681.46	6032.47
ath-miR5012	152.32	52.78	138.84	180.74
ath-miR1888	1357.07	617.17	1206.54	1670.01
ath-miR168	42414.29	37657.05	36271.51	50407.94
ath-miR863-5p	45.61	0.00	165.24	230.31
ath-miR162	26801.51	4597.10	20406.57	28864.14
ath-miR172e	117.03	52.78	70.40	102.25
ath-miR156e	23883.42	3945.01	11763.28	17336.25
ath-miR156	23883.42	3945.01	11763.28	17336.25
ath-miR169a	38411.92	6634.57	1685.64	2489.00
ath-miR156j	101.54	16.24	73.33	109.47
ath-miR157d	9441.84	1656.61	6472.69	10401.13
ath-miR843	1348.47	1277.38	8430.14	13619.27
ath-miR403	18745.14	2726.10	9811.70	16367.50
ath-miR825-3p	681.89	1120.62	159.53	42.84
ath-miR824	16303.79	9851.15	76733.64	129300.98
ath-miR156g	104.13	29.23	76.26	129.10
ath-miR400	5960.96	1960.32	122.22	207.59
ath-miR833-5p	152.32	341.88	132.97	236.51
ath-miR5634	222.88	153.48	145.68	266.46
ath-miR171	6349.06	2238.05	1229.03	2325.82
ath-miR838	931.10	677.26	243.46	508.13
ath-miR166	272530.38	101996.11	72633.94	156076.84
ath-miR397b	2510.19	1784.92	129.06	279.88
ath-miR5651	318.40	228.19	165.24	360.44
ath-miR161.2	18745.14	5361.25	2829.60	6856.63
ath-miR408	6898.09	3491.07	1645.55	4012.35

ath-miR391	4280.33	792.57	747.00	1919.94
ath-miR866-3p	314.10	1.62	116.35	315.00
ath-miR827	431.13	61.72	62.58	171.44
ath-miR3434	33.56	0.00	101.69	287.11
ath-miR1886.2	947.45	531.09	65.51	185.90
ath-miR844*	753.83	119.37	123.20	373.87
ath-miR160	3813.05	1461.72	3833.75	12828.16
ath-miR159c	9000.39	3344.89	1419.69	4764.22
ath-miR165	22617.57	7995.59	4489.82	16407.78
ath-miR865-5p	112.73	41.42	28.35	110.51
ath-miR844	1160.01	73.09	63.55	253.03
ath-miR319c	6625.30	664.27	2072.83	8883.98
ath-miR858b	212.55	245.24	114.40	588.68
ath-miR837-5p	7.74	0.00	14.67	81.59
ath-miR158a	349637.34	29318.78	99445.74	593309.50
ath-miR775	1149.68	52.78	275.72	1721.64
ath-miR398b	24408.35	8167.74	751.89	5138.08
ath-miR172b*	3419.79	993.15	120.26	853.08
ath-miR158b	1721.94	64.97	367.63	2996.10
ath-miR5654	703.06	35.73	57.69	550.47
ath-miR319	19203.81	1313.11	863.35	10989.81
ath-miR779.2	210.83	41.42	19.55	269.56
ath-miR858	229.76	488.86	46.93	705.39
ath-miR393b	15241.88	283.41	327.55	6807.05
ath-miR2112-3p	232.35	0.00	10.76	265.42
ath-miR398a	2147.05	687.01	32.27	803.50
ath-miR394	427.69	57.66	19.55	1422.14
ath-miR172	99.82	0.00	1.96	178.67
ath-miR2111b	6.02	52.78	0.00	0.00
ath-miR5658	16.35	0.00	0.00	0.00
ath-miR833-3p	12.91	63.34	0.00	0.00
ath-miR771	12.05	0.00	0.00	63.00
ath-miR5643b	129.08	85.27	0.00	0.00
ath-miR5024-3p	24.96	32.48	0.00	0.00
ath-miR5014-3p	50.77	0.00	0.00	0.00
ath-miR833b	28.40	18.68	0.00	0.00
ath-miR5648-5p	43.89	0.00	0.00	0.00
ath-miR402	31.84	0.00	0.00	0.00
ath-miR3933	50.77	35.73	0.00	0.00
ath-miR859	18.93	0.00	0.00	1.03
ath-miR842	176.41	0.81	0.00	84.69
ath-miR830	30.98	32.48	0.00	0.00
ath-miR851-5p	13.77	0.00	0.00	0.00
ath-miR5643a	129.08	85.27	0.00	0.00
ath-miR5635d	3.44	0.00	0.00	0.00
ath-miR829.1	54.21	0.00	0.00	0.00
ath-miR3434*	109.29	61.72	0.00	0.00
ath-miR837-3p	145.43	41.42	0.00	0.00
ath-miR830*	257.30	54.41	0.00	196.23
ath-miR1886.1	33.56	38.17	0.00	0.00

ath-miR3440b-5p	20.65	0.00	0.00	0.00
ath-miR5637	0.00	27.61	0.00	0.00
ath-miR397a	427.69	321.58	0.00	0.00
ath-miR862-5p	305.49	203.83	0.00	0.00
ath-miR5014-5p	21.51	0.00	0.00	0.00
ath-miR869.2	33.56	32.48	0.00	57.84
ath-miR829.2	26.68	0.00	0.00	0.00
ath-miR845a	98.96	0.00	0.00	0.00
ath-miR839	370.89	0.00	0.00	85.72
ath-miR2111a	6.02	52.78	0.00	0.00
ath-miR780.2	16.35	0.00	0.00	0.00
ath-miR2112-5p	103.26	1.62	0.00	0.00
ath-miR857	30.12	0.00	0.00	0.00
ath-miR5020c	15.49	30.86	0.00	0.00
ath-miR1886.3	23.23	0.00	0.00	0.00
ath-miR831	0.00	78.77	0.00	0.00
ath-miR828	234.93	223.32	0.00	99.15
ath-miR170	721.99	160.79	0.00	202.42
ath-miR5028	0.00	47.91	0.00	91.92
ath-miR835-5p	19.79	0.00	0.00	0.00
ath-miR849	46.47	86.89	0.00	0.00

Note: miRNAs identified in this research are listed. Reads are normalized to library size and presented in read per million (RPM).

Table S2: Summary of predicted genes targeted by miRNAs with significant differential expression.

ID	Target	Target Description
ath-miR848	AT1G33790	jacalin lectin family protein
	AT1G66960	Terpenoid cyclases family protein
ath-miR773	AT4G14140	MET2, DMT02, DMT2, MET02 | DNA methyltransferase 2
	AT4G08990	DNA (cytosine-5-)-methyltransferase family protein
	AT5G45200	Disease resistance protein (TIR-NBS-LRR class) family
	AT5G64270	splicing factor, putative
	AT1G64060	ATRBOH F, ATRBOHF, RBOHAP108, RBOHF, RBOH F | respiratory burst oxidase protein F
	AT5G57350	AHA3, ATAHA3, HA3 | H(+)-ATPase 3
	AT5G26150	protein kinase family protein
	AT1G79950	RAD3-like DNA-binding helicase protein
	AT5G16680	RING/FYVE/PHD zinc finger superfamily protein
	AT1G03080	kinase interacting (KIP1-like) family protein
ath-miR5629	AT3G43083	LCR33 | low-molecular-weight cysteine-rich 33
ath-miR864-5p	AT1G02840	SR1, ATSRP34, SRP34, SR34, At-SR34 | RNA-binding (RRM/RBD/RNP motifs) family protein
	AT5G57450	XRCC3, ATXRCC3 | homolog of X-ray repair cross complementing 3 (XRCC3)
	AT1G09410	pentatricopeptide (PPR) repeat-containing protein
ath-miR863-3p	AT2G27100	SE | C2H2 zinc-finger protein SERRATE (SE)
	AT2G29980	FAD3 | fatty acid desaturase 3
	AT5G14750	WER, ATMYB66, WER1, MYB66 | myb domain protein 66
ath-miR825*	AT5G38850	Disease resistance protein (TIR-NBS-LRR class)
	AT4G14370	Disease resistance protein (TIR-NBS-LRR class) family
	AT5G40920	pseudogene, disease resistance protein (TIR-NBS-LRR class), putative
	AT1G63750	Disease resistance protein (TIR-NBS-LRR class) family
	AT4G11170	Disease resistance protein (TIR-NBS-LRR class) family
	AT1G63740	Disease resistance protein (TIR-NBS-LRR class) family
	AT1G63730	Disease resistance protein (TIR-NBS-LRR class) family
	AT4G08450	Disease resistance protein (TIR-NBS-LRR class) family
	AT5G41550	Disease resistance protein (TIR-NBS-LRR class) family
	AT5G51630	Disease resistance protein (TIR-NBS-LRR class) family
	AT5G40910	Disease resistance protein (TIR-NBS-LRR class) family
	AT3G04220	Disease resistance protein (TIR-NBS-LRR class) family
	AT5G40060	Disease resistance protein (NBS-LRR class) family
	AT1G66090	Disease resistance protein (TIR-NBS class)
	AT5G18360	Disease resistance protein (TIR-NBS-LRR class) family
ath-miR847	AT2G15130	Plant basic secretory protein (BSP) family protein
	AT1G74620	RING/U-box superfamily protein
	AT1G53340	Cysteine/Histidine-rich C1 domain family protein
	AT3G61340	F-box and associated interaction domains-containing protein
ath-miR395	AT5G10180	AST68, SULTR2;1 | slufate transporter 2;1 | chr5
	AT4G23840	Leucine-rich repeat (LRR) family protein
	AT2G21230	Basic-leucine zipper (bZIP) transcription factor family protein
	AT3G45630	RNA binding (RRM/RBD/RNP motifs) family protein
	AT3G57300	INO80, ATINO80 | INO80 ortholog
ath-miR825	AT5G55970	RING/U-box superfamily protein
	AT5G44940	F-box/RNI-like superfamily protein

ath-miR844*	AT3G46540	ENTH/VHS family protein
	AT5G16880	Target of Myb protein 1
ath-miR160	AT1G77850	ARF17 | auxin response factor 17
	AT2G28350	ARF10 | auxin response factor 10
	AT4G30080	ARF16 | auxin response factor 16
ath-miR159c	AT3G60460	DUO1 | myb-like HTH transcriptional regulator family protein
	AT2G26950	AtMYB104, MYB104 | myb domain protein 104
	AT4G31240	protein kinase C-like zinc finger protein
ath-miR165	AT5G06350	ARM repeat superfamily protein
	AT1G34575	FAD-binding Berberine family protein
	AT5G52620	F-box associated ubiquitination effector family protein
	AT5G57035	U-box domain-containing protein kinase family protein
ath-miR865-5p	AT5G07140	Protein kinase superfamily protein
	AT1G51805	Leucine-rich repeat protein kinase family protein
ath-miR844	AT4G26770	Phosphatidate cytidylyltransferase family protein
	AT1G51480	Disease resistance protein (CC-NBS-LRR class) family
ath-miR319c	AT2G31070	TCP10TCP domain protein 10
	AT3G66658	ALDH22A1 | aldehyde dehydrogenase 22A1 | chr3
	AT2G26950	AtMYB104, MYB104 | myb domain protein 104
	AT3G15030	TCP4 | TCP family transcription factor 4
ath-miR858b	AT1G34670	AtMYB93, MYB93 | myb domain protein 93
	AT5G35550	TT2, ATMYB123, MYB123, ATTT2 | Duplicated homeodomain-like superfamily protein
	AT1G17760	CSTF77, ATCSTF77 | Tetratricopeptide repeat (TPR)-like superfamily protein
ath-miR158a	AT3G03580	Tetratricopeptide repeat (TPR)-like superfamily protein
	AT4G17565	F-box family protein with a domain of unknown function (DUF295)
ath-miR775	AT1G53290	Galactosyltransferase family protein
	AT1G01040	DCL1 | dicer-like 1
	AT1G21245	Protein kinase superfamily protein
ath-miR398b	AT1G08830	Encodes a cytosolic copper/zinc superoxide dismutase CSD1 that can detoxify superoxide radicals.
	AT2G28190	Encodes a chloroplastic copper/zinc superoxide dismutase CSD2 that can
ath-miR172b*	AT2G16500	ADC1, ARGDC1, ARGDC, SPE1 | arginine decarboxylase 1
	AT3G57330	ACA11 | autoinhibited Ca2+-ATPase 11
	AT5G48410	ATGLR1.3, GLR1.3 | glutamate receptor 1.3
ath-miR158b	AT2G46590	DAG2 | Dof-type zinc finger DNA-binding family protein
	AT3G03580	Tetratricopeptide repeat (TPR)-like superfamily protein
ath-miR5654	AT1G52770	Phototropic-responsive NPH3 family protein
	AT3G21070	NADK1, ATNADK-1 | NAD kinase 1
	AT1G12300	Tetratricopeptide repeat (TPR)-like superfamily protein
ath-miR319	AT2G26950	AtMYB104, MYB104 | myb domain protein 104
	AT5G06100	MYB33, ATMYB33 | myb domain protein 33
	AT5G67090	Subtilisin-like serine endopeptidase family protein
ath-miR779.2	AT1G51300	alpha/beta-Hydrolases superfamily protein
	AT1G18370	HIK, ATNACK1, NACK1 | ATP binding microtubule motor family protein
ath-miR858	AT2G26950	AtMYB104, MYB104 | myb domain protein 104
	AT1G17760	CSTF77, ATCSTF77 | Tetratricopeptide repeat (TPR)-like superfamily protein

ath-miR393b	AT1G12820	AFB3 | auxin signaling F-box 3
	AT3G26810	AFB2 | auxin signaling F-box 2
	AT3G62980	TIR1 | F-box/RNI-like superfamily protein
ath-miR398a	AT1G36078	unknown protein; FUNCTIONS IN biological_process unknown
ath-miR394b	AT1G27340	Galactose oxidase/kelch repeat superfamily protein
	AT4G20430	Subtilase family protein
	AT1G01320	Tetratricopeptide repeat (TPR)-like superfamily protein

Note: Prediction targets of miRNAs with significant expression alteration (Table 2) are listed, with gene ID, predicted function, and base-paring patterns shown. A ":" represents a perfect match; a "." represents a wobble (G: U pairs); a " "(a space) represents an imperfect match.

Table S3: siRNA aligned to the At5G38850 locus

#. Reads	Strand	Position	Sequence (5' to 3')	Length	Register
3	+	5	AAACGCAATCTCTCACGACC	20	5
2	+	46	AACTTGGAGATACAACGTCTTCCC	24	4
3	+	108	CTCATTTACGTAAGCAGTTCAACTCAA	27	3
2	+	118	TAAGCAGTTCAACTCAAATGGG	22	13
4	+	149	TTTGATGATCAAGGAATCGAGAG	23	2
18	+	221	ATATCGATTGTGGTTCTTTCA	21	11
7	+	253	TTCTTCGAGTTGGTGCTTGAATGA	24	1
5	+	283	GGAGATTTTGAAATGCAAAGACGT	24	10
10	+	284	GAGATTTTGAAATGCAAAGA	20	11
13	+	284	GAGATTTTGAAATGCAAAGACGT	23	11
31	+	284	GAGATTTTGAAATGCAAAGAC	21	11
2	+	285	AGATTTTGAAATGCAAAGACG	21	12
16	+	288	TTTTGAAATGCAAAGACGTAGT	22	15
6	+	291	TGAAATGCAAAGACGTAGTGATGC	24	18
5	+	292	GAAATGCAAAGACGTAGTGAT	21	19
7	+	293	AAATGCAAAGACGTAGTGATG	21	20
237	+	294	AATGCAAAGACGTAGTGATGC	21	0
2	+	296	TGCAAAGACGTAGTGATGCCG	21	2
11	+	298	CAAAGACGTAGTGATGCCGAT	21	4
11	+	304	CGTAGTGATGCCGATCTTCTA	21	10
22	+	305	GTAGTGATGCCGATCTTCTAT	21	11
4	+	305	GTAGTGATGCCGATCTTCTATG	22	11
1419	+	306	TAGTGATGCCGATCTTCTATG	21	12
1	+	306	AGTGATGCCGATCTTCTATGAAGTAGATC	31	12
21	+	306	TAGTGATGCCGATCTTCTAT	20	12
240	+	306	TAGTGATGCCGATCTTCTATGA	22	12
6	+	306	TAGTGATGCCGATCTTCTATGAAGTAGATC	30	12
16	+	307	AGTGATGCCGATCTTCTATGA	21	13
1	+	307	AGTGATGCCGATCTTCTATG	20	13
7	+	310	GATGCCGATCTTCTATGAAGTAGA	24	16
24	+	311	ATGCCGATCTTCTATGAAGTA	21	17
18	+	312	TGCCGATCTTCTATGAAGTAGA	22	18
4	+	313	GCCGATCTTCTATGAAGTAGA	21	19
7	+	321	TCTATGAAGTAGATCCATCCG	21	6
7	+	323	TATGAAGTAGATCCATCCGAT	21	8
14	+	325	TGAAGTAGATCCATCCGATGTA	22	10
23	+	325	TGAAGTAGATCCATCCGATGT	21	10
1073	+	326	GAAGTAGATCCATCCGATGTA	21	11
2	+	326	GAAGTAGATCCATCCGATGT	20	11
14	+	327	AAGTAGATCCATCCGATGTACGGA	24	12
200	+	327	AAGTAGATCCATCCGATGTA	20	12
35	+	327	AAGTAGATCCATCCGATGTACG	22	12

56	+	327	AAGTAGATCCATCCGATGTAC	21	12
13	+	328	AGTAGATCCATCCGATGTACG	21	13
9	+	330	TAGATCCATCCGATGTA	17	15
8	+	337	ATCCGATGTACGGAAACAGACC	22	1
56	+	342	ATGTACGGAAACAGACCGGAGA	22	6
4	+	343	TGTACGGAAACAGACCGGAGATT	23	7
75	+	343	TGTACGGAAACAGACCGGAGA	21	7
4	+	345	TACGGAAACAGACCGGAGATTTTGGGA	27	9
1	+	347	CGGAAACAGACCGGAGATTTTGGG	24	11
161	+	348	GGAAACAGACCGGAGATTTTGG	22	12
17	+	348	GGAAACAGACCGGAGATTTTGGG	23	12
1	+	348	GGAAACAGACCGGAGATTTT	20	12
6	+	348	GGAAACAGACCGGAGATTTTGGGA	24	12
78	+	348	GGAAACAGACCGGAGATTTTG	21	12
1	+	349	GAAACAGACCGGAGATTTTGGGAAGGCCTT	30	13
10	+	352	ACAGACCGGAGATTTTGGGAAGGC	24	16
3	+	368	GGGAAGGCCTTCAAAAATAGT	21	11
4	+	370	GAAGGCCTTCAAAAATAGTTG	21	13
2	+	371	AAGGCCTTCAAAAATAGTT	19	14
32	+	378	TCAAAAATAGTTGTAAAAGTA	21	0
1	+	379	CAAAAATAGTTGTAAAAGTA	20	1
13	+	380	AAAAATAGTTGTAAAAGTAAA	21	2
4	+	381	AAAATAGTTGTAAAAGTAAAA	21	3
82	+	388	TTGTAAAAGTAAAACTAAGGA	21	10
27	+	389	TGTAAAAGTAAAACTAAGGA	20	11
299	+	389	TGTAAAAGTAAAACTAAGGAGG	22	11
30	+	389	TGTAAAAGTAAAACTAAGGAGGAGA	25	11
98	+	389	TGTAAAAGTAAAACTAAGGAG	21	11
133	+	390	GTAAAAGTAAAACTAAGGAGG	21	12
1	+	390	GTAAAAGTAAAACTAAGGAGGA	22	12
1	+	391	TAAAAGTAAAACTAAGGAGG	20	13
825	+	391	TAAAAGTAAAACTAAGGAGGA	21	13
187	+	392	AAAAGTAAAACTAAGGAGGAG	21	14
57	+	392	AAAAGTAAAACTAAGGAGGAGA	22	14
26	+	393	AAAGTAAAACTAAGGAGGAGA	21	15
1	+	396	GTAAAACTAAGGAGGAG	17	18
6	+	396	GTAAAACTAAGGAGGAGAGGCAGA	24	18
33	+	398	AAAACTAAGGAGGAGAGGCAGA	22	20
508	+	399	AAACTAAGGAGGAGAGGCAGA	21	0
19	+	400	AACTAAGGAGGAGAGGCAGAG	21	1
2	+	400	AACTAAGGAGGAGAGGCAGA	20	1
6	+	400	AACTAAGGAGGAGAGGCAGAGA	22	1
110	+	401	ACTAAGGAGGAGAGGCAGAGA	21	2
2	+	402	CTAAGGAGGAGAGGCAGAGATG	22	3

8	+	402	CTAAGGAGGAGAGGCAGAGAT	21	3
14	+	403	TAAGGAGGAGAGGCAGAGATG	21	4
16	+	403	TAAGGAGGAGAGGCAGAGATGG	22	4
5	+	405	AGGAGGAGAGGCAGAGATGGA	21	6
18	+	409	GGAGAGGCAGAGATGGATCC	20	10
15	+	410	GAGAGGCAGAGATGGATCCAA	21	11
111	+	411	AGAGGCAGAGATGGATCCAAGC	22	12
73	+	411	AGAGGCAGAGATGGATCCAAG	21	12
11	+	412	GAGGCAGAGATGGATCCAAGC	21	13
43	+	413	AGGCAGAGATGGATCCAAGCT	21	14
20	+	414	GGCAGAGATGGATCCAAGCTT	21	15
3	+	415	GCAGAGATGGATCCAAG	17	16
23	+	419	AGATGGATCCAAGCTTTAATT	21	20
3	+	420	GATGGATCCAAGCTTTAATTT	21	0
13	+	422	TGGATCCAAGCTTTAATTTTT	21	2
109	+	428	CAAGCTTTAATTTTTGTTGGC	21	8
14	+	429	AAGCTTTAATTTTTGTTGGCA	21	9
1	+	430	AGCTTTAATTTTTGTTGGC	19	10
70	+	432	CTTTAATTTTTGTTGGCAACA	21	12
252	+	433	TTTAATTTTTGTTGGCAACAT	21	13
59	+	433	TTTAATTTTTGTTGGCAACA	20	13
6	+	433	TTTAATTTTTGTTGGCAAC	19	13
80	+	433	TTTAATTTTTGTTGGCAACATAGC	24	13
3	+	434	TTAATTTTTGTTGGCAACATAGC	23	14
6	+	434	TTAATTTTTGTTGGCAACATAGCT	24	14
70	+	434	TTAATTTTTGTTGGCAACATA	21	14
2	+	435	TAATTTTTGTTGGCAACATAG	21	15
147	+	436	AATTTTTGTTGGCAACATAGC	21	16
37	+	439	TTTTGTTGGCAACATAGCTGGA	22	19
4	+	439	TTTTGTTGGCAACATAGCTGGAG	23	19
284	+	440	TTTGTTGGCAACATAGCTGGA	21	20
37	+	440	TTTGTTGGCAACATAGCTGGAG	22	20
2	+	441	TTGTTGGCAACATAGCTGGAGAA	23	0
366	+	441	TTGTTGGCAACATAGCTGGAG	21	0
683	+	441	TTGTTGGCAACATAGCTGGAGA	22	0
1	+	442	TGTTGGCAACATAGCTGGAGA	21	1
20	+	443	GTTGGCAACATAGCTGGAGA	20	2
24	+	443	GTTGGCAACATAGCTGGAGAA	21	2
13	+	444	TTGGCAACATAGCTGGAGAACA	22	3
9	+	444	TTGGCAACATAGCTGGAGAAC	21	3
29	+	447	GCAACATAGCTGGAGAACACT	21	6
13	+	449	AACATAGCTGGAGAACACTCG	21	8
5	+	449	AACATAGCTGGAGAACACTCGC	22	8
11	+	450	ACATAGCTGGAGAACACTCGCT	22	9

18	+	450	ACATAGCTGGAGAACACTCGC	21	9
3	+	450	ACATAGCTGGAGAACACTCGCTGAAATG	28	9
97	+	451	CATAGCTGGAGAACACTCGCT	21	10
191	+	452	ATAGCTGGAGAACACTCGCTGA	22	11
63	+	452	ATAGCTGGAGAACACTCGCTG	21	11
2287	+	453	TAGCTGGAGAACACTCGCTGA	21	12
2	+	453	TAGCTGGAGAACACTCGCTGAA	22	12
38	+	453	TAGCTGGAGAACACTCG	17	12
1	+	454	AGCTGGAGAACACTCGCTGA	20	13
288	+	454	AGCTGGAGAACACTCGCTGAA	21	13
30	+	454	AGCTGGAGAACACTCGCTGAAA	22	13
13	+	456	CTGGAGAACACTCGCTGAAATG	22	15
53	+	457	TGGAGAACACTCGCTGAAATGG	22	16
10	+	477	GGGAAAATGAAGCGGATA	18	15
19	+	478	GGAAAATGAAGCGGATA	17	16
71	+	478	GGAAAATGAAGCGGATATGAT	21	16
22	+	479	GAAAATGAAGCGGATATGATT	21	17
6	+	479	GAAAATGAAGCGGATATGATTGA	23	17
21	+	480	AAAATGAAGCGGATATGATTG	21	18
6	+	480	AAAATGAAGCGGATATGATTGA	22	18
47	+	481	AAATGAAGCGGATATGATTGA	21	19
13	+	482	AATGAAGCGGATATGATTGAA	21	20
3	+	483	ATGAAGCGGATATGATTGAA	20	0
3	+	483	ATGAAGCGGATATGATTGA	19	0
401	+	483	ATGAAGCGGATATGATTGAAA	21	0
6	+	483	ATGAAGCGGATATGATTGAAAA	22	0
6	+	484	TGAAGCGGATATGATTGAAAAGAT	24	1
6	+	484	TGAAGCGGATATGATTGAAAA	21	1
8	+	484	TGAAGCGGATATGATTGAAAAG	22	1
16	+	485	GAAGCGGATATGATTGAAAAGA	22	2
515	+	486	AAGCGGATATGATTGAAAAGA	21	3
9	+	486	AAGCGGATATGATTGAAAAGAT	22	3
342	+	487	AGCGGATATGATTGAAAAGAT	21	4
5	+	489	CGGATATGATTGAAAAGATAGC	22	6
25	+	494	ATGATTGAAAAGATAGCCAAA	21	11
37	+	495	TGATTGAAAAGATAGCCAAAGA	22	12
9	+	495	TGATTGAAAAGATAGCCAAAG	21	12
275	+	497	ATTGAAAAGATAGCCAAAGAT	21	14
68	+	497	ATTGAAAAGATAGCCAAAGATG	22	14
1	+	498	TTGAAAAGATAGCCAAAGATG	21	15
71	+	499	TGAAAAGATAGCCAAAGATGT	21	16
6	+	500	GAAAAGATAGCCAAAGATG	19	17
7	+	500	GAAAAGATAGCCAAAGATGTT	21	17
4	+	501	AAAAGATAGCCAAAGATGTTT	21	18

169	+	504	AGATAGCCAAAGATGTTTCAGA	22	0
37	+	504	AGATAGCCAAAGATGTTTCAG	21	0
249	+	505	GATAGCCAAAGATGTTTCAGA	21	1
12	+	506	ATAGCCAAAGATGTTTCAGATA	22	2
29	+	506	ATAGCCAAAGATGTTTCAGAT	21	2
136	+	507	TAGCCAAAGATGTTTCAGATA	21	3
3	+	507	TAGCCAAAGATGTTTCAGATAA	22	3
5	+	512	AAAGATGTTTCAGATAAACTGA	22	8
11	+	513	AAGATGTTTCAGATAAACTGA	21	9
68	+	531	TGAATGCTACACCTTCTAAAGA	22	6
6	+	533	AATGCTACACCTTCTAAAGAT	21	8
3	+	537	CTACACCTTCTAAAGATTTTG	21	12
8	+	537	CTACACCTTCTAAAGATTTTGA	22	12
78	+	538	TACACCTTCTAAAGATTTTGA	21	13
5	+	539	ACACCTTCTAAAGATTTTGATG	22	14
73	+	539	ACACCTTCTAAAGATTTTGAT	21	14
9	+	542	CCTTCTAAAGATTTTGATGCA	21	17
12	+	544	TTCTAAAGATTTTGATGCATT	21	19
3	+	547	TAAAGATTTTGATGCATTTGTGG	23	1
41	+	547	TAAAGATTTTGATGCATTTGT	21	1
65	+	548	AAAGATTTTGATGCATTTGTG	21	2
277	+	549	AAGATTTTGATGCATTTGTGG	21	3
3	+	549	AAGATTTTGATGCATTTGTGGG	22	3
1	+	550	AGATTTTGATGCATTTGTGG	20	4
63	+	550	AGATTTTGATGCATTTGTGGG	21	4
224	+	551	GATTTTGATGCATTTGTGGGA	21	5
2	+	552	ATTTTGATGCATTTGTGGGACT	22	6
5	+	552	ATTTTGATGCATTTGTGGGAC	21	6
4	+	553	TTTTGATGCATTTGTGGGACTT	22	7
9	+	553	TTTTGATGCATTTGTGGGACT	21	7
202	+	554	TTTGATGCATTTGTGGGACTT	21	8
16	+	555	TTGATGCATTTGTGGGACTTGA	22	9
4	+	555	TTGATGCATTTGTGGGACTTGAGT	24	9
72	+	555	TTGATGCATTTGTGGGACTTG	21	9
15	+	556	TGATGCATTTGTGGGACTTGAGT	23	10
64	+	556	TGATGCATTTGTGGGACTTGA	21	10
109	+	557	GATGCATTTGTGGGACTTGAG	21	11
7	+	557	GATGCATTTGTGGGACTTGAGT	22	11
1058	+	558	ATGCATTTGTGGGACTTGAGT	21	12
18	+	558	ATGCATTTGTGGGACTTGAGTT	22	12
1	+	558	ATGCATTTGTGGGACTTGAG	20	12
4	+	558	ATGCATTTGTGGGACTTGAGTTTC	24	12
5	+	558	ATGCATTTGTGGGACTTGAGTTTCA	25	12
122	+	559	TGCATTTGTGGGACTTGAGTTT	22	13

1546	+	559	TGCATTTGTGGGACTTGAGTT	21	13
17	+	559	TGCATTTGTGGGACTTGAGTTTCA	24	13
137	+	560	GCATTTGTGGGACTTGAGTTT	21	14
2	+	560	GCATTTGTGGGACTTGAGTTTC	22	14
108	+	561	CATTTGTGGGACTTGAGTTTC	21	15
20	+	561	CATTTGTGGGACTTGAGTTTCA	22	15
17	+	562	ATTTGTGGGACTTGAGTTTC	20	16
3961	+	562	ATTTGTGGGACTTGAGTTTCA	21	16
4	+	562	ATTTGTGGGACTTGAGTTT	19	16
6	+	562	ATTTGTGGGACTTGAGT	17	16
8	+	562	ATTTGTGGGACTTGAGTTTCACAT	24	16
116	+	563	TTTGTGGGACTTGAGTTTCACA	22	17
14	+	563	TTTGTGGGACTTGAGTTTCA	20	17
1	+	566	GTGGGACTTGAGTTTCACATTAGGG	25	20
4	+	567	TGGGACTTGAGTTTCACATTAGGG	24	0
2	+	568	GGGACTTGAGTTTCACATTAGGGA	24	1
2	+	568	GGGACTTGAGTTTCACATTAG	21	1
7	+	568	GGGACTTGAGTTTCACATTAGG	22	1
18	+	569	GGACTTGAGTTTCACATTAGGG	22	2
108	+	570	GACTTGAGTTTCACATTAGGG	21	3
2	+	570	GACTTGAGTTTCACATTAGG	20	3
17	+	571	ACTTGAGTTTCACATTAGGGAA	22	4
59	+	571	ACTTGAGTTTCACATTAGGGA	21	4
5	+	571	ACTTGAGTTTCACATTAGGGAATT	24	4
105	+	572	CTTGAGTTTCACATTAGGGAA	21	5
10	+	572	CTTGAGTTTCACATTAGGGAAT	22	5
1	+	572	CTTGAGTTTCACATTAGGGA	20	5
7	+	572	CTTGAGTTTCACATTAGGGAATT	23	5
98	+	573	TTGAGTTTCACATTAGGGAAT	21	6
7	+	578	TTTCACATTAGGGAATTAAGT	21	11
16	+	579	TTCACATTAGGGAATTAAGTT	21	12
19	+	580	TCACATTAGGGAATTAAGTTC	21	13
1	+	580	TCACATTAGGGAATTAAGTTCT	22	13
13	+	581	CACATTAGGGAATTAAGTTCT	21	14
26	+	590	GAATTAAGTTCTCTGCTATAC	21	2
140	+	591	AATTAAGTTCTCTGCTATACC	21	3
59	+	592	ATTAAGTTCTCTGCTATACCT	21	4
4	+	593	TTAAGTTCTCTGCTATACCTA	21	5
5	+	596	AGTTCTCTGCTATACCTAGAC	21	8
22	+	597	GTTCTCTGCTATACCTAGACT	21	9
317	+	598	TTCTCTGCTATACCTAGACTA	21	10
1	+	599	TCTCTGCTATACCTAGACTATG	22	11
10	+	600	CTCTGCTATACCTAGACTATGA	22	12
16	+	601	TCTGCTATACCTAGACTATGAG	22	13

20	+	601	TCTGCTATACCTAGACTATGA	21	13
1	+	602	CTGCTATACCTAGACTATGAGCAA	24	14
1	+	602	CTGCTATACCTAGACTATGA	20	14
417	+	602	CTGCTATACCTAGACTATGAG	21	14
54	+	602	CTGCTATACCTAGACTATGAGC	22	14
2	+	603	TGCTATACCTAGACTATGAG	20	15
98	+	603	TGCTATACCTAGACTATGAGC	21	15
106	+	606	TATACCTAGACTATGAGCAAG	21	18
31	+	607	ATACCTAGACTATGAGCAAGTG	22	19
1	+	608	TACCTAGACTATGAGCAAGTGA	22	20
2	+	608	TACCTAGACTATGAGCAAGTGAG	23	20
61	+	608	TACCTAGACTATGAGCAAGTG	21	20
89	+	609	ACCTAGACTATGAGCAAGTGA	21	0
128	+	610	CCTAGACTATGAGCAAGTGAG	21	1
15	+	610	CCTAGACTATGAGCAAGTGAGG	22	1
8	+	610	CCTAGACTATGAGCAAGTGA	20	1
5	+	611	CTAGACTATGAGCAAGTGAGG	21	2
1	+	612	TAGACTATGAGCAAGTGAGG	20	3
673	+	612	TAGACTATGAGCAAGTGAGGA	21	3
20	+	613	AGACTATGAGCAAGTGAGGAT	21	4
4	+	616	CTATGAGCAAGTGAGGATAGTAGGAATC	28	7
1	+	617	TATGAGCAAGTGAGGATAGTA	21	8
22	+	617	TATGAGCAAGTGAGGATAGTAG	22	8
5	+	618	ATGAGCAAGTGAGGATAGTAGG	22	9
73	+	618	ATGAGCAAGTGAGGATAGTAG	21	9
156	+	619	TGAGCAAGTGAGGATAGTAGG	21	10
3	+	620	GAGCAAGTGAGGATAGTAGGA	21	11
191	+	621	AGCAAGTGAGGATAGTAGGAA	21	12
13	+	622	GCAAGTGAGGATAGTAGG	18	13
2	+	622	GCAAGTGAGGATAGTAGGAA	20	13
3	+	622	GCAAGTGAGGATAGTAGGAATCTG	24	13
461	+	622	GCAAGTGAGGATAGTAGGAAT	21	13
47	+	622	GCAAGTGAGGATAGTAGGAATC	22	13
22	+	623	CAAGTGAGGATAGTAGGAATCT	22	14
36	+	623	CAAGTGAGGATAGTAGGAATC	21	14
1	+	624	AAGTGAGGATAGTAGGAAT	19	15
297	+	624	AAGTGAGGATAGTAGGAATCT	21	15
34	+	624	AAGTGAGGATAGTAGGAATCTG	22	15
1628	+	625	AGTGAGGATAGTAGGAATCTG	21	16
80	+	625	AGTGAGGATAGTAGGAATCTGT	22	16
51	+	626	GTGAGGATAGTAGGAATCTGT	21	17
7	+	626	GTGAGGATAGTAGGAATCTG	20	17
51	+	627	TGAGGATAGTAGGAATCTGTGG	22	18
84	+	627	TGAGGATAGTAGGAATCTGTG	21	18

24	+	628	GAGGATAGTAGGAATCTGTGGC	22	19
7	+	628	GAGGATAGTAGGAATCTGTGG	21	19
24	+	629	AGGATAGTAGGAATCTGTGGC	21	20
43	+	629	AGGATAGTAGGAATCTGTGGCC	22	20
29	+	630	GGATAGTAGGAATCTGTGGCC	21	0
42	+	630	GGATAGTAGGAATCTGTGGCCCTG	24	0
23	+	631	GATAGTAGGAATCTGTGGC	19	1
255	+	631	GATAGTAGGAATCTGTGGCCC	21	1
4	+	631	GATAGTAGGAATCTGTGGCCCTGCA	25	1
120	+	632	ATAGTAGGAATCTGTGGCCCTG	22	2
187	+	632	ATAGTAGGAATCTGTGGCCCT	21	2
10	+	633	TAGTAGGAATCTGTGGCC	18	3
1	+	633	TAGTAGGAATCTGTGGCCCTGCAGGAATT	29	3
258	+	633	TAGTAGGAATCTGTGGCCCTGC	22	3
350	+	633	TAGTAGGAATCTGTGGCCCTG	21	3
122	+	634	AGTAGGAATCTGTGGCCCTGC	21	4
9	+	634	AGTAGGAATCTGTGGCCCTGCA	22	4
61	+	636	TAGGAATCTGTGGCCCTGCAG	21	6
7	+	637	AGGAATCTGTGGCCCTGCAGGAATC	25	7
9	+	638	GGAATCTGTGGCCCTGCAGGA	21	8
19	+	640	AATCTGTGGCCCTGCAGGAAT	21	10
129	+	642	TCTGTGGCCCTGCAGGAATCGG	22	12
29	+	642	TCTGTGGCCCTGCAGGAATCG	21	12
10	+	643	CTGTGGCCCTGCAGGAATCGGTA	23	13
256	+	643	CTGTGGCCCTGCAGGAATCGGT	22	13
704	+	643	CTGTGGCCCTGCAGGAATCGG	21	13
8	+	643	CTGTGGCCCTGCAGGAATCG	20	13
873	+	644	TGTGGCCCTGCAGGAATCGGT	21	14
8	+	644	TGTGGCCCTGCAGGAATCGG	20	14
12	+	645	GTGGCCCTGCAGGAATCGGT	20	15
1	+	645	GTGGCCCTGCAGGAATCGG	19	15
67	+	645	GTGGCCCTGCAGGAATCGGTA	21	15
290	+	646	TGGCCCTGCAGGAATCGGTAA	21	16
308	+	646	TGGCCCTGCAGGAATCGGTAAG	22	16
12	+	647	GGCCCTGCAGGAATCGGTAAG	21	17
4	+	648	GCCCTGCAGGAATCGGTAAGA	21	18
16	+	649	CCCTGCAGGAATCGGTAAGAC	21	19
6	+	649	CCCTGCAGGAATCGGTAAGACT	22	19
12	+	650	CCTGCAGGAATCGGTAAGACTA	22	20
39	+	650	CCTGCAGGAATCGGTAAGACT	21	20
335	+	651	CTGCAGGAATCGGTAAGACTA	21	0
3	+	651	CTGCAGGAATCGGTAAGACTACC	23	0
240	+	652	TGCAGGAATCGGTAAGACTAC	21	1
371	+	652	TGCAGGAATCGGTAAGACTACC	22	1

1	+	653	GCAGGAATCGGTAAGACTACCA	22	2
1	+	653	GCAGGAATCGGTAAGACTAC	20	2
20	+	653	GCAGGAATCGGTAAGACTACC	21	2
27	+	654	CAGGAATCGGTAAGACTACCA	21	3
16	+	655	AGGAATCGGTAAGACTACCAT	21	4
28	+	655	AGGAATCGGTAAGACTACCATT	22	4
55	+	659	ATCGGTAAGACTACCATTGCT	21	8
14	+	660	TCGGTAAGACTACCATTGCTCG	22	9
35	+	660	TCGGTAAGACTACCATTGCTC	21	9
11	+	661	CGGTAAGACTACCATTGCTCGTGC	24	10
4	+	661	CGGTAAGACTACCATTGCTCG	21	10
44	+	663	GTAAGACTACCATTGCTCGTG	21	12
8	+	663	GTAAGACTACCATTGCTCGTGC	22	12
18	+	664	TAAGACTACCATTGCTCGTG	20	13
1	+	664	TAAGACTACCATTGCTC	17	13
22	+	664	TAAGACTACCATTGCTCGTGCTTT	24	13
2673	+	664	TAAGACTACCATTGCTCGTGC	21	13
64	+	664	TAAGACTACCATTGCTCGTGCT	22	13
10	+	665	AAGACTACCATTGCTCGTGC	20	14
2	+	665	AAGACTACCATTGCTCGTGCTTT	23	14
774	+	665	AAGACTACCATTGCTCGTGCT	21	14
8	+	665	AAGACTACCATTGCTCGTGCTT	22	14
135	+	666	AGACTACCATTGCTCGTGCTT	21	15
1	+	666	AGACTACCATTGCTCGTGCTTT	22	15
14	+	667	GACTACCATTGCTCGTGCTTT	21	16
42	+	668	ACTACCATTGCTCGTGCTTTAC	22	17
64	+	668	ACTACCATTGCTCGTGCTTTA	21	17
33	+	669	CTACCATTGCTCGTGCTTTAC	21	18
8	+	672	CCATTGCTCGTGCTTTACAAA	21	0
23	+	673	CATTGCTCGTGCTTTACAAAGC	22	1
247	+	674	ATTGCTCGTGCTTTACAAAGC	21	2
16	+	675	TTGCTCGTGCTTTACAAAGCC	21	3
8	+	675	TTGCTCGTGCTTTACAAAGCCT	22	3
65	+	684	CTTTACAAAGCCTACTCTCTA	21	12
124	+	685	TTTACAAAGCCTACTCTCTAG	21	13
395	+	685	TTTACAAAGCCTACTCTCTAGC	22	13
6	+	685	TTTACAAAGCCTACTCTCTA	20	13
20	+	686	TTACAAAGCCTACTCTCTAGCA	22	14
485	+	686	TTACAAAGCCTACTCTCTAGC	21	14
16	+	687	TACAAAGCCTACTCTCTAGCAATT	24	15
6	+	687	TACAAAGCCTACTCTCTAGC	20	15
70	+	687	TACAAAGCCTACTCTCTAGCA	21	15
33	+	688	ACAAAGCCTACTCTCTAGCAA	21	16
2	+	689	CAAAGCCTACTCTCTAGCAAT	21	17

44	+	690	AAAGCCTACTCTCTAGCAATT	21	18
21	+	695	CTACTCTCTAGCAATTTTCAGC	22	2
58	+	695	CTACTCTCTAGCAATTTTCAG	21	2
7	+	695	CTACTCTCTAGCAATTTTCA	20	2
11	+	696	TACTCTCTAGCAATTTTCAGCG	22	3
21	+	696	TACTCTCTAGCAATTTTCAGC	21	3
2	+	696	TACTCTCTAGCAATTTTCAGCGA	23	3
14	+	697	ACTCTCTAGCAATTTTCAGCG	21	4
25	+	698	CTCTCTAGCAATTTTCAGCGA	21	5
2	+	701	TCTAGCAATTTTCAGCGAAGT	21	8
15	+	702	CTAGCAATTTTCAGCGAAGTTG	22	9
7	+	702	CTAGCAATTTTCAGCGAAGTT	21	9
74	+	705	GCAATTTTCAGCGAAGTTGTT	21	12
27	+	707	AATTTTCAGCGAAGTTGTTTT	21	14
15	+	708	ATTTTCAGCGAAGTTGTTTTA	21	15
29	+	708	ATTTTCAGCGAAGTTGTTTTATGGAG	26	15
20	+	709	TTTTCAGCGAAGTTGTTTTATG	22	16
8	+	709	TTTTCAGCGAAGTTGTTTTAT	21	16
15	+	710	TTTCAGCGAAGTTGTTTTATGG	22	17
36	+	710	TTTCAGCGAAGTTGTTTTATG	21	17
145	+	711	TTCAGCGAAGTTGTTTTATGG	21	18
197	+	712	TCAGCGAAGTTGTTTTATGGA	21	19
44	+	712	TCAGCGAAGTTGTTTTATGGAG	22	19
93	+	713	CAGCGAAGTTGTTTTATGGAG	21	20
257	+	714	AGCGAAGTTGTTTTATGGAGA	21	0
29	+	714	AGCGAAGTTGTTTTATGGAGAA	22	0
197	+	715	GCGAAGTTGTTTTATGGAGAA	21	1
212	+	716	CGAAGTTGTTTTATGGAGAATG	22	2
2	+	718	AAGTTGTTTTATGGAGAATGTT	22	4
5	+	718	AAGTTGTTTTATGGAGAATGTTAGG	25	4
169	+	719	AGTTGTTTTATGGAGAATGTT	21	5
1	+	719	AGTTGTTTTATGGAGAATGTTA	22	5
57	+	721	TTGTTTTATGGAGAATGTTAGG	22	7
27	+	722	TGTTTTATGGAGAATGTTAGG	21	8
7	+	722	TGTTTTATGGAGAATGTTAGGG	22	8
11	+	723	GTTTTATGGAGAATGTTAGGG	21	9
1	+	723	GTTTTATGGAGAATGTTAGG	20	9
55	+	723	GTTTTATGGAGAATGTTAGGGG	22	9
102	+	724	TTTTATGGAGAATGTTAGGGG	21	10
63	+	724	TTTTATGGAGAATGTTAGGGGA	22	10
20	+	725	TTTATGGAGAATGTTAGGGGA	21	11
4	+	726	TTATGGAGAATGTTAGGGGA	20	12
84	+	726	TTATGGAGAATGTTAGGGGAA	21	12
63	+	727	TATGGAGAATGTTAGGGGAAG	21	13

540	+	728	ATGGAGAATGTTAGGGGAAGT	21	14
230	+	729	TGGAGAATGTTAGGGGAAGTC	21	15
9	+	730	GGAGAATGTTAGGGGAAGT	19	16
34	+	731	GAGAATGTTAGGGGAAGTCTT	21	17
4	+	731	GAGAATGTTAGGGGAAGTC	19	17
2	+	732	AGAATGTTAGGGGAAGTCTTA	21	18
152	+	735	ATGTTAGGGGAAGTCTTAATA	21	0
3	+	738	TTAGGGGAAGTCTTAATATTG	21	3
4	+	738	TTAGGGGAAGTCTTAATATTGGGC	24	3
53	+	738	TTAGGGGAAGTCTTAATATTGG	22	3
7	+	738	TTAGGGGAAGTCTTAATATTGGG	23	3
114	+	739	TAGGGGAAGTCTTAATATTGG	21	4
131	+	739	TAGGGGAAGTCTTAATATTGGG	22	4
1012	+	740	AGGGGAAGTCTTAATATTGGG	21	5
1	+	740	AGGGGAAGTCTTAATATTGGGC	22	5
81	+	741	GGGGAAGTCTTAATATTGGGC	21	6
48	+	745	AAGTCTTAATATTGGGCTTGA	21	10
1	+	747	GTCTTAATATTGGGCTTGACG	21	12
416	+	748	TCTTAATATTGGGCTTGACGA	21	13
43	+	748	TCTTAATATTGGGCTTGACGAG	22	13
73	+	749	CTTAATATTGGGCTTGACGA	20	14
800	+	749	CTTAATATTGGGCTTGACGAG	21	14
97	+	749	CTTAATATTGGGCTTGACGAGT	22	14
192	+	750	TTAATATTGGGCTTGACGAGTA	22	15
1	+	750	TTAATATTGGGCTTGACGAGTAT	23	15
4	+	750	TTAATATTGGGCTTGACGAG	20	15
566	+	750	TTAATATTGGGCTTGACGAGT	21	15
1	+	751	TAATATTGGGCTTGACGAG	19	16
1	+	751	TAATATTGGGCTTGACGAGT	20	16
309	+	751	TAATATTGGGCTTGACGAGTA	21	16
4	+	751	TAATATTGGGCTTGACGAGTAT	22	16
10	+	752	AATATTGGGCTTGACGAGTATG	22	17
12	+	752	AATATTGGGCTTGACGAGTAT	21	17
6	+	752	AATATTGGGCTTGACGAGTATGGT	24	17
10	+	753	ATATTGGGCTTGACGAGTA	19	18
136	+	753	ATATTGGGCTTGACGAGTATG	21	18
5	+	753	ATATTGGGCTTGACGAGTATGGT	23	18
8	+	753	ATATTGGGCTTGACGAGTATGG	22	18
32	+	754	TATTGGGCTTGACGAGTATGG	21	19
50	+	754	TATTGGGCTTGACGAGTATGGT	22	19
1	+	755	ATTGGGCTTGACGAGTATGGTCTGA	25	20
2	+	755	ATTGGGCTTGACGAGTATGGTCT	23	20
605	+	755	ATTGGGCTTGACGAGTATGGT	21	20
125	+	756	TTGGGCTTGACGAGTATGGTCT	22	0

627	+	756	TTGGGCTTGACGAGTATGGTC	21	0
6	+	756	TTGGGCTTGACGAGTATGGT	20	0
154	+	757	TGGGCTTGACGAGTATGGTCT	21	1
15	+	757	TGGGCTTGACGAGTATGGTCTG	22	1
1	+	757	TGGGCTTGACGAGTATGGTC	20	1
10	+	758	GGGCTTGACGAGTATGGTCTG	21	2
1	+	758	GGGCTTGACGAGTATGGTC	19	2
5	+	759	GGCTTGACGAGTATGGTCTGAAG	23	3
16	+	760	GCTTGACGAGTATGGTCTGAAG	22	4
52	+	760	GCTTGACGAGTATGGTCTGAA	21	4
28	+	761	CTTGACGAGTATGGTCTGAAGT	22	5
50	+	762	TTGACGAGTATGGTCTGAAGT	21	6
2	+	763	TGACGAGTATGGTCTGAAGTTAGATT	26	7
11	+	765	ACGAGTATGGTCTGAAGTTAG	21	9
43	+	765	ACGAGTATGGTCTGAAGTTAGA	22	9
4	+	765	ACGAGTATGGTCTGAAGTTAGATT	24	9
22	+	766	CGAGTATGGTCTGAAGTTAGAT	22	10
11	+	767	GAGTATGGTCTGAAGTTAGAT	21	11
3	+	767	GAGTATGGTCTGAAGTTAGATT	22	11
10	+	768	AGTATGGTCTGAAGTTAGA	19	12
2	+	768	AGTATGGTCTGAAGTTAGATTT	22	12
91	+	768	AGTATGGTCTGAAGTTAGATT	21	12
2	+	769	GTATGGTCTGAAGTTAGATTT	21	13
2	+	770	TATGGTCTGAAGTTAGATTTAC	22	14
84	+	770	TATGGTCTGAAGTTAGATTTA	21	14
27	+	771	ATGGTCTGAAGTTAGATTTACA	22	15
5	+	771	ATGGTCTGAAGTTAGATTTAC	21	15
11	+	772	TGGTCTGAAGTTAGATTTACAA	22	16
2	+	772	TGGTCTGAAGTTAGATTTACAAGA	24	16
3	+	772	TGGTCTGAAGTTAGATTTACAAG	23	16
99	+	772	TGGTCTGAAGTTAGATTTACA	21	16
12	+	773	GGTCTGAAGTTAGATTTACAA	21	17
1	+	774	GTCTGAAGTTAGATTTACAAGAACG	25	18
28	+	774	GTCTGAAGTTAGATTTACAAGAAC	24	18
29	+	776	CTGAAGTTAGATTTACAAGAA	21	20
4	+	776	CTGAAGTTAGATTTACAAGA	20	20
199	+	777	TGAAGTTAGATTTACAAGAACG	22	0
7	+	777	TGAAGTTAGATTTACAAGAAC	21	0
7	+	779	AAGTTAGATTTACAAGAACGA	21	2
18	+	780	AGTTAGATTTACAAGAACGAC	21	3
7	+	780	AGTTAGATTTACAAGAACGACT	22	3
57	+	782	TTAGATTTACAAGAACGACTT	21	5
10	+	783	TAGATTTACAAGAACGACTTCT	22	6
2	+	783	TAGATTTACAAGAACGACTTC	21	6

18	+	787	TTTACAAGAACGACTTCTTTC	21	10
1	+	788	TTACAAGAACGACTTCTTTC	20	11
6	+	790	ACAAGAACGACTTCTTTCAAA	21	13
199	+	792	AAGAACGACTTCTTTCAAAGA	21	15
1	+	793	AGAACGACTTCTTTCAAAGA	20	16
2	+	793	AGAACGACTTCTTTCAAAGATT	22	16
3	+	793	AGAACGACTTCTTTCAAAGAT	21	16
1	+	801	TTCTTTCAAAGATTATGAACC	21	3
3	+	801	TTCTTTCAAAGATTATGAACCA	22	3
4	+	802	TCTTTCAAAGATTATGAACCA	21	4
4	+	806	TCAAAGATTATGAACCAAAAG	21	8
12	+	807	CAAAGATTATGAACCAAAA	19	9
6	+	807	CAAAGATTATGAACCAAAAGGG	22	9
71	+	808	AAAGATTATGAACCAAAAGGG	21	10
16	+	809	AAGATTATGAACCAAAAGGGT	21	11
1	+	809	AAGATTATGAACCAAAAGGGTAT	23	11
5	+	809	AAGATTATGAACCAAAAGGGTA	22	11
46	+	810	AGATTATGAACCAAAAGGGTA	21	12
1	+	811	GATTATGAACCAAAAGGGTA	20	13
23	+	812	ATTATGAACCAAAAGGGTATG	21	14
51	+	813	TTATGAACCAAAAGGGTATGA	21	15
36	+	814	TATGAACCAAAAGGGTATGAGG	22	16
59	+	814	TATGAACCAAAAGGGTATGAG	21	16
36	+	815	ATGAACCAAAAGGGTATGAGGA	22	17
66	+	815	ATGAACCAAAAGGGTATGAGG	21	17
127	+	816	TGAACCAAAAGGGTATGAGGA	21	18
60	+	816	TGAACCAAAAGGGTATGAGGAT	22	18
18	+	817	GAACCAAAAGGGTATGAGGAT	21	19
42	+	818	AACCAAAAGGGTATGAGGATA	21	20
1	+	819	ACCAAAAGGGTATGAGGATAG	21	0
61	+	821	CAAAAGGGTATGAGGATAGAGC	22	2
8	+	821	CAAAAGGGTATGAGGATAGAG	21	2
130	+	822	AAAAGGGTATGAGGATAGAGCA	22	3
162	+	822	AAAAGGGTATGAGGATAGAGC	21	3
7	+	822	AAAAGGGTATGAGGATAGAG	20	3
1819	+	823	AAAGGGTATGAGGATAGAGCA	21	4
1	+	823	AAAGGGTATGAGGATAGAGC	20	4
23	+	823	AAAGGGTATGAGGATAGAGCAT	22	4
10	+	824	AAGGGTATGAGGATAGAGCATTTAG	25	5
1	+	824	AAGGGTATGAGGATAGAGCA	20	5
6	+	824	AAGGGTATGAGGATAGAGCATT	22	5
86	+	824	AAGGGTATGAGGATAGAGCAT	21	5
11	+	825	AGGGTATGAGGATAGAGCATT	21	6
2	+	825	AGGGTATGAGGATAGAGCATTTAG	24	6

6	+	828	GTATGAGGATAGAGCATTTAG	21	9
39	+	829	TATGAGGATAGAGCATTTAGGC	22	10
70	+	829	TATGAGGATAGAGCATTTAGG	21	10
125	+	830	ATGAGGATAGAGCATTTAGGC	21	11
1	+	831	TGAGGATAGAGCATTTAGGC	20	12
443	+	831	TGAGGATAGAGCATTTAGGCA	21	12
1	+	832	GAGGATAGAGCATTTAGGCA	20	13
61	+	832	GAGGATAGAGCATTTAGGCACA	22	13
7	+	832	GAGGATAGAGCATTTAGGCAC	21	13
156	+	833	AGGATAGAGCATTTAGGCACA	21	14
1	+	833	AGGATAGAGCATTTAGGCACAA	22	14
1	+	834	GGATAGAGCATTTAGGCACA	20	15
3	+	834	GGATAGAGCATTTAGGCAC	19	15
8	+	834	GGATAGAGCATTTAGGCACAA	21	15
12	+	836	ATAGAGCATTTAGGCACAATA	21	17
7	+	837	TAGAGCATTTAGGCACAATAAG	22	18
3	+	839	GAGCATTTAGGCACAATAAGAG	22	20
1	+	841	GCATTTAGGCACAATAAGAGA	21	1
2	+	841	GCATTTAGGCACAATAAGAGATAGGTTACT	30	1
34	+	842	CATTTAGGCACAATAAGAGAT	21	2
42	+	843	ATTTAGGCACAATAAGAGATA	21	3
4	+	843	ATTTAGGCACAATAAGAGATAGGT	24	3
22	+	844	TTTAGGCACAATAAGAGATAGG	22	4
4	+	844	TTTAGGCACAATAAGAGATA	20	4
52	+	844	TTTAGGCACAATAAGAGATAG	21	4
137	+	845	TTAGGCACAATAAGAGATAGG	21	5
17	+	845	TTAGGCACAATAAGAGATAGGT	22	5
258	+	846	TAGGCACAATAAGAGATAGGT	21	6
6	+	846	TAGGCACAATAAGAGATAGGTT	22	6
19	+	847	AGGCACAATAAGAGATAGGTT	21	7
3	+	848	GGCACAATAAGAGATAGG	18	8
1	+	849	GCACAATAAGAGATAGGTTACA	22	9
7	+	849	GCACAATAAGAGATAGGTTAC	21	9
19	+	852	CAATAAGAGATAGGTTACATGA	22	12
13	+	853	AATAAGAGATAGGTTACATGA	21	13
22	+	854	ATAAGAGATAGGTTACATGACC	22	14
2	+	854	ATAAGAGATAGGTTACATGACCA	23	14
302	+	854	ATAAGAGATAGGTTACATGAC	21	14
16	+	856	AAGAGATAGGTTACATGACCA	21	16
27	+	856	AAGAGATAGGTTACATGA	18	16
2	+	859	AGATAGGTTACATGACCAAAA	21	19
5	+	865	GTTACATGACCAAAAAGTGCT	21	4
7	+	871	TGACCAAAAAGTGCTTATCAT	21	10
15	+	875	CAAAAAGTGCTTATCATTCTAG	22	14

2	+	875	CAAAAAGTGCTTATCATTCTA	21	14
129	+	876	AAAAAGTGCTTATCATTCTAG	21	15
435	+	876	AAAAAGTGCTTATCATTCTAGA	22	15
1	+	877	AAAAGTGCTTATCATTCTAGAT	22	16
4	+	877	AAAAGTGCTTATCATTCTAGATGA	24	16
612	+	877	AAAAGTGCTTATCATTCTAGA	21	16
26	+	878	AAAGTGCTTATCATTCTAGATGA	23	17
8	+	878	AAAGTGCTTATCATTCTAGATG	22	17
34	+	879	AAGTGCTTATCATTCTAGATG	21	18
47	+	879	AAGTGCTTATCATTCTAGATGA	22	18
937	+	880	AGTGCTTATCATTCTAGATGA	21	19
1	+	881	GTGCTTATCATTCTAGATGA	20	20
5	+	883	GCTTATCATTCTAGATGATGT	21	1
2	+	889	CATTCTAGATGATGTTAATGAT	22	7
7	+	890	ATTCTAGATGATGTTAATGAT	21	8
144	+	891	TTCTAGATGATGTTAATGATC	21	9
5	+	891	TTCTAGATGATGTTAATGATCT	22	9
4	+	892	TCTAGATGATGTTAATGATCT	21	10
1	+	893	CTAGATGATGTTAATGATCTC	21	11
3	+	894	TAGATGATGTTAATGATCTCG	21	12
3	+	896	GATGATGTTAATGATCTCGAT	21	14
28	+	897	ATGATGTTAATGATCTCGATT	21	15
15	+	898	TGATGTTAATGATCTCGATTT	21	16
41	+	900	ATGTTAATGATCTCGATTTGTA	22	18
58	+	900	ATGTTAATGATCTCGATTTGT	21	18
273	+	901	TGTTAATGATCTCGATTTGTA	21	19
50	+	903	TTAATGATCTCGATTTGTATGC	22	0
87	+	903	TTAATGATCTCGATTTGTATG	21	0
30	+	904	TAATGATCTCGATTTGTATGCT	22	1
36	+	904	TAATGATCTCGATTTGTATGC	21	1
1068	+	905	AATGATCTCGATTTGTATGCT	21	2
24	+	905	AATGATCTCGATTTGTATGCTT	22	2
3	+	905	AATGATCTCGATTTGTA	17	2
101	+	906	ATGATCTCGATTTGTATGCTT	21	3
14	+	906	ATGATCTCGATTTGTATGCTTT	22	3
2	+	906	ATGATCTCGATTTGTATGCT	20	3
279	+	907	TGATCTCGATTTGTATGCTTT	21	4
9	+	907	TGATCTCGATTTGTATGCTTTG	22	4
244	+	909	ATCTCGATTTGTATGCTTTGG	21	6
55	+	909	ATCTCGATTTGTATGCTTTGGC	22	6
348	+	910	TCTCGATTTGTATGCTTTGGC	21	7
63	+	911	CTCGATTTGTATGCTTTGGCT	21	8
116	+	912	TCGATTTGTATGCTTTGGCTG	21	9
8	+	912	TCGATTTGTATGCTTTGGCTGA	22	9

107	+	913	CGATTTGTATGCTTTGGCTGA	21	10
10	+	914	GATTTGTATGCTTTGGCTGAT	21	11
41	+	915	ATTTGTATGCTTTGGCTGATC	21	12
65	+	915	ATTTGTATGCTTTGGCTGATCA	22	12
12	+	916	TTTGTATGCTTTGGCTGATCA	21	13
3	+	916	TTTGTATGCTTTGGCTGATCAG	22	13
16	+	917	TTGTATGCTTTGGCTGATCAG	21	14
50	+	917	TTGTATGCTTTGGCTGATCAGA	22	14
5	+	918	TGTATGCTTTGGCTGATCAGAC	22	15
88	+	918	TGTATGCTTTGGCTGATCAGA	21	15
20	+	919	GTATGCTTTGGCTGATCAGA	20	16
86	+	919	GTATGCTTTGGCTGATCAGAC	21	16
50	+	920	TATGCTTTGGCTGATCAGACAACG	24	17
6	+	920	TATGCTTTGGCTGATCAGACAAC	23	17
92	+	920	TATGCTTTGGCTGATCAGACA	21	17
185	+	921	ATGCTTTGGCTGATCAGACA	20	18
48	+	921	ATGCTTTGGCTGATCAGACAA	21	18
109	+	922	TGCTTTGGCTGATCAGACAAC	21	19
1	+	922	TGCTTTGGCTGATCAGACAACGTG	24	19
10	+	923	GCTTTGGCTGATCAGACAACGT	22	20
104	+	924	CTTTGGCTGATCAGACAACGT	21	0
123	+	925	TTTGGCTGATCAGACAACGTG	21	1
19	+	925	TTTGGCTGATCAGACAACGTGG	22	1
8	+	925	TTTGGCTGATCAGACAACGTGGT	23	1
273	+	926	TTGGCTGATCAGACAACGTGGT	22	2
312	+	926	TTGGCTGATCAGACAACGTGG	21	2
1217	+	927	TGGCTGATCAGACAACGTGGT	21	3
160	+	927	TGGCTGATCAGACAACGTGGTT	22	3
1	+	927	TGGCTGATCAGACAACGTGG	20	3
14	+	928	GGCTGATCAGACAACGTGGTTT	22	4
17	+	928	GGCTGATCAGACAACGTGG	19	4
669	+	928	GGCTGATCAGACAACGTGGTT	21	4
4	+	929	GCTGATCAGACAACGTGGTT	20	5
23	+	930	CTGATCAGACAACGTGGTTTGG	22	6
308	+	931	TGATCAGACAACGTGGTTTGG	21	7
6	+	932	GATCAGACAACGTGGTTTGGT	21	8
38	+	934	TCAGACAACGTGGTTTGGTCC	21	10
3	+	934	TCAGACAACGTGGTTTGGTCCTGG	24	10
3	+	934	TCAGACAACGTGGTTTGGTC	20	10
7	+	935	CAGACAACGTGGTTTGGTCC	20	11
7	+	936	AGACAACGTGGTTTGGTCCTGG	22	12
1	+	937	GACAACGTGGTTTGGTCCTGGA	22	13
61	+	937	GACAACGTGGTTTGGTCCTGG	21	13
417	+	938	ACAACGTGGTTTGGTCCTGGA	21	14

24	+	939	CAACGTGGTTTGGTCCTGGAAG	22	15
68	+	939	CAACGTGGTTTGGTCCTGGAA	21	15
7	+	939	CAACGTGGTTTGGTCCTGGA	20	15
42	+	940	AACGTGGTTTGGTCCTGGAAG	21	16
51	+	940	AACGTGGTTTGGTCCTGGAAGT	22	16
19	+	948	TTGGTCCTGGAAGTAGGATTATCGTGACA	29	3
39	+	952	TCCTGGAAGTAGGATTATCGTG	22	7
1	+	953	CCTGGAAGTAGGATTATCGTGA	22	8
36	+	953	CCTGGAAGTAGGATTATCGTG	21	8
22	+	954	CTGGAAGTAGGATTATCGTGAC	22	9
45	+	954	CTGGAAGTAGGATTATCGTGA	21	9
44	+	955	TGGAAGTAGGATTATCGTGACA	22	10
84	+	955	TGGAAGTAGGATTATCGTGAC	21	10
119	+	957	GAAGTAGGATTATCGTGACAA	21	12
54	+	957	GAAGTAGGATTATCGTGACA	20	12
53	+	958	AAGTAGGATTATCGTGACAACAGA	24	13
7	+	958	AAGTAGGATTATCGTGACAAC	21	13
1	+	959	AGTAGGATTATCGTGACAACAGA	23	14
27	+	959	AGTAGGATTATCGTGACAACA	21	14
10	+	960	GTAGGATTATCGTGACAACA	20	15
20	+	960	GTAGGATTATCGTGACAACAG	21	15
2	+	961	TAGGATTATCGTGACAACAGAAGACAA	27	16
312	+	961	TAGGATTATCGTGACAACAGA	21	16
6	+	961	TAGGATTATCGTGACAACAGAA	22	16
18	+	962	AGGATTATCGTGACAACAGAAG	22	17
1	+	962	AGGATTATCGTGACAACAGA	20	17
68	+	962	AGGATTATCGTGACAACAGAA	21	17
26	+	963	GGATTATCGTGACAACAGAAG	21	18
3	+	963	GGATTATCGTGACAACAGA	19	18
33	+	965	ATTATCGTGACAACAGAAGAC	21	20
44	+	965	ATTATCGTGACAACAGAAGACA	22	20
4	+	965	ATTATCGTGACAACAGAAGACAAC	24	20
34	+	966	TTATCGTGACAACAGAAGACA	21	0
22	+	967	TATCGTGACAACAGAAGACAA	21	1
15	+	968	ATCGTGACAACAGAAGACAACG	22	2
824	+	968	ATCGTGACAACAGAAGACAAC	21	2
14	+	969	TCGTGACAACAGAAGACAACG	21	3
12	+	970	CGTGACAACAGAAGACAACG	20	4
440	+	970	CGTGACAACAGAAGACAACGA	21	4
10	+	971	GTGACAACAGAAGACAACGA	20	5
4	+	971	GTGACAACAGAAGACAACG	19	5
5	+	971	GTGACAACAGAAGACAACGAGC	22	5
75	+	971	GTGACAACAGAAGACAACGAG	21	5
353	+	972	TGACAACAGAAGACAACGAGCT	22	6

63	+	972	TGACAACAGAAGACAACGAGC	21	6
3	+	973	GACAACAGAAGACAACGAGCT	21	7
10	+	974	ACAACAGAAGACAACGAGCTT	21	8
5	+	974	ACAACAGAAGACAACGAGCT	20	8
7	+	976	AACAGAAGACAACGAGCTTTT	21	10
4	+	980	GAAGACAACGAGCTTTTGCAG	21	14
276	+	981	AAGACAACGAGCTTTTGCAGA	21	15
54	+	982	AGACAACGAGCTTTTGCAGAA	21	16
5	+	982	AGACAACGAGCTTTTGCAGA	20	16
11	+	983	GACAACGAGCTTTTGCAGAAA	21	17
11	+	988	CGAGCTTTTGCAGAAACATGAT	22	1
11	+	989	GAGCTTTTGCAGAAACATGAT	21	2
4	+	989	GAGCTTTTGCAGAAACATGA	20	2
99	+	992	CTTTTGCAGAAACATGATATT	21	5
19	+	993	TTTTGCAGAAACATGATATTA	21	6
3	+	993	TTTTGCAGAAACATGATATT	20	6
14	+	994	TTTGCAGAAACATGATATTAA	21	7
2	+	994	TTTGCAGAAACATGATATTA	20	7
10	+	995	TTGCAGAAACATGATATTAAC	21	8
39	+	995	TTGCAGAAACATGATATTAACA	22	8
4	+	996	TGCAGAAACATGATATTAACA	21	9
61	+	1008	ATATTAACAATGTCTACCATG	21	0
3	+	1009	TATTAACAATGTCTACCATGTGGA	24	1
10	+	1010	ATTAACAATGTCTACCA	17	2
11	+	1010	ATTAACAATGTCTACCATGTGG	22	2
12	+	1010	ATTAACAATGTCTACCATGTGGATT	25	2
24	+	1010	ATTAACAATGTCTACCATGTG	21	2
109	+	1011	TTAACAATGTCTACCATGTGG	21	3
329	+	1011	TTAACAATGTCTACCATGTGGA	22	3
1050	+	1012	TAACAATGTCTACCATGTGGA	21	4
13	+	1012	TAACAATGTCTACCATGTGGAT	22	4
1	+	1012	TAACAATGTCTACCATGTGG	20	4
4	+	1012	TAACAATGTCTACCATGTGGATT	23	4
140	+	1013	AACAATGTCTACCATGTGGATT	22	5
1	+	1013	AACAATGTCTACCATGTGGA	20	5
75	+	1013	AACAATGTCTACCATGTGGAT	21	5
265	+	1014	ACAATGTCTACCATGTGGATT	21	6
6	+	1017	ATGTCTACCATGTGGATT	18	9
3	+	1023	ACCATGTGGATTTTCCATCTAG	22	15
16	+	1026	ATGTGGATTTTCCATCTAGAA	21	18
5	+	1033	TTTTCCATCTAGAAAAGA	18	4
3	+	1034	TTTCCATCTAGAAAAGAAGCT	21	5
11	+	1035	TTCCATCTAGAAAAGAAGCTC	21	6
60	+	1035	TTCCATCTAGAAAAGAAGCTCT	22	6

11	+	1036	TCCATCTAGAAAAGAAGCTCT	21	7
18	+	1037	CCATCTAGAAAAGAAGCTCTT	21	8
7	+	1037	CCATCTAGAAAAGAAGCTCTTG	22	8
4	+	1038	CATCTAGAAAAGAAGCTCTTG	21	9
6	+	1038	CATCTAGAAAAGAAGCTCTTGA	22	9
28	+	1039	ATCTAGAAAAGAAGCTCTTGA	21	10
34	+	1039	ATCTAGAAAAGAAGCTCT	18	10
1	+	1040	TCTAGAAAAGAAGCTCTTGAG	21	11
92	+	1040	TCTAGAAAAGAAGCTCTTGAGA	22	11
82	+	1041	CTAGAAAAGAAGCTCTTGAGA	21	12
23	+	1042	TAGAAAAGAAGCTCTTGAGAT	21	13
68	+	1042	TAGAAAAGAAGCTCTTGAGATC	22	13
77	+	1042	TAGAAAAGAAGCTCTTGAG	19	13
1	+	1043	AGAAAAGAAGCTCTTGAG	18	14
6	+	1043	AGAAAAGAAGCTCTTGAGATC	21	14
27	+	1045	AAAAGAAGCTCTTGAGATCTT	21	16
49	+	1050	AAGCTCTTGAGATCTTTTGCA	21	0
13	+	1051	AGCTCTTGAGATCTTTTGCAG	21	1
27	+	1051	AGCTCTTGAGATCTTTTGCAGA	22	1
1	+	1053	CTCTTGAGATCTTTTGCAGAT	21	3
4	+	1054	TCTTGAGATCTTTTGCAGATGTGC	24	4
53	+	1054	TCTTGAGATCTTTTGCAGATG	21	4
9	+	1054	TCTTGAGATCTTTTGCAGATGT	22	4
44	+	1055	CTTGAGATCTTTTGCAGATGTG	22	5
44	+	1056	TTGAGATCTTTTGCAGATGTG	21	6
56	+	1056	TTGAGATCTTTTGCAGATGTGC	22	6
62	+	1057	TGAGATCTTTTGCAGATGTGC	21	7
21	+	1058	GAGATCTTTTGCAGATGTGCT	21	8
15	+	1062	TCTTTTGCAGATGTGCTTTTA	21	12
21	+	1064	TTTTGCAGATGTGCTTTTAGAC	22	14
93	+	1064	TTTTGCAGATGTGCTTTTAGA	21	14
39	+	1065	TTTGCAGATGTGCTTTTAGACA	22	15
76	+	1065	TTTGCAGATGTGCTTTTAGAC	21	15
273	+	1066	TTGCAGATGTGCTTTTAGACA	21	16
11	+	1067	TGCAGATGTGCTTTTAGACAA	21	17
4	+	1069	CAGATGTGCTTTTAGACAAA	20	19
75	+	1069	CAGATGTGCTTTTAGACAAAGC	22	19
13	+	1075	TGCTTTTAGACAAAGCTCTGCA	22	4
13	+	1077	CTTTTAGACAAAGCTCTGCAC	21	6
32	+	1077	CTTTTAGACAAAGCTCTGCACC	22	6
109	+	1078	TTTTAGACAAAGCTCTGCACC	21	7
7	+	1078	TTTTAGACAAAGCTCTGCAC	20	7
20	+	1079	TTTAGACAAAGCTCTGCACCTG	22	8
40	+	1079	TTTAGACAAAGCTCTGCACCTGA	23	8

77	+	1079	TTTAGACAAAGCTCTGCACCT	21	8
3	+	1080	TTAGACAAAGCTCTGCACCTG	21	9
91	+	1080	TTAGACAAAGCTCTGCACCTGA	22	9
101	+	1081	TAGACAAAGCTCTGCACCTGA	21	10
1	+	1081	TAGACAAAGCTCTGCACCTGAT	22	10
4	+	1082	AGACAAAGCTCTGCACCTGAT	21	11
9	+	1083	GACAAAGCTCTGCACCTGATAC	22	12
27	+	1084	ACAAAGCTCTGCACCTGATAC	21	13
2	+	1086	AAAGCTCTGCACCTGATACGAT	22	15
459	+	1086	AAAGCTCTGCACCTGATACGA	21	15
135	+	1087	AAGCTCTGCACCTGATACGAT	21	16
3	+	1087	AAGCTCTGCACCTGATACGA	20	16
2	+	1088	AGCTCTGCACCTGATACGATT	21	17
2	+	1089	GCTCTGCACCTGATACGATTC	21	18
6	+	1090	CTCTGCACCTGATACGATTCTA	22	19
161	+	1091	TCTGCACCTGATACGATTCTAA	22	20
18	+	1091	TCTGCACCTGATACGATTCTA	21	20
1	+	1092	CTGCACCTGATACGATTCTA	20	0
22	+	1093	TGCACCTGATACGATTCTAAAG	22	1
2	+	1095	CACCTGATACGATTCTAAAGC	21	3
1	+	1096	ACCTGATACGATTCTAAAG	19	4
99	+	1096	ACCTGATACGATTCTAAAGCT	21	4
114	+	1097	CCTGATACGATTCTAAAGCTTG	22	5
29	+	1097	CCTGATACGATTCTAAAGCTT	21	5
7	+	1099	TGATACGATTCTAAAGCTTGCA	22	7
84	+	1099	TGATACGATTCTAAAGCTTGC	21	7
17	+	1100	GATACGATTCTAAAGCTTGCA	21	8
26	+	1100	GATACGATTCTAAAGCT	17	8
190	+	1101	ATACGATTCTAAAGCTTGCAGA	22	9
3	+	1101	ATACGATTCTAAAGCTTGCAGAA	23	9
79	+	1101	ATACGATTCTAAAGCTTGCAG	21	9
495	+	1102	TACGATTCTAAAGCTTGCAGA	21	10
13	+	1103	ACGATTCTAAAGCTTGCAG	19	11
19	+	1103	ACGATTCTAAAGCTTGCAGAA	21	11
1	+	1103	ACGATTCTAAAGCTTGCAGA	20	11
35	+	1104	CGATTCTAAAGCTTGCAGAAC	21	12
258	+	1106	ATTCTAAAGCTTGCAGAACGA	21	14
59	+	1106	ATTCTAAAGCTTGCAGAACGAG	22	14
1	+	1107	TTCTAAAGCTTGCAGAACGA	20	15
359	+	1107	TTCTAAAGCTTGCAGAACGAG	21	15
6	+	1108	TCTAAAGCTTGCAGAACGAGTA	22	16
9	+	1108	TCTAAAGCTTGCAGAACGAGT	21	16
9	+	1109	CTAAAGCTTGCAGAACGAGTA	21	17
8	+	1110	TAAAGCTTGCAGAACGAGTAAC	22	18

10	+	1113	AGCTTGCAGAACGAGTAACAGA	22	0
43	+	1113	AGCTTGCAGAACGAGTAACAG	21	0
34	+	1115	CTTGCAGAACGAGTAACAGAG	21	2
5	+	1115	CTTGCAGAACGAGTAACAGAGCT	23	2
62	+	1115	CTTGCAGAACGAGTAACAGAGC	22	2
1166	+	1116	TTGCAGAACGAGTAACAGAGC	21	3
11	+	1116	TTGCAGAACGAGTAACA	17	3
15	+	1116	TTGCAGAACGAGTAACAGAGCT	22	3
3	+	1116	TTGCAGAACGAGTAACAGA	19	3
7	+	1117	TGCAGAACGAGTAACAGA	18	4
821	+	1117	TGCAGAACGAGTAACAGAGCT	21	4
26	+	1118	GCAGAACGAGTAACAGAGCTT	21	5
7	+	1118	GCAGAACGAGTAACAGAGC	19	5
5	+	1119	CAGAACGAGTAACAGAGCTTT	21	6
48	+	1122	AACGAGTAACAGAGCTTTGTG	21	9
19	+	1123	ACGAGTAACAGAGCTTTGTGGT	22	10
3	+	1123	ACGAGTAACAGAGCTTTGTGGTAA	24	10
55	+	1123	ACGAGTAACAGAGCTTTGTGG	21	10
14	+	1124	CGAGTAACAGAGCTTTGTGGTA	22	11
38	+	1124	CGAGTAACAGAGCTTTGTGGT	21	11
133	+	1125	GAGTAACAGAGCTTTGTGGTA	21	12
30	+	1126	AGTAACAGAGCTTTGTGGTAA	21	13
2	+	1127	GTAACAGAGCTTTGTGGTAATC	22	14
24	+	1128	TAACAGAGCTTTGTGGTAATCT	22	15
7	+	1128	TAACAGAGCTTTGTGGTAATC	21	15
12	+	1130	ACAGAGCTTTGTGGTAATCTTCCA	24	17
1	+	1130	ACAGAGCTTTGTGGTAATCTT	21	17
7	+	1130	ACAGAGCTTTGTGGTAATC	19	17
12	+	1133	GAGCTTTGTGGTAATCTTCCA	21	20
1	+	1138	TTGTGGTAATCTTCCATTGGGTCTCTGTGT	30	4
142	+	1141	TGGTAATCTTCCATTGGGTCTC	22	7
5	+	1142	GGTAATCTTCCATTGGGTCTC	21	8
120	+	1144	TAATCTTCCATTGGGTCTCTGT	22	10
16	+	1144	TAATCTTCCATTGGGTCTCTG	21	10
105	+	1145	AATCTTCCATTGGGTCTCTGT	21	11
11	+	1145	AATCTTCCATTGGGTCTCTGTG	22	11
2	+	1145	AATCTTCCATTGGGTCTCTGTGTC	24	11
51	+	1146	ATCTTCCATTGGGTCTCTGTGT	22	12
66	+	1146	ATCTTCCATTGGGTCTCTGTG	21	12
4	+	1147	TCTTCCATTGGGTCTCTGTGT	21	13
97	+	1147	TCTTCCATTGGGTCTCTGTGTC	22	13
2	+	1148	CTTCCATTGGGTCTCTGTG	19	14
2	+	1148	CTTCCATTGGGTCTCTGTGTCA	22	14
89	+	1148	CTTCCATTGGGTCTCTGTGTC	21	14

16	+	1150	TCCATTGGGTCTCTGTGTCAT	21	16
13	+	1151	CCATTGGGTCTCTGTGTCATAGG	23	17
8	+	1151	CCATTGGGTCTCTGTGTCATA	21	17
5	+	1152	CATTGGGTCTCTGTGTCATAGG	22	18
529	+	1153	ATTGGGTCTCTGTGTCATAGG	21	19
8	+	1153	ATTGGGTCTCTGTGTCATAGGT	22	19
18	+	1154	TTGGGTCTCTGTGTCATAGGTT	22	20
517	+	1154	TTGGGTCTCTGTGTCATAGGT	21	20
6	+	1154	TTGGGTCTCTGTGTCATAGG	20	20
1	+	1155	TGGGTCTCTGTGTCATAGGT	20	0
345	+	1155	TGGGTCTCTGTGTCATAGGTT	21	0
4	+	1156	GGGTCTCTGTGTCATAGGTTC	21	1
8	+	1158	GTCTCTGTGTCATAGGTTCAT	21	3
9	+	1158	GTCTCTGTGTCATAGGTTCATC	22	3
133	+	1159	TCTCTGTGTCATAGGTTCATC	21	4
9	+	1159	TCTCTGTGTCATAGGTTCAT	20	4
1	+	1160	CTCTGTGTCATAGGTTCAT	19	5
8	+	1160	CTCTGTGTCATAGGTTCATCT	21	5
48	+	1161	TCTGTGTCATAGGTTCATC	19	6
65	+	1161	TCTGTGTCATAGGTTCATCTT	21	6
13	+	1162	CTGTGTCATAGGTTCATCTTT	21	7
1	+	1162	CTGTGTCATAGGTTCATCTT	20	7
182	+	1163	TGTGTCATAGGTTCATCTTTA	21	8
9	+	1165	TGTCATAGGTTCATCTTTACA	21	10
59	+	1167	TCATAGGTTCATCTTTACACG	21	12
6	+	1167	TCATAGGTTCATCTTTACAC	20	12
99	+	1167	TCATAGGTTCATCTTTACACGG	22	12
1	+	1168	CATAGGTTCATCTTTACACGGG	22	13
85	+	1168	CATAGGTTCATCTTTACACGG	21	13
25	+	1169	ATAGGTTCATCTTTACACGGGA	22	14
365	+	1169	ATAGGTTCATCTTTACACGGG	21	14
2	+	1170	TAGGTTCATCTTTACACGGGAAA	23	15
341	+	1170	TAGGTTCATCTTTACACGGGA	21	15
9	+	1170	TAGGTTCATCTTTACACGGGAA	22	15
5	+	1171	AGGTTCATCTTTACACGGGAAA	22	16
99	+	1171	AGGTTCATCTTTACACGGGAA	21	16
31	+	1172	GGTTCATCTTTACACGGGAAA	21	17
31	+	1172	GGTTCATCTTTACACGGGA	19	17
3	+	1176	CATCTTTACACGGGAAAACTG	21	0
219	+	1177	ATCTTTACACGGGAAAACTGA	21	1
6	+	1177	ATCTTTACACGGGAAAA	17	1
17	+	1178	TCTTTACACGGGAAAACTGAGG	22	2
19	+	1178	TCTTTACACGGGAAAACTGAG	21	2
74	+	1179	CTTTACACGGGAAAACTGAGGA	22	3

8	+	1179	CTTTACACGGGAAAACTGAGG	21	3
2	+	1180	TTTACACGGGAAAACTGAGGATG	23	4
3312	+	1180	TTTACACGGGAAAACTGAGGA	21	4
3	+	1180	TTTACACGGGAAAACTGAGGAT	22	4
21	+	1181	TTACACGGGAAAACTGAGGAT	21	5
3	+	1181	TTACACGGGAAAACTGAGGA	20	5
4	+	1181	TTACACGGGAAAACTGAGGATGAG	24	5
201	+	1182	TACACGGGAAAACTGAGGATG	21	6
10	+	1183	ACACGGGAAAACTGAGGATGAGTG	24	7
10	+	1183	ACACGGGAAAACTGAGGATGA	21	7
55	+	1183	ACACGGGAAAACTGAGGATGAG	22	7
10	+	1184	CACGGGAAAACTGAGGATGAGT	22	8
673	+	1184	CACGGGAAAACTGAGGATGAG	21	8
11	+	1185	ACGGGAAAACTGAGGATGAGTG	22	9
1	+	1185	ACGGGAAAACTGAGGATGAG	20	9
32	+	1185	ACGGGAAAACTGAGGATGAGTGGG	24	9
45	+	1185	ACGGGAAAACTGAGGATGAGT	21	9
461	+	1186	CGGGAAAACTGAGGATGAGTG	21	10
1	+	1187	GGGAAAACTGAGGATGAGTG	20	11
5	+	1188	GGAAAACTGAGGATGAGTGGGA	22	12
859	+	1188	GGAAAACTGAGGATGAGTGGG	21	12
1	+	1189	GAAAACTGAGGATGAGTGGGAA	22	13
90	+	1189	GAAAACTGAGGATGAGTGGGA	21	13
1	+	1190	AAAACTGAGGATGAGTGGGAAA	22	14
831	+	1190	AAAACTGAGGATGAGTGGGAA	21	14
1	+	1191	AAACTGAGGATGAGTGGGAA	20	15
61	+	1191	AAACTGAGGATGAGTGGGAAA	21	15
48	+	1192	AACTGAGGATGAGTGGGAAAT	21	16
29	+	1193	ACTGAGGATGAGTGGGAAATT	21	17
5	+	1193	ACTGAGGATGAGTGGGAAATTT	22	17
1	+	1194	CTGAGGATGAGTGGGAAATTTTA	23	18
59	+	1194	CTGAGGATGAGTGGGAAATTTT	22	18
29	+	1195	TGAGGATGAGTGGGAAATTTTA	22	19
82	+	1195	TGAGGATGAGTGGGAAATTTT	21	19
2	+	1197	AGGATGAGTGGGAAATTTTAA	21	0
127	+	1200	ATGAGTGGGAAATTTTAATTC	21	3
165	+	1201	TGAGTGGGAAATTTTAATTCGC	22	4
19	+	1201	TGAGTGGGAAATTTTAATTCG	21	4
1	+	1201	TGAGTGGGAAATTTTAATTCGCA	23	4
36	+	1202	GAGTGGGAAATTTTAATTCGC	21	5
78	+	1203	AGTGGGAAATTTTAATTCGCA	21	6
8	+	1204	GTGGGAAATTTTAATTCGCAGA	22	7
23	+	1205	TGGGAAATTTTAATTCGCAGAC	22	8
36	+	1205	TGGGAAATTTTAATTCGCAGA	21	8

5	+	1205	TGGGAAATTTTAATTCGCAGACT	23	8
3	+	1206	GGGAAATTTTAATTCGCAGAC	21	9
4	+	1206	GGGAAATTTTAATTCGCAGACTAGA	25	9
112	+	1209	AAATTTTAATTCGCAGACTAGA	22	12
18	+	1209	AAATTTTAATTCGCAGACTAG	21	12
188	+	1210	AATTTTAATTCGCAGACTAGA	21	13
109	+	1211	ATTTTAATTCGCAGACTAGAAA	22	14
65	+	1211	ATTTTAATTCGCAGACTAGAA	21	14
22	+	1212	TTTTAATTCGCAGACTAGAAA	21	15
55	+	1212	TTTTAATTCGCAGACTAGAAAT	22	15
258	+	1213	TTTAATTCGCAGACTAGAAAT	21	16
54	+	1213	TTTAATTCGCAGACTAGAAATT	22	16
421	+	1214	TTAATTCGCAGACTAGAAATT	21	17
8	+	1214	TTAATTCGCAGACTAGAAAT	20	17
44	+	1216	AATTCGCAGACTAGAAATTAG	21	19
125	+	1217	ATTCGCAGACTAGAAATTAGT	21	20
3	+	1217	ATTCGCAGACTAGAAATTAG	20	20
7	+	1223	AGACTAGAAATTAGTCTTGAT	21	5
11	+	1226	CTAGAAATTAGTCTTGATCGAG	22	8
2	+	1226	CTAGAAATTAGTCTTGATCGA	21	8
100	+	1227	TAGAAATTAGTCTTGATCGAGA	22	9
48	+	1227	TAGAAATTAGTCTTGATCGAG	21	9
212	+	1228	AGAAATTAGTCTTGATCGAGA	21	10
4	+	1229	GAAATTAGTCTTGATCGAGAT	21	11
276	+	1230	AAATTAGTCTTGATCGAGATA	21	12
6	+	1231	AATTAGTCTTGATCGAGATAA	21	13
36	+	1233	TTAGTCTTGATCGAGATAACGA	22	15
24	+	1234	TAGTCTTGATCGAGATAACGA	21	16
388	+	1235	AGTCTTGATCGAGATAACGAG	21	17
8	+	1235	AGTCTTGATCGAGATAACGAGGC	23	17
95	+	1235	AGTCTTGATCGAGATAACGAGG	22	17
17	+	1236	GTCTTGATCGAGATAACGAGG	21	18
24	+	1236	GTCTTGATCGAGATAACGAGGC	22	18
430	+	1237	TCTTGATCGAGATAACGAGGC	21	19
5	+	1237	TCTTGATCGAGATAACGAGGCA	22	19
21	+	1238	CTTGATCGAGATAACGAGGCA	21	20
3	+	1238	CTTGATCGAGATAACGAGGC	20	20
7	+	1239	TTGATCGAGATAACGAGGCAC	21	0
24	+	1241	GATCGAGATAACGAGGCACAA	21	2
9	+	1242	ATCGAGATAACGAGGCACAAC	21	3
10	+	1243	TCGAGATAACGAGGCACAACT	21	4
5	+	1244	CGAGATAACGAGGCACAACTT	21	5
5	+	1246	AGATAACGAGGCACAACTTAGA	22	7
179	+	1248	ATAACGAGGCACAACTTAGAG	21	9

3	+	1248	ATAACGAGGCACAACTTAGAGT	22	9
15	+	1249	TAACGAGGCACAACTTAGAGT	21	10
19	+	1249	TAACGAGGCACAACTTAGAGTT	22	10
2	+	1250	AACGAGGCACAACTTAGAGTT	21	11
1	+	1252	CGAGGCACAACTTAGAGTTGG	21	13
85	+	1252	CGAGGCACAACTTAGAGTTGGG	22	13
45	+	1253	GAGGCACAACTTAGAGTTGGG	21	14
9	+	1253	GAGGCACAACTTAGAGTTGGGT	22	14
14	+	1254	AGGCACAACTTAGAGTTGGGTA	22	15
6	+	1254	AGGCACAACTTAGAGTTGGGT	21	15
14	+	1255	GGCACAACTTAGAGTTGGGTA	21	16
1	+	1255	GGCACAACTTAGAGTTGGG	19	16
1	+	1256	GCACAACTTAGAGTTGGG	18	17
5	+	1256	GCACAACTTAGAGTTGGGTA	20	17
5	+	1258	ACAACTTAGAGTTGGGTATGAT	22	19
7	+	1258	ACAACTTAGAGTTGGGTATGA	21	19
213	+	1259	CAACTTAGAGTTGGGTATGAT	21	20
49	+	1260	AACTTAGAGTTGGGTATGATAG	22	0
94	+	1260	AACTTAGAGTTGGGTATGATA	21	0
168	+	1261	ACTTAGAGTTGGGTATGATAGC	22	1
28	+	1261	ACTTAGAGTTGGGTATGATAGCTT	24	1
416	+	1261	ACTTAGAGTTGGGTATGATAG	21	1
11	+	1262	CTTAGAGTTGGGTATGATAGC	21	2
1	+	1262	CTTAGAGTTGGGTATGATAGCTT	23	2
37	+	1262	CTTAGAGTTGGGTATGATAGCT	22	2
1239	+	1263	TTAGAGTTGGGTATGATAGCT	21	3
40	+	1263	TTAGAGTTGGGTATGATAGCTT	22	3
5	+	1263	TTAGAGTTGGGTATGATAG	19	3
8	+	1263	TTAGAGTTGGGTATGATAGC	20	3
2	+	1264	TAGAGTTGGGTATGATAGCTTA	22	4
914	+	1264	TAGAGTTGGGTATGATAGCTT	21	4
6	+	1265	AGAGTTGGGTATGATAGCTTA	21	5
2	+	1266	GAGTTGGGTATGATAGCTTACATG	24	6
475	+	1269	TTGGGTATGATAGCTTACATG	21	9
16	+	1270	TGGGTATGATAGCTTACATGA	21	10
21	+	1271	GGGTATGATAGCTTACATGAG	21	11
33	+	1272	GGTATGATAGCTTACATGAGA	21	12
3	+	1273	GTATGATAGCTTACATGAGAA	21	13
5	+	1273	GTATGATAGCTTACATGAGAAC	22	13
149	+	1274	TATGATAGCTTACATGAGAACG	22	14
96	+	1274	TATGATAGCTTACATGAGAAC	21	14
13	+	1275	ATGATAGCTTACATGAGAACGA	22	15
59	+	1275	ATGATAGCTTACATGAGAACG	21	15
132	+	1276	TGATAGCTTACATGAGAACGA	21	16

66	+	1276	TGATAGCTTACATGAGAACGAG	22	16
86	+	1277	GATAGCTTACATGAGAACGAG	21	17
52	+	1278	ATAGCTTACATGAGAACGAGCA	22	18
552	+	1278	ATAGCTTACATGAGAACGAGC	21	18
5	+	1278	ATAGCTTACATGAGAACGAG	20	18
2	+	1280	AGCTTACATGAGAACGAGCAA	21	20
107	+	1283	TTACATGAGAACGAGCAAGCT	21	2
1	+	1283	TTACATGAGAACGAGCAAGCTT	22	2
9	+	1284	TACATGAGAACGAGCAAGCTT	21	3
59	+	1285	ACATGAGAACGAGCAAGCTTT	21	4
28	+	1296	AGCAAGCTTTATTTCTCAGCA	21	15
4	+	1297	GCAAGCTTTATTTCTCAGCAT	21	16
29	+	1302	CTTTATTTCTCAGCATTGCAGT	22	0
68	+	1302	CTTTATTTCTCAGCATTGCAG	21	0
142	+	1303	TTTATTTCTCAGCATTGCAGT	21	1
4	+	1303	TTTATTTCTCAGCATTGCAGTC	22	1
104	+	1304	TTATTTCTCAGCATTGCAGTC	21	2
14	+	1305	TATTTCTCAGCATTGCAGTCTT	22	3
29	+	1305	TATTTCTCAGCATTGCAGTCT	21	3
47	+	1306	ATTTCTCAGCATTGCAGTCTT	21	4
14	+	1307	TTTCTCAGCATTGCAGTCTTCT	22	5
77	+	1307	TTTCTCAGCATTGCAGTCTTC	21	5
13	+	1308	TTCTCAGCATTGCAGTCTTCTT	22	6
8	+	1308	TTCTCAGCATTGCAGTCTTCT	21	6
65	+	1309	TCTCAGCATTGCAGTCTTCTT	21	7
23	+	1311	TCAGCATTGCAGTCTTCTTCA	21	9
43	+	1312	CAGCATTGCAGTCTTCTTCAA	21	10
29	+	1313	AGCATTGCAGTCTTCTTCAAC	21	11
3	+	1315	CATTGCAGTCTTCTTCAACTA	21	13
21	+	1321	AGTCTTCTTCAACTATAAAGA	21	19
15	+	1323	TCTTCTTCAACTATAAAGACC	21	0
23	+	1324	CTTCTTCAACTATAAAGACCGT	22	1
24	+	1325	TTCTTCAACTATAAAGACCGTC	22	2
8	+	1325	TTCTTCAACTATAAAGACCGT	21	2
188	+	1326	TCTTCAACTATAAAGACCGTC	21	3
1	+	1326	TCTTCAACTATAAAGACCGTCA	22	3
6	+	1326	TCTTCAACTATAAAGACCGTCAGCT	25	3
7	+	1327	CTTCAACTATAAAGACCGTCAG	22	4
208	+	1328	TTCAACTATAAAGACCGTCAGC	22	5
39	+	1328	TTCAACTATAAAGACCGTCAG	21	5
1	+	1329	TCAACTATAAAGACCGTCA	19	6
227	+	1329	TCAACTATAAAGACCGTCAGC	21	6
45	+	1329	TCAACTATAAAGACCGTCAGCT	22	6
35	+	1330	CAACTATAAAGACCGTCAGCT	21	7

37	+	1331	AACTATAAAGACCGTCAGCTT	21	8
35	+	1332	ACTATAAAGACCGTCAGCTTGT	22	9
3	+	1332	ACTATAAAGACCGTCAGCTTGTGA	24	9
96	+	1332	ACTATAAAGACCGTCAGCTTG	21	9
6	+	1333	CTATAAAGACCGTCAGCTTGT	21	10
122	+	1334	TATAAAGACCGTCAGCTTGTG	21	11
2	+	1334	TATAAAGACCGTCAGCTTGTGA	22	11
148	+	1335	ATAAAGACCGTCAGCTTGTGA	21	12
22	+	1335	ATAAAGACCGTCAGCTTGTGAT	22	12
12	+	1336	TAAAGACCGTCAGCTTGTGATG	22	13
211	+	1336	TAAAGACCGTCAGCTTGTGAT	21	13
4	+	1336	TAAAGACCGTCAGCTTGTGA	20	13
176	+	1337	AAAGACCGTCAGCTTGTGATG	21	14
1	+	1338	AAGACCGTCAGCTTGTGATGGCCA	24	15
23	+	1338	AAGACCGTCAGCTTGTGATGG	21	15
25	+	1338	AAGACCGTCAGCTTGTGATGGC	22	15
13	+	1344	GTCAGCTTGTGATGGCCATGC	21	0
13	+	1345	TCAGCTTGTGATGGCCATGCT	21	1
16	+	1346	CAGCTTGTGATGGCCATGCTC	21	2
178	+	1349	CTTGTGATGGCCATGCTCCTT	21	5
11	+	1350	TTGTGATGGCCATGCTCCTTG	21	6
12	+	1350	TTGTGATGGCCATGCTCCTT	20	6
3	+	1350	TTGTGATGGCCATGCTCCTTGA	22	6
10	+	1351	TGTGATGGCCATGCTCCTTGAC	22	7
66	+	1351	TGTGATGGCCATGCTCCTTGA	21	7
1	+	1355	ATGGCCATGCTCCTTGACAGT	21	11
10	+	1356	TGGCCATGCTCCTTGACAGTAA	22	12
13	+	1356	TGGCCATGCTCCTTGACAGTA	21	12
10	+	1358	GCCATGCTCCTTGACAGTAAC	21	14
3	+	1359	CCATGCTCCTTGACAGTAACCT	22	15
5	+	1360	CATGCTCCTTGACAGTAACCTA	22	16
61	+	1360	CATGCTCCTTGACAGTAACCT	21	16
13	+	1361	ATGCTCCTTGACAGTAACCTA	21	17
18	+	1361	ATGCTCCTTGACAGTAACCTAGA	23	17
63	+	1362	TGCTCCTTGACAGTAACCTAGA	22	18
7	+	1362	TGCTCCTTGACAGTAACCTAG	21	18
14	+	1364	CTCCTTGACAGTAACCTAGATG	22	20
26	+	1365	TCCTTGACAGTAACCTAGATG	21	0
8	+	1365	TCCTTGACAGTAACCTAGATGT	22	0
35	+	1366	CCTTGACAGTAACCTAGATGT	21	1
1	+	1367	CTTGACAGTAACCTAGATGTC	21	2
3	+	1369	TGACAGTAACCTAGATGTCGAGT	23	4
69	+	1370	GACAGTAACCTAGATGTCGAG	21	5
9	+	1370	GACAGTAACCTAGATGTCGAGT	22	5

114	+	1371	ACAGTAACCTAGATGTCGAGT	21	6
262	+	1371	ACAGTAACCTAGATGTCGAGTA	22	6
134	+	1372	CAGTAACCTAGATGTCGAGTA	21	7
5	+	1372	CAGTAACCTAGATGTCGAGT	20	7
15	+	1373	AGTAACCTAGATGTCGAGTA	20	8
31	+	1373	AGTAACCTAGATGTCGAGTAT	21	8
3	+	1373	AGTAACCTAGATGTCGAGTATG	22	8
153	+	1374	GTAACCTAGATGTCGAGTATGG	22	9
15	+	1374	GTAACCTAGATGTCGAGTATG	21	9
16	+	1375	TAACCTAGATGTCGAGTATGGG	22	10
1	+	1376	AACCTAGATGTCGAGTATGGGT	22	11
230	+	1376	AACCTAGATGTCGAGTATGGG	21	11
9	+	1376	AACCTAGATGTCGAGTATGG	20	11
9	+	1378	CCTAGATGTCGAGTATGGGTT	21	13
127	+	1380	TAGATGTCGAGTATGGGTTAAG	22	15
2	+	1380	TAGATGTCGAGTATGGGTTAA	21	15
4	+	1380	TAGATGTCGAGTATGGGTTA	20	15
3	+	1381	AGATGTCGAGTATGGGTTAAGAAC	24	16
4	+	1381	AGATGTCGAGTATGGGTTAA	20	16
70	+	1381	AGATGTCGAGTATGGGTTAAGA	22	16
79	+	1381	AGATGTCGAGTATGGGTTAAG	21	16
9	+	1382	GATGTCGAGTATGGGTTAAGA	21	17
257	+	1383	ATGTCGAGTATGGGTTAAGAA	21	18
2	+	1383	ATGTCGAGTATGGGTTAAGAACC	23	18
1	+	1384	TGTCGAGTATGGGTTAAGAA	20	19
8	+	1384	TGTCGAGTATGGGTTAAGAAC	21	19
9	+	1384	TGTCGAGTATGGGTTAAGAACC	22	19
11	+	1387	CGAGTATGGGTTAAGAACCCT	21	1
1	+	1398	TAAGAACCCTCGCCAATAAATCTCT	25	12
2	+	1398	TAAGAACCCTCGCCAATAAATCTC	24	12
45	+	1401	GAACCCTCGCCAATAAATCTC	21	15
18	+	1402	AACCCTCGCCAATAAATCTCT	21	16
1	+	1402	AACCCTCGCCAATAAATCTCTA	22	16
3	+	1403	ACCCTCGCCAATAAATCTCTA	21	17
7	+	1407	TCGCCAATAAATCTCTAATAC	21	0
10	+	1417	ATCTCTAATACATATATCTAGG	22	10
4	+	1417	ATCTCTAATACATATATCTAG	21	10
51	+	1417	ATCTCTAATACATATATCTAGGA	23	10
10	+	1418	TCTCTAATACATATATCTAGGAAT	24	11
130	+	1418	TCTCTAATACATATATCTAGGA	22	11
8	+	1418	TCTCTAATACATATATCTAGG	21	11
128	+	1419	CTCTAATACATATATCTAGGA	21	12
2	+	1420	TCTAATACATATATCTAGGA	20	13
26	+	1421	CTAATACATATATCTAGGAAT	21	14

81	+	1422	TAATACATATATCTAGGAATG	21	15
8	+	1423	AATACATATATCTAGGAATGA	21	16
37	+	1424	ATACATATATCTAGGAATGAG	21	17
84	+	1424	ATACATATATCTAGGAATGAGA	22	17
6	+	1429	TATATCTAGGAATGAGAAAATAGT	24	1
104	+	1430	ATATCTAGGAATGAGAAAATA	21	2
128	+	1433	TCTAGGAATGAGAAAATAGTG	21	5
6	+	1433	TCTAGGAATGAGAAAATAGTGA	22	5
1	+	1434	CTAGGAATGAGAAAATAGTGA	21	6
114	+	1435	TAGGAATGAGAAAATAGTGATG	22	7
5	+	1436	AGGAATGAGAAAATAGTGATG	21	8
7	+	1441	TGAGAAAATAGTGATGCATAAC	22	13
5	+	1444	GAAAATAGTGATGCATAACTT	21	16
17	+	1451	GTGATGCATAACTTACTACAA	21	2
4	+	1451	GTGATGCATAACTTACTACAAC	22	2
8	+	1454	ATGCATAACTTACTACAACATG	22	5
6	+	1457	CATAACTTACTACAACATGTG	21	8
14	+	1458	ATAACTTACTACAACATGTGGG	22	9
63	+	1458	ATAACTTACTACAACATGTGG	21	9
9	+	1459	TAACTTACTACAACATGTGGG	21	10
3	+	1460	AACTTACTACAACATGTGGG	20	11
3	+	1460	AACTTACTACAACATGTGGGT	21	11
37	+	1463	TTACTACAACATGTGGGTAGA	21	14
12	+	1467	TACAACATGTGGGTAGACAAGC	22	18
9	+	1467	TACAACATGTGGGTAGACAAG	21	18
43	+	1468	ACAACATGTGGGTAGACAAGC	21	19
4	+	1468	ACAACATGTGGGTAGACAAGCC	22	19
1	+	1469	CAACATGTGGGTAGACAAGC	20	20
2	+	1469	CAACATGTGGGTAGACAAGCC	21	20
153	+	1470	AACATGTGGGTAGACAAGCCA	21	0
9	+	1471	ACATGTGGGTAGACAAGCCATT	22	1
10	+	1476	TGGGTAGACAAGCCATTCAAA	21	6
1	+	1476	TGGGTAGACAAGCCATTCAA	20	6
27	+	1476	TGGGTAGACAAGCCATTCAAAG	22	6
7	+	1477	GGGTAGACAAGCCATTCAAAGA	22	7
2	+	1478	GGTAGACAAGCCATTCAAAGA	21	8
79	+	1479	GTAGACAAGCCATTCAAAGAC	21	9
4	+	1480	TAGACAAGCCATTCAAAGACA	21	10
6	+	1480	TAGACAAGCCATTCAAAGAC	20	10
3	+	1483	ACAAGCCATTCAAAGACAAGA	21	13
4	+	1484	CAAGCCATTCAAAGACAAGA	20	14
240	+	1486	AGCCATTCAAAGACAAGAACCT	22	16
5	+	1486	AGCCATTCAAAGACAAGAACC	21	16
4	+	1487	GCCATTCAAAGACAAGAACCTT	22	17

52	+	1487	GCCATTCAAAGACAAGAACCT	21	17
19	+	1488	CCATTCAAAGACAAGAACCTT	21	18
36	+	1490	ATTCAAAGACAAGAACCTTGG	21	20
184	+	1491	TTCAAAGACAAGAACCTTGGA	21	0
31	+	1492	TCAAAGACAAGAACCTTGGAA	21	1
15	+	1494	AAAGACAAGAACCTTGGAAACG	22	3
6	+	1494	AAAGACAAGAACCTTGGAAACGC	23	3
75	+	1494	AAAGACAAGAACCTTGGAAAC	21	3
15	+	1495	AAGACAAGAACCTTGGAAACG	21	4
2	+	1495	AAGACAAGAACCTTGGAAACGC	22	4
47	+	1496	AGACAAGAACCTTGGAAACGC	21	5
94	+	1497	GACAAGAACCTTGGAAACGCC	21	6
1	+	1498	ACAAGAACCTTGGAAACGCC	20	7
4	+	1498	ACAAGAACCTTGGAAACGCCAC	22	7
7	+	1498	ACAAGAACCTTGGAAACGCCA	21	7
9	+	1500	AAGAACCTTGGAAACGCCACA	21	9
6	+	1501	AGAACCTTGGAAACGCCACATC	22	10
34	+	1503	AACCTTGGAAACGCCACATCTT	22	12
3	+	1504	ACCTTGGAAACGCCACATCTT	21	13
3	+	1507	TTGGAAACGCCACATCTTAATA	22	16
1	+	1510	GAAACGCCACATCTTAATAGA	21	19
9	+	1519	CATCTTAATAGATGCTGACGA	21	7
36	+	1520	ATCTTAATAGATGCTGACGAG	21	8
21	+	1521	TCTTAATAGATGCTGACGAGA	21	9
36	+	1521	TCTTAATAGATGCTGACGAGAT	22	9
30	+	1522	CTTAATAGATGCTGACGAGAT	21	10
11	+	1523	TTAATAGATGCTGACGAGATAT	22	11
19	+	1523	TTAATAGATGCTGACGAGATA	21	11
4	+	1524	TAATAGATGCTGACGAGATAT	21	12
29	+	1525	AATAGATGCTGACGAGATATG	21	13
22	+	1526	ATAGATGCTGACGAGATATGCA	22	14
66	+	1526	ATAGATGCTGACGAGATATGC	21	14
55	+	1527	TAGATGCTGACGAGATATGCA	21	15
6	+	1528	AGATGCTGACGAGATATGCAA	21	16
42	+	1530	ATGCTGACGAGATATGCAATG	21	18
26	+	1531	TGCTGACGAGATATGCAATGTC	22	19
3	+	1531	TGCTGACGAGATATGCAATGT	21	19
4	+	1532	GCTGACGAGATATGCAATGTC	21	20
33	+	1533	CTGACGAGATATGCAATGTCCT	22	0
12	+	1534	TGACGAGATATGCAATGTCCTT	22	1
6	+	1534	TGACGAGATATGCAATGTCCT	21	1
16	+	1536	ACGAGATATGCAATGTCCTTG	21	3
2	+	1537	CGAGATATGCAATGTCCTTGAA	22	4
3	+	1538	GAGATATGCAATGTCCTTGAA	21	5

2	+	1541	ATATGCAATGTCCTTGAAAAT	21	8
76	+	1541	ATATGCAATGTCCTTGAAAATG	22	8
22	+	1542	TATGCAATGTCCTTGAAAATGA	22	9
213	+	1543	ATGCAATGTCCTTGAAAATGA	21	10
1	+	1544	TGCAATGTCCTTGAAAATGAT	21	11
4	+	1544	TGCAATGTCCTTGAAAATGATA	22	11
28	+	1568	GATGCTAGAATTGTGTCAGGG	21	14
1	+	1569	ATGCTAGAATTGTGTCAGGGAT	22	15
377	+	1569	ATGCTAGAATTGTGTCAGGGA	21	15
1	+	1570	TGCTAGAATTGTGTCAGGGA	20	16
20	+	1570	TGCTAGAATTGTGTCAGGGAT	21	16
9	+	1570	TGCTAGAATTGTGTCAGGGATA	22	16
2	+	1571	GCTAGAATTGTGTCAGGGATA	21	17
5	+	1571	GCTAGAATTGTGTCAGGGA	19	17
1	+	1572	CTAGAATTGTGTCAGGGATATC	22	18
93	+	1573	TAGAATTGTGTCAGGGATATC	21	19
1	+	1575	GAATTGTGTCAGGGATATCATT	22	0
4	+	1575	GAATTGTGTCAGGGATATCATTTGAT	26	0
6	+	1575	GAATTGTGTCAGGGATATC	19	0
8	+	1575	GAATTGTGTCAGGGATATCAT	21	0
110	+	1576	AATTGTGTCAGGGATATCATT	21	1
36	+	1576	AATTGTGTCAGGGATATCATTT	22	1
103	+	1577	ATTGTGTCAGGGATATCATTT	21	2
1	+	1577	ATTGTGTCAGGGATATC	17	2
10	+	1578	TTGTGTCAGGGATATCATTTG	21	3
48	+	1578	TTGTGTCAGGGATATCATTTGA	22	3
36	+	1579	TGTGTCAGGGATATCATTTGA	21	4
7	+	1579	TGTGTCAGGGATATCATTTGAT	22	4
37	+	1580	GTGTCAGGGATATCATTTGAT	21	5
48	+	1581	TGTCAGGGATATCATTTGATA	21	6
43	+	1583	TCAGGGATATCATTTGATATA	21	8
7	+	1589	ATATCATTTGATATATCCAGA	21	14
16	+	1592	TCATTTGATATATCCAGAATC	21	17
18	+	1592	TCATTTGATATATCCAGAATCGGC	24	17
7	+	1594	ATTTGATATATCCAGAATCGGC	22	19
8	+	1594	ATTTGATATATCCAGAATCGG	21	19
41	+	1595	TTTGATATATCCAGAATCGGC	21	20
7	+	1595	TTTGATATATCCAGAATCGGCG	22	20
57	+	1596	TTGATATATCCAGAATCGGCGA	22	0
5	+	1596	TTGATATATCCAGAATCGGCG	21	0
1	+	1597	TGATATATCCAGAATCGGCGAA	22	1
3	+	1597	TGATATATCCAGAATCGGCGAAGT	24	1
49	+	1597	TGATATATCCAGAATCGGCGA	21	1
9	+	1598	GATATATCCAGAATCGGCGAA	21	2

137	+	1599	ATATATCCAGAATCGGCGAAG	21	3
3	+	1599	ATATATCCAGAATCGGCGAAGT	22	3
174	+	1600	TATATCCAGAATCGGCGAAGTT	22	4
39	+	1600	TATATCCAGAATCGGCGAAGT	21	4
237	+	1601	ATATCCAGAATCGGCGAAGTT	21	5
24	+	1601	ATATCCAGAATCGGCGAAGTTT	22	5
2	+	1602	TATCCAGAATCGGCGAAGTT	20	6
35	+	1602	TATCCAGAATCGGCGAAGTTTT	22	6
88	+	1602	TATCCAGAATCGGCGAAGTTT	21	6
10	+	1603	ATCCAGAATCGGCGAAGTTTT	21	7
38	+	1604	TCCAGAATCGGCGAAGTTTTTT	22	8
57	+	1604	TCCAGAATCGGCGAAGTTTTT	21	8
57	+	1607	AGAATCGGCGAAGTTTTTTTA	21	11
87	+	1609	AATCGGCGAAGTTTTTTTAAG	21	13
16	+	1610	ATCGGCGAAGTTTTTTTAAGCG	22	14
85	+	1610	ATCGGCGAAGTTTTTTTAAGC	21	14
1	+	1611	TCGGCGAAGTTTTTTTAAGCGA	22	15
21	+	1611	TCGGCGAAGTTTTTTTAAGCG	21	15
29	+	1612	CGGCGAAGTTTTTTTAAGCGA	21	16
3	+	1612	CGGCGAAGTTTTTTTAAGCGAG	22	16
3	+	1613	GGCGAAGTTTTTTTAAGCGAGA	22	17
4	+	1617	AAGTTTTTTTAAGCGAGAGAG	21	0
3	+	1619	GTTTTTTTAAGCGAGAGAGCT	21	2
6	+	1625	TTAAGCGAGAGAGCTTTTAAA	21	8
12	+	1632	AGAGAGCTTTTAAAAGATTGT	21	15
3	+	1633	GAGAGCTTTTAAAAGATTGTGT	22	16
3	+	1634	AGAGCTTTTAAAAGATTGTGTA	22	17
4	+	1637	GCTTTTAAAAGATTGTGTAAT	21	20
3	+	1649	TTGTGTAATCTCCAATTCCTC	21	11
1	+	1650	TGTGTAATCTCCAATTCCT	19	12
36	+	1650	TGTGTAATCTCCAATTCCTCAG	22	12
3	+	1651	GTGTAATCTCCAATTCCTCAG	21	13
16	+	1652	TGTAATCTCCAATTCCTCAGG	21	14
65	+	1652	TGTAATCTCCAATTCCTCAGGG	22	14
13	+	1653	GTAATCTCCAATTCCTCAGGG	21	15
49	+	1654	TAATCTCCAATTCCTCAGGGTG	22	16
7	+	1654	TAATCTCCAATTCCTCAGGGT	21	16
3	+	1656	ATCTCCAATTCCTCAGGGTGT	21	18
10	+	1657	TCTCCAATTCCTCAGGGTGTT	21	19
82	+	1662	AATTCCTCAGGGTGTTTAAGA	21	3
42	+	1664	TTCCTCAGGGTGTTTAAGACT	21	5
5	+	1664	TTCCTCAGGGTGTTTAAGACTG	22	5
83	+	1665	TCCTCAGGGTGTTTAAGACTG	21	6
1015	+	1667	CTCAGGGTGTTTAAGACTGGA	21	8

1	+	1667	CTCAGGGTGTTTAAGACTGGAT	22	8
1	+	1668	TCAGGGTGTTTAAGACTGGA	20	9
25	+	1668	TCAGGGTGTTTAAGACTGGATA	22	9
9	+	1668	TCAGGGTGTTTAAGACTGGAT	21	9
25	+	1669	CAGGGTGTTTAAGACTGGATA	21	10
1	+	1670	AGGGTGTTTAAGACTGGATATGA	23	11
24	+	1670	AGGGTGTTTAAGACTGGATATG	22	11
4	+	1670	AGGGTGTTTAAGACTGGATAT	21	11
1	+	1671	GGGTGTTTAAGACTGGATATG	21	12
4	+	1671	GGGTGTTTAAGACTGGATATGA	22	12
3	+	1672	GGTGTTTAAGACTGGATATGAT	22	13
5	+	1672	GGTGTTTAAGACTGGATATGA	21	13
129	+	1673	GTGTTTAAGACTGGATATGAT	21	14
4	+	1673	GTGTTTAAGACTGGATATGATG	22	14
14	+	1674	TGTTTAAGACTGGATATGATGA	22	15
175	+	1674	TGTTTAAGACTGGATATGATG	21	15
97	+	1675	GTTTAAGACTGGATATGATGA	21	16
32	+	1676	TTTAAGACTGGATATGATGAAA	22	17
99	+	1676	TTTAAGACTGGATATGATGAA	21	17
112	+	1677	TTAAGACTGGATATGATGAAA	21	18
12	+	1677	TTAAGACTGGATATGATGAAAA	22	18
39	+	1678	TAAGACTGGATATGATGAAAA	21	19
2	+	1679	AAGACTGGATATGATGAAAAAAAC	24	20
5	+	1679	AAGACTGGATATGATGAAAAA	21	20
173	+	1680	AGACTGGATATGATGAAAAAA	21	0
117	+	1682	ACTGGATATGATGAAAAAAAC	21	2
2	+	1684	TGGATATGATGAAAAAAACAG	21	4
33	+	1684	TGGATATGATGAAAAAAACAGA	22	4
11	+	1686	GATATGATGAAAAAAACAGAG	21	6
18	+	1687	ATATGATGAAAAAAACAGAGT	21	7
3	+	1689	ATGATGAAAAAAACAGAGTGC	21	9
17	+	1690	TGATGAAAAAAACAGAGTGCGC	22	10
2	+	1690	TGATGAAAAAAACAGAGTGCG	21	10
5	+	1690	TGATGAAAAAAACAGAGTGCGCA	23	10
15	+	1691	GATGAAAAAAACAGAGTGCGC	21	11
8	+	1691	GATGAAAAAAACAGAGTGCGCA	22	11
335	+	1692	ATGAAAAAAACAGAGTGCGCA	21	12
4	+	1696	AAAAAACAGAGTGCGCATACC	21	16
24	+	1697	AAAAACAGAGTGCGCATACCG	21	17
149	+	1698	AAAACAGAGTGCGCATACCGG	21	18
84	+	1698	AAAACAGAGTGCGCATACCGGA	22	18
1	+	1699	AAACAGAGTGCGCATACCGGAG	22	19
70	+	1699	AAACAGAGTGCGCATACCGGA	21	19
3	+	1700	AACAGAGTGCGCATACCGGAGA	22	20

65	+	1700	AACAGAGTGCGCATACCGGAG	21	20
396	+	1701	ACAGAGTGCGCATACCGGAGA	21	0
63	+	1702	CAGAGTGCGCATACCGGAGAA	21	1
18	+	1703	AGAGTGCGCATACCGGAGAACA	22	2
35	+	1703	AGAGTGCGCATACCGGAGAAC	21	2
12	+	1705	AGTGCGCATACCGGAGAACAT	21	4
6	+	1706	GTGCGCATACCGGAGAACATGG	22	5
113	+	1707	TGCGCATACCGGAGAACATGGA	22	6
59	+	1707	TGCGCATACCGGAGAACATGG	21	6
125	+	1708	GCGCATACCGGAGAACATGGA	21	7
5	+	1708	GCGCATACCGGAGAACATGGAG	22	7
17	+	1709	CGCATACCGGAGAACATGGAG	21	8
58	+	1709	CGCATACCGGAGAACATGGAGT	22	8
14	+	1710	GCATACCGGAGAACATGGAGTT	22	9
31	+	1710	GCATACCGGAGAACATGGAGT	21	9
135	+	1711	CATACCGGAGAACATGGAGTT	21	10
5	+	1711	CATACCGGAGAACATGGAGTTTC	23	10
14	+	1712	ATACCGGAGAACATGGAGTTTC	22	11
78	+	1712	ATACCGGAGAACATGGAGTTT	21	11
178	+	1713	TACCGGAGAACATGGAGTTTC	21	12
1	+	1713	TACCGGAGAACATGGAGTTT	20	12
5	+	1713	TACCGGAGAACATGGAGTTTCC	22	12
12	+	1714	ACCGGAGAACATGGAGTTTCC	21	13
1	+	1715	CCGGAGAACATGGAGTTTCCAC	22	14
8	+	1715	CCGGAGAACATGGAGTTTC	19	14
22	+	1720	GAACATGGAGTTTCCACCTCGTCTA	25	19
12	+	1721	AACATGGAGTTTCCACCTCGT	21	20
4	+	1721	AACATGGAGTTTCCACCTCGTC	22	20
54	+	1722	ACATGGAGTTTCCACCTCGTC	21	0
19	+	1724	ATGGAGTTTCCACCTCGTCTA	21	2
7	+	1734	CACCTCGTCTAAGGTTACTAC	21	12
26	+	1736	CCTCGTCTAAGGTTACTACAG	21	14
62	+	1737	CTCGTCTAAGGTTACTACAGT	21	15
4	+	1738	TCGTCTAAGGTTACTACAGTGG	22	16
9	+	1738	TCGTCTAAGGTTACTACAGTG	21	16
17	+	1739	CGTCTAAGGTTACTACAGTGG	21	17
28	+	1740	GTCTAAGGTTACTACAGTGGG	21	18
75	+	1741	TCTAAGGTTACTACAGTGGGA	21	19
59	+	1743	TAAGGTTACTACAGTGGGAAG	21	0
9	+	1743	TAAGGTTACTACAGTGGGAAGC	22	0
18	+	1745	AGGTTACTACAGTGGGAAGCA	21	2
1	+	1748	TTACTACAGTGGGAAGCATATC	22	5
24	+	1751	CTACAGTGGGAAGCATATCCG	21	8
2	+	1753	ACAGTGGGAAGCATATCCGAGG	22	10

13	+	1754	CAGTGGGAAGCATATCCGAGG	21	11
1	+	1754	CAGTGGGAAGCATATCCGAGGA	22	11
2	+	1754	CAGTGGGAAGCATATCCGAGGAGA	24	11
506	+	1755	AGTGGGAAGCATATCCGAGGA	21	12
5	+	1755	AGTGGGAAGCATATCCGAGG	20	12
19	+	1756	GTGGGAAGCATATCCGAGGAG	21	13
3	+	1756	GTGGGAAGCATATCCGAGGAGA	22	13
56	+	1757	TGGGAAGCATATCCGAGGAGAA	22	14
80	+	1757	TGGGAAGCATATCCGAGGAGA	21	14
3	+	1758	GGGAAGCATATCCGAGGAGAA	21	15
6	+	1758	GGGAAGCATATCCGAGGAGA	20	15
8	+	1758	GGGAAGCATATCCGAGG	17	15
3	+	1760	GAAGCATATCCGAGGAGAAGTC	22	17
38	+	1761	AAGCATATCCGAGGAGAAGTC	21	18
3	+	1762	AGCATATCCGAGGAGAAGTCTT	22	19
9	+	1762	AGCATATCCGAGGAGAAGTCT	21	19
19	+	1763	GCATATCCGAGGAGAAGTCTT	21	20
38	+	1765	ATATCCGAGGAGAAGTCTTTC	21	1
5	+	1765	ATATCCGAGGAGAAGTC	17	1
1	+	1766	TATCCGAGGAGAAGTCTTTCTC	22	2
11	+	1778	AGTCTTTCTCTTAAACTTAAC	21	14
26	+	1782	TTTCTCTTAAACTTAACCTGG	21	18
142	+	1783	TTCTCTTAAACTTAACCTGGA	21	19
1	+	1783	TTCTCTTAAACTTAACCTGGAA	22	19
31	+	1784	TCTCTTAAACTTAACCTGGAA	21	20
5	+	1785	CTCTTAAACTTAACCTGGAATA	22	0
8	+	1785	CTCTTAAACTTAACCTGGAAT	21	0
12	+	1786	TCTTAAACTTAACCTGGAATA	21	1
65	+	1786	TCTTAAACTTAACCTGGA	18	1
16	+	1787	CTTAAACTTAACCTGGAATAT	21	2
2	+	1790	AAACTTAACCTGGAATATCTT	21	5
5	+	1791	AACTTAACCTGGAATATCTTG	21	6
10	+	1792	ACTTAACCTGGAATATCTTGT	21	7
13	+	1793	CTTAACCTGGAATATCTTGTC	21	8
28	+	1794	TTAACCTGGAATATCTTGTCG	21	9
355	+	1794	TTAACCTGGAATATCTTGTCGA	22	9
7	+	1795	TAACCTGGAATATCTTG	17	10
16	+	1796	AACCTGGAATATCTTGTCGAA	21	11
22	+	1797	ACCTGGAATATCTTGTCGAAC	21	12
26	+	1799	CTGGAATATCTTGTCGAACTT	21	14
11	+	1800	TGGAATATCTTGTCGAACTTGA	22	15
206	+	1800	TGGAATATCTTGTCGAACTTG	21	15
1	+	1801	GGAATATCTTGTCGAACTTG	20	16
20	+	1801	GGAATATCTTGTCGAACTTGA	21	16

3	+	1802	GAATATCTTGTCGAACTTGAT	21	17
6	+	1803	AATATCTTGTCGAACTTGATA	21	18
10	+	1805	TATCTTGTCGAACTTGATATG	21	20
8	+	1806	ATCTTGTCGAACTTGATATGG	21	0
713	+	1807	TCTTGTCGAACTTGATATGGA	21	1
4	+	1808	CTTGTCGAACTTGATATGGAA	21	2
48	+	1809	TTGTCGAACTTGATATGGAAGG	22	3
99	+	1809	TTGTCGAACTTGATATGGAAG	21	3
14	+	1811	GTCGAACTTGATATGGAAGGT	21	5
2	+	1811	GTCGAACTTGATATGGAAGG	20	5
21	+	1812	TCGAACTTGATATGGAAGGTA	21	6
4	+	1813	CGAACTTGATATGGAAGGTAG	21	7
9	+	1813	CGAACTTGATATGGAAGGTAGC	22	7
11	+	1814	GAACTTGATATGGAAGGTAGC	21	8
30	+	1814	GAACTTGATATGGAAGGTAGCC	22	8
29	+	1815	AACTTGATATGGAAGGTAGCC	21	9
22	+	1816	ACTTGATATGGAAGGTAGCCT	21	10
17	+	1817	CTTGATATGGAAGGTAGCCTG	21	11
369	+	1818	TTGATATGGAAGGTAGCCTGC	21	12
41	+	1818	TTGATATGGAAGGTAGCCTGCT	22	12
1	+	1819	TGATATGGAAGGTAGCC	17	13
25	+	1819	TGATATGGAAGGTAGCCTGCT	21	13
19	+	1820	GATATGGAAGGTAGCCTGCTC	21	14
29	+	1821	ATATGGAAGGTAGCCTGCTCGA	22	15
4	+	1821	ATATGGAAGGTAGCCTGCTCGAGA	24	15
59	+	1821	ATATGGAAGGTAGCCTGCTCG	21	15
154	+	1822	TATGGAAGGTAGCCTGCTCGA	21	16
1	+	1822	TATGGAAGGTAGCCTGCTCGAGAA	24	16
72	+	1822	TATGGAAGGTAGCCTGCTCGAG	22	16
9	+	1822	TATGGAAGGTAGCCTGCTCGAGA	23	16
26	+	1823	ATGGAAGGTAGCCTGCTCGAGA	22	17
533	+	1823	ATGGAAGGTAGCCTGCTCGAG	21	17
176	+	1824	TGGAAGGTAGCCTGCTCGAGA	21	18
1	+	1824	TGGAAGGTAGCCTGCTCGAG	20	18
24	+	1824	TGGAAGGTAGCCTGCTCGAGAA	22	18
6	+	1826	GAAGGTAGCCTGCTCGAGAAG	21	20
10	+	1832	AGCCTGCTCGAGAAGCTATGG	21	5
15	+	1832	AGCCTGCTCGAGAAGCTATGGG	22	5
116	+	1833	GCCTGCTCGAGAAGCTATGGG	21	6
1	+	1833	GCCTGCTCGAGAAGCTATGGGA	22	6
9	+	1835	CTGCTCGAGAAGCTATGGGAT	21	8
4	+	1838	CTCGAGAAGCTATGGGATGG	20	11
81	+	1838	CTCGAGAAGCTATGGGATGGA	21	11
170	+	1839	TCGAGAAGCTATGGGATGGAA	21	12

37	+	1839	TCGAGAAGCTATGGGATGGAAC	22	12
37	+	1840	CGAGAAGCTATGGGATGGAAC	21	13
9	+	1841	GAGAAGCTATGGGATGGAACT	21	14
12	+	1842	AGAAGCTATGGGATGGAACTC	21	15
162	+	1844	AAGCTATGGGATGGAACTCAG	21	17
4	+	1863	AGCCCCTTGCAAATCTCAAGA	21	15
11	+	1864	GCCCCTTGCAAATCTCAAGA	20	16
2	+	1864	GCCCCTTGCAAATCTCAAGAA	21	16
3	+	1865	CCCCTTGCAAATCTCAAGAAG	21	17
10	+	1866	CCCTTGCAAATCTCAAGAAGA	21	18
4	+	1867	CCTTGCAAATCTCAAGAAGATG	22	19
8	+	1868	CTTGCAAATCTCAAGAAGATG	21	20
14	+	1870	TGCAAATCTCAAGAAGATGTC	21	1
32	+	1876	TCTCAAGAAGATGTCTTTGTC	21	7
14	+	1880	AAGAAGATGTCTTTGTCAAGT	21	11
7	+	1880	AAGAAGATGTCTTTGTCAAGTT	22	11
134	+	1881	AGAAGATGTCTTTGTCAAGTT	21	12
1	+	1883	AAGATGTCTTTGTCAAGTTCA	21	14
29	+	1886	ATGTCTTTGTCAAGTTCATGG	21	17
221	+	1887	TGTCTTTGTCAAGTTCATGGT	21	18
117	+	1888	GTCTTTGTCAAGTTCATGGTA	21	19
1	+	1888	GTCTTTGTCAAGTTCATGGT	20	19
15	+	1889	TCTTTGTCAAGTTCATGGTAT	21	20
61	+	1889	TCTTTGTCAAGTTCATGGTATT	22	20
28	+	1891	TTTGTCAAGTTCATGGTATTT	21	1
52	+	1891	TTTGTCAAGTTCATGGTATTTA	22	1
59	+	1891	TTTGTCAAGTTCATGGTAT	19	1
3	+	1895	TCAAGTTCATGGTATTTAAAG	21	5
108	+	1897	AAGTTCATGGTATTTAAAGAA	21	7
22	+	1897	AAGTTCATGGTATTTAAAGA	20	7
2	+	1899	GTTCATGGTATTTAAAGAAAC	21	9
17	+	1900	TTCATGGTATTTAAAGAAACT	21	10
1	+	1901	TCATGGTATTTAAAGAAACT	20	11
7	+	1903	ATGGTATTTAAAGAAACTTCC	21	13
9	+	1904	TGGTATTTAAAGAAACTTCCGG	22	14
1	+	1905	GGTATTTAAAGAAACTTCCGGATCTGT	27	15
111	+	1907	TATTTAAAGAAACTTCCGGAT	21	17
2	+	1907	TATTTAAAGAAACTTCCGGATC	22	17
101	+	1908	ATTTAAAGAAACTTCCGGATC	21	18
11	+	1910	TTAAAGAAACTTCCGGATCTG	21	20
15	+	1911	TAAAGAAACTTCCGGATCTGT	21	0
119	+	1912	AAAGAAACTTCCGGATCTGTC	21	1
4	+	1913	AAGAAACTTCCGGATCTGTCA	21	2
9	+	1913	AAGAAACTTCCGGATCTGTC	20	2

19	+	1914	AGAAACTTCCGGATCTGTCAA	21	3
12	+	1915	GAAACTTCCGGATCTGTCAAA	21	4
126	+	1916	AAACTTCCGGATCTGTCAAAT	21	5
4	+	1916	AAACTTCCGGATCTGTCAAATG	22	5
39	+	1917	AACTTCCGGATCTGTCAAATG	21	6
63	+	1918	ACTTCCGGATCTGTCAAATGC	21	7
40	+	1919	CTTCCGGATCTGTCAAATGCT	21	8
11	+	1920	TTCCGGATCTGTCAAATGCTA	21	9
51	+	1921	TCCGGATCTGTCAAATGCTACA	22	10
5	+	1921	TCCGGATCTGTCAAATGCTAC	21	10
8	+	1922	CCGGATCTGTCAAATGCTACAAATC	25	11
28	+	1923	CGGATCTGTCAAATGCTACAA	21	12
4	+	1923	CGGATCTGTCAAATGCTACAAA	22	12
13	+	1926	ATCTGTCAAATGCTACAAATC	21	15
10	+	1928	CTGTCAAATGCTACAAATCTC	21	17
4	+	1929	TGTCAAATGCTACAAATCTCGAAGAA	26	18
4	+	1929	TGTCAAATGCTACAAATCTCG	21	18
7	+	1930	GTCAAATGCTACAAATCTCGA	21	19
22	+	1931	TCAAATGCTACAAATCTCGAAG	22	20
33	+	1931	TCAAATGCTACAAATCTCGAA	21	20
23	+	1933	AAATGCTACAAATCTCGAAGAA	22	1
70	+	1933	AAATGCTACAAATCTCGAAGA	21	1
64	+	1934	AATGCTACAAATCTCGAAGAA	21	2
27	+	1935	ATGCTACAAATCTCGAAGAAT	21	3
6	+	1936	TGCTACAAATCTCGAAGAATTGGAT	25	4
77	+	1938	CTACAAATCTCGAAGAATTGGA	22	6
408	+	1939	TACAAATCTCGAAGAATTGGA	21	7
6	+	1943	AATCTCGAAGAATTGGATCTG	21	11
61	+	1944	ATCTCGAAGAATTGGATCTGA	21	12
1	+	1945	TCTCGAAGAATTGGATC	17	13
6	+	1947	TCGAAGAATTGGATCTGAGAG	21	15
3	+	1949	GAAGAATTGGATCTGAGAGCTT	22	17
5	+	1949	GAAGAATTGGATCTGAGAGCT	21	17
2	+	1950	AAGAATTGGATCTGAGAG	18	18
54	+	1950	AAGAATTGGATCTGAGAGCTTG	22	18
59	+	1950	AAGAATTGGATCTGAGAGCTT	21	18
5	+	1951	AGAATTGGATCTGAGAGCTTG	21	19
1	+	1952	GAATTGGATCTGAGAGCTTGCC	22	20
2	+	1952	GAATTGGATCTGAGAGCTTGC	21	20
1	+	1953	AATTGGATCTGAGAGCTTGCCA	22	0
230	+	1953	AATTGGATCTGAGAGCTTGCC	21	0
27	+	1954	ATTGGATCTGAGAGCTTGCCA	21	1
2	+	1954	ATTGGATCTGAGAGCTTGCC	20	1
5	+	1954	ATTGGATCTGAGAGCTTGC	19	1

140	+	1955	TTGGATCTGAGAGCTTGCCAGA	22	2
15	+	1955	TTGGATCTGAGAGCTTGC	18	2
332	+	1955	TTGGATCTGAGAGCTTGCCAG	21	2
270	+	1956	TGGATCTGAGAGCTTGCCAGA	21	3
1	+	1957	GGATCTGAGAGCTTGCCAGA	20	4
2	+	1957	GGATCTGAGAGCTTGCCAG	19	4
4	+	1957	GGATCTGAGAGCTTGCCAGAA	21	4
2	+	1962	TGAGAGCTTGCCAGAATTTAGT	22	9
6	+	1964	AGAGCTTGCCAGAATTTAGTA	21	11
31	+	1966	AGCTTGCCAGAATTTAGTAGA	21	13
25	+	1967	GCTTGCCAGAATTTAGTAGAG	21	14
6	+	1968	CTTGCCAGAATTTAGTAGAGC	21	15
11	+	1969	TTGCCAGAATTTAGTAGAGCTT	22	16
1	+	1969	TTGCCAGAATTTAGTAGAGCTTCC	24	16
44	+	1969	TTGCCAGAATTTAGTAGAGCT	21	16
196	+	1970	TGCCAGAATTTAGTAGAGCTT	21	17
1	+	1971	GCCAGAATTTAGTAGAGCTT	20	18
4	+	1973	CAGAATTTAGTAGAGCTTCCTT	22	20
8	+	1973	CAGAATTTAGTAGAGCTTCCT	21	20
158	+	1974	AGAATTTAGTAGAGCTTCCTT	21	0
4	+	1974	AGAATTTAGTAGAGCTTCCTTC	22	0
20	+	1976	AATTTAGTAGAGCTTCCTTCC	21	2
11	+	1977	ATTTAGTAGAGCTTCCTTCCT	21	3
16	+	1978	TTTAGTAGAGCTTCCTTCCTC	21	4
7	+	1979	TTAGTAGAGCTTCCTTCCTCC	21	5
120	+	1980	TAGTAGAGCTTCCTTCCTCCT	21	6
22	+	1989	TTCCTTCCTCCTTTTCTTATC	21	15
6	+	1993	TTCCTCCTTTTCTTATCTGCA	21	19
14	+	2006	TATCTGCATAAGCTAAAGTAT	21	11
5	+	2017	GCTAAAGTATTTGAATATGAT	21	1
2	+	2018	CTAAAGTATTTGAATATGATGG	22	2
198	+	2019	TAAAGTATTTGAATATGATGG	21	3
27	+	2020	AAAGTATTTGAATATGATGGG	21	4
267	+	2021	AAGTATTTGAATATGATGGGA	21	5
13	+	2022	AGTATTTGAATATGATGGGAT	21	6
1	+	2022	AGTATTTGAATATGATGGGA	20	6
11	+	2024	TATTTGAATATGATGGGATGCA	22	8
8	+	2024	TATTTGAATATGATGGGATGC	21	8
25	+	2025	ATTTGAATATGATGGGATGCA	21	9
161	+	2026	TTTGAATATGATGGGATGCAGA	22	10
21	+	2026	TTTGAATATGATGGGATGCAG	21	10
235	+	2027	TTGAATATGATGGGATGCAGA	21	11
1	+	2028	TGAATATGATGGGATGCAGA	20	12
3	+	2028	TGAATATGATGGGATGCAGAA	21	12

53	+	2030	AATATGATGGGATGCAGAAGG	21	14
103	+	2031	ATATGATGGGATGCAGAAGGC	21	15
12	+	2037	TGGGATGCAGAAGGCTAAAAG	21	0
36	+	2037	TGGGATGCAGAAGGCTAAAAGA	22	0
16	+	2039	GGATGCAGAAGGCTAAAAGAA	21	2
10	+	2040	GATGCAGAAGGCTAAAAGAAG	21	3
12	+	2041	ATGCAGAAGGCTAAAAGAAGTT	22	4
69	+	2041	ATGCAGAAGGCTAAAAGAAGT	21	4
2	+	2042	TGCAGAAGGCTAAAAGAAGTTC	22	5
40	+	2042	TGCAGAAGGCTAAAAGAAGTT	21	5
1	+	2043	GCAGAAGGCTAAAAGAAGTTC	21	6
18	+	2048	AGGCTAAAAGAAGTTCCACCT	21	11
1	+	2054	AAAGAAGTTCCACCTCATATCA	22	17
34	+	2054	AAAGAAGTTCCACCTCATATC	21	17
12	+	2059	AGTTCCACCTCATATCAACTT	21	1
7	+	2061	TTCCACCTCATATCAACTTGA	21	3
2	+	2062	TCCACCTCATATCAACTTGAA	21	4
1	+	2067	CTCATATCAACTTGAAGTCTCT	22	9
6	+	2067	CTCATATCAACTTGAAGTCTC	21	9
2	+	2069	CATATCAACTTGAAGTCTCT	20	11
10	+	2070	ATATCAACTTGAAGTCTCTTG	21	12
1	+	2070	ATATCAACTTGAAGTCTCTTGA	22	12
16	+	2071	TATCAACTTGAAGTCTCTTGA	21	13
19	+	2073	TCAACTTGAAGTCTCTTGAATT	22	15
6	+	2073	TCAACTTGAAGTCTCTTGAAT	21	15
15	+	2076	ACTTGAAGTCTCTTGAATTGG	21	18
14	+	2077	CTTGAAGTCTCTTGAATTGGT	21	19
2	+	2077	CTTGAAGTCTCTTGAATTGGTC	22	19
1	+	2078	TTGAAGTCTCTTGAATTGGT	20	20
48	+	2078	TTGAAGTCTCTTGAATTGGTC	21	20
4	+	2079	TGAAGTCTCTTGAATTGGTCA	21	0
4	+	2080	GAAGTCTCTTGAATTGGTCA	20	1
12	+	2081	AAGTCTCTTGAATTGGTCAACA	22	2
4	+	2086	TCTTGAATTGGTCAACATGTA	21	7
1	+	2087	CTTGAATTGGTCAACATGTATGG	23	8
9	+	2088	TTGAATTGGTCAACATGTATGG	22	9
11	+	2089	TGAATTGGTCAACATGTATGG	21	10
51	+	2089	TGAATTGGTCAACATGTATGGA	22	10
100	+	2090	GAATTGGTCAACATGTATGGA	21	11
7	+	2090	GAATTGGTCAACATGTATGG	20	11
9	+	2090	GAATTGGTCAACATGTATGGATGC	24	11
37	+	2091	AATTGGTCAACATGTATGGATG	22	12
149	+	2092	ATTGGTCAACATGTATGGATG	21	13
15	+	2092	ATTGGTCAACATGTATGGA	19	13

3	+	2092	ATTGGTCAACATGTATGGATGC	22	13
101	+	2093	TTGGTCAACATGTATGGATGC	21	14
24	+	2094	TGGTCAACATGTATGGATGCT	21	15
45	+	2099	AACATGTATGGATGCTCAAGA	21	20
16	+	2100	ACATGTATGGATGCTCAAGAT	21	0
4	+	2100	ACATGTATGGATGCTCAAGATT	22	0
12	+	2103	TGTATGGATGCTCAAGATTAA	21	3
1	+	2103	TGTATGGATGCTCAAGATTAAAAAG	25	3
3	+	2103	TGTATGGATGCTCAAGATTAAAAA	24	3
4	+	2103	TGTATGGATGCTCAAGATTAAAA	23	3
5	+	2106	ATGGATGCTCAAGATTAAAAAG	22	6
38	+	2107	TGGATGCTCAAGATTAAAAAG	21	7
8	+	2107	TGGATGCTCAAGATTAAAAAGC	22	7
5	+	2109	GATGCTCAAGATTAAAAAGCT	21	9
1	+	2111	TGCTCAAGATTAAAAAGCTTT	21	11
1	+	2116	AAGATTAAAAAGCTTTCCAGA	21	16
7	+	2119	ATTAAAAAGCTTTCCAGATAT	21	19
5	+	2122	AAAAAGCTTTCCAGATATTT	20	1
7	+	2129	TTTCCAGATATTTCTACAAAC	21	8
2	+	2133	CAGATATTTCTACAAACATCAGT	23	12
17	+	2136	ATATTTCTACAAACATCAGTT	21	15
2	+	2139	TTTCTACAAACATCAGTTCAC	21	18
2	+	2143	TACAAACATCAGTTCACTCGAC	22	1
38	+	2143	TACAAACATCAGTTCACTCGA	21	1
9	+	2144	ACAAACATCAGTTCACTCGAC	21	2
20	+	2147	AACATCAGTTCACTCGACATAT	22	5
3	+	2148	ACATCAGTTCACTCGACATAT	21	6
21	+	2151	TCAGTTCACTCGACATATCATA	22	9
6	+	2154	GTTCACTCGACATATCATACA	21	12
4	+	2155	TTCACTCGACATATCATACACTG	23	13
6	+	2155	TTCACTCGACATATCATACACT	22	13
86	+	2159	CTCGACATATCATACACTGATG	22	17
12	+	2174	ACTGATGTGGAAGAACTACCT	21	11
6	+	2175	CTGATGTGGAAGAACTACCTG	21	12
84	+	2175	CTGATGTGGAAGAACTACCTGA	22	12
23	+	2176	TGATGTGGAAGAACTACCTGA	21	13
4	+	2176	TGATGTGGAAGAACTACCTGAA	22	13
16	+	2177	GATGTGGAAGAACTACCTGAA	21	14
9	+	2178	ATGTGGAAGAACTACCTGAAT	21	15
6	+	2179	TGTGGAAGAACTACCTGAATC	21	16
34	+	2181	TGGAAGAACTACCTGAATCAAT	22	18
77	+	2184	AAGAACTACCTGAATCAATGA	21	0
4	+	2185	AGAACTACCTGAATCAATGAC	21	1
1	+	2188	ACTACCTGAATCAATGACGAT	21	4

11	+	2190	TACCTGAATCAATGACGATGT	21	6
2	+	2192	CCTGAATCAATGACGATGTGG	21	8
18	+	2193	CTGAATCAATGACGATGTGGT	21	9
24	+	2198	TCAATGACGATGTGGTCTCGC	21	14
48	+	2198	TCAATGACGATGTGGTCTCGCC	22	14
2	+	2199	CAATGACGATGTGGTCTCGCC	21	15
11	+	2202	TGACGATGTGGTCTCGCCTACG	22	18
2	+	2205	CGATGTGGTCTCGCCTACGTA	21	0
6	+	2205	CGATGTGGTCTCGCCTACGTAC	22	0
21	+	2210	TGGTCTCGCCTACGTACTCTCG	22	5
8	+	2237	TACAAAAGTAGAAACCTCAAG	21	11
2	+	2241	AAAGTAGAAACCTCAAGATAG	21	15
3	+	2241	AAAGTAGAAACCTCAAGATAGT	22	15
8	+	2242	AAGTAGAAACCTCAAGATAGT	21	16
6	+	2245	TAGAAACCTCAAGATAGTAAC	21	19
6	+	2248	AAACCTCAAGATAGTAACACA	21	1
14	+	2253	TCAAGATAGTAACACATGTGC	21	6
19	+	2254	CAAGATAGTAACACATGTGCC	21	7
5	+	2258	ATAGTAACACATGTGCCCCTA	21	11
6	+	2274	CCCTAAACCTAACATATCTAGA	22	6
2	+	2277	TAAACCTAACATATCTAGACC	21	9
13	+	2281	CCTAACATATCTAGACCTCAG	21	13
19	+	2282	CTAACATATCTAGACCTCAGCG	22	14
17	+	2283	TAACATATCTAGACCTCAGCGA	22	15
21	+	2283	TAACATATCTAGACCTCAGCG	21	15
2	+	2284	AACATATCTAGACCTCAGCGA	21	16
7	+	2285	ACATATCTAGACCTCAGCGAG	21	17
7	+	2287	ATATCTAGACCTCAGCGAGAC	21	19
24	+	2292	TAGACCTCAGCGAGACTAGAA	21	3
18	+	2297	CTCAGCGAGACTAGAATTGAG	21	8
23	+	2297	CTCAGCGAGACTAGAATTGAGA	22	8
56	+	2297	CTCAGCGAGACTAGAATTGAGAA	23	8
1	+	2298	TCAGCGAGACTAGAATTGAGAA	22	9
283	+	2298	TCAGCGAGACTAGAATTGAGA	21	9
27	+	2299	CAGCGAGACTAGAATTGAGAA	21	10
60	+	2301	GCGAGACTAGAATTGAGAAGA	21	12
14	+	2302	CGAGACTAGAATTGAGAAGAT	21	13
13	+	2311	AATTGAGAAGATTCCAGATGA	21	1
4	+	2311	AATTGAGAAGATTCCAGATGAC	22	1
3	+	2312	ATTGAGAAGATTCCAGATGA	20	2
7	+	2312	ATTGAGAAGATTCCAGATGAC	21	2
28	+	2333	ATCAAAAATGTTCATGGGCTG	21	2
31	+	2334	TCAAAAATGTTCATGGGCTGC	21	3
61	+	2334	TCAAAAATGTTCATGGGCTGCA	22	3

2	+	2336	AAAAATGTTCATGGGCTGCAAA	22	5
8	+	2336	AAAAATGTTCATGGGCTGCAA	21	5
9	+	2337	AAAATGTTCATGGGCTGCAAA	21	6
35	+	2338	AAATGTTCATGGGCTGCAAAT	21	7
13	+	2339	AATGTTCATGGGCTGCAAATT	21	8
5	+	2341	TGTTCATGGGCTGCAAATTTT	21	10
17	+	2343	TTCATGGGCTGCAAATTTTATT	22	12
18	+	2343	TTCATGGGCTGCAAATTTTAT	21	12
12	+	2344	TCATGGGCTGCAAATTTTATT	21	13
16	+	2346	ATGGGCTGCAAATTTTATTTC	21	15
11	+	2347	TGGGCTGCAAATTTTATTTCT	21	16
8	+	2353	GCAAATTTTATTTCTAGGTGG	21	1
7	+	2354	CAAATTTTATTTCTAGGTGGC	21	2
11	+	2356	AATTTTATTTCTAGGTGG	18	4
34	+	2356	AATTTTATTTCTAGGTGGCTG	21	4
7	+	2356	AATTTTATTTCTAGGTGGCTGC	22	4
23	+	2357	ATTTTATTTCTAGGTGGCTGC	21	5
94	+	2360	TTATTTCTAGGTGGCTGCAGA	21	8
13	+	2363	TTTCTAGGTGGCTGCAGAAAA	21	11
34	+	2367	TAGGTGGCTGCAGAAAACTCGC	22	15
102	+	2368	AGGTGGCTGCAGAAAACTCGC	21	16
1	+	2369	GGTGGCTGCAGAAAACTCGC	20	17
2	+	2370	GTGGCTGCAGAAAACTCGCAT	21	18
132	+	2371	TGGCTGCAGAAAACTCGCATC	21	19
6	+	2377	CAGAAAACTCGCATCATTGCC	21	4
20	+	2380	AAAACTCGCATCATTGCCAGA	21	7
7	+	2385	TCGCATCATTGCCAGAGCTTC	21	12
27	+	2389	ATCATTGCCAGAGCTTCCTGG	21	16
20	+	2407	TGGTTCGCTCTTGTACTTATC	21	13
9	+	2409	GTTCGCTCTTGTACTTATCAG	21	15
38	+	2410	TTCGCTCTTGTACTTATCAGCA	22	16
5	+	2410	TTCGCTCTTGTACTTATCAGC	21	16
84	+	2417	TTGTACTTATCAGCAAACGAG	21	2
51	+	2427	CAGCAAACGAGTGTGAATCAC	21	12
14	+	2438	TGTGAATCACTTGAGAGCGTA	21	2
2	+	2442	AATCACTTGAGAGCGTATCTT	21	6
10	+	2443	ATCACTTGAGAGCGTATCTTG	21	7
3	+	2443	ATCACTTGAGAGCGTATCTTGC	22	7
5	+	2447	CTTGAGAGCGTATCTTGCCCT	21	11
13	+	2465	CCTTTTAATACTTCATACATG	21	8
64	+	2467	TTTTAATACTTCATACATGGA	21	10
2	+	2468	TTTAATACTTCATACATGGAA	21	11
9	+	2470	TAATACTTCATACATGGAACT	21	13
5	+	2471	AATACTTCATACATGGAACTC	21	14

3	+	2472	ATACTTCATACATGGAACTCAGC	23	15
11	+	2473	TACTTCATACATGGAACTCAG	21	16
10	+	2474	ACTTCATACATGGAACTCAGC	21	17
93	+	2475	CTTCATACATGGAACTCAGCT	21	18
4	+	2476	TTCATACATGGAACTCAGCTTC	22	19
58	+	2476	TTCATACATGGAACTCAGCTT	21	19
6	+	2479	ATACATGGAACTCAGCTTCACC	22	1
39	+	2481	ACATGGAACTCAGCTTCACCAA	22	3
9	+	2483	ATGGAACTCAGCTTCACCAAC	21	5
4	+	2485	GGAACTCAGCTTCACCAACTG	21	7
12	+	2486	GAACTCAGCTTCACCAACTGC	21	8
13	+	2488	ACTCAGCTTCACCAACTGCTT	21	10
1	+	2495	TTCACCAACTGCTTCAAACTA	21	17
30	+	2508	TCAAACTAAACCAAGAAGCACGCAGAG	27	9
1	+	2511	AACTAAACCAAGAAGCACGCAG	22	12
5	+	2511	AACTAAACCAAGAAGCACGCA	21	12
2	+	2512	ACTAAACCAAGAAGCACGCAGA	22	13
4	+	2513	CTAAACCAAGAAGCACGCAGAG	22	14
4	+	2514	TAAACCAAGAAGCACGCAGAG	21	15
29	+	2517	ACCAAGAAGCACGCAGAGGAA	21	18
55	+	2527	ACGCAGAGGAATTATTCAACA	21	7
5	+	2541	TTCAACAATCATTTTCTCATGG	22	0
1	+	2546	CAATCATTTTCTCATGGGTGG	21	5
4	+	2547	AATCATTTTCTCATGGGTGGG	21	6
15	+	2551	ATTTTCTCATGGGTGGGCATC	21	10
11	+	2552	TTTTCTCATGGGTGGGCATCCT	22	11
5	+	2557	TCATGGGTGGGCATCCTTACC	21	16
4	+	2560	TGGGTGGGCATCCTTACCTGGA	22	19
5	+	2563	GTGGGCATCCTTACCTGGAA	20	1
31	+	2572	CTTACCTGGAAGAGAGTTGCC	21	10
9	+	2573	TTACCTGGAAGAGAGTTGCCC	21	11
24	+	2574	TACCTGGAAGAGAGTTGCCCA	21	12
3	+	2575	ACCTGGAAGAGAGTTGCCCAC	21	13
4	+	2576	CCTGGAAGAGAGTTGCCC	18	14
1	+	2578	TGGAAGAGAGTTGCCCACTGAC	22	16
9	+	2578	TGGAAGAGAGTTGCCCACTGA	21	16
7	+	2581	AAGAGAGTTGCCCACTGACTT	21	19
11	+	2595	CTGACTTATACCACCGATCTA	21	12
3	+	2595	CTGACTTATACCACCGATCTAC	22	12
53	+	2596	TGACTTATACCACCGATCTAC	21	13
4	+	2599	CTTATACCACCGATCTACCGG	21	16
27	+	2602	ATACCACCGATCTACCGGACA	21	19
1	+	2607	ACCGATCTACCGGACATTCCA	21	3
11	+	2611	ATCTACCGGACATTCCATCAC	21	7

44	+	2611	ATCTACCGGACATTCCATCA	20	7
34	+	2612	TCTACCGGACATTCCATCACC	21	8
28	+	2614	TACCGGACATTCCATCACCGTT	22	10
5	+	2615	ACCGGACATTCCATCACCGTT	21	11
4	+	2618	GGACATTCCATCACCGTTCGTC	22	14
5	+	2623	TTCCATCACCGTTCGTCTCGAG	22	19
90	+	2623	TTCCATCACCGTTCGTCTCGA	21	19
25	+	2624	TCCATCACCGTTCGTCTCGAG	21	20
5	+	2625	CCATCACCGTTCGTCTCGAGGGC	23	0
1	+	2626	CATCACCGTTCGTCTCGAGGGC	22	1
6	+	2626	CATCACCGTTCGTCTCGAGGG	21	1
1	+	2627	ATCACCGTTCGTCTCGAGGGCAA	23	2
38	+	2627	ATCACCGTTCGTCTCGAGGGC	21	2
5	+	2627	ATCACCGTTCGTCTCGAGGGCA	22	2
5	+	2628	TCACCGTTCGTCTCGAGGGCA	21	3
4	+	2630	ACCGTTCGTCTCGAGGGCAAGA	22	5
5	+	2632	CGTTCGTCTCGAGGGCAAGAC	21	7
4	+	2634	TTCGTCTCGAGGGCAAGACTC	21	9
9	+	2638	TCTCGAGGGCAAGACTCCTTT	21	13
37	+	2647	CAAGACTCCTTTTTCTGCATT	21	1
52	+	2649	AGACTCCTTTTTCTGCATTCT	21	3
1	+	2652	CTCCTTTTTCTGCATTCTTTGG	22	6
15	+	2653	TCCTTTTTCTGCATTCTTTGG	21	7
9	+	2656	TTTTTCTGCATTCTTTGGATT	21	10
46	+	2658	TTTCTGCATTCTTTGGATTTAAGG	24	12
9	+	2658	TTTCTGCATTCTTTGGATTTA	21	12
5	+	2660	TCTGCATTCTTTGGATTTAAG	21	14
19	+	2662	TGCATTCTTTGGATTTAAGGT	21	16
5	+	2662	TGCATTCTTTGGATTTAAGGTT	22	16
1	+	2663	GCATTCTTTGGATTTAAGGTT	21	17
22	+	2675	TTTAAGGTTTTCCTCGTGATT	21	8
43	+	2682	TTTTCCTCGTGATTTCCCCTAA	22	15
6	+	2682	TTTTCCTCGTGATTTCCCCTA	21	15
11	+	2684	TTCCTCGTGATTTCCCCTAAC	21	17
2	+	2686	CCTCGTGATTTCCCCTAACCA	21	19
35	+	2689	CGTGATTTCCCCTAACCATGA	21	1
6	+	2691	TGATTTCCCCTAACCATGATGC	22	3
15	+	2694	TTTCCCCTAACCATGATGCTG	21	6
41	+	2702	AACCATGATGCTGAAGAAACT	21	14
3	+	2703	ACCATGATGCTGAAGAAACTA	21	15
17	+	2704	CCATGATGCTGAAGAAACTAG	21	16
4	+	2726	AATTCTCCCTTATTTTGTCCT	21	17
11	+	2730	CTCCCTTATTTTGTCCTCGCA	21	0
5	+	2735	TTATTTTGTCCTCGCATTGGC	21	5

3	+	2736	TATTTTGTCCTCGCATTGGCA	21	6
14	+	2743	TCCTCGCATTGGCAAAATCGG	21	13
18	+	2746	TCGCATTGGCAAAATCGGTTGC	22	16
20	+	2746	TCGCATTGGCAAAATCGGTTG	21	16
10	+	2747	CGCATTGGCAAAATCGGTTGC	21	17
3	+	2748	GCATTGGCAAAATCGGTTGCT	21	18
11	+	2764	TTGCTCCGATGACGAAACACC	21	13
5	+	2779	AACACCTATTTATATTATCCC	21	7
21	+	2790	ATATTATCCCCAAACCTCGAG	21	18
6	+	2791	TATTATCCCCAAACCTCGA	19	19
30	+	2793	TTATCCCCAAACCTCGAGCAGA	22	0
5	+	2823	TTATGTTTCACTCTGACTTGC	21	9
6	+	2826	TGTTTCACTCTGACTTGCATA	21	12
2	+	2845	TAACAAGGAAAAATGTCATGA	21	10
4	+	2847	ACAAGGAAAAATGTCATGAAG	21	12
9	+	2847	ACAAGGAAAAATGTCATGAAGT	22	12
6	+	2849	AAGGAAAAATGTCATGAAGTAGG	23	14
1	+	2852	GAAAAATGTCATGAAGTAGGC	21	17
30	+	2854	AAAATGTCATGAAGTAGGCAA	21	19
26	+	2855	AAATGTCATGAAGTAGGCAAC	21	20
17	+	2859	GTCATGAAGTAGGCAACGAGA	21	3
29	+	2860	TCATGAAGTAGGCAACGAGAT	21	4
11	+	2862	ATGAAGTAGGCAACGAGATACT	22	6
6	+	2863	TGAAGTAGGCAACGAGATACTG	22	7
8	+	2869	AGGCAACGAGATACTGTTTGA	21	13
10	+	2874	ACGAGATACTGTTTGAATTCA	21	18
4	+	2875	CGAGATACTGTTTGAATTCAG	21	19
10	+	2876	GAGATACTGTTTGAATTCAGC	21	20
5	+	2901	TATCCGACACCTATGAGATTA	21	3
1	+	2908	CACCTATGAGATTATTGAGTG	21	10
10	+	2909	ACCTATGAGATTATTGAGTGT	21	11
8	+	2910	CCTATGAGATTATTGAGTGTGG	22	12
3	+	2912	TATGAGATTATTGAGTGTGGT	21	14
8	+	2913	ATGAGATTATTGAGTGTGGTGT	22	15
1	+	2914	TGAGATTATTGAGTGTGGTGT	21	16
9	+	2914	TGAGATTATTGAGTGTGGTGTC	22	16
24	+	2918	ATTATTGAGTGTGGTGTCAGA	21	20
29	+	2929	TGGTGTCAGATTCTATACAGA	21	10
5	+	2932	TGTCAGATTCTATACAGATGA	21	13
3	+	2937	GATTCTATACAGATGAACAGGT	22	18
73	+	2939	TTCTATACAGATGAACAGGTG	21	20
6	+	2942	TATACAGATGAACAGGTGAAA	21	2
5	+	2949	ATGAACAGGTGAAATCAGTGA	21	9
1	+	2950	TGAACAGGTGAAATCAGTGA	20	10

12	+	2953	ACAGGTGAAATCAGTGAAAGG	21	13
3	+	2955	AGGTGAAATCAGTGAAAGGAG	21	15
12	+	2956	GGTGAAATCAGTGAAAGGAGA	21	16
1	+	2957	GTGAAATCAGTGAAAGGAGA	20	17
5	+	2967	TGAAAGGAGAAATGAATATGA	21	6
8	+	2969	AAAGGAGAAATGAATATGAAA	21	8
3	+	2972	GGAGAAATGAATATGAAATAGA	22	11
10	+	2984	ATGAAATAGACCAAGTTTGTG	21	2
2	+	2987	AAATAGACCAAGTTTGTGAAG	21	5
5	+	2987	AAATAGACCAAGTTTGTGAAGA	22	5
61	+	2988	AATAGACCAAGTTTGTGAAGA	21	6
5	+	2997	AGTTTGTGAAGATGAAAACGA	21	15
15	+	2999	TTTGTGAAGATGAAAACGATT	21	17
25	+	3001	TGTGAAGATGAAAACGATTGG	21	19
6	+	3003	TGAAGATGAAAACGATTGGAGC	22	0
12	+	3004	GAAGATGAAAACGATTGGAGC	21	1
18	+	3005	AAGATGAAAACGATTGGAGCT	21	2
2	+	3005	AAGATGAAAACGATTGGAGCTA	22	2
30	+	3008	ATGAAAACGATTGGAGCTATG	21	5
7	+	3010	GAAAACGATTGGAGCTATGAG	21	7
4	+	3017	ATTGGAGCTATGAGTTTGGACC	22	14
42	+	3022	AGCTATGAGTTTGGACCCGTG	21	19
4	+	3023	GCTATGAGTTTGGACCCGTGG	21	20
5	+	3025	TATGAGTTTGGACCCGTGGAAG	22	1
6	+	3027	TGAGTTTGGACCCGTGGAAGC	21	3
1	+	3029	AGTTTGGACCCGTGGAAGCAT	21	5
4	+	3039	CGTGGAAGCATTGGAATGCTC	21	15
5	+	3039	CGTGGAAGCATTGGAATGCTCT	22	15
111	+	3062	AAAATAATGGACATAATGATA	21	17
8	+	3063	AAATAATGGACATAATGATAGC	22	18
3	+	3074	ATAATGATAGCCTAATCTGTA	21	8
9	+	3080	ATAGCCTAATCTGTACTTCGA	21	14
16	+	3081	TAGCCTAATCTGTACTTCGAA	21	15
9	+	3084	CCTAATCTGTACTTCGAACGAA	22	18
33	+	3087	AATCTGTACTTCGAACGAAGA	21	0
11	+	3096	TTCGAACGAAGACAAGATCGA	21	9
5	+	3104	AAGACAAGATCGAAGCCAACA	21	17
3	+	3105	AGACAAGATCGAAGCCAACAAATACACA	28	18
9	+	3112	ATCGAAGCCAACAAATACACA	21	4
3	+	3115	GAAGCCAACAAATACACAGAT	21	7
29	+	3123	CAAATACACAGATTGTTGGAG	21	15
2	+	3123	CAAATACACAGATTGTTGGAGT	22	15
1	+	3124	AAATACACAGATTGTTGGAG	20	16
93	+	3125	AATACACAGATTGTTGGAGTT	21	17

49	+	3127	TACACAGATTGTTGGAGTTGGC	22	19
4	+	3128	ACACAGATTGTTGGAGTTGGC	21	20
50	+	3130	ACAGATTGTTGGAGTTGGCTC	21	1
2	+	3136	TGTTGGAGTTGGCTCATCATC	21	7
27	+	3139	TGGAGTTGGCTCATCATCTGTT	22	10
17	+	3157	TGTTTTGATGTCTCCCATATT	21	7
10	+	3159	TTTTGATGTCTCCCATATTGT	21	9
17	+	3179	TGAGAAGCATCGGAAGTTTAG	21	8
2	+	3184	AGCATCGGAAGTTTAGTTTGGG	22	13
11	+	3190	GGAAGTTTAGTTTGGGGAGGA	21	19
4	+	3200	TTTGGGGAGGAAGATGAGAGA	21	8
1	+	3210	AAGATGAGAGAAGCAAGAAGG	21	18
3	+	3227	AAGGAGAATATCAAAGTGGAG	21	14
1	+	3228	AGGAGAATATCAAAGTGGAGAA	22	15
93	+	3228	AGGAGAATATCAAAGTGGAGA	21	15
5	+	3236	ATCAAAGTGGAGAAGTCGAAC	21	2
6	+	3244	GGAGAAGTCGAACGAATTTGC	21	10
13	+	3265	AAGTGAGGAAAGAATATCTGTT	22	10
6	+	3266	AGTGAGGAAAGAATATCTGTT	21	11
3	-	92	GTAAATGAGAGAGAAAAGTCTTACG	25	8
2	-	215	AACCACAATCGATATCCTAGA	21	5
4	-	215	AGAACCACAATCGATATCCTAGA	23	5
1	-	252	TCAAGCACCAACTCGAAGAAG	21	0
143	-	282	TCTTTGCATTTCAAAATCTCCA	22	9
83	-	282	CTTTGCATTTCAAAATCTCCA	21	9
164	-	283	TCTTTGCATTTCAAAATCTCC	21	10
4	-	283	GTCTTTGCATTTCAAAATCTCC	22	10
1	-	286	TACGTCTTTGCATTTCAAAATC	22	13
3	-	290	ACTACGTCTTTGCATTTCAA	20	17
23	-	299	AGATCGGCATCACTACGTCTTT	22	5
1	-	300	AGAAGATCGGCATCACTACGTCTT	24	6
3	-	301	GAAGATCGGCATCACTACGTCT	22	7
21	-	302	AGAAGATCGGCATCACTACGTC	22	8
43	-	302	GAAGATCGGCATCACTACGTC	21	8
1	-	303	ATAGAAGATCGGCATCACTACGT	23	9
2023	-	303	AGAAGATCGGCATCACTACGT	21	9
259	-	303	TAGAAGATCGGCATCACTACGT	22	9
1664	-	304	TAGAAGATCGGCATCACTACG	21	10
168	-	304	ATAGAAGATCGGCATCACTACG	22	10
8	-	304	TCATAGAAGATCGGCATCACTACG	24	10
20	-	305	TCATAGAAGATCGGCATCACTAC	23	11
21	-	305	ATAGAAGATCGGCATCACTAC	21	11
4	-	306	TAGAAGATCGGCATCACTA	19	12
4	-	306	TCATAGAAGATCGGCATCACTA	22	12

6	-	307	TCATAGAAGATCGGCATCACT	21	13
12	-	309	ATAGAAGATCGGCATCA	17	15
9	-	309	CTTCATAGAAGATCGGCATCA	21	15
2	-	310	TACTTCATAGAAGATCGGCATC	22	16
1	-	312	ATCTACTTCATAGAAGATCGGCA	23	18
1	-	312	TCTACTTCATAGAAGATCGGCA	22	18
114	-	313	ATCTACTTCATAGAAGATCGGC	22	19
2	-	313	CTACTTCATAGAAGATCGGC	20	19
846	-	313	TCTACTTCATAGAAGATCGGC	21	19
12	-	314	ATCTACTTCATAGAAGATCGG	21	20
9	-	317	ATGGATCTACTTCATAGAAGAT	22	2
53	-	318	ATGGATCTACTTCATAGAAGA	21	3
2	-	321	TCGGATGGATCTACTTCATAGA	22	6
13	-	323	ATCGGATGGATCTACTTCATA	21	8
4	-	323	CATCGGATGGATCTACTTCATA	22	8
1086	-	324	CATCGGATGGATCTACTTCAT	21	9
3	-	324	ATCGGATGGATCTACTTCAT	20	9
4	-	324	GTACATCGGATGGATCTACTTCAT	24	9
1065	-	325	ACATCGGATGGATCTACTTCA	21	10
327	-	325	TACATCGGATGGATCTACTTCA	22	10
5	-	325	CATCGGATGGATCTACTTCA	20	10
1005	-	326	TACATCGGATGGATCTACTTC	21	11
11	-	326	CATCGGATGGATCTACTTC	19	11
3	-	326	GTACATCGGATGGATCTACTTC	22	11
5	-	326	CTGTTTCCGTACATCGGATGGATCTACTTC	30	11
95	-	334	TGTTTCCGTACATCGGATGGA	21	19
9	-	336	TCTGTTTCCGTACATCGGATG	21	0
1	-	339	CGGTCTGTTTCCGTACATCGG	21	3
11	-	341	TCCGGTCTGTTTCCGTACATC	21	5
2	-	342	AATCTCCGGTCTGTTTCCGTACAT	24	6
4	-	342	CTCCGGTCTGTTTCCGTACAT	21	6
8	-	342	TCTCCGGTCTGTTTCCGTACAT	22	6
20	-	343	TCTCCGGTCTGTTTCCGTACA	21	7
30	-	344	ATCTCCGGTCTGTTTCCGTAC	21	8
1449	-	345	AATCTCCGGTCTGTTTCCGTA	21	9
15	-	345	AAATCTCCGGTCTGTTTCCGTA	22	9
1	-	345	AAAATCTCCGGTCTGTTTCCGTA	23	9
2	-	345	ATCTCCGGTCTGTTTCCGTA	20	9
3	-	345	CAAAATCTCCGGTCTGTTTCCGTA	24	9
1254	-	346	AAATCTCCGGTCTGTTTCCGT	21	10
1	-	346	AATCTCCGGTCTGTTTCCGT	20	10
44	-	346	AAAATCTCCGGTCTGTTTCCGT	22	10
5	-	346	CAAAATCTCCGGTCTGTTTCCGT	23	10
1	-	347	AAATCTCCGGTCTGTTTCCG	20	11

246	-	347	CAAAATCTCCGGTCTGTTTCCG	22	11
582	-	347	AAAATCTCCGGTCTGTTTCCG	21	11
2	-	348	CAAAATCTCCGGTCTGTTTCC	21	12
190	-	366	TATTTTTGAAGGCCTTCCCAA	21	9
1	-	366	ATTTTTGAAGGCCTTCCCAA	20	9
8	-	366	CTATTTTTGAAGGCCTTCCCAA	22	9
171	-	367	CTATTTTTGAAGGCCTTCCCA	21	10
17	-	367	ACTATTTTTGAAGGCCTTCCCA	22	10
94	-	368	ACTATTTTTGAAGGCCTTCCC	21	11
1	-	369	CAACTATTTTTGAAGGCCTTCC	22	12
37	-	369	AACTATTTTTGAAGGCCTTCC	21	12
10	-	374	TTTTACAACTATTTTTGAAGGC	22	17
35	-	374	TTTACAACTATTTTTGAAGGC	21	17
2	-	375	CTTTTACAACTATTTTTGAAGG	22	18
28	-	376	CTTTTACAACTATTTTTGAAG	21	19
7	-	380	TTTACTTTTACAACTATTTTT	21	2
17	-	387	CCTTAGTTTTACTTTTACAAC	21	9
154	-	388	TCCTTAGTTTTACTTTTACAA	21	10
6	-	389	TCCTTAGTTTTACTTTTACA	20	11
1	-	402	CATCTCTGCCTCTCCTCCTTAG	22	3
1	-	408	TTGGATCCATCTCTGCCTCTCCT	23	9
21	-	408	GGATCCATCTCTGCCTCTCCT	21	9
146	-	409	TTGGATCCATCTCTGCCTCTCC	22	10
300	-	409	TGGATCCATCTCTGCCTCTCC	21	10
15	-	410	CTTGGATCCATCTCTGCCTCTC	22	11
1	-	410	TGGATCCATCTCTGCCTCTC	20	11
772	-	410	TTGGATCCATCTCTGCCTCTC	21	11
1	-	411	TTGGATCCATCTCTGCCTCT	20	12
229	-	411	CTTGGATCCATCTCTGCCTCT	21	12
7	-	412	GCTTGGATCCATCTCTGCCTC	21	13
104	-	417	TTAAAGCTTGGATCCATCTCT	21	18
4	-	417	ATTAAAGCTTGGATCCATCTCT	22	18
1	-	418	AAAATTAAAGCTTGGATCCATCTC	24	19
216	-	418	ATTAAAGCTTGGATCCATCTC	21	19
1	-	419	AAATTAAAGCTTGGATCCATCT	22	20
1	-	419	TTAAAGCTTGGATCCATCT	19	20
3	-	419	AATTAAAGCTTGGATCCATCT	21	20
40	-	420	AAAATTAAAGCTTGGATCCATC	22	0
6	-	420	AAATTAAAGCTTGGATCCATC	21	0
36	-	421	TTAAAGCTTGGATCCAT	17	1
4	-	422	AAAAATTAAAGCTTGGATCCA	21	2
15	-	429	TGCCAACAAAAATTAAAGCTT	21	9
1	-	430	TGCCAACAAAAATTAAAGCT	20	10
236	-	430	TTGCCAACAAAAATTAAAGCT	21	10

38	-	431	GTTGCCAACAAAAATTAAAGC	21	11
1	-	432	TTGCCAACAAAAATTAAAG	19	12
8	-	432	TGTTGCCAACAAAAATTAAAG	21	12
23	-	439	TCCAGCTATGTTGCCAACAAAA	22	19
3	-	440	TCCAGCTATGTTGCCAACAAA	21	20
8	-	442	TCTCCAGCTATGTTGCCAACA	21	1
4	-	445	TGTTCTCCAGCTATGTTGCCA	21	4
22	-	447	AGTGTTCTCCAGCTATGTTGC	21	6
54	-	449	CGAGTGTTCTCCAGCTATGTT	21	8
18	-	451	AGCGAGTGTTCTCCAGCTATG	21	10
46	-	452	TCAGCGAGTGTTCTCCAGCTAT	22	11
106	-	453	TCAGCGAGTGTTCTCCAGCTA	21	12
14	-	454	TTCAGCGAGTGTTCTCCAGCT	21	13
6	-	454	TTTCAGCGAGTGTTCTCCAGCT	22	13
51	-	455	TTTCAGCGAGTGTTCTCCAGC	21	14
1	-	456	ATTTCAGCGAGTGTTCTCCAG	21	15
2	-	456	CATTTCAGCGAGTGTTCTCCAG	22	15
19	-	457	TTTCAGCGAGTGTTCTCCA	19	16
2	-	478	ATCATATCCGCTTCATTTTCC	21	16
15	-	481	TCAATCATATCCGCTTCATTT	21	19
13	-	482	TTCAATCATATCCGCTTCATT	21	20
23	-	483	TTTCAATCATATCCGCTTCAT	21	0
2	-	486	TCTTTTCAATCATATCCGCTT	21	3
121	-	489	CTATCTTTTCAATCATATCCG	21	6
7	-	489	CTTTTCAATCATATCCG	17	6
4	-	492	TTGGCTATCTTTTCAATCATAT	22	9
62	-	493	TTTGGCTATCTTTTCAATCATA	22	10
65	-	493	TTGGCTATCTTTTCAATCATA	21	10
18	-	494	TTTGGCTATCTTTTCAATCAT	21	11
123	-	496	TCTTTGGCTATCTTTTCAATC	21	13
4	-	496	TTTGGCTATCTTTTCAATC	19	13
9	-	501	AAACATCTTTGGCTATCTTTT	21	18
113	-	502	TGAAACATCTTTGGCTATCTTT	22	19
22	-	503	TGAAACATCTTTGGCTATCTT	21	20
3	-	504	TATCTGAAACATCTTTGGCTATCT	24	0
70	-	505	TCTGAAACATCTTTGGCTATC	21	1
9	-	505	ATCTGAAACATCTTTGGCTATC	22	1
15	-	506	ATCTGAAACATCTTTGGCTAT	21	2
29	-	507	TATCTGAAACATCTTTGGCTA	21	3
29	-	508	TTATCTGAAACATCTTTGGCT	21	4
2	-	509	GTTTATCTGAAACATCTTTGGC	22	5
5	-	509	TTTATCTGAAACATCTTTGGC	21	5
7	-	528	TTAGAAGGTGTAGCATTCAGTT	22	3
53	-	529	TTAGAAGGTGTAGCATTCAGT	21	4

8	-	529	TTTAGAAGGTGTAGCATTCAGT	22	4
1	-	530	TTAGAAGGTGTAGCATTCAG	20	5
23	-	530	TTTAGAAGGTGTAGCATTCAG	21	5
37	-	532	TCTTTAGAAGGTGTAGCATTC	21	7
2	-	533	AAAATCTTTAGAAGGTGTAGCATT	24	8
74	-	533	ATCTTTAGAAGGTGTAGCATT	21	8
26	-	535	AAATCTTTAGAAGGTGTAGCA	21	10
4	-	536	TCAAAATCTTTAGAAGGTGTAGC	23	11
68	-	536	AAAATCTTTAGAAGGTGTAGC	21	11
58	-	537	TCAAAATCTTTAGAAGGTGTAG	22	12
165	-	538	TCAAAATCTTTAGAAGGTGTA	21	13
6	-	538	ATCAAAATCTTTAGAAGGTGTA	22	13
31	-	539	ATCAAAATCTTTAGAAGGTGT	21	14
24	-	540	CATCAAAATCTTTAGAAGGTG	21	15
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3	-	544	AATGCATCAAAATCTTTAGAA	21	19
286	-	545	AAATGCATCAAAATCTTTAGA	21	20
8	-	549	CCACAAATGCATCAAAATCTT	21	3
8	-	551	CCACAAATGCATCAAAATC	19	5
5	-	554	AAGTCCCACAAATGCATCAAA	21	8
31	-	555	CAAGTCCCACAAATGCATCAA	21	9
21	-	556	TCAAGTCCCACAAATGCATCA	21	10
43	-	557	CTCAAGTCCCACAAATGCATC	21	11
6	-	557	ACTCAAGTCCCACAAATGCATC	22	11
21	-	558	ACTCAAGTCCCACAAATGCAT	21	12
4	-	558	AACTCAAGTCCCACAAATGCAT	22	12
113	-	559	AACTCAAGTCCCACAAATGCA	21	13
1	-	559	AAACTCAAGTCCCACAAATGCA	22	13
11	-	560	AAACTCAAGTCCCACAAATGC	21	14
7	-	561	TGAAACTCAAGTCCCACAAATG	22	15
15	-	566	AATGTGAAACTCAAGTCCCAC	21	20
6	-	566	TAATGTGAAACTCAAGTCCCAC	22	20
101	-	567	TAATGTGAAACTCAAGTCCCA	21	0
1	-	567	CTAATGTGAAACTCAAGTCCCA	22	0
3	-	567	TTAATTCCCTAATGTGAAACTCAAGTCCC	31	0
17	-	568	TCCCTAATGTGAAACTCAAGTCCC	24	1
85	-	568	CTAATGTGAAACTCAAGTCCC	21	1
6	-	569	CCCTAATGTGAAACTCAAGTCC	22	2
16	-	570	CCCTAATGTGAAACTCAAGTC	21	3
109	-	573	ATTCCCTAATGTGAAACTCAA	21	6
2	-	573	TTCCCTAATGTGAAACTCAA	20	6
2	-	578	ACTTAATTCCCTAATGTGAAA	21	11
44	-	579	AACTTAATTCCCTAATGTGAA	21	12
4	-	579	ACTTAATTCCCTAATGTGAA	20	12

5	-	580	GAACTTAATTCCCTAATGTGA	21	13
7	-	580	AGAACTTAATTCCCTAATGTGA	22	13
83	-	587	TAGCAGAGAACTTAATTCCCT	21	20
12	-	588	ATAGCAGAGAACTTAATTCCC	21	0
5	-	588	TATAGCAGAGAACTTAATTCCC	22	0
33	-	589	TATAGCAGAGAACTTAATTCC	21	1
18	-	594	CTAGGTATAGCAGAGAACTTA	21	6
182	-	595	TCTAGGTATAGCAGAGAACTT	21	7
108	-	597	TAGTCTAGGTATAGCAGAGAAC	22	9
19	-	598	TAGTCTAGGTATAGCAGAGAA	21	10
4	-	598	ATAGTCTAGGTATAGCAGAGAA	22	10
53	-	599	CATAGTCTAGGTATAGCAGAGA	22	11
6059	-	599	ATAGTCTAGGTATAGCAGAGA	21	11
9	-	599	TAGTCTAGGTATAGCAGAGA	20	11
1	-	600	TAGTCTAGGTATAGCAGAG	19	12
1	-	600	TCATAGTCTAGGTATAGCAGAG	22	12
6	-	600	ATAGTCTAGGTATAGCAGAG	20	12
92	-	600	CATAGTCTAGGTATAGCAGAG	21	12
1139	-	601	TCATAGTCTAGGTATAGCAGA	21	13
29	-	601	ATAGTCTAGGTATAGCAGA	19	13
3	-	601	CATAGTCTAGGTATAGCAGA	20	13
533	-	601	CTCATAGTCTAGGTATAGCAGA	22	13
71	-	602	CTCATAGTCTAGGTATAGCAG	21	14
1	-	603	GCTCATAGTCTAGGTATAGCA	21	15
3	-	603	TGCTCATAGTCTAGGTATAGCA	22	15
72	-	604	TTGCTCATAGTCTAGGTATAGC	22	16
9	-	604	TGCTCATAGTCTAGGTATAGC	21	16
8	-	605	TTGCTCATAGTCTAGGTATAG	21	17
1	-	607	ACTTGCTCATAGTCTAGGTAT	21	19
26	-	608	CACTTGCTCATAGTCTAGGTA	21	20
4	-	608	TCACTTGCTCATAGTCTAGGTA	22	20
102	-	609	TCACTTGCTCATAGTCTAGGT	21	0
12	-	609	CTCACTTGCTCATAGTCTAGGT	22	0
1	-	610	CCTCACTTGCTCATAGTCTAGG	22	1
39	-	610	CTCACTTGCTCATAGTCTAGG	21	1
12	-	611	CCTCACTTGCTCATAGTCTAG	21	2
6	-	611	TCCTCACTTGCTCATAGTCTAG	22	2
22	-	612	TCCTCACTTGCTCATAGTCTA	21	3
13	-	614	TATCCTCACTTGCTCATAGTC	21	5
4	-	614	CTATCCTCACTTGCTCATAGTC	22	5
24	-	616	TACTATCCTCACTTGCTCATAG	22	7
4	-	616	ACTATCCTCACTTGCTCATAG	21	7
5	-	617	TACTATCCTCACTTGCTCATA	21	8
55	-	618	CTACTATCCTCACTTGCTCAT	21	9

14	-	619	CCTACTATCCTCACTTGCTCA	21	10
52	-	619	TCCTACTATCCTCACTTGCTCA	22	10
39	-	620	TCCTACTATCCTCACTTGCTC	21	11
9	-	620	TTCCTACTATCCTCACTTGCTC	22	11
116	-	621	TTCCTACTATCCTCACTTGCT	21	12
144	-	622	ATTCCTACTATCCTCACTTGC	21	13
4	-	622	CAGATTCCTACTATCCTCACTTGC	24	13
12	-	625	CAGATTCCTACTATCCTCACT	21	16
17	-	625	ACAGATTCCTACTATCCTCACT	22	16
24	-	629	GCCACAGATTCCTACTATCCT	21	20
7	-	633	CAGGGCCACAGATTCCTACTA	21	3
132	-	636	CTGCAGGGCCACAGATTCCTA	21	6
1	-	637	CCTGCAGGGCCACAGATTCCT	21	7
62	-	640	CTGCAGGGCCACAGATT	17	10
70	-	640	ATTCCTGCAGGGCCACAGATT	21	10
3	-	642	GATTCCTGCAGGGCCACAGA	20	12
22	-	644	ACCGATTCCTGCAGGGCCACA	21	14
31	-	644	TACCGATTCCTGCAGGGCCACA	22	14
64	-	646	TTACCGATTCCTGCAGGGCCA	21	16
13	-	647	CTTACCGATTCCTGCAGGGCC	21	17
86	-	648	TCTTACCGATTCCTGCAGGGC	21	18
24	-	649	GTCTTACCGATTCCTGCAGGG	21	19
13	-	650	AGTCTTACCGATTCCTGCAGG	21	20
1	-	650	GTCTTACCGATTCCTGCAGG	20	20
49	-	650	TAGTCTTACCGATTCCTGCAGG	22	20
3	-	651	GTAGTCTTACCGATTCCTGCAG	22	0
43	-	651	TAGTCTTACCGATTCCTGCAG	21	0
12	-	652	GTAGTCTTACCGATTCCTGCA	21	1
4	-	659	AGCAATGGTAGTCTTACCGAT	21	8
7	-	660	AGCAATGGTAGTCTTACCGA	20	9
1	-	661	GAGCAATGGTAGTCTTACCG	20	10
40	-	661	CGAGCAATGGTAGTCTTACCG	21	10
1	-	663	GCACGAGCAATGGTAGTCTTAC	22	12
10	-	664	GCACGAGCAATGGTAGTCTTA	21	13
109	-	665	AGCACGAGCAATGGTAGTCTT	21	14
4	-	665	AAGCACGAGCAATGGTAGTCTT	22	14
23	-	666	AAGCACGAGCAATGGTAGTCT	21	15
3	-	666	AAAGCACGAGCAATGGTAGTCT	22	15
41	-	667	AAAGCACGAGCAATGGTAGTC	21	16
17	-	668	TAAAGCACGAGCAATGGTAGT	21	17
5	-	668	TTGTAAAGCACGAGCAATGGTAGT	24	17
40	-	670	TGTAAAGCACGAGCAATGGTA	21	19
26	-	671	TTGTAAAGCACGAGCAATGGT	21	20
4	-	672	CTTTGTAAAGCACGAGCAATGG	22	0

87	-	672	TTTGTAAAGCACGAGCAATGG	21	0
2	-	675	GGCTTTGTAAAGCACGAGCAA	21	3
13	-	676	AGGCTTTGTAAAGCACGAGCA	21	4
1	-	680	TAGAGAGTAGGCTTTGTAAAGCACG	25	8
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15	-	682	GAGAGTAGGCTTTGTAAAGCA	21	10
11	-	683	AGAGAGTAGGCTTTGTAAAGC	21	11
142	-	683	TAGAGAGTAGGCTTTGTAAAGC	22	11
1	-	684	AGAGAGTAGGCTTTGTAAAG	20	12
1	-	684	GAGAGTAGGCTTTGTAAAG	19	12
615	-	684	TAGAGAGTAGGCTTTGTAAAG	21	12
6	-	684	CTAGAGAGTAGGCTTTGTAAAG	22	12
38	-	685	CTAGAGAGTAGGCTTTGTAAA	21	13
147	-	687	TTGCTAGAGAGTAGGCTTTGTA	22	15
438	-	687	TGCTAGAGAGTAGGCTTTGTA	21	15
22	-	688	TTGCTAGAGAGTAGGCTTTGT	21	16
30	-	688	ATTGCTAGAGAGTAGGCTTTGT	22	16
7	-	689	ATTGCTAGAGAGTAGGCTTTG	21	17
27	-	690	AATTGCTAGAGAGTAGGCTTT	21	18
9	-	691	AAATTGCTAGAGAGTAGGCTT	21	19
10	-	692	GAAAATTGCTAGAGAGTAGGCT	22	20
137	-	692	AAAATTGCTAGAGAGTAGGCT	21	20
126	-	693	GAAAATTGCTAGAGAGTAGGC	21	0
15	-	693	TGAAAATTGCTAGAGAGTAGGC	22	0
1	-	693	AAAATTGCTAGAGAGTAGGC	20	0
599	-	694	TGAAAATTGCTAGAGAGTAGG	21	1
1	-	695	AAAATTGCTAGAGAGTAG	18	2
3	-	695	CTGAAAATTGCTAGAGAGTAG	21	2
10	-	696	GAAAATTGCTAGAGAGTA	18	3
15	-	696	GCTGAAAATTGCTAGAGAGTA	21	3
26	-	697	TCGCTGAAAATTGCTAGAGAGT	22	4
92	-	697	CGCTGAAAATTGCTAGAGAGT	21	4
2	-	698	ACTTCGCTGAAAATTGCTAGAGAG	24	5
2	-	698	TTCGCTGAAAATTGCTAGAGAG	22	5
289	-	699	TTCGCTGAAAATTGCTAGAGA	21	6
19	-	701	AACTTCGCTGAAAATTGCTAGA	22	8
80	-	701	ACTTCGCTGAAAATTGCTAGA	21	8
5	-	702	AACTTCGCTGAAAATTGCTAG	21	9
21	-	703	CAACTTCGCTGAAAATTGCTA	21	10
141	-	704	ACAACTTCGCTGAAAATTGCT	21	11
2	-	705	AACAACTTCGCTGAAAATTGC	21	12
7	-	707	TAAAACAACTTCGCTGAAAATT	22	14
8	-	707	AAAACAACTTCGCTGAAAATT	21	14
1	-	708	ACAACTTCGCTGAAAAT	17	15

6	-	708	TAAAACAACTTCGCTGAAAAT	21	15
4	-	709	ATAAAACAACTTCGCTGAAAA	21	16
3	-	711	CCATAAAACAACTTCGCTGAA	21	18
4	-	711	TCCATAAAACAACTTCGCTGAA	22	18
39	-	712	CTCCATAAAACAACTTCGCTGA	22	19
90	-	712	TCCATAAAACAACTTCGCTGA	21	19
4	-	713	CTCCATAAAACAACTTCGCTG	21	20
40	-	714	TTCTCCATAAAACAACTTCGCT	22	0
91	-	714	TCTCCATAAAACAACTTCGCT	21	0
107	-	715	TTCTCCATAAAACAACTTCGC	21	1
118	-	715	ATTCTCCATAAAACAACTTCGC	22	1
46	-	716	ATTCTCCATAAAACAACTTCG	21	2
4	-	726	TCCCCTAACATTCTCCATAA	20	12
12	-	727	TTCCCCTAACATTCTCCATA	20	13
6	-	728	ACTTCCCCTAACATTCTCCAT	21	14
1	-	729	AGACTTCCCCTAACATTCTCCA	22	15
10	-	730	AGACTTCCCCTAACATTCTCC	21	16
6	-	730	GACTTCCCCTAACATTCTCC	20	16
1	-	731	AAGACTTCCCCTAACATTCTC	21	17
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11	-	732	TTAAGACTTCCCCTAACATTCT	22	18
3	-	733	TTAAGACTTCCCCTAACATTC	21	19
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30	-	734	TATTAAGACTTCCCCTAACATT	22	20
40	-	735	TATTAAGACTTCCCCTAACAT	21	0
133	-	736	AATATTAAGACTTCCCCTAACA	22	1
251	-	736	ATATTAAGACTTCCCCTAACA	21	1
2	-	736	TATTAAGACTTCCCCTAACA	20	1
3	-	737	CAATATTAAGACTTCCCCTAAC	22	2
87	-	737	AATATTAAGACTTCCCCTAAC	21	2
1	-	738	CCAATATTAAGACTTCCCCTAA	22	3
3	-	741	GCCCAATATTAAGACTTCCCC	21	6
9	-	742	AAGCCCAATATTAAGACTTCCC	22	7
2	-	746	CTCGTCAAGCCCAATATTAAGACT	24	11
5	-	747	CTCGTCAAGCCCAATATTAAGAC	23	12
15	-	748	ACTCGTCAAGCCCAATATTAAGA	23	13
3	-	748	TCGTCAAGCCCAATATTAAGA	21	13
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7	-	749	ATACTCGTCAAGCCCAATATTAAG	24	14
83	-	752	ATACTCGTCAAGCCCAATATT	21	17
27	-	753	CCATACTCGTCAAGCCCAATAT	22	18
5	-	754	ACCATACTCGTCAAGCCCAATA	22	19
16	-	755	ACCATACTCGTCAAGCCCAAT	21	20
17	-	757	AGACCATACTCGTCAAGCCCA	21	1

5	-	757	GACCATACTCGTCAAGCCCA	20	1
48	-	758	CAGACCATACTCGTCAAGCCC	21	2
8	-	758	TCAGACCATACTCGTCAAGCCC	22	2
13	-	759	TTCAGACCATACTCGTCAAGCC	22	3
61	-	759	TCAGACCATACTCGTCAAGCC	21	3
2	-	760	TCAGACCATACTCGTCAAGC	20	4
4	-	760	TTCAGACCATACTCGTCAAGC	21	4
38	-	761	CTTCAGACCATACTCGTCAAG	21	5
9	-	761	ACTTCAGACCATACTCGTCAAG	22	5
8	-	762	ACTTCAGACCATACTCGTCAA	21	6
6	-	763	AACTTCAGACCATACTCGTCA	21	7
107	-	764	TAACTTCAGACCATACTCGTC	21	8
4	-	765	CTAACTTCAGACCATACTCGT	21	9
85	-	765	TCTAACTTCAGACCATACTCGT	22	9
142	-	766	TCTAACTTCAGACCATACTCG	21	10
37	-	766	ATCTAACTTCAGACCATACTCG	22	10
100	-	767	ATCTAACTTCAGACCATACTC	21	11
16	-	768	AATCTAACTTCAGACCATACT	21	12
2	-	768	TAAATCTAACTTCAGACCATACT	23	12
3	-	769	TAAATCTAACTTCAGACCATAC	22	13
159	-	770	TAAATCTAACTTCAGACCATA	21	14
13	-	772	TGTAAATCTAACTTCAGACCA	21	16
1	-	772	TTGTAAATCTAACTTCAGACCA	22	16
31	-	773	TTGTAAATCTAACTTCAGACC	21	17
9	-	775	TTCTTGTAAATCTAACTTCAGA	22	19
5	-	776	TTCTTGTAAATCTAACTTCAG	21	20
132	-	778	TCGTTCTTGTAAATCTAACTTC	22	1
59	-	778	CGTTCTTGTAAATCTAACTTC	21	1
232	-	779	TCGTTCTTGTAAATCTAACTT	21	2
12	-	781	AGTCGTTCTTGTAAATCTAAC	21	4
22	-	783	GAAGTCGTTCTTGTAAATCTA	21	6
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33	-	789	TTGAAAGAAGTCGTTCTTGTA	21	12
33	-	789	TTTGAAAGAAGTCGTTCTTGTA	22	12
63	-	790	TTTGAAAGAAGTCGTTCTTGT	21	13
2	-	792	TCTTTGAAAGAAGTCGTTCTT	21	15
6	-	792	ATCTTTGAAAGAAGTCGTTCTT	22	15
10	-	794	AATCTTTGAAAGAAGTCGTTC	21	17
7	-	795	TAATCTTTGAAAGAAGTCGTT	21	18
5	-	798	TCATAATCTTTGAAAGAAGTC	21	0
4	-	799	TTCATAATCTTTGAAAGAAGT	21	1
13	-	802	GGTTCATAATCTTTGAAAGA	20	4

57	-	804	TTTGGTTCATAATCTTTGAAA	21	6
1	-	805	TTTGGTTCATAATCTTTGAA	20	7
38	-	805	TTTTGGTTCATAATCTTTGAA	21	7
13	-	806	CTTTTGGTTCATAATCTTTGA	21	8
17	-	808	ACCCTTTTGGTTCATAATCTTT	22	10
13	-	809	ACCCTTTTGGTTCATAATCTT	21	11
5	-	809	TACCCTTTTGGTTCATAATCTT	22	11
3	-	814	CCTCATACCCTTTTGGTTCATA	22	16
8	-	814	CTCATACCCTTTTGGTTCATA	21	16
5	-	815	TCCTCATACCCTTTTGGTTCAT	22	17
8	-	816	TCCTCATACCCTTTTGGTTCA	21	18
52	-	818	TATCCTCATACCCTTTTGGTT	21	20
13	-	819	TCTATCCTCATACCCTTTTGGT	22	0
44	-	819	CTATCCTCATACCCTTTTGGT	21	0
4	-	820	CTCTATCCTCATACCCTTTTGG	22	1
62	-	820	TCTATCCTCATACCCTTTTGG	21	1
5	-	822	CTATCCTCATACCCTTTT	18	3
7	-	824	ATGCTCTATCCTCATACCCTT	21	5
22	-	825	AATGCTCTATCCTCATACCCT	21	6
7	-	826	AAATGCTCTATCCTCATACCC	21	7
22	-	827	TAAATGCTCTATCCTCATACC	21	8
28	-	829	CCTAAATGCTCTATCCTCATA	21	10
40	-	830	TGCCTAAATGCTCTATCCTCAT	22	11
5	-	830	GCCTAAATGCTCTATCCTCAT	21	11
18	-	831	TGCCTAAATGCTCTATCCTCA	21	12
13	-	833	TTGTGCCTAAATGCTCTATCCT	22	14
42	-	833	TGTGCCTAAATGCTCTATCCT	21	14
39	-	834	TTGTGCCTAAATGCTCTATCC	21	15
114	-	835	ATTGTGCCTAAATGCTCTATC	21	16
2	-	835	TTATTGTGCCTAAATGCTCTATC	23	16
10	-	836	TATTGTGCCTAAATGCTCTAT	21	17
7	-	836	TTATTGTGCCTAAATGCTCTAT	22	17
28	-	837	TTATTGTGCCTAAATGCTCTA	21	18
7	-	838	CTTATTGTGCCTAAATGCTCT	21	19
3	-	839	TCTTATTGTGCCTAAATGCTC	21	20
30	-	840	CTCTTATTGTGCCTAAATGCT	21	0
18	-	842	ATCTCTTATTGTGCCTAAATG	21	2
41	-	843	TATCTCTTATTGTGCCTAAAT	21	3
12	-	846	ACCTATCTCTTATTGTGCCTA	21	6
21	-	847	AACCTATCTCTTATTGTGCCT	21	7
31	-	850	TGTAACCTATCTCTTATTGTG	21	10
18	-	853	TCATGTAACCTATCTCTTATT	21	13
13	-	855	TCATGTAACCTATCTCTTA	19	15
6	-	855	TGGTCATGTAACCTATCTCTTA	22	15

27	-	856	TGGTCATGTAACCTATCTCTT	21	16
5	-	856	TTGGTCATGTAACCTATCTCTT	22	16
23	-	857	TTGGTCATGTAACCTATCTCT	21	17
24	-	857	TTTGGTCATGTAACCTATCTCT	22	17
1	-	862	ACTTTTTGGTCATGTAACCTA	21	1
12	-	865	AGCACTTTTTGGTCATGTAAC	21	4
9	-	867	TAAGCACTTTTTGGTCATGTA	21	6
10	-	868	ATAAGCACTTTTTGGTCATGT	21	7
9	-	869	TGATAAGCACTTTTTGGTCATG	22	8
27	-	871	AATGATAAGCACTTTTTGGTCA	22	10
4	-	871	ATGATAAGCACTTTTTGGTCA	21	10
26	-	874	TAGAATGATAAGCACTTTTTGG	22	13
6	-	875	TAGAATGATAAGCACTTTTTG	21	14
121	-	878	ATCTAGAATGATAAGCACTTT	21	17
1	-	878	TCTAGAATGATAAGCACTTT	20	17
2	-	879	ATCTAGAATGATAAGCACTT	20	18
16	-	888	TCATTAACATCATCTAGAATGA	22	6
5	-	889	TCATTAACATCATCTAGAATG	21	7
12	-	892	GAGATCATTAACATCATCTAGA	22	10
14	-	892	AGATCATTAACATCATCTAGA	21	10
8	-	893	GAGATCATTAACATCATCTAG	21	11
10	-	894	CGAGATCATTAACATCATCTA	21	12
1	-	895	CGAGATCATTAACATCATCT	20	13
42	-	895	TCGAGATCATTAACATCATCT	21	13
22	-	896	ATCGAGATCATTAACATCATC	21	14
12	-	897	AATCGAGATCATTAACATCAT	21	15
2	-	898	AAATCGAGATCATTAACATCA	21	16
3	-	899	CAAATCGAGATCATTAACATC	21	17
4	-	900	ACAAATCGAGATCATTAACAT	21	18
12	-	901	TACAAATCGAGATCATTAACA	21	19
182	-	901	ATACAAATCGAGATCATTAACA	22	19
18	-	902	ATACAAATCGAGATCATTAAC	21	20
3	-	905	AAGCATACAAATCGAGATCATT	22	2
5	-	906	AAAGCATACAAATCGAGATCAT	22	3
4	-	907	AAAGCATACAAATCGAGATCA	21	4
1	-	908	AGCCAAAGCATACAAATCGAGATC	24	5
4	-	908	CCAAAGCATACAAATCGAGATC	22	5
1	-	910	CCAAAGCATACAAATCGAGA	20	7
41	-	910	GCCAAAGCATACAAATCGAGA	21	7
326	-	911	AGCCAAAGCATACAAATCGAG	21	8
3	-	911	ATCAGCCAAAGCATACAAATCGAG	24	8
7	-	911	CAGCCAAAGCATACAAATCGAG	22	8
23	-	912	CAGCCAAAGCATACAAATCGA	21	9
9	-	912	TCAGCCAAAGCATACAAATCGA	22	9

19	-	913	TCAGCCAAAGCATACAAATCG	21	10
3	-	913	ATCAGCCAAAGCATACAAATCG	22	10
22	-	914	ATCAGCCAAAGCATACAAATC	21	11
1	-	916	TGATCAGCCAAAGCATACAAA	21	13
13	-	917	CTGATCAGCCAAAGCATACAA	21	14
114	-	918	TCTGATCAGCCAAAGCATACA	21	15
1	-	918	CTGATCAGCCAAAGCATACA	20	15
2	-	918	CCACGTTGTCTGATCAGCCAAAGCATACA	29	15
42	-	920	TGTCTGATCAGCCAAAGCATA	21	17
5	-	920	TTGTCTGATCAGCCAAAGCATA	22	17
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8	-	922	TTGTCTGATCAGCCAAAGCA	20	19
11	-	923	CGTTGTCTGATCAGCCAAAGC	21	20
4	-	924	TTGTCTGATCAGCCAAAG	18	0
39	-	926	CCACGTTGTCTGATCAGCCAA	21	2
5	-	926	ACCACGTTGTCTGATCAGCCAA	22	2
32	-	927	ACCACGTTGTCTGATCAGCCA	21	3
62	-	927	AACCACGTTGTCTGATCAGCCA	22	3
6	-	927	CCACGTTGTCTGATCAGCCA	20	3
7	-	927	AAACCACGTTGTCTGATCAGCCA	23	3
23	-	928	CCACGTTGTCTGATCAGCC	19	4
33	-	928	AAACCACGTTGTCTGATCAGCC	22	4
3	-	928	CACGTTGTCTGATCAGCC	18	4
562	-	928	AACCACGTTGTCTGATCAGCC	21	4
13	-	929	CAAACCACGTTGTCTGATCAGC	22	5
158	-	929	AAACCACGTTGTCTGATCAGC	21	5
5	-	930	AACCACGTTGTCTGATCAG	19	6
16	-	933	GACCAAACCACGTTGTCTGAT	21	9
222	-	934	GGACCAAACCACGTTGTCTGA	21	10
7	-	934	AGGACCAAACCACGTTGTCTGA	22	10
15	-	935	AGGACCAAACCACGTTGTCTG	21	11
20	-	936	CAGGACCAAACCACGTTGTCT	21	12
130	-	937	TCCAGGACCAAACCACGTTGTC	22	13
217	-	937	CCAGGACCAAACCACGTTGTC	21	13
5	-	937	ACTTCCAGGACCAAACCACGTTGTC	25	13
320	-	938	TTCCAGGACCAAACCACGTTGT	22	14
4	-	938	CCAGGACCAAACCACGTTGT	20	14
50	-	938	ACTTCCAGGACCAAACCACGTTGT	24	14
544	-	938	TCCAGGACCAAACCACGTTGT	21	14
115	-	939	TTCCAGGACCAAACCACGTTG	21	15
15	-	940	ACTTCCAGGACCAAACCACGTT	22	16
218	-	940	CTTCCAGGACCAAACCACGTT	21	16
10	-	952	ACGATAATCCTACTTCCAGGA	21	7
13	-	953	TCACGATAATCCTACTTCCAGG	22	8

17	-	953	CACGATAATCCTACTTCCAGG	21	8
20	-	954	TCACGATAATCCTACTTCCAG	21	9
18	-	955	GTCACGATAATCCTACTTCCA	21	10
8	-	955	TCACGATAATCCTACTTCCA	20	10
27	-	956	TTGTCACGATAATCCTACTTCC	22	11
8	-	956	TGTCACGATAATCCTACTTCC	21	11
31	-	957	TTGTCACGATAATCCTACTTC	21	12
27	-	958	TGTTGTCACGATAATCCTACTT	22	13
31	-	959	TGTTGTCACGATAATCCTACT	21	14
126	-	960	CTGTTGTCACGATAATCCTAC	21	15
2	-	960	TCTGTTGTCACGATAATCCTAC	22	15
42	-	961	TCTGTTGTCACGATAATCCTA	21	16
41	-	962	TTCTGTTGTCACGATAATCCT	21	17
11	-	963	CTTCTGTTGTCACGATAATCC	21	18
27	-	963	TGTCTTCTGTTGTCACGATAATCC	24	18
80	-	964	TCTTCTGTTGTCACGATAATC	21	19
1	-	966	TTGTCTTCTGTTGTCACGATAA	22	0
2	-	966	TGTCTTCTGTTGTCACGATAA	21	0
512	-	967	TTGTCTTCTGTTGTCACGATA	21	1
18	-	968	GTTGTCTTCTGTTGTCACGAT	21	2
37	-	969	CGTTGTCTTCTGTTGTCACGA	21	3
381	-	970	TCGTTGTCTTCTGTTGTCACG	21	4
185	-	971	CTCGTTGTCTTCTGTTGTCAC	21	5
1	-	972	AAGCTCGTTGTCTTCTGTTGTCA	23	6
2	-	972	CTCGTTGTCTTCTGTTGTCA	20	6
106	-	973	AGCTCGTTGTCTTCTGTTGTC	21	7
81	-	973	AAGCTCGTTGTCTTCTGTTGTC	22	7
22	-	974	AAAGCTCGTTGTCTTCTGTTGT	22	8
81	-	974	AAGCTCGTTGTCTTCTGTTGT	21	8
40	-	975	AAAGCTCGTTGTCTTCTGTTG	21	9
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4	-	976	CAAAAGCTCGTTGTCTTCTGTT	22	10
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186	-	978	GCAAAAGCTCGTTGTCTTCTG	21	12
388	-	978	TGCAAAAGCTCGTTGTCTTCTG	22	12
144	-	979	TGCAAAAGCTCGTTGTCTTCT	21	13
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1343	-	981	TCTGCAAAAGCTCGTTGTCTT	21	15
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58	-	982	TTTCTGCAAAAGCTCGTTGTCT	22	16

356	-	983	TTTCTGCAAAAGCTCGTTGTC	21	17
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36	-	984	GTTTCTGCAAAAGCTCGTTGT	21	18
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12	-	986	CATGTTTCTGCAAAAGCTCGTT	22	20
24	-	986	ATGTTTCTGCAAAAGCTCGTT	21	20
25	-	987	CATGTTTCTGCAAAAGCTCGT	21	0
11	-	988	TCATGTTTCTGCAAAAGCTCG	21	1
181	-	989	TATCATGTTTCTGCAAAAGCTC	22	2
38	-	989	ATCATGTTTCTGCAAAAGCTC	21	2
101	-	990	TATCATGTTTCTGCAAAAGCT	21	3
1	-	990	AATATCATGTTTCTGCAAAAGCT	23	3
11	-	991	ATATCATGTTTCTGCAAAAGC	21	4
1	-	992	AATATCATGTTTCTGCAAAAG	21	5
8	-	993	TTAATATCATGTTTCTGCAAAA	22	6
13	-	994	TTAATATCATGTTTCTGCAAA	21	7
7	-	994	AATATCATGTTTCTGCAAA	19	7
14	-	995	GTTAATATCATGTTTCTGCAA	21	8
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3	-	996	TTGTTAATATCATGTTTCTGCA	22	9
5	-	997	TTGTTAATATCATGTTTCTGC	21	10
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9	-	1003	TAGACATTGTTAATATCATGT	21	16
9	-	1006	TGGTAGACATTGTTAATATCA	21	19
36	-	1007	ATGGTAGACATTGTTAATATC	21	20
86	-	1009	ACATGGTAGACATTGTTAATA	21	1
28	-	1010	CACATGGTAGACATTGTTAAT	21	2
5	-	1012	TCCACATGGTAGACATTGTTA	21	4
41	-	1013	ATCCACATGGTAGACATTGTT	21	5
44	-	1015	AAATCCACATGGTAGACATTG	21	7
36	-	1016	AAAATCCACATGGTAGACATT	21	8
12	-	1017	GAAAATCCACATGGTAGACAT	21	9
45	-	1018	TGGAAAATCCACATGGTAGACA	22	10
4	-	1018	GGAAAATCCACATGGTAGACA	21	10
16	-	1019	TGGAAAATCCACATGGTAGAC	21	11
8	-	1019	AGATGGAAAATCCACATGGTAGAC	24	11
28	-	1022	AGATGGAAAATCCACATGGTA	21	14
5	-	1022	TAGATGGAAAATCCACATGGTA	22	14
36	-	1023	TAGATGGAAAATCCACATGGT	21	15
4	-	1023	CTAGATGGAAAATCCACATGGT	22	15
11	-	1024	TCTAGATGGAAAATCCACATGG	22	16

4	-	1025	TCTAGATGGAAAATCCACATG	21	17
9	-	1025	TTCTAGATGGAAAATCCACATG	22	17
28	-	1034	AGCTTCTTTTCTAGATGGAAA	21	5
5	-	1035	GAGCTTCTTTTCTAGATGGAA	21	6
22	-	1036	AGAGCTTCTTTTCTAGATGGA	21	7
33	-	1037	AAGAGCTTCTTTTCTAGATGG	21	8
4	-	1038	TCAAGAGCTTCTTTTCTAGATG	22	9
15	-	1039	TCAAGAGCTTCTTTTCTAGAT	21	10
2	-	1040	CTCAAGAGCTTCTTTTCTAGA	21	11
61	-	1040	TCTCAAGAGCTTCTTTTCTAGA	22	11
38	-	1042	ATCTCAAGAGCTTCTTTTCTA	21	13
4	-	1045	AAGATCTCAAGAGCTTCTTTT	21	16
12	-	1049	TGCAAAAGATCTCAAGAGCTTC	22	20
9	-	1049	GCAAAAGATCTCAAGAGCTTC	21	20
159	-	1050	TGCAAAAGATCTCAAGAGCTT	21	0
17	-	1050	CTGCAAAAGATCTCAAGAGCTT	22	0
3	-	1050	TCTGCAAAAGATCTCAAGAGCTT	23	0
117	-	1051	CTGCAAAAGATCTCAAGAGCT	21	1
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32	-	1052	TCTGCAAAAGATCTCAAGAGC	21	2
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1	-	1062	GTCTAAAAGCACATCTGCAAAAGA	24	12
10	-	1067	TTGTCTAAAAGCACATCTGCA	21	17
19	-	1067	TTTGTCTAAAAGCACATCTGCA	22	17
23	-	1068	TTTGTCTAAAAGCACATCTGC	21	18
8	-	1078	AGGTGCAGAGCTTTGTCTAAAA	22	7
59	-	1079	AGGTGCAGAGCTTTGTCTAAA	21	8
116	-	1081	TCAGGTGCAGAGCTTTGTCTA	21	10
17	-	1081	ATCAGGTGCAGAGCTTTGTCTA	22	10
58	-	1082	ATCAGGTGCAGAGCTTTGTCT	21	11
57	-	1083	TATCAGGTGCAGAGCTTTGTC	21	12
32	-	1086	TCGTATCAGGTGCAGAGCTTT	21	15
130	-	1087	ATCGTATCAGGTGCAGAGCTT	21	16
146	-	1087	AATCGTATCAGGTGCAGAGCTT	22	16
74	-	1088	AATCGTATCAGGTGCAGAGCT	21	17
39	-	1089	AGAATCGTATCAGGTGCAGAGC	22	18
39	-	1089	TTAGAATCGTATCAGGTGCAGAGC	24	18
27	-	1090	TAGAATCGTATCAGGTGCAGAG	22	19

12	-	1091	ATCGTATCAGGTGCAGA	17	20
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1	-	1091	AATCGTATCAGGTGCAGA	18	20
41	-	1091	TAGAATCGTATCAGGTGCAGA	21	20
11	-	1092	CTTTAGAATCGTATCAGGTGCAG	23	0
161	-	1092	TTAGAATCGTATCAGGTGCAG	21	0
1	-	1092	TAGAATCGTATCAGGTGCAG	20	0
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1	-	1093	CTTTAGAATCGTATCAGGTGCA	22	1
313	-	1093	TTTAGAATCGTATCAGGTGCA	21	1
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3	-	1094	CTGCAAGCTTTAGAATCGTATCAGGTGC	28	2
3	-	1094	GCTTTAGAATCGTATCAGGTGC	22	2
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589	-	1094	CTTTAGAATCGTATCAGGTGC	21	2
28	-	1095	GCTTTAGAATCGTATCAGGTG	21	3
65	-	1095	AGCTTTAGAATCGTATCAGGTG	22	3
6	-	1095	AAGCTTTAGAATCGTATCAGGTG	23	3
15	-	1096	GCTTTAGAATCGTATCAGGT	20	4
1	-	1096	AAGCTTTAGAATCGTATCAGGT	22	4
59	-	1096	AGCTTTAGAATCGTATCAGGT	21	4
1448	-	1097	AAGCTTTAGAATCGTATCAGG	21	5
184	-	1097	CAAGCTTTAGAATCGTATCAGG	22	5
2	-	1097	AGCTTTAGAATCGTATCAGG	20	5
7	-	1097	GCAAGCTTTAGAATCGTATCAGG	23	5
2	-	1098	GCAAGCTTTAGAATCGTATCAG	22	6
48	-	1098	CAAGCTTTAGAATCGTATCAG	21	6
2	-	1099	GCAAGCTTTAGAATCGTATCA	21	7
1	-	1100	GCAAGCTTTAGAATCGTATC	20	8
240	-	1100	TGCAAGCTTTAGAATCGTATC	21	8
228	-	1102	TCTGCAAGCTTTAGAATCGTA	21	10
75	-	1102	TTCTGCAAGCTTTAGAATCGTA	22	10
24	-	1103	TTCTGCAAGCTTTAGAATCGT	21	11
305	-	1105	TCGTTCTGCAAGCTTTAGAATC	22	13
93	-	1106	TCGTTCTGCAAGCTTTAGAAT	21	14
19	-	1107	ACTCGTTCTGCAAGCTTTAGAA	22	15
1	-	1107	TCGTTCTGCAAGCTTTAGAA	20	15
49	-	1107	CTCGTTCTGCAAGCTTTAGAA	21	15
673	-	1108	ACTCGTTCTGCAAGCTTTAGA	21	16
47	-	1109	TACTCGTTCTGCAAGCTTTAG	21	17
5	-	1109	TTACTCGTTCTGCAAGCTTTAG	22	17
6	-	1109	GTTACTCGTTCTGCAAGCTTTAG	23	17
56	-	1110	TTACTCGTTCTGCAAGCTTTA	21	18
101	-	1111	GTTACTCGTTCTGCAAGCTTT	21	19

2	-	1112	TGTTACTCGTTCTGCAAGCTT	21	20
166	-	1113	CTGTTACTCGTTCTGCAAGCT	21	0
4	-	1113	TCTGTTACTCGTTCTGCAAGCT	22	0
173	-	1114	TCTGTTACTCGTTCTGCAAGC	21	1
12	-	1115	TCTGTTACTCGTTCTGCAAG	20	2
63	-	1115	CTCTGTTACTCGTTCTGCAAG	21	2
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13	-	1116	AAGCTCTGTTACTCGTTCTGCAA	23	3
24	-	1116	GCTCTGTTACTCGTTCTGCAA	21	3
1	-	1117	GCTCTGTTACTCGTTCTGCA	20	4
377	-	1117	AGCTCTGTTACTCGTTCTGCA	21	4
59	-	1117	AAGCTCTGTTACTCGTTCTGCA	22	4
14	-	1118	AAAGCTCTGTTACTCGTTCTGC	22	5
416	-	1118	AAGCTCTGTTACTCGTTCTGC	21	5
88	-	1119	AAAGCTCTGTTACTCGTTCTG	21	6
25	-	1121	ACAAAGCTCTGTTACTCGTTC	21	8
18	-	1122	AAGCTCTGTTACTCGTT	17	9
2	-	1122	CACAAAGCTCTGTTACTCGTT	21	9
8	-	1122	CCACAAAGCTCTGTTACTCGTT	22	9
75	-	1123	CCACAAAGCTCTGTTACTCGT	21	10
15	-	1124	ACCACAAAGCTCTGTTACTCG	21	11
8	-	1124	TACCACAAAGCTCTGTTACTCG	22	11
110	-	1125	TTACCACAAAGCTCTGTTACTC	22	12
83	-	1125	TACCACAAAGCTCTGTTACTC	21	12
226	-	1126	TTACCACAAAGCTCTGTTACT	21	13
30	-	1126	ATTACCACAAAGCTCTGTTACT	22	13
52	-	1127	ATTACCACAAAGCTCTGTTAC	21	14
5	-	1127	GATTACCACAAAGCTCTGTTAC	22	14
1	-	1128	AGATTACCACAAAGCTCTGTTA	22	15
124	-	1129	AGATTACCACAAAGCTCTGTT	21	16
13	-	1129	AAGATTACCACAAAGCTCTGTT	22	16
25	-	1130	AAGATTACCACAAAGCTCTGT	21	17
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1	-	1133	TGGAAGATTACCACAAAGCTC	21	20
2	-	1134	GAAGATTACCACAAAGCT	18	0
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7	-	1135	AATGGAAGATTACCACAAAGC	21	1
9	-	1135	CAATGGAAGATTACCACAAAGC	22	1
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1	-	1145	ACAGAGACCCAATGGAAGATT	21	11
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39	-	1146	CACAGAGACCCAATGGAAGAT	21	12
217	-	1147	ACACAGAGACCCAATGGAAGA	21	13

2	-	1147	CTATGACACAGAGACCCAATGGAAGA	26	13
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32	-	1148	TGACACAGAGACCCAATGGAAG	22	14
4	-	1148	GACACAGAGACCCAATGGAAG	21	14
326	-	1149	TGACACAGAGACCCAATGGAA	21	15
47	-	1149	ATGACACAGAGACCCAATGGAA	22	15
17	-	1150	TATGACACAGAGACCCAATGGA	22	16
2	-	1150	CTATGACACAGAGACCCAATGGA	23	16
423	-	1150	ATGACACAGAGACCCAATGGA	21	16
33	-	1151	TATGACACAGAGACCCAATGG	21	17
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13	-	1158	GATGAACCTATGACACAGAGAC	22	3
15	-	1158	AAGATGAACCTATGACACAGAGAC	24	3
22	-	1158	ATGAACCTATGACACAGAGAC	21	3
3	-	1159	AGATGAACCTATGACACAGAGA	22	4
60	-	1159	GATGAACCTATGACACAGAGA	21	4
104	-	1160	AGATGAACCTATGACACAGAG	21	5
559	-	1161	AAGATGAACCTATGACACAGA	21	6
8	-	1161	AGATGAACCTATGACACAGA	20	6
96	-	1161	AAAGATGAACCTATGACACAGA	22	6
8	-	1162	AAAGATGAACCTATGACACAG	21	7
40	-	1163	TAAAGATGAACCTATGACACA	21	8
52	-	1165	TGTAAAGATGAACCTATGACA	21	10
49	-	1166	GTGTAAAGATGAACCTATGAC	21	11
36	-	1168	CCGTGTAAAGATGAACCTATG	21	13
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3	-	1169	CCCGTGTAAAGATGAACCTAT	21	14
24	-	1170	TTCCCGTGTAAAGATGAACCTA	22	15
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30	-	1171	TTTCCCGTGTAAAGATGAACCT	22	16
78	-	1171	TTCCCGTGTAAAGATGAACCT	21	16
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48	-	1173	TTTTCCCGTGTAAAGATGAAC	21	18
105	-	1174	GTTTTCCCGTGTAAAGATGAA	21	19
5	-	1175	AGTTTTCCCGTGTAAAGATGA	21	20
7	-	1175	CAGTTTTCCCGTGTAAAGATGA	22	20
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4	-	1177	TCAGTTTTCCCGTGTAAAGAT	21	1
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50	-	1178	CTCAGTTTTCCCGTGTAAAGA	21	2
11	-	1180	TCCTCAGTTTTCCCGTGTAAA	21	4
3	-	1181	ATCCTCAGTTTTCCCGTGTAA	21	5
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127	-	1182	CATCCTCAGTTTTCCCGTGTA	21	6
137	-	1182	TCATCCTCAGTTTTCCCGTGTA	22	6
7	-	1182	CTCAGTTTTCCCGTGTA	17	6
10	-	1183	TCATCCTCAGTTTTCCCGTGT	21	7
47	-	1183	CTCATCCTCAGTTTTCCCGTGT	22	7
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7	-	1184	ACTCATCCTCAGTTTTCCCGTG	22	8
26	-	1186	CACTCATCCTCAGTTTTCCCG	21	10
79	-	1191	TTTCCCACTCATCCTCAGTTT	21	15
26	-	1192	ATTTCCCACTCATCCTCAGTT	21	16
6	-	1192	AATTTCCCACTCATCCTCAGTT	22	16
65	-	1193	AATTTCCCACTCATCCTCAGT	21	17
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9	-	1196	TAAAATTTCCCACTCATCCTC	21	20
24	-	1197	TTAAAATTTCCCACTCATCCT	21	0
4	-	1197	ATTAAAATTTCCCACTCATCCT	22	0
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44	-	1212	TTTCTAGTCTGCGAATTAAAA	21	15
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27	-	1228	TCTCGATCAAGACTAATTTCT	21	10
4	-	1228	ATCTCGATCAAGACTAATTTCT	22	10
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42	-	1230	TATCTCGATCAAGACTAATTT	21	12
53	-	1231	TTATCTCGATCAAGACTAATT	21	13
106	-	1233	TCGTTATCTCGATCAAGACTAA	22	15
19	-	1234	CGTTATCTCGATCAAGACTA	20	16
41	-	1234	TCGTTATCTCGATCAAGACTA	21	16
22	-	1235	CTCGTTATCTCGATCAAGACT	21	17
25	-	1235	CCTCGTTATCTCGATCAAGACT	22	17
17	-	1236	CCTCGTTATCTCGATCAAGAC	21	18
34	-	1237	TGCCTCGTTATCTCGATCAAGA	22	19
32	-	1238	TGCCTCGTTATCTCGATCAAG	21	20
5	-	1238	GTGCCTCGTTATCTCGATCAAG	22	20
4	-	1239	GTGCCTCGTTATCTCGATCAA	21	0

1	-	1240	TTGTGCCTCGTTATCTCGATCA	22	1
6	-	1240	TGTGCCTCGTTATCTCGATCA	21	1
10	-	1241	TGTGCCTCGTTATCTCGATC	20	2
137	-	1241	TTGTGCCTCGTTATCTCGATC	21	2
167	-	1242	GTTGTGCCTCGTTATCTCGAT	21	3
17	-	1242	TTGTGCCTCGTTATCTCGAT	20	3
17	-	1243	AAGTTGTGCCTCGTTATCTCGA	22	4
460	-	1243	AGTTGTGCCTCGTTATCTCGA	21	4
7	-	1243	GTTGTGCCTCGTTATCTCGA	20	4
1	-	1244	TAAGTTGTGCCTCGTTATCTCG	22	5
14	-	1245	TAAGTTGTGCCTCGTTATCTC	21	6
21	-	1247	TCTAAGTTGTGCCTCGTTATC	21	8
6	-	1247	CTCTAAGTTGTGCCTCGTTATC	22	8
20	-	1249	ACTCTAAGTTGTGCCTCGTTA	21	10
11	-	1251	CAACTCTAAGTTGTGCCTCGT	21	12
4	-	1256	ATACCCAACTCTAAGTTGTGC	21	17
10	-	1257	TCATACCCAACTCTAAGTTGTG	22	18
19	-	1257	CATACCCAACTCTAAGTTGTG	21	18
9	-	1260	TATCATACCCAACTCTAAGTT	21	0
2	-	1264	AAGCTATCATACCCAACTCTA	21	4
1	-	1271	TCTCATGTAAGCTATCATACCC	22	11
21	-	1271	CTCATGTAAGCTATCATACCC	21	11
17	-	1272	ATGTAAGCTATCATACC	17	12
32	-	1272	TCTCATGTAAGCTATCATACC	21	12
48	-	1272	TTCTCATGTAAGCTATCATACC	22	12
12	-	1273	TTCTCATGTAAGCTATCATAC	21	13
14	-	1275	CGTTCTCATGTAAGCTATCAT	21	15
34	-	1276	TCGTTCTCATGTAAGCTATCA	21	16
43	-	1277	CTCGTTCTCATGTAAGCTATC	21	17
46	-	1279	TGCTCGTTCTCATGTAAGCTA	21	19
121	-	1280	TTGCTCGTTCTCATGTAAGCT	21	20
6	-	1281	CTTGCTCGTTCTCATGTAAGC	21	0
8	-	1282	GCTTGCTCGTTCTCATGTAAG	21	1
7	-	1283	AGCTTGCTCGTTCTCATGTAA	21	2
10	-	1284	AAAGCTTGCTCGTTCTCATGTA	22	3
116	-	1284	AAGCTTGCTCGTTCTCATGTA	21	3
73	-	1285	AAAGCTTGCTCGTTCTCATGT	21	4
37	-	1286	ATAAAGCTTGCTCGTTCTCATG	22	5
81	-	1286	TAAAGCTTGCTCGTTCTCATG	21	5
19	-	1287	ATAAAGCTTGCTCGTTCTCAT	21	6
3	-	1288	AAATAAAGCTTGCTCGTTCTCA	22	7
98	-	1288	AATAAAGCTTGCTCGTTCTCA	21	7
34	-	1289	AAATAAAGCTTGCTCGTTCTC	21	8
24	-	1293	TGAGAAATAAAGCTTGCTCGT	21	12

4	-	1294	CTGAGAAATAAAGCTTGCTCG	21	13
2	-	1301	CTGCAATGCTGAGAAATAAAGC	22	20
5	-	1303	ACTGCAATGCTGAGAAATAAA	21	1
13	-	1305	AGACTGCAATGCTGAGAAATA	21	3
1	-	1305	GTTGAAGAAGACTGCAATGCTGAGAAATA	29	3
11	-	1306	AAGACTGCAATGCTGAGAAAT	21	4
20	-	1307	GAAGACTGCAATGCTGAGAAA	21	5
120	-	1308	AGAAGACTGCAATGCTGAGAA	21	6
9	-	1308	GAAGACTGCAATGCTGAGAA	20	6
1171	-	1309	AAGAAGACTGCAATGCTGAGA	21	7
1	-	1309	GAAGAAGACTGCAATGCTGAGA	22	7
4	-	1310	AAGAAGACTGCAATGCTGAG	20	8
6	-	1310	TGAAGAAGACTGCAATGCTGAG	22	8
73	-	1310	GAAGAAGACTGCAATGCTGAG	21	8
7	-	1310	TTGAAGAAGACTGCAATGCTGAG	23	8
125	-	1311	TGAAGAAGACTGCAATGCTGA	21	9
229	-	1311	TTGAAGAAGACTGCAATGCTGA	22	9
26	-	1312	TTGAAGAAGACTGCAATGCTG	21	10
5	-	1312	GTTGAAGAAGACTGCAATGCTG	22	10
1	-	1313	TTGAAGAAGACTGCAATGCT	20	11
5	-	1313	AGTTGAAGAAGACTGCAATGCT	22	11
12	-	1318	TTTATAGTTGAAGAAGACTGCA	22	16
3	-	1318	TTATAGTTGAAGAAGACTGCA	21	16
19	-	1319	TTTATAGTTGAAGAAGACTGC	21	17
14	-	1323	GGTCTTTATAGTTGAAGAAGA	21	0
40	-	1325	ACGGTCTTTATAGTTGAAGAA	21	2
1	-	1326	GACGGTCTTTATAGTTGAAGA	21	3
20	-	1326	TGACGGTCTTTATAGTTGAAGA	22	3
59	-	1327	TGACGGTCTTTATAGTTGAAG	21	4
5	-	1327	AGCTGACGGTCTTTATAGTTGAAG	24	4
5	-	1327	CTGACGGTCTTTATAGTTGAAG	22	4
22	-	1328	CTGACGGTCTTTATAGTTGAA	21	5
19	-	1329	AGCTGACGGTCTTTATAGTTGA	22	6
32	-	1329	GCTGACGGTCTTTATAGTTGA	21	6
1	-	1330	AAGCTGACGGTCTTTATAGTTG	22	7
30	-	1330	AGCTGACGGTCTTTATAGTTG	21	7
3	-	1330	GCTGACGGTCTTTATAGTTG	20	7
63	-	1331	AAGCTGACGGTCTTTATAGTT	21	8
6	-	1332	ACAAGCTGACGGTCTTTATAGT	22	9
18	-	1334	TCACAAGCTGACGGTCTTTATA	22	11
1	-	1335	TCACAAGCTGACGGTCTTTAT	21	12
2	-	1335	ATCACAAGCTGACGGTCTTTAT	22	12
15	-	1336	ATCACAAGCTGACGGTCTTTA	21	13
28	-	1337	CATCACAAGCTGACGGTCTTT	21	14

1	-	1338	CCATCACAAGCTGACGGTCTT	21	15
15	-	1341	ATGGCCATCACAAGCTGACGGT	22	18
41	-	1341	TGGCCATCACAAGCTGACGGT	21	18
26	-	1342	CATGGCCATCACAAGCTGACGG	22	19
2	-	1342	GCCATCACAAGCTGACGG	18	19
747	-	1342	ATGGCCATCACAAGCTGACGG	21	19
22	-	1344	GCATGGCCATCACAAGCTGAC	21	0
13	-	1345	AGCATGGCCATCACAAGCTGA	21	1
10	-	1347	AGGAGCATGGCCATCACAAGCT	22	3
4	-	1348	AAGGAGCATGGCCATCACAAGC	22	4
56	-	1349	AAGGAGCATGGCCATCACAAG	21	5
63	-	1351	TCAAGGAGCATGGCCATCACA	21	7
10	-	1352	GTCAAGGAGCATGGCCATCAC	21	8
16	-	1354	ACTGTCAAGGAGCATGGCCATC	22	10
115	-	1357	TTACTGTCAAGGAGCATGGCC	21	13
3	-	1358	GTTACTGTCAAGGAGCATGGC	21	14
13	-	1359	GGTTACTGTCAAGGAGCATGG	21	15
1	-	1360	CTAGGTTACTGTCAAGGAGCATG	23	16
3	-	1360	AGGTTACTGTCAAGGAGCATG	21	16
99	-	1360	TAGGTTACTGTCAAGGAGCATG	22	16
43	-	1361	CTAGGTTACTGTCAAGGAGCAT	22	17
5	-	1361	TAGGTTACTGTCAAGGAGCAT	21	17
10	-	1362	CATCTAGGTTACTGTCAAGGAGCA	24	18
167	-	1362	TCTAGGTTACTGTCAAGGAGCA	22	18
1	-	1362	ATCTAGGTTACTGTCAAGGAGCA	23	18
800	-	1362	CTAGGTTACTGTCAAGGAGCA	21	18
194	-	1363	ATCTAGGTTACTGTCAAGGAGC	22	19
27	-	1363	CTAGGTTACTGTCAAGGAGC	20	19
480	-	1363	TCTAGGTTACTGTCAAGGAGC	21	19
78	-	1363	ACATCTAGGTTACTGTCAAGGAGC	24	19
147	-	1364	ATCTAGGTTACTGTCAAGGAG	21	20
170	-	1365	CATCTAGGTTACTGTCAAGGA	21	0
11	-	1366	CGACATCTAGGTTACTGTCAAGG	23	1
152	-	1366	ACATCTAGGTTACTGTCAAGG	21	1
29	-	1367	TCGACATCTAGGTTACTGTCAAG	23	2
2	-	1367	CGACATCTAGGTTACTGTCAAG	22	2
8	-	1368	CGACATCTAGGTTACTGTCAA	21	3
1	-	1369	CTCGACATCTAGGTTACTGTCA	22	4
49	-	1369	TCGACATCTAGGTTACTGTCA	21	4
7	-	1369	TACTCGACATCTAGGTTACTGTCA	24	4
216	-	1370	CTCGACATCTAGGTTACTGTC	21	5
3	-	1370	ATACTCGACATCTAGGTTACTGTC	24	5
101	-	1371	ACTCGACATCTAGGTTACTGT	21	6
32	-	1371	TACTCGACATCTAGGTTACTGT	22	6

3	-	1371	ATACTCGACATCTAGGTTACTGT	23	6
9	-	1371	CTCGACATCTAGGTTACTGT	20	6
147	-	1372	TACTCGACATCTAGGTTACTG	21	7
36	-	1372	ATACTCGACATCTAGGTTACTG	22	7
32	-	1373	CCCATACTCGACATCTAGGTTACT	24	8
92	-	1373	ATACTCGACATCTAGGTTACT	21	8
2	-	1376	ACCCATACTCGACATCTAGGTT	22	11
31	-	1376	CCCATACTCGACATCTAGGTT	21	11
20	-	1377	ACCCATACTCGACATCTAGGT	21	12
17	-	1378	TAACCCATACTCGACATCTAGG	22	13
1	-	1378	ACCCATACTCGACATCTAGG	20	13
258	-	1378	AACCCATACTCGACATCTAGG	21	13
64	-	1378	CCCATACTCGACATCTAGG	19	13
1	-	1379	TAACCCATACTCGACATCTAG	21	14
3	-	1379	TTAACCCATACTCGACATCTAG	22	14
2	-	1380	CTTAACCCATACTCGACATCTA	22	15
45	-	1380	TTAACCCATACTCGACATCTA	21	15
4	-	1381	TTAACCCATACTCGACATCT	20	16
6	-	1381	CTTAACCCATACTCGACATCT	21	16
14	-	1382	TTAACCCATACTCGACATC	19	17
5	-	1382	TCTTAACCCATACTCGACATC	21	17
6	-	1382	TTCTTAACCCATACTCGACATC	22	17
4	-	1383	TTCTTAACCCATACTCGACAT	21	18
21	-	1393	TTGGCGAGGGTTCTTAACCCA	21	7
5	-	1396	TTATTGGCGAGGGTTCTTAAC	21	10
13	-	1397	TTTATTGGCGAGGGTTCTTAA	21	11
17	-	1398	ATTTATTGGCGAGGGTTCTTA	21	12
6	-	1398	GATTTATTGGCGAGGGTTCTTA	22	12
3	-	1401	AGAGATTTATTGGCGAGGGTTC	22	15
3	-	1402	TTAGAGATTTATTGGCGAGGGTT	23	16
9	-	1402	AGAGATTTATTGGCGAGGGTT	21	16
13	-	1403	TTAGAGATTTATTGGCGAGGGT	22	17
3	-	1403	TAGAGATTTATTGGCGAGGGT	21	17
454	-	1404	TTAGAGATTTATTGGCGAGGG	21	18
9	-	1404	ATTAGAGATTTATTGGCGAGGG	22	18
24	-	1405	TATTAGAGATTTATTGGCGAGG	22	19
3	-	1405	AGAGATTTATTGGCGAGG	18	19
77	-	1405	ATTAGAGATTTATTGGCGAGG	21	19
203	-	1406	TATTAGAGATTTATTGGCGAG	21	20
10	-	1407	GTATTAGAGATTTATTGGCGA	21	0
10	-	1407	TGTATTAGAGATTTATTGGCGA	22	0
13	-	1407	TATTAGAGATTTATTGGCGA	20	0
267	-	1408	TGTATTAGAGATTTATTGGCG	21	1
5	-	1408	ATGTATTAGAGATTTATTGGCG	22	1

30	-	1409	ATGTATTAGAGATTTATTGGC	21	2
9	-	1409	TATGTATTAGAGATTTATTGGC	22	2
15	-	1410	TATGTATTAGAGATTTATTGG	21	3
27	-	1410	ATATGTATTAGAGATTTATTGG	22	3
10	-	1412	ATATATGTATTAGAGATTTATT	22	5
5	-	1415	CCTAGATATATGTATTAGAGATTT	24	8
5	-	1416	TAGATATATGTATTAGAGATT	21	9
18	-	1417	CTAGATATATGTATTAGAGAT	21	10
2	-	1417	CCTAGATATATGTATTAGAGAT	22	10
7	-	1418	TCCTAGATATATGTATTAGAGA	22	11
169	-	1420	TTCCTAGATATATGTATTAGA	21	13
50	-	1423	TCATTCCTAGATATATGTATT	21	16
10	-	1425	TCTCATTCCTAGATATATGTA	21	18
15	-	1425	TTCTCATTCCTAGATATATGTA	22	18
48	-	1425	TTTTCTCATTCCTAGATATATGTA	24	18
8	-	1426	TTTCTCATTCCTAGATATATGT	22	19
91	-	1426	TTCTCATTCCTAGATATATGT	21	19
9	-	1426	TCTCATTCCTAGATATATGT	20	19
21	-	1427	TTTTCTCATTCCTAGATATATG	22	20
39	-	1427	TTTCTCATTCCTAGATATATG	21	20
10	-	1429	TATTTTCTCATTCCTAGATATA	22	1
14	-	1429	ATTTTCTCATTCCTAGATATA	21	1
1	-	1429	TTTTCTCATTCCTAGATATA	20	1
7	-	1430	TATTTTCTCATTCCTAGATAT	21	2
338	-	1431	ACTATTTTCTCATTCCTAGATA	22	3
8	-	1431	TCACTATTTTCTCATTCCTAGATA	24	3
34	-	1432	ATTTTCTCATTCCTAGAT	18	4
58	-	1432	CACTATTTTCTCATTCCTAGAT	22	4
68	-	1432	ACTATTTTCTCATTCCTAGAT	21	4
123	-	1433	TCACTATTTTCTCATTCCTAGA	22	5
5	-	1433	CACTATTTTCTCATTCCTAGA	21	5
12	-	1434	ATCACTATTTTCTCATTCCTAG	22	6
37	-	1434	TCACTATTTTCTCATTCCTAG	21	6
20	-	1435	CATCACTATTTTCTCATTCCTA	22	7
6	-	1435	ATCACTATTTTCTCATTCCTA	21	7
23	-	1436	CATCACTATTTTCTCATTCCT	21	8
3	-	1437	TGCATCACTATTTTCTCATTCC	22	9
1	-	1438	TGCATCACTATTTTCTCATTC	21	10
12	-	1440	TATGCATCACTATTTTCTCAT	21	12
1	-	1441	TATGCATCACTATTTTCTCA	20	13
32	-	1441	TTATGCATCACTATTTTCTCA	21	13
10	-	1443	TTATGCATCACTATTTTCT	19	15
8	-	1445	AAGTTATGCATCACTATTTT	20	17
130	-	1450	TTGTAGTAAGTTATGCATCACT	22	1

18	-	1450	TGTAGTAAGTTATGCATCACT	21	1
14	-	1451	TTGTAGTAAGTTATGCATCAC	21	2
32	-	1453	TGTTGTAGTAAGTTATGCATC	21	4
46	-	1455	CATGTTGTAGTAAGTTATGCA	21	6
6	-	1455	ACATGTTGTAGTAAGTTATGCA	22	6
13	-	1456	CACATGTTGTAGTAAGTTATGC	22	7
41	-	1456	ACATGTTGTAGTAAGTTATGC	21	7
13	-	1457	CCACATGTTGTAGTAAGTTATG	22	8
5	-	1459	ACCCACATGTTGTAGTAAGTTA	22	10
4	-	1460	ACCCACATGTTGTAGTAAGTT	21	11
21	-	1461	TACCCACATGTTGTAGTAAGT	21	12
6	-	1464	TCTACCCACATGTTGTAGTA	20	15
11	-	1465	TTGTCTACCCACATGTTGTAGT	22	16
6	-	1465	TGTCTACCCACATGTTGTAGT	21	16
18	-	1466	TTGTCTACCCACATGTTGTAG	21	17
4	-	1467	CTTGTCTACCCACATGTTGTA	21	18
7	-	1468	CTTGTCTACCCACATGTTGT	20	19
33	-	1470	TGGCTTGTCTACCCACATGTT	21	0
5	-	1471	ATGGCTTGTCTACCCACATGT	21	1
4	-	1472	AATGGCTTGTCTACCCACATG	21	2
10	-	1474	TGAATGGCTTGTCTACCCACA	21	4
8	-	1475	TTGAATGGCTTGTCTACCCAC	21	5
24	-	1476	TTTGAATGGCTTGTCTACCCA	21	6
1	-	1477	GTCTTTGAATGGCTTGTCTACCC	23	7
5	-	1477	CTTTGAATGGCTTGTCTACCC	21	7
66	-	1477	TCTTTGAATGGCTTGTCTACCC	22	7
3	-	1478	TCTTTGAATGGCTTGTCTACC	21	8
160	-	1479	GTCTTTGAATGGCTTGTCTAC	21	9
24	-	1480	TGTCTTTGAATGGCTTGTCTA	21	10
72	-	1480	TTGTCTTTGAATGGCTTGTCTA	22	10
1	-	1481	TGTCTTTGAATGGCTTGTCT	20	11
211	-	1481	TTGTCTTTGAATGGCTTGTCT	21	11
3	-	1482	CTTGTCTTTGAATGGCTTGTC	21	12
1	-	1483	TCTTGTCTTTGAATGGCTTGT	21	13
9	-	1485	GGTTCTTGTCTTTGAATGGCTT	22	15
5	-	1486	AGGTTCTTGTCTTTGAATGGCT	22	16
8	-	1486	GGTTCTTGTCTTTGAATGGCT	21	16
182	-	1487	AGGTTCTTGTCTTTGAATGGC	21	17
95	-	1488	AAGGTTCTTGTCTTTGAATGG	21	18
12	-	1490	CCAAGGTTCTTGTCTTTGAAT	21	20
72	-	1491	TCCAAGGTTCTTGTCTTTGAA	21	0
18	-	1492	TTTCCAAGGTTCTTGTCTTTGA	22	1
110	-	1495	CGTTTCCAAGGTTCTTGTCTT	21	4
27	-	1497	TGGCGTTTCCAAGGTTCTTGTC	22	6

5	-	1498	TGGCGTTTCCAAGGTTCTTGT	21	7
7	-	1499	TGTGGCGTTTCCAAGGTTCTTG	22	8
11	-	1500	TGTGGCGTTTCCAAGGTTCTT	21	9
21	-	1501	ATGTGGCGTTTCCAAGGTTCT	21	10
186	-	1503	AGATGTGGCGTTTCCAAGGTT	21	12
3	-	1503	AAGATGTGGCGTTTCCAAGGTT	22	12
163	-	1504	AAGATGTGGCGTTTCCAAGGT	21	13
26	-	1504	TAAGATGTGGCGTTTCCAAGGT	22	13
107	-	1505	TTAAGATGTGGCGTTTCCAAGG	22	14
46	-	1505	TAAGATGTGGCGTTTCCAAGG	21	14
3	-	1506	ATTAAGATGTGGCGTTTCCAAG	22	15
48	-	1506	TTAAGATGTGGCGTTTCCAAG	21	15
116	-	1507	ATTAAGATGTGGCGTTTCCAA	21	16
1	-	1508	ATTAAGATGTGGCGTTTCCA	20	17
263	-	1508	TATTAAGATGTGGCGTTTCCA	21	17
49	-	1509	TCTATTAAGATGTGGCGTTTCC	22	18
10	-	1511	ATCTATTAAGATGTGGCGTTT	21	20
28	-	1520	CTCGTCAGCATCTATTAAGAT	21	8
7	-	1520	TCTCGTCAGCATCTATTAAGAT	22	8
1	-	1521	CTCGTCAGCATCTATTAAGA	20	9
4	-	1521	ATCTCGTCAGCATCTATTAAGA	22	9
7	-	1521	TCTCGTCAGCATCTATTAAGA	21	9
247	-	1522	TATCTCGTCAGCATCTATTAAG	22	10
7	-	1522	ATCTCGTCAGCATCTATTAAG	21	10
4	-	1523	TATCTCGTCAGCATCTATTAA	21	11
6	-	1524	TATCTCGTCAGCATCTATTA	20	12
70	-	1524	ATATCTCGTCAGCATCTATTA	21	12
38	-	1525	CATATCTCGTCAGCATCTATT	21	13
6	-	1525	GCATATCTCGTCAGCATCTATT	22	13
8	-	1526	GCATATCTCGTCAGCATCTAT	21	14
3	-	1527	TGCATATCTCGTCAGCATCTA	21	15
7	-	1527	TTGCATATCTCGTCAGCATCTA	22	15
2	-	1528	ATTGCATATCTCGTCAGCATCT	22	16
3	-	1528	TGCATATCTCGTCAGCATCT	20	16
73	-	1528	TTGCATATCTCGTCAGCATCT	21	16
29	-	1529	ATTGCATATCTCGTCAGCATC	21	17
3	-	1530	CATTGCATATCTCGTCAGCAT	21	18
15	-	1531	GACATTGCATATCTCGTCAGCA	22	19
192	-	1531	ACATTGCATATCTCGTCAGCA	21	19
10	-	1532	GGACATTGCATATCTCGTCAGC	22	20
2	-	1533	GGACATTGCATATCTCGTCAG	21	0
2	-	1534	AAGGACATTGCATATCTCGTCA	22	1
7	-	1534	AGGACATTGCATATCTCGTCA	21	1
12	-	1535	CAAGGACATTGCATATCTCGTC	22	2

184	-	1535	AAGGACATTGCATATCTCGTC	21	2
7	-	1535	TTCAAGGACATTGCATATCTCGTC	24	2
104	-	1536	CAAGGACATTGCATATCTCGT	21	3
20	-	1537	TTCAAGGACATTGCATATCTCG	22	4
36	-	1537	TCAAGGACATTGCATATCTCG	21	4
46	-	1538	TTCAAGGACATTGCATATCTC	21	5
60	-	1539	TTTCAAGGACATTGCATATCT	21	6
130	-	1540	TTTTCAAGGACATTGCATATC	21	7
65	-	1540	ATTTTCAAGGACATTGCATATC	22	7
46	-	1541	ATTTTCAAGGACATTGCATAT	21	8
5	-	1542	CTGTATCATTTTCAAGGACATTGCATA	27	9
84	-	1542	TCATTTTCAAGGACATTGCATA	22	9
1	-	1544	TCATTTTCAAGGACATTGCA	20	11
232	-	1544	ATCATTTTCAAGGACATTGCA	21	11
32	-	1544	TATCATTTTCAAGGACATTGCA	22	11
124	-	1545	TATCATTTTCAAGGACATTGC	21	12
6	-	1545	GTATCATTTTCAAGGACATTGC	22	12
89	-	1547	TGTATCATTTTCAAGGACATT	21	14
10	-	1548	CTGTATCATTTTCAAGGACAT	21	15
11	-	1568	TCCCTGACACAATTCTAGCATC	22	14
15	-	1570	TATCCCTGACACAATTCTAGCA	22	16
5	-	1570	ATCCCTGACACAATTCTAGCA	21	16
38	-	1571	ATATCCCTGACACAATTCTAGC	22	17
8	-	1571	TATCCCTGACACAATTCTAGC	21	17
6	-	1572	ATATCCCTGACACAATTCTAG	21	18
3	-	1573	GATATCCCTGACACAATTCTA	21	19
1	-	1575	ATGATATCCCTGACACAATTC	21	0
18	-	1576	AATGATATCCCTGACACAATT	21	1
17	-	1577	AAATGATATCCCTGACACAAT	21	2
8	-	1578	CAAATGATATCCCTGACACAA	21	3
8	-	1578	TCAAATGATATCCCTGACACAA	22	3
9	-	1579	TCAAATGATATCCCTGACACA	21	4
3	-	1581	AAATGATATCCCTGACA	17	6
77	-	1583	TATATCAAATGATATCCCTGA	21	8
17	-	1588	CTGGATATATCAAATGATATC	21	13
7	-	1590	TTCTGGATATATCAAATGATA	21	15
4	-	1593	CGATTCTGGATATATCAAATG	21	18
12	-	1598	CTTCGCCGATTCTGGATATATC	22	2
1	-	1598	TCGCCGATTCTGGATATATC	20	2
53	-	1598	TTCGCCGATTCTGGATATATC	21	2
138	-	1600	ACTTCGCCGATTCTGGATATA	21	4
5	-	1600	AACTTCGCCGATTCTGGATATA	22	4
110	-	1602	AAACTTCGCCGATTCTGGATA	21	6
37	-	1602	AAAACTTCGCCGATTCTGGATA	22	6

1	-	1603	AAAACTTCGCCGATTCTGGAT	21	7
176	-	1604	AAAAACTTCGCCGATTCTGGA	21	8
1	-	1604	AAAAAACTTCGCCGATTCTGGA	22	8
1	-	1605	AAAAACTTCGCCGATTCTGG	20	9
412	-	1605	AAAAAACTTCGCCGATTCTGG	21	9
4	-	1605	AAAAAAACTTCGCCGATTCTGG	22	9
31	-	1606	TAAAAAAACTTCGCCGATTCTG	22	10
54	-	1606	AAAAAAACTTCGCCGATTCTG	21	10
8	-	1607	TAAAAAAACTTCGCCGATTCT	21	11
134	-	1608	TTAAAAAAACTTCGCCGATTC	21	12
1	-	1608	TAAAAAAACTTCGCCGATTC	20	12
45	-	1610	GCTTAAAAAAACTTCGCCGAT	21	14
30	-	1611	CGCTTAAAAAAACTTCGCCGA	21	15
88	-	1611	TCGCTTAAAAAAACTTCGCCGA	22	15
67	-	1612	TCGCTTAAAAAAACTTCGCCG	21	16
32	-	1613	CTCGCTTAAAAAAACTTCGCC	21	17
57	-	1614	TCTCGCTTAAAAAAACTTCGC	21	18
9	-	1614	CTCTCGCTTAAAAAAACTTCGC	22	18
16	-	1615	CTCTCGCTTAAAAAAACTTCG	21	19
2	-	1616	CTCTCTCGCTTAAAAAAACTTC	22	20
3	-	1617	CTCTCTCGCTTAAAAAAACTT	21	0
26	-	1624	TTAAAAGCTCTCTCGCTTAAA	21	7
2	-	1625	TTAAAAGCTCTCTCGCTTAA	20	8
20	-	1626	TTTTAAAAGCTCTCTCGCTTA	21	9
10	-	1627	CTTTTAAAAGCTCTCTCGCTT	21	10
4	-	1627	AATCTTTTAAAAGCTCTCTCGCTT	24	10
13	-	1628	ATCTTTTAAAAGCTCTCTCGCT	22	11
9	-	1628	TCTTTTAAAAGCTCTCTCGCT	21	11
118	-	1629	ATCTTTTAAAAGCTCTCTCGC	21	12
5	-	1630	AATCTTTTAAAAGCTCTCTCG	21	13
7	-	1630	TCTTTTAAAAGCTCTCTCG	19	13
46	-	1631	CAATCTTTTAAAAGCTCTCTC	21	14
8	-	1632	ACAATCTTTTAAAAGCTCTCT	21	15
19	-	1633	CACAATCTTTTAAAAGCTCTC	21	16
20	-	1634	ACACAATCTTTTAAAAGCTCT	21	17
19	-	1648	AGGAATTGGAGATTACACAAT	21	10
4	-	1649	GAGGAATTGGAGATTACACAA	21	11
102	-	1650	CTGAGGAATTGGAGATTACACA	22	12
99	-	1650	TGAGGAATTGGAGATTACACA	21	12
24	-	1651	CTGAGGAATTGGAGATTACAC	21	13
22	-	1656	ACACCCTGAGGAATTGGAGAT	21	18
212	-	1657	AACACCCTGAGGAATTGGAGA	21	19
34	-	1658	AAACACCCTGAGGAATTGGAG	21	20
137	-	1659	TAAACACCCTGAGGAATTGGA	21	0

9	-	1659	TTAAACACCCTGAGGAATTGGA	22	0
4	-	1660	CTTAAACACCCTGAGGAATTGG	22	1
6	-	1660	TTAAACACCCTGAGGAATTGG	21	1
16	-	1664	CAGTCTTAAACACCCTGAGGAA	22	5
1	-	1665	AGTCTTAAACACCCTGAGGA	20	6
234	-	1665	CAGTCTTAAACACCCTGAGGA	21	6
94	-	1666	CCAGTCTTAAACACCCTGAGG	21	7
3	-	1667	TCCAGTCTTAAACACCCTGAG	21	8
115	-	1668	ATCCAGTCTTAAACACCCTGA	21	9
1	-	1668	CAGTCTTAAACACCCTGA	18	9
39	-	1668	TATCCAGTCTTAAACACCCTGA	22	9
6	-	1669	TATCCAGTCTTAAACACCCTG	21	10
10	-	1670	ATATCCAGTCTTAAACACCCT	21	11
5	-	1671	CATATCCAGTCTTAAACACCC	21	12
2	-	1672	CATATCCAGTCTTAAACACC	20	13
3	-	1672	ATCATATCCAGTCTTAAACACC	22	13
61	-	1672	TCATATCCAGTCTTAAACACC	21	13
20	-	1673	ATCATATCCAGTCTTAAACAC	21	14
8	-	1674	TCATCATATCCAGTCTTAAACA	22	15
1	-	1675	TCATCATATCCAGTCTTAAAC	21	16
3	-	1675	TTCATCATATCCAGTCTTAAAC	22	16
7	-	1676	TTCATCATATCCAGTCTTAAA	21	17
10	-	1678	TTTTCATCATATCCAGTCTTA	21	19
5	-	1679	TTTTTCATCATATCCAGTCTT	21	20
10	-	1680	TTTTTTCATCATATCCAGTCT	21	0
58	-	1681	TTTTTTTCATCATATCCAGTC	21	1
10	-	1683	TGTTTTTTTCATCATATCCAG	21	3
1	-	1683	GTTTTTTTCATCATATCCAG	20	3
7	-	1684	CTGTTTTTTTCATCATATCCA	21	4
9	-	1686	CTCTGTTTTTTTCATCATATC	21	6
9	-	1691	TGCGCACTCTGTTTTTTTCATC	22	11
3	-	1692	TGCGCACTCTGTTTTTTTCAT	21	12
12	-	1698	CCGGTATGCGCACTCTGTTTT	21	18
5	-	1698	TCCGGTATGCGCACTCTGTTTT	22	18
51	-	1699	TCCGGTATGCGCACTCTGTTT	21	19
18	-	1700	TCTCCGGTATGCGCACTCTGTT	22	20
19	-	1700	CTCCGGTATGCGCACTCTGTT	21	20
8	-	1700	TCCGGTATGCGCACTCTGTT	20	20
12	-	1701	TCTCCGGTATGCGCACTCTGT	21	0
130	-	1701	TTCTCCGGTATGCGCACTCTGT	22	0
17	-	1702	TTCTCCGGTATGCGCACTCTG	21	1
30	-	1703	CATGTTCTCCGGTATGCGCACTCT	24	2
15	-	1704	TGTTCTCCGGTATGCGCACTC	21	3
19	-	1705	CATGTTCTCCGGTATGCGCACT	22	4

37	-	1705	ATGTTCTCCGGTATGCGCACT	21	4
15	-	1706	CATGTTCTCCGGTATGCGCAC	21	5
61	-	1707	CCATGTTCTCCGGTATGCGCA	21	6
30	-	1708	TCCATGTTCTCCGGTATGCGC	21	7
21	-	1709	CTCCATGTTCTCCGGTATGCG	21	8
9	-	1709	ACTCCATGTTCTCCGGTATGCG	22	8
26	-	1710	AACTCCATGTTCTCCGGTATGC	22	9
5	-	1710	AAACTCCATGTTCTCCGGTATGC	23	9
49	-	1711	AAACTCCATGTTCTCCGGTATG	22	10
65	-	1711	AACTCCATGTTCTCCGGTATG	21	10
47	-	1713	GAAACTCCATGTTCTCCGGTA	21	12
9	-	1714	TGGAAACTCCATGTTCTCCGGT	22	13
26	-	1716	GTGGAAACTCCATGTTCTCCG	21	15
2	-	1717	AGGTGGAAACTCCATGTTCTCC	22	16
13	-	1718	AGGTGGAAACTCCATGTTCTC	21	17
12	-	1721	ACGAGGTGGAAACTCCATGTT	21	20
16	-	1733	TAGTAACCTTAGACGAGGTGG	21	11
1	-	1733	GTAGTAACCTTAGACGAGGTGG	22	11
5	-	1734	GTAGTAACCTTAGACGAGGTG	21	12
5	-	1734	TGTAGTAACCTTAGACGAGGTG	22	12
76	-	1735	TGTAGTAACCTTAGACGAGGT	21	13
1	-	1736	ACTGTAGTAACCTTAGACGAGG	22	14
83	-	1737	ACTGTAGTAACCTTAGACGAG	21	15
94	-	1738	CACTGTAGTAACCTTAGACGA	21	16
45	-	1739	CCACTGTAGTAACCTTAGACG	21	17
73	-	1739	CCCACTGTAGTAACCTTAGACG	22	17
16	-	1740	CCCACTGTAGTAACCTTAGAC	21	18
4	-	1740	TCCCACTGTAGTAACCTTAGAC	22	18
14	-	1741	TCCCACTGTAGTAACCTTAGA	21	19
1	-	1741	CTTCCCACTGTAGTAACCTTAGA	23	19
211	-	1741	TTCCCACTGTAGTAACCTTAGA	22	19
4	-	1741	GCTTCCCACTGTAGTAACCTTAGA	24	19
63	-	1741	CCCACTGTAGTAACCTTAGA	20	19
64	-	1742	TTCCCACTGTAGTAACCTTAG	21	20
36	-	1743	CTTCCCACTGTAGTAACCTTA	21	0
3	-	1743	GCTTCCCACTGTAGTAACCTTA	22	0
28	-	1744	GCTTCCCACTGTAGTAACCTT	21	1
7	-	1744	TGCTTCCCACTGTAGTAACCTT	22	1
238	-	1745	TGCTTCCCACTGTAGTAACCT	21	2
29	-	1745	ATGCTTCCCACTGTAGTAACCT	22	2
21	-	1746	ATGCTTCCCACTGTAGTAACC	21	3
75	-	1746	TATGCTTCCCACTGTAGTAACC	22	3
153	-	1747	TATGCTTCCCACTGTAGTAAC	21	4
6	-	1747	TGCTTCCCACTGTAGTAAC	19	4

34	-	1748	ATATGCTTCCCACTGTAGTAA	21	5
37	-	1748	GATATGCTTCCCACTGTAGTAA	22	5
23	-	1749	GATATGCTTCCCACTGTAGTA	21	6
4	-	1750	GATATGCTTCCCACTGTAGT	20	7
8	-	1750	CGGATATGCTTCCCACTGTAGT	22	7
10	-	1751	TCGGATATGCTTCCCACTGTAG	22	8
16	-	1752	CTCGGATATGCTTCCCACTGTA	22	9
262	-	1752	TCGGATATGCTTCCCACTGTA	21	9
3	-	1753	CTCGGATATGCTTCCCACTGT	21	10
4	-	1753	CCTCGGATATGCTTCCCACTGT	22	10
12	-	1754	CCTCGGATATGCTTCCCACTG	21	11
14	-	1755	TCCTCGGATATGCTTCCCACT	21	12
2	-	1755	CTCCTCGGATATGCTTCCCACT	22	12
12	-	1756	CTCCTCGGATATGCTTCCCAC	21	13
14	-	1757	TCTCCTCGGATATGCTTCCCA	21	14
186	-	1758	CTTCTCCTCGGATATGCTTCCC	22	15
19	-	1758	TTCTCCTCGGATATGCTTCCC	21	15
2	-	1759	ACTTCTCCTCGGATATGCTTCC	22	16
4	-	1759	CTTCTCCTCGGATATGCTTCC	21	16
5	-	1760	ACTTCTCCTCGGATATGCTTC	21	17
10	-	1761	GACTTCTCCTCGGATATGCTT	21	18
14	-	1762	AAGACTTCTCCTCGGATATGCT	22	19
317	-	1762	AGACTTCTCCTCGGATATGCT	21	19
65	-	1763	AAGACTTCTCCTCGGATATGC	21	20
24	-	1764	AAAGACTTCTCCTCGGATATG	21	0
241	-	1768	AAGAGAAAGACTTCTCCTCGGA	22	4
29	-	1768	AGAGAAAGACTTCTCCTCGGA	21	4
16	-	1778	GTTAAGTTTAAGAGAAAGACT	21	14
8	-	1779	GGTTAAGTTTAAGAGAAAGAC	21	15
5	-	1780	AGGTTAAGTTTAAGAGAAAGA	21	16
8	-	1782	TCCAGGTTAAGTTTAAGAGAAA	22	18
10	-	1783	TTCCAGGTTAAGTTTAAGAGAA	22	19
53	-	1783	TCCAGGTTAAGTTTAAGAGAA	21	19
145	-	1784	TTCCAGGTTAAGTTTAAGAGA	21	20
14	-	1784	ATTCCAGGTTAAGTTTAAGAGA	22	20
1	-	1784	TCCAGGTTAAGTTTAAGAGA	20	20
34	-	1785	ATTCCAGGTTAAGTTTAAGAG	21	0
2	-	1786	TATTCCAGGTTAAGTTTAAGA	21	1
11	-	1787	ATATTCCAGGTTAAGTTTAAG	21	2
35	-	1789	AGATATTCCAGGTTAAGTTTA	21	4
44	-	1790	AAGATATTCCAGGTTAAGTTT	21	5
7	-	1791	CAAGATATTCCAGGTTAAGTT	21	6
44	-	1792	ACAAGATATTCCAGGTTAAGT	21	7
142	-	1796	TTCGACAAGATATTCCAGGTT	21	11

27	-	1797	GTTCGACAAGATATTCCAGGT	21	12
4	-	1797	AGTTCGACAAGATATTCCAGGT	22	12
25	-	1798	AAGTTCGACAAGATATTCCAGG	22	13
30	-	1801	TCAAGTTCGACAAGATATTCC	21	16
10	-	1806	TCCATATCAAGTTCGACAAGAT	22	0
112	-	1807	TTCCATATCAAGTTCGACAAGA	22	1
25	-	1808	TTCCATATCAAGTTCGACAAG	21	2
2	-	1809	CTTCCATATCAAGTTCGACAA	21	3
7	-	1810	CTTCCATATCAAGTTCGACA	20	4
3	-	1811	ACCTTCCATATCAAGTTCGAC	21	5
3	-	1812	TACCTTCCATATCAAGTTCGA	21	6
3	-	1815	GGCTACCTTCCATATCAAGTT	21	9
7	-	1820	CGAGCAGGCTACCTTCCATATC	22	14
28	-	1824	TCTCGAGCAGGCTACCTTCCA	21	18
26	-	1825	TTCTCGAGCAGGCTACCTTCC	21	19
37	-	1825	CTTCTCGAGCAGGCTACCTTCC	22	19
159	-	1826	CTTCTCGAGCAGGCTACCTTC	21	20
8	-	1832	CCCATAGCTTCTCGAGCAGGCT	22	5
4	-	1833	TCCCATAGCTTCTCGAGCAGGC	22	6
6	-	1833	CCCATAGCTTCTCGAGCAGGC	21	6
6	-	1834	TCCCATAGCTTCTCGAGCAGG	21	7
1	-	1838	TCCATCCCATAGCTTCTCGAG	21	11
1	-	1838	TTCCATCCCATAGCTTCTCGAG	22	11
98	-	1839	TTCCATCCCATAGCTTCTCGA	21	12
4	-	1841	AGTTCCATCCCATAGCTTCTC	21	14
15	-	1861	TTGAGATTTGCAAGGGGCTGA	21	13
25	-	1864	TTCTTGAGATTTGCAAGGGGC	21	16
9	-	1866	TCTTCTTGAGATTTGCAAGGG	21	18
20	-	1869	ACATCTTCTTGAGATTTGCAA	21	0
6	-	1875	ACAAAGACATCTTCTTGAGAT	21	6
11	-	1878	CTTGACAAAGACATCTTCTTGA	22	9
13	-	1878	TTGACAAAGACATCTTCTTGA	21	9
1	-	1879	CTTGACAAAGACATCTTCTTG	21	10
6	-	1880	ACTTGACAAAGACATCTTCTT	21	11
2	-	1887	TACCATGAACTTGACAAAGACA	22	18
171	-	1889	ATACCATGAACTTGACAAAGA	21	20
13	-	1890	AATACCATGAACTTGACAAAG	21	0
94	-	1892	TAAATACCATGAACTTGACAA	21	2
2	-	1893	TTTAAATACCATGAACTTGACA	22	3
55	-	1893	TTAAATACCATGAACTTGACA	21	3
21	-	1894	TTTAAATACCATGAACTTGAC	21	4
103	-	1900	AGTTTCTTTAAATACCATGAA	21	10
16	-	1901	AAGTTTCTTTAAATACCATGA	21	11
1	-	1904	CGGAAGTTTCTTTAAATACCA	21	14

50	-	1905	TCCGGAAGTTTCTTTAAATACC	22	15
41	-	1906	TCCGGAAGTTTCTTTAAATAC	21	16
10	-	1912	GACAGATCCGGAAGTTTCTTT	21	1
16	-	1912	TGACAGATCCGGAAGTTTCTTT	22	1
13	-	1913	TTGACAGATCCGGAAGTTTCTT	22	2
231	-	1913	TGACAGATCCGGAAGTTTCTT	21	2
24	-	1914	TTGACAGATCCGGAAGTTTCT	21	3
1	-	1915	ATTTGACAGATCCGGAAGTTTC	22	4
81	-	1915	TTTGACAGATCCGGAAGTTTC	21	4
1	-	1916	TTGACAGATCCGGAAGTTT	19	5
4	-	1916	TTTGACAGATCCGGAAGTTT	20	5
5	-	1916	CATTTGACAGATCCGGAAGTTT	22	5
779	-	1916	ATTTGACAGATCCGGAAGTTT	21	5
29	-	1917	CATTTGACAGATCCGGAAGTT	21	6
7	-	1917	TTTGACAGATCCGGAAGTT	19	6
109	-	1918	GCATTTGACAGATCCGGAAGT	21	7
5	-	1918	TAGCATTTGACAGATCCGGAAGT	23	7
23	-	1919	TAGCATTTGACAGATCCGGAAG	22	8
72	-	1920	TAGCATTTGACAGATCCGGAA	21	9
144	-	1921	GTAGCATTTGACAGATCCGGA	21	10
55	-	1921	TGTAGCATTTGACAGATCCGGA	22	10
18	-	1922	TTGTAGCATTTGACAGATCCGG	22	11
31	-	1922	TGTAGCATTTGACAGATCCGG	21	11
20	-	1923	TTTGTAGCATTTGACAGATCCG	22	12
455	-	1923	TTGTAGCATTTGACAGATCCG	21	12
97	-	1924	TTTGTAGCATTTGACAGATCC	21	13
1	-	1926	AGATTTGTAGCATTTGACAGAT	22	15
9	-	1926	GATTTGTAGCATTTGACAGAT	21	15
1	-	1927	GATTTGTAGCATTTGACAGA	20	16
50	-	1927	GAGATTTGTAGCATTTGACAGA	22	16
758	-	1927	AGATTTGTAGCATTTGACAGA	21	16
14	-	1928	GAGATTTGTAGCATTTGACAG	21	17
1	-	1929	TCGAGATTTGTAGCATTTGACA	22	18
273	-	1930	TCGAGATTTGTAGCATTTGAC	21	19
352	-	1931	TTCGAGATTTGTAGCATTTGA	21	20
35	-	1931	CTTCGAGATTTGTAGCATTTGA	22	20
3	-	1933	TTCTTCGAGATTTGTAGCATTT	22	1
6	-	1933	TCTTCGAGATTTGTAGCATTT	21	1
10	-	1934	ATTCTTCGAGATTTGTAGCATT	22	2
238	-	1934	TTCTTCGAGATTTGTAGCATT	21	2
189	-	1935	ATTCTTCGAGATTTGTAGCAT	21	3
193	-	1936	AATTCTTCGAGATTTGTAGCA	21	4
7	-	1936	CAATTCTTCGAGATTTGTAGCA	22	4
11	-	1937	CAATTCTTCGAGATTTGTAGC	21	5

16	-	1939	TCCAATTCTTCGAGATTTGTA	21	7
6	-	1942	AGATCCAATTCTTCGAGATTT	21	10
173	-	1944	TCAGATCCAATTCTTCGAGAT	21	12
11	-	1945	CTCAGATCCAATTCTTCGAGA	21	13
9	-	1947	CTCTCAGATCCAATTCTTCGA	21	15
31	-	1955	CTGGCAAGCTCTCAGATCCAA	21	2
16	-	1956	TCTGGCAAGCTCTCAGATCCA	21	3
105	-	1960	TAAATTCTGGCAAGCTCTCAGA	22	7
112	-	1960	AAATTCTGGCAAGCTCTCAGA	21	7
1	-	1960	AATTCTGGCAAGCTCTCAGA	20	7
19	-	1963	ACTAAATTCTGGCAAGCTCTC	21	10
20	-	1963	TACTAAATTCTGGCAAGCTCTC	22	10
42	-	1964	TACTAAATTCTGGCAAGCTCT	21	11
2	-	1965	TCTACTAAATTCTGGCAAGCTC	22	12
5	-	1965	CTACTAAATTCTGGCAAGCTC	21	12
23	-	1966	TCTACTAAATTCTGGCAAGCT	21	13
8	-	1966	CTACTAAATTCTGGCAAGCT	20	13
21	-	1969	AGCTCTACTAAATTCTGGCAA	21	16
12	-	1970	CTCTACTAAATTCTGGCA	18	17
68	-	1970	AAGCTCTACTAAATTCTGGCA	21	17
18	-	1971	GAAGCTCTACTAAATTCTGGC	21	18
5	-	1972	GGAAGCTCTACTAAATTCTGG	21	19
36	-	1974	AAGGAAGCTCTACTAAATTCT	21	0
1	-	1976	AAGGAAGCTCTACTAAATT	19	2
16	-	1980	AGGAGGAAGGAAGCTCTACTA	21	6
7	-	1981	AAGGAGGAAGGAAGCTCTACT	21	7
9	-	1983	AAAAGGAGGAAGGAAGCTCTA	21	9
227	-	1985	AGAAAAGGAGGAAGGAAGCTC	21	11
2	-	1986	AAGAAAAGGAGGAAGGAAGCT	21	12
65	-	1987	TAAGAAAAGGAGGAAGGAAGC	21	13
11	-	1988	ATAAGAAAAGGAGGAAGGAAG	21	14
4	-	1988	GATAAGAAAAGGAGGAAGGAAG	22	14
69	-	1990	AGATAAGAAAAGGAGGAAGGA	21	16
2	-	1992	TGCAGATAAGAAAAGGAGGAAG	22	18
43	-	1993	TGCAGATAAGAAAAGGAGGAA	21	19
120	-	1994	ATGCAGATAAGAAAAGGAGGA	21	20
7	-	1995	TTATGCAGATAAGAAAAGGAGG	22	0
14	-	1996	TTATGCAGATAAGAAAAGGAG	21	1
2	-	1996	CTTATGCAGATAAGAAAAGGAG	22	1
24	-	2006	ATACTTTAGCTTATGCAGATA	21	11
27	-	2007	AATACTTTAGCTTATGCAGAT	21	12
7	-	2014	CATATTCAAATACTTTAGCTTA	22	19
55	-	2015	CATATTCAAATACTTTAGCTT	21	20
3	-	2017	ATCATATTCAAATACTTTAGC	21	1

64	-	2035	TTTAGCCTTCTGCATCCCATC	21	19
2	-	2038	TTCTTTTAGCCTTCTGCATCCC	22	1
2	-	2039	CTTCTTTTAGCCTTCTGCATCC	22	2
31	-	2042	AACTTCTTTTAGCCTTCTGCA	21	5
5	-	2045	TGGAACTTCTTTTAGCCTTCT	21	8
6	-	2047	GGTGGAACTTCTTTTAGCCTT	21	10
4	-	2049	GAGGTGGAACTTCTTTTAGCC	21	12
6	-	2049	AGGTGGAACTTCTTTTAGCC	20	12
29	-	2050	TGAGGTGGAACTTCTTTTAGC	21	13
11	-	2052	TATGAGGTGGAACTTCTTTTA	21	15
54	-	2055	TTGATATGAGGTGGAACTTCTT	22	18
22	-	2056	TTGATATGAGGTGGAACTTCT	21	19
4	-	2058	AGTTGATATGAGGTGGAACTT	21	0
54	-	2059	CAAGTTGATATGAGGTGGAACT	22	1
75	-	2059	AAGTTGATATGAGGTGGAACT	21	1
170	-	2061	TCAAGTTGATATGAGGTGGAA	21	3
29	-	2062	TTCAAGTTGATATGAGGTGGA	21	4
1	-	2063	TTCAAGTTGATATGAGGTGG	20	5
79	-	2065	GACTTCAAGTTGATATGAGGT	21	7
39	-	2068	AGAGACTTCAAGTTGATATGA	21	10
8	-	2069	AAGAGACTTCAAGTTGATATG	21	11
42	-	2073	ATTCAAGAGACTTCAAGTTGA	21	15
14	-	2075	AATTCAAGAGACTTCAAGTT	20	17
1	-	2077	ACCAATTCAAGAGACTTCAAG	21	19
10	-	2080	TTGACCAATTCAAGAGACTTC	21	1
22	-	2083	ATGTTGACCAATTCAAGAGAC	21	4
40	-	2084	CATGTTGACCAATTCAAGAGA	21	5
20	-	2085	ACATGTTGACCAATTCAAGAG	21	6
17	-	2086	TACATGTTGACCAATTCAAGA	21	7
58	-	2086	ATACATGTTGACCAATTCAAGA	22	7
35	-	2087	ATACATGTTGACCAATTCAAG	21	8
3	-	2088	CATACATGTTGACCAATTCAA	21	9
3	-	2094	AGCATCCATACATGTTGACCA	21	15
1	-	2097	TTGAGCATCCATACATGTTGA	21	18
74	-	2099	TCTTGAGCATCCATACATGTT	21	20
9	-	2099	ATCTTGAGCATCCATACATGTT	22	20
5	-	2100	TAATCTTGAGCATCCATACATGT	23	0
97	-	2100	ATCTTGAGCATCCATACATGT	21	0
103	-	2103	TTTAATCTTGAGCATCCATACA	22	3
2	-	2103	AATCTTGAGCATCCATACA	19	3
8	-	2103	TTAATCTTGAGCATCCATACA	21	3
12	-	2108	CTTTTTAATCTTGAGCATCC	20	8
7	-	2111	AAAGCTTTTTAATCTTGAGCA	21	11
5	-	2113	TGGAAAGCTTTTTAATCTTGAG	22	13

6	-	2113	GGAAAGCTTTTTAATCTTGAG	21	13
4	-	2114	TGGAAAGCTTTTTAATCTTGA	21	14
6	-	2116	TCTGGAAAGCTTTTTAATCTT	21	16
2	-	2120	AATATCTGGAAAGCTTTTTAA	21	20
28	-	2125	GTAGAAATATCTGGAAAGCTT	21	4
7	-	2125	TGTAGAAATATCTGGAAAGCTT	22	4
4	-	2126	TGTAGAAATATCTGGAAAGCT	21	5
21	-	2127	TTTGTAGAAATATCTGGAAAGC	22	6
3	-	2127	TTGTAGAAATATCTGGAAAGC	21	6
16	-	2128	TTTGTAGAAATATCTGGAAAG	21	7
13	-	2129	GTTTGTAGAAATATCTGGAAA	21	8
5	-	2129	TGTTTGTAGAAATATCTGGAAA	22	8
179	-	2130	TGTTTGTAGAAATATCTGGAA	21	9
10	-	2131	ATGTTTGTAGAAATATCTGGA	21	10
104	-	2136	AACTGATGTTTGTAGAAATAT	21	15
5	-	2136	ACTGATGTTTGTAGAAATAT	20	15
2	-	2137	GAACTGATGTTTGTAGAAATA	21	16
15	-	2139	AGTGAACTGATGTTTGTAGAAA	22	18
4	-	2139	GTGAACTGATGTTTGTAGAAA	21	18
1	-	2140	GTGAACTGATGTTTGTAGAA	20	19
357	-	2140	AGTGAACTGATGTTTGTAGAA	21	19
70	-	2141	GAGTGAACTGATGTTTGTAGA	21	20
42	-	2143	TCGAGTGAACTGATGTTTGTA	21	1
82	-	2145	TGTCGAGTGAACTGATGTTTG	21	3
115	-	2147	TATGTCGAGTGAACTGATGTT	21	5
16	-	2147	ATATGTCGAGTGAACTGATGTT	22	5
158	-	2148	ATATGTCGAGTGAACTGATGT	21	6
8	-	2149	TGATATGTCGAGTGAACTGATG	22	7
29	-	2150	ATGATATGTCGAGTGAACTGAT	22	8
67	-	2150	TGATATGTCGAGTGAACTGAT	21	8
173	-	2151	ATGATATGTCGAGTGAACTGA	21	9
9	-	2151	TATGATATGTCGAGTGAACTGA	22	9
2	-	2155	GTGTATGATATGTCGAGTGAA	21	13
1	-	2156	GTGTATGATATGTCGAGTGA	20	14
91	-	2156	AGTGTATGATATGTCGAGTGA	21	14
37	-	2157	CAGTGTATGATATGTCGAGTG	21	15
57	-	2157	TCAGTGTATGATATGTCGAGTG	22	15
272	-	2158	TCAGTGTATGATATGTCGAGT	21	16
5	-	2159	ATCAGTGTATGATATGTCGAG	21	17
8	-	2159	TCAGTGTATGATATGTCGAG	20	17
4	-	2160	CATCAGTGTATGATATGTCGA	21	18
6	-	2161	ACATCAGTGTATGATATGTCG	21	19
2	-	2175	CAGGTAGTTCTTCCACATCAG	21	12
20	-	2182	ATTGATTCAGGTAGTTCTTCC	21	19

3	-	2182	CATTGATTCAGGTAGTTCTTCC	22	19
39	-	2184	TCATTGATTCAGGTAGTTCTT	21	0
162	-	2187	TCGTCATTGATTCAGGTAGTT	21	3
14	-	2190	ACATCGTCATTGATTCAGGTA	21	6
24	-	2191	CACATCGTCATTGATTCAGGT	21	7
11	-	2192	ACCACATCGTCATTGATTCAGG	22	8
37	-	2193	ACCACATCGTCATTGATTCAG	21	9
7	-	2193	AGACCACATCGTCATTGATTCAG	23	9
1	-	2197	CGAGACCACATCGTCATTGAT	21	13
9	-	2204	ACGTAGGCGAGACCACATCGT	21	20
7	-	2205	TACGTAGGCGAGACCACATCG	21	0
15	-	2209	AGAGTACGTAGGCGAGACCAC	21	4
6	-	2211	TCGAGAGTACGTAGGCGAGACC	22	6
261	-	2213	TTTCGAGAGTACGTAGGCGAGA	22	8
92	-	2213	TTCGAGAGTACGTAGGCGAGA	21	8
40	-	2214	TTTCGAGAGTACGTAGGCGAG	21	9
21	-	2215	ATTTCGAGAGTACGTAGGCGA	21	10
5	-	2215	TATTTCGAGAGTACGTAGGCGA	22	10
2	-	2216	ATATTTCGAGAGTACGTAGGCG	22	11
47	-	2216	TATTTCGAGAGTACGTAGGCG	21	11
70	-	2217	ATATTTCGAGAGTACGTAGGC	21	12
62	-	2218	TATATTTCGAGAGTACGTAGG	21	13
13	-	2221	TTGTATATTTCGAGAGTACGT	21	16
8	-	2226	TACTTTTGTATATTTCGAGAG	21	0
7	-	2229	TTCTACTTTTGTATATTTCGA	21	3
12	-	2242	ACTATCTTGAGGTTTCTACTT	21	16
6	-	2245	TGTTACTATCTTGAGGTTTCTA	22	19
11	-	2246	TGTTACTATCTTGAGGTTTCT	21	20
8	-	2247	TGTGTTACTATCTTGAGGTTTC	22	0
68	-	2248	TGTGTTACTATCTTGAGGTTT	21	1
46	-	2250	CATGTGTTACTATCTTGAGGT	21	3
1	-	2251	CACATGTGTTACTATCTTGAGG	22	4
6	-	2251	ACATGTGTTACTATCTTGAGG	21	4
92	-	2252	CACATGTGTTACTATCTTGAG	21	5
2	-	2253	GCACATGTGTTACTATCTTGA	21	6
138	-	2260	TTTAGGGGCACATGTGTTACT	21	13
7	-	2264	TAGGTTTAGGGGCACATGTGT	21	17
6	-	2265	TTAGGTTTAGGGGCACATGTG	21	18
3	-	2270	ATATGTTAGGTTTAGGGGCAC	21	2
1	-	2271	AGATATGTTAGGTTTAGGGGCA	22	3
3	-	2271	GATATGTTAGGTTTAGGGGCA	21	3
44	-	2272	AGATATGTTAGGTTTAGGGGC	21	4
6	-	2273	TAGATATGTTAGGTTTAGGGG	21	5
8	-	2275	TCTAGATATGTTAGGTTTAGG	21	7

1	-	2278	TGAGGTCTAGATATGTTAGGTTT	23	10
6	-	2278	GAGGTCTAGATATGTTAGGTTT	22	10
10	-	2279	GAGGTCTAGATATGTTAGGTT	21	11
35	-	2280	TGAGGTCTAGATATGTTAGGT	21	12
4	-	2281	CTGAGGTCTAGATATGTTAGG	21	13
8	-	2281	GGTCTAGATATGTTAGG	17	13
55	-	2284	TCGCTGAGGTCTAGATATGTT	21	16
1	-	2286	TCTCGCTGAGGTCTAGATATG	21	18
35	-	2293	ATTCTAGTCTCGCTGAGGTCT	21	4
39	-	2293	AATTCTAGTCTCGCTGAGGTCT	22	4
16	-	2294	AATTCTAGTCTCGCTGAGGTC	21	5
12	-	2295	AATTCTAGTCTCGCTGAGGT	20	6
36	-	2295	CAATTCTAGTCTCGCTGAGGT	21	6
38	-	2295	TCAATTCTAGTCTCGCTGAGGT	22	6
123	-	2296	TCAATTCTAGTCTCGCTGAGG	21	7
29	-	2297	CTCAATTCTAGTCTCGCTGAG	21	8
18	-	2298	TTCTCAATTCTAGTCTCGCTGA	22	9
87	-	2298	TCTCAATTCTAGTCTCGCTGA	21	9
5	-	2299	TTCTCAATTCTAGTCTCGCTG	21	10
25	-	2301	TCTTCTCAATTCTAGTCTCGC	21	12
4	-	2301	ATCTTCTCAATTCTAGTCTCGC	22	12
21	-	2302	ATCTTCTCAATTCTAGTCTCG	21	13
23	-	2302	AATCTTCTCAATTCTAGTCTCG	22	13
3	-	2303	AATCTTCTCAATTCTAGTCTC	21	14
12	-	2311	TCATCTGGAATCTTCTCAATT	21	1
23	-	2317	TTGATGTCATCTGGAATCTTC	21	7
27	-	2317	TTTGATGTCATCTGGAATCTTC	22	7
25	-	2321	ATTTTTGATGTCATCTGGAAT	21	11
35	-	2324	AACATTTTTGATGTCATCTGG	21	14
7	-	2330	CCCATGAACATTTTTGATGTC	21	20
20	-	2336	TTGCAGCCCATGAACATTTTT	21	5
13	-	2337	TTTGCAGCCCATGAACATTTT	21	6
26	-	2337	ATTTGCAGCCCATGAACATTTT	22	6
4	-	2338	ATTTGCAGCCCATGAACATTT	21	7
13	-	2344	AATAAAATTTGCAGCCCATGA	21	13
99	-	2365	AGTTTTCTGCAGCCACCTAGA	21	13
13	-	2372	TGATGCGAGTTTTCTGCAGCC	21	20
1	-	2378	TGGCAATGATGCGAGTTTTCT	21	5
46	-	2382	GCTCTGGCAATGATGCGAGTT	21	9
22	-	2384	AAGCTCTGGCAATGATGCGAG	21	11
6	-	2386	GGAAGCTCTGGCAATGATGCG	21	13
10	-	2387	AGGAAGCTCTGGCAATGATGC	21	14
24	-	2394	GCGAACCAGGAAGCTCTGGCA	21	0
4	-	2402	GTACAAGAGCGAACCAGGAAG	21	8

4	-	2403	AGTACAAGAGCGAACCAGGAA	21	9
36	-	2404	AAGTACAAGAGCGAACCAGGA	21	10
42	-	2404	TAAGTACAAGAGCGAACCAGGA	22	10
6	-	2405	ATAAGTACAAGAGCGAACCAGG	22	11
6	-	2405	TAAGTACAAGAGCGAACCAGG	21	11
3	-	2408	CTGATAAGTACAAGAGCGAACC	22	14
4	-	2408	TGATAAGTACAAGAGCGAACC	21	14
1	-	2412	TTTGCTGATAAGTACAAGAGCG	22	18
36	-	2413	TTTGCTGATAAGTACAAGAGC	21	19
46	-	2415	TCGTTTGCTGATAAGTACAAGA	22	0
3	-	2416	TCGTTTGCTGATAAGTACAAG	21	1
7	-	2418	ACTCGTTTGCTGATAAGTACA	21	3
17	-	2425	GATTCACACTCGTTTGCTGAT	21	10
123	-	2426	TGATTCACACTCGTTTGCTGA	21	11
6	-	2428	AGTGATTCACACTCGTTTGCT	21	13
4	-	2434	CTCTCAAGTGATTCACACTCG	21	19
33	-	2443	CAAGATACGCTCTCAAGTGAT	21	7
93	-	2453	ATTAAAAGGGCAAGATACGCT	21	17
5	-	2463	TGTATGAAGTATTAAAAGGGC	21	6
28	-	2464	ATGTATGAAGTATTAAAAGGG	21	7
34	-	2472	TGAGTTCCATGTATGAAGTAT	21	15
40	-	2476	AAGCTGAGTTCCATGTATGAA	21	19
7	-	2478	TGAAGCTGAGTTCCATGTATG	21	0
1	-	2480	GGTGAAGCTGAGTTCCATGTA	21	2
3	-	2492	TTTGAAGCAGTTGGTGAAGCT	21	14
229	-	2493	AGTTTGAAGCAGTTGGTGAAGC	22	15
4	-	2494	AGTTTGAAGCAGTTGGTGAAG	21	16
23	-	2495	TAGTTTGAAGCAGTTGGTGAA	21	17
1	-	2496	TTTAGTTTGAAGCAGTTGGTGA	22	18
53	-	2497	TTTAGTTTGAAGCAGTTGGTG	21	19
9	-	2499	GGTTTAGTTTGAAGCAGTTGG	21	0
27	-	2501	TTGGTTTAGTTTGAAGCAGTT	21	2
6	-	2502	TCTTGGTTTAGTTTGAAGCAGT	22	3
7	-	2503	TCTTGGTTTAGTTTGAAGCAG	21	4
10	-	2504	TTCTTGGTTTAGTTTGAAGCA	21	5
5	-	2507	TGCTTCTTGGTTTAGTTTGAA	21	8
3	-	2508	CGTGCTTCTTGGTTTAGTTTGA	22	9
23	-	2511	TGCGTGCTTCTTGGTTTAGTT	21	12
4	-	2515	CCTCTGCGTGCTTCTTGGTTT	21	16
27	-	2516	TCCTCTGCGTGCTTCTTGGTT	21	17
7	-	2516	TTCCTCTGCGTGCTTCTTGGTT	22	17
5	-	2517	ATTCCTCTGCGTGCTTCTTGGT	22	18
80	-	2518	ATTCCTCTGCGTGCTTCTTGG	21	19
11	-	2521	ATAATTCCTCTGCGTGCTTCT	21	1

9	-	2524	TGAATAATTCCTCTGCGTGCT	21	4
14	-	2526	GTTGAATAATTCCTCTGCGTG	21	6
1	-	2527	TGTTGAATAATTCCTCTGCGT	21	7
10	-	2528	TTGTTGAATAATTCCTCTGCG	21	8
5	-	2529	ATTGTTGAATAATTCCTCTGC	21	9
39	-	2532	ATGATTGTTGAATAATTCCTC	21	12
32	-	2533	AATGATTGTTGAATAATTCCT	21	13
1	-	2534	AATGATTGTTGAATAATTCC	20	14
1	-	2536	GAAAATGATTGTTGAATAATT	21	16
65	-	2537	AGAAAATGATTGTTGAATAAT	21	17
68	-	2540	ATGAGAAAATGATTGTTGAAT	21	20
143	-	2555	TAAGGATGCCCACCCATGAGA	21	14
9	-	2569	AACTCTCTTCCAGGTAAGGAT	21	7
12	-	2574	TGGGCAACTCTCTTCCAGGTA	21	12
4	-	2575	CAGTGGGCAACTCTCTTCCAGGT	23	13
15	-	2578	TCAGTGGGCAACTCTCTTCCA	21	16
94	-	2580	AGTCAGTGGGCAACTCTCTTC	21	18
8	-	2581	AAGTCAGTGGGCAACTCTCTT	21	19
14	-	2582	TAAGTCAGTGGGCAACTCTCT	21	20
5	-	2583	ATAAGTCAGTGGGCAACTCTC	21	0
13	-	2584	TATAAGTCAGTGGGCAACTCT	21	1
1	-	2589	TCGGTGGTATAAGTCAGTGGGCA	23	6
3	-	2589	GGTGGTATAAGTCAGTGGGCA	21	6
8	-	2589	CGGTGGTATAAGTCAGTGGGCA	22	6
11	-	2590	CGGTGGTATAAGTCAGTGGGC	21	7
59	-	2590	TCGGTGGTATAAGTCAGTGGGC	22	7
17	-	2591	ATCGGTGGTATAAGTCAGTGGG	22	8
8	-	2594	TAGATCGGTGGTATAAGTCAGT	22	11
20	-	2595	TAGATCGGTGGTATAAGTCAG	21	12
16	-	2596	GTAGATCGGTGGTATAAGTCA	21	13
19	-	2597	GGTAGATCGGTGGTATAAGTC	21	14
3	-	2597	CGGTAGATCGGTGGTATAAGTC	22	14
11	-	2603	ATGTCCGGTAGATCGGTGGTA	21	20
54	-	2604	AATGTCCGGTAGATCGGTGGT	21	0
11	-	2606	TGGAATGTCCGGTAGATCGGTG	22	2
20	-	2607	TGGAATGTCCGGTAGATCGGT	21	3
8	-	2607	ATGGAATGTCCGGTAGATCGGT	22	3
5	-	2608	ATGGAATGTCCGGTAGATCGG	21	4
5	-	2609	TGATGGAATGTCCGGTAGATCG	22	5
49	-	2610	TGATGGAATGTCCGGTAGATC	21	6
10	-	2615	AACGGTGATGGAATGTCCGGT	21	11
2	-	2616	CGAACGGTGATGGAATGTCCGG	22	12
4	-	2617	CGAACGGTGATGGAATGTCCG	21	13
9	-	2620	AGACGAACGGTGATGGAATGT	21	16

8	-	2621	CGAGACGAACGGTGATGGAATG	22	17
13	-	2623	TCGAGACGAACGGTGATGGAA	21	19
12	-	2624	CTCGAGACGAACGGTGATGGA	21	20
10	-	2625	CCTCGAGACGAACGGTGATGG	21	0
2	-	2625	CCCTCGAGACGAACGGTGATGG	22	0
3	-	2629	TTGCCCTCGAGACGAACGGTG	21	4
12	-	2630	CTTGCCCTCGAGACGAACGGT	21	5
21	-	2631	TCTTGCCCTCGAGACGAACGG	21	6
2	-	2635	GGAGTCTTGCCCTCGAGACGA	21	10
2	-	2638	AAAGGAGTCTTGCCCTCGAGA	21	13
13	-	2639	AAAAGGAGTCTTGCCCTCGAG	21	14
9	-	2643	CAGAAAAAGGAGTCTTGCCCT	21	18
16	-	2647	AATGCAGAAAAAGGAGTCTTG	21	1
8	-	2648	GAATGCAGAAAAAGGAGTCTT	21	2
16	-	2650	AAGAATGCAGAAAAAGGAGTC	21	4
12	-	2651	AAGAATGCAGAAAAAGGAGT	20	5
41	-	2651	CAAAGAATGCAGAAAAAGGAGT	22	5
7	-	2652	CAAAGAATGCAGAAAAAGGAG	21	6
16	-	2653	CCAAAGAATGCAGAAAAAGGA	21	7
6	-	2656	AATCCAAAGAATGCAGAAAAA	21	10
3	-	2660	CCTTAAATCCAAAGAATGCAGA	22	14
1	-	2683	TTAGGGGAAATCACGAGGAAA	21	16
16	-	2686	TGGTTAGGGGAAATCACGAGG	21	19
11	-	2694	TCAGCATCATGGTTAGGGGAAA	22	6
1	-	2694	CAGCATCATGGTTAGGGGAAA	21	6
4	-	2695	TCAGCATCATGGTTAGGGGAA	21	7
34	-	2697	TCTTCAGCATCATGGTTAGGGG	22	9
5	-	2697	CTTCAGCATCATGGTTAGGGG	21	9
42	-	2698	TCTTCAGCATCATGGTTAGGG	21	10
3	-	2699	TTTCTTCAGCATCATGGTTAGG	22	11
6	-	2699	TTCTTCAGCATCATGGTTAGG	21	11
2	-	2715	AGGGAGAATTGCTAGTTTCTT	21	6
2	-	2717	TAAGGGAGAATTGCTAGTTTC	21	8
3	-	2719	AATAAGGGAGAATTGCTAGTT	21	10
5	-	2729	TGCGAGGACAAAATAAGGGAGA	22	20
1	-	2730	ATGCGAGGACAAAATAAGGGAG	22	0
281	-	2731	ATGCGAGGACAAAATAAGGGA	21	1
2	-	2731	TGCGAGGACAAAATAAGGGA	20	1
31	-	2732	AATGCGAGGACAAAATAAGGG	21	2
3	-	2732	CAATGCGAGGACAAAATAAGGG	22	2
1	-	2746	CAACCGATTTTGCCAATGCGA	21	16
11	-	2761	GTTTCGTCATCGGAGCAACCG	21	10
15	-	2765	AGGTGTTTCGTCATCGGAGCA	21	14
24	-	2766	ATAGGTGTTTCGTCATCGGAGC	22	15

7	-	2766	TAGGTGTTTCGTCATCGGAGC	21	15
24	-	2768	AATAGGTGTTTCGTCATCGGA	21	17
17	-	2772	TATAAATAGGTGTTTCGTCAT	21	0
3	-	2773	ATATAAATAGGTGTTTCGTCA	21	1
3	-	2774	AATATAAATAGGTGTTTCGTC	21	2
3	-	2782	TTGGGGATAATATAAATAGGT	21	10
50	-	2796	TGTTCTGCTCGAGGTTTGGGGA	22	3
12	-	2797	TGTTCTGCTCGAGGTTTGGGG	21	4
34	-	2798	ATGTTCTGCTCGAGGTTTGGG	21	5
36	-	2798	GATGTTCTGCTCGAGGTTTGGG	22	5
2	-	2799	AGATGTTCTGCTCGAGGTTTGG	22	6
6	-	2801	TAGATGTTCTGCTCGAGGTTT	21	8
1	-	2803	CTAGATGTTCTGCTCGAGGT	20	10
54	-	2803	ACTAGATGTTCTGCTCGAGGT	21	10
2	-	2804	CTAGATGTTCTGCTCGAGG	19	11
2	-	2804	TAACTAGATGTTCTGCTCGAGG	22	11
2	-	2805	TAACTAGATGTTCTGCTCGAG	21	12
14	-	2814	AGTGAAACATAACTAGATGTT	21	0
1	-	2820	AGAGTGAAACATAACTA	17	6
3	-	2820	AGTCAGAGTGAAACATAACTA	21	6
11	-	2821	CAAGTCAGAGTGAAACATAACT	22	7
4	-	2824	TGCAAGTCAGAGTGAAACATA	21	10
2	-	2829	TGTTATGCAAGTCAGAGTGAA	21	15
11	-	2830	TTGTTATGCAAGTCAGAGTGA	21	16
81	-	2834	TTCCTTGTTATGCAAGTCAGA	21	20
3	-	2859	TCTCGTTGCCTACTTCATGAC	21	3
2	-	2860	ATCTCGTTGCCTACTTCATGA	21	4
27	-	2863	CAGTATCTCGTTGCCTACTTCA	22	7
65	-	2866	AACAGTATCTCGTTGCCTACT	21	10
16	-	2868	CAAACAGTATCTCGTTGCCTA	21	12
4	-	2868	AAACAGTATCTCGTTGCCTA	20	12
5	-	2870	TTCAAACAGTATCTCGTTGCC	21	14
7	-	2880	TGTTGCTGAATTCAAACAGTA	21	3
44	-	2891	GGTGTCGGATATGTTGCTGAA	21	14
30	-	2892	AGGTGTCGGATATGTTGCTGA	21	15
47	-	2892	TAGGTGTCGGATATGTTGCTGA	22	15
18	-	2893	TAGGTGTCGGATATGTTGCTG	21	16
15	-	2894	ATAGGTGTCGGATATGTTGCT	21	17
33	-	2894	TAGGTGTCGGATATGTTGCT	20	17
6	-	2894	CATAGGTGTCGGATATGTTGCT	22	17
10	-	2895	TCATAGGTGTCGGATATGTTGC	22	18
10	-	2896	TAGGTGTCGGATATGTTG	18	19
14	-	2896	TCATAGGTGTCGGATATGTTG	21	19
30	-	2897	TCTCATAGGTGTCGGATATGTT	22	20

1	-	2899	ATCTCATAGGTGTCGGATATG	21	1
19	-	2901	ATAATCTCATAGGTGTCGGATA	22	3
41	-	2904	CAATAATCTCATAGGTGTCGG	21	6
39	-	2906	CTCAATAATCTCATAGGTGTC	21	8
2	-	2909	ACACTCAATAATCTCATAGGT	21	11
7	-	2924	ATAGAATCTGACACCACACTC	21	5
1	-	2930	ATCTGTATAGAATCTGACACC	21	11
7	-	2935	TGTTCATCTGTATAGAATCTG	21	16
3	-	2943	ATTTCACCTGTTCATCTGTAT	21	3
4	-	2946	CTGATTTCACCTGTTCATCTG	21	6
2	-	2952	CTTTCACTGATTTCACCTGTT	21	12
6	-	2953	CCTTTCACTGATTTCACCTGT	21	13
45	-	2958	TTTCTCCTTTCACTGATTTCA	21	18
59	-	2962	TTCATTTCTCCTTTCACTGAT	21	1
19	-	2965	CATATTCATTTCTCCTTTCACT	22	4
27	-	2983	ACAAACTTGGTCTATTTCATA	21	1
4	-	2986	TTCACAAACTTGGTCTATTTC	21	4
3	-	2987	TCTTCACAAACTTGGTCTATTT	22	5
1	-	2988	TCTTCACAAACTTGGTCTATT	21	6
12	-	2989	ATCTTCACAAACTTGGTCTAT	21	7
15	-	2992	TTCATCTTCACAAACTTGGTC	21	10
5	-	2992	TTTCATCTTCACAAACTTGGTC	22	10
11	-	2993	TTTCATCTTCACAAACTTGGT	21	11
12	-	3007	ATAGCTCCAATCGTTTTCATC	21	4
9	-	3007	CATAGCTCCAATCGTTTTCATC	22	4
11	-	3013	AAACTCATAGCTCCAATCGTT	21	10
13	-	3014	CAAACTCATAGCTCCAATCGT	21	11
7	-	3037	GCATTCCAATGCTTCCACGGG	21	13
13	-	3058	ATTATGTCCATTATTTTTAGA	21	13
172	-	3083	CGTTCGAAGTACAGATTAGGC	21	17
1	-	3097	TTCGATCTTGTCTTCGTTCGA	21	10
4	-	3099	GGCTTCGATCTTGTCTTCGTTC	22	12
21	-	3104	TGTTGGCTTCGATCTTGTCTT	21	17
2	-	3105	TTTGTTGGCTTCGATCTTGTCT	22	18
1	-	3106	ATTTGTTGGCTTCGATCTTGTC	22	19
8	-	3107	TGTTGGCTTCGATCTTGT	18	20
25	-	3109	GTATTTGTTGGCTTCGATCTT	21	1
52	-	3112	ATCTGTGTATTTGTTGGCTTCGAT	24	4
10	-	3115	ATCTGTGTATTTGTTGGCTTC	21	7
6	-	3115	AATCTGTGTATTTGTTGGCTTC	22	7
14	-	3118	ACAATCTGTGTATTTGTTGGC	21	10
2	-	3128	GCCAACTCCAACAATCTGTGT	21	20
1	-	3142	AAAACAGATGATGAGCCAACT	21	13
4	-	3153	ATGGGAGACATCAAAACAGATG	22	3

11	-	3155	TATGGGAGACATCAAAACAGA	21	5
1	-	3186	TCCCCAAACTAAACTTCCGATG	22	15
3	-	3202	CTTCTCTCATCTTCCTCCCCA	21	10
3	-	3245	TGCAAATTCGTTCGACTTCTC	21	11
3	-	3246	TTGCAAATTCGTTCGACTTCT	21	12
1	-	3249	TCACTTGCAAATTCGTTCGACT	22	15
3	-	3250	TCACTTGCAAATTCGTTCGAC	21	16

Note: Reads (#) indicate the copy number of the sepcific small RNA in column D5. The "+" strand indicates the same orientation of smal RNA as that of At5G38850 whereas a "-" indicates the reverse strand. Register is the position (column C) module 21.