Bin (kb)	Sum Normalized Reads Replicate 1	Sum Normalized Reads Replicate 2	Sum of PAMs
1	75135.70189	96916.33065	63
2	66514.73417	76101.78315	32
3	96224.79744	134446.2189	67
4	95265.89447	118575.6889	61
5	54582.20622	61719.70813	47
6	61270.23582	64118.26468	60
7	42006.5602	34075.208	56
8	47130.39925	37879.72366	60
9	25662.99897	25369.02567	49
10	44391.47293	34268.87479	48
11	33898.89228	26204.13097	63
12	24281.58934	18828.02919	68
13	24905.19484	15443.05138	54
14	13730.47101	11350.90304	45
15	19452.82799	12257.03421	54
16	22278.96351	16417.12032	67
17	19155.361	18297.76158	66
18	15772.52018	13655.93485	48
19	20416.90775	15547.60497	51
20	14282.79593	9344.532773	47
21	11885.14031	10897.39631	61
22	14721.62943	12499.22798	66
23	12951.56146	8190.472829	58
24	9763.846252	8202.383998	62
25	8350.181168	7839.755071	66
26	8395.577737	6259.539964	67
27	4726.021751	4475.511519	53
28	6818.644291	5157.095086	52
29	2950.378763	3015.731566	41
30	3174.175883	4359.487908	61
31	7468.133799	6112.19439	67
32	5170.430268	4635.65057	56
33	9170.505132	6549.819568	47
34	4910.793751	4822.258887	57
35	7564.501954	7883.429358	78
36	7884.269014	8044.450719	56
37	6287.823008	5962.20189	55
38	10971.2357	7579.032813	51
39	13233.49805	11762.05896	70
40	21049.67221	15586.42656	57
41	6191.454853	9348.944317	31

Spacer Sequence	Location	Strand	PAM	Reads Replicate 1	Reads Replicate 2
CGTTCCATTGAATACTGTGT	2368	-	AGG	52680	43714
AAACATGTTGCGATGATGTC	2048	+	AGG	30908	59970
CAATCCATTCATCTATTGCT	3503	-	TGG	34547	34893
ATAAAAAAACTGCTACTTGT	3239	+	TGG	38980	29511
TCTGATGAATATTCATCTCT	1424	-	CGG	32678	31754
AGCAATTCACACCCGCACAG	998	+	TGG	29015	33743
AGTATGCTTACTTTTTCTTG	3823	-	TGG	15478	35193
TGAAGCATAATACTGCTACT	3088	-	AGG	23825	23247
TAGAGATATAGAACTTCACT	5384	+	GGG	28586	17408
GCGCTTCAATAGTGATAGTA	4338	-	GGG	23891	21139
TTTTAATAACCTCAACATCT	1070	-	TGG	27705	14436
GTCAGTATGTACAGATTAAT	4241	+	AGG	23623	17749
TTCAAAAGTTTAGTATCTAT	698	-	AGG	20913	18997
GAGAACAAAACCATCCTACC	827	+	CGG	21295	17109
ACTTTCCATTACTTAAATCA	9043	+	TGG	20484	16235
GTAGAAGTACAGTATACAAC	2918	+	TGG	13903	20869
GTGAATTGCTAGTAGTGTGT	1181	-	TGG	17596	15299
TTGATTTCGTGCCACTGTGC	993	-	GGG	12816	19034
TTAGAATTGACACCTCAAGA	873	+	AGG	13956	17740
TGAAGAGAACACAGACGAAC	3540	+	AGG	13776	17221
ACCAACTGGCACGGATCAAT	7611	+	TGG	15870	14919
AGTAAGACGCCAAAAGTAAC	2465	+	AGG	14924	14780
TGTCCTTTACCTGTTACTTT	2458	-	TGG	18648	11332
ATATCTGAATTGTTATCAGT	3651	-	TGG	12604	16568
ACTTATTCCGTCGTTGCTAC	5238	+	TGG	7036	20037
CTTTATCTAACATGATACAC	805	+	GGG	11745	15515
ACACCTCAATATATACTTGC	15249	+	TGG	18831	8625
AGAAAAACAAACAACTTAAT	2524	+	AGG	11575	14250
AGCACTCCTAATCGTCATCT	5893	+	TGG	15066	10862
AACACCTATTAACGTAGTAT	1449	-	TGG	6680	17762
GATTCCAATACTACGTTAAT	1461	+	AGG	10539	13894
ACGACATAAGCATGTTTAAT	3441	-	TGG	11300	12864
GGAAGAATACACGATGTTGT	10947	+	AGG	14542	9865
AAGAGAGTTATATAAAGCTT	1876	+	TGG	12238	10403
ATTAGAGCCTCAATATGCTT	16315	-	AGG	12629	10004
CACCTTAAAACGCTAAATCT	5152	-	TGG	14897	6942
GGACAAAAATCAATCAATAG	7069	+	TGG	15414	6461
ATACGTATGCACATTACACA	18135	+	AGG	14115	7229
TTTGATACCAATGATCTTAT	4917	+	TGG	11700	9152
TACTGATATTCAACTTCTGT	9289	-	AGG	11770	8804
ACACAAATCCATCAATTGTT	2890	+	TGG	11505	8805
TGTACACGAGCATAGCTACC	23485	-	AGG	13101	7169
ACTTTATCTAACATGATACA	804	+	CGG	11203	8729
TCACTATAACAATTGCTTGT	12254	-	TGG	13341	6540

ATTGAATTAGTTACTCGATT	4866	+	AGG	8544	10361
CACAACGAGCAACATGCGAT	5751	+	TGG	10590	8348
TTAAAACCCCTAACCTTACT	6272	+	AGG	10403	8348
CCACACCCTTGCGTTTAATA	2334	-	AGG	12777	6202
GTTTAAGATATAGAATGCTT	10634	-	TGG	14243	4653
TCTTGGAAATCATATTTATA	4817	-	CGG	9145	9147
GACAGAAACTATTGAGTACG	3786	+	AGG	7503	10174
CATATTAGATCGAGTCAAGG	12415	+	AGG	9707	8304
ACTCGACGACCAAGATGTTG	1077	+	AGG	9764	8119
TCTACTACGTCCGTAATGCT	4546	-	AGG	8857	8864
ATTAGACGAGTTAATTAAAT	10351	+	GGG	10629	7132
TCCAATTGATCCGTGCCAGT	7596	-	TGG	9158	7773
TCAAAGTGATGTGTTAGCTA	4405	+	GGG	12854	4257
CCTATTACAGATTCATCGTC	11132	-	TGG	6742	9699
GGATATCGAAAAAGAAGCGC	9340	+	TGG	10089	6677
ATATTCATACCGTCATTCTT	6358	+	TGG	12611	3900
ATTGGAGCATGCAAATAACT	1407	+	TGG	6564	9048
AACAAAACGGTATAAACATC	2289	+	GGG	8147	7615
AAATAAAAAGATGCAACAAT	399	-	GGG	8409	7227
CTTAGACCAGAAACACTTTT	7552	+	TGG	8467	7091
TACAAGTGTACTTACAAGTA	1966	+	CGG	7212	7930
AAGTTACTACTCACACACTA	259	-	AGG	7734	7383
ATGTTGTTATCAAATATTTA	1713	-	AGG	8482	6379
TGTACTTGTTTTTCATTTTG	7941	-	TGG	9521	5297
TTATCTAATTGTTTATCGAT	1389	+	TGG	5700	8679
CATTAACGAAGGTGGAACAA	3991	+	CGG	7465	6822
GTAGAATTTTCAGCATCTTT	2686	-	CGG	5714	8306
GGTATGACTTTGGCCGAACT	479	-	AGG	2686	10688
ATATTAATCAGAGTGCCTGT	2982	-	TGG	5350	8273
GAAAAACAAAGATTTGTTTC	6141	-	GGG	11672	2402
AATAGAGCTAGGGAGTTTAA	3709	+	CGG	11354	2603
ATTAAACGAATGAACTCAAT	18056	-	AGG	7023	6481
AGTTTTATAACGGCTCAGCA	4684	+	GGG	6572	6794
CAACCAGCACATTACACATA	9862	+	CGG	5183	8028
TGTTCCATGCTTTTTCAATT	2091	-	TGG	2546	10306
CCATCCTACCCGGTAATAAA	837	+	TGG	7676	5575
CCATTTCGTTATCTCCTTTC	6863	-	TGG	6046	6835
TTGATACGATCCATCAACAT	8124	-	TGG	5946	6695
CATTGGAAACGTTTAAGAAC	12011	+	TGG	8762	3959
TTTTACAAAAGCTTTACCAT	5991	+	AGG	6029	6392
AACTTATATCATTCGTCATA	3618	+	GGG	1147	10766
ACTCCTAATCGTCATCTTGG	5896	+	CGG	5350	6879
TATAATTCATTCATGTTATT	15351	+	TGG	8006	4405
TATTCATACCGTCATTCTTT	6359	+	GGG	3306	8568
ACACCAGAAAACACATATAG	2830	+	AGG	5606	6468

ATTCACCCACAACAATATAT	21829	-	GGG	8722	3648
CGGAAAGCCTCACGCAGACC	5642	+	TGG	7059	4910
TTTTGTATGCGTCAATGAGT	12308	-	TGG	9713	2499
TCTTTATACTCGTAACCATT	7797	-	CGG	7939	4095
ACATCATCGCCCTTTTTGTA	5003	-	AGG	1662	9686
CTTGATGTACTTCTTTGTGT	13373	-	TGG	8380	3498
TATCTTCCGTGCCATCTTCT	8632	-	CGG	7828	3796
TCTTTTCTGCTAATTCATCA	14170	-	CGG	7371	4195
TCTGATTAATATTTCTAAAT	3009	+	TGG	5853	5548
CAAAAGCAGTCAAAGCTAAA	8093	+	GGG	8413	3154
TATTGGTAAGTTTTGTCACT	4934	+	TGG	3218	7715
AATGAAGTTTATTCGCTCAC	8700	+	AGG	6895	4333
TTAATATTGCAAGGTTCATA	8038	+	CGG	7009	4224
GAATGATAACGATCTAATTC	19068	-	AGG	8451	2867
GTCAAGATGTATTACGAAAT	3328	+	AGG	6727	4400
TTTGTTCGGCGAACTTCAAA	2724	-	AGG	4642	6245
TACATTGATTATTCACCAAC	2983	+	AGG	6648	4359
GCTAAGTATTTAAGACATGC	38827	+	AGG	7419	3662
TAGTGGCGTTCAAGAACTTA	7086	+	TGG	6731	4239
CGTCAATATATGCTTTCCGT	14619	-	TGG	5994	4886
TTATTTGCTAATAGTTTGTT	2738	-	CGG	6259	4527
AAGATTTAATAGATCTTAGC	24027	+	AGG	7112	3405
GAATTAGCTATCATAACTTC	1365	+	TGG	6463	3986
TAACTTATATCATTCGTCAT	3617	+	AGG	816	8856
AAATTCCACTTTGTTATTAC	4283	+	AGG	4506	5223
CTTTATACTCGTAACCATTC	7796	-	GGG	5898	3900
GGATCTAAGTCAGTTTCAGC	22166	-	TGG	6933	2923
TAACTTAGTCATGAAATGGT	3573	+	AGG	6055	3643
CTATATGTGTTTTCTGGTGT	2811	-	TGG	109	8989
AAGAAAGTTTTAACTTAAGG	930	+	AGG	5450	4158
AATAAGGAGTTAACTCGTAT	17877	+	AGG	5323	4235
ATTTAAGTGCTAAAGCTAAA	6971	+	GGG	6999	2581
GGTATGAATAGAATGACGTT	14900	+	AGG	7156	2424
ACTAAGACATCAATTTTAGT	2246	+	TGG	3190	5823
GTAGAGATATAGAACTTCAC	5383	+	TGG	6206	3081
TGAATCAATCACACTTATTG	12809	+	AGG	5605	3455
AAGATTTAAATGTAGATAAC	39754	+	AGG	5218	3738
AGCAATCCATTTGAAAGCAG	5127	+	TGG	5730	3213
AATACCACTTGCATGACTCG	5794	+	TGG	2602	6033
AATCACGGAGCAAAGCGTAC	15147	+	AGG	6051	2815
AAATAACTTTATCCACATAA	6704	+	AGG	5790	3047
AAAACTAATAGCATCATCTA	6502	-	TGG	6725	1974
CATGCCTACACAGTATTCAA	2380	+	TGG	4122	4208
AACAGCTGAATGGTTAAACA	7515	+	CGG	6454	2075
AAAAAGAAAAGTGAAATGGT	9072	+	TGG	7409	1211

TGCGCTTCAATAGTGATAGT	4339	-	AGG	2473	5612
CTCAAAGTGATGTGTTAGCT	4404	+	AGG	2916	5169
CCACAATTAGCATTTGCAAT	9934	+	AGG	3966	4208
TATATGACGCAAGCTCGTCC	30146	+	AGG	5246	3016
AATCCTTTTTCGACATGAGT	7713	-	AGG	6141	2100
AAAAATCCACCAGTGCCAGC	39334	+	AGG	6206	2035
TTCTATACTTCACTACAGCA	3154	+	TGG	4609	3397
TGAATTTTACAGTCCTATGA	13169	+	TGG	4255	3715
AGCTAGGGAGTTTAACGGTA	3714	+	TGG	4966	3049
ATTTTCAGCATCTTTCGGTA	2681	-	TGG	2171	5510
TCTAAAAAACCTAAGTCAAC	21416	-	AGG	5245	2733
GTAGTAGAAGCAATTAGAAA	4577	+	TGG	5409	2570
CGACTTAAGCAGGTGCCATA	21278	+	TGG	4230	3534
TGCTTATCTGTCTTCGGAAT	5036	-	AGG	6362	1461
ATTTCCTAATTTCCATCTGC	24053	-	TGG	3656	3857
CTCAACTTTGCGAAGTCACT	13745	-	CGG	2565	4823
GGTTCTTGTAAATTATTTTC	6619	+	AGG	4593	2976
ACTCATCGTTTGAATCGTCT	32540	-	GGG	4389	3005
CTTTGAATGGTTTAATACAT	11994	+	TGG	3593	3679
GCTGTAGTGAAGTATAGAAA	3134	-	CGG	4049	3260
GTTTGAAGATGAAGAAACGT	18313	+	TGG	4972	2284
TCAGCTAAGCGCATGCCATA	9571	-	AGG	5268	1984
CGGATTCCTTATTAAACGCA	2344	+	AGG	5189	2051
GGATTCCTTATTAAACGCAA	2345	+	GGG	3125	3912
AAATCTTCTTTTTCTTCAAT	16429	-	TGG	3083	3934
CTTGGTCGTCATATCCAAAT	5134	-	TGG	6213	1102
AGATACCAGAAAGATAACGA	5214	+	CGG	1085	5638
GCACGTTGCATAATCATTTC	2116	-	TGG	1864	4932
AAAAATAATCATGCGAGTTG	9227	+	AGG	2525	4306
TTTATTAAACCTTACAAAAA	5010	+	GGG	3822	3048
ATATCTATTGATGTTGTAAA	11190	+	TGG	5662	1357
CCATTTATTACCGGGTAGGA	821	-	TGG	1469	5111
ATTGGTCGACGTTTGAATAT	16411	-	TGG	3665	3122
GCGTTTGATGAAATACTTGA	11745	+	GGG	4729	2150
CTAAAGTCATATATACTACG	39928	-	GGG	3992	2811
ATTCAACATTCAGTTAAAGA	11781	+	AGG	2363	4154
TAGGAGTGAACTATATAGCC	40022	+	GGG	1088	5270
TCCTCATGACCATTCTTTAA	9969	-	CGG	5313	1425
AGATTTTATTGAACAAGTAA	9900	+	CGG	4940	1718
GTTAAAATTAAAACTATTTC	12660	+	AGG	4010	2481
AATAAGCGCCATTCACTACA	10138	-	TGG	3974	2484
TTTATCTCTTGTAGCAAACG	3935	-	TGG	4264	2193
CTCTATTATCTCTTCGTACA	18682	-	AGG	3420	2947
TTGTTATCAAATATTTAAGG	1710	-	TGG	2891	3345
TGTTGTATCTGATTCACACA	22667	+	CGG	3938	2305

AGTATAAAAGAATGTTTATA	10613	+	TGG	3338	2789
CTAATACATGTTTGTCATAG	5695	-	TGG	5577	763
TTTAGTTTTTAAAAATTCTT	8442	-	TGG	2337	3634
AACCACAATCCTAAATTAAT	40187	-	AGG	2734	3207
ATCTTTAATGCGATGTCAGC	24590	+	AGG	3099	2873
TACCCATACCGCGTAACACA	17082	-	AGG	2994	2963
TAATTAACTTAGTCATGAAA	3569	+	TGG	3635	2324
AACGCCCTGCTACTAATCAC	2629	-	AGG	1111	4601
AAGAGAACGCAACAAAGAGC	11476	+	TGG	4166	1824
CGCAAAAATATTCATGTTAA	3361	+	CGG	1575	4107
AATGATTCTGACATTGCATT	22286	-	GGG	3506	2358
CATATTCTTCAAAGGCCTTT	14775	-	TGG	3074	2686
TTGGTCGTCGAGTTGTAGCT	1051	-	CGG	1285	4235
TTTTTTACCTCAAATTTTAC	4075	+	AGG	1869	3672
GCAAAGAACGTGAAATAGCT	9651	+	AGG	2787	2836
ATAAAAGTAAATGTTGATAC	18643	+	TGG	3233	2415
AGAAATGTTAAAAAGTGTAT	39712	-	AGG	3115	2501
TTCATTTTAAAAGGTCATAT	3400	+	GGG	2128	3338
GAGTCTAAATTTAAATCGAG	19408	+	TGG	4418	1249
AAAATATCTCTTCCTTCTTG	869	-	AGG	648	4648
GTTTACCCATATATTGTTGT	21840	+	GGG	3591	1989
GAAATCCTATGCAAGGCAGT	331	-	AGG	2141	3288
ATTTGCAAATCCTAGCATTA	4552	+	CGG	2703	2761
ATTTGAATCATCACATTTAT	11324	+	TGG	4288	1306
GATTACTTACGTAATGCGAA	676	+	AGG	2696	2713
TGCCAAGGAAATCCTATGCA	338	-	AGG	1771	3547
TTACGTGCTCTCATTACAGT	18512	-	TGG	3043	2337
AGAAACATCAATCACACATT	2425	+	CGG	1469	3750
AAGAGGTATTTAAATATGTT	16156	+	TGG	3851	1596
TTTAGTTGTTCAGATGTAGT	21085	-	AGG	2785	2536
AAGATTGAACAAATAGATAA	14978	+	AGG	4152	1281
TAACCGTATCGATTAAGATA	40130	-	CGG	3070	2249
TTTATATTCACAACTTGCCA	353	-	AGG	1132	3895
GGAAAAAAGGAGCAAACAAA	37855	+	TGG	3566	1691
CATATCGTACCAGATTGGCA	10188	+	AGG	3196	1996
AACAACAACGAAATATATGC	11088	+	GGG	3400	1793
AATCTCCGTTTAGTTAATAC	5967	+	AGG	1088	3839
AAAGCAATTATGAAAAGAGT	194	-	AGG	4330	889
CGTCTATCTGTCTTTCCCTC	34085	-	TGG	1275	3608
GGTTTGTTAGTTATATAAAT	3630	-	TGG	1263	3579
ATTTAAGGTGGTTATTCTTA	1698	-	TGG	2349	2577
AGCATTGTTGATAACAGAGT	8290	+	AGG	1375	3433
AAACAATAAAACTTTTATGG	11602	+	AGG	2999	1929
AGTGTATAACCTGCTGGCAC	39327	-	TGG	2603	2262
TACACACGATCAATCACAAA	32947	+	CGG	3122	1749

CCGATTAACTGCATAATAGT	25138	-	AGG	3611	1275
GTAAGATGACAGCTATGTTG	17376	+	AGG	3138	1686
TTTAACCTAATAAAATACAT	38598	-	TGG	2688	2065
TACACACATAAGTTTATTGG	234	-	CGG	3690	1151
ATCATCAACACTATTTCTAA	16631	-	TGG	3914	921
AGTTCACTATGAAAACTACG	10991	+	CGG	2333	2347
CGATAGAATCGGAAACCCTT	34564	-	AGG	3380	1399
GTTTTAAACCCAAAGAATGA	6351	-	CGG	3600	1163
GACCATTATTTGATGCTAAC	20142	+	GGG	2738	1924
CAAATACAAGCGTTAATACG	35255	+	TGG	3161	1534
AAAGCATAAAAAATGGTATT	3048	+	AGG	1202	3245
AGGAATCATGAAAGACAAGA	12358	+	TGG	2314	2235
AATACAAAATCTACGGCACA	32585	+	TGG	3043	1549
TTTACTTGTACTAGATGATA	8229	+	TGG	2984	1581
ACGTCATCAAATTCTTTTAT	16181	-	AGG	2986	1574
ACCAACCGAAATGCCATTTT	7188	+	CGG	2625	1869
TTTACGCGCGTTATCTGTCA	10047	-	TGG	2426	2041
TTTATCTTTTCGCTGAATAG	7668	-	TGG	3500	1063
TAAATACAACAGGCTCAATA	17861	+	AGG	3439	1070
TTTTCTAATTGTTCTCGAGT	22997	-	TGG	2580	1843
AATTGGCCACTGCTTTCAAA	5117	-	TGG	3037	1416
TATTACCGCAAAGATAATTT	2947	+	AGG	1855	2461
TCTCCCCAATCATTAAACGT	4186	-	TGG	2243	2075
CCTATTGCAAATGCTAATTG	9918	-	TGG	4104	390
TTGAGTATTGCGAATCAAGT	12100	+	AGG	3557	867
ATTTAAAGTCAAGAAGTATG	20839	+	GGG	2854	1497
GTTCTGAAACTTGTCCCTTC	17520	-	AGG	2075	2198
GTGAAACACGCTGTACAAAC	22371	+	AGG	3135	1228
ACGCAATTTTTCGTACCTTC	14720	-	CGG	3387	986
TGCTAAAGTCATATATACTA	39930	-	CGG	2591	1677
GAACCACAATTTTCTCTTCT	6585	-	AGG	2804	1479
CGATTGTACTTGCTTGATGT	36132	-	TGG	2220	1993
ATTAAAGTACCTTGTTCTGC	19588	-	TGG	2180	1976
ATTCTCATTCAAATCAAAGT	15738	-	CGG	967	3063
TTTGCAGTATACGGAAAAAT	3917	+	TGG	880	3094
TTTAAACGACGTATCGATAT	30713	+	TGG	2622	1456
TTTTTTGATGTCTATTACCC	6033	+	AGG	1604	2353
TATCGCTATTGCGTTAGATT	6829	-	GGG	1844	2111
ACAAGTACGGTTGTTAATAA	1979	+	CGG	1247	2643
CTGAATTCAATAAATACAAC	17851	+	AGG	2037	1929
ATTTAATGATTCTGCAGCTG	308	+	AGG	1197	2683
AGGGTTTCGCAAACTAATTT	37660	+	AGG	2880	1157
ATATATAAAGCAACATGGTT	10250	+	TGG	2824	1199
GATACAAAGACTTACTTTAT	10714	-	AGG	1794	2088
TATTTAATTATGAAAATCAC	4626	+	AGG	2148	1763

CCATTCGGGTGTTTTTTAGT	7782	-	AGG	1810	2050
GTTCCAAACTGCAAGCATAG	10866	+	AGG	2090	1785
GTTTACCATCATACAAGGAT	40369	+	GGG	2212	1674
TATATTTGATTTGTAAGTTC	21725	-	AGG	1983	1843
ATCAGAATTTTAAATCAAGT	18403	+	GGG	2922	989
AACTAAATCAAAATATGAAC	8351	+	TGG	2653	1228
ACTATTTCTAATGGCAAAGT	16622	-	TGG	2422	1421
GTGACATGCTTGGGTGAACA	39861	-	AGG	3092	794
GATGGACGACAACTTTTTGT	27154	+	AGG	2505	1319
AATTAGAAATGTAAATGTAG	9415	+	AGG	3111	750
TCAATACCTTTACCTAAAAT	6805	+	AGG	2687	1125
GAAACGTTCGAGGCACCTAT	8877	+	GGG	2077	1651
CCAAATCGTATCAAGTACAT	25934	-	TGG	2239	1492
TACGAGTGAACTTAAATATC	17454	-	AGG	2367	1368
TTCGTCATTGACATTAACGA	3980	+	AGG	965	2625
CGCTAACATAAAGAACATAT	38272	-	TGG	1867	1800
TCCTAAAATCCCTTTAAGCA	34242	-	TGG	2583	1140
GAAAAACAATAACAGAAGCT	25587	+	TGG	3060	705
TCATTCTGATTGGTTATTTT	17669	-	GGG	1800	1827
GTTGATTTCGTGCCACTGTG	994	-	CGG	1927	1685
TAAAAGAATAGCATCATTTG	6438	+	GGG	876	2623
CCTATCATCTCTTTGTTGTT	16969	-	AGG	620	2845
TTATCATGATGTTACAAAAG	637	-	AGG	1050	2449
AACTTTGAAGCTTCTAGAGC	6577	+	AGG	2676	981
AATACCATTTATTACCGGGT	825	-	AGG	1055	2420
ATTAAACAATAAAACTTTTA	11599	+	TGG	1466	2049
AAGATATAGAATGCTTTGGT	10630	-	AGG	2385	1213
ATTTCTGCTTGTGCATATTC	19753	-	AGG	1812	1686
GTATGCTCAGATGTTAAAAG	14021	+	AGG	1867	1629
TCTTTTCGATTCGATCTAAA	17217	-	TGG	1840	1648
TAAGAATGACATTGAAATAG	14833	+	AGG	3316	306
CTGGCACATTATGAAGCAGT	5661	+	CGG	1547	1888
AACATTCACGTGATCCGTAC	9735	+	TGG	2709	839
TAAATTTAACGAAACGTTCG	8867	+	AGG	1420	1993
TATGAAAAAGATGATGATAA	16832	+	TGG	2415	1091
TCCGATAAAATAACATTGCC	19546	-	TGG	2337	1139
CTGTTCTATGAAAGTTGCAA	5489	+	GGG	1489	1895
CTTAATATTCGACGATAGCG	8572	-	GGG	2057	1377
TGGAAATTCAATGAAGATGA	4965	+	AGG	712	2564
AAAAACCAACGTTTAATGAT	4197	+	TGG	538	2718
GTTCAATATAAAACGAAAAA	3300	+	CGG	3217	285
GATTCTTCTAACTTATTAAC	17482	-	TGG	2349	1055
TCCTTTCACTTATAATCACT	26829	+	TGG	2318	1071
AGATGAAAAAACGACTATAA	165	-	AGG	944	2311
CTTAATGTGTTCATAGATTC	37069	-	AGG	1355	1938

ACATCTGTTTCAATTTCGTT	23689	-	TGG	1222	2044
GCTAAAGTCATATATACTAC	39929	-	GGG	1062	2178
AGCTAGTTATTTCTGTAATT	9166	-	TGG	1432	1824
AAGTAGCGCAATGAGTATGT	16792	-	AGG	1574	1687
TTTTGATGTCTATTACCCAG	6035	+	GGG	870	2311
CAGTTGTGACGTGGAAGGTT	2598	+	TGG	348	2770
AATTTAAAGTCAAGAAGTAT	20838	+	GGG	2034	1227
AATCATCAATAAACTTAAAT	15904	-	TGG	1726	1503
AAGTACCGTCGTTATCTTTC	5203	-	TGG	211	2819
ACTACAGTACCGTTTTTACC	36838	-	GGG	1494	1646
GGATTACCACTATCTTATAC	20177	+	TGG	2347	874
ATAATACTGCTCGTGCAACA	32531	+	TGG	2040	1145
TCATCCAAATTGAAAAAGCA	2103	+	TGG	1001	2077
CATGACCTGTAATAACAAAG	4272	-	TGG	975	2096
GCATATAATTACTTCGGTAT	35948	+	TGG	1905	1255
CTATCTCGTAAGTTCAGCGT	11931	-	TGG	2133	1028
AAGAATTATCTTAAGACGTG	14305	+	GGG	2562	611
TGCTATGCATGCTGTAAAAG	5932	+	TGG	1303	1744
TGCTTGTAACGTCGTTAACG	20288	-	TGG	1535	1476
AAGATTTTATTAAAGCAAGA	7445	+	TGG	1749	1273
GACTCTTATTACAGTCTTGT	20536	+	CGG	1728	1291
TGTTCACCCAAGCATGTCAC	39880	+	TGG	426	2450
GATCTTATACGAAGTAAAGA	13617	+	AGG	2398	668
GATTGGGATTACGCACGTTA	20243	+	CGG	2103	932
GAAAACCTGTGATTAGTAGC	2640	+	AGG	61	2775
AATTTTCTAGTTGATTCTAC	5396	-	TGG	1663	1297
CCACAAATAGAAATAGAGCT	3698	+	AGG	908	1977
CGGACAAGGCAAAGCATTCG	35827	+	CGG	2123	876
GCAAAGATCATTAAACAAAA	2276	+	CGG	1419	1511
TTTGACCAAGCTGTTATCTT	19907	+	TGG	1688	1263
CAAACGTCATTGCATAATCA	35970	-	GGG	1093	1795
AACAACCCTCCTCATCACAA	2575	+	TGG	851	1995
CTGAGAATTTTATTACATGA	12851	+	CGG	1651	1259
ATCCTTGTATGATGGTAAAC	40350	-	CGG	1754	1151
TGTGGTACATTAAACAAATG	9694	-	TGG	2563	406
TTTTATATGAGCAAGAGCTA	8794	+	GGG	1088	1735
TTTGTGTCGTTCATATTCGT	38125	-	AGG	983	1823
TCAATTAGTTTGTCCGCCTA	5991	-	TGG	476	2258
GCATACACACATAAGTTTAT	237	-	TGG	723	2032
GTTTTAGAGAATGTTTCTAC	6754	+	AGG	1746	1086
GTTCAAATAATGATACTGGT	20325	-	TGG	1459	1334
TGAACCTAATAAAAGTTATC	37605	+	AGG	1709	1089
AAAAGCAGAAGTAGAGGTTC	5312	+	CGG	195	2451
CCAAAATCATTAATATTGCA	8029	+	AGG	1309	1443
TATTGTCATCGAGCTTAAAT	15604	-	TGG	1219	1514

TAACCGTATCTTAATCGATA	40143	+	CGG	1792	995
AGAAAAACTTGTGTACTAAA	93	-	AGG	1073	1632
TAGATAACAGGCAGGTACTT	39766	+	CGG	2174	630
TTGACACAACACAAACATCA	27197	+	GGG	1092	1603
TACACAAAATACAAAATCTA	32578	+	CGG	1619	1126
TTTAAAAGAATAGCATCATT	6436	+	TGG	1448	1273
CAAGATGGAATCAAGATTTT	7460	+	AGG	1117	1568
CAGTTTTAATACCGTATTCG	10810	-	TGG	290	2306
CGCTCTTATCAGACGTAGTA	20564	-	CGG	1169	1503
TATAAGTAATATTTTTCTTT	8609	-	CGG	639	1979
GTAAAAGCGTTAGTGGCATT	25184	+	TGG	1430	1264
CATATAAATAAAGGCTCATA	17962	-	AGG	1856	876
AAGAAATCGTTAGCACTAAT	20219	+	GGG	721	1868
TTCTTAAGTTGTCTTTCAGT	30454	-	GGG	1622	1049
AATTTAAGTGCTAAAGCTAA	6970	+	AGG	882	1712
AATAAATTGTTTTTAGCTAT	21163	-	TGG	1021	1577
AACCCTCTATCAACATAGCT	390	+	TGG	1116	1489
CAAGATGGAACAGCAGACGC	12373	+	AGG	1575	1068
TCATACTCTAGTAATTCGTC	9367	-	TGG	1653	996
GTCGAACACTTATTTGTATT	10435	-	TGG	1764	889
CTTTGTTGGTTTGATGCATT	33521	-	CGG	1407	1211
GTATAACGGCAATGACACAG	11681	+	AGG	1982	689
TTGCAAATGTGAAATCTATG	7839	+	AGG	676	1866
GTTAAAAGAATGTTAAAGTC	6108	-	AGG	1405	1200
TCGCCGTATGTGTAATGTGC	9849	-	TGG	2042	618
ACGTAATATCAACGGTATGT	15707	+	GGG	1685	936
CTATCCGGATATTTATTTTT	37527	-	AGG	1864	774
TTTGTCTATCCAGTGCTTGC	35592	-	TGG	1257	1320
AATTATTCAATGGTCAATGT	37782	-	CGG	1653	948
CTCATCTCCTGTAAAATTTG	4066	-	AGG	46	2391
CGATAGTAGACGCAATTAAT	31775	+	GGG	1271	1262
GCCAACAAAAATAACATTAT	16754	-	AGG	1062	1435
GAACTTGTATCAGTACTACT	34831	-	AGG	1400	1129
TCCGTTTTATCAGTGCCTAT	29215	-	CGG	739	1724
ATGCCTAGTTTAATTGATAC	13233	+	TGG	1890	677
TTTTGTTCTTCTGATTGCTC	19161	-	AGG	2121	468
TGATGAATTAGCTGACATGT	12069	+	TGG	1704	840
ACATCAATCACACATTCGGA	2429	+	CGG	96	2290
TCATGTTCGGTAAATTTATA	9457	-	TGG	1470	1035
TCTAGAGCACCGTTAAAGAA	9976	+	TGG	1773	760
GCCTAAAAATCTATCAACTA	19294	-	AGG	1770	761
TCATACCATCTAAACTAGCG	14868	-	AGG	1628	873
AATTTTTCGTATTCAACTGT	22586	-	AGG	1583	911
CAATATAAAACGAAAAACGG	3303	+	AGG	878	1542
ACCGCTCTATATTTAACGGC	6388	+	AGG	992	1432

GGATTGAAATGTGAGAGATG	7747	+	TGG	1713	780
TTCCCTCACACTATTTCTAT	20996	+	TGG	1532	933
GCTTTAATTCAGTTGCTTAC	25886	+	TGG	1274	1161
GTGCTTTCACAAGTATTTCT	25485	+	TGG	1559	883
TATAGTTGGGATCAATGTTG	13006	+	AGG	1109	1283
TCATAACTTTCAACGCTACC	32832	-	TGG	1109	1270
CGCTATTAATGTTAGTACAA	27769	+	AGG	1626	803
ATGTATCAAGATACTGCATA	38893	+	CGG	556	1759
CCATTCATGTTCGTGCCGTT	33943	-	TGG	633	1689
AAAAAGAAAGTTTTAACTTA	927	+	AGG	1106	1245
ATAACAAAAAACTAGCCCGA	39803	-	AGG	2228	228
TCACGATGTTTTTGTAGTGT	18080	-	TGG	1346	1021
GAAGTACGACGAAAGTTATT	7641	+	GGG	1187	1155
CCTGTCCAAATTTTAACCGT	37312	-	CGG	1725	656
CGACACAAATGATTTAGGGT	38155	+	AGG	1884	511
GCATAAAAAATGGTATTAGG	3051	+	AGG	1571	793
AAACAATCAAGAGAAAAACA	500	-	AGG	1689	683
TTTAAATGTAGATAACAGGC	39758	+	AGG	1884	505
GCGAGAAAAGTAAGAGTAAT	8404	+	CGG	1375	964
CCAGAAAGGAGATAACGAAA	6879	+	TGG	1736	637
TCAAAGGTTTACAGTCGTTG	12525	+	AGG	1529	818
TCTTTCAACAACCAATGCTC	15539	-	GGG	1296	1018
TAAAACCGCTCTATATTTAA	6384	+	CGG	706	1539
AGAAAAACAAGGTATGACTT	489	-	TGG	785	1455
GAATGACGGTATGAATATAT	6337	-	CGG	1369	910
GCAACGTGATGAGCTTATTG	11440	+	GGG	1579	711
TTCGACCATGATTTAAGTAA	9032	-	TGG	1462	811
CGCTGATAAAAGTAAACTAT	16058	+	CGG	199	1950
GTTTCAGAACGAACAAGGTT	17549	+	AGG	869	1344
TATTAGTAGTACGCCCTTTT	7244	-	CGG	317	1842
AAATTACCTGACATAGATGA	17645	+	AGG	1215	1017
GAAAATACAGATCCTAAAGC	15585	+	AGG	1166	1052
TTCATACTACGCCAAATATT	35320	-	AGG	1459	784
CCGAAAGCGTTTAGAGATGC	31061	+	AGG	1399	832
CTAATCGTTACATTCACAAT	26638	-	AGG	1452	766
TTATTTCAGTGTACTTTTTC	13048	-	GGG	1554	671
AATAACAATACTAATAATGA	7312	+	TGG	1207	984
GGTAAACATCACGGAATGTT	22440	+	TGG	1151	1029
ACATTTTACAACACTAACTC	27367	+	AGG	1618	603
CGTTCATAGAACATACCTGA	15671	-	TGG	624	1491
TAATTAAGGGGTGATTTTTA	37404	+	TGG	718	1405
CCAAAAACACTGTTGTATCA	40303	-	AGG	380	1697
TAGCGTCCATTACACCTAGT	11361	-	TGG	1430	748
TTATCGAGTGTATAACCTGC	39333	-	TGG	1510	674
TAATTATTTCAACAAATGAA	6470	+	TGG	80	1962

ATAACTAGCTCAAAGCGTTA	9195	+	TGG	1156	969
ACTCACGATAAGTCATGAAT	18559	-	GGG	1819	358
AGATGAGAATGACTTAGATA	3480	+	TGG	1258	861
TATTACTTATACCGAGAAGA	8637	+	TGG	1429	704
ATTTATTAAACCTTACAAAA	5009	+	AGG	384	1628
TGCCAACGCTTAAGTTGTTA	38624	-	GGG	736	1309
ACAACTTCACGACGCAATAA	15028	+	CGG	1378	726
AAAATCCGGAGCTATCACAA	10380	+	GGG	986	1071
GAAACAATAAGTAAACTTTC	6075	-	TGG	1319	763
ACTATGAAGGGGATATCAAT	10471	-	TGG	522	1481
GTTTGATGTTCCGAGTAAAG	18026	+	AGG	1233	835
GTTGATTCTTCTATGCTATC	37542	-	CGG	1258	806
TGGAACTGGTGCAAGAATAT	15512	+	TGG	1133	918
ATCTTTCAACAACCAATGCT	15540	-	CGG	1268	789
TTTGTAGCACGACTACCACC	21548	-	AGG	1109	918
TAATTTATACGTAGACCTTT	20017	+	CGG	1141	875
GTTCCGTTTCCTACTGCTCC	38745	-	AGG	896	1091
TTCATCCGTTTAAATCAATA	20938	+	AGG	1198	813
TTACAAACAAAATCGAACAT	1802	+	CGG	1407	616
CTAATAAAAATGATATGGAT	39203	+	TGG	1483	536
GAAGTAAAATCGAATACACC	31385	+	GGG	850	1105
AGCAAACGCAAAAACAAGAT	15112	+	TGG	1215	772
GTCACCTGATAACTTTTATT	37593	-	AGG	1669	361
AGCTAGGCAACGACGTAAAG	9667	+	AGG	1220	764
CCTGCTTCACCTTTTGCACC	36793	-	AGG	650	1277
TCATTTGGTCAAAACTGGAA	38512	+	CGG	1608	410
TTCTTTCGCCATTTCTTCAA	19468	-	TGG	1360	632
TGAACAAAGGTTATATAGTT	12993	+	GGG	829	1109
GACACCAATTTCTTCAGAAA	756	-	GGG	508	1398
ATGGAATCAAGATTTTAGGT	7464	+	TGG	742	1184
CTATGCTTGCAGTTTGGAAC	10847	-	GGG	1331	648
GGCAACGCAGATTGTTTGAG	2310	+	TGG	588	1310
TATATTTAAATAACCTCTAT	27568	-	AGG	1203	722
TATAACGGCAATGACACAGA	11682	+	GGG	1256	669
AACTATCATTAAAAGTTAAA	22519	+	TGG	1429	501
GTTTTCCGAAAATGGCATTT	7177	-	CGG	1545	393
TTATCTGCATTAAAGCGTAA	17417	+	AGG	1069	814
AAATAAATACCATTTATTAC	830	-	CGG	353	1454
CTGGATAGACAAATGTCTAG	35618	+	GGG	971	895
ACGCCAAAAGTAACAGGTAA	2471	+	AGG	117	1661
CATATCTCCTCCTATTCAGT	20425	-	TGG	388	1415
TGAAGTACGACGAAAGTTAT	7640	+	TGG	363	1437
TTAAAAGAATAGCATCATTT	6437	+	GGG	569	1251
GAGTGATGTCTGTTGTTACC	30829	-	AGG	1062	802
TGCGTCCTGCGTCAATTGCA	21646	-	GGG	1300	587

CTTATCAAATACCGTGTCTT	10514	-	TGG	373	1421
ATTGATCATATAGTTGTAAT	34988	+	GGG	862	979
AAAAAGCTGAAGAAAATAAC	5074	+	GGG	350	1441
GTTTTTTTGGGGCAAAAAAA	40235	+	GGG	910	934
ATATTTGGCAATGTGTTCGC	24980	+	TGG	1064	789
GCTTTTTATTATGCACTTTT	18877	+	CGG	1028	820
TTTGATTACAATCCATTGTT	16958	+	TGG	957	883
TAGAAATAGTGTTGATGATG	16651	+	AGG	984	858
ATGATGATGTGTATGTTACA	17827	+	TGG	987	854
GAGATTTCCAAAGCAACGTA	23652	+	AGG	979	860
AAAACATCCAGTGACATGCT	39871	-	TGG	855	967
GTAGTTAAACATATGAATGA	7048	+	TGG	1105	740
TTTTTCTTTTGTGCTGTCAT	19663	-	TGG	873	948
CAGCCATATTTTGCTTTAAT	32000	-	TGG	785	1003
ATTTTTAAAACATTCAGGCA	31824	+	AGG	1410	437
CTTCCGCCAAGATGACGATT	5883	-	AGG	1231	597
TCTTTCAATATCGTTGATAG	36590	+	TGG	1562	298
GGCGAATGGTACACAACATA	21615	+	TGG	459	1293
CACAAATAGAAATAGAGCTA	3699	+	GGG	891	898
AATTTAAGTTTATTGATGAT	15922	+	TGG	1243	579
ATTCATTTTAAAAGGTCATA	3399	+	TGG	1288	532
GACGTTAATCTGGAAAGATG	10687	+	GGG	1450	372
AGTTATTCAAAAATCACGAA	1154	+	AGG	910	854
TTATGTTATAGCTAGCCTTC	39804	+	GGG	790	959
ACACTGCTAACAGCTGCAAT	25342	-	CGG	1200	565
CAGGTCGTTGATAATACTCT	20788	-	AGG	1085	668
TTTGGAGCACTGTTACAAGT	26100	+	TGG	987	754
CATCCATTAGCACAATTGAT	28409	+	AGG	1493	287
TATGTGTTTTCTGGTGTTGG	2808	-	TGG	124	1510
TATGCACATACCAATGTTGA	8130	+	TGG	720	965
ATTAATATAGATAATTATCG	34463	+	GGG	1229	493
AATCAAAAAATACAACCAAC	7597	+	TGG	686	980
ATTTTCCCTTGTGATAGCTC	10369	-	CGG	939	751
ATTAAGGCTTCAACACCATC	15672	+	AGG	1031	667
CGTACTTAACTTTTGCCATA	21277	-	TGG	281	1343
AAAAGAAGTAACCAAAGACA	10519	+	CGG	1218	493
ATTGAATTGCTATCATATTC	13883	-	CGG	913	766
CAGAATGAACTATGAAACAG	11353	+	GGG	1102	580
AGTCAAAGCTAAAGGGCATA	8100	+	CGG	905	745
AAAAGAAATCGATGTTAAAT	36631	+	TGG	998	658
AGCTTTTACTAAACAACAAG	37273	+	CGG	1137	528
GAATGTTTTAAAAATTCATT	31800	-	CGG	1410	272
TCGGTTGATTCTATATCTAA	6310	+	CGG	401	1180
TGAACGACACAAATGATTTA	38151	+	GGG	686	917
TCCACTAAAAGCAGAAGTAG	5306	+	AGG	693	909

TCATCAACACCATCTTGTCC	32421	-	AGG	1094	544
AAAATTATTACAAACAGAAT	5429	+	TGG	1173	468
GACAAAGAAATGACGAAAGC	23187	+	AGG	758	838
GGAACAACGGTTACTGACGA	4004	+	AGG	117	1414
CATAGAGGTCGAAAAAGTGG	10881	+	AGG	1126	503
TAGTACCAAAGATAACAGCT	19896	-	TGG	1175	458
TTCCCTAACAACTTAAGCGT	38638	+	TGG	1257	381
GTGACATACAACATCCCTGA	37734	-	AGG	1202	429
AACAGAATGAACTATGAAAC	11351	+	AGG	1266	371
AGTTTAATTGATACTGGAGA	13239	+	TGG	1190	439
GATGGTGAAAGAGTTAAATT	11570	+	TGG	1389	254
CGTGGATAAAAGTTGATGAG	5812	+	AGG	1305	328
TACGATTAAAGCAGATGAAC	15776	+	TGG	1244	377
ACATTTAGTAAATCATTACG	39108	-	AGG	858	712
TACGGTGCATATAATTACTT	35942	+	CGG	835	730
ATTCACATTCCAGCAAGCAC	35599	+	TGG	738	813
GCAACGTTGCCGAAACCACA	13941	+	AGG	595	940
AGCGTTTGATGAAATACTTG	11744	+	AGG	1373	236
GGCAAAAGATGAAAAGTCAC	33878	+	AGG	993	564
GAAACAATCTTTATAAACGC	1308	+	AGG	317	1174
AAGCAAGAAAAGTTTGTGCT	14594	+	AGG	806	731
CTGAGAATTTTTCAGCTTTT	22846	-	CGG	1153	406
ACTAACAAAACAAATACTGA	33696	+	GGG	1289	280
TGCAGTAATGCAATCATTTT	30100	+	GGG	708	792
TAAAAGGTATCTACTTCACA	36195	+	AGG	1077	453
ATGAATTGATAAAAAAGAAC	9498	+	GGG	272	1174
GTTAGAAAAACGCGACGCAG	19224	+	AGG	940	571
CTAAATCAATGGCTCAACGA	23769	+	TGG	1204	330
TTTATAGGCTCTCCGTTTGT	16166	-	AGG	749	736
TTTAGTTATAGTAACTTTGT	33295	-	TGG	955	550
GAAACACTTTCTTCATCTAC	37945	-	TGG	953	546
CTGAATGGGTTTCTAACATT	26193	+	TGG	240	1180
CTTTTATATGAGCAAGAGCT	8793	+	AGG	351	1076
CCTTTTGCACCAGGTTGTCC	36784	-	CGG	492	942
TTAATACGTCCATCAACAAG	28432	-	CGG	813	652
GCGATCAGTTAAAAACTACA	24537	+	TGG	518	912
TTGGTATCAAAATCTAAGCT	4889	-	AGG	438	973
TGATTACGAATTAGACGAAA	17596	+	TGG	822	607
TATGAATGAACATGAATTAA	13196	+	GGG	886	549
ATACTTGATAAGTCTACTAT	27938	+	TGG	1156	302
TACTCATCGTTTGAATCGTC	32541	-	TGG	872	558
AGCAATTCAATTGCACAGTA	13911	+	TGG	356	1022
AGATAGAGTGTTTGACTTGT	10032	+	GGG	926	507
CGAGTGTGGGACGAATATAC	10926	+	AGG	294	1076
AGAAAAACAAAGATTTGTTT	6142	-	CGG	1037	405

TGGGAGAAATATAAGCGAAA	18597	+	AGG	1287	177
GTATCTGTTTTAATATACGT	12767	-	TGG	869	552
TGATGCCGAAATATCGAGTG	10912	+	TGG	1062	376
ACAACATTCAAAGATTCAAC	12466	+	AGG	896	521
ATTTGCTATCCTTGAATTGA	461	+	TGG	610	778
AATACTCCACTAATGTAATC	20876	-	AGG	938	473
AGCACAAACTTTTCTTGCTT	14575	-	CGG	980	432
TTTGAAATGTACGAGATGGA	10556	+	AGG	1061	353
AAAACCCTTTCTGAAGAAAT	768	+	TGG	74	1243
ATACAAAAAAGAGCTGAAAA	7129	+	CGG	503	852
CACTCCATTTCTTGAACATT	9759	-	TGG	324	1011
TGATATTTAGAGGTGGCACA	8834	+	TGG	307	1020
TTGATTTTGTCCAATAACTC	36925	-	AGG	1013	382
GCGATCAGTCTGATTTGATG	13783	+	AGG	1149	255
CGAAACGTTCGAGGCACCTA	8876	+	TGG	260	1038
GTCGAAGATTATTTTATCTC	27535	-	CGG	1098	281
GAAATCCATACCAACCATCT	38234	-	GGG	749	592
ACAATAGAAAATGTACGTAG	37630	+	CGG	885	469
CAACGATATTTGATATTTAG	8824	+	AGG	34	1234
CGTCCACGCTTTCGTAATAC	8907	+	AGG	306	984
TCCTAAGTCGTCCTGACAAT	7007	+	TGG	179	1097
AAAGGAGAACAAGGCGCACC	36836	+	CGG	1107	259
GGAAGAAGCGAGTATCAATA	3735	+	TGG	1148	214
GACAAGTTTCAGAACGAACA	17544	+	AGG	380	900
GCCATAAAATGAGTATCCAA	23593	-	AGG	931	401
ATTCATGACTTATCGTGAGT	18578	+	GGG	906	423
AAACAACAACGAAATATATG	11087	+	CGG	1020	319
ACTGCAACTACTGCTAATAT	25492	-	TGG	998	337
TTAACCAAGCAATAGATGAA	3515	+	TGG	451	829
TTAAATATAACATTGAATCC	22901	-	TGG	524	750
ATAATAAAATTATACCAGAA	6865	+	AGG	618	663
ATATGAATGAACATGAATTA	13195	+	AGG	1005	299
CGTTTAAATCAATAAGGTAG	20944	+	AGG	385	857
GTAATTAATCCGTAAGCCAT	29611	-	TGG	522	733
CCTAGCTCTATTTCTATTTG	3682	-	TGG	26	1170
ATTGCAAATGCTAATTGTGG	9915	-	TGG	889	389
AATGACATTTCAAATGATTC	22457	-	TGG	985	301
ACTTGTTCTTTATGATAATA	16121	+	TGG	760	499
ACTAAGCAAGATGTAGTATT	28685	+	AGG	681	566
CAACCTACTCATGTCGAAAA	7726	+	AGG	256	948
ATTAATAACCTAGTAAGGTT	6264	-	AGG	342	869
GAAGAAAAAGAAAAGTGAAA	9068	+	TGG	85	1097
CTTGATTAAGCAAGGTATAC	35377	+	CGG	512	711
TGTACGTCTAACGGCTTACC	12027	-	TGG	74	1105
GATGAACGCTCAGATATTCA	35012	+	AGG	672	559

CTCTAAGAGATATCTGTATC	10109	+	AGG	286	897
CATTCATGACTTATCGTGAG	18577	+	TGG	482	720
AAGAGGTTGAACTACGTAAG	9684	+	AGG	285	895
TATGTTTGGCACCCTACAAA	16170	+	CGG	234	941
CGGATTGTTCTATTTGTTCA	11626	-	CGG	610	589
AAGTTTTATAACGGCTCAGC	4683	+	AGG	34	1106
AATTCTTTGAATATTATCTG	12222	-	TGG	533	651
GGAATATATATAAAGCAACA	10245	+	TGG	719	475
GGCAATACATGCAATCAGTT	25971	+	TGG	937	278
GCGTCACCTTCATCTATGTC	17635	-	AGG	472	689
ATGGAAAGAGAAAAATCTTG	19122	+	AGG	343	798
ACTAAAATGTGGCAAATTGA	36893	+	TGG	939	260
CCTTATTAAACGCAAGGGTG	2350	+	TGG	22	1082
TTATATTGGGTTAAATCACA	38947	+	GGG	813	363
TAGAAATGTAAATGTAGAGG	9418	+	TGG	899	283
ATCTCTTAGAGCCGAAAAAT	10081	-	TGG	968	216
TAATAGAACTATCAAGTAAA	556	-	AGG	993	193
ACAGTATTAGACGCATGTAA	9138	+	TGG	408	715
ATTTCAGGGAGCGAGATGCA	8432	+	TGG	605	535
TGCCTTGCATAGGATTTCCT	352	+	TGG	375	741
AAGCGTTAATACGTGGTGTT	35262	+	TGG	103	983
GCTAAATGAAGATAGTTCTT	27802	+	TGG	588	541
ACCACTAACTTACCTAAGAT	24953	+	TGG	594	525
CAACTAATTCAAGAATTACA	39452	+	GGG	768	364
TGTGAAGCATAAGCAATTTT	26970	-	AGG	279	803
TGATATTGATGAGTATATCG	17705	+	AGG	662	456
ACTCTTTTTGCAACCATTCC	9511	-	AGG	409	677
TTTTTGATGTCTATTACCCA	6034	+	GGG	672	439
TAAATGGAACAAGTGATATT	24174	+	TGG	673	438
TGGATTTAACTAGAATAACT	25431	+	GGG	432	655
TCTATTATAAGGAAAACTTT	588	+	CGG	453	633
TTGTTGAATTACCTTTAACA	32234	-	AGG	754	361
ACGTAACGCTACAAAGTCTA	28520	-	AGG	379	695
TAAAGCTCAATCATTGCGTG	18221	+	TGG	66	976
GCCAATTGTCAGGACGACTT	6992	-	AGG	893	219
CGAAAGATAGCAGACGAAGA	15219	+	AGG	410	648
TGCTCATACTTTGCGTTATC	35380	-	CGG	696	385
GTCGTCGAGTTGTAGCTCGG	1048	-	CGG	23	990
AGTAATCGGAGACGATTTCA	8418	+	GGG	324	716
AAAGTTTACTTATTGTTTCT	6095	+	AGG	515	541
TTATTTCTCCAGTTCTATAT	30321	-	TGG	554	505
TTAGTGAAAACAAACTTTCT	33455	-	AGG	592	470
AGATGGTCCTACTACTATTG	34667	-	CGG	798	284
ACTACAGCATGGTCAATTGC	3165	+	GGG	207	815
TAGAAGAATCAACAGCAAAA	37568	+	TGG	705	363

TTCTATAAATTTGCAGTATA	3908	+	CGG	20	979
TATTCGATAATTTCTTTATA	7356	-	GGG	873	207
AACACGAGCACAAACGAGCT	35680	+	CGG	171	837
TAAAACTTTCGTTATACTCT	28014	-	TGG	337	685
ACAAGTTTACATTCAATGAC	29648	+	AGG	671	383
AACTCTTCTTTAAATTTAAT	33428	-	AGG	705	346
GAGTCAATTGTTAATATGAT	13836	+	AGG	829	231
CTTAAATACTTAGCGATATT	38802	-	AGG	517	508
TTCAGTGATTTCTTAAATGC	26321	+	CGG	703	340
CTAACAAAACAAATACTGAG	33697	+	GGG	456	561
CAGATGAATAACGATAGAAT	34575	-	CGG	668	369
GACGGTATGAGTGATGCACT	26282	+	TGG	422	591
AAAAAAATTATGCTTGTAGC	38722	+	CGG	691	345
CTAATTGTTCTCGAGTTGGT	22993	-	GGG	494	519
TATTACTAATAAAAATGATA	39198	+	TGG	670	359
GCTGAAAACGGTGTGTTTAA	7141	+	AGG	544	467
GGAGAAGAAAGCAAGTGCAT	11497	+	GGG	743	287
TATCTGTCGTTAAATATATT	30373	-	CGG	695	330
AACAATACGCCGTAAAGACA	29368	+	CGG	512	492
CAACGACTCTAAAACGTATA	37030	+	CGG	466	531
ACGGAATACTAGAAGATGTT	20704	+	AGG	655	357
CGTTCAATAAATGTGAAAGG	14452	-	AGG	896	138
ACTGTTGCATCTCTTAAAGA	7905	-	CGG	543	456
TGAAAGAGTTAAATTTGGAA	11575	+	TGG	361	606
TGGTTTATGTTAATTAATCA	15132	+	CGG	535	443
TTGGTAAGTGGAACTTATCC	33094	+	AGG	563	417
ATACGTAATTGTTGTGTTGT	39466	-	TGG	60	867
GATCAGAATTTTAAATCAAG	18402	+	TGG	615	366
TCAATCTTAGCTTTTTCTTC	13094	-	AGG	520	451
TTACAGGAGATGAGAGAAAA	4091	+	CGG	13	907
TATCTGCATTAAAGCGTAAA	17418	+	GGG	362	588
ATGAAAATATAAGGGAGTGT	12626	+	GGG	532	433
AAGCAACGTGATGAGCTTAT	11438	+	TGG	259	673
TTTCAATTAATAACCTAGTA	6269	-	AGG	274	658
ACAGAATGAACTATGAAACA	11352	+	GGG	726	249
CAACTGACAGCTAGATATTT	23282	+	AGG	492	459
TTTACAACGCGCTAAATCAA	23758	+	TGG	386	554
GCCAGTAATTGTTGAGTCAT	34865	-	TGG	492	458
TATTGAAGAAAGGTTATAAC	14104	+	AGG	388	549
TTTACCTTAATATCTTCTGC	20457	-	AGG	431	509
TACTCATCGTCATTTAGATG	18365	+	GGG	34	864
CAATTTGCGGATATGGTGCT	16698	+	AGG	142	766
AAATGGTTTGACAATTCATT	38215	+	AGG	559	389
AACTTCAATTGCAGAACAAA	29258	-	AGG	585	364
TCCTTAGTTGATAGATTTTT	19309	+	AGG	576	372

AGAGATATAGAACTTCACTG	5385	+	GGG	381	545
ATAAATTCGGAACAACGAGC	32705	+	TGG	602	345
GTTTTCCCGTCAAAGTATGG	38437	+	TGG	471	457
CTAAAAATTGATGTGCAGAC	31425	-	GGG	177	720
TAAACCTGAACGATTAAGGA	16256	+	GGG	826	134
ATTAAGTGGTACGTAGACAT	33804	+	GGG	509	420
ATATGACGATGACGTTAATC	10677	+	TGG	441	480
AATGATGGAAGTATATTGTC	7327	+	GGG	688	255
ACAAGAGTGCCGGATTTACC	32830	+	AGG	642	296
GCCAATGACTCAACAATTAC	34880	+	TGG	583	349
CAAGTATCGATGACTGATTC	30923	+	AGG	629	307
TGGAATGAAACTTAAACTTA	17323	+	TGG	269	630
TTAATAGGACGAGGTATAGA	15867	+	TGG	626	301
TGAAATCCATACCAACCATC	38235	-	TGG	812	128
GCATCTGCAAATACAATTTT	2197	-	TGG	73	793
AGCCAATCACGCCATTCAGC	23323	-	AGG	74	790
CTGTCTATAGAAGTACTTAC	26569	-	AGG	642	276
ACAACATCGTCGATAATAAG	36439	-	GGG	363	523
AAGAATGACATTGAAATAGA	14834	+	GGG	739	178
CTTATCTGAAACGACGTTAA	35308	+	AGG	473	416
CGACCTCTATGCTTGCAGTT	10853	-	TGG	544	350
AAAGCAATACGTGATGATGT	18192	+	CGG	575	320
AAAAATACAACCAACTGGCA	7602	+	CGG	34	807
ATGAGAGCACGTAAAGACGA	18537	+	TGG	321	547
GGCAATGTGTTCGCTGGTAT	24986	+	TGG	493	391
GAAGCCTTAAACGCACCTTA	9572	+	TGG	609	286
ACTTATACATCAAGCAAATC	32482	+	TGG	635	259
TTATTAGCTGACTTACAAGA	22218	+	AGG	697	201
GTTGGTTCAGTCGTGTTGCT	26118	+	TGG	790	115
TAAACTACTACGACTTAAGC	21268	+	AGG	486	388
ATACTAAACCTGAACGATTA	16252	+	AGG	590	282
AATCCCTCAATAACGCCACC	33096	-	TGG	368	478
TTAATTTTTAATGTTGTAAT	22772	-	TGG	712	165
TTACTTGTACTAGATGATAT	8230	+	GGG	481	373
GAAAAAGAAGATTTTGAAAC	16454	+	TGG	526	331
AAGTTGAAGATGTTGTTGTG	13978	+	AGG	439	408
TAAAAAGCGTTTTAGCGCTT	1903	+	GGG	102	707
AATAGTTGGACAGGTTCTCC	34751	+	GGG	360	472
TGGTAAGCCTATAGGTGGTT	39276	+	TGG	208	608
TTACTATAACTAAAATTATG	33320	+	GGG	560	290
GGTAAAATGGCAGCAATTTG	16685	+	CGG	330	497
ATTAAAAGATTTTATGTTTG	11219	+	AGG	148	661
ATAATCCAACATCTCAAGAA	38028	+	GGG	521	322
TATTTCAACAAATGAATGGT	6474	+	GGG	359	468
CACAAAGTAGTCAGCGCGGT	26390	+	AGG	258	557

ATGTAGTTGAATTCTTTGAA	11981	+	TGG	813	55
TCGTAATTATCTATTTCTAT	21986	-	AGG	494	342
GAATACTTAAACCAATTTTT	10086	+	CGG	518	319
AACGCTTAAACCAACTGAAT	20431	+	AGG	533	305
ATACGTCCATCAACAAGCGG	28429	-	TGG	525	306
GCGTCTTTAAAAATAAAAAA	69	+	GGG	451	370
GAGAATTACAAGGAAATCAT	23226	+	GGG	501	323
CGGTACTATCTTCGCGCAAC	24268	+	AGG	335	470
CCTGCATCTCTAAACGCTTT	31045	-	CGG	311	486
TGAATATGCACAAGCAGAAA	19771	+	TGG	539	268
GTAGTTGAATATAACGTTAC	26854	+	AGG	663	154
TTCAACACCAGTAGCAACGA	5229	-	CGG	708	113
TGCTATCAAATGCTTAATTT	35741	+	AGG	411	377
AGCCTGTAACACTTACATAA	34773	-	GGG	158	604
GATACTTTGCCGTTATTACA	23067	+	AGG	406	380
CAGGTACCGACCATTTTTCA	27287	-	GGG	619	180
TAATATCACTTAGATATGCT	30960	-	GGG	424	356
ATGGCGTTGCGCAACCTGGT	38549	+	TGG	322	448
TCACATCATTTGGTCAAAAC	38507	+	TGG	645	153
ACGACAATATCCAACTTTTG	38400	-	CGG	195	557
ACCTCTACTTCTGCTTTTAG	5291	-	TGG	555	230
GCAACTCCAACATACACGCC	19544	+	AGG	260	496
ACTTACTTAGCAAAAGGTGT	19706	+	AGG	143	598
AGGAGGCAACCAATGGCTTA	29618	+	CGG	406	359
ATAACCAAATGTTCAAGAAA	9771	+	TGG	447	313
AAGAACTGGAAGAAGAAACC	12025	+	AGG	220	513
GATTTAGCTGAAATAGTACG	22260	+	AGG	510	251
CTTTTGCGATAGCGTATGCT	8060	-	AGG	184	545
GTGTATATTTGCCAATTGTC	7002	-	AGG	524	232
TTGAAAATGATTTAGTTAGT	31919	+	GGG	707	66
CTTTCTTCATCTACTGGTAT	37939	-	CGG	327	409
AACGATTCAAAGGCGCTCAC	8770	+	GGG	427	313
TAAGTGACATCGAACCAGTA	9733	-	CGG	449	293
AAATGAAGCTGATTTAGATA	18759	+	TGG	666	96
GAAATACATTTAGACGCAGC	38986	+	AGG	239	480
GATAACATGTAATGATTACC	30148	-	TGG	360	365
AATCAATCGCAACAGAGATT	14055	+	GGG	187	520
ATTGAACAAGCGCAAGCTAA	23405	+	CGG	494	242
TTACTCAATTGAATCGCGTT	33135	-	AGG	473	258
AATTATCGTTTATCTGAATT	39172	+	AGG	429	296
TTTCTGTTCAATTTAGAGTT	14132	-	AGG	375	342
TGGTTCTTTGATGTACTGCC	31085	+	TGG	417	300
ATGGCGCTTATTACTTTCAC	10165	+	GGG	633	105
AGAAGCGAAAGAGAAGTACG	12561	+	AGG	393	321
CCTATCAAAGAATACTTTGC	15807	+	TGG	309	396

TCAGATACACAACCTATGCA	30587	+	AGG	343	365
CCGATAATTTGAGCGACTGC	25276	-	TGG	411	302
AGTGGTAAACCGCTTGTTGA	19958	+	AGG	283	417
CATCATTCTTTTTATAAAAC	32594	-	GGG	514	207
GAACAACCGGTTTTATATCC	27628	+	AGG	300	397
ACCACAGATCCTATTAATTT	40194	+	AGG	337	362
CGATATTTGATATTTAGAGG	8827	+	TGG	518	196
GGTAAATCCTAGAATTGTTA	27993	-	AGG	417	287
AAAAGAATTTGATGACGTGT	16202	+	TGG	457	248
GCATTAGCTCCTGTTGACTT	21423	+	AGG	382	314
ATGATGTCAGGTACAGAAAA	2060	+	AGG	295	389
GGCTAATTACAGATATCCTA	34564	+	AGG	312	373
TTTTTGAACATACTTGTCAA	19363	-	AGG	168	501
CCGCCCATGATTGCTTTTGC	36016	-	TGG	459	237
TCTAAACTTACAGATGATTA	32287	+	CGG	387	297
GAAAGTGTATTGCAACAGAT	37145	+	TGG	380	302
TAGATAGAGTGTTTGACTTG	10031	+	TGG	21	625
ATAATTATGGATCCTATTTT	6801	-	AGG	230	433
AAAAACTTAAAAATATGGAT	13274	+	TGG	551	142
TTCTTCAATACTGTCTTTAA	28064	+	AGG	596	100
ACAGTTCGCTACACAATACG	21938	+	AGG	363	309
TAATATCGTAAAAGCGTTAG	25177	+	TGG	178	473
AGAATTGGTTAACACCTCTT	30867	-	TGG	416	258
TTGATATCAAAACAGCTGAA	7505	+	TGG	149	499
TAGAAACATTCTCTAAAACT	6734	-	TGG	71	567
GAATCATTTAAATTAACAAT	22317	+	TGG	536	146
AGTTGTCTATAAATATGAGG	11843	+	AGG	179	468
GCATTGATACCAGTGATTGC	24320	+	CGG	575	110
AATTAAACTACCCACCATAT	14403	-	AGG	177	469
TATGGATAGGTTTAAGCAAG	16139	+	AGG	308	349
ACGCTTGTGGAAAAGCTAAA	40280	+	AGG	156	484
TTCAGGCAAGGTGCATGCTC	31836	+	AGG	403	260
AAAAAGTAGAGCTTAAGATA	26954	+	AGG	397	265
CAGGAGAAAGCGCAAGTGGT	39005	+	GGG	248	396
TTAAAAGATTTTATGTTTGA	11220	+	GGG	301	348
TTTACACCAATAAATAGCTT	18425	-	GGG	233	409
AGCAACTAACTTTATTTTAG	10288	+	AGG	243	399
ACACATTGTACCGAATTAGA	36096	+	TGG	401	252
TTTTTCGGGAATTTCATTTT	13034	-	AGG	281	360
GACATCGCAGTTTGGCACCC	34634	+	TGG	114	510
AGTTGGGATCAATGTTGAGG	13009	+	AGG	503	158
TTTGAAAGCAGTGGCCAATT	5136	+	TGG	44	570
CAAAAAGCTGAAGAAAATAA	5073	+	CGG	476	179
GCTTTTTGCTTATCTGTCTT	5042	-	CGG	157	466
AATGCCCCTACATCTTGTGC	14480	-	AGG	412	235

GCGCGCTCTAGATTTAACTT	8981	-	AGG	151	470
CAAATAGATAAAGGTGACAG	14987	+	TGG	148	472
TTAGCATACCTTGTGTTACG	17090	+	CGG	527	127
GGCTCAGCAGGGTTTCAAGC	4695	+	TGG	310	322
GGTGTTGACTTAGGTGACAT	36287	+	TGG	250	372
TTTGACACAACACAAACATC	27196	+	AGG	496	149
AATTTAGATGCATCTACTTT	28096	-	TGG	213	403
TGCAAAAGATTTCTTTAATG	19849	+	AGG	352	277
ATTCAAGAAACACAAAAGAG	17135	+	TGG	272	349
TAAAACAATTAAAGGATTTA	21073	+	TGG	463	176
AGATGTTAAAGCTAATGATA	27465	+	AGG	450	187
CTGTGGTTTTGTTGGTTGTA	40162	-	GGG	9	585
AAGTTAAGAAGTAACGCGCT	19258	+	AGG	260	358
TTATAGCGTTGACCAAAACT	34720	+	GGG	353	273
CTCATCAATATCATTCTGAT	17679	-	TGG	578	67
ACAATCCAATGTATTTTATT	38609	+	AGG	375	247
CATTGATCATATAGTTGTAA	34987	+	TGG	439	189
TGTTTTTGTCCGTGTCTTTA	29361	-	CGG	122	475
TATAATTGCTTTTATATAGT	40003	+	AGG	276	335
TAATTAAGTAAAGTGTATTA	37371	-	GGG	401	222
AGAACTGGAGAAATAACTTA	30344	+	TGG	480	150
GATGATTATAACGTAGATAG	31729	+	AGG	414	209
TATTAGACGAGTTAATTAAA	10350	+	TGG	448	178
ATAGCGCAGACATACAAGCT	13526	+	AGG	204	398
CCTTTAACCGCCATTTTAGC	23980	-	GGG	576	62
TAACAACATCACCTATTTTA	28563	-	GGG	234	369
TAAATCTTTTTAGAGTTATA	32910	-	AGG	436	179
GGATTCTGAAATAGGTAAAA	16672	+	TGG	330	272
AATACTTGTGTTGTGTTACC	31387	-	CGG	241	350
CCTTACAACACTTCAACTAG	19940	+	TGG	232	358
TATCAATTCATTTTCATGTT	9470	-	CGG	410	197
ATGCTTGGTTTTTCGTCTGA	35542	-	TGG	610	14
TTAATTAAGTAAAGTGTATT	37372	-	AGG	152	427
TAGTATTAGGAGACTTTACA	28698	+	AGG	217	368
ATTTAAGTTTATTGATGATT	15923	+	GGG	220	365
CGTATATTTCTTCTTTTTGA	29736	-	TGG	289	302
CAGTATTCCCTGATATAGAC	22054	+	AGG	162	416
AACAATGATTTTATGAAAGA	20736	+	TGG	471	137
TAACGACCCTGAAAAATGGT	27297	+	CGG	422	179
AGATTTAGCGTTTTAAGGTG	5171	+	TGG	125	446
TGTTCAGAACTTATAGATAA	31662	-	CGG	340	251
AATGAATGTTAAGCGAATAT	35704	+	GGG	225	351
CGACGAAAGTTATTGGGATT	7647	+	AGG	48	510
ACATTAGTGGAGTATTAAAC	20899	+	AGG	227	346
TTAACGATAGAAAAAGATTA	12956	+	TGG	477	117

TCATAGAGGGCAAGAGCCAA	14619	+	CGG	180	384
TTATCTAAAGGGACTTAAGA	19002	+	CGG	360	219
CGTTACGAAATAAGAGAACC	23483	+	TGG	195	366
TTGCGTCCTGCGTCAATTGC	21647	-	AGG	423	159
AACGGAAATGTACCTATCAT	17303	+	TGG	289	279
GTGTGATATGCGTCAAACAC	29449	-	TGG	359	214
TCGTCATGATTATGATTTTT	37213	-	TGG	288	278
TGAAAAAGGGCAAACGCTTG	40267	+	TGG	197	358
GCTAATTACAGATATCCTAA	34565	+	GGG	338	230
ACTCTCAATGAGATTAAATT	34024	+	AGG	340	226
CCAATGTACTTGATACGATT	25950	+	TGG	500	81
CTAACAACATCACCTATTTT	28564	-	AGG	311	251
CGTATCGATCTAAAAGCACA	36377	+	TGG	158	388
TTTTCAACAGGATTTAGTGA	10412	+	TGG	274	283
TTGTATTCTAAATTAATAGC	39244	+	CGG	376	189
GCACATATCCATGTAGTGAA	10146	+	TGG	301	255
TTATGATTTGTATAAGCTGT	8936	-	TGG	293	261
AGGAAATATCTCAGTTATTA	27513	+	AGG	354	205
AACAATTCAACCCAGATGGT	38240	+	TGG	166	373
GGTATATATGCTACTGGTCC	21546	+	TGG	225	319
GTATTCGATAATTTCTTTAT	7357	-	AGG	541	32
TCTACCGCTTCTTTACCTAT	29095	-	TGG	255	290
TAAGCGCAGTTAACACATCT	32351	+	AGG	381	176
ACATACTTTTTGATTGAGTA	20756	-	AGG	441	120
AACCAAGCTATGTTGATAGA	376	-	GGG	357	194
GTAAGTCGTAAGGTACATAT	21141	-	AGG	212	324
CGATAAGAAAATAGAAGAGT	21350	+	GGG	140	388
GAAAATCCGGAGCTATCACA	10379	+	AGG	191	340
AATGGTTTGACAATTCATTA	38216	+	GGG	127	395
GACGCAAAGCGCTTTTAATA	30810	+	GGG	396	151
GATAATCCAACATCTCAAGA	38027	+	AGG	465	88
AACTAACAAAACAAATACTG	33695	+	AGG	158	364
TAGGGAATGGAATACACAGT	7338	-	CGG	265	266
TATTAGAATTAACCCAGTTT	34716	-	TGG	291	242
ACTTTAAATATTTCGATGGT	21466	+	GGG	454	94
TAGATTGGTTAACTCAATTG	25653	+	TGG	249	276
AGCAACGTGATGAGCTTATT	11439	+	GGG	323	209
TCAAATGCTTGTTTGTCTTT	27102	-	TGG	62	443
AACGTCCAGCAAATAGTGCT	27008	-	TGG	187	329
TGAGGAAGAAGCCACGAATA	10815	+	CGG	170	344
ATTAATCGGCAAAGTAGCTG	26350	+	AGG	126	373
CTTACTACCTGCCTATATGG	14408	+	TGG	384	140
GACGGTAAACATACCTATAG	27571	+	AGG	272	241
TCTTTGCTTTATTATCAAAC	38333	-	GGG	238	271
TTATTGTTAATTGTTATTGA	4510	-	AGG	13	474

AGCGACAGGAGAGGTAGACA	39576	+	AGG	204	301
AAAAAGGTTATCAAACACGC	36506	+	TGG	365	154
TGAAGAAGAAATATTTAAGA	20675	+	TGG	134	361
TCGCGAGTAAAGTAGCTGAT	26232	+	GGG	289	216
TACAAGGCACTGATGATGAT	29184	+	TGG	304	201
TTGAAATGAGGTGCATACAT	34364	+	GGG	96	388
CTAAAAATTAATTAAAAGGA	4603	+	CGG	353	155
GAGAAATATAAGCGAAAAGG	18600	+	TGG	242	254
AAAACAGTTACAACTGCTAA	28907	+	TGG	260	237
ACTAGTGTTTGCATATAATA	10577	-	CGG	335	169
GTTTTAATGTCTTTAAAAGT	33731	-	TGG	317	185
AGCAAACGCACGCAAGTTTG	24682	+	AGG	65	411
TATACTATCTGTCAAAGTAG	26540	-	AGG	322	179
GCCTTTGGATACTCATTTTA	23608	+	TGG	361	140
GAAGTTGAACAACAAATCAA	32221	+	TGG	368	130
GCTGGAATACTGCGATTATT	13312	+	CGG	249	237
AAAATAAAAAGATGCAACAA	400	-	TGG	184	295
TCGTCCCACACTCGATATTT	10901	-	CGG	293	196
GATTAAAAAACTTAAAAATA	13269	+	TGG	359	136
TTGCCAACGCTTAAGTTGTT	38625	-	AGG	290	198
TTATAGGCTCTCCGTTTGTA	16165	-	GGG	100	369
TAGCACTAACACCTGCTGAA	23328	+	TGG	203	276
TCATTCATATTAGCCATCAT	13166	-	AGG	129	342
CGCTCAGAAACTCATAGATG	8501	+	AGG	30	430
AACTAGGTGTAATGGACGCT	11379	+	AGG	84	381
GAGTTTTCCCCTTGTGGTTT	13934	-	CGG	106	359
AGGTTTAGTATGTGTGTATA	16224	-	TGG	173	298
TCCTGCCGTTAAATATAGAG	6373	-	CGG	338	147
GACCGGTTTACCATCATACA	40364	+	AGG	113	350
ATAGACAGGTTTACTAAGCA	22068	+	TGG	225	248
TAGATATAAAGAGTCTATTA	15656	+	AGG	126	337
CTTGTTTCAGTAACGATGCT	35557	-	TGG	103	357
ATGAAGGCTTTTTCCATACT	37484	-	TGG	433	59
CAAAGCAGAACCTGAGTTAT	36931	+	TGG	147	316
ATGCTCGGGATGGTCAGGGT	15525	-	TGG	208	260
TAAGTACGGTGCTGATAGCA	21308	+	TGG	142	318
GTCGTTTTCCCGTCAAAGTA	38434	+	TGG	426	58
TTTGATACAGCGGAAGAGCT	10224	+	CGG	122	332
AAAGAGTGGTTTGAAGCTGC	22575	+	AGG	318	155
ATCAAGTGGGTGTGTTGGGC	18416	+	AGG	85	365
ATAGAGTTAACTAACAAATA	15306	+	TGG	323	149
ATGAGTGTCGTGAAGATTAA	9446	+	CGG	217	244
GACGTCCAAGCACTATTTGC	27019	+	TGG	252	211
TGTCCTAATACTTGTAATAT	25693	-	AGG	293	173
AACACAACAATTACGTATGA	39487	+	CGG	362	109

CTATAAATATGAGGAGGCAC	11849	+	AGG	379	92
GTGTGAGGGAATTCGTCGTA	20968	-	TGG	48	390
AGAAAGTTTGTTTTCACTAA	33474	+	CGG	262	196
GCTCTCTCGTTGCATAATTC	9614	-	TGG	137	308
CACTGGATAGACAAATGTCT	35616	+	AGG	104	337
CATGAAGTTGCATTATACGG	38851	+	TGG	272	185
AACAACTCATTGAAAGATTA	24206	+	CGG	256	199
GTATACGGAAAAATTGGCTC	3923	+	AGG	13	418
TTAGATCGTTATCATTCGAA	19090	+	AGG	396	72
AATTACGACTTGATTAAGCA	35369	+	AGG	399	69
CGAAAAGGTGGTAATTGATA	18612	+	TGG	380	84
TTAATAATTGTCTTTGATCT	23367	-	AGG	284	170
ATTTTGCTACATTAATTATA	39661	+	GGG	57	374
ATAGATACTTCAGATAAGAA	24634	-	TGG	323	133
ACATTGCCTGGCGTGTATGT	19534	-	TGG	103	331
GATTCACCCACAACAATATA	21830	-	TGG	280	170
GAGTAATCGGAGACGATTTC	8417	+	AGG	40	386
GAAGCGCCACCGCTTGTTGA	28439	+	TGG	205	237
AATAAAAAAGGGCAGAAAAA	80	+	GGG	331	122
ATCTAATCGAACAAGAAGTA	19145	+	CGG	159	277
TAATGTTTGGATTTACCAAA	33944	+	CGG	160	276
TTCTTTACTTCGTATAAGAT	13599	-	CGG	259	185
TGGGAAATTCCACCTTTATG	6700	-	TGG	216	223
TCGCTATTGCGTTAGATTGG	6827	-	GGG	207	231
TAACCTCACAGTCATATCTA	11275	-	AGG	116	313
CGTGGACGAGGCGAGCCCAT	8876	-	AGG	153	278
TGAGTTGTTCGACAAAGATA	17164	+	TGG	161	270
GATTTTCCTAAAGACTTTAA	31343	+	AGG	396	57
TCAATGGACTTTACATTTGA	19452	-	AGG	441	16
CGTTTTAGCAATATGATTCT	29843	+	AGG	275	164
AGCTCCTGCACAAGATGTAG	14492	+	GGG	222	211
CTCTTATCACCTTCGTTTGT	27318	-	AGG	26	387
GGGTGTCTTACTAAACTTCC	34753	-	CGG	316	125
AAAAAGATTATGGCTTATAT	38933	+	TGG	319	122
TATAACGATCCTGGAGCAGT	38752	+	AGG	241	192
CATTGATACCGTCGCCGTTA	29850	-	TGG	121	298
ATTGAAGAAAGGTTATAACA	14105	+	GGG	290	145
CGGAAAGCATATATTGACGC	14639	+	AGG	301	135
GTTTACACCAATAAATAGCT	18426	-	TGG	129	290
TCAGATACATGGCCTCTGCC	40024	-	CGG	89	326
AAAAATGATGGTGTTGACTT	36278	+	AGG	246	184
ACAGTTCTAACATTTTTGAC	25035	+	TGG	180	242
CGATCAGTCTGATTTGATGA	13784	+	GGG	16	390
TTACTCGTTTCTACACTCAT	5540	-	AGG	263	166
AAAGTTACATTACAGCCCCT	6034	-	GGG	161	258

TACGTCAGCGATTTATAATC	30412	+	CGG	214	209
GATATGAAAATGTGGATTCT	34159	+	CGG	129	285
GACTTTAAATATTTCGATGG	21465	+	TGG	73	332
GTTGTTTGAAATGTACGAGA	10552	+	TGG	207	209
TTCTATGAACGTAATATCAA	15699	+	CGG	335	93
ATATCACTGTTCCTATGGCT	25812	-	TGG	206	208
ACTTTTTGGCAGTAAATTTG	7566	+	AGG	13	382
CCAGCAAAAGCAATCATGGG	36032	+	CGG	229	187
TCTGTGGTTTTGTTGGTTGT	40163	-	AGG	5	389
AATACTTTGCTGGTGTCGAC	15817	+	TGG	145	262
ATTCGACTAAAGGTAAGAGT	14664	+	GGG	110	293
GTCATTGACATTAACGAAGG	3983	+	TGG	69	330
CGATTCAAGGTGTAGTAGAT	25638	+	TGG	184	226
TAGCGCGTTGTAAAGCTCTT	23733	-	TGG	144	260
TCAAAGTATGGTGGCGGAGC	38446	+	TGG	154	249
ACAGTTAAGAGTCAGTGCTT	34322	+	CGG	196	210
TGTATTAGCTGATGTAATAC	13880	+	CGG	118	280
TCGTTATATAGCGACAGGAG	39567	+	AGG	174	228
AATCATAAAGCGTATATACA	8967	+	AGG	265	145
GGTAATAGAATAAGTAGTTT	39601	+	TGG	149	249
AATCAAGAAAAGTTTTATAA	4674	+	CGG	308	105
GCAATACCTTTAAAGTCTTT	31333	-	AGG	301	109
GGTATTAAAACAGCAGTTTC	25613	+	CGG	59	327
CATTTCCCTTCTTGAGATGT	38017	-	TGG	183	215
TCATACTACGCCAAATATTA	35319	-	GGG	152	242
ATCAAAATGGACACGCCAAA	14776	+	AGG	54	328
AAAAACCTGTATTAACTAAA	5956	-	CGG	221	176
AGAGCATGGTCAGAACAAGT	25082	+	AGG	39	339
TTTACTCAAGAAAAATGGAG	20639	+	TGG	252	146
CATGCAAGTTTTAGGTGTTT	25738	+	TGG	103	280
TTATCAGATTTAAAAATCGT	31277	+	TGG	187	204
ATGGATTTATTCAGCTGTAT	30283	+	TGG	178	211
ATAAACGAATTTGGCAAAGA	11552	+	TGG	371	36
TGGAACCCTGCAATTGACGC	21657	+	AGG	140	244
TAATAAAACTTTAGAACAAC	27615	+	CGG	205	185
CCGAACCTATTCCGTTGCCA	34635	-	GGG	209	181
AGAGCACCATTATAGTGTCC	31087	-	AGG	210	180
ACGCATGTAATGGTCATGTG	9148	+	TGG	83	294
TATGAAACAGGGGTCCAACT	11363	+	AGG	95	283
GGCGTTATTCCAGCAGAACA	19595	+	AGG	171	214
CAAAAAATCAAGCAGAAAAA	38198	+	TGG	349	53
TTAAAGTGATTTAAAAACTG	6190	+	AGG	295	101
ACTAATGGCGTTGCGCAACC	38545	+	TGG	285	109
TTTGAGTGGTTACGTCAAAA	2324	+	CGG	45	325
AGATATGACTGTGAGGTTAA	11295	+	AGG	167	214

TCATCTAAATCATAAGTAAC	16561	-	AGG	184	198
CGAAAGTTATTGGGATTAGG	7650	+	GGG	216	169
AGATATGCTGGGTTCTGTAT	30949	-	TGG	135	240
GGCGTTCAAGTGGTTCAGAC	15372	+	AGG	136	237
CAACGTTGCCGAAACCACAA	13942	+	GGG	25	337
AATACACTTTACTTAATTAA	37391	+	GGG	190	188
TTAAGTACTGCCATTATTGC	24334	-	AGG	256	128
TACACAGTAGCTAATGTTAA	39406	+	AGG	28	332
ATCAAATCAATTGGAACGAT	28973	+	TGG	172	202
TCATCAAGTTGTACGTCTAA	12036	-	CGG	162	211
TGGAGAAGAAAGCAAGTGCA	11496	+	TGG	35	322
AAAAAGAGTACGTGGTGGCT	9541	+	GGG	58	301
CAGCTTTTTACCGCAAAAGT	38406	+	TGG	124	241
TGGCGTATTTTGGGCTTTAA	25333	+	TGG	267	111
GACGCAGGGTATTCGACTAA	14654	+	AGG	159	207
TTGAACGCTGCAGGAAGATT	24785	+	TGG	109	252
TAAAATGCCTCTGCAATTAG	19861	-	AGG	189	178
TGACACAACACAAACATCAG	27198	+	GGG	238	133
TCTCCAGTATCAATTAAACT	13220	-	AGG	258	114
TTGATACGAATGGTGATGTT	16731	+	AGG	126	233
AAAAAGAACGGGTTAACTCC	9509	+	TGG	67	286
TAAAGGTAGACCCTAATATT	35325	+	TGG	94	260
ATTCTTAAGTTGTCTTTCAG	30455	-	TGG	100	254
CGACTGCTTCATAATGTGCC	5644	-	AGG	66	284
CTAAACCTGAACGATTAAGG	16255	+	AGG	307	61
GAGAAAACATGTTGTTAAGT	23959	+	TGG	40	302
CACATTGACTTACTAGAAAA	5280	+	CGG	16	323
ATTTCTACCTGTGCTGTTTC	31124	-	TGG	51	291
TCAAGTGATTTAGGAATATC	37684	+	AGG	249	112
TGAATATCATACAAGGTTTG	25785	+	TGG	82	261
GAAGCATTTCAAAGAAAATA	1939	+	GGG	208	147
ATAGATAGTTTTTTATTGTC	5315	-	CGG	208	147
AACTGCCATTGTGATGAGGA	2564	-	GGG	15	321
TTGTTCAAATTTGTGTCTCA	24845	+	AGG	235	121
CCGAAAAAATCTCATACATG	35645	+	GGG	346	19
TGCCTTGTTCTTTTTTATAA	39365	-	GGG	299	61
CAACAGACTTTTGCAGAAGC	28367	+	GGG	191	158
AACCAATGCTCGGGATGGTC	15530	-	AGG	35	297
TTTAATCATGAAAGACATTA	19621	+	TGG	305	53
AAAAAGCGCATCTCAACCGA	37312	+	CGG	195	151
TCCAAAGCCCCTTGTAATAA	23060	-	CGG	148	193
GTATTGTTGTACCACTCATA	29337	-	GGG	155	186
CTTTTTGGCAGTAAATTTGA	7567	+	GGG	32	297
ACTAAAAATTGATGTGCAGA	31426	-	CGG	259	92
ACAACATTAAAAATTAATGA	22794	+	CGG	220	127

CAGTGCCTTGTAATATGATT	29157	-	AGG	150	190
GCATTCCTCGCTAGTTTAGA	14879	+	TGG	162	179
AAAACCAACGTTTAATGATT	4198	+	GGG	41	287
AGAAACATTCTCTAAAACTT	6733	-	GGG	270	80
AAGTCACGTTGTAGTGGAAC	15498	+	TGG	144	193
GCGAATGTAGTTGACTCAGA	33175	+	CGG	181	157
TTAAATCAAGTGGGTGTGTT	18412	+	GGG	63	263
TATAAATAATTTTCGTTCTA	30111	-	GGG	274	72
TGATTGGTTACACGGTTATT	29200	+	GGG	100	227
TGTGGATTCTCGGTTTGATA	34169	+	GGG	153	177
CTACCATACTTTGAAAGTGT	27250	+	CGG	218	117
CAGTCTTGTCGGTTACAAAG	20547	+	AGG	163	164
ACCTAGATTACATTTGTTTA	36406	+	TGG	176	151
CATTAAAACTTTTTATGTGT	33761	+	GGG	133	189
AACTAATTCAAGAATTACAG	39453	+	GGG	193	133
GCACGTTACGGTATCTTACA	20255	+	AGG	104	213
AAAATAGAATAGTTTGTGTA	33054	-	CGG	292	43
TTAAATCTGACGCACTTTGT	33535	-	TGG	108	208
TCCTAATGAACATAAATCAA	32994	+	CGG	69	243
ATGATGCAGGTATCTTATAT	30618	+	TGG	70	240
GCAAAAGCAGTCAAAGCTAA	8092	+	AGG	3	300
ATATAAATAATTTTCGTTCT	30112	-	AGG	27	278
AGCAGTATTTTTCATAGAGG	21694	+	TGG	70	238
ATGCTTTTAGTTCTTTAGAT	28776	-	GGG	115	196
AGTGCTAACAATTCATGTTC	23296	-	AGG	277	49
GTAGCTCCTGCACAAGATGT	14490	+	AGG	63	240
AGGGATAAATATAAATAAAG	36215	+	AGG	159	153
TGACGTTAATCTGGAAAGAT	10686	+	GGG	69	234
GACGGCTAATGATGATGTAG	13736	+	AGG	183	130
GGCAGAGCAATGTCACAAGC	18258	+	TGG	70	231
AACGTTGCCGAAACCACAAG	13943	+	GGG	71	230
GCATTCTCTGTCGCAGGTCT	24416	+	TGG	93	209
GCCAACCCTAACTACTTACA	30662	+	AGG	192	119
TTTAATTCTGACGAGTTTAA	17285	+	CGG	270	48
GAGTTTATTCGAGGGAAAGG	31498	+	TGG	207	104
AGTAAATATAGAAAAGCAAC	38090	+	AGG	13	279
TCATACTTAATTGAATTGTC	27063	-	TGG	239	73
AATCTATCAACTAAGGATGT	19287	-	TGG	195	112
ACAAGTGCTAATTAACCTGA	17521	+	AGG	92	202
ACTAGATGCTTTCACTAAAA	29968	+	AGG	144	155
CTAAAGCTACTGTCGAAGCT	23937	+	TGG	34	254
GTTGTCTCAAATGTAGGTGA	26264	+	CGG	237	70
CGATAATTTGAGCGACTGCT	25275	-	GGG	135	162
TTATGTTAGCGACAGGCGAA	38300	+	AGG	219	85
AATTTTATTAAAAAGTCTAC	27736	+	AGG	132	163

CCAGCTACCAAACCACCTAT	39267	-	AGG	160	137
TTATCCAGTGTTATAAGTGT	21489	+	CGG	150	146
TTATTTCAACAAATGAATGG	6473	+	TGG	145	148
ACCGAATATGGCCAAAAGCG	23165	+	AGG	98	190
CGCACGATATAGAAGTAATA	26777	+	AGG	157	135
GCAGCTTCAAACCACTCTTT	22556	-	CGG	86	199
TTCCTAAAAGCTGGATTGTA	29485	-	TGG	109	178
ACCTTGTAAGTAGTTAGGGT	30647	-	TGG	174	116
TCAACTCGCATGATTATTTT	9209	-	TGG	209	84
TTGAACAAAGGTTATATAGT	12992	+	TGG	140	145
CTTTTTAATAAAATTGGCAT	27712	-	AGG	156	130
CGGATTAGTACCTGCAATAA	24340	+	TGG	54	222
ACAAGACAATGCCCTATGAG	29342	+	TGG	65	211
TAAAGACGATAGAGAGAGAA	16363	+	TGG	173	113
AGGCACAGGGCGATGAAAAT	8521	+	AGG	122	159
GAGATTAAGTCACGTTGTAG	15492	+	TGG	162	120
GCGATTCATGGTAAGCCTAT	39268	+	AGG	104	172
ATGCACTTTTCGGACTGTTA	18887	+	GGG	121	156
TAAAGTAGTGCTACTTGTTT	33214	-	TGG	63	208
TGTAAAGTCCATTGAAGAAA	19476	+	TGG	101	172
GCACCAGCAAGTATATATTG	15236	-	AGG	175	104
CACTAAGTCGTTATATCCTA	28601	-	TGG	94	177
CGTATTGATAATACAGGTTA	29903	+	TGG	74	195
TCAACAACCAATGCTCGGGA	15535	-	TGG	165	112
AGAGGGAGAGTCGCTCGTAC	23125	+	TGG	124	148
TTTTTGGCAGTAAATTTGAG	7568	+	GGG	207	72
TCACAACTGCCATTGTGATG	2568	-	AGG	107	162
TAAGTTTATTGATGATTGGG	15926	+	TGG	242	40
CGTAACTATTCTGATATAGA	26890	+	GGG	141	131
TTACTAAGCATGGCACGATA	22078	+	CGG	135	136
CCTACTATTATGCAGTTAAT	25154	+	CGG	179	96
ACAATAACAGAAGCTTGGAA	25592	+	CGG	138	132
GTAAAGAAACTTATTTACGA	37444	+	AGG	167	104
CACAAATGATTTAGGGTAGG	38158	+	TGG	57	202
TAACTAGCCACTGTGTATAT	13350	-	AGG	133	133
CATGTTATTTGGCGTTCAAG	15362	+	TGG	219	55
AAAGTAAAAGTTAAGACGAT	13564	+	TGG	103	159
TAGTAAACCTGTCTATATCA	22045	-	GGG	179	90
TAAGAATTATCTTAAGACGT	14304	+	GGG	190	80
TTAAGAAACTCTTTTGATAA	19804	-	CGG	256	19
GAGTGGGCAAAGTCGAATAT	34433	+	TGG	26	226
AATCGAACGCTTTCAATGTT	26027	+	TGG	52	201
GCTACAAGCATAATTTTTTT	38703	-	AGG	95	161
CCAGCAAAGTATTCTTTGAT	15791	-	AGG	75	179
TCGTTTGTAGGCAATCTATC	27306	-	AGG	98	158

AGAGGATAGCTCTTTATTAA	26522	-	AGG	172	91
ATACGTGGTATGACATCGTT	15423	+	TGG	205	61
TATTTTTGAGTAATCGTGTA	23240	-	AGG	98	156
TTAATTAAGTTATCGATATC	9098	-	CGG	173	86
GATTTTAGGATATAGCTTCT	34271	+	GGG	117	136
CAGGCGCCCAAGCTATTTAT	18435	+	TGG	76	173
AAAGGAACGCTCGACGGACA	35813	+	AGG	51	195
CTTTTAATAGGGGTAACTAT	30821	+	TGG	158	98
AGAGTTATTACAAATACAAA	11907	+	AGG	162	94
GTATTACGAAAGCGTGGACG	8888	-	AGG	91	158
TAACTTTATTTTAGAGGAGA	10294	+	TGG	225	37
GGACACACCGCAATAGTAGT	34676	+	AGG	96	152
TCAGTTGTATGAAAATATAA	12618	+	GGG	162	91
GGACGCAAAGCGCTTTTAAT	30809	+	AGG	157	94
AAAGGCGAACCGGGACAACC	36791	+	TGG	117	130
TGAATAAACCTACTATGATT	25845	-	TGG	60	181
ATGACCCGCGTCACCCTAAT	35175	+	TGG	130	117
AACATCTCAAGAAGGGAAAT	38035	+	GGG	49	190
ATCGAAAGGAGGTTAGCCTT	23593	+	TGG	97	146
AATATGATTCTAGGCCATAA	29852	+	CGG	149	97
GCCGTTATTACAAGGGGCTT	23075	+	TGG	114	127
CTCCGCCACCATACTTTGAC	38426	-	GGG	71	165
TTCCCGTTAGCATCAAATAA	20128	-	TGG	93	145
TGGCGTTGCGCAACCTGGTT	38550	+	GGG	52	182
CTTAATTTAGGCAAGTATCA	35753	+	AGG	6	223
TATAAACAAATCGGCTTAAA	36179	+	AGG	61	173
ATTTTATTAAAAAGTCTACA	27737	+	GGG	31	200
TAACCGACACTTTCAAAGTA	27237	-	TGG	190	56
CTAGCCAATTAGGGTGACGC	35163	-	GGG	28	202
ACCGTTGATTTATGTTCATT	32979	-	AGG	129	110
TGAAGCATTTCAAAGAAAAT	1938	+	AGG	4	222
ATACGCACTAGCACTTATAA	11646	-	CGG	109	127
ATAATTTTGTAATATTCTTA	31242	-	GGG	145	94
TCCGAACCTATTCCGTTGCC	34636	-	AGG	77	155
AGATGGCACGGAAGATATTA	8654	+	AGG	58	171
GGGAGAAAAGGAGCAATGCC	22899	+	AGG	50	178
CGTTTGCTAAAAATAAAGGT	36003	+	TGG	26	199
AACACAAAGAAGTACATCAA	13391	+	GGG	162	76
GAAACGAGAATAAAAAATGA	36266	+	TGG	116	117
GAACGGGTTAACTCCTGGAA	9514	+	TGG	70	158
CGACTAAAGGAGGCAACCAA	29611	+	TGG	81	148
ATATCAGTATTTTGATGATG	9319	+	TGG	188	51
GAATTTAAAGTCAAGAAGTA	20837	+	TGG	114	116
CGATTCTATCGTTATTCATC	34592	+	TGG	151	82
CTATTTTAGGGTTAGCTTCT	28551	-	GGG	49	174

TACCTTGTGTTACGCGGTAT	17096	+	GGG	61	163
TGTAGGCGATTCTGTAGATC	21229	+	AGG	6	212
TCTTAGGATTCCATCTAATT	36090	-	CGG	82	143
AACAATTTATTTGAGTATGA	21191	+	GGG	156	75
GTTTTTCGTCTGATGGAGTA	35535	-	GGG	118	109
ACTTTCAAAGTATGGTAGTT	27229	-	CGG	78	145
AGAAAGGATTACATCAATAA	36068	+	AGG	93	129
GAGCGTAATAAACGTGCAGA	22419	+	CGG	178	51
AAAAGCTGAAGAAAATAACG	5075	+	GGG	135	89
CTGATGTTTGTGTCAATAAT	31578	-	TGG	130	93
AAAGCGTAAAGGGTACAACT	17428	+	TGG	90	129
TCATTTAGATGGGGAATCAG	18374	+	TGG	50	165
GCAACATGGTTTGGAATACG	10259	+	AGG	37	176
CTTCCTTAGATATGACTGTG	11288	+	AGG	17	194
AAAAGGTGTAGGCGCCTACT	19717	+	GGG	70	146
TTATTGAAGGCGCATCAAAA	6761	-	GGG	122	99
ACAGTTATTAAATAACTATT	39690	+	TGG	108	109
TTATCTAGATTGAAGCCCAA	30182	+	CGG	109	108
TGCAAACCCCGCTAAAATGG	23989	+	CGG	141	79
GGCGTTGCGCAACCTGGTTG	38551	+	GGG	28	180
TCATAAGTGATACCTTGCAT	30583	-	AGG	90	124
GTAGAACTTATGCAAAGTAC	11052	+	AGG	96	118
GTGAATGATAGTGCGACAAA	32062	+	AGG	140	78
GGACATGAAGTTGCATTATA	38848	+	CGG	122	94
CCTAACAACAAAGAGATGAT	16985	+	AGG	102	112
TTTTTCAATATCAACTATGA	10484	-	AGG	83	129
TGCAAGAGGTGGCGCAACAA	29080	+	TGG	159	60
AAGTAAACTATCGGGTGTAG	16067	+	AGG	146	69
AATTTTGCTACATTAATTAT	39660	+	AGG	127	86
AAGTAGCTGAACAATCAAAA	14763	+	TGG	20	182
GTTGACTCAGACGGCAACGG	33184	+	TGG	110	100
CTACCTGTATTACGAAAGCG	8894	-	TGG	161	53
GTGTCTGTTGATGACGTTAA	19024	+	AGG	104	104
TACTACACCTTGAATCGCAC	25616	-	CGG	120	89
AAGCCTGTAACACTTACATA	34774	-	AGG	62	141
GCAGTCATTGGTGTATTCAT	25526	+	TGG	109	98
AGTTGTTGGCTTTGGTGCAA	24439	+	TGG	107	99
AAACTTACCAATAAGATCAT	4908	-	TGG	142	67
ATTGGAAGTATCAAAAAAGT	21014	+	AGG	115	91
ATTTGCCACATTTTAGTGTC	36871	-	AGG	34	164
GCAAGTATATATTATGATGA	13718	+	CGG	138	70
AACTATCGCTTGTTAGATGA	29699	+	AGG	21	175
ACAAAGCGTTCTTGTATAAT	21028	-	TGG	91	111
AATGGCAGTTGTGACGTGGA	2593	+	AGG	9	184
GAGCTTTCCTTACGTTGCTT	23643	-	TGG	81	119

TTAGCAAATAGTTGTTCTAT	17735	-	TGG	128	76
TTTGCCGATTAATTCCGCTC	26324	-	CGG	67	131
ATCTATTAGTTTACATAGAA	22678	-	TGG	69	129
CTTATATTGGGTTAAATCAC	38946	+	AGG	18	175
GCGTGTTTGATAACCTTTTT	36487	-	AGG	80	119
AAGGTAATTCAACAACAAAT	32258	+	TGG	126	77
GAAATGTACGAGATGGAAGG	10559	+	AGG	110	91
GACTACTTTGTGCGCAGCAT	26363	-	TGG	83	115
TGATGAGGAACTTCGCGGAA	33575	+	TGG	66	130
GGCTTATTGGTGGTCAGGAT	23358	+	AGG	48	145
AGATCGAGTCAAGGAGGTTT	12421	+	TGG	20	170
TGAATCATCACATTTATTGG	11327	+	AGG	156	47
TTTATAGCGTTGACCAAAAC	34719	+	TGG	179	26
TTTTCAATATCAACTATGAA	10483	-	GGG	129	71
TATTGGGCAGGCGTACCGAT	29216	+	AGG	54	137
TTTAATATCAGTTGTTACAA	39	+	AGG	5	181
ATTATCGACGATGTTGTAAA	36461	+	AGG	6	179
GGTAGAATCTTTAGTATTGT	21212	+	AGG	61	129
AATGAATTTTTAAAACATTC	31819	+	AGG	116	79
TTAACAAACTAGTTGATGAT	21790	+	AGG	45	142
CACAAATTATATTTTAGATA	27700	+	AGG	148	49
GTCAAGCGCCACAGCCATTT	21637	+	TGG	30	155
TAGTAGCCATTAATGCCGAA	20016	-	AGG	9	173
TCCATAAACAAATGTAATCT	36391	-	AGG	93	97
GGCTATTAGCGCTCTTAAAA	24460	+	TGG	84	105
AGCTGGACTTGATAGCGCAA	18275	+	TGG	157	38
TCTAGTAATTTACTAGCTAT	25204	-	AGG	47	137
TAATACACTTTACTTAATTA	37390	+	AGG	109	81
GGTATGTGGGTGTCTGGTGA	15720	+	CGG	113	77
CAGCGACGAAAAGAAAATCA	8732	+	TGG	12	168
TTAACAATTGGTAATGTGCC	22329	+	TGG	43	140
AATGCCGGAGCGGAATTAAT	26336	+	CGG	40	142
CTGAATAGGAGGAGATATGA	20445	+	TGG	105	83
GACGAAAGTTATTGGGATTA	7648	+	GGG	42	139
TCAAGTTGTCTATAAATATG	11840	+	AGG	156	36
GTTTACATTCAATGACAGGT	29652	+	CGG	76	108
TCTGATATAGAGGGTATTGA	26899	+	TGG	38	142
GGTTTACCATCATACAAGGA	40368	+	TGG	94	91
TAAACTTTTGAAATCTAAAA	725	+	TGG	4	172
GCTACTAAAATCCGAACTTT	24248	+	CGG	61	120
AATTTAGGTTCAAGTGATTT	37675	+	AGG	82	101
TTCTTTATGATAATATGGAT	16126	+	AGG	64	117
TTGCCTTGTTCTTTTTTATA	39366	-	AGG	26	151
TTTAGAACGATAAAAGAAAG	6907	+	TGG	119	67
ACCAATGCTCGGGATGGTCA	15529	-	GGG	58	121

AACGGTAAAGGTTGGACTAA	38530	+	TGG	151	37
ACCTCGTGACCTTTTTCGTT	29533	-	AGG	116	68
TATGCAATATACGTTGAATA	21519	+	CGG	138	47
TCTATCAATAAATTGTCCGT	30182	-	TGG	67	111
CTATCAATAAATTGTCCGTT	30181	-	GGG	26	148
ATAACAATTGCTTGTTGGTC	12249	-	GGG	74	104
ACAAGGTATTATGAGTGGAG	18152	+	AGG	134	49
GGTACTGGTATATATGCTAC	21540	+	TGG	124	58
TTAGTTAGAAACTTTGGTAC	31460	+	TGG	144	39
CTCAACCGACGGTTAAAATT	37323	+	TGG	13	157
AAGTTATGAGGGTTATTTAT	32862	+	CGG	66	109
GTTAGCACTAATGGGTGATT	20227	+	GGG	39	133
AAGAGTCAGTGCTTCGGCAC	34328	+	TGG	41	131
GGTCAAAACTGGAACGGTAA	38518	+	AGG	167	17
ACAGTTTCAGGACCCCAACC	38547	-	AGG	69	105
GCTTTACTAAGAACTATTTT	34216	+	TGG	39	132
TCTATTGTGTTAATAGGACG	15858	+	AGG	42	129
TGAAGCAGTAGGGATTATGA	11816	+	CGG	145	36
ATATCGCTGAGAAAAATAAA	3882	+	AGG	3	164
ATCTTCGCGCAACAGGTCAA	24275	+	AGG	57	114
CTAATTTTGTTAGCAGTATT	26082	+	TGG	27	141
CCACACTATTAGCCCAATTT	24876	-	TGG	38	131
GAAATCAACAGAATTATTGA	1024	+	CGG	182	1
ATTGACGCTTTGCAAGAAGT	16919	+	TGG	111	65
AATTTCTGTCCGCAAAACGC	31220	+	CGG	19	148
GGATTTAACTAGAATAACTG	25432	+	GGG	41	128
CATATCGCCTATATACACAG	13359	+	TGG	75	97
ACAGCAATAGAGTACGTACA	7990	+	AGG	56	114
TATTCGACTAAAGGTAAGAG	14663	+	TGG	58	112
AAAGACTTTAAAGGTATTGC	31352	+	AGG	86	86
GAAACTCATAGATGAGGCAC	8507	+	AGG	22	142
ACTGGATAGACAAATGTCTA	35617	+	GGG	53	114
TTTCTTTTCGTCGCTGAAAT	8709	-	GGG	160	17
AGCCCAATTTTGGAAAGCTA	24866	-	TGG	80	89
AGTTAGTACAGAAGATTTTG	37174	+	AGG	144	31
TAGCTCCTGCACAAGATGTA	14491	+	GGG	117	55
TTAGGTAAAACATCAGGTTC	33280	+	TGG	67	100
CGTATTGTTGTACCACTCAT	29338	-	AGG	92	77
AAAGTAATTGCTACAGACTT	26510	+	TGG	65	100
AGCTTTTAGGAAAGCGAGCA	29512	+	TGG	50	113
AGGCCTTTGAAGAATATGAG	14796	+	TGG	82	84
AGCGTTGGCAATAAAGCTAA	38653	+	AGG	115	54
ATTATCGGGGCAGTCAATGT	34476	+	TGG	33	128
GAGGCCATGTATCTGACTGT	40047	+	TGG	78	87
ATAAGTGCTAGTGCGTATAA	11667	+	CGG	109	59

CAATATTAGAAAATAAAGTG	19509	+	AGG	7	151
TAGCTTAGGTAAAGGTTTAG	26476	+	CGG	102	65
CCCTGGCAACGGAATAGGTT	34651	+	CGG	128	41
GGTACTAATCCGGCAATCAC	24313	-	TGG	68	95
AGATAGTTTAAAAAAAGCAA	28477	+	TGG	145	24
CTTGCTCTTTTGGTTCGAAT	30024	-	CGG	67	94
AAAACGACTAATCTTGCAAG	29066	+	AGG	160	10
ACTGCATACGGTGTTAATGT	38905	+	AGG	99	64
ATTATGAGAAAAGAAGTAAA	24158	+	TGG	3	150
CAACTGCCATTGTGATGAGG	2565	-	AGG	5	148
AGTGGTATAGGAGCTATACG	15408	+	TGG	53	103
GACGGTGCATATTGTATTAA	39505	+	TGG	37	117
TTTTTAATTTAACACAAAGT	33916	+	AGG	104	56
TCAACTTTAGTAATCCTTCA	37736	+	GGG	56	99
AACCTGGAGACATCGCAGTT	34626	+	TGG	15	136
AGTTCGGATTTTAGTAGCTA	24227	-	AGG	129	33
GGAAAAACGGAAAACCGAAA	7246	+	AGG	103	56
TTGAAACTGGTGGAAATGTA	16467	+	AGG	65	90
GCCAGGCAATGTTATTTTAT	19561	+	CGG	153	10
ATACCTTGTGTTACGCGGTA	17095	+	TGG	125	35
AAAGAATGGTCATGAGGATA	9990	+	TGG	46	106
CCTAAGATTGGTCAGATATT	24965	+	TGG	16	133
TAACTTTATCCACATAAAGG	6707	+	TGG	131	29
CTTTAACCGCCATTTTAGCG	23979	-	GGG	90	66
ATTATTTCAGTGTACTTTTT	13049	-	CGG	80	75
AGGCTTACCATGAATCGCAC	39247	-	CGG	44	107
ACAATGGCAACAGTTCCAAT	29096	+	AGG	20	128
TTTCAATATCAACTATGAAG	10482	-	GGG	134	25
GCGATGTCAGCAGGTATCAG	24599	+	AGG	73	80
TGCATTACTGCATTTGTATA	30073	-	TGG	60	91
CGGTGCTAGCTTCGTAAGAA	36052	+	AGG	5	140
ATCTTTGCTTTATTATCAAA	38334	-	CGG	129	28
TGGAGTGTGGCTGAAAAAAT	26138	+	GGG	18	128
ACAGTTGAATACGAAAAATT	22605	+	CGG	126	30
CAAAGTCGAATATTGGTAAG	34440	+	AGG	87	65
ATACTGCTTGACTATCGATA	22021	-	CGG	118	37
GCTTCAATTCCTTTATCTCC	22331	-	AGG	108	46
AGGCTCAATAAAATGTTGAA	5832	+	AGG	78	73
AAAACTTGGGAACTTGTCTT	6720	-	TGG	141	15
TGGTTACACGGTTATTGGGC	29204	+	AGG	26	117
TCCGAAAATGGCATTTCGGT	7173	-	TGG	57	89
ACTAATTTCACAGAAATGTT	29027	+	AGG	143	11
GCAACAATGAGAGAAACAGT	21894	+	CGG	95	54
AAAACGGATTATCGGCAAAC	7211	+	GGG	102	47
AAACATCCAGTGACATGCTT	39870	-	GGG	96	52

ATATATGCTACTGGTCCTGG	21549	+	TGG	77	69
GCGAGTACGTTTGACGCAAT	27845	+	AGG	58	86
AGTCACAGGTGTAATGCTTG	33892	+	AGG	133	18
CCTTGCAATATTAATGATTT	8013	-	TGG	99	48
ACCGTTAAAGAATGGTCATG	9984	+	AGG	8	130
AACCGCAACTGTGTAATATG	5622	+	CGG	15	123
CGTGTACGTTAGAGAATGAC	40347	+	CGG	28	110
GTGTCGTACACTTATAACGA	20865	+	TGG	42	97
GGAATATCAGGAGTCAATAG	37696	+	CGG	66	75
ATCGGTGTTATCGGTATTTT	25310	+	AGG	46	93
ATCAATATCGCAAATGTTGA	36959	+	AGG	17	119
TTCTGGGCGTGCTTCTGGTT	34287	+	TGG	50	89
CTACAAACGAAGGTGATAAG	27335	+	AGG	80	61
AATATTGCCTAAGCATATTG	16324	+	AGG	26	109
AATGAATTGATAAAAAAGAA	9497	+	CGG	1	131
GCAACAACATAAGATGACAG	32727	+	AGG	33	101
TCAACTAGTTTGTTAATGTT	21767	-	AGG	47	88
GTTGTAGCTTTTCTAGCTTT	1646	-	AGG	71	66
GGCTTGAGAGAGCAAATAAA	13999	+	AGG	73	64
TCTCTATCGACATATAAATG	35104	-	CGG	23	109
AGAGAACTTGTATTGAACAA	12980	+	AGG	102	37
AGAAGTAAAAGATTATCTAA	18990	+	AGG	84	52
AAAATCTCATACATGGGGCT	35650	+	GGG	36	95
TATTTTAGGTGGCGTATTTT	25324	+	GGG	24	105
AACCGGTTTTATATCCAGGC	27632	+	TGG	47	83
GTCCGCAAAACGCCGGTTAT	31227	+	TGG	21	106
CAGTCGTGTTGCTTGGAGTG	26125	+	TGG	22	105
CAAGGTATCACTTATGATGC	30605	+	AGG	84	49
TTACTGCCAAAAAGTGTTTC	7542	-	TGG	31	96
GACTTTTCATCTTTTGCCTC	33857	-	TGG	53	76
AATTAAGTGGTACGTAGACA	33803	+	TGG	13	112
ACTAGCCAATTAGGGTGACG	35164	-	CGG	65	65
TTATCCACGAGTCATGCAAG	5782	-	TGG	56	73
AACTGATTAAACTGTGTTAA	27399	-	AGG	59	69
TTTGAAGCATTGAATAGCAT	24740	+	AGG	49	77
AAGCTCATTTTAAGCGCGAT	21963	+	AGG	70	58
TCAATATCGCAAATGTTGAA	36960	+	GGG	40	85
AAAAGGTATCTACTTCACAA	36196	+	GGG	42	83
ACTTTAAAGGTATTGCAGGT	31356	+	TGG	50	75
GTTGGTGGTACTATGATTTT	2793	-	TGG	41	83
TCACACTTATTGAGGAGCAT	12817	+	GGG	65	61
TGAACTATATAGCCGGGCAG	40028	+	AGG	6	114
AAAAGATTATGGCTTATATT	38934	+	GGG	78	49
GATAGATTGCCTACAAACGA	27325	+	AGG	40	83
AACGATAAAAACGAAGTTAT	33366	+	CGG	74	52

ACAGCAAAATGGACAATAAA	37579	+	TGG	85	42
ATAGGGGTAACTATTGGACC	30827	+	TGG	44	79
TTCGCGAGTAAAGTAGCTGA	26231	+	TGG	128	3
GACTATTACTGTTACAAAGA	20508	+	AGG	15	105
TCCTCGCTTTTGGCCATATT	23150	-	CGG	39	83
TCACTTACTACCTGCCTATA	14405	+	TGG	34	87
ATTGAAATGAGGTGCATACA	34363	+	TGG	19	100
GTGCCTATATCCGTCTTTTC	32388	-	TGG	35	85
TATGCACTTTTCGGACTGTT	18886	+	AGG	50	71
GATGATGAGGATTCTGAAAT	16664	+	AGG	42	77
CTGTAGGCTTTCTAGTCTTT	34380	-	GGG	30	87
AGGAGACTTCCAAGAAGCTG	30757	+	AGG	104	20
TGTTTACCCATATATTGTTG	21839	+	TGG	3	111
GTTGGCGCATTCTCTGTCGC	24410	+	AGG	8	106
AGTCGTTTAAAATTATTCAA	37792	-	TGG	91	31
ATACTCCACTAATGTAATCA	20875	-	GGG	71	49
TATTGGGGTTTTGTAACATG	34526	+	GGG	31	85
TATCTGACTGTTGGTCCCAC	40056	+	AGG	24	91
CAATGAATGTTAAGCGAATA	35703	+	TGG	28	87
TTTGACAAGTATGTTCAAAA	19381	+	AGG	8	105
ACGACTAATCTTGCAAGAGG	29069	+	TGG	83	37
ATACAAGCTAGGTTAAAAGT	13537	+	AGG	43	73
TAAAGTGAGGTAATAAAATA	19522	+	TGG	105	17
GCAGTTTGGCACCCTGGCAA	34640	+	CGG	27	86
TTTGAGCTTGATTATGTTGA	27136	+	TGG	48	67
AGGAAAGCGAGCATGGAGGA	29519	+	CGG	38	76
ATGATTGGTTACACGGTTAT	29199	+	TGG	51	64
ATTGAAAATGATTTAGTTAG	31918	+	TGG	52	63
ATCACCATAACCTTTAATAA	28319	-	AGG	43	71
AACTTCGCTAATGGTAGATA	35924	+	CGG	33	80
ACGATAGTAGACGCAATTAA	31774	+	TGG	7	103
TAAAAAGTCTACAGGGTGTA	27744	+	GGG	18	93
ACAGGAGAGGTAGACAAGGC	39580	+	AGG	49	65
AGAGAATTACAAGGAAATCA	23225	+	TGG	50	64
TACGGATATCACTGTTCCTA	25817	-	TGG	71	45
ATAAGAAAAACAACGGAGCA	31197	+	TGG	30	82
GATAATTTTGTAATATTCTT	31243	-	AGG	10	100
GGTTAAACCTCTAATTGCAG	19870	+	AGG	24	87
TGTAACATGGGGCAATGCTA	34537	+	AGG	25	86
AACTTTGGTACTGGTGGCGT	31469	+	TGG	33	78
TTTGTGCTAGGACTCATAGA	14606	+	GGG	13	96
CTACGTTCAATAAATGTGAA	14455	-	AGG	75	40
GGTTTTTCGTCTGATGGAGT	35536	-	AGG	26	84
ACTGGGTTAATTCTAATAGT	34737	+	TGG	41	70
AAAATCGGAAGGTTTCCGGA	14721	+	AGG	44	67

CGCACGCAAGTTTGAGGATT	24688	+	GGG	36	74
ATCAACGGTATGTGGGTGTC	15714	+	TGG	29	80
AAAGAAGATTTTGAAACTGG	16457	+	TGG	5	101
GTATCTGAAGTGTATTCCAT	30556	-	AGG	72	40
TCGAAACCTTGTAAGTAGTT	30652	-	AGG	24	83
TGCGCACAAAGTAGTCAGCG	26386	+	CGG	78	34
TGTTTTGTTAGTTTTCAGTT	33669	-	CGG	31	76
CGATTAGAAATCTTTAAAAA	28160	+	AGG	2	102
AAACTACCCACCATATAGGC	14399	-	AGG	58	51
GGAGACCTAATCATATTACA	29168	+	AGG	58	51
CATAAGATGACAGAGGCGAA	32734	+	TGG	58	51
GTAATATCACTTAGATATGC	30961	-	TGG	49	59
GATTGGTTAACTCAATTGTG	25655	+	GGG	65	44
TGATGGAGTAGGGCCTCGTG	35525	-	TGG	24	81
ATAAAAATGAGCAAATTAAG	33790	+	TGG	25	80
TGGGTGTGCTTCGAATAGTT	25256	-	TGG	40	66
CCCGCTATCGTCGAATATTA	8589	+	AGG	63	45
GCTTAGTACAAGCTTCTAAG	23427	+	AGG	43	63
ATACTCAAAGTAATCATTTT	11235	-	CGG	64	44
GACTGGGGTTACGAGCACTA	15834	+	TGG	69	39
TCGAGCAGTATTTTTCATAG	21691	+	AGG	93	17
GAAAAATTCGGCGAAAAAGT	22617	+	CGG	1	100
TTGTTAGGTACACCAAACAA	16954	-	TGG	40	64
TTTATAAAAAAATTGAAAAG	22742	+	AGG	96	13
ATGCCTATATTACAAGTATT	25706	+	AGG	23	78
ATGCAGTAATGCAATCATTT	30099	+	TGG	65	40
ACAAGGAAGATGTCTCCTGT	40055	-	GGG	35	67
TAACAAAACAAATACTGAGG	33698	+	GGG	67	38
ATTGAACAAAGCACCGAATA	23153	+	TGG	39	63
TTATTAAATAACTATTTGGA	39694	+	TGG	20	79
ACCCTGACCATCCCGAGCAT	15544	+	TGG	23	76
CGTTAGCACTAATGGGTGAT	20226	+	TGG	6	91
TTACTACCTGCCTATATGGT	14409	+	GGG	38	62
AGTTTCTATGAATCAGATAG	31615	+	AGG	26	72
GGAGCAGTTAAACGTTCTTT	24122	+	CGG	42	57
TTTGTAACAACTGATATTAA	21	-	AGG	23	74
TCTCAGAAGATAGCGAAGAT	22879	+	GGG	51	48
CAAACTAGGGTTAACACTTG	29398	+	AGG	10	85
TGGAGTTTTAAAGGTGATGA	21594	+	CGG	68	32
GCTTAAACCAACTGAATAGG	20434	+	AGG	20	75
GGAACAGCAGACGCAGGAAA	12379	+	AGG	33	63
TGGGTAATAGACATCAAAAA	6015	-	AGG	96	6
CCTGGTGCAAAAGGTGAAGC	36809	+	AGG	28	67
GACGCGCGTATTGATAATAC	29897	+	AGG	71	28
CAAAAAGTGTTTCTGGTCTA	7535	-	AGG	62	36

TGTAAACTAATAGATCAAGG	22702	+	GGG	93	8
AAATGATTCTGACATTGCAT	22287	-	TGG	44	52
CGTTTTTTTGGGGCAAAAAA	40234	+	AGG	3	89
TTAGCTATTGGTAAGTCGTA	21151	-	AGG	59	38
AAAGATATTGTAAGTAGATA	15957	+	TGG	51	45
ACTGCGATGTCTCCAGGTTC	34606	-	CGG	23	70
ATCATTCTGATTGGTTATTT	17670	-	TGG	13	79
ATTACACAAGGTATTATGAG	18147	+	TGG	44	51
TTGATGACCTTAACAATTCT	28002	+	AGG	5	86
ATTATTGAAGGCGCATCAAA	6762	-	AGG	89	10
GTCAGTTGTATGAAAATATA	12617	+	AGG	91	8
AATGGCGCTGACCTTGTTAA	32239	+	AGG	20	72
AAACAAAACGGTATAAACAT	2288	+	CGG	4	86
ATCGGATTCGTTAATACTGG	33384	+	CGG	46	48
ACACGTGTTGGTTATTTACA	16550	+	TGG	35	57
TTGAACTTGATGAAGCAGTA	11806	+	GGG	26	65
TCATTTTATGGCAAAGATTA	23620	+	TGG	78	18
TGATTTCTTAAATGCCGGAG	26326	+	CGG	58	36
TAAAGTTACATTACAGCCCC	6035	-	TGG	8	81
ACTGTTCTATGAAAGTTGCA	5488	+	AGG	46	46
ATTGACTTTAAATATTTCGA	21462	+	TGG	40	51
CAACGTCGTTATATAGCGAC	39562	+	AGG	61	32
GATGAGCTTATTGGGGATAT	11447	+	AGG	45	46
AAAGGTGATAAAGGCGAACC	36782	+	GGG	45	45
AGTAGATTTAAAGGTGCGAA	36764	+	AGG	67	25
GTTGAAGGCGCAGAAGAGAA	19973	+	AGG	70	22
AGGTAGCGTTGAAAGTTATG	32850	+	AGG	3	82
ATGGGGCAATGCTAAGGATA	34543	+	TGG	34	54
GCAAGCGACTACAAAAAAAG	38685	+	AGG	37	51
GACGGTGGCGCAAATGGTGT	33025	+	AGG	38	50
AGCCATACAATCCAGCTTTT	29499	+	AGG	18	68
TCGCCTCTATATGTGTTTTC	2817	-	TGG	29	58
ATACTTTGCTGGTGTCGACT	15818	+	GGG	29	58
GAAAGATTACGGCGAGAAAA	24217	+	TGG	87	5
TTTAAATTCTTTTTAACTTC	20807	-	AGG	46	42
AGGCATTCTTTACACAAAAC	31856	+	GGG	16	69
GCAAACGTCATTGCATAATC	35971	-	AGG	65	24
GTAGTTGACTCAGACGGCAA	33181	+	CGG	38	48
GTAGCTGTCCAAATCATAGT	25853	+	AGG	41	45
AAACGACGTATCGATATTGG	30716	+	CGG	46	40
ATTACAGTTTTTACGACTAA	29598	+	AGG	9	73
GACTTGAATCGATTCCAGCC	27630	-	TGG	18	64
TTATCGGGGCAGTCAATGTT	34477	+	GGG	18	64
TTGCGATAGCGTATGCTAGG	8057	-	TGG	30	53
TCCGCTCCAGTATAAGATAG	20167	-	TGG	30	53

GATTTAGTTAGTGGGTTTGA	31927	+	TGG	26	56
ATATTTAAGATGGAAGTTGA	20685	+	CGG	37	46
GGTGTCATTACTTCTTTAAT	38104	-	AGG	32	50
CCACTAGTTGAAGTGTTGTA	19924	-	AGG	22	59
AATCTGGAAAGATGGGGAGT	10693	+	TGG	23	58
CGGATATTTATTTTTAGGTA	37522	-	AGG	14	66
GATAATCCGTTTTCCGAAAA	7185	-	TGG	25	56
TTCCGCATATTACACAGTTG	5608	-	CGG	36	46
TCCTTAATATTCGACGATAG	8574	-	CGG	13	66
CAAGTGCTAATTAACCTGAA	17522	+	GGG	24	56
CAACTAGTTTGTTAATGTTA	21766	-	GGG	30	50
AATAGGTGATGTTGTTAGAG	28585	+	TGG	52	30
TTAATCGGCAAAGTAGCTGA	26351	+	GGG	34	46
GTATCGATGACTGATTCAGG	30926	+	CGG	43	37
ACAATTGCGTTCCAAGCCAT	25817	+	AGG	23	55
GAGCCTTTATTTATATGAAA	17984	+	TGG	76	7
GTACTTACCAGAAACAGCAC	31133	+	AGG	28	50
AAAGGTAATAATGTAAGAGA	39424	+	CGG	21	56
TTGCTAGTATCTTTTGAATA	34807	-	TGG	74	8
GCATCTAAATTCGAGGGATT	28124	+	AGG	23	54
ACGCAAAGCGCTTTTAATAG	30811	+	GGG	22	54
GTTAACTTAAATAATGCGCA	32770	+	AGG	23	53
GAATATACAAAAGTATATGC	37471	+	TGG	54	25
AATCAATTCTTAGCGAATAA	37925	+	AGG	3	71
CTTCAATAACTAGCCAATTA	35172	-	GGG	6	68
TGAGACACAAATTTGAACAA	24826	-	CGG	27	49
TGGCACCCTGGCAACGGAAT	34646	+	AGG	7	67
CTTAATGCGGTTGGTGTATT	24368	+	AGG	32	44
TTAAATACTTTCACATCATT	38497	+	TGG	32	44
GTTGCAAAAAGAGTACGTGG	9536	+	TGG	36	40
AGCTAGTGAAGTGGTGGAGT	34417	+	GGG	27	48
ATTCTAGGCCATAACGGCGA	29858	+	CGG	24	50
TACTTTGCTGGTGTCGACTG	15819	+	GGG	5	67
TTAGTAAACCTGTCTATATC	22046	-	AGG	47	29
CATTATTGCAGGTACTAATC	24323	-	CGG	28	46
CCAAAATTGGGCTAATAGTG	24892	+	TGG	12	60
TCCAAGTGATTATAAGTGAA	26814	-	AGG	43	32
GCGCTTAACAAAATACTTAA	35789	+	AGG	43	32
TCTGTAACTTCATTCGTAAG	26438	+	TGG	34	40
ACGCACGCAAGTTTGAGGAT	24687	+	TGG	6	65
TCTATCTACGTTATAATCAT	31711	-	CGG	11	60
AGACAAAGTATTGTATCAAA	30544	+	TGG	32	41
ATTATGCTTGTAGCCGGTCA	38728	+	TGG	13	58
AAGATAACTTGCCGAAAGAG	22561	+	TGG	46	28
CAAAAGGTGTAGGCGCCTAC	19716	+	TGG	37	36

TGGTAACTTTTATTTTATTG	15887	+	AGG	7	63
AGGATCGTTATAACCATGAC	38725	-	CGG	31	41
TTCTTAGAGTTATTGAAGAA	14094	+	AGG	21	49
GAATTCGTTGAACTTTGTTG	30490	+	AGG	44	28
AAACGAAGGAGTGTATTAAA	22130	+	TGG	36	35
TGGCGACTTCTCAGGTGCTT	25906	+	GGG	16	53
GGATTCAATGTTATATTTAA	22920	+	CGG	52	20
CTCTAAACGCTTTCGGTAAC	31038	-	GGG	11	57
GTATAACCTGCTGGCACTGG	39324	-	TGG	6	61
AGCGTCGTTAGCGCATGAAG	15461	+	AGG	40	30
AAGGAAGTTGATTTAAAAGC	27532	+	CGG	55	16
AGAAGTAAAATCGAATACAC	31384	+	CGG	47	23
GCTCAAATTATCGGTGTTAT	25301	+	CGG	52	18
TGGACGATCACTCATGTTGA	27884	+	AGG	23	44
ATGGTTGCAAAAAGAGTACG	9533	+	TGG	15	51
ACATGTCTTGTCACAGTTTC	38559	-	AGG	19	47
TTGAATCGCGTTAGGTAATG	33127	-	CGG	9	56
TATTATGTACGAGTTAATCA	29572	+	AGG	22	44
CTATGTAAACTAATAGATCA	22699	+	AGG	14	51
CATCACTCAATTTATTCCAT	30860	+	CGG	4	60
TGCGCTTAAAACGCTATCTA	32320	-	TGG	35	32
TAAAAATAACTTTTATTAGA	34684	-	TGG	5	58
GTGGTGTTTGGTTATTGTCA	35274	+	GGG	21	43
AATGGAACAAGTGATATTTG	24176	+	GGG	13	50
TCTATGCTTGCAGTTTGGAA	10848	-	CGG	26	38
TAACGCGCTAGGTAAAGCGC	19269	+	AGG	26	38
GTGACGCGGGTCATCAAAAT	35150	-	TGG	26	38
TCAACGCTACCTGGTAAATC	32823	-	CGG	29	35
ATGGATCCTATTTTAGGTAA	6795	-	AGG	19	44
TGTCCATAGCTTTCCAAAAT	24879	+	TGG	3	58
GGTTTTATTACAAAAGATGA	37500	-	AGG	35	29
GTTGACAGTGCGTCCACACG	35528	+	AGG	15	47
TAACTTCTCAATTTAGAGCA	25068	+	TGG	57	9
GATAGATTGCTTGTTAAAAA	30215	+	CGG	7	54
CAAGGCGCACCCGGTAAAAA	36845	+	CGG	10	51
TTAAGCGTTGCGAACGCTTC	20401	-	TGG	13	48
AAACCAACGTTTAATGATTG	4199	+	GGG	55	10
ATGTTCTTTATGTTAGCGAC	38293	+	AGG	14	47
ACCAGCTTTAATGTAATAAT	28247	-	TGG	26	36
TTAGCTGACATGTTGGCGTT	12076	+	TGG	29	33
GTGCTAACAATTCATGTTCA	23295	-	GGG	21	40
GAAGTTTCAACTTATTATAA	26736	+	GGG	11	49
ATCAACTTTAGTAATCCTTC	37735	+	AGG	34	28
ACTGATGATGATTGGTTACA	29192	+	CGG	16	44
GGAGATAAAATAATCTTCGA	27553	+	CGG	58	6

ACTTCATTCGTAAGTGGACA	26444	+	CGG	9	50
TTACAACATCGTCGATAATA	36441	-	AGG	52	11
GGAAAGCATATATTGACGCA	14640	+	GGG	11	48
ATGACGTTTGCTAAAAATAA	35999	+	AGG	59	4
GGTGTCCCTGATTACATTAG	20886	+	TGG	19	40
ATCGCTATTGCGTTAGATTG	6828	-	GGG	22	37
TCGTAACTATTCTGATATAG	26889	+	AGG	54	8
ACAATAGTGGTTTTTTCAAG	23107	+	AGG	3	54
TCTGGATTTGTACCGGAACC	34610	+	TGG	24	35
AACAGATGCGCCAGAAAAGA	32394	+	CGG	15	43
GGCGATTTTTCTTCCTAGTT	482	+	CGG	16	42
GCTGTAGGCTTTCTAGTCTT	34381	-	TGG	28	31
ATAGCTTCTGGGCGTGCTTC	34282	+	TGG	18	40
AGGGGTCCAACTAGGTGTAA	11371	+	TGG	19	39
CAACACAAAGAAGTACATCA	13390	+	AGG	9	48
CCCATGTATGAGATTTTTTC	35628	-	GGG	23	35
ATTGAAGAATTTGATGATAA	4433	+	CGG	38	21
AGGGATATGTTCCCAATAAC	31223	-	CGG	31	27
TAGGTTATTAATTGAAATTT	6291	+	CGG	1	54
ACGAAAGTTATTGGGATTAG	7649	+	GGG	32	26
TGACACCAATTTCTTCAGAA	757	-	AGG	3	52
AGCAGTTTAACGACATGCTA	18841	-	AGG	24	33
TCAATTATCGGCTTTTTAAC	25997	+	TGG	28	28
AATGATGAAAGAGAATTACA	23216	+	AGG	50	8
AATTGGGCTAATAGTGTGGC	24896	+	TGG	12	42
AACGTAATATCAACGGTATG	15706	+	TGG	13	41
GAATGTAACGATTAGAAATG	26662	+	AGG	34	22
ATAGATGATATTGAAGCACA	16301	+	AGG	21	33
CACGGTGGAGGTAGTAGCTT	26462	+	AGG	21	33
GGATTTTAGGATATAGCTTC	34270	+	TGG	22	32
TATGAATCAGATAGAGGAAC	31621	+	TGG	13	40
TCTAATTGTTCTCGAGTTGG	22994	-	TGG	3	49
AGACATAAAAAGAAAAACGA	22116	+	AGG	15	38
TTTCAATGTTTGGTACAAGT	26037	+	TGG	36	19
AGATGCAAACCCCGCTAAAA	23986	+	TGG	10	42
ATCACACTTATTGAGGAGCA	12816	+	TGG	16	36
AAACTTGGGAACTTGTCTTT	6719	-	GGG	6	45
ATACACTTTACTTAATTAAG	37392	+	GGG	19	33
ATGAACGACACAAATGATTT	38150	+	AGG	52	3
GAATATAACGTTACAGGCGC	26860	+	AGG	22	30
GTAAGAATTATCTTAAGACG	14303	+	TGG	37	16
TTACAAGCATCAGATGCTTC	20318	+	TGG	38	15
CGAAACCTTGTAAGTAGTTA	30651	-	GGG	20	31
AGATTGGGGGTGAATAATTA	6814	-	TGG	33	19
GTAAGTGGAACTTATCCAGG	33097	+	TGG	33	19

GTACAAGTTGGTCACAGATA	26049	+	TGG	13	37
ATATACGTTGAATACGGTAC	21525	+	TGG	15	35
AGATTGGTTAACTCAATTGT	25654	+	GGG	16	34
TTATCGCTATTGCGTTAGAT	6830	-	TGG	29	22
AAAGATTTAATAAACGAATT	11543	+	TGG	9	40
GTACTGGTGGCGTTGGTAAA	31476	+	TGG	12	37
TGCGCCGACACTTATAACAC	21477	-	TGG	27	23
GCGCCAGAAAAGACGGATAT	32401	+	AGG	8	40
GTTAACACCTCTTTGGCCGA	30860	-	TGG	20	29
CGTGGTGTTTGGTTATTGTC	35273	+	AGG	21	28
TTACCTATCAATTGTGCTAA	28396	-	TGG	33	17
TAAGGCTTGATATCAAAGCT	27969	+	AGG	5	42
TCAGTCTGATTTGATGAGGG	13787	+	CGG	37	13
AACAAAATACTTAAAGGAAA	35795	+	AGG	37	13
GAAAGGTGATAAAGGCGAAC	36781	+	CGG	19	29
GCAGGAGAAAGCGCAAGTGG	39004	+	TGG	41	9
TTTAAATCAAGTGGGTGTGT	18411	+	TGG	4	42
TCAACGGTATTGTTCGACGG	33010	+	TGG	15	32
TACTATGATTTGGACAGCTA	25835	-	CGG	3	42
GGCGATTCTGTAGATCAGGG	21233	+	CGG	15	31
TTAGCATATATTGATACGAA	16721	+	TGG	17	29
GCATTTATATGTCGATAGAG	35122	+	AGG	18	28
ACCACTATCTTATACTGGAG	20182	+	CGG	9	36
AAATGTTATACCTTTATTAA	28325	+	AGG	27	19
CTCTACCTTATTGATTTAAA	20927	-	CGG	29	17
GGGATTACTAAAAGAGATTG	11702	+	AGG	32	14
AATGGTTACGAGTATAAAGA	7816	+	CGG	27	18
AATAATGCGCAAGGCGATTT	32779	+	GGG	9	34
AAATCAATCGCAACAGAGAT	14054	+	TGG	22	22
GCGATGCGATTTCATCAGCT	26412	+	TGG	12	31
CCAAACGGCACGAACATGAA	33959	+	TGG	12	31
TTATTCATCTGGATTTGTAC	34603	+	CGG	14	29
GGAGACTTCCAAGAAGCTGA	30758	+	GGG	16	27
CCGGGACAACCTGGTGCAAA	36800	+	AGG	17	26
CATACAAAAAGAAAATGAAA	12338	+	AGG	41	4
GCAGGTAAAAAAGGAGAACA	36827	+	AGG	21	22
GATAATTTCTTTATAGGGAA	7351	-	TGG	4	37
GCTGATAAAAGTAAACTATC	16059	+	GGG	16	26
GATAAATCAGTGATAAATTC	30049	-	CGG	6	35
TTTATGTTATAGCTAGCCTT	39803	+	CGG	6	35
AATGGTTGAAGATGGAACAT	24478	+	TGG	17	25
TAATAACCTAGTAAGGTTAG	6262	-	GGG	11	30
CGATGCGATTTCATCAGCTT	26413	+	GGG	3	37
ATGTACGTAGCGGTATAATG	37640	+	AGG	35	8
GCAATGGTTGCTAAAGATAA	18291	+	CGG	25	17

ACCGATAGGCACTGATAAAA	29230	+	CGG	17	24
CCGACGGTTAAAATTTGGAC	37328	+	AGG	7	33
ATGTCGATAGAGAGGCTACA	35130	+	TGG	18	23
CGAAGATAGTACCGAAAGTT	24243	-	CGG	19	22
GTACTGCCTGGACACTATAA	31097	+	TGG	9	31
AAACAATTTATTTGAGTATG	21190	+	AGG	40	3
TTGATATTGATTCCAGCAGA	24057	+	TGG	30	12
AAAACTGGAACGGTAAAGGT	38522	+	TGG	10	30
TTAGAGAAGCCTGGACAAGA	32428	+	TGG	11	29
AAAGCAAAGATTGAAAAATA	38362	+	TGG	11	29
GATACATTGATGGAGAATTA	30264	+	TGG	20	20
TTTTGTGCAAAGTACGAATG	10797	+	AGG	10	29
ACACGGACAAAAACAAACTA	29385	+	GGG	3	35
GTGCAATGTTTTTTAAGAAT	30882	-	TGG	15	24
CACCTGCTGAATGGCGTGAT	23337	+	TGG	10	28
TCAACTAATTCAAGAATTAC	39451	+	AGG	23	16
GGGAAACAATTCAACCCAGA	38236	+	TGG	14	24
CGGACTGTTAGGGTACGCGA	18897	+	AGG	5	32
ATCACTAGTATTTTTGAATC	29296	-	TGG	16	22
AGACATATTAGATCGAGTCA	12412	+	AGG	18	20
GCGACAGGCGAAAGGCTGCA	38308	+	AGG	11	26
TTAAGTTTCATTCCAATGAT	17299	-	AGG	22	16
TTGCAAGGTTCATACGGAAC	8044	+	TGG	14	23
CCTATAGGTGGTTTGGTAGC	39283	+	TGG	26	12
AATTCCGGTTCTTGCTCTTT	30034	-	TGG	17	20
GATATTGATGAGTATATCGA	17706	+	GGG	18	19
CTAGTATCTTTTGAATATGG	34804	-	AGG	12	24
GATCCTGGAGCAGTAGGAAA	38758	+	CGG	4	31
GTCTGATTTGATGAGGGCGG	13790	+	AGG	15	21
CATTTCTTTGTCCTCGCTTT	23160	-	TGG	17	19
GCAGGGTTCCAAAATGGCTG	21629	-	TGG	19	17
CATGCCATAAGGTGCGTTTA	9560	-	AGG	11	24
TGATTTCATCACTGAAAACG	23045	+	AGG	11	24
AATGTAACGATTAGAAATGA	26663	+	GGG	22	14
TTACTATGCAACAAGAGTGC	32820	+	CGG	12	23
ACATTAAAACTTTTTATGTG	33760	+	TGG	12	23
TACTTTGTTAACAAGTTTTT	2501	+	AGG	23	13
AATGCTTTTAGTTCTTTAGA	28777	-	TGG	14	21
GAATCAAGATTTTAGGTTGG	7467	+	AGG	9	25
GAAAAAGACATTTGATACAG	10214	+	CGG	30	6
ACAGGTCACAGTAAAGTAAG	15390	+	TGG	11	23
GTCCATAGCTTTCCAAAATT	24880	+	GGG	22	13
ATGTAAACTAATAGATCAAG	22701	+	GGG	5	28
TGGCGTGATTGGCTTATTGG	23348	+	TGG	17	17
TGATTGGCTTATTGGTGGTC	23353	+	AGG	21	13

GCCTACAGCTAGTGAAGTGG	34411	+	TGG	11	22
AGCATATCTAAGTGATATTA	30979	+	CGG	22	12
TATTATGTATTTCGAGGAGA	16895	+	AGG	3	29
TGGCTAGTTATTGAAGTATG	35195	+	TGG	3	29
GTTACTATAACTAAAATTAT	33319	+	GGG	15	18
AATGGCGCTTATTACTTTCA	10164	+	CGG	5	27
AAAGGTGCGAAAGGTGATAA	36773	+	AGG	16	17
ACCATGCTTAAAGGGATTTT	34257	+	AGG	10	22
CAATACTGTCTTTAAAGGAA	28069	+	CGG	22	11
ATAGGTATCAATGACAAACA	36353	+	AGG	22	11
GTATCAAATGGATATACCTA	30556	+	TGG	12	20
TAAATGGGCGCGAGAAAATC	10366	+	CGG	3	28
AAACTTTTACTCAAGAAAAA	20634	+	TGG	4	27
GATACTCATCGTCATTTAGA	18363	+	TGG	6	25
GGACCTAGAAGAGAAAATTG	6598	+	TGG	9	22
ACAGTTTTTACGACTAAAGG	29601	+	AGG	9	22
TCAATCCTGACACTAAAATG	36882	+	TGG	21	11
GTTTTAGGTGTTTTGGTAAT	25745	+	AGG	11	20
TGTGGTTTTGTTGGTTGTAG	40161	-	GGG	24	8
TACCTACAAGATACCTAAAA	36490	+	AGG	5	25
TTGGTATTCTTGTTTATTTA	25545	+	TGG	7	23
TCAGTTTGGGAGTCAATTAT	25985	+	CGG	18	13
GGACAAGATGGTGTTGATGA	32440	+	CGG	9	21
ATGTGGATTCTCGGTTTGAT	34168	+	AGG	15	15
GTCGCAGGTCTTGGAGTTGT	24425	+	TGG	20	10
TGGTAAATGGAGTTTATTCG	31489	+	AGG	4	24
GATATTGGGGTTTTGTAACA	34524	+	TGG	5	23
GGAGATTTATTGAACGCTGC	24776	+	AGG	6	22
GAAACTAAAAATTAATTAAA	4599	+	AGG	23	6
TTACTTGAGTTTTCCCCTTG	13940	-	TGG	4	23
AAAATTAAAACTATTTCAGG	12663	+	TGG	15	13
GCTCCGCCACCATACTTTGA	38427	-	CGG	5	22
TGATAGCATGGTTGTTGAAT	21320	+	TGG	16	12
GAATCAGTCATCGATACTTG	30904	-	AGG	6	21
TTGCTTACTGGCGACTTCTC	25898	+	AGG	7	20
ATAGGCACGTTAGAGAAGCC	32419	+	TGG	7	20
CAAGGTATTATGAGTGGAGA	18153	+	GGG	8	19
AATAGGATCTGTGGTTTTGT	40170	-	TGG	8	19
TCGATAAGAAAATAGAAGAG	21349	+	TGG	13	14
GATTATTTAACGTATTTAAA	29819	+	TGG	13	14
AACCTTTTTAGGTATCTTGT	36476	-	AGG	15	12
CAACATCTCAAGAAGGGAAA	38034	+	TGG	15	12
CACTGGTGAAAAATATCCAG	33857	+	AGG	6	20
TATCCAGGTGGCGTTATTGA	33109	+	GGG	7	19
TTCGACTAAAGGTAAGAGTG	14665	+	GGG	9	17

GAAAGAATGACGAGTTTTAA	12729	+	TGG	20	7
AATACTGTCTTTAAAGGAAC	28070	+	GGG	10	16
CTGGCGACTTCTCAGGTGCT	25905	+	TGG	11	15
AGATTGCTTGTTAAAAACGG	30218	+	CGG	11	15
GATAGCGAAGATGGGAGAAA	22887	+	AGG	2	23
AAAATCATTAAATTTTCTAC	30415	-	CGG	5	20
GTAGGCAATAAAAAAGATTA	38923	+	TGG	6	19
CGAACCAAAAGAGCAAGAAC	30046	+	CGG	20	6
GATTCCAGCAGATGGAAATT	24065	+	AGG	2	22
TGTAGACTTTTTAATAAAAT	27718	-	TGG	2	22
GAACAAGTAGGACAATCACA	25094	+	AGG	3	21
TTGGCGACTCTGTAGCTAGA	28992	+	GGG	4	20
CTAAGTGATATTACGGAAGT	30986	+	TGG	16	9
ACGGCAGACTTGAGCAACAG	32966	+	TGG	7	17
ATGGCAGTACTTAATGCGGT	24359	+	TGG	12	12
TTCACTTTCTATACAGATAA	27493	+	AGG	15	9
AGTGCTGACGATATTGATAA	30518	+	AGG	5	18
ACTTCAATAACTAGCCAATT	35173	-	AGG	5	18
TATGTAAACTAATAGATCAA	22700	+	GGG	8	15
TTAATAGCCGGTGCGATTCA	39256	+	TGG	9	14
GTAGGAGTGAACTATATAGC	40021	+	CGG	9	14
GGGACCAACAGTCAGATACA	40035	-	TGG	9	14
ATTTATTCCATCGGCCAAAG	30869	+	AGG	5	17
GGTCTTGGAGTTGTTGGCTT	24431	+	TGG	17	6
AGTGGCATTTGGTACTGCAA	25195	+	TGG	7	15
TAATAGTTGGACAGGTTCTC	34750	+	CGG	7	15
TCACGTTCAAATAATGATAC	20329	-	TGG	12	10
ATCTCCAGCAAAAGCAATCA	36028	+	TGG	2	19
CAATAGTGGTTTTTTCAAGA	23108	+	GGG	3	18
ATACTTGCTGGTGCAACATT	15261	+	AGG	15	7
ACTTAAGGAGGAACAACAAA	942	+	TGG	16	6
TGCGTCAGATTTAAGTGATG	33560	+	AGG	8	13
AGGTGATTACCATGCTTAAA	34249	+	GGG	8	13
AGTTACTATAACTAAAATTA	33318	+	TGG	9	12
CCCTAACGAAAAAGGTCACG	29548	+	AGG	10	11
ATAGAAGAGTGGGTTAAAAA	21360	+	AGG	12	9
TTTTAGGAAAGCGAGCATGG	29515	+	AGG	2	18
ATTTTCGGAAAACGGATTAT	7203	+	CGG	4	16
TTCAACCCAGATGGTTGGTA	38245	+	TGG	4	16
TAATCCTGCAGAAGATATTA	20469	+	AGG	5	15
GTATTTTAGGTGGCGTATTT	25323	+	TGG	5	15
AAAAGAGTTGTCTCAAATGT	26258	+	AGG	6	14
AGGTGATGTTGTTAGAGTGG	28588	+	TGG	19	2
CAATGGACTTTACATTTGAA	19451	-	GGG	10	10
CTAGAATCATATTGCTAAAA	29826	-	CGG	11	9

CCTCGTGACCTTTTTCGTTA	29532	-	GGG	12	8
ATCAGTTACGTTCAAGAGAA	25130	+	TGG	15	5
ATGTATTACGATCTAGAAAC	30788	+	AGG	15	5
GTAGATGCATCTAAATTCGA	28118	+	GGG	6	13
GCAGCAGGAGAAAGCGCAAG	39001	+	TGG	6	13
TCAGGTACCGACCATTTTTC	27288	-	AGG	7	12
AAAGCCTACAGCTAGTGAAG	34408	+	TGG	9	10
GGCTTACACCCTAACGAAAA	29540	+	AGG	10	9
AATATTCAAGAAAAAGAAAA	1835	+	TGG	1	17
ATACTCATCGTCATTTAGAT	18364	+	GGG	1	17
GCAGTTTCCGGTGCGATTCA	25625	+	AGG	1	17
CTGCAAGTTTTTGGATAAAT	8536	-	AGG	4	14
AAAGGAAAAGGAACGCTCGA	35807	+	CGG	7	11
TCAATTGCAGGGTTCCAAAA	21635	-	TGG	9	9
ATATACGCGATATGAAAATG	34151	+	TGG	12	6
TAATGATGGAAGTATATTGT	7326	+	CGG	3	14
GGTAAATGGAGTTTATTCGA	31490	+	GGG	6	11
GTTTCAACTTATTATAAGGG	26739	+	AGG	9	8
AGAGTGGTGGATTCTGCCAT	28601	+	AGG	3	13
TTAATAACCTAGTAAGGTTA	6263	-	GGG	5	11
TACACGATTACTCAAAAATA	23259	+	AGG	5	11
GCCAATTATTACATTAAAGC	28262	+	TGG	6	10
GTTTTCGGAAAACGGAAAAA	7233	+	CGG	2	13
GTAAGCGATAAAACAATTAA	21065	+	AGG	14	2
GAAGAATATGCATTGATCAC	33840	+	TGG	6	9
TTCCAGCCTGGATATAAAAC	27618	-	CGG	9	6
TAAACTTAAATCTTTATATA	15068	+	CGG	10	5
GGATATTTATTTTTAGGTAA	37521	-	GGG	2	12
TGCTGGACGTTTTTATTTAA	27036	+	GGG	3	11
ATCGATGAGAACATCTAATG	14318	-	TGG	4	10
CCAGCAGTCGCTCAAATTAT	25292	+	CGG	4	10
GCTGGGTTCTGTATTGGTAA	30943	-	CGG	4	10
AGTGACCTAAAACGATTCAA	8760	+	AGG	6	8
TACACTTTTTAAAAATCGGA	14710	+	AGG	7	7
TTTAACTAGAATAACTGGGG	25435	+	TGG	7	7
CAATTTTTAGTTAGAAACTT	31454	+	TGG	9	5
TGATCAGAAAGCATAAAAAA	3041	+	TGG	1	12
AGACCATTATTTGATGCTAA	20141	+	CGG	1	12
TCCTAAATTAATAGGATCTG	40179	-	TGG	1	12
TTAAAAAGTCTACAGGGTGT	27743	+	AGG	2	11
TTCCCGTCAAAGTATGGTGG	38440	+	CGG	3	10
TTAAAAAGCGTTTTAGCGCT	1902	+	TGG	4	9
AAACACGCTGTACAAACAGG	22374	+	TGG	5	8
CTAAAGCTAAGAGTAATCAA	12509	+	AGG	7	6
CCCGAAAAAATCTCATACAT	35644	+	GGG	8	5

TTTTAGTCGTTTTTTTATTT	37834	+	TGG	8	5
ACTTTATTTTTAAAAGATAT	34509	+	TGG	9	4
CATAGAGGTGGTTAAATATG	21706	+	TGG	1	11
GCGGTTGGTGTATTAGGTGG	24374	+	TGG	2	10
ATTGGCGACTCTGTAGCTAG	28991	+	AGG	2	10
ATGTCTTACTTAACAAAAAA	6219	-	AGG	3	9
GAAAACGGATTATCGGCAAA	7210	+	CGG	3	9
AAATTTACTTACTTAGCAAA	19700	+	AGG	3	9
CAGGTGGACAGTTGCGTATA	22390	+	TGG	3	9
GATGATAGGAGATGCTGAAA	16999	+	AGG	4	8
AGACAAGCAGAGCAAATAAG	29147	+	AGG	5	7
GCTCTTAAAATGGTTGAAGA	24470	+	TGG	7	5
AGTAGATGCATCTAAATTCG	28117	+	AGG	2	9
AGCATAGGTGGCGCAATCTT	24755	+	CGG	3	8
GACACGGACAAAAACAAACT	29384	+	AGG	3	8
GAACTATTTTTGGTATTTAA	34226	+	AGG	3	8
ATTCATGGTAAGCCTATAGG	39271	+	TGG	3	8
AAAAATCTCATACATGGGGC	35649	+	TGG	5	6
GCGCACGCTTTCTTAGAAAG	35891	+	TGG	5	6
AATACAGCATCTATAAGAAT	36335	+	AGG	5	6
CTTAGTCATGAAATGGTAGG	3576	+	AGG	6	5
GAGGAGGTAGAACATGACTG	3805	+	AGG	6	5
TAACCAATTAAAGCAAAATA	32013	+	TGG	2	8
AATGTTGAAAGGAGAGAAAA	5843	+	AGG	3	7
CAGGCATTCTTTACACAAAA	31855	+	CGG	3	7
CACTACAGCATGGTCAATTG	3164	+	CGG	4	6
GTAATAACGACCCTGAAAAA	27293	+	TGG	4	6
AATGTTATGAATATCATACA	25778	+	AGG	5	5
GGTAGCGTTGAAAGTTATGA	32851	+	GGG	5	5
GCTAAGTTATATAAACAAAT	36170	+	CGG	5	5
ATTGAACTTGATGAAGCAGT	11805	+	AGG	6	4
CCGTTTTATAAAAAGAATGA	32611	+	TGG	1	8
CTATTTTTGGTATTTAAAGG	34229	+	AGG	1	8
AGTGCTTGCTGGAATGTGAA	35581	-	TGG	1	8
TTTTAGTTCTTTAGATGGGT	28772	-	CGG	3	6
GCTAACCTCCTTTCGATTCA	23571	-	AGG	4	5
AAATTCCTTGAATCGAAAGG	23582	+	AGG	4	5
TGGAAATCATATTTATACGG	4814	-	CGG	5	4
ATGGCAGCAATTTGCGGATA	16691	+	TGG	5	4
TTAAAGGTGATGACGGCGAA	21601	+	TGG	5	4
TTAGCTGACTTACAAGAAGG	22221	+	TGG	6	3
GGAGGTAGTAGCTTAGGTAA	26468	+	AGG	6	3
AAAGAAATCGTTAGCACTAA	20218	+	TGG	1	7
AAAGAATTCAATGAAGTCGA	24101	+	AGG	3	5
AAACGATTCAAAGGCGCTCA	8769	+	CGG	4	4

ATACTTTGCCGTTATTACAA	23068	+	GGG	4	4
ATATTGGGGTTTTGTAACAT	34525	+	GGG	4	4
CTGGATTTAACTAGAATAAC	25430	+	TGG	5	3
GAGTATAACGAAAGTTTTAC	28034	+	AGG	7	1
AAGATAAAGCGTTATTATAT	5590	+	TGG	2	5
GTACGTTTCCAATATAGAAC	30329	+	TGG	2	5
ATTTTCAATAAGAAAAACAA	31190	+	CGG	2	5
TTTGTTATTACAGGTCATGA	4292	+	AGG	3	4
GGATCACGTGAATGTTTTTG	9712	-	TGG	3	4
AAGCATAGAGGTCGAAAAAG	10878	+	TGG	3	4
AGTTCCAATAGGTAAAGAAG	29107	+	CGG	3	4
AATGCGTATAGATACATTGA	30254	+	TGG	3	4
CAGTATGTAGATGATAAATT	32692	+	CGG	3	4
AATAACTTAGGACAAATAAG	39094	+	AGG	3	4
TTTGTCACTTGGTATTGAAA	4945	+	TGG	4	3
TTGTTCGACGGTGGCGCAAA	33019	+	TGG	4	3
TTCCAATAGAAATAGTGTGA	20982	-	GGG	5	2
CGAGTACACTTTTTAAAAAT	14706	+	CGG	2	4
TATGGATCTATTGTGTTAAT	15852	+	AGG	2	4
GGACTGTTAGGGTACGCGAA	18898	+	GGG	2	4
TAACAAACTAGTTGATGATA	21791	+	GGG	2	4
TTCTCAGAAGATAGCGAAGA	22878	+	TGG	2	4
AAAGGTGAAGCAGGTAAAAA	36818	+	AGG	2	4
AATAGTACGAGGCGGTAAAA	22271	+	CGG	3	3
GGTATCTTATATTGGTATAC	30626	+	AGG	3	3
GGTATTGATAAAATTATTGA	6774	-	AGG	4	2
TTTTCTTTTCGTCGCTGAAA	8710	-	TGG	4	2
TAAACGCAACGATTGATATA	9279	+	AGG	1	4
TAGCCACTCATATTCTTCAA	14783	-	AGG	1	4
AACCTGAACGATTAAGGAGG	16258	+	GGG	1	4
GAAATGGAAGCTAAGAAAAT	19787	+	TGG	1	4
GATTAATATAGATAATTATC	34462	+	GGG	1	4
GTTTTAACTTCTTTAAATTG	34900	-	CGG	1	4
TTATCCAGGTGGCGTTATTG	33108	+	AGG	2	3
CAGCTAGTGAAGTGGTGGAG	34416	+	TGG	2	3
GGCAACGGAATAGGTTCGGA	34655	+	CGG	2	3
TAGCTATAACATAAAAAAAT	39779	-	AGG	2	3
GAGCGCCTTTGAATCGTTTT	8749	-	AGG	3	2
TATTCTATTTTGTTGGTAAG	33082	+	TGG	3	2
AGGGTACGCGAAGGGCAAAA	18906	+	AGG	4	1
GGTAATGTGCCTGGAGATAA	22338	+	AGG	4	1
GATTTCGTTACTAATTTAGC	25241	+	TGG	4	1
CATATGGCAAAAGTTAAGTA	21294	+	CGG	1	3
GTTAAAGCTAATGATAAGGA	27469	+	TGG	1	3
GGTGGCGTTATTGAGGGATT	33115	+	CGG	1	3

GAGGTGATTACCATGCTTAA	34248	+	AGG	1	3
ACCCGAAAAAATCTCATACA	35643	+	TGG	1	3
AACAAAGATAAAGATGATGA	4319	+	AGG	2	2
AAATGGAACAAGTGATATTT	24175	+	GGG	2	2
AAAGCGTTCGGTTTATTGAC	25463	+	TGG	2	2
CCAGAAGCTAACCCTAAAAT	28568	+	AGG	2	2
TCTCTAAACGCTTTCGGTAA	31039	-	CGG	2	2
AAAGTAGGTGGCGTAATGTT	33931	+	TGG	2	2
GGGGTGGTAAGTAAAGCGTT	25451	+	CGG	3	1
AGCGTCTTTAAAAATAAAAA	68	+	AGG	1	2
GCAAACGGGTTTTCGGAAAA	7225	+	CGG	1	2
GAATACTTAAATAAAAAAGC	7390	+	AGG	1	2
AATAATGGCAGTACTTAATG	24355	+	CGG	1	2
CTTTCAACATATTTTTCAAA	12695	-	AGG	2	1
CCCTTTAACCGCCATTTTAG	23981	-	CGG	2	1
AGATGAAGGTAAGTATTTTA	4979	+	CGG	1	1
ATGACGTTAATCTGGAAAGA	10685	+	TGG	1	1
GAAGCAGTAGGGATTATGAC	11817	+	GGG	1	1
GATGAAGAGTTAGATCCAAA	20060	+	CGG	1	1
TACTTTGCCGTTATTACAAG	23069	+	GGG	1	1
AAATTCGAGGGATTAGGCAA	28130	+	AGG	1	1
TATACCTTTATTAAAGGTTA	28331	+	TGG	1	1
TTTATCTATAAATAATGAAT	28837	+	TGG	1	1
TCCCAATAACCGGCGTTTTG	31213	-	CGG	1	1
CCCCATGTATGAGATTTTTT	35629	-	CGG	1	1
CTTACCTAAAAATAAATATC	37539	+	CGG	1	1
GTTATTTTTTGCGTTTTTTT	40223	+	GGG	1	1

Normalized Reads Replicate 1	Normalized Reads Replicate 2	Average Normalized Reads
20977.99342	19284.624	20131.30871
12308.04519	26456.03014	19382.03766
13757.15145	15393.20093	14575.17619
15522.44084	13018.90788	14270.67436
13012.88665	14008.41723	13510.65194
11554.22321	14885.87335	13220.04828
6163.579766	15525.54725	10844.56351
9487.484684	10255.51664	9871.50066
11383.38876	7679.616019	9531.502389
9513.766908	9325.563134	9419.665021
11032.56089	6368.505104	8700.532996
9407.045149	7830.049674	8618.547412
8327.881099	8380.610381	8354.24574
8479.999427	7547.71085	8013.855138
8157.046643	7162.141893	7659.594268
5536.390328	9206.451442	7371.420885
7007.000231	6749.221362	6878.110797
5103.530061	8396.933095	6750.231578
5557.49575	7826.079284	6691.787517
5485.816957	7597.120144	6541.468551
6319.680249	6581.582686	6450.631467
5942.96837	6520.262222	6231.615296
7425.922954	4999.161807	6212.54238
5019.108372	7309.046312	6164.077342
2801.844375	8839.410971	5820.627673
4677.041243	6844.510716	5760.775979
7498.796394	3804.956811	5651.876602
4609.344605	6286.450383	5447.897494
5999.514974	4791.819233	5395.667103
2660.079651	7835.784681	5247.932166
4196.79333	6129.399412	5163.096371
4499.835338	5675.010367	5087.422853
5790.850043	4351.988283	5071.419163
4873.361492	4589.329357	4731.345425
5029.063759	4413.308746	4721.186253
5932.216551	3062.493934	4497.355243
6138.093973	2850.298662	4494.196317
5620.812017	3189.105251	4404.958634
4659.121545	4037.445187	4348.283366
4686.996631	3883.923451	4285.460041
4581.469519	3884.364605	4232.917062
5217.021483	3162.635986	4189.828735
4461.208433	3850.83687	4156.022651
5312.593207	2885.14986	4098.871534

3402.353374	4570.800872	3986.577123
4217.102321	3682.757039	3949.92968
4142.636019	3682.757039	3912.696529
5087.999656	2736.039669	3912.019662
5671.783603	2052.691483	3862.237543
3641.6809	4035.239414	3838.460157
2987.811021	4488.304997	3738.058009
3839.873289	3634.970836	3737.422062
3888.176304	3581.732678	3734.954491
3526.994831	3910.392716	3718.693773
4232.632726	3146.313273	3689.472999
3646.857701	3429.093251	3537.975476
5118.662251	1877.994336	3498.328293
2684.769013	4278.75665	3481.762832
4017.596347	2945.588015	3481.592181
5021.89588	1720.50221	3371.199045
2613.886651	3991.565128	3302.725889
3244.261814	3359.390854	3301.826334
3348.594279	3188.222942	3268.408611
3371.690779	3128.225942	3249.95836
2871.930306	3498.354494	3185.1424
3079.798806	3257.04303	3168.420918
3377.664012	2814.124	3095.894006
3791.409934	2336.794925	3064.102429
2269.828445	3828.779149	3049.303797
2972.678832	3009.555405	2991.117118
2275.403462	3664.228553	2969.816008
1069.606878	4715.058365	2892.332621
2130.453014	3649.670458	2890.061736
4647.97151	1059.6529	2853.812205
4521.338976	1148.324937	2834.831956
2796.667573	2859.12175	2827.894662
2617.072375	2997.203081	2807.137728
2063.951023	3541.587627	2802.769325
1013.856705	4546.537379	2780.197042
3056.702306	2459.435852	2758.069079
2407.611014	3015.290412	2711.450713
2367.789462	2953.528794	2660.659128
3489.164357	1746.530321	2617.847339
2400.84135	2819.859007	2610.350178
456.7531976	4749.468409	2603.110803
2130.453014	3034.701206	2582.57711
3188.113426	1943.285189	2565.699307
1316.500498	3779.811009	2548.155754
2232.396186	2853.386742	2542.891464

3473.235736	1609.331298	2541.283517
2811.003332	2166.068167	2488.53575
3867.867313	1102.444878	2485.156095
3161.432987	1806.527321	2483.980154
661.8341886	4273.021643	2467.427916
3337.046029	1543.158136	2440.102083
3117.231064	1674.622151	2395.926608
2935.246573	1850.642762	2392.944668
2330.755419	2447.524683	2389.140051
3350.187141	1391.401018	2370.79408
1281.457533	3403.506295	2342.481914
2745.695987	1911.522071	2328.609029
2791.092556	1863.43624	2327.264398
3365.319331	1264.789702	2315.054516
2678.79578	1941.079417	2309.937598
1848.516428	2755.009308	2301.762868
2647.336755	1922.992086	2285.16442
2954.360918	1615.50746	2284.934189
2680.388642	1870.053556	2275.221099
2386.903807	2155.480461	2271.192134
2492.430919	1997.106027	2244.768473
2832.108754	1502.130776	2167.119765
2573.666884	1758.44149	2166.054187
324.9438616	3906.86348	2115.903671
1794.359118	2304.149498	2049.254308
2348.675117	1720.50221	2034.588664
2760.828177	1289.494349	2025.161263
2411.194953	1607.125526	2009.16024
43.40549131	3965.537017	2004.471254
2170.274566	1834.320049	2002.297307
2119.701195	1868.288938	1993.995067
2787.110401	1138.61954	1962.86497
2849.630237	1069.358297	1959.494267
1270.307498	2568.842146	1919.574822
2471.325496	1359.196746	1915.261121
2231.997971	1524.188496	1878.093234
2077.888566	1649.035195	1863.461881
2281.77491	1417.429129	1849.602019
1036.156774	2661.484573	1848.820674
2409.602091	1241.849672	1825.725882
2305.667841	1344.197496	1824.932669
2677.999349	870.838811	1774.41908
1641.44436	1856.377769	1748.911064
2570.082944	915.3954067	1742.739176
2950.378763	534.237994	1742.308378

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1579.322739	1856.377769	1717.850254
2089.0386	1330.521709	1709.780155
2445.441488	926.424267	1685.932877
2471.325496	897.7492302	1684.537363
1835.375316	1498.601541	1666.988428
1694.407023	1638.888644	1666.647834
1977.538256	1345.079805	1661.30903
864.5258866	2430.760815	1647.643351
2088.640385	1205.67501	1647.157698
2153.947729	1133.766841	1643.857285
1684.451635	1559.039695	1621.745665
2533.447117	644.5265972	1588.986857
1455.875929	1701.53257	1578.70425
1021.4228	2127.687733	1574.555267
1829.003868	1312.875533	1570.9397
1747.767902	1325.669011	1536.718457
1430.788351	1623.007085	1526.897718
1612.374627	1438.163386	1525.269006
1979.927549	1007.596679	1493.762114
2097.799342	875.2503551	1486.524848
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1244.423489	1725.796063	1485.109776
1227.698438	1735.50146	1481.599949
2474.113005	486.152163	1480.132584
432.0638355	2487.22858	1459.646208
742.273723	2175.773564	1459.023644
1005.494179	1899.610902	1452.552541
1521.979705	1344.63865	1433.309177
2254.696255	598.6465383	1426.671397
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1459.459868	1377.284077	1418.371973
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940.9832658	1832.555431	1386.769348
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1697.990963	967.4516274	1332.721295
1361.897067	1300.082055	1330.989561
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1568.172704	1016.860922	1292.516813

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2220.847936	336.600817	1278.724377
930.6296624	1603.155136	1266.892399
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1192.257257	1307.140525	1249.698891
1447.513403	1025.242856	1236.378129
442.417439	2029.751454	1236.084446
1658.965842	804.6656491	1231.815746
627.1894387	1811.821174	1219.505306
1396.143601	1040.242106	1218.192853
1224.114498	1184.940753	1204.527626
511.7069389	1868.288938	1189.997939
744.2648006	1619.919004	1182.091902
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1240.441334	1103.327187	1171.88426
847.4026194	1472.57343	1159.988025
1759.316152	551.0018617	1155.159007
258.0436548	2050.485711	1154.264683
1429.99192	877.4561272	1153.724024
852.5794211	1450.51571	1151.547565
1076.376541	1218.027334	1147.201938
1707.548135	576.1476632	1141.847899
1073.589033	1196.851922	1135.220477
705.2396799	1564.774702	1135.007191
1211.769817	1030.977863	1121.37384
584.9785939	1654.329048	1119.653821
1533.527955	704.0824429	1118.805199
1109.030214	1118.767591	1113.898902
1653.390825	565.1188029	1109.254814
1222.521636	992.1562745	1107.338955
450.7799648	1718.296438	1084.538201
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1353.932757	790.9898623	1072.461309
433.2584821	1693.591791	1063.425137
1724.273187	392.186273	1058.22973
507.7247837	1591.685122	1049.704953
502.9461975	1578.891644	1040.918921
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547.5463354	1514.483099	1031.014717
1194.248334	850.9868624	1022.617598
1036.55499	997.8912819	1017.223136
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1469.415256	507.7687292	988.5919928
1558.615532	406.3032143	982.4593732
929.0368003	1035.389407	982.2131036
1345.968446	617.1750236	981.5717349
1433.57586	513.0625822	973.319221
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1258.759248	676.7308693	967.7450587
478.655051	1431.54607	955.1005604
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1211.769817	683.3481855	947.5590013
1188.275102	697.4651267	942.8701142
1189.071533	694.3770459	941.7242893
1045.315731	824.5175976	934.9166644
966.0708433	900.3961567	933.2335
1393.754308	468.9471409	931.3507245
1369.463162	472.0352218	920.7491917
1027.396033	813.0475829	920.2218079
1209.380524	624.6746486	917.0275863
738.6897833	1085.68101	912.1853967
893.1974038	915.3954067	904.2964052
1634.27648	172.050221	903.1633506
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1248.405645	541.737619	895.0716318
1348.755955	434.9782511	891.867103
1031.776404	739.8159504	885.796177
1116.596309	652.4673766	884.5318426
884.0384469	879.2207448	881.6295959
868.1098262	871.7211198	869.915473
385.0744046	1351.255967	868.1651856
350.4296546	1364.931753	857.680704
1044.121085	642.3208251	843.2209549
638.7376887	1038.036333	838.3870111
734.3094127	931.2769656	832.7931891
496.5747492	1165.971113	831.2729312
811.1650074	850.9868624	831.0759349
476.6639734	1183.61729	830.1406316
1146.860688	510.4156557	828.6381718
1124.560619	528.944141	826.75238
714.3986368	921.1304141	817.7645254
855.3669297	777.7552299	816.5610798

720.7700851	904.3665464	812.5683157
832.2704298	787.460627	809.8655284
880.8527228	738.4924871	809.672605
789.6613695	813.0475829	801.3544762
1163.58574	436.3017143	799.943727
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964.4779813	626.8804207	795.679201
1231.282377	350.2766038	790.7794906
997.5298692	581.8826706	789.7062699
1238.848472	330.8658097	784.8571409
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827.093628	728.3459356	777.7197818
891.6045417	658.202384	774.9034629
942.5761279	603.4992368	773.0376823
384.2779735	1158.030334	771.1541537
743.4683695	794.0779432	768.7731564
1028.590679	502.9160307	765.7533551
1218.539481	311.0138611	764.776671
716.7879299	805.9891123	761.3885211
767.3613005	743.3451857	755.3532431
348.8367926	1157.148025	752.9924088
246.8936203	1255.084305	750.9889625
418.1262925	1080.387157	749.2567248
1065.624722	432.772479	749.1986008
420.11737	1067.593679	743.8555246
583.7839474	903.925392	743.8546697
949.7440072	535.1203028	742.432155
721.5665161	743.7863401	732.6764281
743.4683695	718.6405386	731.0544541
732.7165506	727.0224724	729.8695115
1320.482653	134.9932503	727.7379517
616.0394042	832.8995315	724.4694679
1078.765835	370.1285524	724.4471935
565.4660336	879.2207448	722.3433892
961.6904727	481.2994644	721.4949685
930.6296624	502.4748763	716.5522693
592.9429043	835.9876124	714.4652583
819.1293177	607.4696265	713.2994721
283.5294478	1131.119915	707.3246812
214.2399479	1199.057694	706.6488211
1281.059317	125.7290077	703.3941623
935.4082486	465.4179056	700.4130771
923.0635675	472.4763762	697.7699719
375.9154477	1019.507848	697.7116479
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138.5789998	1221.997724	680.2883617
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398.6137321	916.2777155	657.4457238
388.2601287	924.6596494	656.459889
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189.5505859	996.1266643	592.8386251
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389.8529908	379.3927951	384.6228929
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478.655051	189.2552431	333.9551471
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216.629241	154.4040445	185.5166428
228.9739221	141.1694121	185.0716671
13.53932757	356.0116112	184.7754694
127.8271808	241.3114638	184.5693223
196.3202497	172.4913754	184.4058126
242.5132496	126.1701621	184.3417059
252.8668531	114.2589929	183.562923
277.5562151	88.67203699	183.114126
314.5902581	50.73275748	182.6615078
193.5327411	171.1679122	182.3503266
234.9471548	124.4055444	179.6763496
146.5433101	210.8718094	178.7075597
283.5294478	72.79047812	178.159963
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174.8166118	179.9910004	177.4038061
40.6179827	311.8961699	176.2570763
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223.0006893	127.9347797	175.4677345
131.4111205	219.2537432	175.3324318
58.93589646	291.6030669	175.2694817
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142.9593705	206.4602652	174.7098178
102.7396033	245.723008	174.2313056

323.749215	24.26349271	174.0063539
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212.2488704	134.5520959	173.4004831
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133.4021981	207.342574	170.3723861
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214.6381635	118.2293826	166.4337731
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281.9365858	49.85044865	165.8935172
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62.91805163	266.4572654	164.6876585
161.6754998	167.6386769	164.6570883
246.4954048	79.40779432	162.9515996
168.843379	157.050971	162.947175
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256.8490082	67.49662517	162.1728167
77.65202574	245.723008	161.6875169
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73.27165506	240.429155	156.850405
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119.464655	175.1383019	147.3014784
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219.4167497	62.64392663	141.0303381
237.3364479	44.11544129	140.7259446
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37.03404305	92.20127229	64.61765767
76.45737919	52.49737513	64.47737716
107.5181895	21.17541182	64.34680065
82.43061194	45.88005894	64.15533544
5.176801716	123.0820812	64.12944145
95.17350847	32.20427214	63.68889031
77.65202574	49.40929424	63.53065999
36.63582753	89.1131914	62.87450946
57.34303439	68.37893399	62.86098419
13.53932757	112.0532209	62.79627422
94.37707744	30.8808089	62.62894317
53.75909474	71.46701488	62.61305481
87.20919814	37.49812509	62.35366162
52.56444819	71.9081693	62.23630875

63.71448266	60.43815456	62.07631861
59.73232749	64.40854428	62.07043589
57.74124991	65.2908531	61.51605151
39.02512063	83.81933844	61.42222954
62.51983611	59.55584574	61.03784092
34.24653443	87.78972816	61.0181313
43.40549131	78.52548549	60.9654884
69.28949989	51.17391189	60.23170589
83.22704298	37.05697068	60.14200683
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62.12162059	57.35007367	59.73584713
21.5036379	97.93627966	59.71995878
25.88400858	93.08358112	59.48379485
68.89128438	49.85044865	59.37086652
48.58229303	70.14355165	59.36292234
64.51091369	52.93852954	58.72472162
41.41441373	75.87855901	58.64648637
48.18407751	68.82008841	58.50208296
25.08757755	91.76011788	58.42384771
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69.68771541	45.88005894	57.78388717
37.43225856	78.08433108	57.75829482
29.46794823	86.02511051	57.74652937
65.70556024	49.40929424	57.55742724
49.37872406	65.2908531	57.33478858
82.43061194	31.76311773	57.09686483
42.60906028	71.46701488	57.03803758
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71.28057748	42.35082364	56.81570056
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41.01619821	70.14355165	55.57987493
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37.83047408	71.02586047	54.42816728
29.86616375	78.9666399	54.41640183
39.02512063	69.70239723	54.36375893

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39.02512063	68.82008841	53.92260452
68.89128438	37.93927951	53.41528194
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62.91805163	43.23313246	53.07559204
64.51091369	41.46851481	52.98971425
36.23761201	69.70239723	52.97000462
89.59849124	16.32271328	52.96060226
38.2286896	67.05547076	52.64208018
64.51091369	40.14505157	52.32798263
62.51983611	41.46851481	51.99417546
46.59121545	57.35007367	51.97064456
23.892931	79.84894873	51.87093986
51.76801716	51.61506631	51.69154173
19.51256031	83.81933844	51.66594938
38.62690511	64.40854428	51.5177247
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43.40549131	56.02661043	49.71605087
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23.09649996	75.4374046	49.26695228
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62.12162059	33.08658097	47.60410078
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31.0608103	63.96738987	47.51410008
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53.75909474	39.26274275	46.51091874
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27.87508616	64.40854428	46.14181522
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43.0072758	48.085831	45.5465534
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38.2286896	52.05622072	45.14245516
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42.60906028	43.67428687	43.14167358
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13.53932757	72.34932371	42.94432564
54.95374129	30.8808089	42.9172751
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46.19299993	34.85119862	40.52209927
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13.93754308	29.55734566	21.74744437
26.68043961	16.76386769	21.72215365
15.53040515	27.79272801	21.66156658
7.964310333	34.85119862	21.40775447
9.158956882	33.52773538	21.34334613
2.3892931	40.14505157	21.26717234
15.13218963	27.3515736	21.24188161
10.35360343	31.76311773	21.05836058
16.7250517	25.14580153	20.93542662
9.158956882	32.64542655	20.90219172
20.30899135	21.17541182	20.74220158
3.982155166	37.49812509	20.74014013
27.07865513	14.11694121	20.59779817
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13.14111205	27.79272801	20.46692003
38.2286896	2.646926477	20.43780804
11.15003447	29.55734566	20.35369006
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24.68936203	15.88155886	20.28546045

37.03404305	3.529235303	20.28163917
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9.158956882	30.8808089	20.01988289
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17.52148273	22.49887506	20.01017889
1.991077583	37.93927951	19.96517854
35.44118098	4.411544129	19.92636255
36.23761201	3.529235303	19.88342366
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1.592862067	37.93927951	19.76607079
18.31791376	21.17541182	19.74666279
13.93754308	25.14580153	19.54167231
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31.0608103	7.940779432	19.50079486
23.09649996	15.88155886	19.48902941
3.185724133	35.73350744	19.45961579
18.31791376	20.29310299	19.30550838
15.92862067	22.49887506	19.21374786
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17.91969825	20.29310299	19.10640062
17.91969825	19.85194858	18.88582341
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27.87508616	9.705397083	18.79024162
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13.53932757	23.82233829	18.68083293
14.73397412	22.49887506	18.61642459
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9.158956882	23.38118388	16.27007038
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3.982155166	22.49887506	13.24051511
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21.90185341	4.411544129	13.15669877
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13.14111205	7.499625019	10.32036853
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0.398215517	7.499625019	3.948920268
1.592862067	6.17616178	3.884511923
2.787508616	4.852698542	3.820103579
3.58393965	3.970389716	3.777164683
4.7785862	2.646926477	3.712756338
1.19464655	6.17616178	3.685404165
2.3892931	4.852698542	3.620995821
3.58393965	3.529235303	3.556587476
1.19464655	5.735007367	3.464826959
1.991077583	4.852698542	3.421888062
1.991077583	4.852698542	3.421888062
2.3892931	4.411544129	3.400418614
0.796431033	5.735007367	3.2657192
5.575017233	0.882308826	3.228663029
2.3892931	3.970389716	3.179841408
3.58393965	2.646926477	3.115433063
3.982155166	2.205772064	3.093963615
0.796431033	5.293852954	3.045141994
1.19464655	4.852698542	3.023672546
1.592862067	4.411544129	3.002203098
1.592862067	4.411544129	3.002203098
1.592862067	4.411544129	3.002203098
2.3892931	3.529235303	2.959264201
2.787508616	3.08808089	2.937794753
2.787508616	3.08808089	2.937794753
3.58393965	2.205772064	2.894855857
0.398215517	5.293852954	2.846034236
0.398215517	5.293852954	2.846034236
0.398215517	5.293852954	2.846034236
0.796431033	4.852698542	2.824564787
1.19464655	4.411544129	2.803095339
1.592862067	3.970389716	2.781625891
1.991077583	3.529235303	2.760156443
2.787508616	2.646926477	2.717217547
3.185724133	2.205772064	2.695748099

3.185724133	2.205772064	2.695748099
3.58393965	1.764617651	2.674278651
0.398215517	4.852698542	2.625457029
0.796431033	4.411544129	2.603987581
0.796431033	4.411544129	2.603987581
1.19464655	3.970389716	2.582518133
1.19464655	3.970389716	2.582518133
1.19464655	3.970389716	2.582518133
1.19464655	3.970389716	2.582518133
1.592862067	3.529235303	2.561048685
1.991077583	3.08808089	2.539579237
2.787508616	2.205772064	2.49664034
0.796431033	3.970389716	2.383410375
1.19464655	3.529235303	2.361940926
1.19464655	3.529235303	2.361940926
1.19464655	3.529235303	2.361940926
1.19464655	3.529235303	2.361940926
1.991077583	2.646926477	2.31900203
1.991077583	2.646926477	2.31900203
1.991077583	2.646926477	2.31900203
2.3892931	2.205772064	2.297532582
2.3892931	2.205772064	2.297532582
0.796431033	3.529235303	2.162833168
1.19464655	3.08808089	2.14136372
1.19464655	3.08808089	2.14136372
1.592862067	2.646926477	2.119894272
1.592862067	2.646926477	2.119894272
1.991077583	2.205772064	2.098424824
1.991077583	2.205772064	2.098424824
1.991077583	2.205772064	2.098424824
2.3892931	1.764617651	2.076955376
0.398215517	3.529235303	1.96372541
0.398215517	3.529235303	1.96372541
0.398215517	3.529235303	1.96372541
1.19464655	2.646926477	1.920786514
1.592862067	2.205772064	1.899317065
1.592862067	2.205772064	1.899317065
1.991077583	1.764617651	1.877847617
1.991077583	1.764617651	1.877847617
1.991077583	1.764617651	1.877847617
2.3892931	1.323463239	1.856378169
2.3892931	1.323463239	1.856378169
0.398215517	3.08808089	1.743148203
1.19464655	2.205772064	1.700209307
1.592862067	1.764617651	1.678739859

1.592862067	1.764617651	1.678739859
1.592862067	1.764617651	1.678739859
1.991077583	1.323463239	1.657270411
2.787508616	0.441154413	1.614331515
0.796431033	2.205772064	1.501101549
0.796431033	2.205772064	1.501101549
0.796431033	2.205772064	1.501101549
1.19464655	1.764617651	1.479632101
1.19464655	1.764617651	1.479632101
1.19464655	1.764617651	1.479632101
1.19464655	1.764617651	1.479632101
1.19464655	1.764617651	1.479632101
1.19464655	1.764617651	1.479632101
1.19464655	1.764617651	1.479632101
1.592862067	1.323463239	1.458162653
1.592862067	1.323463239	1.458162653
1.991077583	0.882308826	1.436693204
0.796431033	1.764617651	1.280524342
0.796431033	1.764617651	1.280524342
0.796431033	1.764617651	1.280524342
0.796431033	1.764617651	1.280524342
0.796431033	1.764617651	1.280524342
0.796431033	1.764617651	1.280524342
1.19464655	1.323463239	1.259054894
1.19464655	1.323463239	1.259054894
1.592862067	0.882308826	1.237585446
1.592862067	0.882308826	1.237585446
0.398215517	1.764617651	1.081416584
0.398215517	1.764617651	1.081416584
0.398215517	1.764617651	1.081416584
0.398215517	1.764617651	1.081416584
0.398215517	1.764617651	1.081416584
0.398215517	1.764617651	1.081416584
0.796431033	1.323463239	1.059947136
0.796431033	1.323463239	1.059947136
0.796431033	1.323463239	1.059947136
0.796431033	1.323463239	1.059947136
1.19464655	0.882308826	1.038477688
1.19464655	0.882308826	1.038477688
1.592862067	0.441154413	1.01700824
1.592862067	0.441154413	1.01700824
1.592862067	0.441154413	1.01700824
0.398215517	1.323463239	0.860839378
0.398215517	1.323463239	0.860839378
0.398215517	1.323463239	0.860839378

0.398215517	1.323463239	0.860839378
0.398215517	1.323463239	0.860839378
0.796431033	0.882308826	0.839369929
0.796431033	0.882308826	0.839369929
0.796431033	0.882308826	0.839369929
0.796431033	0.882308826	0.839369929
0.796431033	0.882308826	0.839369929
0.796431033	0.882308826	0.839369929
1.19464655	0.441154413	0.817900481
0.398215517	0.882308826	0.640262171
0.398215517	0.882308826	0.640262171
0.398215517	0.882308826	0.640262171
0.398215517	0.882308826	0.640262171
0.796431033	0.441154413	0.618792723
0.796431033	0.441154413	0.618792723
0.398215517	0.441154413	0.419684965
0.398215517	0.441154413	0.419684965
0.398215517	0.441154413	0.419684965
0.398215517	0.441154413	0.419684965
0.398215517	0.441154413	0.419684965
0.398215517	0.441154413	0.419684965
0.398215517	0.441154413	0.419684965
0.398215517	0.441154413	0.419684965
0.398215517	0.441154413	0.419684965
0.398215517	0.441154413	0.419684965
0.398215517	0.441154413	0.419684965
0.398215517	0.441154413	0.419684965

ATGAATGGATTGAAGAGAACACAGACGAAC			**Uncut Band**		
Cas9 Concentration (nM)		**replicate 1**	**replicate 2**	**replicate 3**	**replicate 1**
	6.25	3340	3453	2522	123
	12.5	3103	3220	2411	276
	25	2416	2844	2078	471.5
	50	2416	2023	1746	471.5
	100	1896	1310	1135	932

AGAAATTATCGAATACTTAAATAAAAAAGC			**Uncut Band**		
Cas9 Concentration (nM)		**replicate 1**	**replicate 2**	**replicate 3**	**replicate 1**
	6.25	1464	2182	2336	26.5
	12.5	1619	1603	2276	61
	25	1484	1577	2264	167.5
	50	1225	1174	1681	416
	100	608	492	905	788.5

ATACGTGTAAAGACATATTAGATCGAGTCA			**Uncut Band**		
Cas9 Concentration (nM)		**replicate 1**	**replicate 2**	**replicate 3**	**replicate 1**
	6.25	1059	909	778	126
	12.5	817	658	747	241.5
	25	730	491	581	303
	50	226	308	258	407.5
	100	163	48	163	401.5

CGTGTAAAGACATATTAGATCGAGTCAAGG			**Uncut Band**		
Cas9 Concentration (nM)		**replicate 1**	**replicate 2**	**replicate 3**	**replicate 1**
	6.25	2064	1505	1505	148
	12.5	1899	1079	1836	333
	25	1622	839	1698	549
	50	1285	577	1142	744.5
	100	339	209	987	894.5

Cut Band		Percentage Cut			Average	St. Dev.
replicate 2	**replicate 3**	**replicate 1**	**replicate 2**	**replicate 3**		
140.5	94.5	3.55183367	3.909837206	3.611695012	3.691121963	0.19176317
282	217.5	8.16809707	8.052541405	8.274681377	8.165106617	0.111100175
505.5	359	16.32900433	15.09180475	14.73122692	15.384012	0.838010723
797	410	16.32900433	28.26241135	19.01669759	21.20270442	6.259833878
1011	653.5	32.95615276	43.55881086	36.53899916	37.68465426	5.393374073

Cut Band		Percentage Cut			Average	St. Dev.
replicate 2	**replicate 3**	**replicate 1**	**replicate 2**	**replicate 3**		
56.5	47.5	1.77792687	2.524011615	1.992867632	2.098268706	0.38404772
90	73	3.630952381	5.316007088	3.107705407	4.018221625	1.153963682
215	222	10.14229488	11.99776786	8.930008045	10.35669026	1.545076568
481	436.5	25.3503961	29.06344411	20.61393152	25.00925724	4.235073497
666.5	858.5	56.46258503	57.53129046	48.68159909	54.2251582	4.830509132

Cut Band		Percentage Cut			Average	St. Dev.
replicate 2	**replicate 3**	**replicate 1**	**replicate 2**	**replicate 3**		
110.5	80	10.63291139	10.8386464	9.324009324	10.26518904	0.821551071
190.5	128.5	22.81530468	22.4513848	14.67732724	19.9813389	4.597011444
273.5	231.5	29.33204259	35.77501635	28.49230769	31.19978888	3.984447074
326.5	337.5	64.32517758	51.45784082	56.67506297	57.48602713	6.471888133
428	439	71.12488928	89.91596639	72.92358804	77.9881479	10.36887022

Cut Band		Percentage Cut			Average	St. Dev.
replicate 2	**replicate 3**	**replicate 1**	**replicate 2**	**replicate 3**		
82.5	90.5	6.690777577	5.196850394	5.672203071	5.853277014	0.763246642
128	198	14.91935484	10.6048053	9.734513274	11.75289114	2.776548456
232	324	25.28788577	21.66199813	16.02373887	20.99120759	4.668358853
411.5	570	36.68391229	41.6287304	33.29439252	37.20234507	4.191285766
495.5	769	72.5172274	70.33356991	43.79271071	62.21450267	15.99105701

Spacer	Replicate 1	Replicate 2	Replicate 3
None (control)	45000000000	30000000000	30000000000
ATGAATGGATTGAAGAGAACACAGACGAAC	750000	400000	900000
AGAAATTATCGAATACTTAAATAAAAAAGC	1500000	950000	1400000

Spacer	Replicate 1	Replicate 2	Replicate 3
None (control)	55000000000	55000000000	50000000000
CGTGTAAAGACATATTAGATCGAGTCAAGG	450000	450000	750000
ATACGTGTAAAGACATATTAGATCGAGTCA	1150000	900000	850000

Average	StDev
35000000000	8660254038
683333.3333	256580.072
1283333.333	292973.2639

Average	StDev
53333333333	2886751346
550000	173205.0808
966666.6667	160727.5127

Sample	Oligo	Number of Reads		
		Replicate 1	Replicate 2	Replicate 3
1	ATGAATGGATTGAAGAGAACACAGACGAAC	31	29	25
	AGAAATTATCGAATACTTAAATAAAAAAGC	1	1	1
2	CGTGTAAAGACATATTAGATCGAGTCAAGG	36	6	43
	ATACGTGTAAAGACATATTAGATCGAGTCA	0	0	1

Percent Acquired			Percent Acquired	St. Dev.
Replicate 1	Replicate 2	Replicate 3		
96.875	96.666667	96.153846	96.56517094	0.371135763
3.125	3.3333333	3.8461538	3.43482906	0.371135763
100	100	97.727273	99.24242424	1.312159703
0	0	2.2727273	0.757575758	1.312159703

Oligo	Number of Reads			Pe
	Replicate 1	Replicate 2	Replicate 3	Replicate 1
ATGAATGGATTGAAGAGAACACAGACGAAC	103	115	122	23.409091
ATGAATGGATGAATACTTAAACAGACGAAC	58	65	66	13.181818
AGAAATTATCGAATACTTAAACAGACGAAC	52	59	51	11.818182
AGAAATTATCTGAAGAGAACACAGACGAAC	62	44	55	14.090909
AGAAATTATCGAATAAGAACACAGACGAAC	59	52	14	13.409091
ATGAATGGATTGAAGAGAACATAAAAAAGC	27	19	18	6.1363636
ATGAATGGATGAATACTTAAATAAAAAAGC	14	32	17	3.1818182
ATGAATGGATTGAAGCTTAAATAAAAAAGC	26	8	25	5.9090909
AGAAATTATCGAATACTTAAATAAAAAAGC	19	12	26	4.3181818
AGAAATTATCTGAAGAGAACATAAAAAAGC	20	22	15	4.5454545

rcent Acquired		Percent Acquired	St. Dev.
Replicate 2	Replicate 3		
26.869159	29.828851	26.70236688	3.213128401
15.186916	16.136919	14.8352178	1.508616697
13.785047	12.469438	12.69088873	1.001957998
10.280374	13.447433	12.60623856	2.039791779
12.149533	3.4229829	9.660535501	5.438466576
4.4392523	4.400978	4.992197989	0.991061301
7.4766355	4.1564792	4.938310971	2.25162378
1.8691589	6.1124694	4.630239742	2.393327465
2.8037383	6.3569682	4.492962784	1.783051308
5.1401869	3.6674817	4.451041041	0.740878278

Spacer Sequence	Location	PAM	Early Time Point Reads	Late Time Point Reads
CAATCCATTCATCTATTGCT	3503	TGG	11641	220287
TTTTAATAACCTCAACATCT	1070	TGG	9243	181490
CGTTCCATTGAATACTGTGT	2368	AGG	7845	223481
TGAAGCATAATACTGCTACT	3088	AGG	7621	125781
ATAAAAAAACTGCTACTTGT	3239	TGG	7600	121667
AAACATGTTGCGATGATGTC	2048	AGG	6812	172152
GCGCTTCAATAGTGATAGTA	4338	GGG	5691	39818
AGTATGCTTACTTTTTCTTG	3823	TGG	5401	105921
TTCAAAAGTTTAGTATCTAT	698	AGG	5120	40111
AGAAAAACAAACAACTTAAT	2524	AGG	5040	125782
TCTGATGAATATTCATCTCT	1424	CGG	5034	177336
GTAGAAGTACAGTATACAAC	2918	TGG	4662	81725
ACTTTCCATTACTTAAATCA	17090	CGG	4462	82822
AGCAATTCACACCCGCACAG	998	TGG	4211	100312
TGAAGAGAACACAGACGAAC	3540	AGG	4123	99045
TAGAGATATAGAACTTCACT	5384	GGG	4084	84992
TACATTGATTATTCACCAAC	2983	AGG	3955	111321
TGTACACGAGCATAGCTACC	23485	AGG	3773	170810
ATTGGAGCATGCAAATAACT	1407	TGG	3728	65144
ACACCTCAATATATACTTGC	15249	TGG	3409	71755
TTGATTTCGTGCCACTGTGC	993	GGG	3245	67452
GTCAGTATGTACAGATTAAT	4241	AGG	3211	82107
ATTAATTATGCTCGTAAGAA	1241	CGG	3108	94112
ACTTTATCTAACATGATACA	804	CGG	3077	55382
AGCAATTCACACCCGCACAG	998	TGG	3017	34010
GTGAATTGCTAGTAGTGTGT	1181	TGG	2881	63717
TTAGAATTGACACCTCAAGA	873	AGG	2640	91081
ATTGAATTAGTTACTCGATT	4866	AGG	2583	92039
TACATTGATTATTCACCAAC	2983	AGG	2544	52290
AGTAAGACGCCAAAAGTAAC	2465	AGG	2451	25848
AGATGAAAAAACGACTATAA	165	AGG	2413	32340
AGCAATTCACACCCGCACAG	998	TGG	2334	28651
AATAAGGAGTTAACTCGTAT	17877	AGG	2316	55672
ATAAAAAAACTGCTACTTGT	3239	TGG	2173	55155
TGAAGCATAATACTGCTACT	3088	AGG	2072	58120
AATTTAAGTGCTAAAGCTAA	6970	AGG	1908	47371
AAATTACCTGACATAGATGA	17645	AGG	1867	78248
AAACAATAAAACTTTTATGG	11602	AGG	1840	55614
CATTAACGAAGGTGGAACAA	3991	CGG	1816	41668
CATATTAGATCGAGTCAAGG	12415	AGG	1803	16873
TTTTTTACCTCAAATTTTAC	4075	AGG	1748	83851
GAGAACAAAACCATCCTACC	827	CGG	1711	89221
TTCATTTTAAAAGGTCATAT	3400	GGG	1663	10348
CTTTATCTAACATGATACAC	805	GGG	1659	62364

CATTAACGAAGGTGGAACAA	3991	CGG	1654	30996
ACTTTATCTAACATGATACA	804	CGG	1629	64525
ATTAGAGCCTCAATATGCTT	16315	AGG	1620	69342
ACGTGTAGTTAATACTCCGT	20059	TGG	1591	68130
AAGTTACTACTCACACACTA	259	AGG	1557	87758
ATTAAACGAATGAACTCAAT	18056	AGG	1544	9831
ATTGGAGCATGCAAATAACT	1407	TGG	1501	16770
AAGAAATCGTTAGCACTAAT	20219	GGG	1482	2615
TTAATACGTCCATCAACAAG	28432	CGG	1470	69662
TCTAAATTCAGTGATGTATT	15995	AGG	1464	55595
ACACCTCAATATATACTTGC	15249	TGG	1462	69532
CCACACCCTTGCGTTTAATA	2334	AGG	1442	53782
CAAAAAGCTGAAGAAAATAA	5073	CGG	1386	65236
ACAACATCGTCGATAATAAG	36439	GGG	1356	67907
TCTTTTCGATTCGATCTAAA	17217	TGG	1331	51710
AAATAAAAAGATGCAACAAT	399	GGG	1319	31521
AAACAATCAAGAGAAAAACA	500	AGG	1300	7027
GGATCTAAGTCAGTTTCAGC	22166	TGG	1268	63346
TGAATCAATCACACTTATTG	12809	AGG	1266	39587
AAATTCCACTTTGTTATTAC	4283	AGG	1255	365
GATTCCAATACTACGTTAAT	1461	AGG	1239	27552
GAGTCAATTGTTAATATGAT	13836	AGG	1192	457
AAGAAAGTTTTAACTTAAGG	930	AGG	1191	214
GCATACACACATAAGTTTAT	237	TGG	1185	26573
TTTAGTTTTTAAAAATTCTT	8442	TGG	1173	28991
TCTAAAAAACCTAAGTCAAC	21416	AGG	1171	57115
AGAAAAACAAACAACTTAAT	2524	AGG	1155	271
TAATTTATACGTAGACCTTT	20017	CGG	1153	1616
AGATGAGAATGACTTAGATA	3480	TGG	1140	45738
TACGAGTGAACTTAAATATC	17454	AGG	1134	54375
TCCAATTGATCCGTGCCAGT	7596	TGG	1133	46544
TCTCCCCAATCATTAAACGT	4186	TGG	1099	6284
TAACCGTATCGATTAAGATA	40130	CGG	1084	54015
ACGTGTAGTTAATACTCCGT	20059	TGG	1069	32629
AGTAAGACGCCAAAAGTAAC	2465	AGG	1062	37539
CGCTGATAAAAGTAAACTAT	16058	CGG	1056	55948
TTTGATACCAATGATCTTAT	4917	TGG	1052	23591
ATCATCAACACTATTTCTAA	16631	TGG	1051	47347
ATTGGTCGACGTTTGAATAT	16411	TGG	1044	43673
ATTAGAGCCTCAATATGCTT	16315	AGG	1027	16084
ATTTCCTAATTTCCATCTGC	24053	TGG	1007	35972
AACGCTTAAACCAACTGAAT	20431	AGG	1004	803
ATTTAAGTGCTAAAGCTAAA	6971	GGG	996	17644
AAGTAGCGCAATGAGTATGT	16792	AGG	992	892
ATTAAACAATAAAACTTTTA	11599	TGG	991	55660

TATTGAAGAAAGGTTATAAC	14104	AGG	979	33749
CATGCCTACACAGTATTCAA	2380	TGG	971	17652
AACACCTATTAACGTAGTAT	1449	TGG	970	29057
GGATATCGAAAAAGAAGCGC	9340	TGG	953	15822
TTTTAAAAATCGGAAGGTTT	14717	CGG	952	46518
ATCTAATCGAACAAGAAGTA	19145	CGG	951	34436
CACCTTAAAACGCTAAATCT	5152	TGG	927	37572
AAAAATAATCATGCGAGTTG	9227	AGG	924	40368
AGTGGTATAGGAGCTATACG	15408	TGG	913	39382
TATAGTTGGGATCAATGTTG	13006	AGG	899	231
CGCTAACATAAAGAACATAT	38272	TGG	892	6315
GACACCAATTTCTTCAGAAA	756	GGG	892	203
AACTAAGTAACACTGAATTA	23899	TGG	883	48211
GCATAAAAAATGGTATTAGG	3051	AGG	880	17411
TGCCAAGGAAATCCTATGCA	338	AGG	872	263
GATTCACCCACAACAATATA	21830	TGG	871	19576
CTTAGACCAGAAACACTTTT	7552	TGG	846	10051
TACCCATACCGCGTAACACA	17082	AGG	844	24605
GGACAAAAATCAATCAATAG	7069	TGG	821	16777
CCCTATAATGTTATTTTTGT	16769	TGG	820	32970
GTAGAAGTACAGTATACAAC	2918	TGG	812	15450
AAGAGGTATTTAAATATGTT	16156	TGG	804	38024
ATTAAACAATAAAACTTTTA	11599	TGG	802	44412
AAGATTTAATAGATCTTAGC	24027	AGG	801	26657
GTCAAGATGTATTACGAAAT	3328	AGG	793	36730
TGCTAAAGTCATATATACTA	39930	CGG	792	11506
ATAATAAAATTATACCAGAA	6865	AGG	778	29041
TTTTGTATGCGTCAATGAGT	12308	TGG	771	21751
TATATGACGCAAGCTCGTCC	30146	AGG	770	41224
TTTGTTCGGCGAACTTCAAA	2724	AGG	765	5235
TAACTTAGTCATGAAATGGT	3573	AGG	751	41721
AAGATTTAATAGATCTTAGC	24027	AGG	749	276
AACACCTATTAACGTAGTAT	1449	TGG	746	38449
TATAATTCATTCATGTTATT	15351	TGG	731	6034
ATTGAATTAGTTACTCGATT	4866	AGG	731	168
GGACAAAAATCAATCAATAG	7069	TGG	727	23198
TACTGATATTCAACTTCTGT	9289	AGG	726	743
ATATTTGGCAATGTGTTCGC	24980	TGG	720	32414
TCTTTTCTGCTAATTCATCA	14170	CGG	712	18310
AAGAAAGTTTTAACTTAAGG	930	AGG	702	1162
TAACTTATATCATTCGTCAT	3617	AGG	695	9229
CAATATAAAACGAAAAACGG	3303	AGG	679	24455
CCGAAAGCGTTTAGAGATGC	31061	AGG	678	25933
TGGATTTAACTAGAATAACT	25431	GGG	664	32380
TAATTAACTTAGTCATGAAA	3569	TGG	661	178

AGCGTTTGATGAAATACTTG	11744	AGG	660	33684
AAATAACTTTATCCACATAA	6704	AGG	652	11834
TTCTATACTTCACTACAGCA	3154	TGG	650	27934
GCGTTTGATGAAATACTTGA	11745	GGG	648	1870
TCTTTATACTCGTAACCATT	7797	CGG	638	12034
CATTGGAAACGTTTAAGAAC	12011	TGG	636	12664
TTGATACGAATGGTGATGTT	16731	AGG	629	30676
TGGAAATTCAATGAAGATGA	4965	AGG	627	15182
TGCGCTTCAATAGTGATAGT	4339	AGG	619	31706
TCTTTTCGATTCGATCTAAA	17217	TGG	619	21649
CCATCCTACCCGGTAATAAA	837	TGG	618	9689
AATAGAGCTAGGGAGTTTAA	3709	CGG	615	17383
AGAAACTATTGAGTACGAGG	3789	AGG	612	23209
AGACGTGAACTCTTCAAAGA	23552	AGG	597	21547
CGTTCATAGAACATACCTGA	15671	TGG	594	14384
TTAATATTGCAAGGTTCATA	8038	CGG	592	11408
GTTTGATGTTCCGAGTAAAG	18026	AGG	588	28740
ACTACAGTACCGTTTTTACC	36838	GGG	587	30546
TATTACTTATACCGAGAAGA	8637	TGG	586	257
TTCGTCATTGACATTAACGA	3980	AGG	584	19503
TTAACCAAGCAATAGATGAA	3515	TGG	581	27680
TATGAAAAAGATGATGATAA	16832	TGG	580	13797
GTTAAAATTAAAACTATTTC	12660	AGG	579	26943
ATATCTGAATTGTTATCAGT	3651	TGG	579	14565
ACTAAGACATCAATTTTAGT	2246	TGG	579	531
GGTATGAATAGAATGACGTT	14900	AGG	576	2570
TCAACTAATTCAAGAATTAC	39451	AGG	574	28649
TTGACACAACACAAACATCA	27197	GGG	571	8341
AAAAACAAACAACTTAATAG	2527	AGG	570	29704
AAAATAAAAAGATGCAACAA	400	TGG	569	5218
ACATTTTACAACACTAACTC	27367	AGG	567	17935
TCAATTAGTTTGTCCGCCTA	5991	TGG	564	28605
ATTGAAGAATTTGATGATAA	4433	CGG	555	8327
GTTCAAATAATGATACTGGT	20325	TGG	553	13918
ATTCACCCACAACAATATAT	21829	GGG	551	20633
AGTTCACTATGAAAACTACG	10991	CGG	550	13711
GGATTACCACTATCTTATAC	20177	TGG	549	20976
ATTGAATTGCTATCATATTC	13883	CGG	544	5486
ATTTCCTAATTTCCATCTGC	24053	TGG	544	1641
AGGCTTACCATGAATCGCAC	39247	CGG	542	26333
GTCGAAGATTATTTTATCTC	27535	CGG	541	2729
TTGATACGATCCATCAACAT	8124	TGG	535	16000
TTTGATACCAATGATCTTAT	4917	TGG	530	8972
CAACCTACTCATGTCGAAAA	7726	AGG	525	24799
GCGATCAGTTAAAAACTACA	24537	TGG	522	3311

GTGAAACACGCTGTACAAAC	22371	AGG	516	25605
TTTAAACGACGTATCGATAT	30713	TGG	512	21869
TTACAAACAAAATCGAACAT	1802	CGG	510	27958
TTATCTAATTGTTTATCGAT	1389	TGG	502	25583
TACACACGATCAATCACAAA	32947	CGG	502	20547
GAAAAACAAAGATTTGTTTC	6141	GGG	501	26275
TTTTTTACCTCAAATTTTAC	4075	AGG	500	13768
TTTCAATGTTTGGTACAAGT	26037	TGG	500	11966
CTTTGTTTCAAACGTATTAG	4474	AGG	497	16668
CACAACGAGCAACATGCGAT	5751	TGG	493	22783
ATTCTCATTCAAATCAAAGT	15738	CGG	485	24796
ATTTGAATCATCACATTTAT	11324	TGG	483	3625
TCCTTTCACTTATAATCACT	26829	TGG	482	26031
TTCATCCGTTTAAATCAATA	20938	AGG	482	13330
ACAGAATGAACTATGAAACA	11352	GGG	481	7986
AGGAATCATGAAAGACAAGA	12358	TGG	477	23416
AGAAATGTTAAAAAGTGTAT	39712	AGG	475	9163
ATAACAACATTATACACGAA	2773	AGG	472	147
AGAAAGCAAGTGCATGGGAT	11502	AGG	467	222
GTTAGAAAAACGCGACGCAG	19224	AGG	466	120
TTAATATTGCAAGGTTCATA	8038	CGG	464	15644
AACTAGAGTAATTAACATAA	14532	AGG	460	23430
AGAAACTATTGAGTACGAGG	3789	AGG	452	1649
AATCACGGAGCAAAGCGTAC	15147	AGG	448	1343
CGCTATTAATGTTAGTACAA	27769	AGG	443	17038
TCACTATAACAATTGCTTGT	12254	TGG	443	6247
ACAGTTCGCTACACAATACG	21938	AGG	442	16850
AAGAGAGTTATATAAAGCTT	1876	TGG	442	10576
TGCAAAAGATTTCTTTAATG	19849	AGG	442	101
GACCGGTTTACCATCATACA	40364	AGG	432	19493
TTACGTGCTCTCATTACAGT	18512	TGG	432	16963
AAATAACTTTATCCACATAA	6704	AGG	432	10460
AGTAGATTTAAAGGTGCGAA	36764	AGG	426	21128
AAAAAAATTATGCTTGTAGC	38722	CGG	426	20829
AATTAGAAATGTAAATGTAG	9415	AGG	420	16839
TTATCTGCATTAAAGCGTAA	17417	AGG	416	19173
ACGACATAAGCATGTTTAAT	3441	TGG	415	10339
GTTTCAGAACGAACAAGGTT	17549	AGG	413	486
GATACTTTGCCGTTATTACA	23067	AGG	409	19478
ATGAATTGATAAAAAAGAAC	9498	GGG	407	113
CCAACAAAAATAACATTATA	16753	GGG	406	8839
AACTAAATCAAAATATGAAC	8351	TGG	405	20687
TCTACTACGTCCGTAATGCT	4546	AGG	405	16491
GACTCTTATTACAGTCTTGT	20536	CGG	405	5674
GAAAATACAGATCCTAAAGC	15585	AGG	401	7212

ATGTATCAAGATACTGCATA	38893	CGG	396	13718
AGTATAAAAGAATGTTTATA	10613	TGG	393	1978
GCATACACACATAAGTTTAT	237	TGG	390	20218
GTCACCTGATAACTTTTATT	37593	AGG	390	15201
TCATCCAAATTGAAAAAGCA	2103	TGG	388	19001
GTAGAGATATAGAACTTCAC	5383	TGG	388	4288
CCGATTAACTGCATAATAGT	25138	AGG	387	16541
GTAGTAGAAGCAATTAGAAA	4577	TGG	385	3287
GGTATGAATAGAATGACGTT	14900	AGG	384	17371
TCTGATTAATATTTCTAAAT	3009	TGG	383	2664
AATCCTTTTTCGACATGAGT	7713	AGG	383	1784
CCCTATAATGTTATTTTTGT	16769	TGG	376	6122
TCATTTGGTCAAAACTGGAA	38512	CGG	375	19802
GAATATAAGCAAAACAAGCA	7862	CGG	375	11880
AATCTCCGTTTAGTTAATAC	5967	AGG	373	18333
GAATGACGGTATGAATATAT	6337	CGG	373	14595
TCCTAAAATCCCTTTAAGCA	34242	TGG	372	20879
CTTAATGTGTTCATAGATTC	37069	AGG	372	19097
GAAACACTTTCTTCATCTAC	37945	TGG	371	537
GAGAAATATAAGCGAAAAGG	18600	TGG	371	99
TAGATATAAAGAGTCTATTA	15656	AGG	370	15015
TCCAAGTGATTATAAGTGAA	26814	AGG	370	140
TCATCCAAATTGAAAAAGCA	2103	TGG	369	148
TACGTCAGCGATTTATAATC	30412	CGG	368	18001
CTGAGAATTTTATTACATGA	12851	CGG	364	12524
GTTTTAAACCCAAAGAATGA	6351	CGG	364	9996
TTATCGAGTGTATAACCTGC	39333	TGG	363	13922
CATTGGAAACGTTTAAGAAC	12011	TGG	361	394
CTGTTCTATGAAAGTTGCAA	5489	GGG	359	11712
GCCTAAAAATCTATCAACTA	19294	AGG	359	7887
TTAATTAAGTAAAGTGTATT	37372	AGG	358	20701
TATTTAATTATGAAAATCAC	4626	AGG	358	19345
TTTATCTCTTGTAGCAAACG	3935	TGG	358	14247
AGCAAACGCACGCAAGTTTG	24682	AGG	354	39
CTTTGTTTCAAACGTATTAG	4474	AGG	353	16203
AATAAGCGCCATTCACTACA	10138	TGG	351	247
ATCTTTAATGCGATGTCAGC	24590	AGG	348	16209
TTTAAAAGAATAGCATCATT	6436	TGG	347	9621
GAGTATAACGAAAGTTTTAC	28034	AGG	347	5305
AATTGGCCACTGCTTTCAAA	5117	TGG	345	17672
AAGATTGAACAAATAGATAA	14978	AGG	345	14655
ATATATAAAGCAACATGGTT	10250	TGG	343	386
GTTGATTCTTCTATGCTATC	37542	CGG	342	17002
TATGAATGAACATGAATTAA	13196	GGG	341	15457
GAAGTAAAATCGAATACACC	31385	GGG	340	11001

AACTAAGTAACACTGAATTA	23899	TGG	339	18840
TTGATACGATCCATCAACAT	8124	TGG	339	16229
TCCAATTGATCCGTGCCAGT	7596	TGG	339	15071
CGCAAAAATATTCATGTTAA	3361	CGG	335	17524
ATACACATGTAACAGAGAAA	138	TGG	333	16965
AATGATTCTGACATTGCATT	22286	GGG	333	16956
TTGCAAATGTGAAATCTATG	7839	AGG	332	3430
TGAACCTAATAAAAGTTATC	37605	AGG	331	9037
TCGCCTCTATATGTGTTTTC	2817	TGG	330	15598
AATACTTGTGTTGTGTTACC	31387	CGG	329	282
TAAATACAACAGGCTCAATA	17861	AGG	328	10711
ACTCGACGACCAAGATGTTG	1077	AGG	327	7875
ACAACTTCACGACGCAATAA	15028	CGG	326	14312
GTTTAAGATATAGAATGCTT	10634	TGG	325	13463
CTTTGAATGGTTTAATACAT	11994	TGG	324	5702
GGAAGAATACACGATGTTGT	10947	AGG	323	6795
GGGTGTCTTACTAAACTTCC	34753	CGG	323	3031
TCACTATAACAATTGCTTGT	12254	TGG	321	15950
GTAGAGATATAGAACTTCAC	5383	TGG	321	199
CTCAACTTTGCGAAGTCACT	13745	CGG	319	7718
CGAGTGTGGGACGAATATAC	10926	AGG	314	3676
GTTTTAGAGAATGTTTCTAC	6754	AGG	314	3113
AAGATTTTATTAAAGCAAGA	7445	TGG	310	493
AAACAATTGATGGATTTGTG	2871	AGG	308	388
TTTACTTGTACTAGATGATA	8229	TGG	307	3190
TAATTAACTTAGTCATGAAA	3569	TGG	305	15300
GAGTGATGTCTGTTGTTACC	30829	AGG	305	2462
TTTACCTTAATATCTTCTGC	20457	AGG	302	13819
TCTATCAATAAATTGTCCGT	30182	TGG	302	111
TACACACGATCAATCACAAA	32947	CGG	301	12514
AAATGGTTTGACAATTCATT	38215	AGG	300	12340
AACAGCTGAATGGTTAAACA	7515	CGG	299	1243
CAACCAGCACATTACACATA	9862	CGG	298	6274
ACTGTTCTATGAAAGTTGCA	5488	AGG	297	14011
CCATTCGGGTGTTTTTTAGT	7782	AGG	297	2373
TCTTATCTGAAGTATCTATG	24655	TGG	294	12735
GATCTTATACGAAGTAAAGA	13617	AGG	293	15039
ATCAGAATTTTAAATCAAGT	18403	GGG	292	1966
AGATATGCTGGGTTCTGTAT	30949	TGG	292	381
AACCACAATCCTAAATTAAT	40187	AGG	291	13543
TAATGATGGAAGTATATTGT	7326	CGG	291	2746
AGATTTTATTGAACAAGTAA	9900	CGG	288	556
AATAGAGCTAGGGAGTTTAA	3709	CGG	288	165
GTATCTGTTTTAATATACGT	12767	TGG	287	2399
ATTAATTATGCTCGTAAGAA	1241	CGG	285	11646

GATTAAAAAACTTAAAAATA	13269	TGG	285	1581
GAAAAACAATAACAGAAGCT	25587	TGG	283	12953
GCTGTAGTGAAGTATAGAAA	3134	CGG	281	6844
GTTAAAATTAAAACTATTTC	12660	AGG	280	10324
ATATCTATTGATGTTGTAAA	11190	TGG	280	9566
GACCATTATTTGATGCTAAC	20142	GGG	274	997
TATAATTGCTTTTATATAGT	40003	AGG	273	13365
AACTAACAAAACAAATACTG	33695	AGG	273	5667
ACTCATCGTTTGAATCGTCT	32540	GGG	272	8457
ATCTTTCAACAACCAATGCT	15540	CGG	270	12519
AGCACTCCTAATCGTCATCT	5893	TGG	270	4102
AGCAAACGCAAAAACAAGAT	15112	TGG	270	222
CTTAGACCAGAAACACTTTT	7552	TGG	267	4035
ATAACTAGCTCAAAGCGTTA	9195	TGG	265	4947
TGAATTTTACAGTCCTATGA	13169	TGG	264	12917
GTGACATACAACATCCCTGA	37734	AGG	264	2962
TTGAGTATTGCGAATCAAGT	12100	AGG	262	5413
GAAGTACGACGAAAGTTATT	7641	GGG	261	12686
TGCTAAAGTCATATATACTA	39930	CGG	261	3782
AAACAATTGATGGATTTGTG	2871	AGG	260	11983
TGCAAAAGATTTCTTTAATG	19849	AGG	259	11390
TACACAAAATACAAAATCTA	32578	CGG	258	12851
TCTAGAGCACCGTTAAAGAA	9976	TGG	258	9190
ATTTTTAAAACATTCAGGCA	31824	AGG	258	77
TACATACTCCAAACAATTGA	2882	TGG	258	76
TAAATACAACAGGCTCAATA	17861	AGG	257	14666
CTGAGAATTTTATTACATGA	12851	CGG	257	4752
TAATTAAGGGGTGATTTTTA	37404	TGG	254	14326
TGTGGATTCTCGGTTTGATA	34169	GGG	253	13215
TTCTATACTTCACTACAGCA	3154	TGG	252	12199
AATAACAATACTAATAATGA	7312	TGG	252	7671
GGAAGAATACACGATGTTGT	10947	AGG	251	5583
GAAAGGTGATAAAGGCGAAC	36781	CGG	250	11473
GAGTCTAAATTTAAATCGAG	19408	TGG	250	67
AAATGATTCTGACATTGCAT	22287	TGG	249	3132
TATGAAAAAGATGATGATAA	16832	TGG	246	311
GTATGCTCAGATGTTAAAAG	14021	AGG	246	51
GTCAGTATGTACAGATTAAT	4241	AGG	245	205
ATTCAACATTCAGTTAAAGA	11781	AGG	244	8972
AATCTCCGTTTAGTTAATAC	5967	AGG	244	1359
TTTGTTCGGCGAACTTCAAA	2724	AGG	243	11092
AGCAATCCATTTGAAAGCAG	5127	TGG	241	11467
ACTTATTCCGTCGTTGCTAC	5238	TGG	240	2628
TGTAGGCGATTCTGTAGATC	21229	AGG	238	166
GGATTCTGAAATAGGTAAAA	16672	TGG	237	291

ATTAAAGTACCTTGTTCTGC	19588	TGG	236	12740
ATTCTCATTCAAATCAAAGT	15738	CGG	236	11930
GAACGGGTTAACTCCTGGAA	9514	TGG	235	9981
GAGATTTCCAAAGCAACGTA	23652	AGG	235	128
CGAGTGTGGGACGAATATAC	10926	AGG	234	6968
TAATATCACTTAGATATGCT	30960	GGG	233	10395
AAAGGAGAACAAGGCGCACC	36836	CGG	233	9368
AGATTTTATTGAACAAGTAA	9900	CGG	233	7191
TAATTATTTCAACAAATGAA	6470	TGG	233	155
ATATGAATGAACATGAATTA	13195	AGG	232	4221
TCTCCAGTATCAATTAAACT	13220	AGG	232	2457
TGTTCCATGCTTTTTCAATT	2091	TGG	231	262
TCATACTTAATTGAATTGTC	27063	TGG	229	59
TATGCAATATACGTTGAATA	21519	CGG	228	8265
CGTAGACCTTTCGGCATTAA	20026	TGG	228	192
TTTGAGCTTGATTATGTTGA	27136	TGG	226	12628
AGAAGTAAAATCGAATACAC	31384	CGG	225	8268
ACTTGTTCTTTATGATAATA	16121	TGG	225	3251
TTTGTCACTTGGTATTGAAA	4945	TGG	224	10276
ATGTAGTTGAATTCTTTGAA	11981	TGG	224	65
TATTACTTATACCGAGAAGA	8637	TGG	223	11483
TTGCCAACGCTTAAGTTGTT	38625	AGG	223	210
TAACCGTATCTTAATCGATA	40143	CGG	222	11980
AATCCCTCAATAACGCCACC	33096	TGG	222	146
AAATGAAGCTGATTTAGATA	18759	TGG	220	11013
ATAGAGGTGGTTAAATATGT	21707	GGG	220	7629
ATCATCAACACTATTTCTAA	16631	TGG	217	3899
ATTGAAGAAAGGTTATAACA	14105	GGG	213	9203
TTTTCTAATTGTTCTCGAGT	22997	TGG	213	2278
ACATTTAGTAAATCATTACG	39108	AGG	211	6081
TCACGTTCAAATAATGATAC	20329	TGG	211	132
TCAATTAGTTTGTCCGCCTA	5991	TGG	210	10442
ATATCTGAATTGTTATCAGT	3651	TGG	210	1214
CTATCTCGTAAGTTCAGCGT	11931	TGG	209	9164
ATTCAACATTCAGTTAAAGA	11781	AGG	208	9714
GGTAAACATCACGGAATGTT	22440	TGG	208	302
TGGAGAAGAAAGCAAGTGCA	11496	TGG	206	9121
CTAAAAATTAATTAAAAGGA	4603	CGG	206	534
GAAGAAAAAGAAAAGTGAAA	9068	TGG	206	45
GCTTTAATTCAGTTGCTTAC	25886	TGG	205	10840
AGAATTGGTTAACACCTCTT	30867	TGG	203	8684
ATTGAATTGCTATCATATTC	13883	CGG	203	264
ATTAAGGCTTCAACACCATC	15672	AGG	202	10266
TTCCCTCACACTATTTCTAT	20996	TGG	202	9682
GAAAGAATGACGAGTTTTAA	12729	TGG	202	9340

GGTTTGTTAGTTATATAAAT	3630	TGG	202	204
AAAACCAACGTTTAATGATT	4198	GGG	201	11318
TATAAGTAATATTTTTCTTT	8609	CGG	201	10164
TAAGAATGACATTGAAATAG	14833	AGG	201	345
TCTAAAAAACCTAAGTCAAC	21416	AGG	200	9574
ATGGAAAGAGAAAAATCTTG	19122	AGG	198	44
GTAAGATGACAGCTATGTTG	17376	AGG	197	6177
AAAAAGAAAAGTGAAATGGT	9072	TGG	196	9105
GTATAACGGCAATGACACAG	11681	AGG	196	3748
AAGCCTGTAACACTTACATA	34774	AGG	195	10916
TATATTTGATTTGTAAGTTC	21725	AGG	195	4149
GACAAAGAAATGACGAAAGC	23187	AGG	194	7995
TATTACTAATAAAAATGATA	39198	TGG	192	5650
TTAATAGGACGAGGTATAGA	15867	TGG	192	2213
GGCTTGAGAGAGCAAATAAA	13999	AGG	190	4661
TGAAGTACGACGAAAGTTAT	7640	TGG	189	7365
TGAAATCCATACCAACCATC	38235	TGG	189	7297
TTCATCCGTTTAAATCAATA	20938	AGG	189	5430
CGCTAACATAAAGAACATAT	38272	TGG	189	377
CCATTCGGGTGTTTTTTAGT	7782	AGG	188	9469
GCAATACATGCAATCAGTTT	25972	GGG	188	1512
GAAACAATCTTTATAAACGC	1308	AGG	187	9827
GAATATAAGCAAAACAAGCA	7862	CGG	187	9772
CCTATTACAGATTCATCGTC	11132	TGG	186	8380
TACTTATTATTATGTATTTC	16889	AGG	186	1569
AGGAAATATCTCAGTTATTA	27513	AGG	185	9841
GATTCCAATACTACGTTAAT	1461	AGG	185	8989
AGTTATTCAAAAATCACGAA	1154	AGG	185	656
TTGAGTATTGCGAATCAAGT	12100	AGG	185	617
TTTACAACGCGCTAAATCAA	23758	TGG	185	112
AACTTATATCATTCGTCATA	3618	GGG	184	8497
AATTGGCCACTGCTTTCAAA	5117	TGG	184	8417
TTGAAAATGATTTAGTTAGT	31919	GGG	183	9227
AAGAGAGTTATATAAAGCTT	1876	TGG	183	7527
TGCGTCCTGCGTCAATTGCA	21646	GGG	183	7438
TTCCCTCACACTATTTCTAT	20996	TGG	178	4332
CACATTGACTTACTAGAAAA	5280	CGG	177	9113
AGAGCATGGTCAGAACAAGT	25082	AGG	177	575
GTAAGAATTATCTTAAGACG	14303	TGG	177	103
GTTCAATATAAAACGAAAAA	3300	CGG	175	10658
GAAAGAATGACGAGTTTTAA	12729	TGG	175	518
AGATACCAGAAAGATAACGA	5214	CGG	173	7625
ATACAAAAAAGAGCTGAAAA	7129	CGG	173	50
ACGCAATTTTTCGTACCTTC	14720	CGG	172	8212
ATTTTCAGCATCTTTCGGTA	2681	TGG	172	35

ATAGACAGGTTTACTAAGCA	22068	TGG	170	2367
GAAATCCTATGCAAGGCAGT	331	AGG	170	67
ACACCAGAAAACACATATAG	2830	AGG	169	9626
TATAAGTAATATTTTTCTTT	8609	CGG	169	8353
GCCAACAAAAATAACATTAT	16754	AGG	168	6426
AATACAAAATCTACGGCACA	32585	TGG	168	1159
TACACAGTAGCTAATGTTAA	39406	AGG	168	126
TATATTTGATTTGTAAGTTC	21725	AGG	166	95
AACCCTCTATCAACATAGCT	390	TGG	165	179
ATAACTAGCTCAAAGCGTTA	9195	TGG	164	6708
CCAAATCGTATCAAGTACAT	25934	TGG	164	5353
TTTGCCGATTAATTCCGCTC	26324	CGG	164	2751
TTATCCACGAGTCATGCAAG	5782	TGG	164	53
CAGTGCCTTGTAATATGATT	29157	AGG	163	9676
GCTTCAATTCCTTTATCTCC	22331	AGG	163	4080
TACTACAGTACCGTTTTTAC	36839	CGG	163	2769
TTTAGTTATAGTAACTTTGT	33295	TGG	162	8104
TACTTACGTAATGCGAAAGG	679	TGG	162	6638
TGGGTGTGCTTCGAATAGTT	25256	TGG	161	6497
GTTAAAAGAATGTTAAAGTC	6108	AGG	160	5978
ACGGAATACTAGAAGATGTT	20704	AGG	160	4960
TAAAGACGATAGAGAGAGAA	16363	TGG	160	1473
TTGAACGCTGCAGGAAGATT	24785	TGG	160	258
ACTCCTAATCGTCATCTTGG	5896	CGG	160	63
ACTAAAAATTGATGTGCAGA	31426	CGG	159	7297
CTCATCAATATCATTCTGAT	17679	TGG	159	6393
TGCGCTTCAATAGTGATAGT	4339	AGG	159	4498
CTGGCACATTATGAAGCAGT	5661	CGG	159	3645
TATTGTCATCGAGCTTAAAT	15604	TGG	159	113
TTTGATTACAATCCATTGTT	16958	TGG	158	9583
GATAATTTTGTAATATTCTT	31243	AGG	158	7138
GCCAACAAAAATAACATTAT	16754	AGG	157	8228
TGGAACCCTGCAATTGACGC	21657	AGG	156	6252
GAATGATAACGATCTAATTC	19068	AGG	156	3709
AGAACTGGAGAAATAACTTA	30344	TGG	155	7829
TGGTAACTTTTATTTTATTG	15887	AGG	155	7653
TTTGACACAACACAAACATC	27196	AGG	155	5377
ACAGTATTAGACGCATGTAA	9138	TGG	155	1343
AAGATTTTATTAAAGCAAGA	7445	TGG	154	3645
TGCTTATCTGTCTTCGGAAT	5036	AGG	153	1930
ATGAGAGCACGTAAAGACGA	18537	TGG	152	252
AACAGCTGAATGGTTAAACA	7515	CGG	152	109
ATCTCCAGCAAAAGCAATCA	36028	TGG	152	42
GATTTGATTACCTCTTTACT	18020	CGG	151	6757
GTATAACGGCAATGACACAG	11681	AGG	151	6369

CACAAAGTAGTCAGCGCGGT	26390	AGG	151	3337
AAGTTAAGAAGTAACGCGCT	19258	AGG	151	134
CGATAGTAGACGCAATTAAT	31775	GGG	150	7237
TTATCTGCATTAAAGCGTAA	17417	AGG	150	4153
ATAATCCAACATCTCAAGAA	38028	GGG	149	2601
AAACAATAAAACTTTTATGG	11602	AGG	149	1695
TTAAAACCCCTAACCTTACT	6272	AGG	149	540
ATTATTTCAGTGTACTTTTT	13049	CGG	149	363
TCATAACTTTCAACGCTACC	32832	TGG	148	5413
ATTGAACAAGCGCAAGCTAA	23405	CGG	147	192
AATTTTCTAGTTGATTCTAC	5396	TGG	145	7483
TACACAAAATACAAAATCTA	32578	CGG	145	518
TCGGTTGATTCTATATCTAA	6310	CGG	144	8551
GGAAGAAGCGAGTATCAATA	3735	TGG	144	616
CTGGATAGACAAATGTCTAG	35618	GGG	144	65
AGAAAAACAAAGATTTGTTT	6142	CGG	143	8395
CAACGATATTTGATATTTAG	8824	AGG	143	6332
TTCATACTACGCCAAATATT	35320	AGG	142	3348
CGTTCATAGAACATACCTGA	15671	TGG	141	8142
GTAAAAGCGTTAGTGGCATT	25184	TGG	141	6525
TCTTTGCTTTATTATCAAAC	38333	GGG	141	1774
GTTTACCCATATATTGTTGT	21840	GGG	141	1418
ACACAAATCCATCAATTGTT	2890	TGG	140	7017
CCACTCACGATAAGTCATGA	18560	TGG	139	6407
TTTACTCAAGAAAAATGGAG	20639	TGG	138	35
TGCTTGTAACGTCGTTAACG	20288	TGG	137	6429
TTAACCAAGCAATAGATGAA	3515	TGG	137	3224
TCTAAACTTACAGATGATTA	32287	CGG	137	3140
TTGAACAAAGGTTATATAGT	12992	TGG	136	2321
GATTACTTACGTAATGCGAA	676	AGG	136	63
AGCAATTCAATTGCACAGTA	13911	TGG	136	35
AAACGAAGGAGTGTATTAAA	22130	TGG	134	7363
TATTGGTAAGTTTTGTCACT	4934	TGG	134	6951
TATATTGGGTTAAATCACAG	38948	GGG	134	6395
AATTTAAGTTTATTGATGAT	15922	TGG	134	4421
AAACAACAACGAAATATATG	11087	CGG	134	3997
AGTTGTCTATAAATATGAGG	11843	AGG	134	320
ACATCAATCACACATTCGGA	2429	CGG	133	7740
GCATAAAAAATGGTATTAGG	3051	AGG	133	142
TCAGATACACAACCTATGCA	30587	AGG	132	1976
AAAATTATTACAAACAGAAT	5429	TGG	132	809
TCTATCAATAAATTGTCCGT	30182	TGG	130	6556
TCCTGCCGTTAAATATAGAG	6373	CGG	130	61
TAACGAAATAGTATTTGTTT	12907	TGG	129	5456
ATTAATATAGATAATTATCG	34463	GGG	129	3542

CAAGATGGAATCAAGATTTT	7460	AGG	129	3453
AGGAAATATCTCAGTTATTA	27513	AGG	128	5448
TTTATCTTTTCGCTGAATAG	7668	TGG	128	58
TGCTATGCATGCTGTAAAAG	5932	TGG	127	6756
ACTAAAATGTGGCAAATTGA	36893	TGG	127	4341
AATACTCCACTAATGTAATC	20876	AGG	126	5607
TTGTTGAATTACCTTTAACA	32234	AGG	125	4219
TTCTTTACTTCGTATAAGAT	13599	CGG	125	158
TGATGAATTAGCTGACATGT	12069	TGG	125	36
TTACAACATCGTCGATAATA	36441	AGG	124	5154
TAGTATTAGGAGACTTTACA	28698	AGG	124	1894
TGCATTACTGCATTTGTATA	30073	TGG	124	111
TGATGAATTAGCTGACATGT	12069	TGG	123	4130
ATAAAAGTAAATGTTGATAC	18643	TGG	122	287
AAAGCGTAAAGGGTACAACT	17428	TGG	122	73
AATCACGGAGCAAAGCGTAC	15147	AGG	122	31
TTATTTCTCCAGTTCTATAT	30321	TGG	121	4885
CAAAAGCAGTCAAAGCTAAA	8093	GGG	121	638
TAACAAACTAGTTGATGATA	21791	GGG	121	30
CCAAATATCTGACCAATCTT	24949	AGG	120	5768
GGTTCTTGTAAATTATTTTC	6619	AGG	120	2738
TACCCATACCGCGTAACACA	17082	AGG	120	1635
CATATTATATCGAGTCAAGG	12415	AGG	120	1420
ACAAGAGTGCCGGATTTACC	32830	AGG	120	1356
TCTTATCTGAAGTATCTATG	24655	TGG	119	6766
TTTGTCTATCCAGTGCTTGC	35592	TGG	118	5281
ATGATGATGTGTATGTTACA	17827	TGG	118	1816
TTTTCTAATTGTTCTCGAGT	22997	TGG	118	1041
CCTACTATTATGCAGTTAAT	25154	CGG	117	5819
GTTTGATGTTCCGAGTAAAG	18026	AGG	116	3120
ACAACTTCACGACGCAATAA	15028	CGG	115	5538
GAAAATCCGGAGCTATCACA	10379	AGG	115	164
TCATGTTCGGTAAATTTATA	9457	TGG	114	5319
AAAGCAATACGTGATGATGT	18192	CGG	113	6324
TAATTAAGTAAAGTGTATTA	37371	GGG	113	42
ACAATAGAAAATGTACGTAG	37630	CGG	112	5168
ATTTATTAAACCTTACAAAA	5009	AGG	112	4572
CGACTAAAGGAGGCAACCAA	29611	TGG	112	2098
TAATACACTTTACTTAATTA	37390	AGG	112	790
GTAAGATGACAGCTATGTTG	17376	AGG	112	760
TCAACAACCAATGCTCGGGA	15535	TGG	112	210
ACAATAGAAAATGTACGTAG	37630	CGG	112	56
ATTTAAGTTTATTGATGATT	15923	GGG	110	5702
TTCAGGCAAGGTGCATGCTC	31836	AGG	110	5510
TATATGTATCGAGTGATGAC	40072	AGG	110	4984

CTAAAAATTGATGTGCAGAC	31425	GGG	110	4906
TCTAAATTCAGTGATGTATT	15995	AGG	110	4509
TACTTTGTTAACAAGTTTTT	2501	AGG	110	614
AAGCAACGTGATGAGCTTAT	11438	TGG	109	98
TCCTTAGTTGATAGATTTTT	19309	AGG	109	87
CTCGCCATTTCATATAAATA	17971	AGG	109	39
CATATAAATAAAGGCTCATA	17962	AGG	108	4427
TGAAAGAGTTAAATTTGGAA	11575	TGG	108	3375
TTGCTTACTGGCGACTTCTC	25898	AGG	107	5878
AATGAAGTTTATTCGCTCAC	8700	AGG	107	4104
TAAAACTTTCGTTATACTCT	28014	TGG	107	3299
ATTTTTAAAACATTCAGGCA	31824	AGG	107	54
TTCTTAGAGTTATTGAAGAA	14094	AGG	106	5016
TAAAACTTTCGTTATACTCT	28014	TGG	106	4855
TACTTATTATTATGTATTTC	16889	AGG	106	2818
TATAATTCATTCATGTTATT	15351	TGG	106	2289
TCATCAACACCATCTTGTCC	32421	AGG	106	571
ATTTAAAGTCAAGAAGTATG	20839	GGG	105	5100
GGCTTTTTAGATACAGAAGA	19045	AGG	105	40
GGCAAAAGATGAAAAGTCAC	33878	AGG	104	4391
GGCAATGTGTTCGCTGGTAT	24986	TGG	104	3489
ATAATACTGCTCGTGCAACA	32531	TGG	104	2056
TATGCACTTTTCGGACTGTT	18886	AGG	104	49
ATCTTCGCGCAACAGGTCAA	24275	AGG	103	55
TTTACCTTAATATCTTCTGC	20457	AGG	102	5012
ACAGCAATAGAGTACGTACA	7990	AGG	102	4900
GTTGTTTGAAATGTACGAGA	10552	TGG	102	4166
GTGTATATTTGCCAATTGTC	7002	AGG	102	1417
CGTTACGAAATAAGAGAACC	23483	TGG	101	5066
CATTGATACCGTCGCCGTTA	29850	TGG	101	5039
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AATTAAACTACCCACCATAT	14403	AGG	100	5326
TGAATTTTACAGTCCTATGA	13169	TGG	100	5089
TGAACAAAGGTTATATAGTT	12993	GGG	100	4588
GACGGTAAACATACCTATAG	27571	AGG	100	4241
AAACGAAGGAGTGTATTAAA	22130	TGG	100	687
TTGGTATCAAAATCTAAGCT	4889	AGG	99	5142
TTCTTAAGTTGTCTTTCAGT	30454	GGG	99	4548
AAGAGAACGCAACAAAGAGC	11476	TGG	99	3042
CTCTATTATCTCTTCGTACA	18682	AGG	98	5299
GGTAAATCCTAGAATTGTTA	27993	AGG	98	5052
TAAAACCGCTCTATATTTAA	6384	CGG	98	54
TCACAGTAAAGTAAGTGGTA	15396	AGG	98	40
AAAAAGCTGAAGAAAATAAC	5074	GGG	97	4608

CAGTTTTAATACCGTATTCG	10810	TGG	97	2977
ATAATAAAATTATACCAGAA	6865	AGG	97	55
TTCCTAAAAGCTGGATTGTA	29485	TGG	96	2527
CCAAAATCATTAATATTGCA	8029	AGG	95	5144
ACTTGTTCTTTATGATAATA	16121	TGG	95	2563
ATTCAATCAATTGTTTTTCT	4834	TGG	95	204
GCGATGTCAGCAGGTATCAG	24599	AGG	94	4113
CAAGATGGAACAGCAGACGC	12373	AGG	94	2876
TATAGTTGGGATCAATGTTG	13006	AGG	94	2750
TAATTATTTCAACAAATGAA	6470	TGG	94	113
GTAGTTAAACATATGAATGA	7048	TGG	93	6310
TTTGTAACAACTGATATTAA	21	AGG	93	4404
ACTAAAAATTGATGTGCAGA	31426	CGG	93	3153
AATACTCCACTAATGTAATC	20876	AGG	93	62
AAACTTACCAATAAGATCAT	4908	TGG	92	4542
AGATGAAAAAACGACTATAA	165	AGG	92	2767
TAAAAGGTATCTACTTCACA	36195	AGG	92	472
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ATTAAACGAATGAACTCAAT	18056	AGG	91	3304
AAAACTAATAGCATCATCTA	6502	TGG	91	1377
GTCGAACACTTATTTGTATT	10435	TGG	90	3693
CTATCCGGATATTTATTTTT	37527	AGG	90	3136
CATGACCTGTAATAACAAAG	4272	TGG	90	209
TCTGATATAGAGGGTATTGA	26899	TGG	90	49
GGTTCTTGTAAATTATTTTC	6619	AGG	90	48
AATCATCAATAAACTTAAAT	15904	TGG	89	5306
CACAACGAGCAACATGCGAT	5751	TGG	89	3764
GTAAGTCGTAAGGTACATAT	21141	AGG	88	3809
GGATATCGAAAAAGAAGCGC	9340	TGG	88	218
CGGAAAGCCTCACGCAGACC	5642	TGG	88	88
CGGATTGTTCTATTTGTTCA	11626	CGG	87	4032
AGAGAACTTGTATTGAACAA	12980	AGG	87	3682
TTTTAAAAATCGGAAGGTTT	14717	CGG	87	3667
ATACTTGATAAGTCTACTAT	27938	TGG	87	120
CTGAATGGGTTTCTAACATT	26193	TGG	86	3692
ATTTCAGGGAGCGAGATGCA	8432	TGG	86	3197
GAATCATTTAAATTAACAAT	22317	TGG	86	38
TTTTATATGAGCAAGAGCTA	8794	GGG	85	3896
CTTGATGTACTTCTTTGTGT	13373	TGG	85	797
AAATGAAGCTGATTTAGATA	18759	TGG	85	49
ATTGGAAGTATCAAAAAAGT	21014	AGG	84	5141
AGAGAACTTGTATTGAACAA	12980	AGG	84	1823
ATTCATTTTAAAAGGTCATA	3399	TGG	84	203
CTTTGAATGGTTTAATACAT	11994	TGG	84	170
TATCAAAAGAGTTTCTTAAA	19824	TGG	83	4858

TTAGCAAATAGTTGTTCTAT	17735	TGG	83	4517
TCTAGAGCACCGTTAAAGAA	9976	TGG	83	4451
CGTATATTTCTTCTTTTTGA	29736	TGG	83	3896
AAAATTAAAACTATTTCAGG	12663	TGG	83	3781
CATATCGTACCAGATTGGCA	10188	AGG	83	3425
ACACTGCTAACAGCTGCAAT	25342	CGG	83	1140
GTAGTTGAATATAACGTTAC	26854	AGG	83	82
GAGAAAACATGTTGTTAAGT	23959	TGG	83	75
GTTTGAAGATGAAGAAACGT	18313	TGG	82	4561
GGCGTTCAAGTGGTTCAGAC	15372	AGG	82	4549
AAAAAGTAGAGCTTAAGATA	26954	AGG	82	217
TTTAACCTAATAAAATACAT	38598	TGG	82	116
CTATATGTGTTTTCTGGTGT	2811	TGG	82	71
TGCTCATACTTTGCGTTATC	35380	CGG	82	35
AATTTAAGTTTATTGATGAT	15922	TGG	81	4441
GCTGATAAAAGTAAACTATC	16059	GGG	81	3567
GAATCAAGATTTTAGGTTGG	7467	AGG	81	3411
CTTAATGTGTTCATAGATTC	37069	AGG	81	2672
AAAAGAATTTGATGACGTGT	16202	TGG	81	2319
ACATTATGAAGCAGTCGGCA	5667	AGG	81	1877
ATATCACTGTTCCTATGGCT	25812	TGG	80	3837
GTATTGTTGTACCACTCATA	29337	GGG	80	3113
CCATTTCGTTATCTCCTTTC	6863	TGG	80	2449
ACACATTGTACCGAATTAGA	36096	TGG	80	1802
ATTTGAATCATCACATTTAT	11324	TGG	80	80
AAACAACAACGAAATATATG	11087	CGG	79	3839
CTAATAAAAATGATATGGAT	39203	TGG	79	2387
ATCAAATCAATTGGAACGAT	28973	TGG	79	680
TAATAAAACTTTAGAACAAC	27615	CGG	78	4535
GCATTCCTCGCTAGTTTAGA	14879	TGG	78	3412
TATGCACATACCAATGTTGA	8130	TGG	78	3247
ACGTAACGCTACAAAGTCTA	28520	AGG	78	1726
GTTACTATAACTAAAATTAT	33319	GGG	78	1490
TTAATTTTTAATGTTGTAAT	22772	TGG	77	3850
CGCTCTTATCAGACGTAGTA	20564	CGG	77	3442
TTAAAAGAATAGCATCATTT	6437	GGG	77	3408
ACTTTAAATATTTCGATGGT	21466	GGG	76	4089
CAACCAGCACATTACACATA	9862	CGG	76	3733
TAGCGTCCATTACACCTAGT	11361	TGG	76	3537
TTTACACCAATAAATAGCTT	18425	GGG	76	2560
ATATTGGGGTTTTGTAACAT	34525	GGG	76	2108
CAAGATGGAACAGCAGACGC	12373	AGG	76	970
CCAAAATCATTAATATTGCA	8029	AGG	76	37
AAAAAGATTATGGCTTATAT	38933	TGG	75	4474
CTTAAATACTTAGCGATATT	38802	AGG	75	981

TCAAAGTGATGTGTTAGCTA	4405	GGG	75	399
TAATAGAACTATCAAGTAAA	556	AGG	75	47
GTATCAAATGGATATACCTA	30556	TGG	74	4270
TTAAATCTGACGCACTTTGT	33535	TGG	74	3972
GCTAAGTATTTAAGACATGC	38827	AGG	74	2232
TCGCCTCTATATGTGTTTTC	2817	TGG	73	3080
CGTGTGGCTCGTAAAGAAGC	18237	AGG	73	2251
CATAGAGGTGGTTAAATATG	21706	TGG	73	133
GATTGGGATTACGCACGTTA	20243	CGG	73	116
CCAGCAAAAGCAATCATGGG	36032	CGG	72	2928
ATTGGTCGACGTTTGAATAT	16411	TGG	72	1682
TGTATTAGCTGATGTAATAC	13880	CGG	71	4364
AAAAAGATTATGGCTTATAT	38933	TGG	71	3120
TTACTATAACTAAAATTATG	33320	GGG	71	2936
GCCAATGACTCAACAATTAC	34880	TGG	71	928
AACAATTTATTTGAGTATGA	21191	GGG	71	330
TGAACGACACAAATGATTTA	38151	GGG	70	3490
TACTCATCGTTTGAATCGTC	32541	TGG	70	3305
GATTCTTCTAACTTATTAAC	17482	TGG	70	3140
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CCAGACGATGAATCTGTAAT	11148	AGG	70	2675
GTTTAAGATATAGAATGCTT	10634	TGG	70	1942
ATAAGAAACATCAAATCAAT	28964	TGG	70	1307
CGGATTCCTTATTAAACGCA	2344	AGG	70	158
TCGCCGTATGTGTAATGTGC	9849	TGG	69	2156
TATGCAATATACGTTGAATA	21519	CGG	69	1369
TTTACTCAAGAAAAATGGAG	20639	TGG	69	796
CATTCGAAAGGATTAGAATC	19103	TGG	68	4251
AGCTAGTTATTTCTGTAATT	9166	TGG	68	4111
CGATTGTACTTGCTTGATGT	36132	TGG	68	3735
CCTGGTGCAAAAGGTGAAGC	36809	AGG	68	3329
TTATTTGCTAATAGTTTGTT	2738	CGG	68	3202
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ATCGGTGTTATCGGTATTTT	25310	AGG	68	184
GTACTGCCTGGACACTATAA	31097	TGG	68	67
GGTATATATGCTACTGGTCC	21546	TGG	67	2791
GACTCTTATTACAGTCTTGT	20536	CGG	67	2689
TTAGAATTGACACCTCAAGA	873	AGG	67	2651
AGCAACTAACTTTATTTTAG	10288	AGG	67	2587
CTTATCAAATACCGTGTCTT	10514	TGG	67	57
GATGAACGCTCAGATATTCA	35012	AGG	66	2553
GAGGAGGTAGAACATGACTG	3805	AGG	66	568
CGCTCAGAAACTCATAGATG	8501	AGG	66	157
GATGATTATAACGTAGATAG	31729	AGG	65	3389
CTTCCGCCAAGATGACGATT	5883	AGG	65	3013

TGAATATGCACAAGCAGAAA	19771	TGG	65	2661
TCAGATACATGGCCTCTGCC	40024	CGG	65	858
CTGAATTCAATAAATACAAC	17851	AGG	65	76
GAATGTTGTCAAAAGAATAC	25411	TGG	65	27
GCGAGAAAAGTAAGAGTAAT	8404	CGG	64	410
TTAATTAAGTAAAGTGTATT	37372	AGG	64	271
TTAGAGAAGCCTGGACAAGA	32428	TGG	63	2311
GTGTGATATGCGTCAAACAC	29449	TGG	63	1312
GATACAAAGACTTACTTTAT	10714	AGG	63	781
ACCACTAACTTACCTAAGAT	24953	TGG	63	119
TTTAATTCTGACGAGTTTAA	17285	CGG	61	4021
TTAGGTAAAACATCAGGTTC	33280	TGG	61	2398
AAAGTAAAAGTTAAGACGAT	13564	TGG	61	335
GATCCTGGAGCAGTAGGAAA	38758	CGG	60	2997
GCCGTTATTACAAGGGGCTT	23075	TGG	60	2189
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TGGTTCTTTGATGTACTGCC	31085	TGG	60	471
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GGATTCTGAAATAGGTAAAA	16672	TGG	60	63
GAAAACCTGTGATTAGTAGC	2640	AGG	59	3051
TAGCACTAACACCTGCTGAA	23328	TGG	59	2782
TTAGCTATTGGTAAGTCGTA	21151	AGG	59	2371
GTTGATTCTTCTATGCTATC	37542	CGG	59	2216
AATGGCAGTTGTGACGTGGA	2593	AGG	59	1809
CTCAAAGTGATGTGTTAGCT	4404	AGG	59	1445
TTAAATATAACATTGAATCC	22901	TGG	59	927
AATCATAAAGCGTATATACA	8967	AGG	59	879
ACATACTTTTTGATTGAGTA	20756	AGG	58	3341
GATTTGGGATATTTAACTGC	32794	TGG	58	3062
GTCCGCAAAACGCCGGTTAT	31227	TGG	58	2437
GAAACGTTCGAGGCACCTAT	8877	GGG	58	2137
AATACACTTTACTTAATTAA	37391	GGG	58	1163
AGAACTGGAGAAATAACTTA	30344	TGG	58	35
AACTATCATTAAAAGTTAAA	22519	TGG	57	3270
GAGTGGGCAAAGTCGAATAT	34433	TGG	57	1772
CGTACTTAACTTTTGCCATA	21277	TGG	56	3490
TGGTTTATGTTAATTAATCA	15132	CGG	56	2831
CAGTATTCCCTGATATAGAC	22054	AGG	56	348
ACACAAATCCATCAATTGTT	2890	TGG	56	228
AACAATACGCCGTAAAGACA	29368	CGG	56	206
GTTTATCCTACTGCCTTGCA	342	AGG	56	132
AAAATTAAAACTATTTCAGG	12663	TGG	55	2288
GCAGCTTCAAACCACTCTTT	22556	CGG	55	1895
ACACGTGTTGGTTATTTACA	16550	TGG	55	1225
TACAAGTGTACTTACAAGTA	1966	CGG	55	130

TCATTTGGTCAAAACTGGAA	38512	CGG	55	59
TAACGATGTGTACTTTGATT	33262	AGG	54	3276
GAATGTTTTAAAAATTCATT	31800	CGG	54	2658
CAAGATACTATCGAAGCTGT	31981	CGG	54	2504
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CCTTTTGCACCAGGTTGTCC	36784	CGG	54	1305
CTTGTTTCAGTAACGATGCT	35557	TGG	54	195
TCAAAGTATGGTGGCGGAGC	38446	TGG	54	123
AATTATTCAATGGTCAATGT	37782	CGG	53	2462
TTCTATGAACGTAATATCAA	15699	CGG	53	2263
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TAATTTATACGTAGACCTTT	20017	CGG	53	129
ACAAAGCGTTCTTGTATAAT	21028	TGG	53	92
CATTCATGACTTATCGTGAG	18577	TGG	52	2234
GTGCCAAACTGCGATGTCTC	34612	AGG	52	1164
TTTGTCTATCCAGTGCTTGC	35592	TGG	52	1011
TGTACTTGTTTTTCATTTTG	7941	TGG	52	247
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CTTTATACTCGTAACCATTC	7796	GGG	51	1516
GGCAAAAGATGAAAAGTCAC	33878	AGG	51	1339
ATACTGCTTGACTATCGATA	22021	CGG	51	168
TACGATTAAAGCAGATGAAC	15776	TGG	51	127
CGTACTTAACTTTTGCCATA	21277	TGG	51	124
GATGGACGACAACTTTTTGT	27154	AGG	51	101
CACAAATAGAAATAGAGCTA	3699	GGG	51	39
GCGCGCTCTAGATTTAACTT	8981	AGG	50	2543
ATAGCGCAGACATACAAGCT	13526	AGG	50	2218
TTTGAAATGTACGAGATGGA	10556	AGG	50	2079
ACTGCAACTACTGCTAATAT	25492	TGG	50	2015
TCAACTTTAGTAATCCTTCA	37736	GGG	50	2009
AAAATCCGGAGCTATCACAA	10380	GGG	50	1355
GCACGTTGCATAATCATTTC	2116	TGG	50	230
ATTAAAAGATTTTATGTTTG	11219	AGG	50	149
TTAAGTACTGCCATTATTGC	24334	AGG	50	118
GCCTAAAAATCTATCAACTA	19294	AGG	50	86
ATACTAAACCTGAACGATTA	16252	AGG	50	50
ATATCGCTGAGAAAAATAAA	3882	AGG	49	2526
TCAAAGTATGGTGGCGGAGC	38446	TGG	49	2257
GCGATCAGTTAAAAACTACA	24537	TGG	49	2158
CTTTTGCGATAGCGTATGCT	8060	AGG	49	1687
AGAAAAATCGCCATCAATTC	454	AGG	49	465
TGTACTTGTTTTTCATTTTG	7941	TGG	49	452
ATTTGCTATCCTTGAATTGA	461	TGG	49	138
ACTACAGCATGGTCAATTGC	3165	GGG	49	69

ACAATAACAGAAGCTTGGAA	25592	CGG	49	14
ACGACATAAGCATGTTTAAT	3441	TGG	48	2711
AACAATACGCCGTAAAGACA	29368	CGG	48	1791
AAAAAGCGCATCTCAACCGA	37312	CGG	48	644
CAGTGCCTTGTAATATGATT	29157	AGG	48	171
ACAGTTCTAACATTTTTGAC	25035	TGG	47	2036
CGACTAAAGGAGGCAACCAA	29611	TGG	47	1012
TTATTTCAGTGTACTTTTTC	13048	GGG	47	131
TCTGATATAGAGGGTATTGA	26899	TGG	47	56
GAACCACAATTTTCTCTTCT	6585	AGG	47	52
CGTATTGATAATACAGGTTA	29903	TGG	47	37
GAACCACAATTTTCTCTTCT	6585	AGG	46	1935
TGAAAAAGGGCAAACGCTTG	40267	TGG	46	1843
TCCGTTTTATCAGTGCCTAT	29215	CGG	46	1818
TAAACTTAAATCTTTATATA	15068	CGG	46	1712
ACGCTTGTGGAAAAGCTAAA	40280	AGG	46	1535
AAAGATATTGTAAGTAGATA	15957	TGG	46	1412
AGTGTATAACCTGCTGGCAC	39327	TGG	46	999
TAAAAGAATAGCATCATTTG	6438	GGG	46	104
TTTGCCGATTAATTCCGCTC	26324	CGG	45	2307
CCACAATTAGCATTTGCAAT	9934	AGG	45	2289
CAAATAGATAAAGGTGACAG	14987	TGG	45	2137
AGAGCATGGTCAGAACAAGT	25082	AGG	45	2123
AAATTACCTGACATAGATGA	17645	AGG	45	2042
TAGGAGTGAACTATATAGCC	40022	GGG	45	1801
CGATTCAAGGTGTAGTAGAT	25638	TGG	45	1498
TGCAGTAATGCAATCATTTT	30100	GGG	45	1453
TATCTGTCGTTAAATATATT	30373	CGG	45	1388
AAGTCACGTTGTAGTGGAAC	15498	TGG	45	1199
GGAGACCTAATCATATTACA	29168	AGG	45	546
AACTTTGAAGCTTCTAGAGC	6577	AGG	45	159
AAAAACCAACGTTTAATGAT	4197	TGG	45	85
AAAAACAAACAACTTAATAG	2527	AGG	45	60
TTAATAATTGTCTTTGATCT	23367	AGG	44	2570
TTCAGTGATTTCTTAAATGC	26321	CGG	44	1563
TATCTGCATTAAAGCGTAAA	17418	GGG	44	1533
TAAATGGAACAAGTGATATT	24174	TGG	44	1420
GTTGATTTCGTGCCACTGTG	994	CGG	44	585
TTATCTAAAGGGACTTAAGA	19002	CGG	43	2721
TTTCAATGTTTGGTACAAGT	26037	TGG	43	2260
AAGATAACTTGCCGAAAGAG	22561	TGG	43	2259
AAAAAGAAAAGTGAAATGGT	9072	TGG	43	1685
AGCTTTAGTTGCATTATATT	23906	TGG	43	1574
GCATTGATACCAGTGATTGC	24320	CGG	43	1077
TAAAGACGATAGAGAGAGAA	16363	TGG	43	363

CTTGATTAAGCAAGGTATAC	35377	CGG	43	227
GACCAAGATTTAGCGTTTTA	5166	AGG	43	129
CAAGATACTATCGAAGCTGT	31981	CGG	42	1881
TCGCCGTATGTGTAATGTGC	9849	TGG	42	1616
ATTATCGGGGCAGTCAATGT	34476	TGG	42	1201
CGATTGTACTTGCTTGATGT	36132	TGG	42	1145
GAGTAATCGGAGACGATTTC	8417	AGG	42	580
TGCTTGTAACGTCGTTAACG	20288	TGG	42	236
GTAGTTAAACATATGAATGA	7048	TGG	42	55
AAATCAATCGCAACAGAGAT	14054	TGG	42	12
ACTCTCAATGAGATTAAATT	34024	AGG	41	2577
CAACTGACAGCTAGATATTT	23282	AGG	41	2247
CAACACAAAGAAGTACATCA	13390	AGG	41	2232
TTAATTTTTAATGTTGTAAT	22772	TGG	41	2060
TCAATTATCGGCTTTTTAAC	25997	TGG	41	1961
ATGATGATGTGTATGTTACA	17827	TGG	41	1384
GATAACATGTAATGATTACC	30148	TGG	41	891
TAACCTCACAGTCATATCTA	11275	AGG	41	806
ATTCAAGAAACACAAAAGAG	17135	TGG	41	743
GTCAAGATGTATTACGAAAT	3328	AGG	41	302
GACAGAAACTATTGAGTACG	3786	AGG	41	174
TGAGTTGTTCGACAAAGATA	17164	TGG	41	127
TAATAAAACTTTAGAACAAC	27615	CGG	41	50
AAAACTGGAACGGTAAAGGT	38522	TGG	41	22
AAAGACTTTAAAGGTATTGC	31352	AGG	40	1471
ACTGCAACTACTGCTAATAT	25492	TGG	40	1355
TCATAGAGGGCAAGAGCCAA	14619	CGG	40	515
CTGGCACATTATGAAGCAGT	5661	CGG	40	455
GGCAATACATGCAATCAGTT	25971	TGG	40	327
TAGTGGCGTTCAAGAACTTA	7086	TGG	40	146
TCAGTTGTATGAAAATATAA	12618	GGG	40	87
AAATTCCACTTTGTTATTAC	4283	AGG	40	32
GCGATGCGATTTCATCAGCT	26412	TGG	40	20
GGAATATATATAAAGCAACA	10245	TGG	39	2488
CTTTGTTGGTTTGATGCATT	33521	CGG	39	1480
GATGGACGACAACTTTTTGT	27154	AGG	39	606
GACGGTATGAGTGATGCACT	26282	TGG	39	356
GATTTTCCTAAAGACTTTAA	31343	AGG	39	53
CTTAATGCGGTTGGTGTATT	24368	AGG	39	44
GAGAAAACATGTTGTTAAGT	23959	TGG	38	2290
ACAGTTAAGAGTCAGTGCTT	34322	CGG	38	2122
CACCGGGTAAACTGTTATAC	39955	GGG	38	1893
CACCCTTATGTAAGTGTTAC	34787	AGG	38	1864
TTATCAGATTTAAAAATCGT	31277	TGG	38	1831
GTATCAGGATAACGAGCGAG	10124	TGG	38	1647

GCTGGAATACTGCGATTATT	13312	CGG	38	1005
TTTGACCAAGCTGTTATCTT	19907	TGG	38	468
CTCAACTTTGCGAAGTCACT	13745	CGG	38	452
TAAAGGTAGACCCTAATATT	35325	TGG	38	157
TTTATAGGCTCTCCGTTTGT	16166	AGG	38	147
CGGATTCCTTATTAAACGCA	2344	AGG	38	110
GCGACAGGCGAAAGGCTGCA	38308	AGG	38	13
TGAATGGCGTGATTGGCTTA	23345	TGG	37	1588
CAAAAAGAGTACGTGGTGGC	9540	TGG	37	1303
TGCTATCAAATGCTTAATTT	35741	AGG	37	1169
AAGTTTTATAACGGCTCAGC	4683	AGG	37	124
TTGAACTTGATGAAGCAGTA	11806	GGG	37	13
ATAGATACTTCAGATAAGAA	24634	TGG	36	2068
ACTGGATAGACAAATGTCTA	35617	GGG	36	1905
ACGGAATACTAGAAGATGTT	20704	AGG	36	1675
AAGTACCGTCGTTATCTTTC	5203	TGG	36	1649
CAATTTGCGGATATGGTGCT	16698	AGG	36	1644
CCATTCATGTTCGTGCCGTT	33943	TGG	36	1341
CCAGAAAGGAGATAACGAAA	6879	TGG	36	1322
TTATAGGCTCTCCGTTTGTA	16165	GGG	36	280
ACAATTGCGTTCCAAGCCAT	25817	AGG	36	175
TAGATATAAAGAGTCTATTA	15656	AGG	36	40
TTAAGCGTTGCGAACGCTTC	20401	TGG	35	1317
AATAGTTGGACAGGTTCTCC	34751	GGG	35	1223
TCATCAACACCATCTTGTCC	32421	AGG	35	1143
TTATCTAAAGGGACTTAAGA	19002	CGG	35	1037
AGAAAAACAAAGATTTGTTT	6142	CGG	35	988
TCATACTACGCCAAATATTA	35319	GGG	35	555
AAGAATTATCTTAAGACGTG	14305	GGG	35	415
TTGTTAGGTACACCAAACAA	16954	TGG	35	297
CGTATTGTTGTACCACTCAT	29338	AGG	35	205
TTTGTGCTAGGACTCATAGA	14606	GGG	35	28
CAAAAAGCTGAAGAAAATAA	5073	CGG	35	20
CGAAAGTTATTGGGATTAGG	7650	GGG	35	15
AACTATCGCTTGTTAGATGA	29699	AGG	34	2254
CAGCCATATTTTGCTTTAAT	32000	TGG	34	1453
AGGGTTTCGCAAACTAATTT	37660	AGG	34	1397
CATTTCCCTTCTTGAGATGT	38017	TGG	34	1149
TGAATCAATCACACTTATTG	12809	AGG	34	1127
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TTGGTAAGTGGAACTTATCC	33094	AGG	34	723
ACAGTTCTAACATTTTTGAC	25035	TGG	34	314
TCATAGAGGGCAAGAGCCAA	14619	CGG	34	178
TCAACTAGTTTGTTAATGTT	21767	AGG	34	49
GGTTAATTCTAATAGTTGGA	34742	AGG	33	1637

GACGGTGCATATTGTATTAA	39505	TGG	33	1632
GGCGAATGGTACACAACATA	21615	TGG	33	1429
AAAAGAAGTAACCAAAGACA	10519	CGG	33	1055
GAGTTTATTCGAGGGAAAGG	31498	TGG	33	1026
TTGCGTCCTGCGTCAATTGC	21647	AGG	33	811
GAAACTCATAGATGAGGCAC	8507	AGG	33	805
GTAGGAGTGAACTATATAGC	40021	CGG	33	599
GCCTTTGGATACTCATTTTA	23608	TGG	33	446
AAAAACCTGTATTAACTAAA	5956	CGG	33	367
ATGCTTTTAGTTCTTTAGAT	28776	GGG	33	31
TCACATCATTTGGTCAAAAC	38507	TGG	33	12
GACGGTGCATATTGTATTAA	39505	TGG	32	1992
AATGCCGGAGCGGAATTAAT	26336	CGG	32	1579
GAGTTTTCCCCTTGTGGTTT	13934	CGG	32	1064
TAATAGAACTATCAAGTAAA	556	AGG	32	723
AAAGCAATACGTGATGATGT	18192	CGG	32	685
TTATTTCTCCAGTTCTATAT	30321	TGG	32	149
TTCTATAAATTTGCAGTATA	3908	CGG	32	53
CGAAAGATAGCAGACGAAGA	15219	AGG	32	18
ATTAATCGGCAAAGTAGCTG	26350	AGG	32	14
ATGGATCCTATTTTAGGTAA	6795	AGG	31	1447
CGACTAAAGGAGGCAACCAA	29611	TGG	31	1402
AACTCTTCTTTAAATTTAAT	33428	AGG	31	1281
TCCAAAGCCCCTTGTAATAA	23060	CGG	31	992
TCCGAACCTATTCCGTTGCC	34636	AGG	31	648
ACGCAATTTTTCGTACCTTC	14720	CGG	31	620
AGAGGGAGAGTCGCTCGTAC	23125	TGG	31	113
TTATTTTTTGCGTTTTTTTG	40224	GGG	31	53
AATGATGGAAGTATATTGTC	7327	GGG	31	33
TTGATTTTGTCCAATAACTC	36925	AGG	30	2177
ATACTTGATAAGTCTACTAT	27938	TGG	30	2061
GACTACTTTGTGCGCAGCAT	26363	TGG	30	1553
CTTAAATACTTAGCGATATT	38802	AGG	30	1535
GAAAGTGTATTGCAACAGAT	37145	TGG	30	1433
AATGGTTGAAGATGGAACAT	24478	TGG	30	1405
ATAGAGTTAACTAACAAATA	15306	TGG	30	1140
TGTTCAGAACTTATAGATAA	31662	CGG	30	974
CATCATTCTTTTTATAAAAC	32594	GGG	30	917
CGAAAGATAGCAGACGAAGA	15219	AGG	30	432
TAACGACCCTGAAAAATGGT	27297	CGG	30	154
AAATCTTCTTTTTCTTCAAT	16429	TGG	30	131
ACTAGATGCTTTCACTAAAA	29968	AGG	30	92
ATTATTTCAGTGTACTTTTT	13049	CGG	30	49
TAGAAGAATCAACAGCAAAA	37568	TGG	30	13
AACGCTTAAACCAACTGAAT	20431	AGG	29	1600

TCGAGCAGTATTTTTCATAG	21691	AGG	29	1097
TTGTTGAATTACCTTTAACA	32234	AGG	29	1055
TTCCCGTATAACAGTTTACC	39969	CGG	29	1025
TCATCTAAATCATAAGTAAC	16561	AGG	29	894
CCGACGGTTAAAATTTGGAC	37328	AGG	29	840
AACTTCAATTGCAGAACAAA	29258	AGG	29	831
AATCCTTTTTCGACATGAGT	7713	AGG	29	604
GGTATGTGGGTGTCTGGTGA	15720	CGG	29	386
AAGATATAGAATGCTTTGGT	10630	AGG	29	87
CGGACAAGGCAAAGCATTCG	35827	CGG	29	74
AAACAAAACGGTATAAACAT	2288	CGG	29	51
GAATGACGGTATGAATATAT	6337	CGG	29	43
GGCTAATTACAGATATCCTA	34564	AGG	28	1306
TGAGACACAAATTTGAACAA	24826	CGG	28	1241
AATTATTCAATGGTCAATGT	37782	CGG	28	1221
GTTTACCATCATACAAGGAT	40369	GGG	28	1179
ATACGTCCATCAACAAGCGG	28429	TGG	28	1110
GTTAGAAAAACGCGACGCAG	19224	AGG	28	591
ACAGTTCGCTACACAATACG	21938	AGG	28	259
CGTCTATCTGTCTTTCCCTC	34085	TGG	28	192
TCGTTTGTAGGCAATCTATC	27306	AGG	28	58
TTTAAACGACGTATCGATAT	30713	TGG	28	28
TCTTTCAATATCGTTGATAG	36590	TGG	27	1491
TCCGAAAATGGCATTTCGGT	7173	TGG	27	1472
ATAGACAGGTTTACTAAGCA	22068	TGG	27	1266
GGTAAACATCACGGAATGTT	22440	TGG	27	907
AATTAAACTACCCACCATAT	14403	AGG	27	374
TAATTAAGGGGTGATTTTTA	37404	TGG	27	335
AAAGTTACATTACAGCCCCT	6034	GGG	27	247
GCACATATCCATGTAGTGAA	10146	TGG	27	193
GGTTTTATTACAAAAGATGA	37500	AGG	27	167
AAAAGCAGAAGTAGAGGTTC	5312	CGG	27	142
GAGAAATATAAGCGAAAAGG	18600	TGG	27	113
TATGTTTGGCACCCTACAAA	16170	CGG	27	66
AATAAATTGTTTTTAGCTAT	21163	TGG	26	1586
TCGTCCCACACTCGATATTT	10901	CGG	26	1127
TAACCTCACAGTCATATCTA	11275	AGG	26	1081
GCAACAATGAGAGAAACAGT	21894	CGG	26	1010
AGTTTAATTGATACTGGAGA	13239	TGG	26	789
TTGAAACTGGTGGAAATGTA	16467	AGG	26	743
AAGTCACGTTGTAGTGGAAC	15498	TGG	26	688
ATATCTATTGATGTTGTAAA	11190	TGG	26	400
GCAACGTTGCCGAAACCACA	13941	AGG	26	338
TGGTTCGATATCTTTATTGC	13294	TGG	26	294
GATTCTTCTAACTTATTAAC	17482	TGG	26	134

TGACACCAATTTCTTCAGAA	757	AGG	26	17
TCATACTTAATTGAATTGTC	27063	TGG	26	15
AGGTGATTACCATGCTTAAA	34249	GGG	26	13
TAGAAACATTCTCTAAAACT	6734	TGG	25	1626
TTAATACGTCCATCAACAAG	28432	CGG	25	1166
AAACTACCCACCATATAGGC	14399	AGG	25	1117
GCAACGTGATGAGCTTATTG	11440	GGG	25	1020
TTTTGTTCTTCTGATTGCTC	19161	AGG	25	980
TTGATTTTGTCCAATAACTC	36925	AGG	25	704
GAAATCCATACCAACCATCT	38234	GGG	25	693
AGCGACAGGAGAGGTAGACA	39576	AGG	25	678
AGAGCACCATTATAGTGTCC	31087	AGG	25	594
TCATCTAAATCATAAGTAAC	16561	AGG	25	390
AGCGACAGGAGAGGTAGACA	39576	AGG	25	366
TAAGTACGGTGCTGATAGCA	21308	TGG	25	250
TTACTAGCAATGTATGAGCT	13680	AGG	25	197
ATTCGACTAAAGGTAAGAGT	14664	GGG	25	129
AGCTGGACTTGATAGCGCAA	18275	TGG	25	51
GTAAAAGCGTTAGTGGCATT	25184	TGG	24	1267
TAGCGTCCATTACACCTAGT	11361	TGG	24	1244
GATTACTTACGTAATGCGAA	676	AGG	24	1172
ACCAGCTTTAATGTAATAAT	28247	TGG	24	1082
GCTAAGTTATATAAACAAAT	36170	CGG	24	1022
GGAACAACGGTTACTGACGA	4004	AGG	24	793
AAGTAGCGCAATGAGTATGT	16792	AGG	24	709
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CATCCATTAGCACAATTGAT	28409	AGG	24	105
AGGGATATGTTCCCAATAAC	31223	CGG	24	94
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AGAAAGGATTACATCAATAA	36068	AGG	24	19
AATGTTGAAAGGAGAGAAAA	5843	AGG	24	12
GCGCTTAACAAAATACTTAA	35789	AGG	23	1280
TTAAATCAAGTGGGTGTGTT	18412	GGG	23	1140
CTAATCGTTACATTCACAAT	26638	AGG	23	1095
TTTCTGTTCAATTTAGAGTT	14132	AGG	23	1079
CCTTTTGCACCAGGTTGTCC	36784	CGG	23	1014
GCAACAATGAGAGAAACAGT	21894	CGG	23	876
TGTTTTTGTCCGTGTCTTTA	29361	CGG	23	833
GCACGTTACGGTATCTTACA	20255	AGG	23	776
GGATTGAAATGTGAGAGATG	7747	TGG	23	699
TCAAAGGTTTACAGTCGTTG	12525	AGG	23	630

AGGGTTTCGCAAACTAATTT	37660	AGG	23	542
AAGTACCGTCGTTATCTTTC	5203	TGG	23	509
TGGAACTGGTGCAAGAATAT	15512	TGG	23	462
GTTAGCACTAATGGGTGATT	20227	GGG	23	316
TTACTTGTACTAGATGATAT	8230	GGG	23	285
CAGGAGAAAGCGCAAGTGGT	39005	GGG	23	199
TCCTTTCACTTATAATCACT	26829	TGG	23	198
TATAACGATCCTGGAGCAGT	38752	AGG	23	198
CGGAAAGCCTCACGCAGACC	5642	TGG	23	194
TGCATTACTGCATTTGTATA	30073	TGG	23	135
GGTACTAATCCGGCAATCAC	24313	TGG	23	98
CAGAATGAACTATGAAACAG	11353	GGG	23	92
TACGTCAGCGATTTATAATC	30412	CGG	23	92
TCGTAATTATCTATTTCTAT	21986	AGG	23	73
ATTTAATGATTCTGCAGCTG	308	AGG	23	58
GTACAAGTTGGTCACAGATA	26049	TGG	23	52
TGCAAACCCCGCTAAAATGG	23989	CGG	23	19
CTTTTATATGAGCAAGAGCT	8793	AGG	22	1324
CACTGGATAGACAAATGTCT	35616	AGG	22	1277
ACAAGTGCTAATTAACCTGA	17521	AGG	22	1040
TCAGCTAAGCGCATGCCATA	9571	AGG	22	914
CCTAACAACAAAGAGATGAT	16985	AGG	22	874
TGGAACTGGTGCAAGAATAT	15512	TGG	22	700
CACAAATGATTTAGGGTAGG	38158	TGG	22	687
TTACTAAGCATGGCACGATA	22078	CGG	22	537
CATATCGTACCAGATTGGCA	10188	AGG	22	536
AACATTCACGTGATCCGTAC	9735	TGG	22	238
TGATGAGGAACTTCGCGGAA	33575	TGG	22	208
GACGCAGGGTATTCGACTAA	14654	AGG	22	175
ACAACATTAAAAATTAATGA	22794	CGG	22	91
GTGTATATTTGCCAATTGTC	7002	AGG	22	87
AGATGTTAAAGCTAATGATA	27465	AGG	22	85
ATAGATAGTTTTTTATTGTC	5315	CGG	22	58
ATTTAAGGTGGTTATTCTTA	1698	TGG	22	46
GTACTTACCAGAAACAGCAC	31133	AGG	22	46
GTTGTCTCAAATGTAGGTGA	26264	CGG	22	35
CTACGTTCAATAAATGTGAA	14455	AGG	22	30
CTAACAAAACAAATACTGAG	33697	GGG	22	12
GCAAAGATCATTAAACAAAA	2276	CGG	21	1200
AGTGGTAAACCGCTTGTTGA	19958	AGG	21	1088
GTATCAAATGGATATACCTA	30556	TGG	21	1025
AATTAAGTGGTACGTAGACA	33803	TGG	21	705
ATTGAAATGAGGTGCATACA	34363	TGG	21	392
AGCTTTTAGGAAAGCGAGCA	29512	TGG	21	89
TTGCGATAGCGTATGCTAGG	8057	TGG	21	66

ATTAATAACCTAGTAAGGTT	6264	AGG	21	57
AAGATTTAAATGTAGATAAC	39754	AGG	21	49
GACCAATCTTAGGTAAGTTA	24938	TGG	20	968
TATTATGTATTTCGAGGAGA	16895	AGG	20	930
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TCAAGTGATTTAGGAATATC	37684	AGG	20	817
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GCATATAATTACTTCGGTAT	35948	TGG	20	444
ACATCTGTTTCAATTTCGTT	23689	TGG	20	426
GACGGTATGAGTGATGCACT	26282	TGG	20	409
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TATATGTATCGAGTGATGAC	40072	AGG	20	164
TTACAACATCGTCGATAATA	36441	AGG	20	79
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CAAATAGATAAAGGTGACAG	14987	TGG	20	30
AAAAAGCGCATCTCAACCGA	37312	CGG	20	30
CTCTATTATCTCTTCGTACA	18682	AGG	19	1313
AAAATAGAATAGTTTGTGTA	33054	CGG	19	1194
GGCGTTGCGCAACCTGGTTG	38551	GGG	19	971
ACGTCATCAAATTCTTTTAT	16181	AGG	19	919
ACTTACTTAGCAAAAGGTGT	19706	AGG	19	893
AAACTACCCACCATATAGGC	14399	AGG	19	772
ATAGGGGTAACTATTGGACC	30827	TGG	19	634
CTTATCAAATACCGTGTCTT	10514	TGG	19	548
CTAACAACATCACCTATTTT	28564	AGG	19	530
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TCAATTAGTTTGTCCGCCTA	5991	TGG	19	385
ACAAGGTATTATGAGTGGAG	18152	AGG	19	321
ACTCTTTTTGCAACCATTCC	9511	AGG	19	211
ATCAAGTGGGTGTGTTGGGC	18416	AGG	19	174
AACATCTCAAGAAGGGAAAT	38035	GGG	19	166
AAGTTATGAGGGTTATTTAT	32862	CGG	19	126
AAACTTACCAATAAGATCAT	4908	TGG	19	116
TGTTTACCCATATATTGTTG	21839	TGG	19	75
CTCATCAATATCATTCTGAT	17679	TGG	19	70
ATAAGTGCTAGTGCGTATAA	11667	CGG	19	60
TTCAGTGATTTCTTAAATGC	26321	CGG	19	40

ATTGCAAATGCTAATTGTGG	9915	TGG	19	37
TAAATCAACGGTATTGTTCG	33007	CGG	19	33
GCAATACCTTTAAAGTCTTT	31333	AGG	18	1039
GTTATCGGATTCGTTAATAC	33381	TGG	18	947
GGATTCAATGTTATATTTAA	22920	CGG	18	879
TCTATCAATAAATTGTCCGT	30182	TGG	18	824
TGTTTTTGTCCGTGTCTTTA	29361	CGG	18	777
CCAAATATCTGACCAATCTT	24949	AGG	18	743
AGTATAAAAGAATGTTTATA	10613	TGG	18	590
CTTTTGCGATAGCGTATGCT	8060	AGG	18	507
AGAATTGGTTAACACCTCTT	30867	TGG	18	483
CTAAATCAATGGCTCAACGA	23769	TGG	18	447
CCTATCATCTCTTTGTTGTT	16969	AGG	18	323
GGCGAATGGTACACAACATA	21615	TGG	18	309
ATGAAAATATAAGGGAGTGT	12626	GGG	18	229
GATTGGGATTACGCACGTTA	20243	CGG	18	222
AAAGACTTTAAAGGTATTGC	31352	AGG	18	211
TTAATAACCTAGTAAGGTTA	6263	GGG	18	132
ACCGTTGATTTATGTTCATT	32979	AGG	18	126
AAACTCATAGATGAGGCACA	8508	GGG	18	104
TTATCAGATTTAAAAATCGT	31277	TGG	18	24
GCGCTTAACAAAATACTTAA	35789	AGG	18	18
TTTATGTTATAGCTAGCCTT	39803	CGG	17	969
TCAACGCTACCTGGTAAATC	32823	CGG	17	967
TTCTTTATGATAATATGGAT	16126	AGG	17	947
ATTGATCATATAGTTGTAAT	34988	GGG	17	497
GCAGTCATTGGTGTATTCAT	25526	TGG	17	439
GTAGAACTTATGCAAAGTAC	11052	AGG	17	325
TATGTTTGGCACCCTACAAA	16170	CGG	17	320
CCGAAAGCGTTTAGAGATGC	31061	AGG	17	195
CGTATTGTTGTACCACTCAT	29338	AGG	17	168
AAAAGAATTTGATGACGTGT	16202	TGG	17	95
GCAAGCGACTACAAAAAAAG	38685	AGG	17	95
GATGACATGAACGCTATAGA	26714	CGG	17	59
ACCCTGACCATCCCGAGCAT	15544	TGG	17	58
TTCCCGTATAACAGTTTACC	39969	CGG	17	52
ATTGAAGAATTTGATGATAA	4433	CGG	17	35
GTACAAGTTGGTCACAGATA	26049	TGG	17	35
CTCAACCGACGGTTAAAATT	37323	TGG	17	14
AAATAAATACCATTTATTAC	830	CGG	16	928
TTTTCAACAGGATTTAGTGA	10412	TGG	16	776
TAAATCTTTTTAGAGTTATA	32910	AGG	16	701
GTGAAACACGCTGTACAAAC	22371	AGG	16	653
TTTGGAGCACTGTTACAAGT	26100	TGG	16	645
GGTACTAATCCGGCAATCAC	24313	TGG	16	626

TTTATTAAACCTTACAAAAA	5010	GGG	16	546
CAACGACTCTAAAACGTATA	37030	CGG	16	519
TGGTTCTTTGATGTACTGCC	31085	TGG	16	487
TAAAGTTACATTACAGCCCC	6035	TGG	16	483
AATAGGATCTGTGGTTTTGT	40170	TGG	16	442
TGAGGAAGAAGCCACGAATA	10815	CGG	16	406
AGCGTCGTTAGCGCATGAAG	15461	AGG	16	402
AAAACCTGTGATTAGTAGCA	2641	GGG	16	299
CCGATTAACTGCATAATAGT	25138	AGG	16	232
AATAAGGAGTTAACTCGTAT	17877	AGG	16	225
ACATTATGAAGCAGTCGGCA	5667	AGG	16	159
AATGCCCCTACATCTTGTGC	14480	AGG	16	148
CGCGGGTCATCAAAATTGGT	35146	TGG	16	131
ACCTTGTAAGTAGTTAGGGT	30647	TGG	16	121
TACAAGTGTACTTACAAGTA	1966	CGG	16	120
ATAAGTGCTAGTGCGTATAA	11667	CGG	16	105
AACTTCAATTGCAGAACAAA	29258	AGG	16	66
TCGGTTGATTCTATATCTAA	6310	CGG	16	63
TGTTTTGTTAGTTTTCAGTT	33669	CGG	16	58
ACAATAACAGAAGCTTGGAA	25592	CGG	16	43
GCTCTCTCGTTGCATAATTC	9614	TGG	16	41
CGACCTCTATGCTTGCAGTT	10853	TGG	16	39
TATGTGTTTTCTGGTGTTGG	2808	TGG	16	38
CTATAAATATGAGGAGGCAC	11849	AGG	16	33
CTTAATTTAGGCAAGTATCA	35753	AGG	15	942
AATGGTTACGAGTATAAAGA	7816	CGG	15	847
ATATTTGGCAATGTGTTCGC	24980	TGG	15	842
TTAGGTAAAACATCAGGTTC	33280	TGG	15	835
GACAGAAACTATTGAGTACG	3786	AGG	15	721
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GCAACGTTGCCGAAACCACA	13941	AGG	15	636
AATCAAGAAAAGTTTTATAA	4674	CGG	15	617
GCATATAATTACTTCGGTAT	35948	TGG	15	568
TGAGGAAGAAGCCACGAATA	10815	CGG	15	546
ATGCTTGGTTTTTCGTCTGA	35542	TGG	15	542
CTAAATCAATGGCTCAACGA	23769	TGG	15	539
CCGATAATTTGAGCGACTGC	25276	TGG	15	457
CCTATCATCTCTTTGTTGTT	16969	AGG	15	441
AGAAAAATCGCCATCAATTC	454	AGG	15	437
GGATCACGTGAATGTTTTTG	9712	TGG	15	403
GAAACACTTTCTTCATCTAC	37945	TGG	15	402
CTAATACATGTTTGTCATAG	5695	TGG	15	388
TTATCTAATTGTTTATCGAT	1389	TGG	15	346
AAAGGAACGCTCGACGGACA	35813	AGG	15	340
TTTGAAATGTACGAGATGGA	10556	AGG	15	322

TCATAGAGGGCAAGAGCCAA	14619	CGG	15	313
GAGCTTTCCTTACGTTGCTT	23643	TGG	15	290
TTATGATTTGTATAAGCTGT	8936	TGG	15	273
CTATCTCGTAAGTTCAGCGT	11931	TGG	15	251
GGTATATATGCTACTGGTCC	21546	TGG	15	211
TTTGTGTCGTTCATATTCGT	38125	AGG	15	208
GAGAATTACAAGGAAATCAT	23226	GGG	15	182
ACAAAGCGATTTTACAATTT	22960	TGG	15	155
TAGATAACAGGCAGGTACTT	39766	CGG	15	123
CGTATATTTCTTCTTTTTGA	29736	TGG	15	100
GCAAGTATATATTATGATGA	13718	CGG	15	87
CCAGAAAGGAGATAACGAAA	6879	TGG	15	84
ACTAAGACATCAATTTTAGT	2246	TGG	15	69
CGCTATTAATGTTAGTACAA	27769	AGG	15	69
CTTGGTCGTCATATCCAAAT	5134	TGG	15	65
CCATCATTCTTTTTATAAAA	32595	CGG	15	63
GATATTGATGAGTATATCGA	17706	GGG	15	32
TAACTTAGTCATGAAATGGT	3573	AGG	14	821
CAACGACTCTAAAACGTATA	37030	CGG	14	746
TGATTTCATCACTGAAAACG	23045	AGG	14	719
ACAAGAGTGCCGGATTTACC	32830	AGG	14	689
GTCAAGCGCCACAGCCATTT	21637	TGG	14	667
TCTACTACGTCCGTAATGCT	4546	AGG	14	629
AGAGTTATTACAAATACAAA	11907	AGG	14	582
ATTTCTGCTTGTGCATATTC	19753	AGG	14	513
AAATTCGAGGGATTAGGCAA	28130	AGG	14	479
AACAACTCATTGAAAGATTA	24206	CGG	14	465
TTGAAATGAGGTGCATACAT	34364	GGG	14	445
ACAGTTTCAGGACCCCAACC	38547	AGG	14	414
TCCGATAAAATAACATTGCC	19546	TGG	14	409
AACTAGGTGTAATGGACGCT	11379	AGG	14	362
ACAGAATTGGAAATTATGAA	5442	AGG	14	347
GCATTCTCTGTCGCAGGTCT	24416	TGG	14	338
TTATGTTATAGCTAGCCTTC	39804	GGG	14	330
AGCAATTCAATTGCACAGTA	13911	TGG	14	329
GAAGCCTTAAACGCACCTTA	9572	TGG	14	300
AACAAAACGGTATAAACATC	2289	GGG	14	261
TCACAACTGCCATTGTGATG	2568	AGG	14	245
GGTCAAAACTGGAACGGTAA	38518	AGG	14	235
CGACGAAAGTTATTGGGATT	7647	AGG	14	206
AGCTAGGGAGTTTAACGGTA	3714	TGG	14	178
TAAAACAATTAAAGGATTTA	21073	TGG	14	152
TCCGCAAAACGCCGGTTATT	31228	GGG	14	145
GTAAGTGGAACTTATCCAGG	33097	TGG	14	111
TCAATACCTTTACCTAAAAT	6805	AGG	14	101

AGATTGCTTGTTAAAAACGG	30218	CGG	14	93
ATCATAAAGCGTATATACAA	8968	GGG	14	89
CGATAAGAAAATAGAAGAGT	21350	GGG	14	83
GTAGTAGAAGCAATTAGAAA	4577	TGG	14	54
AACTATCATTAAAAGTTAAA	22519	TGG	14	26
ATTACTTATATTGCTAATCT	39538	GGG	14	14
AAAAGAGTTGTCTCAAATGT	26258	AGG	14	13
GCTAAATGAAGATAGTTCTT	27802	TGG	13	1098
ATGTACGTAGCGGTATAATG	37640	AGG	13	837
TGAATCATCACATTTATTGG	11327	AGG	13	825
AATACTGTCTTTAAAGGAAC	28070	GGG	13	734
ACAACATTCAAAGATTCAAC	12466	AGG	13	673
AACGCCCTGCTACTAATCAC	2629	AGG	13	633
TCATAAGTGATACCTTGCAT	30583	AGG	13	581
ATTCACATTCCAGCAAGCAC	35599	TGG	13	505
GTGTCTGTTGATGACGTTAA	19024	AGG	13	480
TAACTAGCCACTGTGTATAT	13350	AGG	13	474
TTATTTGCTAATAGTTTGTT	2738	CGG	13	452
TCAAGTTGTCTATAAATATG	11840	AGG	13	355
AGCACAAACTTTTCTTGCTT	14575	CGG	13	354
ATTAAAGTACCTTGTTCTGC	19588	TGG	13	262
ATGGATTTATTCAGCTGTAT	30283	TGG	13	194
TTAATAATTGTCTTTGATCT	23367	AGG	13	178
GCTGTAGTGAAGTATAGAAA	3134	CGG	13	155
TCCGTTTTATCAGTGCCTAT	29215	CGG	13	125
CCACAATTAGCATTTGCAAT	9934	AGG	13	118
ATACCTTGTGTTACGCGGTA	17095	TGG	13	105
CATTAAAACTTTTTATGTGT	33761	GGG	13	96
TAAAGTTACATTACAGCCCC	6035	TGG	13	92
TCATAGAGGGCAAGAGCCAA	14619	CGG	13	92
ATAATTATGGATCCTATTTT	6801	AGG	13	75
TCATCACCTTTAAAACTCCA	21575	CGG	13	72
CATGTTATTTGGCGTTCAAG	15362	TGG	13	71
AGCTAGGGAGTTTAACGGTA	3714	TGG	13	69
TATTACCGCAAAGATAATTT	2947	AGG	13	62
TCCCAATAACCGGCGTTTTG	31213	CGG	13	60
GTTATTTTTTGCGTTTTTTT	40223	GGG	13	41
ACTTAAGGAGGAACAACAAA	942	TGG	13	18
AGCTTTAGTTGCATTATATT	23906	TGG	13	18
TTGATATCAAAACAGCTGAA	7505	TGG	13	13
AACAGAATGAACTATGAAAC	11351	AGG	12	736
ATTGAACAAAGCACCGAATA	23153	TGG	12	565
ATTTCAGGGAGCGAGATGCA	8432	TGG	12	529
CAAGGTATCACTTATGATGC	30605	AGG	12	519
CATTCGAAAGGATTAGAATC	19103	TGG	12	515

TGTACGTCTAACGGCTTACC	12027	TGG	12	498
CGGAATACTAGAAGATGTTA	20705	GGG	12	486
TAATATCGTAAAAGCGTTAG	25177	TGG	12	471
TTTAAATCAAGTGGGTGTGT	18411	TGG	12	462
GCCAATTGTCAGGACGACTT	6992	AGG	12	442
AGGGTACGCGAAGGGCAAAA	18906	AGG	12	418
CACAAATGATTTAGGGTAGG	38158	TGG	12	401
AAAGATATTGTAAGTAGATA	15957	TGG	12	368
CATTGATCATATAGTTGTAA	34987	TGG	12	340
GGACATGAAGTTGCATTATA	38848	CGG	12	282
TTAGTGAAAACAAACTTTCT	33455	AGG	12	275
GAGATTAAGTCACGTTGTAG	15492	TGG	12	273
TACCTTGTGTTACGCGGTAT	17096	GGG	12	261
CCGCCCATGATTGCTTTTGC	36016	TGG	12	259
GCATTCCTCGCTAGTTTAGA	14879	TGG	12	257
CGATTCTATCGTTATTCATC	34592	TGG	12	254
CGACTAAAGGAGGCAACCAA	29611	TGG	12	246
GTTTTCCCGTCAAAGTATGG	38437	TGG	12	229
AACTCTTCTTTAAATTTAAT	33428	AGG	12	226
TGAATATCATACAAGGTTTG	25785	TGG	12	188
ATATCACTGTTCCTATGGCT	25812	TGG	12	180
TCGTCATGATTATGATTTTT	37213	TGG	12	177
AAGAGAACGCAACAAAGAGC	11476	TGG	12	167
TCCGAAAATGGCATTTCGGT	7173	TGG	12	156
GGATCTAAGTCAGTTTCAGC	22166	TGG	12	140
TAAGCGCAGTTAACACATCT	32351	AGG	12	114
CCAAATCGTATCAAGTACAT	25934	TGG	12	113
GCCTTTGGATACTCATTTTA	23608	TGG	12	108
GTTAAATGGAATACAGCAGA	22533	AGG	12	81
ATACACATGTAACAGAGAAA	138	TGG	12	73
GTTTTAATGTCTTTAAAAGT	33731	TGG	12	56
CCTGGTGCAAAAGGTGAAGC	36809	AGG	12	51
TTAGTGAAAACAAACTTTCT	33455	AGG	12	39
CTTTTTCACACCTTGCCAAT	10181	TGG	12	38
GAAGAAAAAGAAAAGTGAAA	9068	TGG	12	34
AACATTCACGTGATCCGTAC	9735	TGG	12	19
GCGCACGCTTTCTTAGAAAG	35891	TGG	12	11
TTTGAAAGCAGTGGCCAATT	5136	TGG	12	10
AAATGATTCTGACATTGCAT	22287	TGG	11	924
TTCTATGAACGTAATATCAA	15699	CGG	11	884
ACGACTAATCTTGCAAGAGG	29069	TGG	11	701
TGTAGACTTTTTAATAAAAT	27718	TGG	11	569
GTACTGGTGGCGTTGGTAAA	31476	TGG	11	529
ATACTTGCTGGTGCAACATT	15261	AGG	11	525
TACAACATCGTCGATAATAA	36440	GGG	11	490

CCTTAATATTCGACGATAGC	8573	GGG	11	479
ACCGAATATGGCCAAAAGCG	23165	AGG	11	477
TGGACGATCACTCATGTTGA	27884	AGG	11	471
TCCTAAAATCCCTTTAAGCA	34242	TGG	11	460
GACGCAAAGCGCTTTTAATA	30810	GGG	11	374
ATTTTCAATAAGAAAAACAA	31190	CGG	11	347
CAGCCATATTTTGCTTTAAT	32000	TGG	11	347
AGGTTTAGTATGTGTGTATA	16224	TGG	11	342
GCTAAATGAAGATAGTTCTT	27802	TGG	11	316
AAAGTAATTGCTACAGACTT	26510	TGG	11	303
GTTTACACCAATAAATAGCT	18426	TGG	11	290
TAGAAATAGTGTTGATGATG	16651	AGG	11	289
TTAAATACTTTCACATCATT	38497	TGG	11	277
GACAAGTTTCAGAACGAACA	17544	AGG	11	275
ATAGATACTTCAGATAAGAA	24634	TGG	11	243
TGATATTGATGAGTATATCG	17705	AGG	11	218
GTCACCTGATAACTTTTATT	37593	AGG	11	218
TCAGCTAAGCGCATGCCATA	9571	AGG	11	195
GTGGTGTTTGGTTATTGTCA	35274	GGG	11	171
TTAAAACCCCTAACCTTACT	6272	AGG	11	169
CAGTTGTGACGTGGAAGGTT	2598	TGG	11	165
ACACCAGAAAACACATATAG	2830	AGG	11	133
ATGGCGTTGCGCAACCTGGT	38549	TGG	11	128
GTGCCTATATCCGTCTTTTC	32388	TGG	11	114
GTATCAAATGGATATACCTA	30556	TGG	11	107
TCTGATTAATATTTCTAAAT	3009	TGG	11	105
AAAAGAAATCGATGTTAAAT	36631	TGG	11	104
GTGCCAAACTGCGATGTCTC	34612	AGG	11	102
CGATATTTGATATTTAGAGG	8827	TGG	11	96
ACCGATAGGCACTGATAAAA	29230	CGG	11	71
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CACTACAGCATGGTCAATTG	3164	CGG	11	41
TGGAGTTTTAAAGGTGATGA	21594	CGG	11	41
ATAGGTATCAATGACAAACA	36353	AGG	11	37
TACTTACGTAATGCGAAAGG	679	TGG	11	28
TGAAGCAGTAGGGATTATGA	11816	CGG	11	26
TAAACTACTACGACTTAAGC	21268	AGG	11	25
TAGCTATAACATAAAAAAAT	39779	AGG	11	22
CATAAGATGACAGAGGCGAA	32734	TGG	11	14
AAAAGATTATGGCTTATATT	38934	GGG	10	732
ATAAACGAATTTGGCAAAGA	11552	TGG	10	647
ATACGCACTAGCACTTATAA	11646	CGG	10	645
AAAGCCTACAGCTAGTGAAG	34408	TGG	10	630
TCAAATGCTTGTTTGTCTTT	27102	TGG	10	548

ATTGAACTTGATGAAGCAGT	11805	AGG	10	514
AAGAATGACATTGAAATAGA	14834	GGG	10	503
AAGCATAGAGGTCGAAAAAG	10878	TGG	10	494
GCGTGTTTGATAACCTTTTT	36487	AGG	10	462
CTAGCCAATTAGGGTGACGC	35163	GGG	10	441
AACACGAGCACAAACGAGCT	35680	CGG	10	435
GCTTTTTGCTTATCTGTCTT	5042	CGG	10	381
AAACGTTCTTTCGGAAGAAT	24131	TGG	10	363
TTAATAGGACGAGGTATAGA	15867	TGG	10	346
AAAGAAGATTTTGAAACTGG	16457	TGG	10	343
ATGCAGTAATGCAATCATTT	30099	TGG	10	331
AAAAAGAACGGGTTAACTCC	9509	TGG	10	318
CTGATGTTTGTGTCAATAAT	31578	TGG	10	299
GAATTAGCTATCATAACTTC	1365	TGG	10	291
AAAAGGTGTAGGCGCCTACT	19717	GGG	10	235
CTGGATTTAACTAGAATAAC	25430	TGG	10	226
AAAACATCCAGTGACATGCT	39871	TGG	10	200
AAAAGGTATCTACTTCACAA	36196	GGG	10	185
AATCGAACGCTTTCAATGTT	26027	TGG	10	171
GGAGAAGAAAGCAAGTGCAT	11497	GGG	10	128
TTAATTAAGTTATCGATATC	9098	CGG	10	124
TCACAACTGCCATTGTGATG	2568	AGG	10	117
ATTCTTAAGTTGTCTTTCAG	30455	TGG	10	103
CAACACAAAGAAGTACATCA	13390	AGG	10	98
GAGCCTTTATTTATATGAAA	17984	TGG	10	92
TAACTTCTCAATTTAGAGCA	25068	TGG	10	71
CGGATTAGTACCTGCAATAA	24340	TGG	10	70
AAAAAGAGTACGTGGTGGCT	9541	GGG	10	63
TTACCTATCAATTGTGCTAA	28396	TGG	10	62
TTAAAGTGATTTAAAAACTG	6190	AGG	10	61
TTACTTGATAGTTCTATTAT	577	AGG	10	53
TCTGGATTTGTACCGGAACC	34610	TGG	10	40
CCTAAGATTGGTCAGATATT	24965	TGG	10	30
CGTGGATAAAAGTTGATGAG	5812	AGG	9	0
CTTATACCGAGAAGATGGCA	8642	CGG	9	0
TATGAAAATATAAGGGAGTG	12625	TGG	9	0
ATACTTTGCTGGTGTCGACT	15818	GGG	9	0
GGTGTCCCTGATTACATTAG	20886	TGG	9	0
GAAAGATTACGGCGAGAAAA	24217	TGG	9	0
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TACTACACCTTGAATCGCAC	25616	CGG	9	0
TGGCGACTTCTCAGGTGCTT	25906	GGG	9	0
TGCGCTTAAAACGCTATCTA	32320	TGG	9	0
AGTCACAGGTGTAATGCTTG	33892	AGG	9	0
CTTTATTTTTAAAAGATATT	34510	GGG	9	0

TTTTAGTCGTTTTTTTATTT	37834	TGG	9	0
AAAAATCCACCAGTGCCAGC	39334	AGG	9	0
AATCAAAAAATACAACCAAC	7597	TGG	8	0
ATAACCAAATGTTCAAGAAA	9771	TGG	8	0
TTAGCATATATTGATACGAA	16721	TGG	8	0
GATTCCAGCAGATGGAAATT	24065	AGG	8	0
AGAGTGGTGGATTCTGCCAT	28601	AGG	8	0
CACTGGTGAAAAATATCCAG	33857	AGG	8	0
TAATGTTTGGATTTACCAAA	33944	CGG	8	0
GCCAGTAATTGTTGAGTCAT	34865	TGG	8	0
ATGAACGACACAAATGATTT	38150	AGG	8	0
AAACCAACGTTTAATGATTG	4199	GGG	7	0
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CTAATTTTGTTAGCAGTATT	26082	TGG	7	0
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AGTGCTGACGATATTGATAA	30518	AGG	7	0
TCAACGGTATTGTTCGACGG	33010	TGG	7	0
CAAAGTCGAATATTGGTAAG	34440	AGG	7	0
GCAAACGTCATTGCATAATC	35971	AGG	7	0
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ATCGTATTTGAAAATGATGA	4779	AGG	6	0
GAACAAGTAGGACAATCACA	25094	AGG	6	0
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CGATGCGATTTCATCAGCTT	26413	GGG	6	0
ACTTTCAAAGTATGGTAGTT	27229	CGG	6	0
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GGTAAATGGAGTTTATTCGA	31490	GGG	6	0
AATGAATTTTTAAAACATTC	31819	AGG	6	0
TAAAGTAGTGCTACTTGTTT	33214	TGG	6	0
GCTGTAGGCTTTCTAGTCTT	34381	TGG	6	0
TACGTAATTGTTGTGTTGTT	39465	GGG	6	0
GGACCTAGAAGAGAAAATTG	6598	TGG	5	0
TATTCGACTAAAGGTAAGAG	14663	TGG	5	0
GTGCTTTCACAAGTATTTCT	25485	TGG	5	0
GTTGACTCAGACGGCAACGG	33184	TGG	5	0
AGTTACTATAACTAAAATTA	33318	TGG	5	0
AGTTTTATAACGGCTCAGCA	4684	GGG	4	0
ATCACACTTATTGAGGAGCA	12816	TGG	4	0
GTAGGCGATTCTGTAGATCA	21230	GGG	4	0
CTGAGAATTTTTCAGCTTTT	22846	CGG	4	0
TTATCACAAAAGGTTCTGAA	26178	TGG	4	0
CGTAACTATTCTGATATAGA	26890	GGG	4	0
ATTTTATTAAAAAGTCTACA	27737	GGG	4	0
CCCGAAAAAATCTCATACAT	35644	GGG	4	0
AACAAAATACTTAAAGGAAA	35795	AGG	4	0

ACTGCATACGGTGTTAATGT	38905	AGG	4	0
AATTTTGCTACATTAATTAT	39660	AGG	4	0
CTGTGGTTTTGTTGGTTGTA	40162	GGG	4	0
AAAGCAATTATGAAAAGAGT	194	AGG	3	0
AAAGCATAAAAAATGGTATT	3048	AGG	3	0
AGGGGTCCAACTAGGTGTAA	11371	TGG	3	0
CTTACTACCTGCCTATATGG	14408	TGG	3	0
GATCAGAATTTTAAATCAAG	18402	TGG	3	0
CTAATTGTTCTCGAGTTGGT	22993	GGG	3	0
ATCGAAAGGAGGTTAGCCTT	23593	TGG	3	0
AATTGGGCTAATAGTGTGGC	24896	TGG	3	0
TAGGTGCTATAACTAAAATG	27864	TGG	3	0
ATAAATTCGGAACAACGAGC	32705	TGG	3	0
ATAACAAAAAACTAGCCCGA	39803	AGG	3	0
AAACATCCAGTGACATGCTT	39870	GGG	3	0
ATATGTATCGAGTGATGACA	40072	AGG	3	0
GAAAAATCGCCATCAATTCA	454	AGG	2	0
TAAACTTTTGAAATCTAAAA	725	TGG	2	0
GAATACTTAAATAAAAAAGC	7390	AGG	2	0
CCCGCTAAAATGGCGGTTAA	23996	AGG	2	0
TGGCGTATTTTGGGCTTTAA	25333	TGG	2	0
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CATCACTCAATTTATTCCAT	30860	CGG	2	0
AAACTTTAGATGCTATCCAG	34085	AGG	2	0
CTTCAATAACTAGCCAATTA	35172	GGG	2	0
AATCAATTCTTAGCGAATAA	37925	AGG	2	0
GAGGCCATGTATCTGACTGT	40047	TGG	2	0
GGCAACGCAGATTGTTTGAG	2310	TGG	1	0
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CTTTTTGGCAGTAAATTTGA	7567	GGG	1	0
TTTGATACAGCGGAAGAGCT	10224	CGG	1	0
ACTATTTCTAATGGCAAAGT	16622	TGG	1	0
TAGTAAACCTGTCTATATCA	22045	GGG	1	0
AAACACGCTGTACAAACAGG	22374	TGG	1	0
AGCCCAATTTTGGAAAGCTA	24866	TGG	1	0
TAGATTGGTTAACTCAATTG	25653	TGG	1	0
GAATATAACGTTACAGGCGC	26860	AGG	1	0
GATAGATTGCCTACAAACGA	27325	AGG	1	0
AACAGATGCGCCAGAAAAGA	32394	CGG	1	0
GAAATACATTTAGACGCAGC	38986	AGG	1	0
ATGACGTTAATCTGGAAAGA	10685	TGG	0	10
ACGTAATATCAACGGTATGT	15707	GGG	0	10
GACTGGGGTTACGAGCACTA	15834	TGG	0	10
ATTCATGACTTATCGTGAGT	18578	GGG	0	10
ACAGTTGAATACGAAAAATT	22605	CGG	0	10

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CATGCAAGTTTTAGGTGTTT	25738	TGG	0	10
TAGCTTAGGTAAAGGTTTAG	26476	CGG	0	10
TAACCGACACTTTCAAAGTA	27237	TGG	0	10
GGAGATAAAATAATCTTCGA	27553	CGG	0	10
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CGAAACCTTGTAAGTAGTTA	30651	GGG	0	10
ACGCAAAGCGCTTTTAATAG	30811	GGG	0	10
GTGCAATGTTTTTTAAGAAT	30882	TGG	0	10
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CCCATGTATGAGATTTTTTC	35628	GGG	0	10
ACCTAGATTACATTTGTTTA	36406	TGG	0	10
CAGCTTTTTACCGCAAAAGT	38406	TGG	0	10
TTCCCTAACAACTTAAGCGT	38638	TGG	0	10
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AAAATATCTCTTCCTTCTTG	869	AGG	0	9
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CAGGTGGACAGTTGCGTATA	22390	TGG	0	9
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CTCTTATCACCTTCGTTTGT	27318	AGG	0	9
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ACCACAGATCCTATTAATTT	40194	AGG	0	7

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TTAATTATGCTCGTAAGAAT	1241	CGG	0	6
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CACTCACGATAAGTCATGAA	18560	TGG	0	6
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ACTTCATTCGTAAGTGGACA	26444	CGG	0	4
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GAAGTTTCAACTTATTATAA	26736	GGG	0	3
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AATACCATTTATTACCGGGT	825	AGG	0	1
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AGTTGTTGGCTTTGGTGCAA	24439	TGG	0	1
GGCTATTAGCGCTCTTAAAA	24460	TGG	0	1
ACGCACGCAAGTTTGAGGAT	24687	TGG	0	1
GAAGCATTGAATAGCATAGG	24743	TGG	0	1
GATTTCGTTACTAATTTAGC	25241	TGG	0	1
GGTGTTATCGGTATTTTAGG	25313	TGG	0	1
GGATTTAACTAGAATAACTG	25432	GGG	0	1
AGATTGGTTAACTCAATTGT	25654	GGG	0	1
GATTGGTTAACTCAATTGTG	25655	GGG	0	1

CAAGTATTCATGCAAGTTTT	25730	AGG	0	1
TACTATGATTTGGACAGCTA	25835	CGG	0	1
TTGGAGTGTGGCTGAAAAAA	26137	TGG	0	1
TGGAGTGTGGCTGAAAAAAT	26138	GGG	0	1
TTCGCGAGTAAAGTAGCTGA	26231	TGG	0	1
TCGCGAGTAAAGTAGCTGAT	26232	GGG	0	1
TTAATCGGCAAAGTAGCTGA	26351	GGG	0	1
TCTGTAACTTCATTCGTAAG	26438	TGG	0	1
TGACACAACACAAACATCAG	27198	GGG	0	1
CTACCATACTTTGAAAGTGT	27250	CGG	0	1
TCAGGAGAAGTTTATTATAA	27385	CGG	0	1
AAGGAAGTTGATTTAAAAGC	27532	CGG	0	1
CACAAATTATATTTTAGATA	27700	AGG	0	1
TAAAAAGTCTACAGGGTGTA	27744	GGG	0	1
GCGAGTACGTTTGACGCAAT	27845	AGG	0	1
CAATACTGTCTTTAAAGGAA	28069	CGG	0	1
AATTTAGATGCATCTACTTT	28096	TGG	0	1
AGTAGATGCATCTAAATTCG	28117	AGG	0	1
GTAGATGCATCTAAATTCGA	28118	GGG	0	1
GCATCTAAATTCGAGGGATT	28124	AGG	0	1
TATACCTTTATTAAAGGTTA	28331	TGG	0	1
ATTGGCGACTCTGTAGCTAG	28991	AGG	0	1
TTGGCGACTCTGTAGCTAGA	28992	GGG	0	1
TGCAAGAGGTGGCGCAACAA	29080	TGG	0	1
AGTTCCAATAGGTAAAGAAG	29107	CGG	0	1
ACTGATGATGATTGGTTACA	29192	CGG	0	1
ATCACTAGTATTTTTGAATC	29296	TGG	0	1
ACACGGACAAAAACAAACTA	29385	GGG	0	1
ATGCTCGCTTTCCTAAAAGC	29494	TGG	0	1
CCTCGTGACCTTTTTCGTTA	29532	GGG	0	1
CCCTAACGAAAAAGGTCACG	29548	AGG	0	1
GATTATTTAACGTATTTAAA	29819	TGG	0	1
CTAGAATCATATTGCTAAAA	29826	CGG	0	1
ATTCTAGGCCATAACGGCGA	29858	CGG	0	1
CTTGCTCTTTTGGTTCGAAT	30024	CGG	0	1
GATAAATCAGTGATAAATTC	30049	CGG	0	1
TATAAATAATTTTCGTTCTA	30111	GGG	0	1
AATGCGTATAGATACATTGA	30254	TGG	0	1
GTACGTTTCCAATATAGAAC	30329	TGG	0	1
AGACAAAGTATTGTATCAAA	30544	TGG	0	1
GTTAACACCTCTTTGGCCGA	30860	TGG	0	1
ATTTATTCCATCGGCCAAAG	30869	AGG	0	1
GCTGGGTTCTGTATTGGTAA	30943	CGG	0	1
GTAATATCACTTAGATATGC	30961	TGG	0	1
CTAAGTGATATTACGGAAGT	30986	TGG	0	1

TCTCTAAACGCTTTCGGTAA	31039	CGG	0	1
CCTGCATCTCTAAACGCTTT	31045	CGG	0	1
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AATTTCTGTCCGCAAAACGC	31220	CGG	0	1
ATAATTTTGTAATATTCTTA	31242	GGG	0	1
ATGGAGTTTATTCGAGGGAA	31495	AGG	0	1
TATGAATCAGATAGAGGAAC	31621	TGG	0	1
ACGATAGTAGACGCAATTAA	31774	TGG	0	1
AGGCATTCTTTACACAAAAC	31856	GGG	0	1
GAAGTTGAACAACAAATCAA	32221	TGG	0	1
AAGGTAATTCAACAACAAAT	32258	TGG	0	1
GGACAAGATGGTGTTGATGA	32440	CGG	0	1
ACTTATACATCAAGCAAATC	32482	TGG	0	1
GCAACAACATAAGATGACAG	32727	AGG	0	1
TTGTTCGACGGTGGCGCAAA	33019	TGG	0	1
GCGAATGTAGTTGACTCAGA	33175	CGG	0	1
GTAGTTGACTCAGACGGCAA	33181	CGG	0	1
GACTCAGACGGCAACGGTGG	33187	CGG	0	1
AACGATAAAAACGAAGTTAT	33366	CGG	0	1
TTAAGTGATGAGGAACTTCG	33570	CGG	0	1
ACTAACAAAACAAATACTGA	33696	GGG	0	1
ACATTAAAACTTTTTATGTG	33760	TGG	0	1
ATAAAAATGAGCAAATTAAG	33790	TGG	0	1
GAAGAATATGCATTGATCAC	33840	TGG	0	1
ATATACGCGATATGAAAATG	34151	TGG	0	1
GATATGAAAATGTGGATTCT	34159	CGG	0	1
GCTTTACTAAGAACTATTTT	34216	TGG	0	1
GAACTATTTTTGGTATTTAA	34226	AGG	0	1
ACCATGCTTAAAGGGATTTT	34257	AGG	0	1
GGATTTTAGGATATAGCTTC	34270	TGG	0	1
TTCTGGGCGTGCTTCTGGTT	34287	TGG	0	1
AAGAGTCAGTGCTTCGGCAC	34328	TGG	0	1
GCCTACAGCTAGTGAAGTGG	34411	TGG	0	1
ACTTTATTTTTAAAAGATAT	34509	TGG	0	1
CGATAGAATCGGAAACCCTT	34564	AGG	0	1
GGACACACCGCAATAGTAGT	34676	AGG	0	1
TTTATAGCGTTGACCAAAAC	34719	TGG	0	1
CTAGTATCTTTTGAATATGG	34804	AGG	0	1
GTTTTAACTTCTTTAAATTG	34900	CGG	0	1
TCTCTATCGACATATAAATG	35104	CGG	0	1
GCATTTATATGTCGATAGAG	35122	AGG	0	1
ATGTCGATAGAGAGGCTACA	35130	TGG	0	1
ATGACCCGCGTCACCCTAAT	35175	TGG	0	1
CTAGTTATTGAAGTATGTGG	35198	TGG	0	1
AAGCGTTAATACGTGGTGTT	35262	TGG	0	1

AATTACGACTTGATTAAGCA	35369	AGG	0	1
GTTTTTCGTCTGATGGAGTA	35535	GGG	0	1
CCCCATGTATGAGATTTTTT	35629	CGG	0	1
ACCCGAAAAAATCTCATACA	35643	TGG	0	1
AAAATCTCATACATGGGGCT	35650	GGG	0	1
CAATGAATGTTAAGCGAATA	35703	TGG	0	1
CAAACGTCATTGCATAATCA	35970	GGG	0	1
ATGACGTTTGCTAAAAATAA	35999	AGG	0	1
CGTTTGCTAAAAATAAAGGT	36003	TGG	0	1
TCTCCAGCAAAAGCAATCAT	36029	GGG	0	1
CGGTGCTAGCTTCGTAAGAA	36052	AGG	0	1
GGTGTTGACTTAGGTGACAT	36287	TGG	0	1
AATACAGCATCTATAAGAAT	36335	AGG	0	1
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ATTATCGACGATGTTGTAAA	36461	AGG	0	1
AAAAAGGTTATCAAACACGC	36506	TGG	0	1
CAAAGCAGAACCTGAGTTAT	36931	TGG	0	1
ATCAATATCGCAAATGTTGA	36959	AGG	0	1
AGTTAGTACAGAAGATTTTG	37174	AGG	0	1
ATGAAGGCTTTTTCCATACT	37484	TGG	0	1
ATGCTGGAAATATCCAAGTA	37487	TGG	0	1
GGATATTTATTTTTAGGTAA	37521	GGG	0	1
CTTACCTAAAAATAAATATC	37539	CGG	0	1
ACAGCAAAATGGACAATAAA	37579	TGG	0	1
TGTACGTAGCGGTATAATGA	37641	GGG	0	1
GGAATATCAGGAGTCAATAG	37696	CGG	0	1
TTCAACCCAGATGGTTGGTA	38245	TGG	0	1
ATCTTTGCTTTATTATCAAA	38334	CGG	0	1
CTCCGCCACCATACTTTGAC	38426	GGG	0	1
AACGGTAAAGGTTGGACTAA	38530	TGG	0	1
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AGCGTTGGCAATAAAGCTAA	38653	AGG	0	1
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GCGATTCATGGTAAGCCTAT	39268	AGG	0	1
TGGTAAGCCTATAGGTGGTT	39276	TGG	0	1
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AACTAATTCAAGAATTACAG	39453	GGG	0	1
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ATTGTATTAATGGTTATAGA	39515	TGG	0	1
GGTAATAGAATAAGTAGTTT	39601	TGG	0	1
ATTTTGCTACATTAATTATA	39661	GGG	0	1
TGTTCACCCAAGCATGTCAC	39880	TGG	0	1
CTAAAGTCATATATACTACG	39928	GGG	0	1
GCTAAAGTCATATATACTAC	39929	GGG	0	1

GGTTATTTTTTGCGTTTTTT	40222	TGG	0	1
ATCCTTGTATGATGGTAAAC	40350	CGG	0	1
GCGTCTTTAAAAATAAAAAA	69	GGG	0	0
AATAAAAAAGGGCAGAAAAA	80	GGG	0	0
AGAAAAACTTGTGTACTAAA	93	AGG	0	0
AAAACCCTTTCTGAAGAAAT	768	TGG	0	0
GAAATCAACAGAATTATTGA	1024	CGG	0	0
TTAAAAAGCGTTTTAGCGCT	1902	TGG	0	0
GGATTCCTTATTAAACGCAA	2345	GGG	0	0
TGATCAGAAAGCATAAAAAA	3041	TGG	0	0
CCTAGCTCTATTTCTATTTG	3682	TGG	0	0
GAAACTAAAAATTAATTAAA	4599	AGG	0	0
AAAAGCTGAAGAAAATAACG	5075	GGG	0	0
AGATAAAGCGTTATTATATT	5591	GGG	0	0
TACAAAAGCTTTACCATAGG	5994	CGG	0	0
TTTTGATGTCTATTACCCAG	6035	GGG	0	0
AAAACGGATTATCGGCAAAC	7211	GGG	0	0
GCAAACGGGTTTTCGGAAAA	7225	CGG	0	0
AAAAATACAACCAACTGGCA	7602	CGG	0	0
AGTAATCGGAGACGATTTCA	8418	GGG	0	0
CCCGCTATCGTCGAATATTA	8589	AGG	0	0
AGTGACCTAAAACGATTCAA	8760	AGG	0	0
AACGATTCAAAGGCGCTCAC	8770	GGG	0	0
GTTGCAAAAAGAGTACGTGG	9536	TGG	0	0
AGATAGAGTGTTTGACTTGT	10032	GGG	0	0
GCAACATGGTTTGGAATACG	10259	AGG	0	0
TATTAGACGAGTTAATTAAA	10350	TGG	0	0
TGACGTTAATCTGGAAAGAT	10686	GGG	0	0
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TGATGCCGAAATATCGAGTG	10912	TGG	0	0
TTAAAAGATTTTATGTTTGA	11220	GGG	0	0
ATACTCAAAGTAATCATTTT	11235	CGG	0	0
CTTCCTTAGATATGACTGTG	11288	AGG	0	0
AGATATGACTGTGAGGTTAA	11295	AGG	0	0
GATGAGCTTATTGGGGATAT	11447	AGG	0	0
TATAACGGCAATGACACAGA	11682	GGG	0	0
TTAGCTGACATGTTGGCGTT	12076	TGG	0	0
AATTCTTTGAATATTATCTG	12222	TGG	0	0
GATCGAGTCAAGGAGGTTTT	12422	GGG	0	0
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AGTTGGGATCAATGTTGAGG	13009	AGG	0	0
TTACTTGAGTTTTCCCCTTG	13940	TGG	0	0
CGGAAAGCATATATTGACGC	14639	AGG	0	0
GGAAAGCATATATTGACGCA	14640	GGG	0	0

CACAGTAAAGTAAGTGGTAT	15396	AGG	0	0
ATACGTGGTATGACATCGTT	15423	TGG	0	0
TCTTTCAACAACCAATGCTC	15539	GGG	0	0
AACGTAATATCAACGGTATG	15706	TGG	0	0
ATCAACGGTATGTGGGTGTC	15714	TGG	0	0
TACTTTGCTGGTGTCGACTG	15819	GGG	0	0
GAAAAAGAAGATTTTGAAAC	16454	TGG	0	0
GATGATGAGGATTCTGAAAT	16664	AGG	0	0
GGTAAAATGGCAGCAATTTG	16685	CGG	0	0
GATGATAGGAGATGCTGAAA	16999	AGG	0	0
AACGGAAATGTACCTATCAT	17303	TGG	0	0
GCGTCACCTTCATCTATGTC	17635	AGG	0	0
ATACGTATGCACATTACACA	18135	AGG	0	0
TACTCATCGTCATTTAGATG	18365	GGG	0	0
TCATTTAGATGGGGAATCAG	18374	TGG	0	0
GCTTTTTATTATGCACTTTT	18877	CGG	0	0
CGGACTGTTAGGGTACGCGA	18897	AGG	0	0
GAAGTAAAAGATTATCTAAA	18991	GGG	0	0
CAATATTAGAAAATAAAGTG	19509	AGG	0	0
GCAACTCCAACATACACGCC	19544	AGG	0	0
TTTAATCATGAAAGACATTA	19621	TGG	0	0
CAAAAGGTGTAGGCGCCTAC	19716	TGG	0	0
CCACTAGTTGAAGTGTTGTA	19924	AGG	0	0
CCTTACAACACTTCAACTAG	19940	TGG	0	0
GATGAAGAGTTAGATCCAAA	20060	CGG	0	0
CATATCTCCTCCTATTCAGT	20425	TGG	0	0
CTGAATAGGAGGAGATATGA	20445	TGG	0	0
GTGTCGTACACTTATAACGA	20865	TGG	0	0
CTCTACCTTATTGATTTAAA	20927	CGG	0	0
TGATAGCATGGTTGTTGAAT	21320	TGG	0	0
TCGATAAGAAAATAGAAGAG	21349	TGG	0	0
TGCGCCGACACTTATAACAC	21477	TGG	0	0
ATATACGTTGAATACGGTAC	21525	TGG	0	0
TCAATTGCAGGGTTCCAAAA	21635	TGG	0	0
CAACTAGTTTGTTAATGTTA	21766	GGG	0	0
TTAACAATTGGTAATGTGCC	22329	TGG	0	0
CGTGCAGACGGTAAACATCA	22431	CGG	0	0
AATGACATTTCAAATGATTC	22457	TGG	0	0
AAAGAGTGGTTTGAAGCTGC	22575	AGG	0	0
GAAAAATTCGGCGAAAAAGT	22617	CGG	0	0
TGTTGTATCTGATTCACACA	22667	CGG	0	0
TATGTAAACTAATAGATCAA	22700	GGG	0	0
TCTCAGAAGATAGCGAAGAT	22879	GGG	0	0
CAAAGCGATTTTACAATTTT	22961	GGG	0	0
TTGGACAAACTTAACAATAG	23094	TGG	0	0

CAATAGTGGTTTTTTCAAGA	23108	GGG	0	0
TCCTCGCTTTTGGCCATATT	23150	CGG	0	0
GCTAACCTCCTTTCGATTCA	23571	AGG	0	0
GCTTTGGAAATCTCTAATAT	23627	TGG	0	0
CCTTTAACCGCCATTTTAGC	23980	GGG	0	0
CGAAGATAGTACCGAAAGTT	24243	CGG	0	0
ATGGCAGTACTTAATGCGGT	24359	TGG	0	0
AATGCGGTTGGTGTATTAGG	24371	TGG	0	0
GCGGTTGGTGTATTAGGTGG	24374	TGG	0	0
GCTCTTAAAATGGTTGAAGA	24470	TGG	0	0
GCTGCAGGAAGATTTGGCGA	24791	CGG	0	0
CCAAAATTGGGCTAATAGTG	24892	TGG	0	0
CCAGCAGTCGCTCAAATTAT	25292	CGG	0	0
GCTCAAATTATCGGTGTTAT	25301	CGG	0	0
TATTTTAGGTGGCGTATTTT	25324	GGG	0	0
TTTAACTAGAATAACTGGGG	25435	TGG	0	0
AAAGCGTTCGGTTTATTGAC	25463	TGG	0	0
TTGGTATTCTTGTTTATTTA	25545	TGG	0	0
GCAGTTTCCGGTGCGATTCA	25625	AGG	0	0
ATGCCTATATTACAAGTATT	25706	AGG	0	0
TACGGATATCACTGTTCCTA	25817	TGG	0	0
GTTGGTTCAGTCGTGTTGCT	26118	TGG	0	0
CGCACGATATAGAAGTAATA	26777	AGG	0	0
CTACAAACGAAGGTGATAAG	27335	AGG	0	0
AACTGATTAAACTGTGTTAA	27399	AGG	0	0
GAACAACCGGTTTTATATCC	27628	AGG	0	0
AACCGGTTTTATATCCAGGC	27632	TGG	0	0
CTATTTTAGGGTTAGCTTCT	28551	GGG	0	0
CCAGAAGCTAACCCTAAAAT	28568	AGG	0	0
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AGGTGATGTTGTTAGAGTGG	28588	TGG	0	0
ACTAAGCAAGATGTAGTATT	28685	AGG	0	0
ACTAATTTCACAGAAATGTT	29027	AGG	0	0
AAAACGACTAATCTTGCAAG	29066	AGG	0	0
TCTACCGCTTCTTTACCTAT	29095	TGG	0	0
ACAATGGCAACAGTTCCAAT	29096	AGG	0	0
AGACAAGCAGAGCAAATAAG	29147	AGG	0	0
TACAAGGCACTGATGATGAT	29184	TGG	0	0
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ACAAGACAATGCCCTATGAG	29342	TGG	0	0
GACACGGACAAAAACAAACT	29384	AGG	0	0
CAAACTAGGGTTAACACTTG	29398	AGG	0	0
ACCTCGTGACCTTTTTCGTT	29533	AGG	0	0
ATTACAGTTTTTACGACTAA	29598	AGG	0	0

AGGAGGCAACCAATGGCTTA	29618	CGG	0	0
CGTTTTAGCAATATGATTCT	29843	AGG	0	0
CGAACCAAAAGAGCAAGAAC	30046	CGG	0	0
ATATAAATAATTTTCGTTCT	30112	AGG	0	0
GAATTCGTTGAACTTTGTTG	30490	AGG	0	0
AGGAGACTTCCAAGAAGCTG	30757	AGG	0	0
CTTTTAATAGGGGTAACTAT	30821	TGG	0	0
GTATCGATGACTGATTCAGG	30926	CGG	0	0
TCTATCTACGTTATAATCAT	31711	CGG	0	0
CAGGCATTCTTTACACAAAA	31855	CGG	0	0
AATGGCGCTGACCTTGTTAA	32239	AGG	0	0
AATAATGCGCAAGGCGATTT	32779	GGG	0	0
AGGTAGCGTTGAAAGTTATG	32850	AGG	0	0
ACGGCAGACTTGAGCAACAG	32966	TGG	0	0
AAATCAACGGTATTGTTCGA	33007	CGG	0	0
CACAAACTATTCTATTTTGT	33075	TGG	0	0
GGTGGCGTTATTGAGGGATT	33115	CGG	0	0
AACGATGTGTACTTTGATTT	33262	AGG	0	0
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GACTTTTCATCTTTTGCCTC	33857	TGG	0	0
CCAAACGGCACGAACATGAA	33959	TGG	0	0
AACTTTAGATGCTATCCAGA	34086	GGG	0	0
ATGTGGATTCTCGGTTTGAT	34168	AGG	0	0
CTATTTTTGGTATTTAAAGG	34229	AGG	0	0
AGCTAGTGAAGTGGTGGAGT	34417	GGG	0	0
TTATCGGGGCAGTCAATGTT	34477	GGG	0	0
TATTGGGGTTTTGTAACATG	34526	GGG	0	0
CAGATGAATAACGATAGAAT	34575	CGG	0	0
AACCTGGAGACATCGCAGTT	34626	TGG	0	0
CCGAACCTATTCCGTTGCCA	34635	GGG	0	0
GGCAACGGAATAGGTTCGGA	34655	CGG	0	0
AGATGGTCCTACTACTATTG	34667	CGG	0	0
ACTGGGTTAATTCTAATAGT	34737	TGG	0	0
GAACTTGTATCAGTACTACT	34831	AGG	0	0
CGTGGTGTTTGGTTATTGTC	35273	AGG	0	0
CTTATCTGAAACGACGTTAA	35308	AGG	0	0
TGATGGAGTAGGGCCTCGTG	35525	TGG	0	0
AGTGCTTGCTGGAATGTGAA	35581	TGG	0	0
AAAAATCTCATACATGGGGC	35649	TGG	0	0
AAAGGAAAAGGAACGCTCGA	35807	CGG	0	0
TACGGTGCATATAATTACTT	35942	CGG	0	0
AGGGATAAATATAAATAAAG	36215	AGG	0	0
GAAACGAGAATAAAAAATGA	36266	TGG	0	0
CGTATCGATCTAAAAGCACA	36377	TGG	0	0

AAAGGTGCGAAAGGTGATAA	36773	AGG	0	0
AAAGGCGAACCGGGACAACC	36791	TGG	0	0
CCGGGACAACCTGGTGCAAA	36800	AGG	0	0
AGTAAATATAGAAAAGCAAC	38090	AGG	0	0
CAAAAAATCAAGCAGAAAAA	38198	TGG	0	0
GGGAAACAATTCAACCCAGA	38236	TGG	0	0
AACAATTCAACCCAGATGGT	38240	TGG	0	0
ACTAATGGCGTTGCGCAACC	38545	TGG	0	0
GCTACAAGCATAATTTTTTT	38703	AGG	0	0
GGTCATGGTTATAACGATCC	38743	TGG	0	0
CATGAAGTTGCATTATACGG	38851	TGG	0	0
TTATATTGGGTTAAATCACA	38947	GGG	0	0
GCAGCAGGAGAAAGCGCAAG	39001	TGG	0	0
ATTCATGGTAAGCCTATAGG	39271	TGG	0	0
CCTATAGGTGGTTTGGTAGC	39283	TGG	0	0
GTATAACCTGCTGGCACTGG	39324	TGG	0	0
TGCCTTGTTCTTTTTTATAA	39365	GGG	0	0
AAAGGTAATAATGTAAGAGA	39424	CGG	0	0
CAACGTCGTTATATAGCGAC	39562	AGG	0	0
ACAAGGAAGATGTCTCCTGT	40055	GGG	0	0
TGTGGTTTTGTTGGTTGTAG	40161	GGG	0	0
GTTTTTTTGGGGCAAAAAAA	40235	GGG	0	0
CCTTGATACAACAGTGTTTT	40319	TGG	0	0
CGTGTACGTTAGAGAATGAC	40347	CGG	0	0

Early Time Point Normalized Reads	Late Time Point Normalized Reads
27416.00	20187.02
21768.42	16631.67
18475.95	20479.71
17948.40	11526.52
17898.95	11149.52
16043.11	15775.94
13403.01	3648.91
12720.03	9706.56
12058.24	3675.76
11869.83	11526.61
11855.70	16251.00
10979.59	7489.25
10508.57	7589.78
9917.43	9192.55
9710.18	9076.45
9618.33	7788.63
9314.52	10201.41
8885.88	15652.96
8779.90	5969.77
8028.62	6575.60
7642.38	6181.28
7562.30	7524.25
7319.73	8624.39
7246.72	5075.19
7105.41	3116.66
6785.11	5839.00
6217.53	8346.63
6083.29	8434.42
5991.44	4791.84
5772.41	2368.70
5682.92	2963.63
5496.86	2625.57
5454.47	5101.76
5117.69	5054.38
4879.82	5326.09
4493.58	4341.06
4397.02	7170.62
4333.43	5096.45
4276.91	3818.44
4246.29	1546.24
4116.76	7684.07
4029.62	8176.18
3916.57	948.29
3907.15	5715.01

3895.38	2840.46
3836.50	5913.05
3815.30	6354.47
3747.00	6243.41
3666.93	8042.11
3636.31	900.91
3535.04	1536.80
3490.29	239.64
3462.03	6383.80
3447.90	5094.70
3443.19	6371.89
3396.09	4928.56
3264.20	5978.20
3193.55	6222.97
3134.67	4738.68
3106.41	2888.57
3061.66	643.95
2986.30	5805.00
2981.59	3627.74
2955.68	33.45
2918.00	2524.85
2807.31	41.88
2804.95	19.61
2790.82	2435.14
2762.56	2656.72
2757.85	5234.00
2720.17	24.83
2715.46	148.09
2684.84	4191.41
2670.71	4982.90
2668.36	4265.27
2588.28	575.86
2552.95	4949.91
2517.63	2990.11
2501.14	3440.06
2487.01	5127.05
2477.59	2161.87
2475.24	4338.86
2458.75	4002.18
2418.71	1473.93
2371.61	3296.46
2364.55	73.59
2345.70	1616.89
2336.28	81.74
2333.93	5100.66

2305.67	3092.75
2286.83	1617.62
2284.47	2662.77
2244.43	1449.92
2242.08	4262.89
2239.72	3155.70
2183.20	3443.08
2176.14	3699.31
2150.23	3608.95
2117.26	21.17
2100.77	578.70
2100.77	18.60
2079.57	4418.04
2072.51	1595.54
2053.67	24.10
2051.31	1793.94
1992.44	921.07
1987.73	2254.79
1933.56	1537.44
1931.20	3021.36
1912.36	1415.83
1893.52	3484.50
1888.81	4069.90
1886.45	2442.84
1867.61	3365.92
1865.26	1054.41
1832.29	2661.31
1815.80	1993.25
1813.45	3777.75
1801.67	479.73
1768.70	3823.30
1763.99	25.29
1756.92	3523.45
1721.60	552.95
1721.60	15.40
1712.18	2125.86
1709.82	68.09
1695.69	2970.41
1676.85	1677.92
1653.30	106.49
1636.81	845.74
1599.13	2241.05
1596.77	2376.49
1563.80	2967.29
1556.74	16.31

1554.38	3086.79
1535.54	1084.46
1530.83	2559.86
1526.12	171.37
1502.57	1102.79
1497.86	1160.52
1481.37	2811.14
1476.66	1391.27
1457.82	2905.53
1457.82	1983.91
1455.47	887.90
1448.40	1592.97
1441.34	2126.86
1406.01	1974.56
1398.94	1318.14
1394.23	1045.42
1384.81	2633.72
1382.46	2799.22
1380.10	23.55
1375.39	1787.25
1368.33	2536.58
1365.97	1264.35
1363.62	2469.05
1363.62	1334.73
1363.62	48.66
1356.55	235.51
1351.84	2625.38
1344.78	764.37
1342.42	2722.06
1340.07	478.18
1335.36	1643.56
1328.29	2621.35
1307.09	763.08
1302.38	1275.44
1297.67	1890.80
1295.32	1256.47
1292.96	1922.23
1281.19	502.73
1281.19	150.38
1276.48	2413.15
1274.12	250.08
1259.99	1466.23
1248.22	822.19
1236.44	2272.57
1229.37	303.42

1215.24	2346.43
1205.82	2004.07
1201.11	2562.06
1182.27	2344.42
1182.27	1882.92
1179.92	2407.83
1177.56	1261.69
1177.56	1096.56
1170.50	1527.45
1161.08	2087.83
1142.24	2272.30
1137.53	332.19
1135.17	2385.47
1135.17	1221.56
1132.81	731.83
1123.39	2145.83
1118.68	839.69
1111.62	13.47
1099.84	20.34
1097.49	11.00
1092.78	1433.61
1083.36	2147.12
1064.52	151.11
1055.10	123.07
1043.32	1561.36
1043.32	572.47
1040.97	1544.13
1040.97	969.18
1040.97	9.26
1017.41	1786.33
1017.41	1554.48
1017.41	958.55
1003.28	1936.16
1003.28	1908.76
989.15	1543.12
979.73	1757.01
977.38	947.46
972.67	44.54
963.25	1784.96
958.54	10.36
956.18	810.00
953.83	1895.75
953.83	1511.23
953.83	519.96
944.40	660.90

932.63	1257.11
925.56	181.26
918.50	1852.77
918.50	1393.01
913.79	1741.24
913.79	392.95
911.43	1515.81
906.72	301.22
904.37	1591.87
902.01	244.13
902.01	163.49
885.53	561.02
883.17	1814.65
883.17	1088.68
878.46	1680.03
878.46	1337.48
876.11	1913.34
876.11	1750.04
873.75	49.21
873.75	9.07
871.40	1375.97
871.40	12.83
869.04	13.56
866.69	1649.60
857.27	1147.69
857.27	916.03
854.91	1275.81
850.20	36.11
845.49	1073.28
845.49	722.76
843.13	1897.03
843.13	1772.77
843.13	1305.59
833.71	3.57
831.36	1484.84
826.65	22.63
819.58	1485.39
817.23	881.66
817.23	486.15
812.52	1619.46
812.52	1342.98
807.81	35.37
805.45	1558.06
803.10	1416.47
800.74	1008.13

798.39	1726.49
798.39	1487.22
798.39	1381.10
788.97	1605.89
784.26	1554.67
784.26	1553.84
781.90	314.32
779.55	828.15
777.19	1429.39
774.84	25.84
772.48	981.55
770.13	721.66
767.77	1311.55
765.42	1233.74
763.06	522.53
760.71	622.69
760.71	277.76
755.99	1461.65
755.99	18.24
751.28	707.27
739.51	336.87
739.51	285.27
730.09	45.18
725.38	35.56
723.02	292.33
718.31	1402.09
718.31	225.62
711.25	1266.37
711.25	10.17
708.89	1146.78
706.54	1130.83
704.18	113.91
701.83	574.95
699.47	1283.96
699.47	217.46
692.41	1167.03
690.05	1378.17
687.70	180.16
687.70	34.91
685.34	1241.08
685.34	251.64
678.28	50.95
678.28	15.12
675.92	219.84
671.21	1067.23

671.21	144.88
666.50	1187.01
661.79	627.18
659.43	946.09
659.43	876.62
645.30	91.36
642.95	1224.76
642.95	519.32
640.59	775.00
635.88	1147.24
635.88	375.91
635.88	20.34
628.82	369.77
624.11	453.34
621.75	1183.71
621.75	271.44
617.04	496.05
614.69	1162.54
614.69	346.58
612.33	1098.12
609.98	1043.78
607.62	1177.66
607.62	842.17
607.62	7.06
607.62	6.96
605.27	1343.99
605.27	435.47
598.20	1312.83
595.85	1211.02
593.49	1117.91
593.49	702.97
591.14	511.62
588.78	1051.38
588.78	6.14
586.43	287.02
579.36	28.50
579.36	4.67
577.01	18.79
574.65	822.19
574.65	124.54
572.30	1016.47
567.59	1050.83
565.23	240.83
560.52	15.21
558.16	26.67

555.81	1167.49
555.81	1093.26
553.45	914.66
553.45	11.73
551.10	638.54
548.74	952.59
548.74	858.48
548.74	658.98
548.74	14.20
546.39	386.81
546.39	225.16
544.03	24.01
539.32	5.41
536.97	757.40
536.97	17.59
532.26	1157.23
529.90	757.68
529.90	297.92
527.55	941.69
527.55	5.96
525.19	1052.30
525.19	19.24
522.84	1097.84
522.84	13.38
518.13	1009.23
518.13	699.12
511.06	357.30
501.64	843.36
501.64	208.76
496.93	557.26
496.93	12.10
494.58	956.90
494.58	111.25
492.22	839.79
489.87	890.19
489.87	27.68
485.16	835.84
485.16	48.94
485.16	4.12
482.80	993.37
478.09	795.80
478.09	24.19
475.74	940.77
475.74	887.25
475.74	855.91

475.74	18.69
473.38	1037.18
473.38	931.43
473.38	31.62
471.02	877.36
466.31	4.03
463.96	566.06
461.60	834.38
461.60	343.47
459.25	1000.34
459.25	380.21
456.89	732.66
452.18	517.76
452.18	202.80
447.47	427.13
445.12	674.93
445.12	668.69
445.12	497.60
445.12	34.55
442.76	867.74
442.76	138.56
440.41	900.54
440.41	895.50
438.05	767.94
438.05	143.78
435.70	901.83
435.70	823.75
435.70	60.12
435.70	56.54
435.70	10.26
433.34	778.66
433.34	771.33
430.99	845.56
430.99	689.77
430.99	681.62
419.21	396.98
416.86	835.11
416.86	52.69
416.86	9.44
412.15	976.70
412.15	47.47
407.44	698.75
407.44	4.58
405.08	752.54
405.08	3.21

400.37	216.91
400.37	6.14
398.02	882.12
398.02	765.47
395.66	588.88
395.66	106.21
395.66	11.55
390.95	8.71
388.60	16.40
386.24	614.72
386.24	490.55
386.24	252.10
386.24	4.86
383.89	886.70
383.89	373.89
383.89	253.75
381.53	742.65
381.53	608.30
379.18	595.38
376.82	547.82
376.82	454.53
376.82	134.99
376.82	23.64
376.82	5.77
374.46	668.69
374.46	585.85
374.46	412.19
374.46	334.03
374.46	10.36
372.11	878.18
372.11	654.12
369.75	754.01
367.40	572.93
367.40	339.89
365.04	717.45
365.04	701.32
365.04	492.75
365.04	123.07
362.69	334.03
360.33	176.86
357.98	23.09
357.98	9.99
357.98	3.85
355.62	619.21
355.62	583.65

355.62	305.80
355.62	12.28
353.27	663.20
353.27	380.58
350.91	238.35
350.91	155.33
350.91	49.49
350.91	33.27
348.56	496.05
346.20	17.59
341.49	685.74
341.49	47.47
339.14	783.61
339.14	56.45
339.14	5.96
336.78	769.31
336.78	580.26
334.43	306.81
332.07	746.13
332.07	597.95
332.07	162.57
332.07	129.94
329.72	643.04
327.36	587.14
325.01	3.21
322.65	589.15
322.65	295.45
322.65	287.75
320.30	212.70
320.30	5.77
320.30	3.21
315.59	674.74
315.59	636.99
315.59	586.04
315.59	405.14
315.59	366.28
315.59	29.32
313.23	709.29
313.23	13.01
310.88	181.08
310.88	74.14
306.17	600.79
306.17	5.59
303.81	499.99
303.81	324.59

303.81	316.43
301.46	499.25
301.46	5.32
299.10	619.12
299.10	397.81
296.75	513.82
294.39	386.63
294.39	14.48
294.39	3.30
292.04	472.31
292.04	173.57
292.04	10.17
289.68	378.47
287.33	26.30
287.33	6.69
287.33	2.84
284.97	447.66
284.97	58.47
284.97	2.75
282.61	528.58
282.61	250.91
282.61	149.83
282.61	130.13
282.61	124.26
280.26	620.03
277.90	483.95
277.90	166.42
277.90	95.40
275.55	533.25
273.19	285.92
270.84	507.50
270.84	15.03
268.48	487.43
266.13	579.53
266.13	3.85
263.77	473.59
263.77	418.98
263.77	192.26
263.77	72.40
263.77	69.65
263.77	19.24
263.77	5.13
259.06	522.53
259.06	504.93
259.06	456.73

259.06	449.58
259.06	413.20
259.06	56.27
256.71	8.98
256.71	7.97
256.71	3.57
254.35	405.69
254.35	309.28
252.00	538.66
252.00	376.09
252.00	302.32
252.00	4.95
249.64	459.66
249.64	444.91
249.64	258.24
249.64	209.76
249.64	52.33
247.29	467.36
247.29	3.67
244.93	402.39
244.93	319.73
244.93	188.41
244.93	4.49
242.58	5.04
240.22	459.30
240.22	449.03
240.22	381.77
240.22	129.85
237.87	464.25
237.87	461.77
237.87	411.74
237.87	4.03
235.51	488.07
235.51	466.35
235.51	420.44
235.51	388.64
235.51	62.96
233.16	471.21
233.16	416.78
233.16	278.77
230.80	485.60
230.80	462.96
230.80	4.95
230.80	3.67
228.45	422.28

228.45	272.81
228.45	5.04
226.09	231.57
223.74	471.39
223.74	234.87
223.74	18.69
221.38	376.91
221.38	263.56
221.38	252.01
221.38	10.36
219.03	578.25
219.03	403.58
219.03	288.94
219.03	5.68
216.67	416.23
216.67	253.57
216.67	43.25
216.67	28.87
214.32	302.78
214.32	126.19
211.96	338.43
211.96	287.38
211.96	19.15
211.96	4.49
211.96	4.40
209.61	486.24
209.61	344.93
207.25	349.06
207.25	19.98
207.25	8.06
204.90	369.49
204.90	337.42
204.90	336.04
204.90	11.00
202.54	338.33
202.54	292.97
202.54	3.48
200.19	357.03
200.19	73.04
200.19	4.49
197.83	471.12
197.83	167.06
197.83	18.60
197.83	15.58
195.48	445.19

195.48	413.94
195.48	407.89
195.48	357.03
195.48	346.49
195.48	313.87
195.48	104.47
195.48	7.51
195.48	6.87
193.12	417.97
193.12	416.87
193.12	19.89
193.12	10.63
193.12	6.51
193.12	3.21
190.77	406.97
190.77	326.88
190.77	312.58
190.77	244.86
190.77	212.51
190.77	172.01
188.41	351.62
188.41	285.27
188.41	224.43
188.41	165.13
188.41	7.33
186.05	351.80
186.05	218.74
186.05	62.31
183.70	415.59
183.70	312.67
183.70	297.55
183.70	158.17
183.70	136.54
181.34	352.81
181.34	315.42
181.34	312.31
178.99	374.71
178.99	342.09
178.99	324.13
178.99	234.60
178.99	193.18
178.99	88.89
178.99	3.39
176.63	410.00
176.63	89.90

176.63	36.56
176.63	4.31
174.28	391.30
174.28	363.99
174.28	204.54
171.92	282.25
171.92	206.28
171.92	12.19
171.92	10.63
169.57	268.32
169.57	154.14
167.21	399.92
167.21	285.92
167.21	269.05
167.21	85.04
167.21	30.24
164.86	319.82
164.86	302.87
164.86	287.75
164.86	264.66
164.86	245.14
164.86	177.96
164.86	119.77
164.86	14.48
162.50	197.58
162.50	125.45
162.50	72.95
160.15	389.56
160.15	376.73
160.15	342.27
160.15	305.07
160.15	293.43
160.15	196.11
160.15	16.86
160.15	6.14
157.79	255.77
157.79	246.42
157.79	242.94
157.79	237.07
157.79	5.22
155.44	233.96
155.44	52.05
155.44	14.39
153.08	310.57
153.08	276.11

153.08	243.85
153.08	78.63
153.08	6.96
153.08	2.47
150.73	37.57
150.73	24.83
148.37	211.78
148.37	120.23
148.37	71.57
148.37	10.91
143.66	368.48
143.66	219.75
143.66	30.70
141.31	274.64
141.31	200.60
141.31	188.87
141.31	43.16
141.31	7.79
141.31	5.77
138.95	279.59
138.95	254.94
138.95	217.28
138.95	203.07
138.95	165.78
138.95	132.42
138.95	84.95
138.95	80.55
136.60	306.17
136.60	280.60
136.60	223.33
136.60	195.83
136.60	106.58
136.60	3.21
134.24	299.66
134.24	162.39
131.89	319.82
131.89	259.43
131.89	31.89
131.89	20.89
131.89	18.88
131.89	12.10
129.53	209.67
129.53	173.66
129.53	112.26
129.53	11.91

129.53	5.41
127.18	300.21
127.18	243.58
127.18	229.47
127.18	210.50
127.18	119.59
127.18	17.87
127.18	11.27
124.82	225.62
124.82	207.38
124.82	157.71
124.82	11.82
124.82	8.43
122.47	204.72
122.47	106.67
122.47	92.65
122.47	22.63
122.47	3.12
120.11	208.21
120.11	138.93
120.11	122.71
120.11	15.40
120.11	11.64
120.11	11.36
120.11	9.26
120.11	3.57
117.76	233.04
117.76	203.26
117.76	190.52
117.76	184.65
117.76	184.10
117.76	124.17
117.76	21.08
117.76	13.65
117.76	10.81
117.76	7.88
117.76	4.58
115.40	231.48
115.40	206.83
115.40	197.76
115.40	154.60
115.40	42.61
115.40	41.42
115.40	12.65
115.40	6.32

115.40	1.28
113.05	248.44
113.05	164.13
113.05	59.02
113.05	15.67
110.69	186.58
110.69	92.74
110.69	12.00
110.69	5.13
110.69	4.77
110.69	3.39
108.34	177.32
108.34	168.89
108.34	166.60
108.34	156.89
108.34	140.67
108.34	129.40
108.34	91.55
108.34	9.53
105.98	211.41
105.98	209.76
105.98	195.83
105.98	194.55
105.98	187.13
105.98	165.04
105.98	137.28
105.98	133.15
105.98	127.20
105.98	109.88
105.98	50.04
105.98	14.57
105.98	7.79
105.98	5.50
103.63	235.51
103.63	143.23
103.63	140.48
103.63	130.13
103.63	53.61
101.27	249.35
101.27	207.11
101.27	207.01
101.27	154.41
101.27	144.24
101.27	98.70
101.27	33.27

101.27	20.80
101.27	11.82
98.92	172.37
98.92	148.09
98.92	110.06
98.92	104.93
98.92	53.15
98.92	21.63
98.92	5.04
98.92	1.10
96.56	236.16
96.56	205.91
96.56	204.54
96.56	188.78
96.56	179.71
96.56	126.83
96.56	81.65
96.56	73.86
96.56	68.09
96.56	27.68
96.56	15.95
96.56	11.64
96.56	4.58
96.56	2.02
94.20	134.80
94.20	124.17
94.20	47.19
94.20	41.70
94.20	29.97
94.20	13.38
94.20	7.97
94.20	2.93
94.20	1.83
91.85	228.00
91.85	135.63
91.85	55.53
91.85	32.62
91.85	4.86
91.85	4.03
89.49	209.85
89.49	194.46
89.49	173.47
89.49	170.82
89.49	167.79
89.49	150.93

89.49	92.10
89.49	42.89
89.49	41.42
89.49	14.39
89.49	13.47
89.49	10.08
89.49	1.19
87.14	145.52
87.14	119.41
87.14	107.13
87.14	11.36
87.14	1.19
84.78	189.51
84.78	174.57
84.78	153.50
84.78	151.11
84.78	150.66
84.78	122.89
84.78	121.15
84.78	25.66
84.78	16.04
84.78	3.67
82.43	120.69
82.43	112.08
82.43	104.74
82.43	95.03
82.43	90.54
82.43	50.86
82.43	38.03
82.43	27.22
82.43	18.79
82.43	2.57
82.43	1.83
82.43	1.37
80.07	206.56
80.07	133.15
80.07	128.02
80.07	105.29
80.07	103.28
80.07	91.00
80.07	66.26
80.07	28.77
80.07	16.31
80.07	4.49
77.72	150.01

77.72	149.56
77.72	130.95
77.72	96.68
77.72	94.02
77.72	74.32
77.72	73.77
77.72	54.89
77.72	40.87
77.72	33.63
77.72	2.84
77.72	1.10
75.36	182.55
75.36	144.70
75.36	97.50
75.36	66.26
75.36	62.77
75.36	13.65
75.36	4.86
75.36	1.65
75.36	1.28
73.01	132.60
73.01	128.48
73.01	117.39
73.01	90.91
73.01	59.38
73.01	56.82
73.01	10.36
73.01	4.86
73.01	3.02
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70.65	188.87
70.65	142.32
70.65	140.67
70.65	131.32
70.65	128.75
70.65	104.47
70.65	89.26
70.65	84.03
70.65	39.59
70.65	14.11
70.65	12.00
70.65	8.43
70.65	4.49
70.65	1.19
68.30	146.62

68.30	100.53
68.30	96.68
68.30	93.93
68.30	81.93
68.30	76.98
68.30	76.15
68.30	55.35
68.30	35.37
68.30	7.97
68.30	6.78
68.30	4.67
68.30	3.94
65.94	119.68
65.94	113.72
65.94	111.89
65.94	108.04
65.94	101.72
65.94	54.16
65.94	23.73
65.94	17.59
65.94	5.32
65.94	2.57
63.59	136.63
63.59	134.89
63.59	116.02
63.59	83.12
63.59	34.27
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63.59	22.63
63.59	17.69
63.59	15.30
63.59	13.01
63.59	10.36
63.59	6.05
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61.23	72.30
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61.23	63.05
61.23	36.66
61.23	30.97
61.23	26.94
61.23	12.28

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61.23	1.37
61.23	1.19
58.88	149.01
58.88	106.85
58.88	102.36
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58.88	4.67
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56.52	114.00
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56.52	3.30
56.52	1.74
56.52	1.10
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54.17	100.35
54.17	98.88
54.17	92.92
54.17	80.28
54.17	76.34
54.17	71.11
54.17	64.06
54.17	57.73

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54.17	46.64
54.17	42.34
54.17	28.96
54.17	26.12
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54.17	18.14
54.17	18.14
54.17	17.78
54.17	12.37
54.17	8.98
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54.17	8.43
54.17	6.69
54.17	5.32
54.17	4.77
54.17	1.74
51.81	121.33
51.81	117.02
51.81	95.31
51.81	83.76
51.81	80.09
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51.81	62.96
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51.81	21.81
51.81	19.06
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51.81	4.22
51.81	3.21
51.81	2.75
51.81	1.10
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49.46	99.70
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49.46	64.61
49.46	35.92
49.46	8.16
49.46	6.05

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47.10	85.22
47.10	81.74
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47.10	64.51
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47.10	40.69
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47.10	37.48
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47.10	15.03
47.10	7.24
47.10	6.51
47.10	2.75
47.10	2.75
44.75	120.32
44.75	109.42
44.75	88.98
44.75	84.22
44.75	81.83
44.75	70.75
44.75	58.10
44.75	50.22
44.75	48.57
44.75	47.10
44.75	46.83
44.75	42.98
44.75	35.28
44.75	29.42
44.75	19.34
44.75	15.95
44.75	15.21
44.75	11.55
44.75	10.63
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40.04	45.54
40.04	40.23
40.04	29.78
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40.04	3.21
40.04	1.28
37.68	85.04
37.68	71.11
37.68	64.24
37.68	59.84
37.68	59.11
37.68	57.37

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37.68	21.26
37.68	20.62
37.68	14.57
37.68	13.56
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37.68	11.00
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37.68	5.32
37.68	3.94
37.68	3.76
37.68	3.57
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35.33	6.32
35.33	5.96
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32.97	27.49
32.97	23.92
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32.97	18.88
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30.62	8.43
30.62	6.87
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30.62	6.32
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30.62	1.65
30.62	1.19
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28.26	48.48
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28.26	47.19

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25.91	84.68
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25.91	43.71
25.91	43.16
25.91	42.15
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25.91	31.34
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25.91	26.58
25.91	26.48
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25.91	25.20
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25.91	19.98
25.91	19.98
25.91	17.87
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25.91	15.12
25.91	12.19
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Spacer Sequence	**Strand**	**Location**	**PAM**	**Fitness**
TTTGTAACAACTGATATTAA	-	21	AGG	1.842554804
ATACACATGTAACAGAGAAA	-	138	TGG	1.98228312
ATACACATGTAACAGAGAAA	-	138	TGG	0.236699678
AGATGAAAAAACGACTATAA	-	165	AGG	0.521481308
AGATGAAAAAACGACTATAA	-	165	AGG	1.170246589
GCATACACACATAAGTTTAT	-	237	TGG	0.872525824
GCATACACACATAAGTTTAT	-	237	TGG	2.017110256
AAGTTACTACTCACACACTA	-	259	AGG	2.193078397
ATTTAATGATTCTGCAGCTG	+	308	AGG	0.0981197
GAAATCCTATGCAAGGCAGT	-	331	AGG	0.015334935
TGCCAAGGAAATCCTATGCA	-	338	AGG	0.01173533
TGCCAAGGAAATCCTATGCA	-	338	AGG	0.016950689
AACCCTCTATCAACATAGCT	+	390	TGG	0.042210951
AAATAAAAAGATGCAACAAT	-	399	GGG	0.929846464
AAAATAAAAAGATGCAACAA	-	400	TGG	0.356818909
ATTTGCTATCCTTGAATTGA	+	461	TGG	0.109581959
AAACAATCAAGAGAAAAACA	-	500	AGG	0.210321008
TAATAGAACTATCAAGTAAA	-	556	AGG	0.024383309
TAATAGAACTATCAAGTAAA	-	556	AGG	0.87911233
GATTACTTACGTAATGCGAA	+	676	AGG	0.01802427
GATTACTTACGTAATGCGAA	+	676	AGG	1.900082343
TTCAAAAGTTTAGTATCTAT	-	698	AGG	0.304824297
GACACCAATTTCTTCAGAAA	-	756	GGG	0.008854973
TGACACCAATTTCTTCAGAA	-	757	AGG	0.02544085
ACTTTATCTAACATGATACA	+	804	CGG	0.700321068
ACTTTATCTAACATGATACA	+	804	CGG	1.541214127
CTTTATCTAACATGATACAC	+	805	GGG	1.462660823
GAGAACAAAACCATCCTACC	+	827	CGG	2.028958337
AAATAAATACCATTTATTAC	-	830	CGG	2.25675309
CCATCCTACCCGGTAATAAA	+	837	TGG	0.610023454
TTAGAATTGACACCTCAAGA	+	873	AGG	1.342393732
TTAGAATTGACACCTCAAGA	+	873	AGG	1.539540001
AAGAAAGTTTTAACTTAAGG	+	930	AGG	0.006991302
AAGAAAGTTTTAACTTAAGG	+	930	AGG	0.064405813
ACTTAAGGAGGAACAACAAA	+	942	TGG	0.053874742
TTGATTTCGTGCCACTGTGC	-	993	GGG	0.808790763
GTTGATTTCGTGCCACTGTG	-	994	CGG	0.517319968
AGCAATTCACACCCGCACAG	+	998	TGG	0.926880404
AGCAATTCACACCCGCACAG	+	998	TGG	0.438618933
AGCAATTCACACCCGCACAG	+	998	TGG	0.477633726
TTTTAATAACCTCAACATCT	-	1070	TGG	0.764004295
ACTCGACGACCAAGATGTTG	+	1077	AGG	0.937041579
AGTTATTCAAAAATCACGAA	+	1154	AGG	0.137971112
GTGAATTGCTAGTAGTGTGT	-	1181	TGG	0.860534158

ATTAATTATGCTCGTAAGAA	+	1241	CGG	1.178202785
ATTAATTATGCTCGTAAGAA	+	1241	CGG	1.589966515
GAAACAATCTTTATAAACGC	+	1308	AGG	2.04472733
GAATTAGCTATCATAACTTC	+	1365	TGG	1.132267499
TTATCTAATTGTTTATCGAT	+	1389	TGG	1.982913666
TTATCTAATTGTTTATCGAT	+	1389	TGG	0.897513298
ATTGGAGCATGCAAATAACT	+	1407	TGG	0.679914918
ATTGGAGCATGCAAATAACT	+	1407	TGG	0.4347188
TCTGATGAATATTCATCTCT	-	1424	CGG	1.370691594
AACACCTATTAACGTAGTAT	-	1449	TGG	2.005405833
AACACCTATTAACGTAGTAT	-	1449	TGG	1.165561226
GATTCCAATACTACGTTAAT	+	1461	AGG	0.865242564
GATTCCAATACTACGTTAAT	+	1461	AGG	1.890582808
ATTTAAGGTGGTTATTCTTA	-	1698	TGG	0.081356303
TTACAAACAAAATCGAACAT	+	1802	CGG	2.133005507
AAGAGAGTTATATAAAGCTT	+	1876	TGG	0.931011885
AAGAGAGTTATATAAAGCTT	+	1876	TGG	1.600393868
TAAAAAGCGTTTTAGCGCTT	+	1903	GGG	1.591400024
TACAAGTGTACTTACAAGTA	+	1966	CGG	0.091967994
TACAAGTGTACTTACAAGTA	+	1966	CGG	0.29182152
AAACATGTTGCGATGATGTC	+	2048	AGG	0.98331686
TGTTCCATGCTTTTTCAATT	-	2091	TGG	0.044131162
TCATCCAAATTGAAAAAGCA	+	2103	TGG	1.905464161
TCATCCAAATTGAAAAAGCA	+	2103	TGG	0.015605993
GCACGTTGCATAATCATTTC	-	2116	TGG	0.178983866
ACTAAGACATCAATTTTAGT	+	2246	TGG	0.035683875
ACTAAGACATCAATTTTAGT	+	2246	TGG	0.178983866
GCAAAGATCATTAAACAAAA	+	2276	CGG	2.22340206
AAACAAAACGGTATAAACAT	+	2288	CGG	0.068427115
AACAAAACGGTATAAACATC	+	2289	GGG	0.725384922
CCACACCCTTGCGTTTAATA	-	2334	AGG	1.451201572
CGGATTCCTTATTAAACGCA	+	2344	AGG	0.087824381
CGGATTCCTTATTAAACGCA	+	2344	AGG	0.112632867
CGTTCCATTGAATACTGTGT	-	2368	AGG	1.108418359
CATGCCTACACAGTATTCAA	+	2380	TGG	0.707344109
ACATCAATCACACATTCGGA	+	2429	CGG	2.264359466
AGTAAGACGCCAAAAGTAAC	+	2465	AGG	0.410336062
TACTTTGTTAACAAGTTTTT	+	2501	AGG	0.217185956
AGAAAAACAAACAACTTAAT	+	2524	AGG	0.971055409
AGAAAAACAAACAACTTAAT	+	2524	AGG	0.009129424
TCACAACTGCCATTGTGATG	-	2568	AGG	0.680916881
TCACAACTGCCATTGTGATG	-	2568	AGG	0.455241572
AATGGCAGTTGTGACGTGGA	+	2593	AGG	1.193005944
CAGTTGTGACGTGGAAGGTT	+	2598	TGG	0.583643041
AACGCCCTGCTACTAATCAC	-	2629	AGG	1.894595101

GAAAACCTGTGATTAGTAGC	+	2640	AGG	2.012084652
ATTTTCAGCATCTTTCGGTA	-	2681	TGG	0.007917638
TTTGTTCGGCGAACTTCAAA	-	2724	AGG	0.266263296
TTTGTTCGGCGAACTTCAAA	-	2724	AGG	1.776068205
TTATTTGCTAATAGTTTGTT	-	2738	CGG	1.832181388
TTATTTGCTAATAGTTTGTT	-	2738	CGG	1.352854638
ATAACAACATTATACACGAA	+	2773	AGG	0.012118012
TATGTGTTTTCTGGTGTTGG	-	2808	TGG	0.092410148
CTATATGTGTTTTCTGGTGT	-	2811	TGG	0.033689964
TCGCCTCTATATGTGTTTTC	-	2817	TGG	1.83912407
TCGCCTCTATATGTGTTTTC	-	2817	TGG	1.641662617
ACACCAGAAAACACATATAG	+	2830	AGG	2.216231917
ACACCAGAAAACACATATAG	+	2830	AGG	0.470451663
ACACAAATCCATCAATTGTT	+	2890	TGG	1.950201531
ACACAAATCCATCAATTGTT	+	2890	TGG	0.158417397
GTAGAAGTACAGTATACAAC	+	2918	TGG	0.682085335
GTAGAAGTACAGTATACAAC	+	2918	TGG	0.740335384
TATTACCGCAAAGATAATTT	+	2947	AGG	0.185568557
TACATTGATTATTCACCAAC	+	2983	AGG	1.095182923
TACATTGATTATTCACCAAC	+	2983	AGG	0.799756148
TCTGATTAATATTTCTAAAT	+	3009	TGG	0.270639697
TCTGATTAATATTTCTAAAT	+	3009	TGG	0.371409208
GCATAAAAAATGGTATTAGG	+	3051	AGG	0.769834014
GCATAAAAAATGGTATTAGG	+	3051	AGG	0.041542512
TGAAGCATAATACTGCTACT	-	3088	AGG	0.642183487
TGAAGCATAATACTGCTACT	-	3088	AGG	1.091419997
GCTGTAGTGAAGTATAGAAA	-	3134	CGG	0.947675675
GCTGTAGTGAAGTATAGAAA	-	3134	CGG	0.463921391
TTCTATACTTCACTACAGCA	+	3154	TGG	1.672152277
TTCTATACTTCACTACAGCA	+	3154	TGG	1.883561231
CACTACAGCATGGTCAATTG	+	3164	CGG	0.145026453
ACTACAGCATGGTCAATTGC	+	3165	GGG	0.054790979
ATAAAAAAACTGCTACTTGT	+	3239	TGG	0.622895595
ATAAAAAAACTGCTACTTGT	+	3239	TGG	0.987600304
GTTCAATATAAAACGAAAAA	+	3300	CGG	2.369701915
CAATATAAAACGAAAAACGG	+	3303	AGG	1.401373643
GTCAAGATGTATTACGAAAT	+	3328	AGG	1.802203353
GTCAAGATGTATTACGAAAT	+	3328	AGG	0.286601948
CGCAAAAATATTCATGTTAA	+	3361	CGG	2.035375253
ATTCATTTTAAAAGGTCATA	+	3399	TGG	0.094031379
TTCATTTTAAAAGGTCATAT	+	3400	GGG	0.242114179
ACGACATAAGCATGTTTAAT	-	3441	TGG	0.969363116
ACGACATAAGCATGTTTAAT	-	3441	TGG	2.197578171
AGATGAGAATGACTTAGATA	+	3480	TGG	1.561091543
CAATCCATTCATCTATTGCT	-	3503	TGG	0.736299714

TTAACCAAGCAATAGATGAA	+	3515	TGG	1.853727982
TTAACCAAGCAATAGATGAA	+	3515	TGG	0.915652147
TGAAGAGAACACAGACGAAC	+	3540	AGG	0.934706524
TAATTAACTTAGTCATGAAA	+	3569	TGG	1.951855415
TAATTAACTTAGTCATGAAA	+	3569	TGG	0.010477908
TAACTTAGTCATGAAATGGT	+	3573	AGG	2.161577567
TAACTTAGTCATGAAATGGT	+	3573	AGG	2.281766364
TAACTTATATCATTCGTCAT	+	3617	AGG	0.516685048
AACTTATATCATTCGTCATA	+	3618	GGG	1.796816999
GGTTTGTTAGTTATATAAAT	-	3630	TGG	0.039294779
ATATCTGAATTGTTATCAGT	-	3651	TGG	0.978786515
ATATCTGAATTGTTATCAGT	-	3651	TGG	0.224934175
CACAAATAGAAATAGAGCTA	+	3699	GGG	0.029754351
AATAGAGCTAGGGAGTTTAA	+	3709	CGG	1.099779618
AATAGAGCTAGGGAGTTTAA	+	3709	CGG	0.022291922
AGCTAGGGAGTTTAACGGTA	+	3714	TGG	0.494706958
AGCTAGGGAGTTTAACGGTA	+	3714	TGG	0.206519845
GGAAGAAGCGAGTATCAATA	+	3735	TGG	0.166446349
GACAGAAACTATTGAGTACG	+	3786	AGG	0.165128275
GACAGAAACTATTGAGTACG	+	3786	AGG	1.870251699
GAGGAGGTAGAACATGACTG	+	3805	AGG	0.334857825
AGTATGCTTACTTTTTCTTG	-	3823	TGG	0.76306924
ATATCGCTGAGAAAAATAAA	+	3882	AGG	2.005826287
TTCTATAAATTTGCAGTATA	+	3908	CGG	0.064443919
TTTATCTCTTGTAGCAAACG	-	3935	TGG	1.548447374
TTCGTCATTGACATTAACGA	+	3980	AGG	1.299405276
CATTAACGAAGGTGGAACAA	+	3991	CGG	0.892776733
CATTAACGAAGGTGGAACAA	+	3991	CGG	0.729165646
GGAACAACGGTTACTGACGA	+	4004	AGG	1.28563592
TTTTTTACCTCAAATTTTAC	+	4075	AGG	1.866477979
TTTTTTACCTCAAATTTTAC	+	4075	AGG	1.071412984
TCTCCCCAATCATTAAACGT	-	4186	TGG	0.222481824
AAAAACCAACGTTTAATGAT	+	4197	TGG	0.07349579
AAAACCAACGTTTAATGATT	+	4198	GGG	2.190935965
GTCAGTATGTACAGATTAAT	+	4241	AGG	0.9949378
GTCAGTATGTACAGATTAAT	+	4241	AGG	0.032556959
CATGACCTGTAATAACAAAG	-	4272	TGG	0.090356589
AAATTCCACTTTGTTATTAC	+	4283	AGG	0.011316319
AAATTCCACTTTGTTATTAC	+	4283	AGG	0.031127629
GCGCTTCAATAGTGATAGTA	-	4338	GGG	0.934706524
TGCGCTTCAATAGTGATAGT	-	4339	AGG	1.99299798
TGCGCTTCAATAGTGATAGT	-	4339	AGG	1.100723856
CTCAAAGTGATGTGTTAGCT	+	4404	AGG	0.952953891
TCAAAGTGATGTGTTAGCTA	+	4405	GGG	0.206998732
ATTGAAGAATTTGATGATAA	+	4433	CGG	0.583783255

ATTGAAGAATTTGATGATAA	+	4433	CGG	0.080107868
TCTACTACGTCCGTAATGCT	-	4546	AGG	1.584338664
TCTACTACGTCCGTAATGCT	-	4546	AGG	1.748149869
GTAGTAGAAGCAATTAGAAA	+	4577	TGG	0.33219648
GTAGTAGAAGCAATTAGAAA	+	4577	TGG	0.150079639
CTAAAAATTAATTAAAAGGA	+	4603	CGG	0.100862584
TATTTAATTATGAAAATCAC	+	4626	AGG	2.102527862
AATCAAGAAAAGTTTTATAA	+	4674	CGG	1.600478916
AAGTTTTATAACGGCTCAGC	+	4683	AGG	0.130399526
ATTGAATTAGTTACTCGATT	+	4866	AGG	1.386447847
ATTGAATTAGTTACTCGATT	+	4866	AGG	0.008942274
TTGGTATCAAAATCTAAGCT	-	4889	AGG	2.02093772
AAACTTACCAATAAGATCAT	-	4908	TGG	1.920946877
AAACTTACCAATAAGATCAT	-	4908	TGG	0.237552957
TTTGATACCAATGATCTTAT	+	4917	TGG	0.872542647
TTTGATACCAATGATCTTAT	+	4917	TGG	0.658672372
TATTGGTAAGTTTTGTCACT	+	4934	TGG	2.01835959
TTTGTCACTTGGTATTGAAA	+	4945	TGG	1.784974966
TGGAAATTCAATGAAGATGA	+	4965	AGG	0.94214446
ATTTATTAAACCTTACAAAA	+	5009	AGG	1.588342846
TTTATTAAACCTTACAAAAA	+	5010	GGG	1.327787917
TGCTTATCTGTCTTCGGAAT	-	5036	AGG	0.490819638
GCTTTTTGCTTATCTGTCTT	-	5042	CGG	1.482453323
CAAAAAGCTGAAGAAAATAA	+	5073	CGG	1.83138708
CAAAAAGCTGAAGAAAATAA	+	5073	CGG	0.022234021
AAAAAGCTGAAGAAAATAAC	+	5074	GGG	1.848403527
AATTGGCCACTGCTTTCAAA	-	5117	TGG	1.993070495
AATTGGCCACTGCTTTCAAA	-	5117	TGG	1.779899809
AGCAATCCATTTGAAAGCAG	+	5127	TGG	1.851351244
CTTGGTCGTCATATCCAAAT	-	5134	TGG	0.16860799
TTTGAAAGCAGTGGCCAATT	+	5136	TGG	0.032424613
CACCTTAAAACGCTAAATCT	-	5152	TGG	1.577032458
AAGTACCGTCGTTATCTTTC	-	5203	TGG	1.782272915
AAGTACCGTCGTTATCTTTC	-	5203	TGG	0.86108495
AGATACCAGAAAGATAACGA	+	5214	CGG	1.714943424
ACTTATTCCGTCGTTGCTAC	+	5238	TGG	0.42605942
CACATTGACTTACTAGAAAA	+	5280	CGG	2.003291536
AAAAGCAGAAGTAGAGGTTC	+	5312	CGG	0.204635338
ATAGATAGTTTTTTATTGTC	-	5315	CGG	0.102579686
GTAGAGATATAGAACTTCAC	+	5383	TGG	0.430010543
GTAGAGATATAGAACTTCAC	+	5383	TGG	0.024121488
TAGAGATATAGAACTTCACT	+	5384	GGG	0.809745173
AATTTTCTAGTTGATTCTAC	-	5396	TGG	2.008000401
AAAATTATTACAAACAGAAT	+	5429	TGG	0.238468293
ACTGTTCTATGAAAGTTGCA	+	5488	AGG	1.835560638

CTGTTCTATGAAAGTTGCAA	+	5489	GGG	1.26938297
CGGAAAGCCTCACGCAGACC	+	5642	TGG	0.038909536
CGGAAAGCCTCACGCAGACC	+	5642	TGG	0.328193478
CTGGCACATTATGAAGCAGT	+	5661	CGG	0.89198276
CTGGCACATTATGAAGCAGT	+	5661	CGG	0.442595972
CTAATACATGTTTGTCATAG	-	5695	TGG	1.006459999
CACAACGAGCAACATGCGAT	+	5751	TGG	1.798125679
CACAACGAGCAACATGCGAT	+	5751	TGG	1.645567344
TTATCCACGAGTCATGCAAG	-	5782	TGG	0.012574423
AATGTTGAAAGGAGAGAAAA	+	5843	AGG	0.019454768
CTTCCGCCAAGATGACGATT	-	5883	AGG	1.803606648
AGCACTCCTAATCGTCATCT	+	5893	TGG	0.591136729
ACTCCTAATCGTCATCTTGG	+	5896	CGG	0.01532063
TGCTATGCATGCTGTAAAAG	+	5932	TGG	2.069864768
AAAAACCTGTATTAACTAAA	-	5956	CGG	0.432721204
AATCTCCGTTTAGTTAATAC	+	5967	AGG	1.912408912
AATCTCCGTTTAGTTAATAC	+	5967	AGG	0.216713359
TCAATTAGTTTGTCCGCCTA	+	5991	TGG	1.97341716
TCAATTAGTTTGTCCGCCTA	+	5991	TGG	1.934730359
TCAATTAGTTTGTCCGCCTA	-	5991	TGG	0.788430072
AAAGTTACATTACAGCCCCT	+	6034	GGG	0.3559502
TAAAGTTACATTACAGCCCC	-	6035	TGG	1.174581619
TAAAGTTACATTACAGCCCC	+	6035	TGG	0.275359794
GTTAAAAGAATGTTAAAGTC	-	6108	AGG	1.45375754
GAAAAACAAAGATTTGTTTC	-	6141	GGG	2.040614889
AGAAAAACAAAGATTTGTTT	-	6142	CGG	2.284234651
AGAAAAACAAAGATTTGTTT	-	6142	CGG	1.098360617
TTAAAGTGATTTAAAAACTG	+	6190	AGG	0.23734817
TTAATAACCTAGTAAGGTTA	-	6263	GGG	0.285336598
ATTAATAACCTAGTAAGGTT	-	6264	AGG	0.105611598
TTAAAACCCCTAACCTTACT	+	6272	AGG	0.141014426
TTAAAACCCCTAACCTTACT	+	6272	AGG	0.597791963
TCGGTTGATTCTATATCTAA	+	6310	CGG	2.310523908
TCGGTTGATTCTATATCTAA	+	6310	CGG	0.153206298
GAATGACGGTATGAATATAT	-	6337	CGG	1.522479031
GAATGACGGTATGAATATAT	-	6337	CGG	0.05769345
GTTTTAAACCCAAAGAATGA	-	6351	CGG	1.068515721
TCCTGCCGTTAAATATAGAG	-	6373	CGG	0.018257552
TAAAACCGCTCTATATTTAA	+	6384	CGG	0.021439948
TTTAAAAGAATAGCATCATT	+	6436	TGG	1.078814543
TTAAAAGAATAGCATCATTT	+	6437	GGG	1.722125959
TAAAAGAATAGCATCATTTG	+	6438	GGG	0.087969386
TAATTATTTCAACAAATGAA	+	6470	TGG	0.025884026
TAATTATTTCAACAAATGAA	+	6470	TGG	0.046774229
TTATTTCAACAAATGAATGG	+	6473	TGG	0.247606138

AAAACTAATAGCATCATCTA	-	6502	TGG	0.588773968
AACTTTGAAGCTTCTAGAGC	+	6577	AGG	0.137480361
GAACCACAATTTTCTCTTCT	-	6585	AGG	1.636738092
GAACCACAATTTTCTCTTCT	-	6585	AGG	0.043048848
GGTTCTTGTAAATTATTTTC	+	6619	AGG	0.887785914
GGTTCTTGTAAATTATTTTC	+	6619	AGG	0.020751753
AAATAACTTTATCCACATAA	+	6704	AGG	0.706220015
AAATAACTTTATCCACATAA	+	6704	AGG	0.942115155
TAGAAACATTCTCTAAAACT	-	6734	TGG	2.530676224
GTTTTAGAGAATGTTTCTAC	+	6754	AGG	0.385749636
ATGGATCCTATTTTAGGTAA	-	6795	AGG	1.816196731
ATAATTATGGATCCTATTTT	-	6801	AGG	0.224478093
TCAATACCTTTACCTAAAAT	+	6805	AGG	0.28070451
CCATTTCGTTATCTCCTTTC	-	6863	TGG	1.191118172
ATAATAAAATTATACCAGAA	+	6865	AGG	1.452405959
ATAATAAAATTATACCAGAA	+	6865	AGG	0.022062108
CCAGAAAGGAGATAACGAAA	+	6879	TGG	1.428844629
CCAGAAAGGAGATAACGAAA	+	6879	TGG	0.217893402
AATTTAAGTGCTAAAGCTAA	+	6970	AGG	0.966029157
ATTTAAGTGCTAAAGCTAAA	+	6971	GGG	0.689276962
GCCAATTGTCAGGACGACTT	-	6992	AGG	1.433167911
GTGTATATTTGCCAATTGTC	-	7002	AGG	0.540537378
GTGTATATTTGCCAATTGTC	-	7002	AGG	0.153869529
GTAGTTAAACATATGAATGA	+	7048	TGG	2.639991101
GTAGTTAAACATATGAATGA	+	7048	TGG	0.050952964
GGACAAAAATCAATCAATAG	+	7069	TGG	1.241572788
GGACAAAAATCAATCAATAG	+	7069	TGG	0.795109971
TAGTGGCGTTCAAGAACTTA	+	7086	TGG	0.142019807
ATACAAAAAAGAGCTGAAAA	+	7129	CGG	0.011245531
TCCGAAAATGGCATTTCGGT	-	7173	TGG	2.121290261
TCCGAAAATGGCATTTCGGT	-	7173	TGG	0.505823969
AATAACAATACTAATAATGA	+	7312	TGG	1.184424805
TAATGATGGAAGTATATTGT	+	7326	CGG	0.367166962
AATGATGGAAGTATATTGTC	+	7327	GGG	0.041419829
AAGATTTTATTAAAGCAAGA	+	7445	TGG	0.061878714
AAGATTTTATTAAAGCAAGA	+	7445	TGG	0.920943239
CAAGATGGAATCAAGATTTT	+	7460	AGG	1.041508744
GAATCAAGATTTTAGGTTGG	+	7467	AGG	1.638523796
TTGATATCAAAACAGCTGAA	+	7505	TGG	0.038909536
AACAGCTGAATGGTTAAACA	+	7515	CGG	0.161754359
AACAGCTGAATGGTTAAACA	+	7515	CGG	0.027902233
CTTAGACCAGAAACACTTTT	+	7552	TGG	0.462269204
CTTAGACCAGAAACACTTTT	+	7552	TGG	0.588014899
TCCAATTGATCCGTGCCAGT	-	7596	TGG	1.598416104
TCCAATTGATCCGTGCCAGT	-	7596	TGG	1.729810082

TGAAGTACGACGAAAGTTAT	+	7640	TGG	1.516236682
GAAGTACGACGAAAGTTATT	+	7641	GGG	1.891212162
CGACGAAAGTTATTGGGATT	+	7647	AGG	0.57252603
CGAAAGTTATTGGGATTAGG	+	7650	GGG	0.016675515
TTTATCTTTTCGCTGAATAG	-	7668	TGG	0.017630884
AATCCTTTTTCGACATGAGT	-	7713	AGG	0.181239197
AATCCTTTTTCGACATGAGT	-	7713	AGG	0.810391716
CAACCTACTCATGTCGAAAA	+	7726	AGG	1.837938256
GGATTGAAATGTGAGAGATG	+	7747	TGG	1.182511552
CCATTCGGGTGTTTTTTAGT	-	7782	AGG	1.95975743
CCATTCGGGTGTTTTTTAGT	-	7782	AGG	0.310883263
CTTTATACTCGTAACCATTC	-	7796	GGG	1.156605032
TCTTTATACTCGTAACCATT	-	7797	CGG	0.733914352
AATGGTTACGAGTATAAAGA	+	7816	CGG	2.197091802
TTGCAAATGTGAAATCTATG	+	7839	AGG	0.401987074
TGTACTTGTTTTTCATTTTG	-	7941	TGG	0.358920618
TGTACTTGTTTTTCATTTTG	-	7941	TGG	0.184820296
ACAGCAATAGAGTACGTACA	+	7990	AGG	1.869183594
CCAAAATCATTAATATTGCA	+	8029	AGG	2.106848983
CCAAAATCATTAATATTGCA	+	8029	AGG	0.0189428
TTAATATTGCAAGGTTCATA	+	8038	CGG	1.311855133
TTAATATTGCAAGGTTCATA	+	8038	CGG	0.749797276
TTGCGATAGCGTATGCTAGG	-	8057	TGG	0.122287113
CTTTTGCGATAGCGTATGCT	-	8060	AGG	1.339599741
CTTTTGCGATAGCGTATGCT	-	8060	AGG	1.095951932
CAAAAGCAGTCAAAGCTAAA	+	8093	GGG	0.205159372
TTGATACGATCCATCAACAT	-	8124	TGG	1.163649676
TTGATACGATCCATCAACAT	-	8124	TGG	1.862722302
TATGCACATACCAATGTTGA	+	8130	TGG	1.619734148
TTTACTTGTACTAGATGATA	+	8229	TGG	0.4043043
TTTACTTGTACTAGATGATA	+	8229	TGG	1.735365307
TTACTTGTACTAGATGATAT	+	8230	GGG	0.482139903
AACTAAATCAAAATATGAAC	+	8351	TGG	1.987460672
GCGAGAAAAGTAAGAGTAAT	+	8404	CGG	0.249264215
GAGTAATCGGAGACGATTTC	+	8417	AGG	0.537322164
ATTTCAGGGAGCGAGATGCA	+	8432	TGG	1.446439381
ATTTCAGGGAGCGAGATGCA	+	8432	TGG	1.715262047
TTTAGTTTTTAAAAATTCTT	-	8442	TGG	0.9616593
CGCTCAGAAACTCATAGATG	+	8501	AGG	0.092557533
GAAACTCATAGATGAGGCAC	+	8507	AGG	0.949156864
TATAAGTAATATTTTTCTTT	-	8609	CGG	1.967544897
TATAAGTAATATTTTTCTTT	-	8609	CGG	1.92314411
TATTACTTATACCGAGAAGA	+	8637	TGG	2.003579383
TATTACTTATACCGAGAAGA	+	8637	TGG	0.017064421
AATGAAGTTTATTCGCTCAC	+	8700	AGG	1.492380709

CTTTTATATGAGCAAGAGCT	+	8793	AGG	2.341646624
TTTTATATGAGCAAGAGCTA	+	8794	GGG	1.783430028
CAACGATATTTGATATTTAG	+	8824	AGG	1.722903372
CGATATTTGATATTTAGAGG	+	8827	TGG	0.339574133
GAAACGTTCGAGGCACCTAT	+	8877	GGG	1.433615147
TTATGATTTGTATAAGCTGT	-	8936	TGG	0.708153556
AATCATAAAGCGTATATACA	+	8967	AGG	0.579686139
GCGCGCTCTAGATTTAACTT	-	8981	AGG	1.978939003
GAAGAAAAAGAAAAGTGAAA	+	9068	TGG	0.008499656
GAAGAAAAAGAAAAGTGAAA	+	9068	TGG	0.110243685
AAAAAGAAAAGTGAAATGGT	+	9072	TGG	1.807506764
AAAAAGAAAAGTGAAATGGT	+	9072	TGG	1.524710889
TTAATTAAGTTATCGATATC	-	9098	CGG	0.482478247
ACAGTATTAGACGCATGTAA	+	9138	TGG	0.337132303
AGCTAGTTATTTCTGTAATT	-	9166	TGG	2.352310333
ATAACTAGCTCAAAGCGTTA	+	9195	TGG	0.726360282
ATAACTAGCTCAAAGCGTTA	+	9195	TGG	1.591494925
AAAAATAATCATGCGAGTTG	+	9227	AGG	1.699891938
TACTGATATTCAACTTCTGT	-	9289	AGG	0.039820641
GGATATCGAAAAAGAAGCGC	+	9340	TGG	0.645988121
GGATATCGAAAAAGAAGCGC	+	9340	TGG	0.096389532
AATTAGAAATGTAAATGTAG	+	9415	AGG	1.55999447
TCATGTTCGGTAAATTTATA	-	9457	TGG	1.815437037
ATGAATTGATAAAAAAGAAC	+	9498	GGG	0.010802893
AAAAAGAACGGGTTAACTCC	+	9509	TGG	0.478587293
AAAAAGAACGGGTTAACTCC	+	9509	TGG	1.237323246
ACTCTTTTTGCAACCATTCC	-	9511	AGG	0.432100637
GAACGGGTTAACTCCTGGAA	+	9514	TGG	1.652579061
AAAAAGAGTACGTGGTGGCT	+	9541	GGG	0.245130077
TCAGCTAAGCGCATGCCATA	-	9571	AGG	1.616514361
TCAGCTAAGCGCATGCCATA	-	9571	AGG	0.689759957
GAAGCCTTAAACGCACCTTA	+	9572	TGG	0.833775772
GCTCTCTCGTTGCATAATTC	-	9614	TGG	0.099705686
GGATCACGTGAATGTTTTTG	-	9712	TGG	1.045369535
AACATTCACGTGATCCGTAC	+	9735	TGG	0.420930435
AACATTCACGTGATCCGTAC	+	9735	TGG	0.061606765
TCGCCGTATGTGTAATGTGC	-	9849	TGG	1.215782025
TCGCCGTATGTGTAATGTGC	-	9849	TGG	1.49709072
CAACCAGCACATTACACATA	+	9862	CGG	0.819189359
CAACCAGCACATTACACATA	+	9862	CGG	1.911174974
AGATTTTATTGAACAAGTAA	+	9900	CGG	1.200851818
AGATTTTATTGAACAAGTAA	+	9900	CGG	0.075117021
ATTGCAAATGCTAATTGTGG	-	9915	TGG	0.075771202
CCACAATTAGCATTTGCAAT	+	9934	AGG	1.9791984
CCACAATTAGCATTTGCAAT	+	9934	AGG	0.353178866

TCTAGAGCACCGTTAAAGAA	+	9976	TGG	1.385963706
TCTAGAGCACCGTTAAAGAA	+	9976	TGG	2.086582469
TTTACGCGCGTTATCTGTCA	-	10047	TGG	0.960451179
AATAAGCGCCATTCACTACA	-	10138	TGG	0.027380785
GCACATATCCATGTAGTGAA	+	10146	TGG	0.278131128
CATATCGTACCAGATTGGCA	+	10188	AGG	1.605604349
CATATCGTACCAGATTGGCA	+	10188	AGG	0.947977787
GGAATATATATAAAGCAACA	+	10245	TGG	2.482228863
ATATATAAAGCAACATGGTT	+	10250	TGG	0.043787408
AGCAACTAACTTTATTTTAG	+	10288	AGG	1.502372683
GAAAATCCGGAGCTATCACA	+	10379	AGG	0.055488382
AAAATCCGGAGCTATCACAA	+	10380	GGG	1.054448427
TTTTCAACAGGATTTAGTGA	+	10412	TGG	1.887112498
GTCGAACACTTATTTGTATT	-	10435	TGG	1.596587962
CTTATCAAATACCGTGTCTT	-	10514	TGG	0.033102143
CTTATCAAATACCGTGTCTT	-	10514	TGG	1.122232934
AAAAGAAGTAACCAAAGACA	+	10519	CGG	1.243926076
GTTGTTTGAAATGTACGAGA	+	10552	TGG	1.589187521
TTTGAAATGTACGAGATGGA	+	10556	AGG	1.617858509
TTTGAAATGTACGAGATGGA	+	10556	AGG	0.83525804
AGTATAAAAGAATGTTTATA	+	10613	TGG	0.195834764
AGTATAAAAGAATGTTTATA	+	10613	TGG	1.275368126
AAGATATAGAATGCTTTGGT	-	10630	AGG	0.116728608
GTTTAAGATATAGAATGCTT	-	10634	TGG	1.611812565
GTTTAAGATATAGAATGCTT	-	10634	TGG	1.0794617
GATACAAAGACTTACTTTAT	-	10714	AGG	0.482354725
CAGTTTTAATACCGTATTCG	-	10810	TGG	1.19416174
TGAGGAAGAAGCCACGAATA	+	10815	CGG	1.416307112
TGAGGAAGAAGCCACGAATA	+	10815	CGG	0.987329477
CGACCTCTATGCTTGCAGTT	-	10853	TGG	0.094841994
AAGCATAGAGGTCGAAAAAG	+	10878	TGG	1.92213108
TCGTCCCACACTCGATATTT	-	10901	CGG	1.686578735
CGAGTGTGGGACGAATATAC	+	10926	AGG	1.158639518
CGAGTGTGGGACGAATATAC	+	10926	AGG	0.455514186
GGAAGAATACACGATGTTGT	+	10947	AGG	0.818545812
GGAAGAATACACGATGTTGT	+	10947	AGG	0.865465895
AGTTCACTATGAAAACTACG	+	10991	CGG	0.969979361
GTAGAACTTATGCAAAGTAC	+	11052	AGG	0.743858777
AAACAACAACGAAATATATG	+	11087	CGG	1.160607579
AAACAACAACGAAATATATG	+	11087	CGG	1.890806441
CCTATTACAGATTCATCGTC	-	11132	TGG	1.753021032
ATATCTATTGATGTTGTAAA	+	11190	TGG	1.329316506
ATATCTATTGATGTTGTAAA	+	11190	TGG	0.598608247
ATTAAAAGATTTTATGTTTG	+	11219	AGG	0.115950417
TAACCTCACAGTCATATCTA	-	11275	AGG	0.764904538

TAACCTCACAGTCATATCTA	-	11275	AGG	1.617738787
ATTTGAATCATCACATTTAT	+	11324	TGG	0.292022915
ATTTGAATCATCACATTTAT	+	11324	TGG	0.038909536
TGAATCATCACATTTATTGG	+	11327	AGG	2.469259018
AACAGAATGAACTATGAAAC	+	11351	AGG	0.055121843
AACAGAATGAACTATGAAAC	+	11351	AGG	2.386451544
ACAGAATGAACTATGAAACA	+	11352	GGG	0.646011548
CAGAATGAACTATGAAACAG	+	11353	GGG	0.155638144
TAGCGTCCATTACACCTAGT	-	11361	TGG	1.810829329
TAGCGTCCATTACACCTAGT	-	11361	TGG	2.016810951
AACTAGGTGTAATGGACGCT	+	11379	AGG	1.006089432
AAGCAACGTGATGAGCTTAT	+	11438	TGG	0.034982886
GCAACGTGATGAGCTTATTG	+	11440	GGG	1.58750907
AAGAGAACGCAACAAAGAGC	+	11476	TGG	1.195583926
AAGAGAACGCAACAAAGAGC	+	11476	TGG	0.541491043
TGGAGAAGAAAGCAAGTGCA	+	11496	TGG	1.722785817
GGAGAAGAAAGCAAGTGCAT	+	11497	GGG	0.498042061
ATAAACGAATTTGGCAAAGA	+	11552	TGG	2.517446982
TGAAAGAGTTAAATTTGGAA	+	11575	TGG	1.215923001
ATTAAACAATAAAACTTTTA	+	11599	TGG	2.185373134
ATTAAACAATAAAACTTTTA	+	11599	TGG	2.154676203
AAACAATAAAACTTTTATGG	+	11602	AGG	1.176040727
AAACAATAAAACTTTTATGG	+	11602	AGG	0.442628615
CGGATTGTTCTATTTGTTCA	-	11626	CGG	1.803255739
ATACGCACTAGCACTTATAA	-	11646	CGG	2.509665075
ATAAGTGCTAGTGCGTATAA	+	11667	CGG	0.122872219
ATAAGTGCTAGTGCGTATAA	+	11667	CGG	0.25534383
GTATAACGGCAATGACACAG	+	11681	AGG	1.641157848
GTATAACGGCAATGACACAG	+	11681	AGG	0.744045618
AGCGTTTGATGAAATACTTG	+	11744	AGG	1.98580123
GCGTTTGATGAAATACTTGA	+	11745	GGG	0.112285235
ATTCAACATTCAGTTAAAGA	+	11781	AGG	1.430722776
ATTCAACATTCAGTTAAAGA	+	11781	AGG	1.817150159
ATTGAACTTGATGAAGCAGT	+	11805	AGG	1.999950153
TTGAACTTGATGAAGCAGTA	+	11806	GGG	0.013670918
TGAAGCAGTAGGGATTATGA	+	11816	CGG	0.091967994
TCAAGTTGTCTATAAATATG	+	11840	AGG	1.062529638
AGTTGTCTATAAATATGAGG	+	11843	AGG	0.092918295
CTATAAATATGAGGAGGCAC	+	11849	AGG	0.080250918
AGAGTTATTACAAATACAAA	+	11907	AGG	1.262614445
AGAGTTATTACAAATACAAA	+	11907	AGG	1.617524998
CTATCTCGTAAGTTCAGCGT	-	11931	TGG	1.706062145
CTATCTCGTAAGTTCAGCGT	-	11931	TGG	0.651086236
ATGTAGTTGAATTCTTTGAA	+	11981	TGG	0.011290714
CTTTGAATGGTTTAATACAT	+	11994	TGG	0.684759798

CTTTGAATGGTTTAATACAT	+	11994	TGG	0.07874549
CATTGGAAACGTTTAAGAAC	+	12011	TGG	0.774764724
CATTGGAAACGTTTAAGAAC	+	12011	TGG	0.042466363
TGTACGTCTAACGGCTTACC	-	12027	TGG	1.614745746
TGATGAATTAGCTGACATGT	+	12069	TGG	1.306474665
TGATGAATTAGCTGACATGT	+	12069	TGG	0.011205946
TTGAGTATTGCGAATCAAGT	+	12100	AGG	0.803882895
TTGAGTATTGCGAATCAAGT	+	12100	AGG	0.129768561
TCACTATAACAATTGCTTGT	-	12254	TGG	1.933355451
TCACTATAACAATTGCTTGT	-	12254	TGG	0.548685941
TTTTGTATGCGTCAATGAGT	-	12308	TGG	1.09769302
AGGAATCATGAAAGACAAGA	+	12358	TGG	1.910074834
CAAGATGGAACAGCAGACGC	+	12373	AGG	1.19046623
CAAGATGGAACAGCAGACGC	+	12373	AGG	0.496608552
CATATTAGATCGAGTCAAGG	+	12415	AGG	0.359640683
ACAACATTCAAAGATTCAAC	+	12466	AGG	2.01431675
TCAAAGGTTTACAGTCGTTG	+	12525	AGG	1.065782944
TCAGTTGTATGAAAATATAA	+	12618	GGG	0.084628241
ATGAAAATATAAGGGAGTGT	+	12626	GGG	0.495015764
GTTAAAATTAAAACTATTTC	+	12660	AGG	1.810603851
GTTAAAATTAAAACTATTTC	+	12660	AGG	1.434650179
AAAATTAAAACTATTTCAGG	+	12663	TGG	1.772493443
AAAATTAAAACTATTTCAGG	+	12663	TGG	1.618636699
GAAAGAATGACGAGTTTTAA	+	12729	TGG	1.799084488
GAAAGAATGACGAGTTTTAA	+	12729	TGG	0.115172227
GTATCTGTTTTAATATACGT	-	12767	TGG	0.325240338
TGAATCAATCACACTTATTG	+	12809	AGG	1.21667599
TGAATCAATCACACTTATTG	+	12809	AGG	1.28973668
CTGAGAATTTTATTACATGA	+	12851	CGG	1.338744586
CTGAGAATTTTATTACATGA	+	12851	CGG	0.719447919
AGAGAACTTGTATTGAACAA	+	12980	AGG	1.646723123
AGAGAACTTGTATTGAACAA	+	12980	AGG	0.844429574
TTGAACAAAGGTTATATAGT	+	12992	TGG	0.664037008
TGAACAAAGGTTATATAGTT	+	12993	GGG	1.785169514
TATAGTTGGGATCAATGTTG	+	13006	AGG	0.00999789
TATAGTTGGGATCAATGTTG	+	13006	AGG	1.138310895
TTATTTCAGTGTACTTTTTC	-	13048	GGG	0.108449983
ATTATTTCAGTGTACTTTTT	-	13049	CGG	0.094793031
ATTATTTCAGTGTACTTTTT	-	13049	CGG	0.063552242
TGAATTTTACAGTCCTATGA	+	13169	TGG	1.903766959
TGAATTTTACAGTCCTATGA	+	13169	TGG	1.980106289
ATATGAATGAACATGAATTA	+	13195	AGG	0.707918757
TATGAATGAACATGAATTAA	+	13196	GGG	1.763708794
TCTCCAGTATCAATTAAACT	-	13220	AGG	0.412072112
AGTTTAATTGATACTGGAGA	+	13239	TGG	1.180754767

GATTAAAAAACTTAAAAATA	+	13269	TGG	0.215845532
GCTGGAATACTGCGATTATT	+	13312	CGG	1.029054835
TAACTAGCCACTGTGTATAT	-	13350	AGG	1.418701545
CTTGATGTACTTCTTTGTGT	-	13373	TGG	0.36483412
CAACACAAAGAAGTACATCA	+	13390	AGG	2.118197182
CAACACAAAGAAGTACATCA	+	13390	AGG	0.381313453
ATAGCGCAGACATACAAGCT	+	13526	AGG	1.726027019
AAAGTAAAAGTTAAGACGAT	+	13564	TGG	0.213683518
TTCTTTACTTCGTATAAGAT	-	13599	CGG	0.049181654
GATCTTATACGAAGTAAAGA	+	13617	AGG	1.997134855
GCAAGTATATATTATGATGA	+	13718	CGG	0.225675309
CTCAACTTTGCGAAGTCACT	-	13745	CGG	0.94139122
CTCAACTTTGCGAAGTCACT	-	13745	CGG	0.462818692
GAGTCAATTGTTAATATGAT	+	13836	AGG	0.014917498
TGTATTAGCTGATGTAATAC	+	13880	CGG	2.391566412
ATTGAATTGCTATCATATTC	-	13883	CGG	0.392385505
ATTGAATTGCTATCATATTC	-	13883	CGG	0.050601564
AGCAATTCAATTGCACAGTA	+	13911	TGG	0.010013484
AGCAATTCAATTGCACAGTA	+	13911	TGG	0.914374097
GAGTTTTCCCCTTGTGGTTT	-	13934	CGG	1.293742073
GCAACGTTGCCGAAACCACA	+	13941	AGG	1.649764328
GCAACGTTGCCGAAACCACA	+	13941	AGG	0.505823969
GGCTTGAGAGAGCAAATAAA	+	13999	AGG	0.954512355
GTATGCTCAGATGTTAAAAG	+	14021	AGG	0.008066611
AAATCAATCGCAACAGAGAT	+	14054	TGG	0.01111701
TTCTTAGAGTTATTGAAGAA	+	14094	AGG	1.841228611
TATTGAAGAAAGGTTATAAC	+	14104	AGG	1.341325773
ATTGAAGAAAGGTTATAACA	+	14105	GGG	1.6811477
TTTCTGTTCAATTTAGAGTT	-	14132	AGG	0.133222868
TTTCTGTTCAATTTAGAGTT	-	14132	AGG	1.825364756
TCTTTTCTGCTAATTCATCA	-	14170	CGG	1.000608996
GTAAGAATTATCTTAAGACG	+	14303	TGG	0.022642272
AAGAATTATCTTAAGACGTG	+	14305	GGG	0.461355927
AAACTACCCACCATATAGGC	-	14399	AGG	1.73847807
AAACTACCCACCATATAGGC	-	14399	AGG	1.580955885
AATTAAACTACCCACCATAT	-	14403	AGG	2.07232189
AATTAAACTACCCACCATAT	-	14403	AGG	0.538969129
TCACTTACTACCTGCCTATA	+	14405	TGG	1.849499947
CTACGTTCAATAAATGTGAA	-	14455	AGG	0.053058458
AATGCCCCTACATCTTGTGC	-	14480	AGG	0.359913208
AGCACAAACTTTTCTTGCTT	-	14575	CGG	1.059536597
TTTGTGCTAGGACTCATAGA	+	14606	GGG	0.031127629
TCATAGAGGGCAAGAGCCAA	-	14619	CGG	0.500960277
TCATAGAGGGCAAGAGCCAA	-	14619	CGG	0.203702865
TCATAGAGGGCAAGAGCCAA	+	14619	CGG	0.811912319

TCATAGAGGGCAAGAGCCAA	+	14619	CGG	0.275359794
GACGCAGGGTATTCGACTAA	+	14654	AGG	0.309507673
ATTCGACTAAAGGTAAGAGT	+	14664	GGG	0.200773206
ACGCAATTTTTCGTACCTTC	-	14720	CGG	1.857704128
ACGCAATTTTTCGTACCTTC	-	14720	CGG	0.778190721
TAAGAATGACATTGAAATAG	+	14833	AGG	0.066785025
AAGAATGACATTGAAATAGA	+	14834	GGG	1.957149663
GCATTCCTCGCTAGTTTAGA	+	14879	TGG	1.702042782
GCATTCCTCGCTAGTTTAGA	+	14879	TGG	0.833312564
GGTATGAATAGAATGACGTT	+	14900	AGG	1.760149871
GGTATGAATAGAATGACGTT	+	14900	AGG	0.173606784
AAGATTGAACAAATAGATAA	+	14978	AGG	1.652809422
CAAATAGATAAAGGTGACAG	+	14987	TGG	1.847770634
CAAATAGATAAAGGTGACAG	+	14987	TGG	0.058364304
ACAACTTCACGACGCAATAA	+	15028	CGG	1.708200245
ACAACTTCACGACGCAATAA	+	15028	CGG	1.873747918
TAAACTTAAATCTTTATATA	+	15068	CGG	1.448111428
AGCAAACGCAAAAACAAGAT	+	15112	TGG	0.031992285
TGGTTTATGTTAATTAATCA	+	15132	CGG	1.96701601
AATCACGGAGCAAAGCGTAC	+	15147	AGG	0.116641756
AATCACGGAGCAAAGCGTAC	+	15147	AGG	0.009886849
CGAAAGATAGCAGACGAAGA	+	15219	AGG	0.560297319
CGAAAGATAGCAGACGAAGA	+	15219	AGG	0.021886614
ACACCTCAATATATACTTGC	+	15249	TGG	0.818994942
ACACCTCAATATATACTTGC	+	15249	TGG	1.850518372
ATACTTGCTGGTGCAACATT	+	15261	AGG	1.857046038
ATAGAGTTAACTAACAAATA	+	15306	TGG	1.47856237
TATAATTCATTCATGTTATT	+	15351	TGG	0.321176663
TATAATTCATTCATGTTATT	+	15351	TGG	0.840225736
CATGTTATTTGGCGTTCAAG	+	15362	TGG	0.212505928
GGCGTTCAAGTGGTTCAGAC	+	15372	AGG	2.158530237
AGTGGTATAGGAGCTATACG	+	15408	TGG	1.67835197
AGCGTCGTTAGCGCATGAAG	+	15461	AGG	0.977602093
GAGATTAAGTCACGTTGTAG	+	15492	TGG	0.885191945
AAGTCACGTTGTAGTGGAAC	+	15498	TGG	1.036722971
AAGTCACGTTGTAGTGGAAC	+	15498	TGG	1.029606184
TGGAACTGGTGCAAGAATAT	+	15512	TGG	1.238030692
TGGAACTGGTGCAAGAATAT	+	15512	TGG	0.781574159
TCAACAACCAATGCTCGGGA	-	15535	TGG	0.07295538
ATCTTTCAACAACCAATGCT	-	15540	CGG	1.804105488
ACCCTGACCATCCCGAGCAT	+	15544	TGG	0.132750182
GAAAATACAGATCCTAAAGC	+	15585	AGG	0.699789461
TATTGTCATCGAGCTTAAAT	-	15604	TGG	0.027652689
TAGATATAAAGAGTCTATTA	+	15656	AGG	1.578991037
TAGATATAAAGAGTCTATTA	+	15656	AGG	0.043232818

CGTTCATAGAACATACCTGA	-	15671	TGG	0.942213411
CGTTCATAGAACATACCTGA	-	15671	TGG	2.246818741
ATTAAGGCTTCAACACCATC	+	15672	AGG	1.977451965
TTCTATGAACGTAATATCAA	+	15699	CGG	1.661363775
TTCTATGAACGTAATATCAA	+	15699	CGG	3.126911806
GGTATGTGGGTGTCTGGTGA	+	15720	CGG	0.517899342
ATTCTCATTCAAATCAAAGT	-	15738	CGG	1.989280115
ATTCTCATTCAAATCAAAGT	-	15738	CGG	1.966910021
TACGATTAAAGCAGATGAAC	+	15776	TGG	0.096892374
TTAATAGGACGAGGTATAGA	+	15867	TGG	0.448472934
TTAATAGGACGAGGTATAGA	+	15867	TGG	1.346269947
TGGTAACTTTTATTTTATTG	+	15887	AGG	1.921126963
AATCATCAATAAACTTAAAT	-	15904	TGG	2.319707845
AATTTAAGTTTATTGATGAT	+	15922	TGG	1.28372432
AATTTAAGTTTATTGATGAT	+	15922	TGG	2.133299377
ATTTAAGTTTATTGATGATT	+	15923	GGG	2.016928859
AAAGATATTGTAAGTAGATA	+	15957	TGG	1.194353585
AAAGATATTGTAAGTAGATA	+	15957	TGG	1.193225772
CGCTGATAAAAGTAAACTAT	+	16058	CGG	2.061468487
GCTGATAAAAGTAAACTATC	+	16059	GGG	1.71346068
ACTTGTTCTTTATGATAATA	+	16121	TGG	0.562199563
ACTTGTTCTTTATGATAATA	+	16121	TGG	1.049738325
TTCTTTATGATAATATGGAT	+	16126	AGG	2.167490037
AAGAGGTATTTAAATATGTT	+	16156	TGG	1.840169401
TTATAGGCTCTCCGTTTGTA	-	16165	GGG	0.302629725
TTTATAGGCTCTCCGTTTGT	-	16166	AGG	0.150518468
TATGTTTGGCACCCTACAAA	+	16170	CGG	0.095112199
TATGTTTGGCACCCTACAAA	+	16170	CGG	0.732414796
ACGTCATCAAATTCTTTTAT	-	16181	AGG	1.655096376
ACGTCATCAAATTCTTTTAT	-	16181	AGG	1.881992822
AAAAGAATTTGATGACGTGT	+	16202	TGG	1.113965606
AAAAGAATTTGATGACGTGT	+	16202	TGG	0.217435643
AGGTTTAGTATGTGTGTATA	-	16224	TGG	1.209732848
ATACTAAACCTGAACGATTA	+	16252	AGG	0.038909536
ATTAGAGCCTCAATATGCTT	-	16315	AGG	1.665472252
ATTAGAGCCTCAATATGCTT	-	16315	AGG	0.609368041
TAAAGACGATAGAGAGAGAA	+	16363	TGG	0.358210916
TAAAGACGATAGAGAGAGAA	+	16363	TGG	0.328468874
ATTGGTCGACGTTTGAATAT	-	16411	TGG	1.627678321
ATTGGTCGACGTTTGAATAT	-	16411	TGG	0.908969995
AAATCTTCTTTTTCTTCAAT	-	16429	TGG	0.169904974
AAAGAAGATTTTGAAACTGG	+	16457	TGG	1.334597086
TTGAAACTGGTGGAAATGTA	+	16467	AGG	1.111914818
ACACGTGTTGGTTATTTACA	+	16550	TGG	0.866621485
TCATCTAAATCATAAGTAAC	-	16561	AGG	1.199487077

TCATCTAAATCATAAGTAAC	-	16561	AGG	0.606988762
ATCATCAACACTATTTCTAA	-	16631	TGG	1.752854237
ATCATCAACACTATTTCTAA	-	16631	TGG	0.699116502
TAGAAATAGTGTTGATGATG	+	16651	AGG	0.058364304
TAGAAATAGTGTTGATGATG	+	16651	AGG	1.022259629
GGATTCTGAAATAGGTAAAA	+	16672	TGG	0.047775
GGATTCTGAAATAGGTAAAA	+	16672	TGG	0.040855013
CAATTTGCGGATATGGTGCT	+	16698	AGG	1.776868813
TTGATACGAATGGTGATGTT	+	16731	AGG	1.897597659
GCCAACAAAAATAACATTAT	-	16754	AGG	2.039157086
GCCAACAAAAATAACATTAT	-	16754	AGG	1.488289754
AAGTAGCGCAATGAGTATGT	-	16792	AGG	0.034987204
AAGTAGCGCAATGAGTATGT	-	16792	AGG	1.149452544
TATGAAAAAGATGATGATAA	+	16832	TGG	0.92557736
TATGAAAAAGATGATGATAA	+	16832	TGG	0.049190511
TATTATGTATTTCGAGGAGA	+	16895	AGG	1.809293426
TTGTTAGGTACACCAAACAA	-	16954	TGG	0.330175206
TTGTTAGGTACACCAAACAA	-	16954	TGG	0.868979638
TTTGATTACAATCCATTGTT	+	16958	TGG	2.35993724
CCTATCATCTCTTTGTTGTT	-	16969	AGG	1.14394036
CCTATCATCTCTTTGTTGTT	-	16969	AGG	0.698210008
CCTAACAACAAAGAGATGAT	+	16985	AGG	1.54576975
TACCCATACCGCGTAACACA	-	17082	AGG	1.134323619
TACCCATACCGCGTAACACA	-	17082	AGG	0.530142429
ACTTTCCATTACTTAAATCA	+	17090	CGG	0.722224472
ATACCTTGTGTTACGCGGTA	+	17095	TGG	0.31426933
TACCTTGTGTTACGCGGTAT	+	17096	GGG	0.846282409
ATTCAAGAAACACAAAAGAG	+	17135	TGG	0.705116714
TGAGTTGTTCGACAAAGATA	+	17164	TGG	0.12052466
TCTTTTCGATTCGATCTAAA	-	17217	TGG	1.511654477
TCTTTTCGATTCGATCTAAA	-	17217	TGG	1.360828022
TTTAATTCTGACGAGTTTAA	+	17285	CGG	2.564840073
GTAAGATGACAGCTATGTTG	+	17376	AGG	1.220021341
GTAAGATGACAGCTATGTTG	+	17376	AGG	0.264028995
TTATCTGCATTAAAGCGTAA	+	17417	AGG	1.793299362
TTATCTGCATTAAAGCGTAA	+	17417	AGG	1.077275355
TATCTGCATTAAAGCGTAAA	+	17418	GGG	1.355643608
AAAGCGTAAAGGGTACAACT	+	17428	TGG	0.023281936
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GATTCTTCTAACTTATTAAC	-	17482	TGG	1.745370617
GATTCTTCTAACTTATTAAC	-	17482	TGG	0.200533763
ACAAGTGCTAATTAACCTGA	+	17521	AGG	1.839359886
GACAAGTTTCAGAACGAACA	+	17544	AGG	0.972738401
GTTTCAGAACGAACAAGGTT	+	17549	AGG	0.045787009
AAATTACCTGACATAGATGA	+	17645	AGG	1.630740962

AAATTACCTGACATAGATGA	+	17645	AGG	1.76562828
CTCATCAATATCATTCTGAT	-	17679	TGG	1.564457006
CTCATCAATATCATTCTGAT	-	17679	TGG	0.143350922
TGATATTGATGAGTATATCG	+	17705	AGG	0.77111626
GATATTGATGAGTATATCGA	+	17706	GGG	0.08300701
TTAGCAAATAGTTGTTCTAT	-	17735	TGG	2.117522582
ATGATGATGTGTATGTTACA	+	17827	TGG	0.598811165
ATGATGATGTGTATGTTACA	+	17827	TGG	1.313434095
CTGAATTCAATAAATACAAC	+	17851	AGG	0.045494227
TAAATACAACAGGCTCAATA	+	17861	AGG	2.220417337
TAAATACAACAGGCTCAATA	+	17861	AGG	1.27060988
AATAAGGAGTTAACTCGTAT	+	17877	AGG	0.935307293
AATAAGGAGTTAACTCGTAT	+	17877	AGG	0.547165351
CATATAAATAAAGGCTCATA	-	17962	AGG	1.594930704
GAGCCTTTATTTATATGAAA	+	17984	TGG	0.357967732
GTTTGATGTTCCGAGTAAAG	+	18026	AGG	1.901802833
GTTTGATGTTCCGAGTAAAG	+	18026	AGG	1.046532349
ATTAAACGAATGAACTCAAT	-	18056	AGG	0.247745887
ATTAAACGAATGAACTCAAT	-	18056	AGG	1.412715462
TCACGATGTTTTTGTAGTGT	-	18080	TGG	1.136387332
ACAAGGTATTATGAGTGGAG	+	18152	AGG	0.657366372
AAAGCAATACGTGATGATGT	+	18192	CGG	2.17755669
AAAGCAATACGTGATGATGT	+	18192	CGG	0.832907256
AGCTGGACTTGATAGCGCAA	+	18275	TGG	0.079375454
GTTTGAAGATGAAGAAACGT	+	18313	TGG	2.164224316
ATCAGAATTTTAAATCAAGT	+	18403	GGG	0.261973109
TTTAAATCAAGTGGGTGTGT	+	18411	TGG	1.498017138
TTAAATCAAGTGGGTGTGTT	+	18412	GGG	1.928559612
ATCAAGTGGGTGTGTTGGGC	+	18416	AGG	0.356329435
TTTACACCAATAAATAGCTT	-	18425	GGG	1.310637004
GTTTACACCAATAAATAGCT	-	18426	TGG	1.025796859
TTACGTGCTCTCATTACAGT	-	18512	TGG	1.527829768
ATGAGAGCACGTAAAGACGA	+	18537	TGG	0.064507915
CATTCATGACTTATCGTGAG	+	18577	TGG	1.671613529
GAGAAATATAAGCGAAAAGG	+	18600	TGG	0.010382868
GAGAAATATAAGCGAAAAGG	+	18600	TGG	0.162843614
ATAAAAGTAAATGTTGATAC	+	18643	TGG	0.091533089
CTCTATTATCTCTTCGTACA	-	18682	AGG	2.103894199
CTCTATTATCTCTTCGTACA	-	18682	AGG	2.688853727
AAATGAAGCTGATTTAGATA	+	18759	TGG	1.947776002
AAATGAAGCTGATTTAGATA	+	18759	TGG	0.022430203
TATGCACTTTTCGGACTGTT	+	18886	AGG	0.018332378
AGGGTACGCGAAGGGCAAAA	+	18906	AGG	1.355348839
TTATCTAAAGGGACTTAAGA	+	19002	CGG	2.462159246
TTATCTAAAGGGACTTAAGA	+	19002	CGG	1.152833968

GTGTCTGTTGATGACGTTAA	+	19024	AGG	1.436659792
GAATGATAACGATCTAATTC	-	19068	AGG	0.925099161
ATGGAAAGAGAAAAATCTTG	+	19122	AGG	0.008646564
ATCTAATCGAACAAGAAGTA	+	19145	CGG	1.408926165
TTTTGTTCTTCTGATTGCTC	-	19161	AGG	1.525253813
GTTAGAAAAACGCGACGCAG	+	19224	AGG	0.010019623
GTTAGAAAAACGCGACGCAG	+	19224	AGG	0.821269136
AAGTTAAGAAGTAACGCGCT	+	19258	AGG	0.034528992
GCCTAAAAATCTATCAACTA	-	19294	AGG	0.854817579
GCCTAAAAATCTATCAACTA	-	19294	AGG	0.066924402
TCCTTAGTTGATAGATTTTT	+	19309	AGG	0.031056235
GAGTCTAAATTTAAATCGAG	+	19408	TGG	0.010427756
TCCGATAAAATAACATTGCC	-	19546	TGG	1.136714303
ATTAAAGTACCTTGTTCTGC	-	19588	TGG	2.100455463
ATTAAAGTACCTTGTTCTGC	-	19588	TGG	0.784176803
ACTTACTTAGCAAAAGGTGT	+	19706	AGG	1.828748194
AAAAGGTGTAGGCGCCTACT	+	19717	GGG	0.914374097
ATTTCTGCTTGTGCATATTC	-	19753	AGG	1.425756571
TGAATATGCACAAGCAGAAA	+	19771	TGG	1.592896545
TGCAAAAGATTTCTTTAATG	+	19849	AGG	1.711118207
TGCAAAAGATTTCTTTAATG	+	19849	AGG	0.008891093
TTTGACCAAGCTGTTATCTT	+	19907	TGG	0.479201654
AGTGGTAAACCGCTTGTTGA	+	19958	AGG	2.015884534
TAATTTATACGTAGACCTTT	+	20017	CGG	0.054534094
TAATTTATACGTAGACCTTT	+	20017	CGG	0.094704342
GACCATTATTTGATGCTAAC	+	20142	GGG	0.141579589
GGATTACCACTATCTTATAC	+	20177	TGG	1.486641945
AAGAAATCGTTAGCACTAAT	+	20219	GGG	0.068656165
GTTAGCACTAATGGGTGATT	+	20227	GGG	0.534583191
GATTGGGATTACGCACGTTA	+	20243	CGG	0.061828852
GATTGGGATTACGCACGTTA	+	20243	CGG	0.479884278
GCACGTTACGGTATCTTACA	+	20255	AGG	1.312773912
TGCTTGTAACGTCGTTAACG	-	20288	TGG	1.825908082
TGCTTGTAACGTCGTTAACG	-	20288	TGG	0.218634536
GTTCAAATAATGATACTGGT	-	20325	TGG	0.979281958
TCACGTTCAAATAATGATAC	-	20329	TGG	0.024341511
TTAAGCGTTGCGAACGCTTC	-	20401	TGG	1.464110256
AACGCTTAAACCAACTGAAT	+	20431	AGG	0.031119878
AACGCTTAAACCAACTGAAT	+	20431	AGG	2.146733023
TTTACCTTAATATCTTCTGC	-	20457	AGG	1.780433373
TTTACCTTAATATCTTCTGC	-	20457	AGG	1.911907791
GACTCTTATTACAGTCTTGT	+	20536	CGG	0.545117796
GACTCTTATTACAGTCTTGT	+	20536	CGG	1.561608096
CGCTCTTATCAGACGTAGTA	-	20564	CGG	1.739306793
TTTACTCAAGAAAAATGGAG	+	20639	TGG	0.009868361

TTTACTCAAGAAAAATGGAG	+	20639	TGG	0.44886943
ACGGAATACTAGAAGATGTT	+	20704	AGG	1.206195617
ACGGAATACTAGAAGATGTT	+	20704	AGG	1.810374246
ACATACTTTTTGATTGAGTA	-	20756	AGG	2.241323447
ATTTAAAGTCAAGAAGTATG	+	20839	GGG	1.889891751
AATACTCCACTAATGTAATC	-	20876	AGG	1.731474354
AATACTCCACTAATGTAATC	-	20876	AGG	0.025939691
TTCATCCGTTTAAATCAATA	+	20938	AGG	1.07606663
TTCATCCGTTTAAATCAATA	+	20938	AGG	1.117877147
TTCCCTCACACTATTTCTAT	+	20996	TGG	1.864961029
TTCCCTCACACTATTTCTAT	+	20996	TGG	0.946944439
ATTGGAAGTATCAAAAAAGT	+	21014	AGG	2.381356247
ACAAAGCGTTCTTGTATAAT	-	21028	TGG	0.067541081
TAAAACAATTAAAGGATTTA	+	21073	TGG	0.422446391
GTAAGTCGTAAGGTACATAT	-	21141	AGG	1.684163895
TTAGCTATTGGTAAGTCGTA	-	21151	AGG	1.563635762
AATAAATTGTTTTTAGCTAT	-	21163	TGG	2.373481699
AACAATTTATTTGAGTATGA	+	21191	GGG	0.180847139
TGTAGGCGATTCTGTAGATC	+	21229	AGG	0.027138584
TAAACTACTACGACTTAAGC	+	21268	AGG	0.088430764
CGTACTTAACTTTTGCCATA	-	21277	TGG	2.424897871
CGTACTTAACTTTTGCCATA	-	21277	TGG	0.094603578
TAAGTACGGTGCTGATAGCA	+	21308	TGG	0.38909536
CGATAAGAAAATAGAAGAGT	+	21350	GGG	0.230677964
TCTAAAAAACCTAAGTCAAC	-	21416	AGG	1.897795176
TCTAAAAAACCTAAGTCAAC	-	21416	AGG	1.86259949
ACTTTAAATATTTCGATGGT	+	21466	GGG	2.093435433
TTATCCAGTGTTATAAGTGT	+	21489	CGG	1.046461732
TATGCAATATACGTTGAATA	+	21519	CGG	1.410470682
TATGCAATATACGTTGAATA	+	21519	CGG	0.771987751
GGTATATATGCTACTGGTCC	+	21546	TGG	1.620843509
GGTATATATGCTACTGGTCC	+	21546	TGG	0.547327474
TGGAGTTTTAAAGGTGATGA	+	21594	CGG	0.145026453
GGCGAATGGTACACAACATA	+	21615	TGG	1.684900818
GGCGAATGGTACACAACATA	+	21615	TGG	0.667947035
GTCAAGCGCCACAGCCATTT	+	21637	TGG	1.853761467
TGCGTCCTGCGTCAATTGCA	-	21646	GGG	1.581470651
TTGCGTCCTGCGTCAATTGC	-	21647	AGG	0.956231325
TGGAACCCTGCAATTGACGC	+	21657	AGG	1.559374483
TCGAGCAGTATTTTTCATAG	+	21691	AGG	1.471853829
CATAGAGGTGGTTAAATATG	+	21706	TGG	0.070889977
TATATTTGATTTGTAAGTTC	-	21725	AGG	0.827875205
TATATTTGATTTGTAAGTTC	-	21725	AGG	0.022267506
TCAACTAGTTTGTTAATGTT	-	21767	AGG	0.056075508
TAACAAACTAGTTGATGATA	+	21791	GGG	0.009646992

ATTCACCCACAACAATATAT	-	21829	GGG	1.457024423
GATTCACCCACAACAATATA	-	21830	TGG	0.874504107
TGTTTACCCATATATTGTTG	+	21839	TGG	0.153590274
GTTTACCCATATATTGTTGT	+	21840	GGG	0.391302994
GCAACAATGAGAGAAACAGT	+	21894	CGG	1.511485823
GCAACAATGAGAGAAACAGT	+	21894	CGG	1.481945807
ACAGTTCGCTACACAATACG	+	21938	AGG	1.483316023
ACAGTTCGCTACACAATACG	+	21938	AGG	0.359913208
TCGTAATTATCTATTTCTAT	-	21986	AGG	0.123495484
ATACTGCTTGACTATCGATA	-	22021	CGG	0.128172589
CAGTATTCCCTGATATAGAC	+	22054	AGG	0.241794974
ATAGACAGGTTTACTAAGCA	+	22068	TGG	0.541758069
ATAGACAGGTTTACTAAGCA	+	22068	TGG	1.824424912
TTACTAAGCATGGCACGATA	+	22078	CGG	0.949746402
AAACGAAGGAGTGTATTAAA	+	22130	TGG	2.137991895
AAACGAAGGAGTGTATTAAA	+	22130	TGG	0.267308513
GGATCTAAGTCAGTTTCAGC	-	22166	TGG	1.943819771
GGATCTAAGTCAGTTTCAGC	-	22166	TGG	0.453944587
AATGATTCTGACATTGCATT	-	22286	GGG	1.981231511
AAATGATTCTGACATTGCAT	-	22287	TGG	0.489416333
AAATGATTCTGACATTGCAT	-	22287	TGG	3.268401027
GAATCATTTAAATTAACAAT	+	22317	TGG	0.017192586
GCTTCAATTCCTTTATCTCC	-	22331	AGG	0.973931945
GTGAAACACGCTGTACAAAC	+	22371	AGG	1.930772617
GTGAAACACGCTGTACAAAC	+	22371	AGG	1.58799544
GGTAAACATCACGGAATGTT	+	22440	TGG	0.056493653
GGTAAACATCACGGAATGTT	+	22440	TGG	1.307072192
AACTATCATTAAAAGTTAAA	+	22519	TGG	2.232178647
AACTATCATTAAAAGTTAAA	+	22519	TGG	0.072260567
GCAGCTTCAAACCACTCTTT	-	22556	CGG	1.340610378
AAGATAACTTGCCGAAAGAG	+	22561	TGG	2.044107952
TTAATTTTTAATGTTGTAAT	-	22772	TGG	1.945476802
TTAATTTTTAATGTTGTAAT	-	22772	TGG	1.954966933
ACAACATTAAAAATTAATGA	+	22794	CGG	0.16094399
TTAAATATAACATTGAATCC	-	22901	TGG	0.611341354
GGATTCAATGTTATATTTAA	+	22920	CGG	1.900082343
TTTTCTAATTGTTCTCGAGT	-	22997	TGG	0.416131094
TTTTCTAATTGTTCTCGAGT	-	22997	TGG	0.343261246
TGATTTCATCACTGAAAACG	+	23045	AGG	1.998282601
TCCAAAGCCCCTTGTAATAA	-	23060	CGG	1.245105153
GATACTTTGCCGTTATTACA	+	23067	AGG	1.853007196
GCCGTTATTACAAGGGGCTT	+	23075	TGG	1.419549573
AGAGGGAGAGTCGCTCGTAC	+	23125	TGG	0.141831535
ATTGAACAAAGCACCGAATA	+	23153	TGG	1.831990655
ACCGAATATGGCCAAAAGCG	+	23165	AGG	1.687258972

GACAAAGAAATGACGAAAGC	+	23187	AGG	1.603514127
GAGAATTACAAGGAAATCAT	+	23226	GGG	0.472102371
CAACTGACAGCTAGATATTT	+	23282	AGG	2.132432378
TAGCACTAACACCTGCTGAA	+	23328	TGG	1.834683547
TTAATAATTGTCTTTGATCT	-	23367	AGG	2.272670628
TTAATAATTGTCTTTGATCT	-	23367	AGG	0.53276134
ATTGAACAAGCGCAAGCTAA	+	23405	CGG	0.050820619
ATTGAACAAGCGCAAGCTAA	+	23405	CGG	0.173324297
CGTTACGAAATAAGAGAACC	+	23483	TGG	1.951640689
TGTACACGAGCATAGCTACC	-	23485	AGG	1.761499563
GCCTTTGGATACTCATTTTA	+	23608	TGG	0.525868275
GCCTTTGGATACTCATTTTA	+	23608	TGG	0.350185824
GAGCTTTCCTTACGTTGCTT	-	23643	TGG	0.75225103
GAGATTTCCAAAGCAACGTA	+	23652	AGG	0.021193279
ACATCTGTTTCAATTTCGTT	-	23689	TGG	0.828773118
TTTACAACGCGCTAAATCAA	+	23758	TGG	0.023556043
CTAAATCAATGGCTCAACGA	+	23769	TGG	1.398149328
CTAAATCAATGGCTCAACGA	+	23769	TGG	0.966253478
GAGAAAACATGTTGTTAAGT	+	23959	TGG	2.344811514
GAGAAAACATGTTGTTAAGT	+	23959	TGG	0.035159219
TGCAAACCCCGCTAAAATGG	+	23989	CGG	0.03214266
AAGATTTAATAGATCTTAGC	+	24027	AGG	1.294895758
AAGATTTAATAGATCTTAGC	+	24027	AGG	0.014337826
ATTTCCTAATTTCCATCTGC	-	24053	TGG	1.38992436
ATTTCCTAATTTCCATCTGC	-	24053	TGG	0.117372332
TAAATGGAACAAGTGATATT	+	24174	TGG	1.255716845
AACAACTCATTGAAAGATTA	+	24206	CGG	1.292352447
ATCTTCGCGCAACAGGTCAA	+	24275	AGG	0.020776937
GGTACTAATCCGGCAATCAC	-	24313	TGG	1.522335598
GGTACTAATCCGGCAATCAC	-	24313	TGG	0.165788458
GCATTGATACCAGTGATTGC	+	24320	CGG	0.974548147
TTAAGTACTGCCATTATTGC	-	24334	AGG	0.091826505
CGGATTAGTACCTGCAATAA	+	24340	TGG	0.272366752
CTTAATGCGGTTGGTGTATT	+	24368	AGG	0.043897938
GCATTCTCTGTCGCAGGTCT	+	24416	TGG	0.93938737
AATGGTTGAAGATGGAACAT	+	24478	TGG	1.822263271
AATGGTTGAAGATGGAACAT	+	24478	TGG	0.84952487
GCGATCAGTTAAAAACTACA	+	24537	TGG	0.246799758
GCGATCAGTTAAAAACTACA	+	24537	TGG	1.71360773
ATCTTTAATGCGATGTCAGC	+	24590	AGG	1.812312269
GCGATGTCAGCAGGTATCAG	+	24599	AGG	1.702499167
ATAGATACTTCAGATAAGAA	-	24634	TGG	2.235136681
ATAGATACTTCAGATAAGAA	-	24634	TGG	0.859547023
TCTTATCTGAAGTATCTATG	+	24655	TGG	1.685418168
TCTTATCTGAAGTATCTATG	+	24655	TGG	2.212285049

AGCAAACGCACGCAAGTTTG	+	24682	AGG	0.004286644
TTGAACGCTGCAGGAAGATT	+	24785	TGG	0.062741627
TGAGACACAAATTTGAACAA	-	24826	CGG	1.724526222
GACCAATCTTAGGTAAGTTA	-	24938	TGG	1.883221544
ACCACTAACTTACCTAAGAT	+	24953	TGG	0.07349579
CCTAAGATTGGTCAGATATT	+	24965	TGG	0.116728608
ATATTTGGCAATGTGTTCGC	+	24980	TGG	1.751685696
ATATTTGGCAATGTGTTCGC	+	24980	TGG	2.184121956
GGCAATGTGTTCGCTGGTAT	+	24986	TGG	1.305340108
ACAGTTCTAACATTTTTGAC	+	25035	TGG	1.685527987
ACAGTTCTAACATTTTTGAC	+	25035	TGG	0.359341009
TAACTTCTCAATTTAGAGCA	+	25068	TGG	0.276257706
AGAGCATGGTCAGAACAAGT	+	25082	AGG	0.126401035
AGAGCATGGTCAGAACAAGT	+	25082	AGG	1.835665445
CCGATTAACTGCATAATAGT	-	25138	AGG	1.663055906
CCGATTAACTGCATAATAGT	-	25138	AGG	0.564188273
CCTACTATTATGCAGTTAAT	+	25154	CGG	1.935167438
TAATATCGTAAAAGCGTTAG	+	25177	TGG	1.52719929
GTAAAAGCGTTAGTGGCATT	+	25184	TGG	1.80060087
GTAAAAGCGTTAGTGGCATT	+	25184	TGG	2.054099257
TGGGTGTGCTTCGAATAGTT	-	25256	TGG	1.570156867
CCGATAATTTGAGCGACTGC	-	25276	TGG	1.185443865
ATCGGTGTTATCGGTATTTT	+	25310	AGG	0.105284627
ACACTGCTAACAGCTGCAAT	-	25342	CGG	0.534420134
CTGGATTTAACTAGAATAAC	+	25430	TGG	0.879355515
TGGATTTAACTAGAATAACT	+	25431	GGG	1.897425869
ACTGCAACTACTGCTAATAT	-	25492	TGG	1.568054302
ACTGCAACTACTGCTAATAT	-	25492	TGG	1.318060533
GCAGTCATTGGTGTATTCAT	+	25526	TGG	1.004781548
GAAAAACAATAACAGAAGCT	+	25587	TGG	1.780901839
ACAATAACAGAAGCTTGGAA	+	25592	CGG	0.01111701
ACAATAACAGAAGCTTGGAA	+	25592	CGG	0.104569378
CGATTCAAGGTGTAGTAGAT	+	25638	TGG	1.295255222
TGTCCTAATACTTGTAATAT	-	25693	AGG	0.50906643
TGAATATCATACAAGGTTTG	+	25785	TGG	0.609582731
ATATCACTGTTCCTATGGCT	-	25812	TGG	1.866198622
ATATCACTGTTCCTATGGCT	-	25812	TGG	0.583643041
ACAATTGCGTTCCAAGCCAT	-	25817	AGG	0.189143578
GCTTTAATTCAGTTGCTTAC	+	25886	TGG	2.057460345
TTGCTTACTGGCGACTTCTC	+	25898	AGG	2.137478999
CCAAATCGTATCAAGTACAT	-	25934	TGG	1.270016747
CCAAATCGTATCAAGTACAT	-	25934	TGG	0.366398131
GGCAATACATGCAATCAGTT	+	25971	TGG	0.318085457
TCAATTATCGGCTTTTTAAC	+	25997	TGG	1.861014638
AATCGAACGCTTTCAATGTT	+	26027	TGG	0.665353066

TTTCAATGTTTGGTACAAGT	+	26037	TGG	0.931183017
TTTCAATGTTTGGTACAAGT	+	26037	TGG	2.045012825
GTACAAGTTGGTCACAGATA	+	26049	TGG	0.087969386
GTACAAGTTGGTCACAGATA	+	26049	TGG	0.080107868
TTTGGAGCACTGTTACAAGT	+	26100	TGG	1.568540672
CTGAATGGGTTTCTAACATT	+	26193	TGG	1.670395431
AAAAGAGTTGTCTCAAATGT	+	26258	AGG	0.036130283
GTTGTCTCAAATGTAGGTGA	+	26264	CGG	0.061901535
GACGGTATGAGTGATGCACT	+	26282	TGG	0.355174226
GACGGTATGAGTGATGCACT	+	26282	TGG	0.795700012
TTCAGTGATTTCTTAAATGC	+	26321	CGG	1.382172837
TTCAGTGATTTCTTAAATGC	+	26321	CGG	0.081914813
TTTGCCGATTAATTCCGCTC	-	26324	CGG	0.652683742
TTTGCCGATTAATTCCGCTC	-	26324	CGG	1.994762214
AATGCCGGAGCGGAATTAAT	+	26336	CGG	1.919942419
ATTAATCGGCAAAGTAGCTG	+	26350	AGG	0.017022922
GACTACTTTGTGCGCAGCAT	-	26363	TGG	2.014216982
CACAAAGTAGTCAGCGCGGT	+	26390	AGG	0.859874979
GCGATGCGATTTCATCAGCT	+	26412	TGG	0.019454768
AAAGTAATTGCTACAGACTT	+	26510	TGG	1.071780856
AGAGGATAGCTCTTTATTAA	-	26522	AGG	1.369615669
CTGTCTATAGAAGTACTTAC	-	26569	AGG	1.730896489
CTAATCGTTACATTCACAAT	-	26638	AGG	1.852432259
TCCAAGTGATTATAAGTGAA	-	26814	AGG	0.014722527
TCCTTTCACTTATAATCACT	+	26829	TGG	2.101357122
TCCTTTCACTTATAATCACT	+	26829	TGG	0.334960354
GTAGTTGAATATAACGTTAC	+	26854	AGG	0.038440746
TCTGATATAGAGGGTATTGA	+	26899	TGG	0.021184081
TCTGATATAGAGGGTATTGA	+	26899	TGG	0.046360298
AAAAAGTAGAGCTTAAGATA	+	26954	AGG	0.102967919
TCATACTTAATTGAATTGTC	-	27063	TGG	0.010024728
TCATACTTAATTGAATTGTC	-	27063	TGG	0.022447809
TCAAATGCTTGTTTGTCTTT	-	27102	TGG	2.132242575
TTTGAGCTTGATTATGTTGA	+	27136	TGG	2.174113368
GATGGACGACAACTTTTTGT	+	27154	AGG	0.604594329
GATGGACGACAACTTTTTGT	+	27154	AGG	0.07705614
TTTGACACAACACAAACATC	+	27196	AGG	1.349784357
TTGACACAACACAAACATCA	+	27197	GGG	0.568379055
TAACGACCCTGAAAAATGGT	+	27297	CGG	0.199735618
TCGTTTGTAGGCAATCTATC	-	27306	AGG	0.080598325
ACATTTTACAACACTAACTC	+	27367	AGG	1.230762838
AGATGTTAAAGCTAATGATA	+	27465	AGG	0.150332298
GTTAAAGCTAATGATAAGGA	+	27469	TGG	0.02544085
AGGAAATATCTCAGTTATTA	+	27513	AGG	2.069776996
AGGAAATATCTCAGTTATTA	+	27513	AGG	1.656087128

GTCGAAGATTATTTTATCTC	-	27535	CGG	0.196273796
GACGGTAAACATACCTATAG	+	27571	AGG	1.650153424
TAATAAAACTTTAGAACAAC	+	27615	CGG	2.262240333
TAATAAAACTTTAGAACAAC	+	27615	CGG	0.047450654
TGTAGACTTTTTAATAAAAT	-	27718	TGG	2.012684183
CGCTATTAATGTTAGTACAA	+	27769	AGG	1.496480079
CGCTATTAATGTTAGTACAA	+	27769	AGG	0.178983866
GCTAAATGAAGATAGTTCTT	+	27802	TGG	3.286359275
GCTAAATGAAGATAGTTCTT	+	27802	TGG	1.117764854
TGGACGATCACTCATGTTGA	+	27884	AGG	1.666035589
ATACTTGATAAGTCTACTAT	+	27938	TGG	2.673085126
ATACTTGATAAGTCTACTAT	+	27938	TGG	0.053668326
GGTAAATCCTAGAATTGTTA	-	27993	AGG	2.005826287
TAAAACTTTCGTTATACTCT	-	28014	TGG	1.782130165
TAAAACTTTCGTTATACTCT	-	28014	TGG	1.199650088
GAGTATAACGAAAGTTTTAC	+	28034	AGG	0.594856163
TTCTTCAATACTGTCTTTAA	+	28064	AGG	1.412416158
AATACTGTCTTTAAAGGAAC	+	28070	GGG	2.196892266
AAATTCGAGGGATTAGGCAA	+	28130	AGG	1.331261983
ACCAGCTTTAATGTAATAAT	-	28247	TGG	1.754171583
ATCACCATAACCTTTAATAA	-	28319	AGG	1.733381684
TTACCTATCAATTGTGCTAA	-	28396	TGG	0.241239123
CATCCATTAGCACAATTGAT	+	28409	AGG	0.17022922
ATACGTCCATCAACAAGCGG	-	28429	TGG	1.542485179
TTAATACGTCCATCAACAAG	-	28432	CGG	1.843888503
TTAATACGTCCATCAACAAG	-	28432	CGG	1.814740761
ACGTAACGCTACAAAGTCTA	-	28520	AGG	0.860998195
CTAACAACATCACCTATTTT	-	28564	AGG	1.085371269
TAGTATTAGGAGACTTTACA	+	28698	AGG	0.594311784
ATGCTTTTAGTTCTTTAGAT	-	28776	GGG	0.036551382
ATCAAATCAATTGGAACGAT	+	28973	TGG	0.334917525
ACGACTAATCTTGCAAGAGG	+	29069	TGG	2.479598615
CAGTGCCTTGTAATATGATT	-	29157	AGG	2.309746446
CAGTGCCTTGTAATATGATT	-	29157	AGG	0.138615222
GGAGACCTAATCATATTACA	+	29168	AGG	0.472102371
TGATTGGTTACACGGTTATT	+	29200	GGG	1.224505987
TCCGTTTTATCAGTGCCTAT	-	29215	CGG	1.537772533
TCCGTTTTATCAGTGCCTAT	-	29215	CGG	0.374130154
ACCGATAGGCACTGATAAAA	+	29230	CGG	0.359640683
AACTTCAATTGCAGAACAAA	-	29258	AGG	1.114959464
AACTTCAATTGCAGAACAAA	-	29258	AGG	0.160501836
GTATTGTTGTACCACTCATA	-	29337	GGG	1.514067321
CGTATTGTTGTACCACTCAT	-	29338	AGG	0.227898711
CGTATTGTTGTACCACTCAT	-	29338	AGG	0.384517768
TGTTTTTGTCCGTGTCTTTA	-	29361	CGG	1.409201892

TGTTTTTGTCCGTGTCTTTA	-	29361	CGG	1.679594972
AACAATACGCCGTAAAGACA	+	29368	CGG	1.451812064
AACAATACGCCGTAAAGACA	+	29368	CGG	0.143131508
GTGTGATATGCGTCAAACAC	-	29449	TGG	0.810306528
TTCCTAAAAGCTGGATTGTA	-	29485	TGG	1.024212475
AGCTTTTAGGAAAGCGAGCA	+	29512	TGG	0.164902319
AGCTTTTAGGAAAGCGAGCA	+	29512	TGG	0.138128853
CGACTAAAGGAGGCAACCAA	-	29611	TGG	0.728858988
CGACTAAAGGAGGCAACCAA	+	29611	TGG	0.837796819
CGACTAAAGGAGGCAACCAA	+	29611	TGG	1.759715146
CGACTAAAGGAGGCAACCAA	-	29611	TGG	0.797645489
AACTATCGCTTGTTAGATGA	+	29699	AGG	2.57947336
CGTATATTTCTTCTTTTTGA	-	29736	TGG	1.826404246
CGTATATTTCTTCTTTTTGA	-	29736	TGG	0.259396907
CATTGATACCGTCGCCGTTA	-	29850	TGG	1.94123913
CGTATTGATAATACAGGTTA	+	29903	TGG	0.030630911
ACTAGATGCTTTCACTAAAA	+	29968	AGG	0.119322577
TGCATTACTGCATTTGTATA	-	30073	TGG	0.03483031
TGCATTACTGCATTTGTATA	-	30073	TGG	0.228382059
ATGCAGTAATGCAATCATTT	+	30099	TGG	1.287905643
TGCAGTAATGCAATCATTTT	+	30100	GGG	1.256345686
TATATGACGCAAGCTCGTCC	+	30146	AGG	2.083125602
GATAACATGTAATGATTACC	-	30148	TGG	0.845570649
TCTATCAATAAATTGTCCGT	-	30182	TGG	1.962237833
TCTATCAATAAATTGTCCGT	+	30182	TGG	0.014301187
TCTATCAATAAATTGTCCGT	+	30182	TGG	1.781192094
AGATTGCTTGTTAAAAACGG	+	30218	CGG	0.258470489
ATGGATTTATTCAGCTGTAT	+	30283	TGG	0.580649999
TTATTTCTCCAGTTCTATAT	-	30321	TGG	1.57085193
TTATTTCTCCAGTTCTATAT	-	30321	TGG	0.181172527
AGAACTGGAGAAATAACTTA	+	30344	TGG	1.965308114
AGAACTGGAGAAATAACTTA	+	30344	TGG	0.023479892
TATCTGTCGTTAAATATATT	-	30373	CGG	1.200143023
TACGTCAGCGATTTATAATC	+	30412	CGG	1.903289561
TACGTCAGCGATTTATAATC	+	30412	CGG	0.155638144
TTCTTAAGTTGTCTTTCAGT	-	30454	GGG	1.787480504
ATTCTTAAGTTGTCTTTCAG	-	30455	TGG	0.400768221
GTATCAAATGGATATACCTA	+	30556	TGG	2.245185391
GTATCAAATGGATATACCTA	+	30556	TGG	1.899155926
GTATCAAATGGATATACCTA	-	30556	TGG	0.378483669
TCATAAGTGATACCTTGCAT	-	30583	AGG	1.738956957
TCAGATACACAACCTATGCA	+	30587	AGG	0.582463964
CAAGGTATCACTTATGATGC	+	30605	AGG	1.682837434
ACCTTGTAAGTAGTTAGGGT	-	30647	TGG	0.294253366
TTTAAACGACGTATCGATAT	+	30713	TGG	1.661938757

TTTAAACGACGTATCGATAT	+	30713	TGG	0.038909536
GACGCAAAGCGCTTTTAATA	+	30810	GGG	1.322924225
ATAGGGGTAACTATTGGACC	+	30827	TGG	1.298349782
GAGTGATGTCTGTTGTTACC	-	30829	AGG	0.314082878
AGAATTGGTTAACACCTCTT	-	30867	TGG	1.664484783
AGAATTGGTTAACACCTCTT	-	30867	TGG	1.04407255
AGATATGCTGGGTTCTGTAT	-	30949	TGG	0.050768949
TAATATCACTTAGATATGCT	-	30960	GGG	1.735899687
CCGAAAGCGTTTAGAGATGC	+	31061	AGG	1.488261059
CCGAAAGCGTTTAGAGATGC	+	31061	AGG	0.446315266
TGGTTCTTTGATGTACTGCC	+	31085	TGG	0.305439858
TGGTTCTTTGATGTACTGCC	+	31085	TGG	1.184309003
AGAGCACCATTATAGTGTCC	-	31087	AGG	0.924490576
GTACTGCCTGGACACTATAA	+	31097	TGG	0.038337337
ATTTCTACCTGTGCTGTTTC	-	31124	TGG	0.173471682
GTACTTACCAGAAACAGCAC	+	31133	AGG	0.081356303
ATTTTCAATAAGAAAAACAA	+	31190	CGG	1.227419001
TCCCAATAACCGGCGTTTTG	-	31213	CGG	0.179582474
AGGGATATGTTCCCAATAAC	-	31223	CGG	0.152395683
GTCCGCAAAACGCCGGTTAT	+	31227	TGG	1.634871368
GATAATTTTGTAATATTCTT	-	31243	AGG	1.757824483
TTATCAGATTTAAAAATCGT	+	31277	TGG	1.874825276
TTATCAGATTTAAAAATCGT	+	31277	TGG	0.051879381
GCAATACCTTTAAAGTCTTT	-	31333	AGG	2.245944886
GATTTTCCTAAAGACTTTAA	+	31343	AGG	0.052877062
AAAGACTTTAAAGGTATTGC	+	31352	AGG	1.430898188
AAAGACTTTAAAGGTATTGC	+	31352	AGG	0.456106228
AGAAGTAAAATCGAATACAC	+	31384	CGG	1.429795751
GAAGTAAAATCGAATACACC	+	31385	GGG	1.258952371
AATACTTGTGTTGTGTTACC	-	31387	CGG	0.033351031
CTAAAAATTGATGTGCAGAC	-	31425	GGG	1.735365307
ACTAAAAATTGATGTGCAGA	-	31426	CGG	1.785678519
ACTAAAAATTGATGTGCAGA	-	31426	CGG	1.319158786
GTACTGGTGGCGTTGGTAAA	+	31476	TGG	1.871194961
GAGTTTATTCGAGGGAAAGG	+	31498	TGG	1.209732848
CTGATGTTTGTGTCAATAAT	-	31578	TGG	1.163395128
TGTTCAGAACTTATAGATAA	-	31662	CGG	1.263262937
GATGATTATAACGTAGATAG	+	31729	AGG	2.028683348
CGATAGTAGACGCAATTAAT	+	31775	GGG	1.877255416
GAATGTTTTAAAAATTCATT	-	31800	CGG	1.91521383
ATTTTTAAAACATTCAGGCA	+	31824	AGG	0.011612536
ATTTTTAAAACATTCAGGCA	+	31824	AGG	0.019636588
TTCAGGCAAGGTGCATGCTC	+	31836	AGG	1.949014033
TTGAAAATGATTTAGTTAGT	+	31919	GGG	1.961848574
CAGCCATATTTTGCTTTAAT	-	32000	TGG	1.662810467

CAGCCATATTTTGCTTTAAT	-	32000	TGG	1.227419001
TTGTTGAATTACCTTTAACA	-	32234	AGG	1.31327466
TTGTTGAATTACCTTTAACA	-	32234	AGG	1.415502087
TCTAAACTTACAGATGATTA	+	32287	CGG	0.891795206
TAAGCGCAGTTAACACATCT	+	32351	AGG	1.418252589
TAAGCGCAGTTAACACATCT	+	32351	AGG	0.369640592
GTGCCTATATCCGTCTTTTC	-	32388	TGG	0.403244283
TCATCAACACCATCTTGTCC	-	32421	AGG	0.209597595
TCATCAACACCATCTTGTCC	-	32421	AGG	1.270674277
TTAGAGAAGCCTGGACAAGA	+	32428	TGG	1.4273006
ATAATACTGCTCGTGCAACA	+	32531	TGG	0.769211597
ACTCATCGTTTGAATCGTCT	-	32540	GGG	1.209771861
TACTCATCGTTTGAATCGTC	-	32541	TGG	1.837085952
TACACAAAATACAAAATCTA	+	32578	CGG	1.938087006
TACACAAAATACAAAATCTA	+	32578	CGG	0.139000963
AATACAAAATCTACGGCACA	+	32585	TGG	0.268429478
CATCATTCTTTTTATAAAAC	-	32594	GGG	1.189334818
CATAAGATGACAGAGGCGAA	+	32734	TGG	0.049521228
TCAACGCTACCTGGTAAATC	-	32823	CGG	2.213265962
ACAAGAGTGCCGGATTTACC	+	32830	AGG	0.439677757
ACAAGAGTGCCGGATTTACC	+	32830	AGG	1.914905024
TCATAACTTTCAACGCTACC	-	32832	TGG	1.42308999
AAGTTATGAGGGTTATTTAT	+	32862	CGG	0.25803166
TAAATCTTTTTAGAGTTATA	-	32910	AGG	1.704724048
TACACACGATCAATCACAAA	+	32947	CGG	1.592578161
TACACACGATCAATCACAAA	+	32947	CGG	1.617654266
ACCGTTGATTTATGTTCATT	-	32979	AGG	0.272366752
AAAATAGAATAGTTTGTGTA	-	33054	CGG	2.44515716
TTGGTAAGTGGAACTTATCC	+	33094	AGG	0.82739984
AATCCCTCAATAACGCCACC	-	33096	TGG	0.025589154
GTAAGTGGAACTTATCCAGG	+	33097	TGG	0.308497036
TTAGGTAAAACATCAGGTTC	+	33280	TGG	1.529591269
TTAGGTAAAACATCAGGTTC	+	33280	TGG	2.165964173
TTTAGTTATAGTAACTTTGT	-	33295	TGG	1.946437531
GTTACTATAACTAAAATTAT	+	33319	GGG	0.743271906
TTACTATAACTAAAATTATG	+	33320	GGG	1.608991519
AACTCTTCTTTAAATTTAAT	-	33428	AGG	1.607842441
AACTCTTCTTTAAATTTAAT	-	33428	AGG	0.732796262
TTAGTGAAAACAAACTTTCT	-	33455	AGG	0.891676868
TTAGTGAAAACAAACTTTCT	-	33455	AGG	0.126455992
CTTTGTTGGTTTGATGCATT	-	33521	CGG	1.476567009
TTAAATCTGACGCACTTTGT	-	33535	TGG	2.088495637
TGATGAGGAACTTCGCGGAA	+	33575	TGG	0.367871977
TGTTTTGTTAGTTTTCAGTT	-	33669	CGG	0.141047068
AACTAACAAAACAAATACTG	+	33695	AGG	0.807693556

CTAACAAAACAAATACTGAG	+	33697	GGG	0.021223383
GTTTTAATGTCTTTAAAAGT	-	33731	TGG	0.181577835
CATTAAAACTTTTTATGTGT	+	33761	GGG	0.287331958
AATTAAGTGGTACGTAGACA	+	33803	TGG	1.30624871
GGCAAAAGATGAAAAGTCAC	+	33878	AGG	1.642805507
GGCAAAAGATGAAAAGTCAC	+	33878	AGG	1.021566054
CCATTCATGTTCGTGCCGTT	-	33943	TGG	1.449380218
ACTCTCAATGAGATTAAATT	+	34024	AGG	2.445606692
CGTCTATCTGTCTTTCCCTC	-	34085	TGG	0.266808247
TGTGGATTCTCGGTTTGATA	+	34169	GGG	2.032369639
TCCTAAAATCCCTTTAAGCA	-	34242	TGG	2.183850008
TCCTAAAATCCCTTTAAGCA	-	34242	TGG	1.627126053
AGGTGATTACCATGCTTAAA	+	34249	GGG	0.019454768
ACAGTTAAGAGTCAGTGCTT	+	34322	CGG	2.172790407
ATTGAAATGAGGTGCATACA	+	34363	TGG	0.726311339
TTGAAATGAGGTGCATACAT	+	34364	GGG	1.236767396
AAAGCCTACAGCTAGTGAAG	+	34408	TGG	2.451300771
GAGTGGGCAAAGTCGAATAT	+	34433	TGG	1.209608734
ATTAATATAGATAATTATCG	+	34463	GGG	1.068353307
ATTATCGGGGCAGTCAATGT	+	34476	TGG	1.112627447
ATTATCGGGGCAGTCAATGT	+	34476	TGG	1.052605343
ATATTGGGGTTTTGTAACAT	+	34525	GGG	1.079227658
GGCTAATTACAGATATCCTA	+	34564	AGG	1.814851931
CGATTCTATCGTTATTCATC	+	34592	TGG	0.82358518
TCTGGATTTGTACCGGAACC	+	34610	TGG	0.155638144
TCCGAACCTATTCCGTTGCC	-	34636	AGG	0.813334818
AATAGTTGGACAGGTTCTCC	+	34751	GGG	1.359610359
GGGTGTCTTACTAAACTTCC	-	34753	CGG	0.365123231
AAGCCTGTAACACTTACATA	-	34774	AGG	2.178135874
GCCAATGACTCAACAATTAC	+	34880	TGG	0.508564077
CATTGATCATATAGTTGTAA	+	34987	TGG	1.102436855
ATTGATCATATAGTTGTAAT	+	34988	GGG	1.13753173
GATGAACGCTCAGATATTCA	+	35012	AGG	1.505091599
CTAGCCAATTAGGGTGACGC	-	35163	GGG	1.715910539
GTGGTGTTTGGTTATTGTCA	+	35274	GGG	0.604866424
TCATACTACGCCAAATATTA	-	35319	GGG	0.616994072
TTCATACTACGCCAAATATT	-	35320	AGG	0.917388216
TAAAGGTAGACCCTAATATT	+	35325	TGG	0.16075782
CTTGATTAAGCAAGGTATAC	+	35377	CGG	0.205406155
TGCTCATACTTTGCGTTATC	-	35380	CGG	0.016607729
ATGCTTGGTTTTTCGTCTGA	-	35542	TGG	1.405931236
CTTGTTTCAGTAACGATGCT	-	35557	TGG	0.140506658
TTTGTCTATCCAGTGCTTGC	-	35592	TGG	1.741366609
TTTGTCTATCCAGTGCTTGC	-	35592	TGG	0.756491172
ATTCACATTCCAGCAAGCAC	+	35599	TGG	1.511485823

CACTGGATAGACAAATGTCT	+	35616	AGG	2.258521706
ACTGGATAGACAAATGTCTA	+	35617	GGG	2.058962949
CTGGATAGACAAATGTCTAG	+	35618	GGG	0.017563332
AACACGAGCACAAACGAGCT	+	35680	CGG	1.692564818
AATGAATGTTAAGCGAATAT	+	35704	GGG	1.558326918
TGCTATCAAATGCTTAATTT	+	35741	AGG	1.229331017
CTTAATTTAGGCAAGTATCA	+	35753	AGG	2.443518863
GCGCTTAACAAAATACTTAA	+	35789	AGG	2.165400267
GCGCTTAACAAAATACTTAA	+	35789	AGG	0.038909536
AAAGGAACGCTCGACGGACA	+	35813	AGG	0.881949484
CGGACAAGGCAAAGCATTCG	+	35827	CGG	0.099286402
GCGCACGCTTTCTTAGAAAG	+	35891	TGG	0.035667075
GCATATAATTACTTCGGTAT	+	35948	TGG	0.8637917
GCATATAATTACTTCGGTAT	+	35948	TGG	1.473374431
CCGCCCATGATTGCTTTTGC	-	36016	TGG	0.839797486
ATCTCCAGCAAAAGCAATCA	+	36028	TGG	0.010751319
CCAGCAAAAGCAATCATGGG	+	36032	CGG	1.582321132
AGAAAGGATTACATCAATAA	+	36068	AGG	0.030803383
ACACATTGTACCGAATTAGA	+	36096	TGG	0.876437299
CGATTGTACTTGCTTGATGT	-	36132	TGG	2.137163487
CGATTGTACTTGCTTGATGT	-	36132	TGG	1.060748066
GCTAAGTTATATAAACAAAT	+	36170	CGG	1.656897743
TAAAAGGTATCTACTTCACA	+	36195	AGG	0.199622837
AAAAGGTATCTACTTCACAA	+	36196	GGG	0.719826417
ATAGGTATCAATGACAAACA	+	36353	AGG	0.13087753
ACAACATCGTCGATAATAAG	-	36439	GGG	1.948547097
TTACAACATCGTCGATAATA	-	36441	AGG	1.617256038
TTACAACATCGTCGATAATA	-	36441	AGG	0.153692667
GCGTGTTTGATAACCTTTTT	-	36487	AGG	1.797620565
TCTTTCAATATCGTTGATAG	+	36590	TGG	2.148671046
AAAAGAAATCGATGTTAAAT	+	36631	TGG	0.367871977
AGTAGATTTAAAGGTGCGAA	+	36764	AGG	1.929766849
GAAAGGTGATAAAGGCGAAC	+	36781	CGG	1.785636428
CCTTTTGCACCAGGTTGTCC	-	36784	CGG	0.940313788
CCTTTTGCACCAGGTTGTCC	-	36784	CGG	1.715403024
CCTGGTGCAAAAGGTGAAGC	+	36809	AGG	1.904850669
CCTGGTGCAAAAGGTGAAGC	+	36809	AGG	0.165365528
AAAGGAGAACAAGGCGCACC	+	36836	CGG	1.56439714
ACTACAGTACCGTTTTTACC	-	36838	GGG	2.024754153
ACTAAAATGTGGCAAATTGA	+	36893	TGG	1.329970834
TTGATTTTGTCCAATAACTC	-	36925	AGG	2.823535332
TTGATTTTGTCCAATAACTC	-	36925	AGG	1.095692535
CAACGACTCTAAAACGTATA	+	37030	CGG	2.07332242
CAACGACTCTAAAACGTATA	+	37030	CGG	1.262128075
CTTAATGTGTTCATAGATTC	-	37069	AGG	1.997460779

CTTAATGTGTTCATAGATTC	-	37069	AGG	1.283534325
GAAAGTGTATTGCAACAGAT	+	37145	TGG	1.858578838
TCGTCATGATTATGATTTTT	-	37213	TGG	0.573915657
AAAAAGCGCATCTCAACCGA	+	37312	CGG	0.522036275
AAAAAGCGCATCTCAACCGA	-	37312	CGG	0.058364304
CTCAACCGACGGTTAAAATT	+	37323	TGG	0.032043147
CCGACGGTTAAAATTTGGAC	+	37328	AGG	1.127034837
TAATTAAGTAAAGTGTATTA	-	37371	GGG	0.014461951
TTAATTAAGTAAAGTGTATT	-	37372	AGG	2.249905882
TTAATTAAGTAAAGTGTATT	-	37372	AGG	0.164757567
TAATACACTTTACTTAATTA	+	37390	AGG	0.274451192
AATACACTTTACTTAATTAA	+	37391	GGG	0.780203283
TAATTAAGGGGTGATTTTTA	+	37404	TGG	2.194559108
TAATTAAGGGGTGATTTTTA	+	37404	TGG	0.482766466
GGTTTTATTACAAAAGATGA	-	37500	AGG	0.240662686
CTATCCGGATATTTATTTTT	-	37527	AGG	1.355781167
GTTGATTCTTCTATGCTATC	-	37542	CGG	1.934327286
GTTGATTCTTCTATGCTATC	-	37542	CGG	1.461415794
TAGAAGAATCAACAGCAAAA	+	37568	TGG	0.016860799
GTCACCTGATAACTTTTATT	-	37593	AGG	1.516573993
GTCACCTGATAACTTTTATT	-	37593	AGG	0.77111626
TGAACCTAATAAAAGTTATC	+	37605	AGG	1.06231262
ACAATAGAAAATGTACGTAG	+	37630	CGG	1.795397163
ACAATAGAAAATGTACGTAG	+	37630	CGG	0.019454768
ATGTACGTAGCGGTATAATG	+	37640	AGG	2.505175513
AGGGTTTCGCAAACTAATTT	+	37660	AGG	1.598724172
AGGGTTTCGCAAACTAATTT	+	37660	AGG	0.916911675
TCAAGTGATTTAGGAATATC	+	37684	AGG	1.589454547
GTGACATACAACATCCCTGA	-	37734	AGG	0.436553204
TCAACTTTAGTAATCCTTCA	+	37736	GGG	1.563385158
AATTATTCAATGGTCAATGT	-	37782	CGG	1.80745807
AATTATTCAATGGTCAATGT	-	37782	CGG	1.696733697
GAAACACTTTCTTCATCTAC	-	37945	TGG	0.056319194
GAAACACTTTCTTCATCTAC	-	37945	TGG	1.042775566
CATTTCCCTTCTTGAGATGT	-	38017	TGG	1.314913439
ATAATCCAACATCTCAAGAA	+	38028	GGG	0.679219485
AACATCTCAAGAAGGGAAAT	+	38035	GGG	0.339946473
TTTGTGTCGTTCATATTCGT	-	38125	AGG	0.539545566
TGAACGACACAAATGATTTA	+	38151	GGG	1.939918297
CACAAATGATTTAGGGTAGG	+	38158	TGG	1.215038694
CACAAATGATTTAGGGTAGG	+	38158	TGG	1.300226996
AAATGGTTTGACAATTCATT	+	38215	AGG	1.600478916
GAAATCCATACCAACCATCT	-	38234	GGG	1.078572339
TGAAATCCATACCAACCATC	-	38235	TGG	1.502237484
CGCTAACATAAAGAACATAT	-	38272	TGG	0.275463812

CGCTAACATAAAGAACATAT	-	38272	TGG	0.077613202
GCGACAGGCGAAAGGCTGCA	+	38308	AGG	0.013311157
TCTTTGCTTTATTATCAAAC	-	38333	GGG	0.489542673
GTTTTCCCGTCAAAGTATGG	+	38437	TGG	0.742523646
TCAAAGTATGGTGGCGGAGC	+	38446	TGG	1.792220874
TCAAAGTATGGTGGCGGAGC	+	38446	TGG	0.088627277
TTAAATACTTTCACATCATT	+	38497	TGG	0.979812862
TCACATCATTTGGTCAAAAC	+	38507	TGG	0.014148922
TCATTTGGTCAAAACTGGAA	+	38512	CGG	2.054631021
TCATTTGGTCAAAACTGGAA	+	38512	CGG	0.04173932
GGTCAAAACTGGAACGGTAA	+	38518	AGG	0.653124355
AAAACTGGAACGGTAAAGGT	+	38522	TGG	0.020878288
ACAGTTTCAGGACCCCAACC	-	38547	AGG	1.150610566
ATGGCGTTGCGCAACCTGGT	+	38549	TGG	0.45276551
GGCGTTGCGCAACCTGGTTG	+	38551	GGG	1.988482079
TTTAACCTAATAAAATACAT	-	38598	TGG	0.055042758
TTGCCAACGCTTAAGTTGTT	-	38625	AGG	0.036641267
GCAAGCGACTACAAAAAAAG	+	38685	AGG	0.217435643
AAAAAAATTATGCTTGTAGC	+	38722	CGG	1.902457104
TATAACGATCCTGGAGCAGT	+	38752	AGG	0.334960354
GATCCTGGAGCAGTAGGAAA	+	38758	CGG	1.943531325
CTTAAATACTTAGCGATATT	-	38802	AGG	0.508936731
CTTAAATACTTAGCGATATT	-	38802	AGG	1.990871261
GCTAAGTATTTAAGACATGC	+	38827	AGG	1.173595736
GGACATGAAGTTGCATTATA	+	38848	CGG	0.914374097
ATGTATCAAGATACTGCATA	+	38893	CGG	1.347881352
AAAAAGATTATGGCTTATAT	+	38933	TGG	2.321083523
AAAAAGATTATGGCTTATAT	+	38933	TGG	1.709827499
AAAAGATTATGGCTTATATT	+	38934	GGG	2.848178038
CAGGAGAAAGCGCAAGTGGT	+	39005	GGG	0.336652073
ACATTTAGTAAATCATTACG	-	39108	AGG	1.121369141
ACATTTAGTAAATCATTACG	-	39108	AGG	1.171177035
TATTACTAATAAAAATGATA	+	39198	TGG	1.14499416
CTAATAAAAATGATATGGAT	+	39203	TGG	1.175659019
AGGCTTACCATGAATCGCAC	-	39247	CGG	1.890414783
AGTGTATAACCTGCTGGCAC	-	39327	TGG	0.84501362
TTATCGAGTGTATAACCTGC	-	39333	TGG	1.492282537
TACACAGTAGCTAATGTTAA	+	39406	AGG	0.029182152
TCAACTAATTCAAGAATTAC	+	39451	AGG	1.942019683
GACGGTGCATATTGTATTAA	+	39505	TGG	2.422118619
GACGGTGCATATTGTATTAA	+	39505	TGG	1.924253419
AGCGACAGGAGAGGTAGACA	+	39576	AGG	1.055226617
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Bin	**Average Fitness**
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9000	1.12041116
10000	0.938932328
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12000	1.059816567
13000	1.038195691
14000	0.816776126
15000	0.976599074
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19000	1.109850049
20000	1.072830592
21000	1.007050792
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27000	0.813587569
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Bin (kb)	Barcodes Sonication	Normalized Reads Figure 1
1	29310	86026.01627
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5	11450	58150.95717
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Spacer	Location	PAM	Reads Sonication	Barcodes Sonication
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ATAAAAAAACTGCTACTTGT	3239	TGG	20101	4663
TCTGATGAATATTCATCTCT	1424	CGG	19122	3176
AGCAATTCACACCCGCACAG	998	TGG	12651	3690
AGTATGCTTACTTTTTCTTG	3823	TGG	44061	4852
TGAAGCATAATACTGCTACT	3088	AGG	10205	2367
TAGAGATATAGAACTTCACT	5384	GGG	9521	3021
GCGCTTCAATAGTGATAGTA	4338	GGG	8628	1340
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TTCAAAAGTTTAGTATCTAT	698	AGG	27625	5785
GAGAACAAAACCATCCTACC	827	CGG	15152	3299
ACTTTCCATTACTTAAATCA	9043	TGG	14293	3738
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TTAGAATTGACACCTCAAGA	873	AGG	13663	1490
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ACCAACTGGCACGGATCAAT	7611	TGG	4605	96
AGTAAGACGCCAAAAGTAAC	2465	AGG	14789	1240
TGTCCTTTACCTGTTACTTT	2458	TGG	5366	966
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ACTTATTCCGTCGTTGCTAC	5238	TGG	7000	1291
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ACACCTCAATATATACTTGC	15249	TGG	2594	305
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AGCACTCCTAATCGTCATCT	5893	TGG	1969	702
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ACACAAATCCATCAATTGTT	2890	TGG	2691	53
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CCTATTACAGATTCATCGTC	11132	TGG	9938	1670
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ACTAAGACATCAATTTTAGT	2246	TGG	912	66
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AACGCCCTGCTACTAATCAC	2629	AGG	1550	260
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TTCATTTTAAAAGGTCATAT	3400	GGG	304	113
GAGTCTAAATTTAAATCGAG	19408	TGG	1819	286
AAAATATCTCTTCCTTCTTG	869	AGG	767	113
GTTTACCCATATATTGTTGT	21840	GGG	2751	671
GAAATCCTATGCAAGGCAGT	331	AGG	766	265
ATTTGCAAATCCTAGCATTA	4552	CGG	1924	492
ATTTGAATCATCACATTTAT	11324	TGG	791	154
GATTACTTACGTAATGCGAA	676	AGG	1837	298
TGCCAAGGAAATCCTATGCA	338	AGG	1270	7
TTACGTGCTCTCATTACAGT	18512	TGG	7613	2094
AGAAACATCAATCACACATT	2425	CGG	441	119
AAGAGGTATTTAAATATGTT	16156	TGG	2148	378
TTTAGTTGTTCAGATGTAGT	21085	AGG	2423	649
AAGATTGAACAAATAGATAA	14978	AGG	555	6
TAACCGTATCGATTAAGATA	40130	CGG	545	137
TTTATATTCACAACTTGCCA	353	AGG	1327	133
GGAAAAAAGGAGCAAACAAA	37855	TGG	977	52
CATATCGTACCAGATTGGCA	10188	AGG	3996	264
AACAACAACGAAATATATGC	11088	GGG	2211	68
AATCTCCGTTTAGTTAATAC	5967	AGG	2037	526
AAAGCAATTATGAAAAGAGT	194	AGG	260	49
CGTCTATCTGTCTTTCCCTC	34085	TGG	2944	505
GGTTTGTTAGTTATATAAAT	3630	TGG	326	85
ATTTAAGGTGGTTATTCTTA	1698	TGG	685	68
AGCATTGTTGATAACAGAGT	8290	AGG	894	180
AAACAATAAAACTTTTATGG	11602	AGG	894	1
AGTGTATAACCTGCTGGCAC	39327	TGG	14730	1785
TACACACGATCAATCACAAA	32947	CGG	1105	25

CCGATTAACTGCATAATAGT	25138	AGG	1258	190
GTAAGATGACAGCTATGTTG	17376	AGG	3091	126
TTTAACCTAATAAAATACAT	38598	TGG	494	64
TACACACATAAGTTTATTGG	234	CGG	811	47
ATCATCAACACTATTTCTAA	16631	TGG	1060	128
AGTTCACTATGAAAACTACG	10991	CGG	1028	137
CGATAGAATCGGAAACCCTT	34564	AGG	811	78
GTTTTAAACCCAAAGAATGA	6351	CGG	1116	232
GACCATTATTTGATGCTAAC	20142	GGG	4151	922
CAAATACAAGCGTTAATACG	35255	TGG	654	107
AAAGCATAAAAAATGGTATT	3048	AGG	308	73
AGGAATCATGAAAGACAAGA	12358	TGG	603	194
AATACAAAATCTACGGCACA	32585	TGG	3564	475
TTTACTTGTACTAGATGATA	8229	TGG	844	209
ACGTCATCAAATTCTTTTAT	16181	AGG	313	97
ACCAACCGAAATGCCATTTT	7188	CGG	247	42
TTTACGCGCGTTATCTGTCA	10047	TGG	1528	188
TTTATCTTTTCGCTGAATAG	7668	TGG	618	227
TAAATACAACAGGCTCAATA	17861	AGG	1013	183
TTTTCTAATTGTTCTCGAGT	22997	TGG	3987	892
AATTGGCCACTGCTTTCAAA	5117	TGG	1192	308
TATTACCGCAAAGATAATTT	2947	AGG	218	10
TCTCCCCAATCATTAAACGT	4186	TGG	637	48
CCTATTGCAAATGCTAATTG	9918	TGG	578	60
TTGAGTATTGCGAATCAAGT	12100	AGG	1036	258
ATTTAAAGTCAAGAAGTATG	20839	GGG	913	339
GTTCTGAAACTTGTCCCTTC	17520	AGG	3290	528
GTGAAACACGCTGTACAAAC	22371	AGG	4179	558
ACGCAATTTTTCGTACCTTC	14720	CGG	5133	828
TGCTAAAGTCATATATACTA	39930	CGG	569	142
GAACCACAATTTTCTCTTCT	6585	AGG	396	11
CGATTGTACTTGCTTGATGT	36132	TGG	6269	686
ATTAAAGTACCTTGTTCTGC	19588	TGG	8417	1830
ATTCTCATTCAAATCAAAGT	15738	CGG	2249	182
TTTGCAGTATACGGAAAAAT	3917	TGG	312	80
TTTAAACGACGTATCGATAT	30713	TGG	1349	404
TTTTTTGATGTCTATTACCC	6033	AGG	1119	185
TATCGCTATTGCGTTAGATT	6829	GGG	775	96
ACAAGTACGGTTGTTAATAA	1979	CGG	682	74
CTGAATTCAATAAATACAAC	17851	AGG	2271	339
ATTTAATGATTCTGCAGCTG	308	AGG	787	35
AGGGTTTCGCAAACTAATTT	37660	AGG	259	15
ATATATAAAGCAACATGGTT	10250	TGG	554	70
GATACAAAGACTTACTTTAT	10714	AGG	1435	113
TATTTAATTATGAAAATCAC	4626	AGG	1391	292

CCATTCGGGTGTTTTTTAGT	7782	AGG	851	133
GTTCCAAACTGCAAGCATAG	10866	AGG	209	52
GTTTACCATCATACAAGGAT	40369	GGG	1105	142
TATATTTGATTTGTAAGTTC	21725	AGG	3691	678
ATCAGAATTTTAAATCAAGT	18403	GGG	220	58
AACTAAATCAAAATATGAAC	8351	TGG	1639	197
ACTATTTCTAATGGCAAAGT	16622	TGG	2796	790
GTGACATGCTTGGGTGAACA	39861	AGG	468	145
GATGGACGACAACTTTTTGT	27154	AGG	1776	323
AATTAGAAATGTAAATGTAG	9415	AGG	1003	163
TCAATACCTTTACCTAAAAT	6805	AGG	677	145
GAAACGTTCGAGGCACCTAT	8877	GGG	545	63
CCAAATCGTATCAAGTACAT	25934	TGG	2341	603
TACGAGTGAACTTAAATATC	17454	AGG	1932	559
TTCGTCATTGACATTAACGA	3980	AGG	1172	300
CGCTAACATAAAGAACATAT	38272	TGG	634	250
TCCTAAAATCCCTTTAAGCA	34242	TGG	2517	474
GAAAAACAATAACAGAAGCT	25587	TGG	1281	504
TCATTCTGATTGGTTATTTT	17669	GGG	788	162
GTTGATTTCGTGCCACTGTG	994	CGG	276	126
TAAAAGAATAGCATCATTTG	6438	GGG	505	58
CCTATCATCTCTTTGTTGTT	16969	AGG	621	42
TTATCATGATGTTACAAAAG	637	AGG	445	118
AACTTTGAAGCTTCTAGAGC	6577	AGG	891	88
AATACCATTTATTACCGGGT	825	AGG	788	235
ATTAAACAATAAAACTTTTA	11599	TGG	138	47
AAGATATAGAATGCTTTGGT	10630	AGG	987	210
ATTTCTGCTTGTGCATATTC	19753	AGG	5731	549
GTATGCTCAGATGTTAAAAG	14021	AGG	300	49
TCTTTTCGATTCGATCTAAA	17217	TGG	809	200
TAAGAATGACATTGAAATAG	14833	AGG	305	48
CTGGCACATTATGAAGCAGT	5661	CGG	510	161
AACATTCACGTGATCCGTAC	9735	TGG	2762	448
TAAATTTAACGAAACGTTCG	8867	AGG	536	78
TATGAAAAAGATGATGATAA	16832	TGG	1392	312
TCCGATAAAATAACATTGCC	19546	TGG	4144	563
CTGTTCTATGAAAGTTGCAA	5489	GGG	802	18
CTTAATATTCGACGATAGCG	8572	GGG	182	88
TGGAAATTCAATGAAGATGA	4965	AGG	614	154
AAAAACCAACGTTTAATGAT	4197	TGG	962	236
GTTCAATATAAAACGAAAAA	3300	CGG	11	1
GATTCTTCTAACTTATTAAC	17482	TGG	3875	821
TCCTTTCACTTATAATCACT	26829	TGG	1275	241
AGATGAAAAAACGACTATAA	165	AGG	671	170
CTTAATGTGTTCATAGATTC	37069	AGG	2230	506

ACATCTGTTTCAATTTCGTT	23689	TGG	864	165
GCTAAAGTCATATATACTAC	39929	GGG	1596	372
AGCTAGTTATTTCTGTAATT	9166	TGG	488	81
AAGTAGCGCAATGAGTATGT	16792	AGG	2915	288
TTTTGATGTCTATTACCCAG	6035	GGG	503	56
CAGTTGTGACGTGGAAGGTT	2598	TGG	213	2
AATTTAAAGTCAAGAAGTAT	20838	GGG	1012	276
AATCATCAATAAACTTAAAT	15904	TGG	491	152
AAGTACCGTCGTTATCTTTC	5203	TGG	318	14
ACTACAGTACCGTTTTTACC	36838	GGG	3302	571
GGATTACCACTATCTTATAC	20177	TGG	4014	709
ATAATACTGCTCGTGCAACA	32531	TGG	3010	925
TCATCCAAATTGAAAAAGCA	2103	TGG	477	9
CATGACCTGTAATAACAAAG	4272	TGG	496	138
GCATATAATTACTTCGGTAT	35948	TGG	3489	611
CTATCTCGTAAGTTCAGCGT	11931	TGG	1924	251
AAGAATTATCTTAAGACGTG	14305	GGG	508	61
TGCTATGCATGCTGTAAAAG	5932	TGG	483	110
TGCTTGTAACGTCGTTAACG	20288	TGG	235	31
AAGATTTTATTAAAGCAAGA	7445	TGG	184	30
GACTCTTATTACAGTCTTGT	20536	CGG	2819	625
TGTTCACCCAAGCATGTCAC	39880	TGG	1573	137
GATCTTATACGAAGTAAAGA	13617	AGG	369	78
GATTGGGATTACGCACGTTA	20243	CGG	3654	776
GAAAACCTGTGATTAGTAGC	2640	AGG	746	221
AATTTTCTAGTTGATTCTAC	5396	TGG	1728	242
CCACAAATAGAAATAGAGCT	3698	AGG	418	66
CGGACAAGGCAAAGCATTCG	35827	CGG	1225	263
GCAAAGATCATTAAACAAAA	2276	CGG	87	5
TTTGACCAAGCTGTTATCTT	19907	TGG	734	174
CAAACGTCATTGCATAATCA	35970	GGG	2195	317
AACAACCCTCCTCATCACAA	2575	TGG	1373	79
CTGAGAATTTTATTACATGA	12851	CGG	1807	375
ATCCTTGTATGATGGTAAAC	40350	CGG	1071	383
TGTGGTACATTAAACAAATG	9694	TGG	227	40
TTTTATATGAGCAAGAGCTA	8794	GGG	834	157
TTTGTGTCGTTCATATTCGT	38125	AGG	1260	379
TCAATTAGTTTGTCCGCCTA	5991	TGG	565	179
GCATACACACATAAGTTTAT	237	TGG	3236	757
GTTTTAGAGAATGTTTCTAC	6754	AGG	2658	481
GTTCAAATAATGATACTGGT	20325	TGG	2726	487
TGAACCTAATAAAAGTTATC	37605	AGG	1631	295
AAAAGCAGAAGTAGAGGTTC	5312	CGG	277	80
CCAAAATCATTAATATTGCA	8029	AGG	558	68
TATTGTCATCGAGCTTAAAT	15604	TGG	780	219

TAACCGTATCTTAATCGATA	40143	CGG	452	110
AGAAAAACTTGTGTACTAAA	93	AGG	446	46
TAGATAACAGGCAGGTACTT	39766	CGG	702	141
TTGACACAACACAAACATCA	27197	GGG	1187	157
TACACAAAATACAAAATCTA	32578	CGG	440	3
TTTAAAAGAATAGCATCATT	6436	TGG	300	80
CAAGATGGAATCAAGATTTT	7460	AGG	194	66
CAGTTTTAATACCGTATTCG	10810	TGG	407	34
CGCTCTTATCAGACGTAGTA	20564	CGG	2788	512
TATAAGTAATATTTTTCTTT	8609	CGG	131	44
GTAAAAGCGTTAGTGGCATT	25184	TGG	1179	239
CATATAAATAAAGGCTCATA	17962	AGG	773	270
AAGAAATCGTTAGCACTAAT	20219	GGG	1489	294
TTCTTAAGTTGTCTTTCAGT	30454	GGG	1695	213
AATTTAAGTGCTAAAGCTAA	6970	AGG	1049	330
AATAAATTGTTTTTAGCTAT	21163	TGG	771	150
AACCCTCTATCAACATAGCT	390	TGG	247	101
CAAGATGGAACAGCAGACGC	12373	AGG	2463	567
TCATACTCTAGTAATTCGTC	9367	TGG	1866	170
GTCGAACACTTATTTGTATT	10435	TGG	1022	183
CTTTGTTGGTTTGATGCATT	33521	CGG	2034	453
GTATAACGGCAATGACACAG	11681	AGG	1245	65
TTGCAAATGTGAAATCTATG	7839	AGG	643	156
GTTAAAAGAATGTTAAAGTC	6108	AGG	920	316
TCGCCGTATGTGTAATGTGC	9849	TGG	5909	736
ACGTAATATCAACGGTATGT	15707	GGG	2516	807
CTATCCGGATATTTATTTTT	37527	AGG	745	6
TTTGTCTATCCAGTGCTTGC	35592	TGG	9798	1420
AATTATTCAATGGTCAATGT	37782	CGG	1221	169
CTCATCTCCTGTAAAATTTG	4066	AGG	219	58
CGATAGTAGACGCAATTAAT	31775	GGG	639	47
GCCAACAAAAATAACATTAT	16754	AGG	908	163
GAACTTGTATCAGTACTACT	34831	AGG	1128	254
TCCGTTTTATCAGTGCCTAT	29215	CGG	1654	184
ATGCCTAGTTTAATTGATAC	13233	TGG	2899	766
TTTTGTTCTTCTGATTGCTC	19161	AGG	4972	1394
TGATGAATTAGCTGACATGT	12069	TGG	2452	558
ACATCAATCACACATTCGGA	2429	CGG	493	156
TCATGTTCGGTAAATTTATA	9457	TGG	448	116
TCTAGAGCACCGTTAAAGAA	9976	TGG	384	21
GCCTAAAAATCTATCAACTA	19294	AGG	713	93
TCATACCATCTAAACTAGCG	14868	AGG	342	32
AATTTTTCGTATTCAACTGT	22586	AGG	2927	352
CAATATAAAACGAAAAACGG	3303	AGG	786	60
ACCGCTCTATATTTAACGGC	6388	AGG	1311	96

GGATTGAAATGTGAGAGATG	7747	TGG	361	96
TTCCCTCACACTATTTCTAT	20996	TGG	829	146
GCTTTAATTCAGTTGCTTAC	25886	TGG	7230	1240
GTGCTTTCACAAGTATTTCT	25485	TGG	850	28
TATAGTTGGGATCAATGTTG	13006	AGG	726	179
TCATAACTTTCAACGCTACC	32832	TGG	7146	1438
CGCTATTAATGTTAGTACAA	27769	AGG	1102	80
ATGTATCAAGATACTGCATA	38893	CGG	549	76
CCATTCATGTTCGTGCCGTT	33943	TGG	1599	186
AAAAAGAAAGTTTTAACTTA	927	AGG	84	20
ATAACAAAAAACTAGCCCGA	39803	AGG	838	140
TCACGATGTTTTTGTAGTGT	18080	TGG	3233	728
GAAGTACGACGAAAGTTATT	7641	GGG	333	19
CCTGTCCAAATTTTAACCGT	37312	CGG	893	125
CGACACAAATGATTTAGGGT	38155	AGG	598	197
GCATAAAAAATGGTATTAGG	3051	AGG	233	43
AAACAATCAAGAGAAAAACA	500	AGG	366	95
TTTAAATGTAGATAACAGGC	39758	AGG	523	73
GCGAGAAAAGTAAGAGTAAT	8404	CGG	485	49
CCAGAAAGGAGATAACGAAA	6879	TGG	273	37
TCAAAGGTTTACAGTCGTTG	12525	AGG	1023	300
TCTTTCAACAACCAATGCTC	15539	GGG	1578	363
TAAAACCGCTCTATATTTAA	6384	CGG	447	18
AGAAAAACAAGGTATGACTT	489	TGG	402	74
GAATGACGGTATGAATATAT	6337	CGG	455	173
GCAACGTGATGAGCTTATTG	11440	GGG	894	203
TTCGACCATGATTTAAGTAA	9032	TGG	791	138
CGCTGATAAAAGTAAACTAT	16058	CGG	426	37
GTTTCAGAACGAACAAGGTT	17549	AGG	697	123
TATTAGTAGTACGCCCTTTT	7244	CGG	98	8
AAATTACCTGACATAGATGA	17645	AGG	1887	405
GAAAATACAGATCCTAAAGC	15585	AGG	3416	798
TTCATACTACGCCAAATATT	35320	AGG	838	313
CCGAAAGCGTTTAGAGATGC	31061	AGG	4090	716
CTAATCGTTACATTCACAAT	26638	AGG	1588	505
TTATTTCAGTGTACTTTTTC	13048	GGG	1946	99
AATAACAATACTAATAATGA	7312	TGG	660	61
GGTAAACATCACGGAATGTT	22440	TGG	1310	298
ACATTTTACAACACTAACTC	27367	AGG	2808	197
CGTTCATAGAACATACCTGA	15671	TGG	2748	425
TAATTAAGGGGTGATTTTTA	37404	TGG	462	100
CCAAAAACACTGTTGTATCA	40303	AGG	348	43
TAGCGTCCATTACACCTAGT	11361	TGG	1180	150
TTATCGAGTGTATAACCTGC	39333	TGG	3072	520
TAATTATTTCAACAAATGAA	6470	TGG	304	100

ATAACTAGCTCAAAGCGTTA	9195	TGG	1126	207
ACTCACGATAAGTCATGAAT	18559	GGG	672	80
AGATGAGAATGACTTAGATA	3480	TGG	1241	270
TATTACTTATACCGAGAAGA	8637	TGG	484	106
ATTTATTAAACCTTACAAAA	5009	AGG	124	13
TGCCAACGCTTAAGTTGTTA	38624	GGG	1183	325
ACAACTTCACGACGCAATAA	15028	CGG	1808	193
AAAATCCGGAGCTATCACAA	10380	GGG	400	100
GAAACAATAAGTAAACTTTC	6075	TGG	1330	299
ACTATGAAGGGGATATCAAT	10471	TGG	335	73
GTTTGATGTTCCGAGTAAAG	18026	AGG	1502	70
GTTGATTCTTCTATGCTATC	37542	CGG	3407	483
TGGAACTGGTGCAAGAATAT	15512	TGG	1491	123
ATCTTTCAACAACCAATGCT	15540	CGG	1379	130
TTTGTAGCACGACTACCACC	21548	AGG	777	151
TAATTTATACGTAGACCTTT	20017	CGG	642	44
GTTCCGTTTCCTACTGCTCC	38745	AGG	5924	76
TTCATCCGTTTAAATCAATA	20938	AGG	687	24
TTACAAACAAAATCGAACAT	1802	CGG	414	8
CTAATAAAAATGATATGGAT	39203	TGG	293	20
GAAGTAAAATCGAATACACC	31385	GGG	4001	275
AGCAAACGCAAAAACAAGAT	15112	TGG	611	123
GTCACCTGATAACTTTTATT	37593	AGG	144	11
AGCTAGGCAACGACGTAAAG	9667	AGG	859	241
CCTGCTTCACCTTTTGCACC	36793	AGG	1050	242
TCATTTGGTCAAAACTGGAA	38512	CGG	410	89
TTCTTTCGCCATTTCTTCAA	19468	TGG	826	150
TGAACAAAGGTTATATAGTT	12993	GGG	300	50
GACACCAATTTCTTCAGAAA	756	GGG	455	112
ATGGAATCAAGATTTTAGGT	7464	TGG	349	42
CTATGCTTGCAGTTTGGAAC	10847	GGG	2543	302
GGCAACGCAGATTGTTTGAG	2310	TGG	1629	269
TATATTTAAATAACCTCTAT	27568	AGG	567	38
TATAACGGCAATGACACAGA	11682	GGG	437	162
AACTATCATTAAAAGTTAAA	22519	TGG	100	10
GTTTTCCGAAAATGGCATTT	7177	CGG	550	186
TTATCTGCATTAAAGCGTAA	17417	AGG	607	30
AAATAAATACCATTTATTAC	830	CGG	110	16
CTGGATAGACAAATGTCTAG	35618	GGG	812	189
ACGCCAAAAGTAACAGGTAA	2471	AGG	542	44
CATATCTCCTCCTATTCAGT	20425	TGG	1007	133
TGAAGTACGACGAAAGTTAT	7640	TGG	275	27
TTAAAAGAATAGCATCATTT	6437	GGG	286	18
GAGTGATGTCTGTTGTTACC	30829	AGG	5223	1376
TGCGTCCTGCGTCAATTGCA	21646	GGG	3603	249

CTTATCAAATACCGTGTCTT	10514	TGG	458	122
ATTGATCATATAGTTGTAAT	34988	GGG	761	1
AAAAAGCTGAAGAAAATAAC	5074	GGG	144	51
GTTTTTTTGGGGCAAAAAAA	40235	GGG	142	42
ATATTTGGCAATGTGTTCGC	24980	TGG	1497	180
GCTTTTTATTATGCACTTTT	18877	CGG	1427	55
TTTGATTACAATCCATTGTT	16958	TGG	443	65
TAGAAATAGTGTTGATGATG	16651	AGG	675	61
ATGATGATGTGTATGTTACA	17827	TGG	3206	830
GAGATTTCCAAAGCAACGTA	23652	AGG	1133	165
AAAACATCCAGTGACATGCT	39871	TGG	70	10
GTAGTTAAACATATGAATGA	7048	TGG	914	62
TTTTTCTTTTGTGCTGTCAT	19663	TGG	656	58
CAGCCATATTTTGCTTTAAT	32000	TGG	1334	122
ATTTTTAAAACATTCAGGCA	31824	AGG	777	85
CTTCCGCCAAGATGACGATT	5883	AGG	303	53
TCTTTCAATATCGTTGATAG	36590	TGG	915	103
GGCGAATGGTACACAACATA	21615	TGG	550	168
CACAAATAGAAATAGAGCTA	3699	GGG	569	78
AATTTAAGTTTATTGATGAT	15922	TGG	1432	268
ATTCATTTTAAAAGGTCATA	3399	TGG	143	4
GACGTTAATCTGGAAAGATG	10687	GGG	398	61
AGTTATTCAAAAATCACGAA	1154	AGG	143	41
TTATGTTATAGCTAGCCTTC	39804	GGG	1094	170
ACACTGCTAACAGCTGCAAT	25342	CGG	1886	315
CAGGTCGTTGATAATACTCT	20788	AGG	308	32
TTTGGAGCACTGTTACAAGT	26100	TGG	626	88
CATCCATTAGCACAATTGAT	28409	AGG	213	2
TATGTGTTTTCTGGTGTTGG	2808	TGG	713	80
TATGCACATACCAATGTTGA	8130	TGG	1500	329
ATTAATATAGATAATTATCG	34463	GGG	175	28
AATCAAAAAATACAACCAAC	7597	TGG	2261	522
ATTTTCCCTTGTGATAGCTC	10369	CGG	458	15
ATTAAGGCTTCAACACCATC	15672	AGG	1383	423
CGTACTTAACTTTTGCCATA	21277	TGG	1937	110
AAAAGAAGTAACCAAAGACA	10519	CGG	1126	307
ATTGAATTGCTATCATATTC	13883	CGG	1094	249
CAGAATGAACTATGAAACAG	11353	GGG	164	39
AGTCAAAGCTAAAGGGCATA	8100	CGG	92	26
AAAAGAAATCGATGTTAAAT	36631	TGG	533	47
AGCTTTTACTAAACAACAAG	37273	CGG	607	98
GAATGTTTTAAAAATTCATT	31800	CGG	231	53
TCGGTTGATTCTATATCTAA	6310	CGG	414	157
TGAACGACACAAATGATTTA	38151	GGG	339	56
TCCACTAAAAGCAGAAGTAG	5306	AGG	327	48

TCATCAACACCATCTTGTCC	32421	AGG	2799	1024
AAAATTATTACAAACAGAAT	5429	TGG	156	25
GACAAAGAAATGACGAAAGC	23187	AGG	1789	219
GGAACAACGGTTACTGACGA	4004	AGG	320	95
CATAGAGGTCGAAAAAGTGG	10881	AGG	311	8
TAGTACCAAAGATAACAGCT	19896	TGG	550	18
TTCCCTAACAACTTAAGCGT	38638	TGG	1187	172
GTGACATACAACATCCCTGA	37734	AGG	2629	198
AACAGAATGAACTATGAAAC	11351	AGG	299	19
AGTTTAATTGATACTGGAGA	13239	TGG	825	12
GATGGTGAAAGAGTTAAATT	11570	TGG	119	14
CGTGGATAAAAGTTGATGAG	5812	AGG	181	15
TACGATTAAAGCAGATGAAC	15776	TGG	1182	45
ACATTTAGTAAATCATTACG	39108	AGG	983	112
TACGGTGCATATAATTACTT	35942	CGG	220	42
ATTCACATTCCAGCAAGCAC	35599	TGG	4582	705
GCAACGTTGCCGAAACCACA	13941	AGG	671	78
AGCGTTTGATGAAATACTTG	11744	AGG	364	6
GGCAAAAGATGAAAAGTCAC	33878	AGG	1957	359
GAAACAATCTTTATAAACGC	1308	AGG	3111	114
AAGCAAGAAAAGTTTGTGCT	14594	AGG	1083	311
CTGAGAATTTTTCAGCTTTT	22846	CGG	141	1
ACTAACAAAACAAATACTGA	33696	GGG	608	194
TGCAGTAATGCAATCATTTT	30100	GGG	555	103
TAAAAGGTATCTACTTCACA	36195	AGG	628	94
ATGAATTGATAAAAAAGAAC	9498	GGG	551	122
GTTAGAAAAACGCGACGCAG	19224	AGG	1548	88
CTAAATCAATGGCTCAACGA	23769	TGG	1271	12
TTTATAGGCTCTCCGTTTGT	16166	AGG	1463	286
TTTAGTTATAGTAACTTTGT	33295	TGG	818	153
GAAACACTTTCTTCATCTAC	37945	TGG	3217	241
CTGAATGGGTTTCTAACATT	26193	TGG	99	18
CTTTTATATGAGCAAGAGCT	8793	AGG	115	10
CCTTTTGCACCAGGTTGTCC	36784	CGG	2490	637
TTAATACGTCCATCAACAAG	28432	CGG	814	192
GCGATCAGTTAAAAACTACA	24537	TGG	2105	92
TTGGTATCAAAATCTAAGCT	4889	AGG	246	36
TGATTACGAATTAGACGAAA	17596	TGG	437	13
TATGAATGAACATGAATTAA	13196	GGG	153	39
ATACTTGATAAGTCTACTAT	27938	TGG	801	195
TACTCATCGTTTGAATCGTC	32541	TGG	3652	24
AGCAATTCAATTGCACAGTA	13911	TGG	611	19
AGATAGAGTGTTTGACTTGT	10032	GGG	693	127
CGAGTGTGGGACGAATATAC	10926	AGG	1295	321
AGAAAAACAAAGATTTGTTT	6142	CGG	170	42

TGGGAGAAATATAAGCGAAA	18597	AGG	92	35
GTATCTGTTTTAATATACGT	12767	TGG	825	58
TGATGCCGAAATATCGAGTG	10912	TGG	369	37
ACAACATTCAAAGATTCAAC	12466	AGG	1577	460
ATTTGCTATCCTTGAATTGA	461	TGG	979	239
AATACTCCACTAATGTAATC	20876	AGG	1069	108
AGCACAAACTTTTCTTGCTT	14575	CGG	642	134
TTTGAAATGTACGAGATGGA	10556	AGG	998	403
AAAACCCTTTCTGAAGAAAT	768	TGG	58	14
ATACAAAAAAGAGCTGAAAA	7129	CGG	153	29
CACTCCATTTCTTGAACATT	9759	TGG	122	26
TGATATTTAGAGGTGGCACA	8834	TGG	718	93
TTGATTTTGTCCAATAACTC	36925	AGG	709	118
GCGATCAGTCTGATTTGATG	13783	AGG	273	57
CGAAACGTTCGAGGCACCTA	8876	TGG	257	84
GTCGAAGATTATTTTATCTC	27535	CGG	1473	384
GAAATCCATACCAACCATCT	38234	GGG	942	156
ACAATAGAAAATGTACGTAG	37630	CGG	926	266
CAACGATATTTGATATTTAG	8824	AGG	633	182
CGTCCACGCTTTCGTAATAC	8907	AGG	1676	369
TCCTAAGTCGTCCTGACAAT	7007	TGG	350	27
AAAGGAGAACAAGGCGCACC	36836	CGG	913	131
GGAAGAAGCGAGTATCAATA	3735	TGG	212	18
GACAAGTTTCAGAACGAACA	17544	AGG	1342	334
GCCATAAAATGAGTATCCAA	23593	AGG	670	47
ATTCATGACTTATCGTGAGT	18578	GGG	1101	53
AAACAACAACGAAATATATG	11087	CGG	231	33
ACTGCAACTACTGCTAATAT	25492	TGG	1372	24
TTAACCAAGCAATAGATGAA	3515	TGG	547	150
TTAAATATAACATTGAATCC	22901	TGG	3443	949
ATAATAAAATTATACCAGAA	6865	AGG	351	55
ATATGAATGAACATGAATTA	13195	AGG	177	9
CGTTTAAATCAATAAGGTAG	20944	AGG	625	122
GTAATTAATCCGTAAGCCAT	29611	TGG	1049	213
CCTAGCTCTATTTCTATTTG	3682	TGG	166	21
ATTGCAAATGCTAATTGTGG	9915	TGG	1435	256
AATGACATTTCAAATGATTC	22457	TGG	2737	167
ACTTGTTCTTTATGATAATA	16121	TGG	365	118
ACTAAGCAAGATGTAGTATT	28685	AGG	358	99
CAACCTACTCATGTCGAAAA	7726	AGG	74	9
ATTAATAACCTAGTAAGGTT	6264	AGG	203	42
GAAGAAAAAGAAAAGTGAAA	9068	TGG	55	14
CTTGATTAAGCAAGGTATAC	35377	CGG	2772	379
TGTACGTCTAACGGCTTACC	12027	TGG	405	20
GATGAACGCTCAGATATTCA	35012	AGG	1280	239

CTCTAAGAGATATCTGTATC	10109	AGG	103	3
CATTCATGACTTATCGTGAG	18577	TGG	724	139
AAGAGGTTGAACTACGTAAG	9684	AGG	636	49
TATGTTTGGCACCCTACAAA	16170	CGG	800	62
CGGATTGTTCTATTTGTTCA	11626	CGG	895	206
AAGTTTTATAACGGCTCAGC	4683	AGG	162	16
AATTCTTTGAATATTATCTG	12222	TGG	124	16
GGAATATATATAAAGCAACA	10245	TGG	286	99
GGCAATACATGCAATCAGTT	25971	TGG	405	11
GCGTCACCTTCATCTATGTC	17635	AGG	2260	279
ATGGAAAGAGAAAAATCTTG	19122	AGG	34	4
ACTAAAATGTGGCAAATTGA	36893	TGG	1357	113
CCTTATTAAACGCAAGGGTG	2350	TGG	128	42
TTATATTGGGTTAAATCACA	38947	GGG	302	10
TAGAAATGTAAATGTAGAGG	9418	TGG	168	66
ATCTCTTAGAGCCGAAAAAT	10081	TGG	45	11
TAATAGAACTATCAAGTAAA	556	AGG	118	13
ACAGTATTAGACGCATGTAA	9138	TGG	975	105
ATTTCAGGGAGCGAGATGCA	8432	TGG	504	39
TGCCTTGCATAGGATTTCCT	352	TGG	476	81
AAGCGTTAATACGTGGTGTT	35262	TGG	215	37
GCTAAATGAAGATAGTTCTT	27802	TGG	244	11
ACCACTAACTTACCTAAGAT	24953	TGG	546	183
CAACTAATTCAAGAATTACA	39452	GGG	172	77
TGTGAAGCATAAGCAATTTT	26970	AGG	163	26
TGATATTGATGAGTATATCG	17705	AGG	364	9
ACTCTTTTTGCAACCATTCC	9511	AGG	824	196
TTTTTGATGTCTATTACCCA	6034	GGG	549	52
TAAATGGAACAAGTGATATT	24174	TGG	366	63
TGGATTTAACTAGAATAACT	25431	GGG	303	39
TCTATTATAAGGAAAACTTT	588	CGG	64	2
TTGTTGAATTACCTTTAACA	32234	AGG	654	185
ACGTAACGCTACAAAGTCTA	28520	AGG	698	159
TAAAGCTCAATCATTGCGTG	18221	TGG	1052	126
GCCAATTGTCAGGACGACTT	6992	AGG	130	3
CGAAAGATAGCAGACGAAGA	15219	AGG	287	31
TGCTCATACTTTGCGTTATC	35380	CGG	2187	348
GTCGTCGAGTTGTAGCTCGG	1048	CGG	18	8
AGTAATCGGAGACGATTTCA	8418	GGG	273	32
AAAGTTTACTTATTGTTTCT	6095	AGG	334	34
TTATTTCTCCAGTTCTATAT	30321	TGG	798	15
TTAGTGAAAACAAACTTTCT	33455	AGG	422	36
AGATGGTCCTACTACTATTG	34667	CGG	337	71
ACTACAGCATGGTCAATTGC	3165	GGG	2011	558
TAGAAGAATCAACAGCAAAA	37568	TGG	166	53

TTCTATAAATTTGCAGTATA	3908	CGG	190	65
TATTCGATAATTTCTTTATA	7356	GGG	33	3
AACACGAGCACAAACGAGCT	35680	CGG	275	85
TAAAACTTTCGTTATACTCT	28014	TGG	1047	142
ACAAGTTTACATTCAATGAC	29648	AGG	3853	737
AACTCTTCTTTAAATTTAAT	33428	AGG	154	14
GAGTCAATTGTTAATATGAT	13836	AGG	252	39
CTTAAATACTTAGCGATATT	38802	AGG	189	53
TTCAGTGATTTCTTAAATGC	26321	CGG	1431	220
CTAACAAAACAAATACTGAG	33697	GGG	280	55
CAGATGAATAACGATAGAAT	34575	CGG	301	92
GACGGTATGAGTGATGCACT	26282	TGG	1601	142
AAAAAAATTATGCTTGTAGC	38722	CGG	2224	322
CTAATTGTTCTCGAGTTGGT	22993	GGG	958	229
TATTACTAATAAAAATGATA	39198	TGG	57	6
GCTGAAAACGGTGTGTTTAA	7141	AGG	950	14
GGAGAAGAAAGCAAGTGCAT	11497	GGG	399	5
TATCTGTCGTTAAATATATT	30373	CGG	325	59
AACAATACGCCGTAAAGACA	29368	CGG	454	31
CAACGACTCTAAAACGTATA	37030	CGG	451	19
ACGGAATACTAGAAGATGTT	20704	AGG	651	129
CGTTCAATAAATGTGAAAGG	14452	AGG	287	32
ACTGTTGCATCTCTTAAAGA	7905	CGG	568	53
TGAAAGAGTTAAATTTGGAA	11575	TGG	283	64
TGGTTTATGTTAATTAATCA	15132	CGG	559	68
TTGGTAAGTGGAACTTATCC	33094	AGG	1032	216
ATACGTAATTGTTGTGTTGT	39466	TGG	772	23
GATCAGAATTTTAAATCAAG	18402	TGG	32	9
TCAATCTTAGCTTTTTCTTC	13094	AGG	502	9
TTACAGGAGATGAGAGAAAA	4091	CGG	67	37
TATCTGCATTAAAGCGTAAA	17418	GGG	337	2
ATGAAAATATAAGGGAGTGT	12626	GGG	363	83
AAGCAACGTGATGAGCTTAT	11438	TGG	516	136
TTTCAATTAATAACCTAGTA	6269	AGG	53	23
ACAGAATGAACTATGAAACA	11352	GGG	186	63
CAACTGACAGCTAGATATTT	23282	AGG	203	52
TTTACAACGCGCTAAATCAA	23758	TGG	584	116
GCCAGTAATTGTTGAGTCAT	34865	TGG	424	125
TATTGAAGAAAGGTTATAAC	14104	AGG	499	122
TTTACCTTAATATCTTCTGC	20457	AGG	1233	368
TACTCATCGTCATTTAGATG	18365	GGG	628	55
CAATTTGCGGATATGGTGCT	16698	AGG	343	101
AAATGGTTTGACAATTCATT	38215	AGG	215	38
AACTTCAATTGCAGAACAAA	29258	AGG	207	110
TCCTTAGTTGATAGATTTTT	19309	AGG	176	44

AGAGATATAGAACTTCACTG	5385	GGG	173	35
ATAAATTCGGAACAACGAGC	32705	TGG	1533	41
GTTTTCCCGTCAAAGTATGG	38437	TGG	1165	198
CTAAAAATTGATGTGCAGAC	31425	GGG	2622	582
TAAACCTGAACGATTAAGGA	16256	GGG	123	11
ATTAAGTGGTACGTAGACAT	33804	GGG	445	156
ATATGACGATGACGTTAATC	10677	TGG	867	198
AATGATGGAAGTATATTGTC	7327	GGG	586	124
ACAAGAGTGCCGGATTTACC	32830	AGG	1221	306
GCCAATGACTCAACAATTAC	34880	TGG	219	38
CAAGTATCGATGACTGATTC	30923	AGG	926	180
TGGAATGAAACTTAAACTTA	17323	TGG	799	111
TTAATAGGACGAGGTATAGA	15867	TGG	680	129
TGAAATCCATACCAACCATC	38235	TGG	1520	267
GCATCTGCAAATACAATTTT	2197	TGG	68	21
AGCCAATCACGCCATTCAGC	23323	AGG	2521	671
CTGTCTATAGAAGTACTTAC	26569	AGG	1281	10
ACAACATCGTCGATAATAAG	36439	GGG	705	115
AAGAATGACATTGAAATAGA	14834	GGG	578	23
CTTATCTGAAACGACGTTAA	35308	AGG	763	223
CGACCTCTATGCTTGCAGTT	10853	TGG	233	68
AAAGCAATACGTGATGATGT	18192	CGG	583	107
AAAAATACAACCAACTGGCA	7602	CGG	603	163
ATGAGAGCACGTAAAGACGA	18537	TGG	1443	214
GGCAATGTGTTCGCTGGTAT	24986	TGG	1115	378
GAAGCCTTAAACGCACCTTA	9572	TGG	679	91
ACTTATACATCAAGCAAATC	32482	TGG	1375	36
TTATTAGCTGACTTACAAGA	22218	AGG	462	28
GTTGGTTCAGTCGTGTTGCT	26118	TGG	725	90
TAAACTACTACGACTTAAGC	21268	AGG	1412	325
ATACTAAACCTGAACGATTA	16252	AGG	572	43
AATCCCTCAATAACGCCACC	33096	TGG	1650	247
TTAATTTTTAATGTTGTAAT	22772	TGG	334	70
TTACTTGTACTAGATGATAT	8230	GGG	254	3
GAAAAAGAAGATTTTGAAAC	16454	TGG	141	15
AAGTTGAAGATGTTGTTGTG	13978	AGG	209	57
TAAAAAGCGTTTTAGCGCTT	1903	GGG	231	10
AATAGTTGGACAGGTTCTCC	34751	GGG	471	40
TGGTAAGCCTATAGGTGGTT	39276	TGG	452	14
TTACTATAACTAAAATTATG	33320	GGG	370	45
GGTAAAATGGCAGCAATTTG	16685	CGG	517	30
ATTAAAAGATTTTATGTTTG	11219	AGG	547	78
ATAATCCAACATCTCAAGAA	38028	GGG	336	53
TATTTCAACAAATGAATGGT	6474	GGG	703	104
CACAAAGTAGTCAGCGCGGT	26390	AGG	196	93

ATGTAGTTGAATTCTTTGAA	11981	TGG	193	29
TCGTAATTATCTATTTCTAT	21986	AGG	176	35
GAATACTTAAACCAATTTTT	10086	CGG	25	4
AACGCTTAAACCAACTGAAT	20431	AGG	272	37
ATACGTCCATCAACAAGCGG	28429	TGG	1424	83
GCGTCTTTAAAAATAAAAAA	69	GGG	16	1
GAGAATTACAAGGAAATCAT	23226	GGG	401	21
CGGTACTATCTTCGCGCAAC	24268	AGG	1152	92
CCTGCATCTCTAAACGCTTT	31045	CGG	376	65
TGAATATGCACAAGCAGAAA	19771	TGG	631	145
GTAGTTGAATATAACGTTAC	26854	AGG	854	127
TTCAACACCAGTAGCAACGA	5229	CGG	144	41
TGCTATCAAATGCTTAATTT	35741	AGG	95	18
AGCCTGTAACACTTACATAA	34773	GGG	400	114
GATACTTTGCCGTTATTACA	23067	AGG	409	57
CAGGTACCGACCATTTTTCA	27287	GGG	690	201
TAATATCACTTAGATATGCT	30960	GGG	653	212
ATGGCGTTGCGCAACCTGGT	38549	TGG	333	77
TCACATCATTTGGTCAAAAC	38507	TGG	395	107
ACGACAATATCCAACTTTTG	38400	CGG	276	80
ACCTCTACTTCTGCTTTTAG	5291	TGG	392	95
GCAACTCCAACATACACGCC	19544	AGG	4134	878
ACTTACTTAGCAAAAGGTGT	19706	AGG	446	44
AGGAGGCAACCAATGGCTTA	29618	CGG	459	34
ATAACCAAATGTTCAAGAAA	9771	TGG	30	2
AAGAACTGGAAGAAGAAACC	12025	AGG	572	112
GATTTAGCTGAAATAGTACG	22260	AGG	156	38
CTTTTGCGATAGCGTATGCT	8060	AGG	356	54
GTGTATATTTGCCAATTGTC	7002	AGG	4620	631
TTGAAAATGATTTAGTTAGT	31919	GGG	1395	315
CTTTCTTCATCTACTGGTAT	37939	CGG	249	37
AACGATTCAAAGGCGCTCAC	8770	GGG	1083	177
TAAGTGACATCGAACCAGTA	9733	CGG	405	20
AAATGAAGCTGATTTAGATA	18759	TGG	476	130
GAAATACATTTAGACGCAGC	38986	AGG	726	152
GATAACATGTAATGATTACC	30148	TGG	1232	272
AATCAATCGCAACAGAGATT	14055	GGG	30	11
ATTGAACAAGCGCAAGCTAA	23405	CGG	426	151
TTACTCAATTGAATCGCGTT	33135	AGG	512	51
AATTATCGTTTATCTGAATT	39172	AGG	229	5
TTTCTGTTCAATTTAGAGTT	14132	AGG	297	130
TGGTTCTTTGATGTACTGCC	31085	TGG	5512	611
ATGGCGCTTATTACTTTCAC	10165	GGG	636	74
AGAAGCGAAAGAGAAGTACG	12561	AGG	153	11
CCTATCAAAGAATACTTTGC	15807	TGG	1131	122

TCAGATACACAACCTATGCA	30587	AGG	1596	71
CCGATAATTTGAGCGACTGC	25276	TGG	2122	356
AGTGGTAAACCGCTTGTTGA	19958	AGG	1171	231
CATCATTCTTTTTATAAAAC	32594	GGG	241	47
GAACAACCGGTTTTATATCC	27628	AGG	890	220
ACCACAGATCCTATTAATTT	40194	AGG	79	25
CGATATTTGATATTTAGAGG	8827	TGG	227	7
GGTAAATCCTAGAATTGTTA	27993	AGG	247	68
AAAAGAATTTGATGACGTGT	16202	TGG	1801	269
GCATTAGCTCCTGTTGACTT	21423	AGG	283	13
ATGATGTCAGGTACAGAAAA	2060	AGG	111	35
GGCTAATTACAGATATCCTA	34564	AGG	433	48
TTTTTGAACATACTTGTCAA	19363	AGG	406	101
CCGCCCATGATTGCTTTTGC	36016	TGG	1764	267
TCTAAACTTACAGATGATTA	32287	CGG	589	72
GAAAGTGTATTGCAACAGAT	37145	TGG	610	129
TAGATAGAGTGTTTGACTTG	10031	TGG	262	3
ATAATTATGGATCCTATTTT	6801	AGG	75	13
AAAAACTTAAAAATATGGAT	13274	TGG	138	39
TTCTTCAATACTGTCTTTAA	28064	AGG	464	109
ACAGTTCGCTACACAATACG	21938	AGG	508	61
TAATATCGTAAAAGCGTTAG	25177	TGG	487	63
AGAATTGGTTAACACCTCTT	30867	TGG	549	36
TTGATATCAAAACAGCTGAA	7505	TGG	96	1
TAGAAACATTCTCTAAAACT	6734	TGG	38	8
GAATCATTTAAATTAACAAT	22317	TGG	299	42
AGTTGTCTATAAATATGAGG	11843	AGG	581	193
GCATTGATACCAGTGATTGC	24320	CGG	1569	16
AATTAAACTACCCACCATAT	14403	AGG	1335	319
TATGGATAGGTTTAAGCAAG	16139	AGG	685	171
ACGCTTGTGGAAAAGCTAAA	40280	AGG	75	12
TTCAGGCAAGGTGCATGCTC	31836	AGG	218	35
AAAAAGTAGAGCTTAAGATA	26954	AGG	260	54
CAGGAGAAAGCGCAAGTGGT	39005	GGG	407	67
TTAAAAGATTTTATGTTTGA	11220	GGG	428	15
TTTACACCAATAAATAGCTT	18425	GGG	320	97
AGCAACTAACTTTATTTTAG	10288	AGG	158	25
ACACATTGTACCGAATTAGA	36096	TGG	161	30
TTTTTCGGGAATTTCATTTT	13034	AGG	134	39
GACATCGCAGTTTGGCACCC	34634	TGG	2499	851
AGTTGGGATCAATGTTGAGG	13009	AGG	157	20
TTTGAAAGCAGTGGCCAATT	5136	TGG	32	1
CAAAAAGCTGAAGAAAATAA	5073	CGG	3	2
GCTTTTTGCTTATCTGTCTT	5042	CGG	236	2
AATGCCCCTACATCTTGTGC	14480	AGG	1785	379

GCGCGCTCTAGATTTAACTT	8981	AGG	101	14
CAAATAGATAAAGGTGACAG	14987	TGG	1053	158
TTAGCATACCTTGTGTTACG	17090	CGG	655	191
GGCTCAGCAGGGTTTCAAGC	4695	TGG	2325	300
GGTGTTGACTTAGGTGACAT	36287	TGG	812	132
TTTGACACAACACAAACATC	27196	AGG	796	56
AATTTAGATGCATCTACTTT	28096	TGG	413	58
TGCAAAAGATTTCTTTAATG	19849	AGG	31	14
ATTCAAGAAACACAAAAGAG	17135	TGG	562	114
TAAAACAATTAAAGGATTTA	21073	TGG	161	36
AGATGTTAAAGCTAATGATA	27465	AGG	463	73
CTGTGGTTTTGTTGGTTGTA	40162	GGG	7	1
AAGTTAAGAAGTAACGCGCT	19258	AGG	794	267
TTATAGCGTTGACCAAAACT	34720	GGG	82	21
CTCATCAATATCATTCTGAT	17679	TGG	293	46
ACAATCCAATGTATTTTATT	38609	AGG	59	23
CATTGATCATATAGTTGTAA	34987	TGG	246	65
TGTTTTTGTCCGTGTCTTTA	29361	CGG	587	90
TATAATTGCTTTTATATAGT	40003	AGG	211	87
TAATTAAGTAAAGTGTATTA	37371	GGG	370	50
AGAACTGGAGAAATAACTTA	30344	TGG	78	8
GATGATTATAACGTAGATAG	31729	AGG	190	2
TATTAGACGAGTTAATTAAA	10350	TGG	68	1
ATAGCGCAGACATACAAGCT	13526	AGG	269	27
CCTTTAACCGCCATTTTAGC	23980	GGG	1127	186
TAACAACATCACCTATTTTA	28563	GGG	605	85
TAAATCTTTTTAGAGTTATA	32910	AGG	350	105
GGATTCTGAAATAGGTAAAA	16672	TGG	352	108
AATACTTGTGTTGTGTTACC	31387	CGG	1266	168
CCTTACAACACTTCAACTAG	19940	TGG	661	175
TATCAATTCATTTTCATGTT	9470	CGG	81	13
ATGCTTGGTTTTTCGTCTGA	35542	TGG	33	1
TTAATTAAGTAAAGTGTATT	37372	AGG	319	53
TAGTATTAGGAGACTTTACA	28698	AGG	427	69
ATTTAAGTTTATTGATGATT	15923	GGG	352	38
CGTATATTTCTTCTTTTTGA	29736	TGG	544	192
CAGTATTCCCTGATATAGAC	22054	AGG	1352	288
AACAATGATTTTATGAAAGA	20736	TGG	84	8
TAACGACCCTGAAAAATGGT	27297	CGG	289	74
AGATTTAGCGTTTTAAGGTG	5171	TGG	56	28
TGTTCAGAACTTATAGATAA	31662	CGG	397	108
AATGAATGTTAAGCGAATAT	35704	GGG	403	105
CGACGAAAGTTATTGGGATT	7647	AGG	67	8
ACATTAGTGGAGTATTAAAC	20899	AGG	275	29
TTAACGATAGAAAAAGATTA	12956	TGG	110	25

TCATAGAGGGCAAGAGCCAA	14619	CGG	104	11
TTATCTAAAGGGACTTAAGA	19002	CGG	111	8
CGTTACGAAATAAGAGAACC	23483	TGG	402	51
TTGCGTCCTGCGTCAATTGC	21647	AGG	1555	31
AACGGAAATGTACCTATCAT	17303	TGG	1139	218
GTGTGATATGCGTCAAACAC	29449	TGG	1387	308
TCGTCATGATTATGATTTTT	37213	TGG	63	27
TGAAAAAGGGCAAACGCTTG	40267	TGG	49	28
GCTAATTACAGATATCCTAA	34565	GGG	370	105
ACTCTCAATGAGATTAAATT	34024	AGG	89	30
CCAATGTACTTGATACGATT	25950	TGG	178	21
CTAACAACATCACCTATTTT	28564	AGG	98	8
CGTATCGATCTAAAAGCACA	36377	TGG	137	11
TTTTCAACAGGATTTAGTGA	10412	TGG	394	44
TTGTATTCTAAATTAATAGC	39244	CGG	79	9
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TTATGATTTGTATAAGCTGT	8936	TGG	569	78
AGGAAATATCTCAGTTATTA	27513	AGG	398	82
AACAATTCAACCCAGATGGT	38240	TGG	591	113
GGTATATATGCTACTGGTCC	21546	TGG	645	32
GTATTCGATAATTTCTTTAT	7357	AGG	55	2
TCTACCGCTTCTTTACCTAT	29095	TGG	163	53
TAAGCGCAGTTAACACATCT	32351	AGG	148	17
ACATACTTTTTGATTGAGTA	20756	AGG	483	37
AACCAAGCTATGTTGATAGA	376	GGG	778	189
GTAAGTCGTAAGGTACATAT	21141	AGG	321	8
CGATAAGAAAATAGAAGAGT	21350	GGG	243	68
GAAAATCCGGAGCTATCACA	10379	AGG	601	68
AATGGTTTGACAATTCATTA	38216	GGG	178	42
GACGCAAAGCGCTTTTAATA	30810	GGG	108	29
GATAATCCAACATCTCAAGA	38027	AGG	4	1
AACTAACAAAACAAATACTG	33695	AGG	213	62
TAGGGAATGGAATACACAGT	7338	CGG	855	42
TATTAGAATTAACCCAGTTT	34716	TGG	753	110
ACTTTAAATATTTCGATGGT	21466	GGG	416	107
TAGATTGGTTAACTCAATTG	25653	TGG	190	33
AGCAACGTGATGAGCTTATT	11439	GGG	23	12
TCAAATGCTTGTTTGTCTTT	27102	TGG	249	9
AACGTCCAGCAAATAGTGCT	27008	TGG	381	99
TGAGGAAGAAGCCACGAATA	10815	CGG	190	37
ATTAATCGGCAAAGTAGCTG	26350	AGG	332	83
CTTACTACCTGCCTATATGG	14408	TGG	54	1
GACGGTAAACATACCTATAG	27571	AGG	436	92
TCTTTGCTTTATTATCAAAC	38333	GGG	700	147
TTATTGTTAATTGTTATTGA	4510	AGG	185	57

AGCGACAGGAGAGGTAGACA	39576	AGG	329	50
AAAAAGGTTATCAAACACGC	36506	TGG	279	44
TGAAGAAGAAATATTTAAGA	20675	TGG	48	3
TCGCGAGTAAAGTAGCTGAT	26232	GGG	312	36
TACAAGGCACTGATGATGAT	29184	TGG	416	93
TTGAAATGAGGTGCATACAT	34364	GGG	162	42
CTAAAAATTAATTAAAAGGA	4603	CGG	50	1
GAGAAATATAAGCGAAAAGG	18600	TGG	453	71
AAAACAGTTACAACTGCTAA	28907	TGG	1060	316
ACTAGTGTTTGCATATAATA	10577	CGG	288	10
GTTTTAATGTCTTTAAAAGT	33731	TGG	240	87
AGCAAACGCACGCAAGTTTG	24682	AGG	39	28
TATACTATCTGTCAAAGTAG	26540	AGG	361	79
GCCTTTGGATACTCATTTTA	23608	TGG	247	39
GAAGTTGAACAACAAATCAA	32221	TGG	281	31
GCTGGAATACTGCGATTATT	13312	CGG	154	16
AAAATAAAAAGATGCAACAA	400	TGG	120	16
TCGTCCCACACTCGATATTT	10901	CGG	176	25
GATTAAAAAACTTAAAAATA	13269	TGG	33	6
TTGCCAACGCTTAAGTTGTT	38625	AGG	78	14
TTATAGGCTCTCCGTTTGTA	16165	GGG	573	168
TAGCACTAACACCTGCTGAA	23328	TGG	492	105
TCATTCATATTAGCCATCAT	13166	AGG	326	56
CGCTCAGAAACTCATAGATG	8501	AGG	193	10
AACTAGGTGTAATGGACGCT	11379	AGG	222	92
GAGTTTTCCCCTTGTGGTTT	13934	CGG	208	21
AGGTTTAGTATGTGTGTATA	16224	TGG	655	160
TCCTGCCGTTAAATATAGAG	6373	CGG	308	138
GACCGGTTTACCATCATACA	40364	AGG	536	63
ATAGACAGGTTTACTAAGCA	22068	TGG	593	87
TAGATATAAAGAGTCTATTA	15656	AGG	76	15
CTTGTTTCAGTAACGATGCT	35557	TGG	191	52
ATGAAGGCTTTTTCCATACT	37484	TGG	31	6
CAAAGCAGAACCTGAGTTAT	36931	TGG	281	44
ATGCTCGGGATGGTCAGGGT	15525	TGG	814	130
TAAGTACGGTGCTGATAGCA	21308	TGG	571	150
GTCGTTTTCCCGTCAAAGTA	38434	TGG	58	20
TTTGATACAGCGGAAGAGCT	10224	CGG	103	21
AAAGAGTGGTTTGAAGCTGC	22575	AGG	744	63
ATCAAGTGGGTGTGTTGGGC	18416	AGG	1222	163
ATAGAGTTAACTAACAAATA	15306	TGG	144	54
ATGAGTGTCGTGAAGATTAA	9446	CGG	69	14
GACGTCCAAGCACTATTTGC	27019	TGG	1166	239
TGTCCTAATACTTGTAATAT	25693	AGG	152	26
AACACAACAATTACGTATGA	39487	CGG	372	77

CTATAAATATGAGGAGGCAC	11849	AGG	999	258
GTGTGAGGGAATTCGTCGTA	20968	TGG	113	49
AGAAAGTTTGTTTTCACTAA	33474	CGG	313	19
GCTCTCTCGTTGCATAATTC	9614	TGG	349	61
CACTGGATAGACAAATGTCT	35616	AGG	92	38
CATGAAGTTGCATTATACGG	38851	TGG	240	58
AACAACTCATTGAAAGATTA	24206	CGG	209	70
GTATACGGAAAAATTGGCTC	3923	AGG	67	13
TTAGATCGTTATCATTCGAA	19090	AGG	378	107
AATTACGACTTGATTAAGCA	35369	AGG	71	18
CGAAAAGGTGGTAATTGATA	18612	TGG	152	10
TTAATAATTGTCTTTGATCT	23367	AGG	317	5
ATTTTGCTACATTAATTATA	39661	GGG	94	19
ATAGATACTTCAGATAAGAA	24634	TGG	176	23
ACATTGCCTGGCGTGTATGT	19534	TGG	454	172
GATTCACCCACAACAATATA	21830	TGG	200	9
GAGTAATCGGAGACGATTTC	8417	AGG	506	6
GAAGCGCCACCGCTTGTTGA	28439	TGG	1047	357
AATAAAAAAGGGCAGAAAAA	80	GGG	11	1
ATCTAATCGAACAAGAAGTA	19145	CGG	342	81
TAATGTTTGGATTTACCAAA	33944	CGG	145	32
TTCTTTACTTCGTATAAGAT	13599	CGG	123	11
TGGGAAATTCCACCTTTATG	6700	TGG	740	216
TCGCTATTGCGTTAGATTGG	6827	GGG	278	30
TAACCTCACAGTCATATCTA	11275	AGG	465	42
CGTGGACGAGGCGAGCCCAT	8876	AGG	123	18
TGAGTTGTTCGACAAAGATA	17164	TGG	292	50
GATTTTCCTAAAGACTTTAA	31343	AGG	104	15
TCAATGGACTTTACATTTGA	19452	AGG	80	4
CGTTTTAGCAATATGATTCT	29843	AGG	73	8
AGCTCCTGCACAAGATGTAG	14492	GGG	191	9
CTCTTATCACCTTCGTTTGT	27318	AGG	249	18
GGGTGTCTTACTAAACTTCC	34753	CGG	751	185
AAAAAGATTATGGCTTATAT	38933	TGG	185	38
TATAACGATCCTGGAGCAGT	38752	AGG	705	128
CATTGATACCGTCGCCGTTA	29850	TGG	102	18
ATTGAAGAAAGGTTATAACA	14105	GGG	438	56
CGGAAAGCATATATTGACGC	14639	AGG	1062	254
GTTTACACCAATAAATAGCT	18426	TGG	81	5
TCAGATACATGGCCTCTGCC	40024	CGG	536	61
AAAAATGATGGTGTTGACTT	36278	AGG	110	4
ACAGTTCTAACATTTTTGAC	25035	TGG	1166	377
CGATCAGTCTGATTTGATGA	13784	GGG	883	151
TTACTCGTTTCTACACTCAT	5540	AGG	222	61
AAAGTTACATTACAGCCCCT	6034	GGG	258	45

TACGTCAGCGATTTATAATC	30412	CGG	269	27
GATATGAAAATGTGGATTCT	34159	CGG	81	5
GACTTTAAATATTTCGATGG	21465	TGG	354	161
GTTGTTTGAAATGTACGAGA	10552	TGG	883	132
TTCTATGAACGTAATATCAA	15699	CGG	196	20
ATATCACTGTTCCTATGGCT	25812	TGG	1547	294
ACTTTTTGGCAGTAAATTTG	7566	AGG	17	2
CCAGCAAAAGCAATCATGGG	36032	CGG	286	85
TCTGTGGTTTTGTTGGTTGT	40163	AGG	42	8
AATACTTTGCTGGTGTCGAC	15817	TGG	1066	123
ATTCGACTAAAGGTAAGAGT	14664	GGG	223	19
GTCATTGACATTAACGAAGG	3983	TGG	75	9
CGATTCAAGGTGTAGTAGAT	25638	TGG	181	11
TAGCGCGTTGTAAAGCTCTT	23733	TGG	175	58
TCAAAGTATGGTGGCGGAGC	38446	TGG	424	173
ACAGTTAAGAGTCAGTGCTT	34322	CGG	186	37
TGTATTAGCTGATGTAATAC	13880	CGG	290	129
TCGTTATATAGCGACAGGAG	39567	AGG	792	38
AATCATAAAGCGTATATACA	8967	AGG	122	34
GGTAATAGAATAAGTAGTTT	39601	TGG	130	29
AATCAAGAAAAGTTTTATAA	4674	CGG	23	2
GCAATACCTTTAAAGTCTTT	31333	AGG	286	25
GGTATTAAAACAGCAGTTTC	25613	CGG	31	8
CATTTCCCTTCTTGAGATGT	38017	TGG	317	85
TCATACTACGCCAAATATTA	35319	GGG	290	2
ATCAAAATGGACACGCCAAA	14776	AGG	21	1
AAAAACCTGTATTAACTAAA	5956	CGG	57	3
AGAGCATGGTCAGAACAAGT	25082	AGG	486	6
TTTACTCAAGAAAAATGGAG	20639	TGG	359	88
CATGCAAGTTTTAGGTGTTT	25738	TGG	312	91
TTATCAGATTTAAAAATCGT	31277	TGG	127	30
ATGGATTTATTCAGCTGTAT	30283	TGG	216	7
ATAAACGAATTTGGCAAAGA	11552	TGG	171	47
TGGAACCCTGCAATTGACGC	21657	AGG	1419	389
TAATAAAACTTTAGAACAAC	27615	CGG	332	88
CCGAACCTATTCCGTTGCCA	34635	GGG	276	63
AGAGCACCATTATAGTGTCC	31087	AGG	1825	49
ACGCATGTAATGGTCATGTG	9148	TGG	97	22
TATGAAACAGGGGTCCAACT	11363	AGG	89	1
GGCGTTATTCCAGCAGAACA	19595	AGG	329	48
CAAAAAATCAAGCAGAAAAA	38198	TGG	3	1
TTAAAGTGATTTAAAAACTG	6190	AGG	120	11
ACTAATGGCGTTGCGCAACC	38545	TGG	1399	341
TTTGAGTGGTTACGTCAAAA	2324	CGG	28	17
AGATATGACTGTGAGGTTAA	11295	AGG	269	70

TCATCTAAATCATAAGTAAC	16561	AGG	713	297
CGAAAGTTATTGGGATTAGG	7650	GGG	61	16
AGATATGCTGGGTTCTGTAT	30949	TGG	383	58
GGCGTTCAAGTGGTTCAGAC	15372	AGG	1231	118
CAACGTTGCCGAAACCACAA	13942	GGG	107	13
AATACACTTTACTTAATTAA	37391	GGG	217	57
TTAAGTACTGCCATTATTGC	24334	AGG	1424	112
TACACAGTAGCTAATGTTAA	39406	AGG	164	3
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TCATCAAGTTGTACGTCTAA	12036	CGG	838	141
TGGAGAAGAAAGCAAGTGCA	11496	TGG	163	39
AAAAAGAGTACGTGGTGGCT	9541	GGG	946	160
CAGCTTTTTACCGCAAAAGT	38406	TGG	101	18
TGGCGTATTTTGGGCTTTAA	25333	TGG	579	113
GACGCAGGGTATTCGACTAA	14654	AGG	19	6
TTGAACGCTGCAGGAAGATT	24785	TGG	272	68
TAAAATGCCTCTGCAATTAG	19861	AGG	172	9
TGACACAACACAAACATCAG	27198	GGG	271	29
TCTCCAGTATCAATTAAACT	13220	AGG	274	67
TTGATACGAATGGTGATGTT	16731	AGG	133	30
AAAAAGAACGGGTTAACTCC	9509	TGG	256	68
TAAAGGTAGACCCTAATATT	35325	TGG	171	2
ATTCTTAAGTTGTCTTTCAG	30455	TGG	367	23
CGACTGCTTCATAATGTGCC	5644	AGG	219	86
CTAAACCTGAACGATTAAGG	16255	AGG	112	54
GAGAAAACATGTTGTTAAGT	23959	TGG	407	134
CACATTGACTTACTAGAAAA	5280	CGG	38	12
ATTTCTACCTGTGCTGTTTC	31124	TGG	304	14
TCAAGTGATTTAGGAATATC	37684	AGG	97	24
TGAATATCATACAAGGTTTG	25785	TGG	226	45
ATAGATAGTTTTTTATTGTC	5315	CGG	223	22
AACTGCCATTGTGATGAGGA	2564	GGG	313	124
TTGTTCAAATTTGTGTCTCA	24845	AGG	920	102
CCGAAAAAATCTCATACATG	35645	GGG	23	4
TGCCTTGTTCTTTTTTATAA	39365	GGG	34	1
CAACAGACTTTTGCAGAAGC	28367	GGG	1128	288
AACCAATGCTCGGGATGGTC	15530	AGG	914	194
TTTAATCATGAAAGACATTA	19621	TGG	161	1
AAAAAGCGCATCTCAACCGA	37312	CGG	541	165
TCCAAAGCCCCTTGTAATAA	23060	CGG	449	113
GTATTGTTGTACCACTCATA	29337	GGG	841	5
CTTTTTGGCAGTAAATTTGA	7567	GGG	3	3
ACTAAAAATTGATGTGCAGA	31426	CGG	132	41
ACAACATTAAAAATTAATGA	22794	CGG	38	1
CAGTGCCTTGTAATATGATT	29157	AGG	232	48

GCATTCCTCGCTAGTTTAGA	14879	TGG	159	44
AAAACCAACGTTTAATGATT	4198	GGG	113	16
AGAAACATTCTCTAAAACTT	6733	GGG	24	3
AAGTCACGTTGTAGTGGAAC	15498	TGG	1389	267
GCGAATGTAGTTGACTCAGA	33175	CGG	342	87
TTAAATCAAGTGGGTGTGTT	18412	GGG	83	1
TATAAATAATTTTCGTTCTA	30111	GGG	57	33
TGATTGGTTACACGGTTATT	29200	GGG	89	15
TGTGGATTCTCGGTTTGATA	34169	GGG	150	30
CTACCATACTTTGAAAGTGT	27250	CGG	263	55
CAGTCTTGTCGGTTACAAAG	20547	AGG	255	47
ACCTAGATTACATTTGTTTA	36406	TGG	171	35
CATTAAAACTTTTTATGTGT	33761	GGG	336	36
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TCCTAATGAACATAAATCAA	32994	CGG	75	3
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GCAAAAGCAGTCAAAGCTAA	8092	AGG	23	4
ATATAAATAATTTTCGTTCT	30112	AGG	41	8
AGCAGTATTTTTCATAGAGG	21694	TGG	118	35
ATGCTTTTAGTTCTTTAGAT	28776	GGG	110	17
AGTGCTAACAATTCATGTTC	23296	AGG	121	31
GTAGCTCCTGCACAAGATGT	14490	AGG	105	44
AGGGATAAATATAAATAAAG	36215	AGG	64	6
TGACGTTAATCTGGAAAGAT	10686	GGG	143	32
GACGGCTAATGATGATGTAG	13736	AGG	247	39
GGCAGAGCAATGTCACAAGC	18258	TGG	413	93
AACGTTGCCGAAACCACAAG	13943	GGG	29	9
GCATTCTCTGTCGCAGGTCT	24416	TGG	264	85
GCCAACCCTAACTACTTACA	30662	AGG	211	54
TTTAATTCTGACGAGTTTAA	17285	CGG	350	58
GAGTTTATTCGAGGGAAAGG	31498	TGG	84	17
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TCATACTTAATTGAATTGTC	27063	TGG	413	9
AATCTATCAACTAAGGATGT	19287	TGG	232	24
ACAAGTGCTAATTAACCTGA	17521	AGG	639	114
ACTAGATGCTTTCACTAAAA	29968	AGG	145	10
CTAAAGCTACTGTCGAAGCT	23937	TGG	52	13
GTTGTCTCAAATGTAGGTGA	26264	CGG	252	19
CGATAATTTGAGCGACTGCT	25275	GGG	481	34
TTATGTTAGCGACAGGCGAA	38300	AGG	381	72
AATTTTATTAAAAAGTCTAC	27736	AGG	210	29
CCAGCTACCAAACCACCTAT	39267	AGG	136	22

TTATCCAGTGTTATAAGTGT	21489	CGG	356	12
TTATTTCAACAAATGAATGG	6473	TGG	202	86
ACCGAATATGGCCAAAAGCG	23165	AGG	107	31
CGCACGATATAGAAGTAATA	26777	AGG	124	24
GCAGCTTCAAACCACTCTTT	22556	CGG	233	44
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ACCTTGTAAGTAGTTAGGGT	30647	TGG	576	56
TCAACTCGCATGATTATTTT	9209	TGG	166	30
TTGAACAAAGGTTATATAGT	12992	TGG	107	17
CTTTTTAATAAAATTGGCAT	27712	AGG	212	44
CGGATTAGTACCTGCAATAA	24340	TGG	126	13
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TAAAGACGATAGAGAGAGAA	16363	TGG	116	25
AGGCACAGGGCGATGAAAAT	8521	AGG	33	6
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GCGATTCATGGTAAGCCTAT	39268	AGG	217	69
ATGCACTTTTCGGACTGTTA	18887	GGG	649	212
TAAAGTAGTGCTACTTGTTT	33214	TGG	358	76
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GCACCAGCAAGTATATATTG	15236	AGG	100	2
CACTAAGTCGTTATATCCTA	28601	TGG	176	4
CGTATTGATAATACAGGTTA	29903	TGG	180	3
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AGAGGGAGAGTCGCTCGTAC	23125	TGG	1109	138
TTTTTGGCAGTAAATTTGAG	7568	GGG	6	2
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TAAGTTTATTGATGATTGGG	15926	TGG	624	33
CGTAACTATTCTGATATAGA	26890	GGG	327	20
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CCTACTATTATGCAGTTAAT	25154	CGG	95	2
ACAATAACAGAAGCTTGGAA	25592	CGG	115	14
GTAAAGAAACTTATTTACGA	37444	AGG	191	14
CACAAATGATTTAGGGTAGG	38158	TGG	119	29
TAACTAGCCACTGTGTATAT	13350	AGG	459	99
CATGTTATTTGGCGTTCAAG	15362	TGG	259	78
AAAGTAAAAGTTAAGACGAT	13564	TGG	190	29
TAGTAAACCTGTCTATATCA	22045	GGG	521	35
TAAGAATTATCTTAAGACGT	14304	GGG	712	79
TTAAGAAACTCTTTTGATAA	19804	CGG	85	12
GAGTGGGCAAAGTCGAATAT	34433	TGG	33	1
AATCGAACGCTTTCAATGTT	26027	TGG	47	16
GCTACAAGCATAATTTTTTT	38703	AGG	27	9
CCAGCAAAGTATTCTTTGAT	15791	AGG	466	105
TCGTTTGTAGGCAATCTATC	27306	AGG	675	65
AGAGGATAGCTCTTTATTAA	26522	AGG	52	9

ATACGTGGTATGACATCGTT	15423	TGG	499	74
TATTTTTGAGTAATCGTGTA	23240	AGG	352	54
TTAATTAAGTTATCGATATC	9098	CGG	232	47
GATTTTAGGATATAGCTTCT	34271	GGG	153	12
CAGGCGCCCAAGCTATTTAT	18435	TGG	116	1
AAAGGAACGCTCGACGGACA	35813	AGG	95	10
CTTTTAATAGGGGTAACTAT	30821	TGG	284	5
AGAGTTATTACAAATACAAA	11907	AGG	70	25
GTATTACGAAAGCGTGGACG	8888	AGG	38	12
TAACTTTATTTTAGAGGAGA	10294	TGG	51	4
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TCAGTTGTATGAAAATATAA	12618	GGG	124	18
GGACGCAAAGCGCTTTTAAT	30809	AGG	187	20
AAAGGCGAACCGGGACAACC	36791	TGG	202	13
TGAATAAACCTACTATGATT	25845	TGG	228	28
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AACATCTCAAGAAGGGAAAT	38035	GGG	105	6
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GCCGTTATTACAAGGGGCTT	23075	TGG	148	12
CTCCGCCACCATACTTTGAC	38426	GGG	631	183
TTCCCGTTAGCATCAAATAA	20128	TGG	153	17
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CTTAATTTAGGCAAGTATCA	35753	AGG	29	11
TATAAACAAATCGGCTTAAA	36179	AGG	112	11
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TAACCGACACTTTCAAAGTA	27237	TGG	397	52
CTAGCCAATTAGGGTGACGC	35163	GGG	310	61
ACCGTTGATTTATGTTCATT	32979	AGG	84	41
TGAAGCATTTCAAAGAAAAT	1938	AGG	1	1
ATACGCACTAGCACTTATAA	11646	CGG	132	64
ATAATTTTGTAATATTCTTA	31242	GGG	76	18
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GGGAGAAAAGGAGCAATGCC	22899	AGG	260	36
CGTTTGCTAAAAATAAAGGT	36003	TGG	11	4
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GAACGGGTTAACTCCTGGAA	9514	TGG	75	16
CGACTAAAGGAGGCAACCAA	29611	TGG	321	24
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GAATTTAAAGTCAAGAAGTA	20837	TGG	229	33
CGATTCTATCGTTATTCATC	34592	TGG	121	41
CTATTTTAGGGTTAGCTTCT	28551	GGG	80	28
TACCTTGTGTTACGCGGTAT	17096	GGG	298	100

TGTAGGCGATTCTGTAGATC	21229	AGG	1336	435
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AACAATTTATTTGAGTATGA	21191	GGG	118	14
GTTTTTCGTCTGATGGAGTA	35535	GGG	392	4
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AGAAAGGATTACATCAATAA	36068	AGG	67	12
GAGCGTAATAAACGTGCAGA	22419	CGG	169	41
AAAAGCTGAAGAAAATAACG	5075	GGG	79	12
CTGATGTTTGTGTCAATAAT	31578	TGG	115	24
AAAGCGTAAAGGGTACAACT	17428	TGG	194	1
TCATTTAGATGGGGAATCAG	18374	TGG	463	29
GCAACATGGTTTGGAATACG	10259	AGG	52	18
CTTCCTTAGATATGACTGTG	11288	AGG	65	1
AAAAGGTGTAGGCGCCTACT	19717	GGG	286	11
TTATTGAAGGCGCATCAAAA	6761	GGG	81	17
ACAGTTATTAAATAACTATT	39690	TGG	42	6
TTATCTAGATTGAAGCCCAA	30182	CGG	437	88
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GGCGTTGCGCAACCTGGTTG	38551	GGG	50	14
TCATAAGTGATACCTTGCAT	30583	AGG	160	27
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GTGAATGATAGTGCGACAAA	32062	AGG	530	105
GGACATGAAGTTGCATTATA	38848	CGG	231	5
CCTAACAACAAAGAGATGAT	16985	AGG	247	52
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TGCAAGAGGTGGCGCAACAA	29080	TGG	187	37
AAGTAAACTATCGGGTGTAG	16067	AGG	200	13
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CTACCTGTATTACGAAAGCG	8894	TGG	1	1
GTGTCTGTTGATGACGTTAA	19024	AGG	106	19
TACTACACCTTGAATCGCAC	25616	CGG	1170	122
AAGCCTGTAACACTTACATA	34774	AGG	78	15
GCAGTCATTGGTGTATTCAT	25526	TGG	58	3
AGTTGTTGGCTTTGGTGCAA	24439	TGG	257	31
AAACTTACCAATAAGATCAT	4908	TGG	273	47
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ATTTGCCACATTTTAGTGTC	36871	AGG	385	149
GCAAGTATATATTATGATGA	13718	CGG	186	48
AACTATCGCTTGTTAGATGA	29699	AGG	687	194
ACAAAGCGTTCTTGTATAAT	21028	TGG	49	11
AATGGCAGTTGTGACGTGGA	2593	AGG	26	10
GAGCTTTCCTTACGTTGCTT	23643	TGG	166	22
TTAGCAAATAGTTGTTCTAT	17735	TGG	591	170

TTTGCCGATTAATTCCGCTC	26324	CGG	457	15
ATCTATTAGTTTACATAGAA	22678	TGG	105	24
CTTATATTGGGTTAAATCAC	38946	AGG	397	35
GCGTGTTTGATAACCTTTTT	36487	AGG	250	1
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GAAATGTACGAGATGGAAGG	10559	AGG	32	11
GACTACTTTGTGCGCAGCAT	26363	TGG	511	116
TGATGAGGAACTTCGCGGAA	33575	TGG	586	204
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AGATCGAGTCAAGGAGGTTT	12421	TGG	36	4
TGAATCATCACATTTATTGG	11327	AGG	164	20
TTTATAGCGTTGACCAAAAC	34719	TGG	81	2
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GGTAGAATCTTTAGTATTGT	21212	AGG	181	1
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TTAACAAACTAGTTGATGAT	21790	AGG	84	21
CACAAATTATATTTTAGATA	27700	AGG	68	19
GTCAAGCGCCACAGCCATTT	21637	TGG	106	2
TAGTAGCCATTAATGCCGAA	20016	AGG	757	40
TCCATAAACAAATGTAATCT	36391	AGG	93	10
GGCTATTAGCGCTCTTAAAA	24460	TGG	195	50
AGCTGGACTTGATAGCGCAA	18275	TGG	316	83
TCTAGTAATTTACTAGCTAT	25204	AGG	74	33
TAATACACTTTACTTAATTA	37390	AGG	63	9
GGTATGTGGGTGTCTGGTGA	15720	CGG	1661	106
CAGCGACGAAAAGAAAATCA	8732	TGG	15	1
TTAACAATTGGTAATGTGCC	22329	TGG	145	37
AATGCCGGAGCGGAATTAAT	26336	CGG	107	18
CTGAATAGGAGGAGATATGA	20445	TGG	102	24
GACGAAAGTTATTGGGATTA	7648	GGG	56	12
TCAAGTTGTCTATAAATATG	11840	AGG	64	5
GTTTACATTCAATGACAGGT	29652	CGG	147	1
TCTGATATAGAGGGTATTGA	26899	TGG	486	167
GGTTTACCATCATACAAGGA	40368	TGG	92	46
TAAACTTTTGAAATCTAAAA	725	TGG	21	1
GCTACTAAAATCCGAACTTT	24248	CGG	16	2
AATTTAGGTTCAAGTGATTT	37675	AGG	43	3
TTCTTTATGATAATATGGAT	16126	AGG	140	37
TTGCCTTGTTCTTTTTTATA	39366	AGG	42	8
TTTAGAACGATAAAAGAAAG	6907	TGG	67	5
ACCAATGCTCGGGATGGTCA	15529	GGG	160	25
AACGGTAAAGGTTGGACTAA	38530	TGG	171	34

ACCTCGTGACCTTTTTCGTT	29533	AGG	36	7
TATGCAATATACGTTGAATA	21519	CGG	260	100
TCTATCAATAAATTGTCCGT	30182	TGG	233	2
CTATCAATAAATTGTCCGTT	30181	GGG	112	25
ATAACAATTGCTTGTTGGTC	12249	GGG	457	10
ACAAGGTATTATGAGTGGAG	18152	AGG	307	70
GGTACTGGTATATATGCTAC	21540	TGG	26	10
TTAGTTAGAAACTTTGGTAC	31460	TGG	494	124
CTCAACCGACGGTTAAAATT	37323	TGG	29	14
AAGTTATGAGGGTTATTTAT	32862	CGG	102	25
GTTAGCACTAATGGGTGATT	20227	GGG	459	139
AAGAGTCAGTGCTTCGGCAC	34328	TGG	131	29
GGTCAAAACTGGAACGGTAA	38518	AGG	24	13
ACAGTTTCAGGACCCCAACC	38547	AGG	487	125
GCTTTACTAAGAACTATTTT	34216	TGG	45	5
TCTATTGTGTTAATAGGACG	15858	AGG	96	9
TGAAGCAGTAGGGATTATGA	11816	CGG	104	8
ATATCGCTGAGAAAAATAAA	3882	AGG	19	4
ATCTTCGCGCAACAGGTCAA	24275	AGG	71	11
CTAATTTTGTTAGCAGTATT	26082	TGG	84	1
CCACACTATTAGCCCAATTT	24876	TGG	87	38
GAAATCAACAGAATTATTGA	1024	CGG	41	6
ATTGACGCTTTGCAAGAAGT	16919	TGG	284	29
AATTTCTGTCCGCAAAACGC	31220	CGG	1242	33
GGATTTAACTAGAATAACTG	25432	GGG	46	7
CATATCGCCTATATACACAG	13359	TGG	125	24
ACAGCAATAGAGTACGTACA	7990	AGG	83	16
TATTCGACTAAAGGTAAGAG	14663	TGG	20	8
AAAGACTTTAAAGGTATTGC	31352	AGG	427	31
GAAACTCATAGATGAGGCAC	8507	AGG	356	36
ACTGGATAGACAAATGTCTA	35617	GGG	37	10
TTTCTTTTCGTCGCTGAAAT	8709	GGG	2	1
AGCCCAATTTTGGAAAGCTA	24866	TGG	108	9
AGTTAGTACAGAAGATTTTG	37174	AGG	9	1
TAGCTCCTGCACAAGATGTA	14491	GGG	68	18
TTAGGTAAAACATCAGGTTC	33280	TGG	355	131
CGTATTGTTGTACCACTCAT	29338	AGG	142	27
AAAGTAATTGCTACAGACTT	26510	TGG	88	18
AGCTTTTAGGAAAGCGAGCA	29512	TGG	127	37
AGGCCTTTGAAGAATATGAG	14796	TGG	123	17
AGCGTTGGCAATAAAGCTAA	38653	AGG	161	62
ATTATCGGGGCAGTCAATGT	34476	TGG	175	29
GAGGCCATGTATCTGACTGT	40047	TGG	73	14
ATAAGTGCTAGTGCGTATAA	11667	CGG	140	29
CAATATTAGAAAATAAAGTG	19509	AGG	51	14

TAGCTTAGGTAAAGGTTTAG	26476	CGG	177	26
CCCTGGCAACGGAATAGGTT	34651	CGG	51	1
GGTACTAATCCGGCAATCAC	24313	TGG	621	81
AGATAGTTTAAAAAAAGCAA	28477	TGG	189	16
CTTGCTCTTTTGGTTCGAAT	30024	CGG	46	18
AAAACGACTAATCTTGCAAG	29066	AGG	201	55
ACTGCATACGGTGTTAATGT	38905	AGG	765	145
ATTATGAGAAAAGAAGTAAA	24158	TGG	18	1
CAACTGCCATTGTGATGAGG	2565	AGG	140	36
AGTGGTATAGGAGCTATACG	15408	TGG	302	17
GACGGTGCATATTGTATTAA	39505	TGG	99	35
TTTTTAATTTAACACAAAGT	33916	AGG	65	7
TCAACTTTAGTAATCCTTCA	37736	GGG	146	17
AACCTGGAGACATCGCAGTT	34626	TGG	73	10
AGTTCGGATTTTAGTAGCTA	24227	AGG	250	65
GGAAAAACGGAAAACCGAAA	7246	AGG	3	3
TTGAAACTGGTGGAAATGTA	16467	AGG	89	4
GCCAGGCAATGTTATTTTAT	19561	CGG	13	6
ATACCTTGTGTTACGCGGTA	17095	TGG	124	1
AAAGAATGGTCATGAGGATA	9990	TGG	96	27
CCTAAGATTGGTCAGATATT	24965	TGG	94	1
TAACTTTATCCACATAAAGG	6707	TGG	41	12
CTTTAACCGCCATTTTAGCG	23979	GGG	36	14
ATTATTTCAGTGTACTTTTT	13049	CGG	13	3
AGGCTTACCATGAATCGCAC	39247	CGG	6156	1340
ACAATGGCAACAGTTCCAAT	29096	AGG	105	26
TTTCAATATCAACTATGAAG	10482	GGG	259	100
GCGATGTCAGCAGGTATCAG	24599	AGG	212	2
TGCATTACTGCATTTGTATA	30073	TGG	163	27
CGGTGCTAGCTTCGTAAGAA	36052	AGG	2	2
ATCTTTGCTTTATTATCAAA	38334	CGG	69	10
TGGAGTGTGGCTGAAAAAAT	26138	GGG	60	9
ACAGTTGAATACGAAAAATT	22605	CGG	15	2
CAAAGTCGAATATTGGTAAG	34440	AGG	416	34
ATACTGCTTGACTATCGATA	22021	CGG	103	11
GCTTCAATTCCTTTATCTCC	22331	AGG	427	67
AGGCTCAATAAAATGTTGAA	5832	AGG	92	29
AAAACTTGGGAACTTGTCTT	6720	TGG	448	156
TGGTTACACGGTTATTGGGC	29204	AGG	214	17
TCCGAAAATGGCATTTCGGT	7173	TGG	95	17
ACTAATTTCACAGAAATGTT	29027	AGG	42	2
GCAACAATGAGAGAAACAGT	21894	CGG	311	25
AAAACGGATTATCGGCAAAC	7211	GGG	142	12
AAACATCCAGTGACATGCTT	39870	GGG	448	161
ATATATGCTACTGGTCCTGG	21549	TGG	264	16

GCGAGTACGTTTGACGCAAT	27845	AGG	75	11
AGTCACAGGTGTAATGCTTG	33892	AGG	51	2
CCTTGCAATATTAATGATTT	8013	TGG	23	4
ACCGTTAAAGAATGGTCATG	9984	AGG	41	4
AACCGCAACTGTGTAATATG	5622	CGG	52	10
CGTGTACGTTAGAGAATGAC	40347	CGG	623	166
GTGTCGTACACTTATAACGA	20865	TGG	65	17
GGAATATCAGGAGTCAATAG	37696	CGG	27	2
ATCGGTGTTATCGGTATTTT	25310	AGG	177	25
ATCAATATCGCAAATGTTGA	36959	AGG	344	35
TTCTGGGCGTGCTTCTGGTT	34287	TGG	48	7
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AATATTGCCTAAGCATATTG	16324	AGG	136	25
AATGAATTGATAAAAAAGAA	9497	CGG	20	5
GCAACAACATAAGATGACAG	32727	AGG	241	82
TCAACTAGTTTGTTAATGTT	21767	AGG	42	1
GTTGTAGCTTTTCTAGCTTT	1646	AGG	74	15
GGCTTGAGAGAGCAAATAAA	13999	AGG	25	8
TCTCTATCGACATATAAATG	35104	CGG	28	6
AGAGAACTTGTATTGAACAA	12980	AGG	40	21
AGAAGTAAAAGATTATCTAA	18990	AGG	25	4
AAAATCTCATACATGGGGCT	35650	GGG	124	21
TATTTTAGGTGGCGTATTTT	25324	GGG	172	16
AACCGGTTTTATATCCAGGC	27632	TGG	448	56
GTCCGCAAAACGCCGGTTAT	31227	TGG	46	21
CAGTCGTGTTGCTTGGAGTG	26125	TGG	129	45
CAAGGTATCACTTATGATGC	30605	AGG	144	6
TTACTGCCAAAAAGTGTTTC	7542	TGG	36	3
GACTTTTCATCTTTTGCCTC	33857	TGG	116	9
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ACTAGCCAATTAGGGTGACG	35164	CGG	64	17
TTATCCACGAGTCATGCAAG	5782	TGG	217	32
AACTGATTAAACTGTGTTAA	27399	AGG	57	16
TTTGAAGCATTGAATAGCAT	24740	AGG	263	75
AAGCTCATTTTAAGCGCGAT	21963	AGG	1915	310
TCAATATCGCAAATGTTGAA	36960	GGG	133	25
AAAAGGTATCTACTTCACAA	36196	GGG	295	34
ACTTTAAAGGTATTGCAGGT	31356	TGG	396	68
GTTGGTGGTACTATGATTTT	2793	TGG	86	22
TCACACTTATTGAGGAGCAT	12817	GGG	52	7
TGAACTATATAGCCGGGCAG	40028	AGG	14	4
AAAAGATTATGGCTTATATT	38934	GGG	50	13
GATAGATTGCCTACAAACGA	27325	AGG	188	25
AACGATAAAAACGAAGTTAT	33366	CGG	140	5
ACAGCAAAATGGACAATAAA	37579	TGG	34	2

ATAGGGGTAACTATTGGACC	30827	TGG	118	15
TTCGCGAGTAAAGTAGCTGA	26231	TGG	2	1
GACTATTACTGTTACAAAGA	20508	AGG	197	47
TCCTCGCTTTTGGCCATATT	23150	CGG	79	25
TCACTTACTACCTGCCTATA	14405	TGG	85	25
ATTGAAATGAGGTGCATACA	34363	TGG	233	19
GTGCCTATATCCGTCTTTTC	32388	TGG	1103	175
TATGCACTTTTCGGACTGTT	18886	AGG	87	25
GATGATGAGGATTCTGAAAT	16664	AGG	32	2
CTGTAGGCTTTCTAGTCTTT	34380	GGG	54	15
AGGAGACTTCCAAGAAGCTG	30757	AGG	24	4
TGTTTACCCATATATTGTTG	21839	TGG	310	112
GTTGGCGCATTCTCTGTCGC	24410	AGG	83	20
AGTCGTTTAAAATTATTCAA	37792	TGG	2	1
ATACTCCACTAATGTAATCA	20875	GGG	71	1
TATTGGGGTTTTGTAACATG	34526	GGG	64	7
TATCTGACTGTTGGTCCCAC	40056	AGG	326	99
CAATGAATGTTAAGCGAATA	35703	TGG	128	4
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ACGACTAATCTTGCAAGAGG	29069	TGG	178	36
ATACAAGCTAGGTTAAAAGT	13537	AGG	17	4
TAAAGTGAGGTAATAAAATA	19522	TGG	3	1
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TTTGAGCTTGATTATGTTGA	27136	TGG	393	46
AGGAAAGCGAGCATGGAGGA	29519	CGG	484	135
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ATTGAAAATGATTTAGTTAG	31918	TGG	144	8
ATCACCATAACCTTTAATAA	28319	AGG	610	46
AACTTCGCTAATGGTAGATA	35924	CGG	88	17
ACGATAGTAGACGCAATTAA	31774	TGG	14	6
TAAAAAGTCTACAGGGTGTA	27744	GGG	40	9
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AGAGAATTACAAGGAAATCA	23225	TGG	53	9
TACGGATATCACTGTTCCTA	25817	TGG	86	23
ATAAGAAAAACAACGGAGCA	31197	TGG	78	16
GATAATTTTGTAATATTCTT	31243	AGG	14	4
GGTTAAACCTCTAATTGCAG	19870	AGG	976	162
TGTAACATGGGGCAATGCTA	34537	AGG	70	15
AACTTTGGTACTGGTGGCGT	31469	TGG	142	9
TTTGTGCTAGGACTCATAGA	14606	GGG	13	3
CTACGTTCAATAAATGTGAA	14455	AGG	41	13
GGTTTTTCGTCTGATGGAGT	35536	AGG	76	12
ACTGGGTTAATTCTAATAGT	34737	TGG	145	16
AAAATCGGAAGGTTTCCGGA	14721	AGG	58	2
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ATCAACGGTATGTGGGTGTC	15714	TGG	83	1
AAAGAAGATTTTGAAACTGG	16457	TGG	45	19
GTATCTGAAGTGTATTCCAT	30556	AGG	63	5
TCGAAACCTTGTAAGTAGTT	30652	AGG	48	28
TGCGCACAAAGTAGTCAGCG	26386	CGG	18	6
TGTTTTGTTAGTTTTCAGTT	33669	CGG	159	43
AAACTACCCACCATATAGGC	14399	AGG	305	39
CATAAGATGACAGAGGCGAA	32734	TGG	171	63
GGAGACCTAATCATATTACA	29168	AGG	52	11
GTAATATCACTTAGATATGC	30961	TGG	243	73
GATTGGTTAACTCAATTGTG	25655	GGG	33	8
TGATGGAGTAGGGCCTCGTG	35525	TGG	45	4
ATAAAAATGAGCAAATTAAG	33790	TGG	107	24
TGGGTGTGCTTCGAATAGTT	25256	TGG	86	1
CCCGCTATCGTCGAATATTA	8589	AGG	64	27
GCTTAGTACAAGCTTCTAAG	23427	AGG	173	59
ATACTCAAAGTAATCATTTT	11235	CGG	23	7
GACTGGGGTTACGAGCACTA	15834	TGG	56	11
TCGAGCAGTATTTTTCATAG	21691	AGG	36	4
GAAAAATTCGGCGAAAAAGT	22617	CGG	5	3
TTGTTAGGTACACCAAACAA	16954	TGG	123	38
TTTATAAAAAAATTGAAAAG	22742	AGG	19	1
ATGCCTATATTACAAGTATT	25706	AGG	28	4
ATGCAGTAATGCAATCATTT	30099	TGG	40	3
ACAAGGAAGATGTCTCCTGT	40055	GGG	216	19
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ATTGAACAAAGCACCGAATA	23153	TGG	19	4
TTATTAAATAACTATTTGGA	39694	TGG	161	47
ACCCTGACCATCCCGAGCAT	15544	TGG	203	20
CGTTAGCACTAATGGGTGAT	20226	TGG	30	4
TTACTACCTGCCTATATGGT	14409	GGG	49	4
AGTTTCTATGAATCAGATAG	31615	AGG	75	9
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TTTGTAACAACTGATATTAA	21	AGG	141	11
TCTCAGAAGATAGCGAAGAT	22879	GGG	36	1
CAAACTAGGGTTAACACTTG	29398	AGG	47	2
TGGAGTTTTAAAGGTGATGA	21594	CGG	99	21
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GGAACAGCAGACGCAGGAAA	12379	AGG	54	12
TGGGTAATAGACATCAAAAA	6015	AGG	15	1
CCTGGTGCAAAAGGTGAAGC	36809	AGG	91	22
GACGCGCGTATTGATAATAC	29897	AGG	516	141
CAAAAAGTGTTTCTGGTCTA	7535	AGG	37	9
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TTAGCTATTGGTAAGTCGTA	21151	AGG	55	1
AAAGATATTGTAAGTAGATA	15957	TGG	87	6
ACTGCGATGTCTCCAGGTTC	34606	CGG	55	11
ATCATTCTGATTGGTTATTT	17670	TGG	25	2
ATTACACAAGGTATTATGAG	18147	TGG	32	1
TTGATGACCTTAACAATTCT	28002	AGG	107	13
ATTATTGAAGGCGCATCAAA	6762	AGG	22	2
GTCAGTTGTATGAAAATATA	12617	AGG	11	2
AATGGCGCTGACCTTGTTAA	32239	AGG	133	34
AAACAAAACGGTATAAACAT	2288	CGG	8	2
ATCGGATTCGTTAATACTGG	33384	CGG	118	4
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TTGAACTTGATGAAGCAGTA	11806	GGG	135	5
TCATTTTATGGCAAAGATTA	23620	TGG	46	21
TGATTTCTTAAATGCCGGAG	26326	CGG	32	8
TAAAGTTACATTACAGCCCC	6035	TGG	163	45
ACTGTTCTATGAAAGTTGCA	5488	AGG	21	2
ATTGACTTTAAATATTTCGA	21462	TGG	54	12
CAACGTCGTTATATAGCGAC	39562	AGG	67	1
GATGAGCTTATTGGGGATAT	11447	AGG	60	4
AAAGGTGATAAAGGCGAACC	36782	GGG	147	15
AGTAGATTTAAAGGTGCGAA	36764	AGG	3	1
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AGGTAGCGTTGAAAGTTATG	32850	AGG	103	20
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GCAAGCGACTACAAAAAAAG	38685	AGG	68	9
GACGGTGGCGCAAATGGTGT	33025	AGG	85	26
AGCCATACAATCCAGCTTTT	29499	AGG	57	10
TCGCCTCTATATGTGTTTTC	2817	TGG	2861	648
ATACTTTGCTGGTGTCGACT	15818	GGG	210	25
GAAAGATTACGGCGAGAAAA	24217	TGG	8	4
TTTAAATTCTTTTTAACTTC	20807	AGG	386	85
AGGCATTCTTTACACAAAAC	31856	GGG	89	7
GCAAACGTCATTGCATAATC	35971	AGG	114	54
GTAGTTGACTCAGACGGCAA	33181	CGG	177	38
GTAGCTGTCCAAATCATAGT	25853	AGG	50	10
AAACGACGTATCGATATTGG	30716	CGG	97	37
ATTACAGTTTTTACGACTAA	29598	AGG	114	17
GACTTGAATCGATTCCAGCC	27630	TGG	146	40
TTATCGGGGCAGTCAATGTT	34477	GGG	25	13
TCCGCTCCAGTATAAGATAG	20167	TGG	85	7
TTGCGATAGCGTATGCTAGG	8057	TGG	21	7
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ATATTTAAGATGGAAGTTGA	20685	CGG	72	10

GGTGTCATTACTTCTTTAAT	38104	AGG	17	1
CCACTAGTTGAAGTGTTGTA	19924	AGG	179	48
AATCTGGAAAGATGGGGAGT	10693	TGG	54	10
CGGATATTTATTTTTAGGTA	37522	AGG	1	1
GATAATCCGTTTTCCGAAAA	7185	TGG	59	2
TTCCGCATATTACACAGTTG	5608	CGG	25	4
TCCTTAATATTCGACGATAG	8574	CGG	83	22
CAAGTGCTAATTAACCTGAA	17522	GGG	246	25
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AATAGGTGATGTTGTTAGAG	28585	TGG	257	6
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GAGCCTTTATTTATATGAAA	17984	TGG	60	12
GTACTTACCAGAAACAGCAC	31133	AGG	146	53
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GAATATACAAAAGTATATGC	37471	TGG	877	70
AATCAATTCTTAGCGAATAA	37925	AGG	33	3
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TGAGACACAAATTTGAACAA	24826	CGG	69	1
TGGCACCCTGGCAACGGAAT	34646	AGG	26	9
TTAAATACTTTCACATCATT	38497	TGG	84	10
CTTAATGCGGTTGGTGTATT	24368	AGG	23	5
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AGCTAGTGAAGTGGTGGAGT	34417	GGG	89	20
ATTCTAGGCCATAACGGCGA	29858	CGG	151	21
TACTTTGCTGGTGTCGACTG	15819	GGG	5	3
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CCAAAATTGGGCTAATAGTG	24892	TGG	93	3
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GCGCTTAACAAAATACTTAA	35789	AGG	69	39
TCTGTAACTTCATTCGTAAG	26438	TGG	13	5
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TCTATCTACGTTATAATCAT	31711	CGG	24	6
AGACAAAGTATTGTATCAAA	30544	TGG	62	30
ATTATGCTTGTAGCCGGTCA	38728	TGG	89	27
AAGATAACTTGCCGAAAGAG	22561	TGG	114	42
CAAAAGGTGTAGGCGCCTAC	19716	TGG	412	50
TGGTAACTTTTATTTTATTG	15887	AGG	20	4
AGGATCGTTATAACCATGAC	38725	CGG	262	33

TTCTTAGAGTTATTGAAGAA	14094	AGG	12	1
GAATTCGTTGAACTTTGTTG	30490	AGG	37	4
AAACGAAGGAGTGTATTAAA	22130	TGG	93	13
TGGCGACTTCTCAGGTGCTT	25906	GGG	71	7
GGATTCAATGTTATATTTAA	22920	CGG	88	36
CTCTAAACGCTTTCGGTAAC	31038	GGG	17	1
GTATAACCTGCTGGCACTGG	39324	TGG	47	5
AGCGTCGTTAGCGCATGAAG	15461	AGG	88	19
AAGGAAGTTGATTTAAAAGC	27532	CGG	110	9
AGAAGTAAAATCGAATACAC	31384	CGG	76	18
GCTCAAATTATCGGTGTTAT	25301	CGG	71	14
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ACATGTCTTGTCACAGTTTC	38559	AGG	80	20
TTGAATCGCGTTAGGTAATG	33127	CGG	16	5
TATTATGTACGAGTTAATCA	29572	AGG	248	82
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TGCGCTTAAAACGCTATCTA	32320	TGG	26	3
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TCTATGCTTGCAGTTTGGAA	10848	CGG	103	7
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GTTGACAGTGCGTCCACACG	35528	AGG	55	23
TAACTTCTCAATTTAGAGCA	25068	TGG	120	31
GATAGATTGCTTGTTAAAAA	30215	CGG	24	8
CAAGGCGCACCCGGTAAAAA	36845	CGG	41	3
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AAACCAACGTTTAATGATTG	4199	GGG	2	2
ATGTTCTTTATGTTAGCGAC	38293	AGG	216	60
ACCAGCTTTAATGTAATAAT	28247	TGG	50	23
TTAGCTGACATGTTGGCGTT	12076	TGG	44	19
GTGCTAACAATTCATGTTCA	23295	GGG	55	16
GAAGTTTCAACTTATTATAA	26736	GGG	22	9
ATCAACTTTAGTAATCCTTC	37735	AGG	134	35
ACTGATGATGATTGGTTACA	29192	CGG	33	6
GGAGATAAAATAATCTTCGA	27553	CGG	11	4
ACTTCATTCGTAAGTGGACA	26444	CGG	96	7
TTACAACATCGTCGATAATA	36441	AGG	285	96

GGAAAGCATATATTGACGCA	14640	GGG	39	4
ATGACGTTTGCTAAAAATAA	35999	AGG	13	3
GGTGTCCCTGATTACATTAG	20886	TGG	20	10
ATCGCTATTGCGTTAGATTG	6828	GGG	13	6
TCGTAACTATTCTGATATAG	26889	AGG	47	20
ACAATAGTGGTTTTTTCAAG	23107	AGG	1	1
TCTGGATTTGTACCGGAACC	34610	TGG	69	21
AACAGATGCGCCAGAAAAGA	32394	CGG	3	1
GGCGATTTTTCTTCCTAGTT	482	CGG	64	29
GCTGTAGGCTTTCTAGTCTT	34381	TGG	34	9
ATAGCTTCTGGGCGTGCTTC	34282	TGG	175	29
AGGGGTCCAACTAGGTGTAA	11371	TGG	85	34
CAACACAAAGAAGTACATCA	13390	AGG	90	13
CCCATGTATGAGATTTTTTC	35628	GGG	89	4
ATTGAAGAATTTGATGATAA	4433	CGG	407	39
AGGGATATGTTCCCAATAAC	31223	CGG	66	11
TAGGTTATTAATTGAAATTT	6291	CGG	1	1
ACGAAAGTTATTGGGATTAG	7649	GGG	14	5
TGACACCAATTTCTTCAGAA	757	AGG	10	8
AGCAGTTTAACGACATGCTA	18841	AGG	40	10
TCAATTATCGGCTTTTTAAC	25997	TGG	259	49
AATGATGAAAGAGAATTACA	23216	AGG	18	1
AATTGGGCTAATAGTGTGGC	24896	TGG	103	47
AACGTAATATCAACGGTATG	15706	TGG	20	3
GAATGTAACGATTAGAAATG	26662	AGG	29	11
ATAGATGATATTGAAGCACA	16301	AGG	62	5
CACGGTGGAGGTAGTAGCTT	26462	AGG	60	6
GGATTTTAGGATATAGCTTC	34270	TGG	27	1
TATGAATCAGATAGAGGAAC	31621	TGG	135	12
TCTAATTGTTCTCGAGTTGG	22994	TGG	205	47
AGACATAAAAAGAAAAACGA	22116	AGG	19	8
TTTCAATGTTTGGTACAAGT	26037	TGG	77	3
AGATGCAAACCCCGCTAAAA	23986	TGG	10	5
ATCACACTTATTGAGGAGCA	12816	TGG	43	2
AAACTTGGGAACTTGTCTTT	6719	GGG	73	12
ATACACTTTACTTAATTAAG	37392	GGG	24	17
ATGAACGACACAAATGATTT	38150	AGG	1	1
GAATATAACGTTACAGGCGC	26860	AGG	314	105
GTAAGAATTATCTTAAGACG	14303	TGG	10	7
TTACAAGCATCAGATGCTTC	20318	TGG	365	24
CGAAACCTTGTAAGTAGTTA	30651	GGG	41	9
AGATTGGGGGTGAATAATTA	6814	TGG	9	2
GTAAGTGGAACTTATCCAGG	33097	TGG	6	5
GTACAAGTTGGTCACAGATA	26049	TGG	46	17
ATATACGTTGAATACGGTAC	21525	TGG	266	60

AGATTGGTTAACTCAATTGT	25654	GGG	153	19
TTATCGCTATTGCGTTAGAT	6830	TGG	35	7
AAAGATTTAATAAACGAATT	11543	TGG	18	4
GTACTGGTGGCGTTGGTAAA	31476	TGG	57	1
TGCGCCGACACTTATAACAC	21477	TGG	94	8
GCGCCAGAAAAGACGGATAT	32401	AGG	28	17
GTTAACACCTCTTTGGCCGA	30860	TGG	187	36
CGTGGTGTTTGGTTATTGTC	35273	AGG	140	48
TTACCTATCAATTGTGCTAA	28396	TGG	332	69
TAAGGCTTGATATCAAAGCT	27969	AGG	11	1
TCAGTCTGATTTGATGAGGG	13787	CGG	20	1
AACAAAATACTTAAAGGAAA	35795	AGG	13	3
GAAAGGTGATAAAGGCGAAC	36781	CGG	428	21
GCAGGAGAAAGCGCAAGTGG	39004	TGG	24	7
TTTAAATCAAGTGGGTGTGT	18411	TGG	108	16
TCAACGGTATTGTTCGACGG	33010	TGG	128	25
TACTATGATTTGGACAGCTA	25835	CGG	23	9
GGCGATTCTGTAGATCAGGG	21233	CGG	34	6
TTAGCATATATTGATACGAA	16721	TGG	62	3
GCATTTATATGTCGATAGAG	35122	AGG	131	8
ACCACTATCTTATACTGGAG	20182	CGG	91	17
AAATGTTATACCTTTATTAA	28325	AGG	122	4
CTCTACCTTATTGATTTAAA	20927	CGG	75	7
GGGATTACTAAAAGAGATTG	11702	AGG	17	4
AATGGTTACGAGTATAAAGA	7816	CGG	35	4
AATAATGCGCAAGGCGATTT	32779	GGG	15	5
AAATCAATCGCAACAGAGAT	14054	TGG	23	13
CCAAACGGCACGAACATGAA	33959	TGG	70	15
GCGATGCGATTTCATCAGCT	26412	TGG	16	3
TTATTCATCTGGATTTGTAC	34603	CGG	315	80
GGAGACTTCCAAGAAGCTGA	30758	GGG	50	11
CCGGGACAACCTGGTGCAAA	36800	AGG	243	14
CATACAAAAAGAAAATGAAA	12338	AGG	31	11
GCAGGTAAAAAAGGAGAACA	36827	AGG	12	6
GATAATTTCTTTATAGGGAA	7351	TGG	12	1
GCTGATAAAAGTAAACTATC	16059	GGG	238	26
GATAAATCAGTGATAAATTC	30049	CGG	216	50
TTTATGTTATAGCTAGCCTT	39803	CGG	8	1
AATGGTTGAAGATGGAACAT	24478	TGG	99	13
TAATAACCTAGTAAGGTTAG	6262	GGG	54	3
CGATGCGATTTCATCAGCTT	26413	GGG	9	2
ATGTACGTAGCGGTATAATG	37640	AGG	16	1
GCAATGGTTGCTAAAGATAA	18291	CGG	30	6
ACCGATAGGCACTGATAAAA	29230	CGG	17	11
CCGACGGTTAAAATTTGGAC	37328	AGG	296	51

ATGTCGATAGAGAGGCTACA	35130	TGG	41	1
CGAAGATAGTACCGAAAGTT	24243	CGG	24	1
GTACTGCCTGGACACTATAA	31097	TGG	18	9
AAACAATTTATTTGAGTATG	21190	AGG	2	1
TTGATATTGATTCCAGCAGA	24057	TGG	30	5
AAAACTGGAACGGTAAAGGT	38522	TGG	49	11
TTAGAGAAGCCTGGACAAGA	32428	TGG	65	11
AAAGCAAAGATTGAAAAATA	38362	TGG	42	9
GATACATTGATGGAGAATTA	30264	TGG	11	4
TTTTGTGCAAAGTACGAATG	10797	AGG	12	3
ACACGGACAAAAACAAACTA	29385	GGG	10	3
GTGCAATGTTTTTTAAGAAT	30882	TGG	64	10
CACCTGCTGAATGGCGTGAT	23337	TGG	19	1
TCAACTAATTCAAGAATTAC	39451	AGG	64	7
GGGAAACAATTCAACCCAGA	38236	TGG	184	24
CGGACTGTTAGGGTACGCGA	18897	AGG	21	2
ATCACTAGTATTTTTGAATC	29296	TGG	413	43
AGACATATTAGATCGAGTCA	12412	AGG	43	9
GCGACAGGCGAAAGGCTGCA	38308	AGG	24	1
TTAAGTTTCATTCCAATGAT	17299	AGG	17	1
TTGCAAGGTTCATACGGAAC	8044	TGG	68	24
CCTATAGGTGGTTTGGTAGC	39283	TGG	122	18
AATTCCGGTTCTTGCTCTTT	30034	TGG	25	12
GATATTGATGAGTATATCGA	17706	GGG	20	8
CTAGTATCTTTTGAATATGG	34804	AGG	61	9
GATCCTGGAGCAGTAGGAAA	38758	CGG	7	3
GTCTGATTTGATGAGGGCGG	13790	AGG	311	62
CATTTCTTTGTCCTCGCTTT	23160	TGG	75	11
GCAGGGTTCCAAAATGGCTG	21629	TGG	8	1
CATGCCATAAGGTGCGTTTA	9560	AGG	84	2
TGATTTCATCACTGAAAACG	23045	AGG	8	2
AATGTAACGATTAGAAATGA	26663	GGG	66	11
TTACTATGCAACAAGAGTGC	32820	CGG	133	1
ACATTAAAACTTTTTATGTG	33760	TGG	17	4
TACTTTGTTAACAAGTTTTT	2501	AGG	572	97
AATGCTTTTAGTTCTTTAGA	28777	TGG	37	7
GAATCAAGATTTTAGGTTGG	7467	AGG	5	2
GAAAAAGACATTTGATACAG	10214	CGG	13	12
ACAGGTCACAGTAAAGTAAG	15390	TGG	19	1
ATGTAAACTAATAGATCAAG	22701	GGG	11	5
TGGCGTGATTGGCTTATTGG	23348	TGG	14	1
TGATTGGCTTATTGGTGGTC	23353	AGG	49	1
GCCTACAGCTAGTGAAGTGG	34411	TGG	48	4
AGCATATCTAAGTGATATTA	30979	CGG	159	7
TATTATGTATTTCGAGGAGA	16895	AGG	84	7

TGGCTAGTTATTGAAGTATG	35195	TGG	7	2
GTTACTATAACTAAAATTAT	33319	GGG	20	5
AATGGCGCTTATTACTTTCA	10164	CGG	7	4
AAAGGTGCGAAAGGTGATAA	36773	AGG	81	45
ACCATGCTTAAAGGGATTTT	34257	AGG	16	1
CAATACTGTCTTTAAAGGAA	28069	CGG	64	17
ATAGGTATCAATGACAAACA	36353	AGG	40	22
GTATCAAATGGATATACCTA	30556	TGG	37	8
TAAATGGGCGCGAGAAAATC	10366	CGG	11	1
AAACTTTTACTCAAGAAAAA	20634	TGG	18	7
GATACTCATCGTCATTTAGA	18363	TGG	165	13
GGACCTAGAAGAGAAAATTG	6598	TGG	44	9
ACAGTTTTTACGACTAAAGG	29601	AGG	17	1
TCAATCCTGACACTAAAATG	36882	TGG	33	3
GTTTTAGGTGTTTTGGTAAT	25745	AGG	14	4
TGTGGTTTTGTTGGTTGTAG	40161	GGG	66	12
TACCTACAAGATACCTAAAA	36490	AGG	9	1
TTGGTATTCTTGTTTATTTA	25545	TGG	1	1
TCAGTTTGGGAGTCAATTAT	25985	CGG	6	1
GGACAAGATGGTGTTGATGA	32440	CGG	32	8
ATGTGGATTCTCGGTTTGAT	34168	AGG	76	1
GTCGCAGGTCTTGGAGTTGT	24425	TGG	157	23
TGGTAAATGGAGTTTATTCG	31489	AGG	22	6
GATATTGGGGTTTTGTAACA	34524	TGG	40	11
GGAGATTTATTGAACGCTGC	24776	AGG	210	50
GAAACTAAAAATTAATTAAA	4599	AGG	12	4
TTACTTGAGTTTTCCCCTTG	13940	TGG	8	2
AAAATTAAAACTATTTCAGG	12663	TGG	43	10
GCTCCGCCACCATACTTTGA	38427	CGG	35	18
TGATAGCATGGTTGTTGAAT	21320	TGG	32	1
GAATCAGTCATCGATACTTG	30904	AGG	123	35
TTGCTTACTGGCGACTTCTC	25898	AGG	58	1
ATAGGCACGTTAGAGAAGCC	32419	TGG	41	10
AATAGGATCTGTGGTTTTGT	40170	TGG	231	51
CAAGGTATTATGAGTGGAGA	18153	GGG	36	4
GATTATTTAACGTATTTAAA	29819	TGG	33	4
TCGATAAGAAAATAGAAGAG	21349	TGG	21	2
AACCTTTTTAGGTATCTTGT	36476	AGG	44	17
CAACATCTCAAGAAGGGAAA	38034	TGG	5	2
CACTGGTGAAAAATATCCAG	33857	AGG	7	1
TTCGACTAAAGGTAAGAGTG	14665	GGG	25	1
GAAAGAATGACGAGTTTTAA	12729	TGG	1502	233
AATACTGTCTTTAAAGGAAC	28070	GGG	275	106
CTGGCGACTTCTCAGGTGCT	25905	TGG	53	2
AGATTGCTTGTTAAAAACGG	30218	CGG	45	6

GATAGCGAAGATGGGAGAAA	22887	AGG	9	1
AAAATCATTAAATTTTCTAC	30415	CGG	72	25
CGAACCAAAAGAGCAAGAAC	30046	CGG	44	7
TGTAGACTTTTTAATAAAAT	27718	TGG	31	8
GATTCCAGCAGATGGAAATT	24065	AGG	2	2
GAACAAGTAGGACAATCACA	25094	AGG	2	2
TTGGCGACTCTGTAGCTAGA	28992	GGG	143	42
CTAAGTGATATTACGGAAGT	30986	TGG	15	5
ACGGCAGACTTGAGCAACAG	32966	TGG	57	18
ATGGCAGTACTTAATGCGGT	24359	TGG	29	1
TTCACTTTCTATACAGATAA	27493	AGG	15	4
AGTGCTGACGATATTGATAA	30518	AGG	69	39
ACTTCAATAACTAGCCAATT	35173	AGG	6	5
TATGTAAACTAATAGATCAA	22700	GGG	8	1
GTAGGAGTGAACTATATAGC	40021	CGG	30	2
TTAATAGCCGGTGCGATTCA	39256	TGG	21	3
GGGACCAACAGTCAGATACA	40035	TGG	15	3
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GGTCTTGGAGTTGTTGGCTT	24431	TGG	30	3
TAATAGTTGGACAGGTTCTC	34750	CGG	129	27
AGTGGCATTTGGTACTGCAA	25195	TGG	14	3
TCACGTTCAAATAATGATAC	20329	TGG	83	11
ATCTCCAGCAAAAGCAATCA	36028	TGG	9	7
CAATAGTGGTTTTTTCAAGA	23108	GGG	19	3
ATACTTGCTGGTGCAACATT	15261	AGG	26	11
ACTTAAGGAGGAACAACAAA	942	TGG	64	4
AGGTGATTACCATGCTTAAA	34249	GGG	214	8
TGCGTCAGATTTAAGTGATG	33560	AGG	45	24
AGTTACTATAACTAAAATTA	33318	TGG	16	3
CCCTAACGAAAAAGGTCACG	29548	AGG	34	3
ATAGAAGAGTGGGTTAAAAA	21360	AGG	19	3
TTTTAGGAAAGCGAGCATGG	29515	AGG	58	9
TTCAACCCAGATGGTTGGTA	38245	TGG	9	1
ATTTTCGGAAAACGGATTAT	7203	CGG	8	1
GTATTTTAGGTGGCGTATTT	25323	TGG	38	10
TAATCCTGCAGAAGATATTA	20469	AGG	18	3
AAAAGAGTTGTCTCAAATGT	26258	AGG	12	4
AGGTGATGTTGTTAGAGTGG	28588	TGG	44	1
CAATGGACTTTACATTTGAA	19451	GGG	11	8
CTAGAATCATATTGCTAAAA	29826	CGG	13	1
CCTCGTGACCTTTTTCGTTA	29532	GGG	33	1
ATGTATTACGATCTAGAAAC	30788	AGG	98	3
ATCAGTTACGTTCAAGAGAA	25130	TGG	40	13
GCAGCAGGAGAAAGCGCAAG	39001	TGG	27	1
GTAGATGCATCTAAATTCGA	28118	GGG	6	1

TCAGGTACCGACCATTTTTC	27288	AGG	11	2
AAAGCCTACAGCTAGTGAAG	34408	TGG	5	1
GGCTTACACCCTAACGAAAA	29540	AGG	23	5
ATACTCATCGTCATTTAGAT	18364	GGG	5	3
GCAGTTTCCGGTGCGATTCA	25625	AGG	4	3
AATATTCAAGAAAAAGAAAA	1835	TGG	1	1
CTGCAAGTTTTTGGATAAAT	8536	AGG	2	1
AAAGGAAAAGGAACGCTCGA	35807	CGG	96	12
TCAATTGCAGGGTTCCAAAA	21635	TGG	19	5
ATATACGCGATATGAAAATG	34151	TGG	57	25
TAATGATGGAAGTATATTGT	7326	CGG	41	9
GGTAAATGGAGTTTATTCGA	31490	GGG	13	1
GTTTCAACTTATTATAAGGG	26739	AGG	225	35
AGAGTGGTGGATTCTGCCAT	28601	AGG	23	15
TTAATAACCTAGTAAGGTTA	6263	GGG	9	8
TACACGATTACTCAAAAATA	23259	AGG	8	3
GCCAATTATTACATTAAAGC	28262	TGG	85	26
GTTTTCGGAAAACGGAAAAA	7233	CGG	23	6
GTAAGCGATAAAACAATTAA	21065	AGG	10	1
GAAGAATATGCATTGATCAC	33840	TGG	291	50
TTCCAGCCTGGATATAAAAC	27618	CGG	23	13
TAAACTTAAATCTTTATATA	15068	CGG	52	11
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TGCTGGACGTTTTTATTTAA	27036	GGG	2	1
ATCGATGAGAACATCTAATG	14318	TGG	16	8
GCTGGGTTCTGTATTGGTAA	30943	CGG	15	3
CCAGCAGTCGCTCAAATTAT	25292	CGG	6	3
AGTGACCTAAAACGATTCAA	8760	AGG	41	10
TTTAACTAGAATAACTGGGG	25435	TGG	27	1
TACACTTTTTAAAAATCGGA	14710	AGG	3	1
CAATTTTTAGTTAGAAACTT	31454	TGG	27	2
TGATCAGAAAGCATAAAAAA	3041	TGG	42	8
AGACCATTATTTGATGCTAA	20141	CGG	14	4
TCCTAAATTAATAGGATCTG	40179	TGG	13	1
TTAAAAAGTCTACAGGGTGT	27743	AGG	5	2
TTAAAAAGCGTTTTAGCGCT	1902	TGG	7	3
AAACACGCTGTACAAACAGG	22374	TGG	24	1
CTAAAGCTAAGAGTAATCAA	12509	AGG	41	10
TTTTAGTCGTTTTTTTATTT	37834	TGG	4	1
CCCGAAAAAAATCTCATACAT	35644	GGG	2	1
ACTTTATTTTTAAAAGATAT	34509	TGG	8	3
CATAGAGGTGGTTAAATATG	21706	TGG	1	1
ATTGGCGACTCTGTAGCTAG	28991	AGG	33	1
GCGGTTGGTGTATTAGGTGG	24374	TGG	21	3
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CAGGTGGACAGTTGCGTATA	22390	TGG	7	2
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GAAAACGGATTATCGGCAAA	7210	CGG	4	2
GATGATAGGAGATGCTGAAA	16999	AGG	17	7
AGACAAGCAGAGCAAATAAG	29147	AGG	329	48
GCTCTTAAAATGGTTGAAGA	24470	TGG	2	2
AGTAGATGCATCTAAATTCG	28117	AGG	1	1
ATTCATGGTAAGCCTATAGG	39271	TGG	107	6
GAACTATTTTTGGTATTTAA	34226	AGG	38	20
GACACGGACAAAAACAAACT	29384	AGG	11	1
AGCATAGGTGGCGCAATCTT	24755	CGG	4	3
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GAGGAGGTAGAACATGACTG	3805	AGG	8	2
CTTAGTCATGAAATGGTAGG	3576	AGG	6	1
TAACCAATTAAAGCAAAATA	32013	TGG	8	1
AATGTTGAAAGGAGAGAAAA	5843	AGG	5	3
CAGGCATTCTTTACACAAAA	31855	CGG	1	1
CACTACAGCATGGTCAATTG	3164	CGG	30	1
GTAATAACGACCCTGAAAAA	27293	TGG	3	1
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GCTAAGTTATATAAACAAAT	36170	CGG	15	5
GGTAGCGTTGAAAGTTATGA	32851	GGG	10	1
ATTGAACTTGATGAAGCAGT	11805	AGG	157	13
CCGTTTTATAAAAAGAATGA	32611	TGG	34	13
AGTGCTTGCTGGAATGTGAA	35581	TGG	19	1
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TTTTAGTTCTTTAGATGGGT	28772	CGG	58	1
AAATTCCTTGAATCGAAAGG	23582	AGG	5	1
GCTAACCTCCTTTCGATTCA	23571	AGG	3	2
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TTAAAGGTGATGACGGCGAA	21601	TGG	4	1
TTAGCTGACTTACAAGAAGG	22221	TGG	5	2
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AAAGAAATCGTTAGCACTAA	20218	TGG	76	20
AAAGAATTCAATGAAGTCGA	24101	AGG	17	4
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ATACTTTGCCGTTATTACAA	23068	GGG	17	1
AAACGATTCAAAGGCGCTCA	8769	CGG	4	1
CTGGATTTAACTAGAATAAC	25430	TGG	7	3
GAGTATAACGAAAGTTTTAC	28034	AGG	4857	1139
GTACGTTTCCAATATAGAAC	30329	TGG	71	7
AAGATAAAGCGTTATTATAT	5590	TGG	17	12
ATTTTCAATAAGAAAAACAA	31190	CGG	3	2

GGATCACGTGAATGTTTTTG	9712	TGG	275	98
TTTGTTATTACAGGTCATGA	4292	AGG	43	12
AATGCGTATAGATACATTGA	30254	TGG	6	1
AGTTCCAATAGGTAAAGAAG	29107	CGG	3	1
AAGCATAGAGGTCGAAAAAG	10878	TGG	1	1
TTGTTCGACGGTGGCGCAAA	33019	TGG	3	1
TTCCAATAGAAATAGTGTGA	20982	GGG	115	34
CGAGTACACTTTTTAAAAAT	14706	CGG	24	1
TATGGATCTATTGTGTTAAT	15852	AGG	21	3
TAACAAACTAGTTGATGATA	21791	GGG	19	13
GGACTGTTAGGGTACGCGAA	18898	GGG	5	1
TTCTCAGAAGATAGCGAAGA	22878	TGG	3	1
GGTATCTTATATTGGTATAC	30626	AGG	56	5
AATAGTACGAGGCGGTAAAA	22271	CGG	2	1
GGTATTGATAAAATTATTGA	6774	AGG	9	4
TTTTCTTTTCGTCGCTGAAA	8710	TGG	3	2
TAGCCACTCATATTCTTCAA	14783	AGG	51	5
TAAACGCAACGATTGATATA	9279	AGG	13	7
GATTAATATAGATAATTATC	34462	GGG	10	1
AACCTGAACGATTAAGGAGG	16258	GGG	9	5
GAAATGGAAGCTAAGAAAAT	19787	TGG	1	1
GTTTTAACTTCTTTAAATTG	34900	CGG	1	1
GGCAACGGAATAGGTTCGGA	34655	CGG	4	2
CAGCTAGTGAAGTGGTGGAG	34416	TGG	3	1
TTATCCAGGTGGCGTTATTG	33108	AGG	1	1
TAGCTATAACATAAAAAAAT	39779	AGG	1	1
GAGCGCCTTTGAATCGTTTT	8749	AGG	138	22
TATTCTATTTTGTTGGTAAG	33082	TGG	44	5
GATTTCGTTACTAATTTAGC	25241	TGG	39	18
GGTAATGTGCCTGGAGATAA	22338	AGG	13	3
AGGGTACGCGAAGGGCAAAA	18906	AGG	6	4
GAGGTGATTACCATGCTTAA	34248	AGG	27	16
GGTGGCGTTATTGAGGGATT	33115	CGG	9	1
CATATGGCAAAAGTTAAGTA	21294	CGG	9	3
GTTAAAGCTAATGATAAGGA	27469	TGG	8	3
ACCCGAAAAAATCTCATACA	35643	TGG	2	1
AAAGCGTTCGGTTTATTGAC	25463	TGG	66	1
AAAGTAGGTGGCGTAATGTT	33931	TGG	19	5
AACAAAGATAAAGATGATGA	4319	AGG	18	3
AAATGGAACAAGTGATATTT	24175	GGG	4	1
TCTCTAAACGCTTTCGGTAA	31039	CGG	4	4
CCAGAAGCTAACCCTAAAAT	28568	AGG	3	1
GAATACTTAAATAAAAAAGC	7390	AGG	9	1
AATAATGGCAGTACTTAATG	24355	CGG	5	3
GCAAACGGGTTTTCGGAAAA	7225	CGG	2	1

CCCTTTAACCGCCATTTTAG	23981	CGG	23	7
CTTTCAACATATTTTTCAAA	12695	AGG	13	3
TCCCAATAACCGGCGTTTTG	31213	CGG	180	24
GTTATTTTTTGCGTTTTTTT	40223	GGG	135	8
GAAGCAGTAGGGATTATGAC	11817	GGG	32	13
ATGACGTTAATCTGGAAAGA	10685	TGG	10	3
TTTATCTATAAATAATGAAT	28837	TGG	9	4
CTTACCTAAAAATAAATATC	37539	CGG	7	3
AGATGAAGGTAAGTATTTTA	4979	CGG	6	3
AAATTCGAGGGATTAGGCAA	28130	AGG	4	1
TACTTTGCCGTTATTACAAG	23069	GGG	4	2
CCCCATGTATGAGATTTTTT	35629	CGG	3	1
GATGAAGAGTTAGATCCAAA	20060	CGG	2	1
TATACCTTTATTAAAGGTTA	28331	TGG	2	2

Normalized Reads Sonication	Normalized Reads Figure 1
7579.247183	20131.30871
12247.64208	19382.03766
11105.76113	14575.17619
9988.22839	14270.67436
9501.761269	13510.65194
6286.308013	13220.04828
21894.00185	10844.56351
5070.885564	9871.50066
4731.004552	9531.502389
4287.271009	9419.665021
7950.433025	8700.532996
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9.441139218	7.263461089
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8.944237153	1.678739859
8.447335089	1.678739859
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3.478314449	1.657270411
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1.490706192	1.501101549

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1.490706192	1.280524342
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1.490706192	1.237585446
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4.969020641	1.081416584
4.472118577	1.081416584
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0.496902064	1.081416584
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0.496902064	1.059947136
68.57248484	1.038477688
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2.981412384	1.01700824
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4.472118577	0.860839378
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0.993804128	0.860839378
32.79553623	0.839369929
9.441139218	0.839369929
8.944237153	0.839369929
1.987608256	0.839369929
1.987608256	0.839369929
1.490706192	0.839369929
4.472118577	0.640262171
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0.993804128	0.640262171

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4.472118577	0.419684965
3.478314449	0.419684965
2.981412384	0.419684965
1.987608256	0.419684965
1.987608256	0.419684965
1.490706192	0.419684965
0.993804128	0.419684965
0.993804128	0.419684965

Spacer Sequence	Location	Strand	PAM	Reads Replicate 1
TTTGTAACAACTGATATTAA	21	-	AGG	23
TTTAATATCAGTTGTTACAA	39	+	AGG	5
AGCGTCTTTAAAAATAAAAA	68	+	AGG	1
GCGTCTTTAAAAATAAAAAA	69	+	GGG	451
AATAAAAAAGGGCAGAAAAA	80	+	GGG	331
AGAAAAACTTGTGTACTAAA	93	-	AGG	1073
AGATGAAAAAACGACTATAA	165	-	AGG	944
AAAGCAATTATGAAAAGAGT	194	-	AGG	4330
TACACACATAAGTTTATTGG	234	-	CGG	3690
GCATACACACATAAGTTTAT	237	-	TGG	723
AAGTTACTACTCACACACTA	259	-	AGG	7734
ATTTAATGATTCTGCAGCTG	308	+	AGG	1197
GAAATCCTATGCAAGGCAGT	331	-	AGG	2141
TGCCAAGGAAATCCTATGCA	338	-	AGG	1771
TGCCTTGCATAGGATTTCCT	352	+	TGG	375
TTTATATTCACAACTTGCCA	353	-	AGG	1132
AACCAAGCTATGTTGATAGA	376	-	GGG	357
GAACCAAGCTATGTTGATAG	377	-	AGG	3
AACCCTCTATCAACATAGCT	390	+	TGG	1116
AAATAAAAAGATGCAACAAT	399	-	GGG	8409
AAAATAAAAAGATGCAACAA	400	-	TGG	184
ATTTGCTATCCTTGAATTGA	461	+	TGG	610
GGTATGACTTTGGCCGAACT	479	-	AGG	2686
GGCGATTTTTCTTCCTAGTT	482	+	CGG	16
AGAAAAACAAGGTATGACTT	489	-	TGG	785
AAACAATCAAGAGAAAAACA	500	-	AGG	1689
TAATAGAACTATCAAGTAAA	556	-	AGG	993
TCTATTATAAGGAAAACTTT	588	+	CGG	453
TTATCATGATGTTACAAAAG	637	-	AGG	1050
GATTACTTACGTAATGCGAA	676	+	AGG	2696
TTCAAAAGTTTAGTATCTAT	698	-	AGG	20913
TAAACTTTTGAAATCTAAAA	725	+	TGG	4
GACACCAATTTCTTCAGAAA	756	-	GGG	508
TGACACCAATTTCTTCAGAA	757	-	AGG	3
AAAACCCTTTCTGAAGAAAT	768	+	TGG	74
ACTTTATCTAACATGATACA	804	+	CGG	11203
CTTTATCTAACATGATACAC	805	+	GGG	11745
CCATTTATTACCGGGTAGGA	821	-	TGG	1469
AATACCATTTATTACCGGGT	825	-	AGG	1055
GAGAACAAAACCATCCTACC	827	+	CGG	21295
AAATAAATACCATTTATTAC	830	-	CGG	353
CCATCCTACCCGGTAATAAA	837	+	TGG	7676

AAAATATCTCTTCCTTCTTG	869	-	AGG	648
TTAGAATTGACACCTCAAGA	873	+	AGG	13956
AAAAAGAAAGTTTTAACTTA	927	+	AGG	1106
AAGAAAGTTTTAACTTAAGG	930	+	AGG	5450
ACTTAAGGAGGAACAACAAA	942	+	TGG	16
TTGATTTCGTGCCACTGTGC	993	-	GGG	12816
GTTGATTTCGTGCCACTGTG	994	-	CGG	1927
AGCAATTCACACCCGCACAG	998	+	TGG	29015
GAAATCAACAGAATTATTGA	1024	+	CGG	182
GTCGTCGAGTTGTAGCTCGG	1048	-	CGG	23
TTGGTCGTCGAGTTGTAGCT	1051	-	CGG	1285
TTTTAATAACCTCAACATCT	1070	-	TGG	27705
ACTCGACGACCAAGATGTTG	1077	+	AGG	9764
AGTTATTCAAAAATCACGAA	1154	+	AGG	910
GTGAATTGCTAGTAGTGTGT	1181	-	TGG	17596
GAAACAATCTTTATAAACGC	1308	+	AGG	317
GAATTAGCTATCATAACTTC	1365	+	TGG	6463
TTATCTAATTGTTTATCGAT	1389	+	TGG	5700
ATTGGAGCATGCAAATAACT	1407	+	TGG	6564
TCTGATGAATATTCATCTCT	1424	-	CGG	32678
AACACCTATTAACGTAGTAT	1449	-	TGG	6680
GATTCCAATACTACGTTAAT	1461	+	AGG	10539
GTTGTAGCTTTTCTAGCTTT	1646	-	AGG	71
ATTTAAGGTGGTTATTCTTA	1698	-	TGG	2349
TTGTTATCAAATATTTAAGG	1710	-	TGG	2891
ATGTTGTTATCAAATATTTA	1713	-	AGG	8482
TTACAAACAAAATCGAACAT	1802	+	CGG	1407
AATATTCAAGAAAAAGAAAA	1835	+	TGG	1
AAGAGAGTTATATAAAGCTT	1876	+	TGG	12238
TTAAAAAGCGTTTTAGCGCT	1902	+	TGG	4
TAAAAAGCGTTTTAGCGCTT	1903	+	GGG	102
TGAAGCATTTCAAAGAAAAT	1938	+	AGG	4
GAAGCATTTCAAAGAAAATA	1939	+	GGG	208
TACAAGTGTACTTACAAGTA	1966	+	CGG	7212
ACAAGTACGGTTGTTAATAA	1979	+	CGG	1247
AAACATGTTGCGATGATGTC	2048	+	AGG	30908
ATGATGTCAGGTACAGAAAA	2060	+	AGG	295
TGTTCCATGCTTTTTCAATT	2091	-	TGG	2546
TCATCCAAATTGAAAAAGCA	2103	+	TGG	1001
GCACGTTGCATAATCATTTC	2116	-	TGG	1864
GCATCTGCAAATACAATTTT	2197	-	TGG	73
ACTAAGACATCAATTTTAGT	2246	+	TGG	3190
GCAAAGATCATTAAACAAAA	2276	+	CGG	1419

AAACAAAACGGTATAAACAT	2288	+	CGG	4
AACAAAACGGTATAAACATC	2289	+	GGG	8147
GGCAACGCAGATTGTTTGAG	2310	+	TGG	588
TTTGAGTGGTTACGTCAAAA	2324	+	CGG	45
CCACACCCTTGCGTTTAATA	2334	-	AGG	12777
CGGATTCCTTATTAAACGCA	2344	+	AGG	5189
GGATTCCTTATTAAACGCAA	2345	+	GGG	3125
CCTTATTAAACGCAAGGGTG	2350	+	TGG	22
CGTTCCATTGAATACTGTGT	2368	-	AGG	52680
CATGCCTACACAGTATTCAA	2380	+	TGG	4122
AGAAACATCAATCACACATT	2425	+	CGG	1469
ACATCAATCACACATTCGGA	2429	+	CGG	96
TGTCCTTTACCTGTTACTTT	2458	-	TGG	18648
AGTAAGACGCCAAAAGTAAC	2465	+	AGG	14924
ACGCCAAAAGTAACAGGTAA	2471	+	AGG	117
TACTTTGTTAACAAGTTTTT	2501	+	AGG	23
AGAAAAACAAACAACTTAAT	2524	+	AGG	11575
AACTGCCATTGTGATGAGGA	2564	-	GGG	15
CAACTGCCATTGTGATGAGG	2565	-	AGG	5
TCACAACTGCCATTGTGATG	2568	-	AGG	107
AACAACCCTCCTCATCACAA	2575	+	TGG	851
AATGGCAGTTGTGACGTGGA	2593	+	AGG	9
CAGTTGTGACGTGGAAGGTT	2598	+	TGG	348
AACGCCCTGCTACTAATCAC	2629	-	AGG	1111
GAAAACCTGTGATTAGTAGC	2640	+	AGG	61
ATTTTCAGCATCTTTCGGTA	2681	-	TGG	2171
GTAGAATTTTCAGCATCTTT	2686	-	CGG	5714
TTTGTTCGGCGAACTTCAAA	2724	-	AGG	4642
TTATTTGCTAATAGTTTGTT	2738	-	CGG	6259
GTTGGTGGTACTATGATTTT	2793	-	TGG	41
TATGTGTTTTCTGGTGTTGG	2808	-	TGG	124
CTATATGTGTTTTCTGGTGT	2811	-	TGG	109
TCGCCTCTATATGTGTTTTC	2817	-	TGG	29
ACACCAGAAAACACATATAG	2830	+	AGG	5606
ACACAAATCCATCAATTGTT	2890	+	TGG	11505
GTAGAAGTACAGTATACAAC	2918	+	TGG	13903
TATTACCGCAAAGATAATTT	2947	+	AGG	1855
ATATTAATCAGAGTGCCTGT	2982	-	TGG	5350
TACATTGATTATTCACCAAC	2983	+	AGG	6648
TCTGATTAATATTTCTAAAT	3009	+	TGG	5853
TGATCAGAAAGCATAAAAAA	3041	+	TGG	1
AAAGCATAAAAAATGGTATT	3048	+	AGG	1202
GCATAAAAAATGGTATTAGG	3051	+	AGG	1571

TGAAGCATAATACTGCTACT	3088	-	AGG	23825
GCTGTAGTGAAGTATAGAAA	3134	-	CGG	4049
TTCTATACTTCACTACAGCA	3154	+	TGG	4609
CACTACAGCATGGTCAATTG	3164	+	CGG	4
ACTACAGCATGGTCAATTGC	3165	+	GGG	207
ATAAAAAAACTGCTACTTGT	3239	+	TGG	38980
GTTCAATATAAAACGAAAAA	3300	+	CGG	3217
CAATATAAAACGAAAAACGG	3303	+	AGG	878
GTCAAGATGTATTACGAAAT	3328	+	AGG	6727
CGCAAAAATATTCATGTTAA	3361	+	CGG	1575
ATTCATTTTAAAAGGTCATA	3399	+	TGG	1288
TTCATTTTAAAAGGTCATAT	3400	+	GGG	2128
ACGACATAAGCATGTTTAAT	3441	-	TGG	11300
AGATGAGAATGACTTAGATA	3480	+	TGG	1258
CAATCCATTCATCTATTGCT	3503	-	TGG	34547
TTAACCAAGCAATAGATGAA	3515	+	TGG	451
TGAAGAGAACACAGACGAAC	3540	+	AGG	13776
TAATTAACTTAGTCATGAAA	3569	+	TGG	3635
TAACTTAGTCATGAAATGGT	3573	+	AGG	6055
CTTAGTCATGAAATGGTAGG	3576	+	AGG	6
TAACTTATATCATTCGTCAT	3617	+	AGG	816
AACTTATATCATTCGTCATA	3618	+	GGG	1147
GGTTTGTTAGTTATATAAAT	3630	-	TGG	1263
ATATCTGAATTGTTATCAGT	3651	-	TGG	12604
CCTAGCTCTATTTCTATTTG	3682	-	TGG	26
CCACAAATAGAAATAGAGCT	3698	+	AGG	908
CACAAATAGAAATAGAGCTA	3699	+	GGG	891
AATAGAGCTAGGGAGTTTAA	3709	+	CGG	11354
AGCTAGGGAGTTTAACGGTA	3714	+	TGG	4966
GGAAGAAGCGAGTATCAATA	3735	+	TGG	1148
GACAGAAACTATTGAGTACG	3786	+	AGG	7503
GAGGAGGTAGAACATGACTG	3805	+	AGG	6
AGTATGCTTACTTTTTCTTG	3823	-	TGG	15478
ATATCGCTGAGAAAAATAAA	3882	+	AGG	3
TTCTATAAATTTGCAGTATA	3908	+	CGG	20
TTTGCAGTATACGGAAAAAT	3917	+	TGG	880
GTATACGGAAAAATTGGCTC	3923	+	AGG	13
TTTATCTCTTGTAGCAAACG	3935	-	TGG	4264
TTCGTCATTGACATTAACGA	3980	+	AGG	965
GTCATTGACATTAACGAAGG	3983	+	TGG	69
CATTAACGAAGGTGGAACAA	3991	+	CGG	7465
GGAACAACGGTTACTGACGA	4004	+	AGG	117
CTCATCTCCTGTAAAATTTG	4066	-	AGG	46

TTTTTTACCTCAAATTTTAC	4075	+	AGG	1869
TTACAGGAGATGAGAGAAAA	4091	+	CGG	13
TCTCCCCAATCATTAAACGT	4186	-	TGG	2243
AAAAACCAACGTTTAATGAT	4197	+	TGG	538
AAAACCAACGTTTAATGATT	4198	+	GGG	41
AAACCAACGTTTAATGATTG	4199	+	GGG	55
GTCAGTATGTACAGATTAAT	4241	+	AGG	23623
CATGACCTGTAATAACAAAG	4272	-	TGG	975
AAATTCCACTTTGTTATTAC	4283	+	AGG	4506
TTTGTTATTACAGGTCATGA	4292	+	AGG	3
AACAAAGATAAAGATGATGA	4319	+	AGG	2
GCGCTTCAATAGTGATAGTA	4338	-	GGG	23891
TGCGCTTCAATAGTGATAGT	4339	-	AGG	2473
CTCAAAGTGATGTGTTAGCT	4404	+	AGG	2916
TCAAAGTGATGTGTTAGCTA	4405	+	GGG	12854
ATTGAAGAATTTGATGATAA	4433	+	CGG	38
TTATTGTTAATTGTTATTGA	4510	-	AGG	13
TCTACTACGTCCGTAATGCT	4546	-	AGG	8857
ATTTGCAAATCCTAGCATTA	4552	+	CGG	2703
GTAGTAGAAGCAATTAGAAA	4577	+	TGG	5409
GAAACTAAAAATTAATTAAA	4599	+	AGG	23
CTAAAAATTAATTAAAAGGA	4603	+	CGG	353
TATTTAATTATGAAAATCAC	4626	+	AGG	2148
AATCAAGAAAAGTTTTATAA	4674	+	CGG	308
AAGTTTTATAACGGCTCAGC	4683	+	AGG	34
AGTTTTATAACGGCTCAGCA	4684	+	GGG	6572
GGCTCAGCAGGGTTTCAAGC	4695	+	TGG	310
TGGAAATCATATTTATACGG	4814	-	CGG	5
TCTTGGAAATCATATTTATA	4817	-	CGG	9145
ATTGAATTAGTTACTCGATT	4866	+	AGG	8544
TTGGTATCAAAATCTAAGCT	4889	-	AGG	438
AAACTTACCAATAAGATCAT	4908	-	TGG	142
TTTGATACCAATGATCTTAT	4917	+	TGG	11700
TATTGGTAAGTTTTGTCACT	4934	+	TGG	3218
TTTGTCACTTGGTATTGAAA	4945	+	TGG	4
TGGAAATTCAATGAAGATGA	4965	+	AGG	712
AGATGAAGGTAAGTATTTTA	4979	+	CGG	1
ACATCATCGCCCTTTTTGTA	5003	-	AGG	1662
ATTTATTAAACCTTACAAAA	5009	+	AGG	384
TTTATTAAACCTTACAAAAA	5010	+	GGG	3822
TGCTTATCTGTCTTCGGAAT	5036	-	AGG	6362
GCTTTTTGCTTATCTGTCTT	5042	-	CGG	157
CAAAAAGCTGAAGAAAATAA	5073	+	CGG	476

AAAAAGCTGAAGAAAATAAC	5074	+	GGG	350
AAAAGCTGAAGAAAATAACG	5075	+	GGG	135
AATTGGCCACTGCTTTCAAA	5117	-	TGG	3037
AGCAATCCATTTGAAAGCAG	5127	+	TGG	5730
CTTGGTCGTCATATCCAAAT	5134	-	TGG	6213
TTTGAAAGCAGTGGCCAATT	5136	+	TGG	44
CACCTTAAAACGCTAAATCT	5152	-	TGG	14897
AGATTTAGCGTTTTAAGGTG	5171	+	TGG	125
AAGTACCGTCGTTATCTTTC	5203	-	TGG	211
AGATACCAGAAAGATAACGA	5214	+	CGG	1085
TTCAACACCAGTAGCAACGA	5229	-	CGG	708
ACTTATTCCGTCGTTGCTAC	5238	+	TGG	7036
CACATTGACTTACTAGAAAA	5280	+	CGG	16
ACCTCTACTTCTGCTTTTAG	5291	-	TGG	555
TCCACTAAAAGCAGAAGTAG	5306	+	AGG	693
AAAAGCAGAAGTAGAGGTTC	5312	+	CGG	195
ATAGATAGTTTTTTATTGTC	5315	-	CGG	208
GTAGAGATATAGAACTTCAC	5383	+	TGG	6206
TAGAGATATAGAACTTCACT	5384	+	GGG	28586
AGAGATATAGAACTTCACTG	5385	+	GGG	381
AATTTTCTAGTTGATTCTAC	5396	-	TGG	1663
AAAATTATTACAAACAGAAT	5429	+	TGG	1173
ACAGAATTGGAAATTATGAA	5442	+	AGG	3
ACTGTTCTATGAAAGTTGCA	5488	+	AGG	46
CTGTTCTATGAAAGTTGCAA	5489	+	GGG	1489
TTACTCGTTTCTACACTCAT	5540	-	AGG	263
AAGATAAAGCGTTATTATAT	5590	+	TGG	2
TTCCGCATATTACACAGTTG	5608	-	CGG	36
AACCGCAACTGTGTAATATG	5622	+	CGG	15
CGGAAAGCCTCACGCAGACC	5642	+	TGG	7059
CGACTGCTTCATAATGTGCC	5644	-	AGG	66
CTGGCACATTATGAAGCAGT	5661	+	CGG	1547
CTAATACATGTTTGTCATAG	5695	-	TGG	5577
CACAACGAGCAACATGCGAT	5751	+	TGG	10590
TTATCCACGAGTCATGCAAG	5782	-	TGG	56
AATACCACTTGCATGACTCG	5794	+	TGG	2602
CGTGGATAAAAGTTGATGAG	5812	+	AGG	1305
AGGCTCAATAAAATGTTGAA	5832	+	AGG	78
AATGTTGAAAGGAGAGAAAA	5843	+	AGG	3
CTTCCGCCAAGATGACGATT	5883	-	AGG	1231
AGCACTCCTAATCGTCATCT	5893	+	TGG	15066
ACTCCTAATCGTCATCTTGG	5896	+	CGG	5350
TGCTATGCATGCTGTAAAAG	5932	+	TGG	1303

AAAAACCTGTATTAACTAAA	5956	-	CGG	221
AATCTCCGTTTAGTTAATAC	5967	+	AGG	1088
TTTTACAAAAGCTTTACCAT	5991	+	AGG	6029
TCAATTAGTTTGTCCGCCTA	5991	-	TGG	476
TGGGTAATAGACATCAAAAA	6015	-	AGG	96
TTTTTTGATGTCTATTACCC	6033	+	AGG	1604
TTTTTGATGTCTATTACCCA	6034	+	GGG	672
AAAGTTACATTACAGCCCCT	6034	-	GGG	161
TTTTGATGTCTATTACCCAG	6035	+	GGG	870
TAAAGTTACATTACAGCCCC	6035	-	TGG	8
GAAACAATAAGTAAACTTTC	6075	-	TGG	1319
AAAGTTTACTTATTGTTTCT	6095	+	AGG	515
GTTAAAAGAATGTTAAAGTC	6108	-	AGG	1405
GAAAAACAAAGATTTGTTTC	6141	-	GGG	11672
AGAAAAACAAAGATTTGTTT	6142	-	CGG	1037
TTAAAGTGATTTAAAAACTG	6190	+	AGG	295
ATGTCTTACTTAACAAAAAA	6219	-	AGG	3
TAATAACCTAGTAAGGTTAG	6262	-	GGG	11
TTAATAACCTAGTAAGGTTA	6263	-	GGG	5
ATTAATAACCTAGTAAGGTT	6264	-	AGG	342
TTTCAATTAATAACCTAGTA	6269	-	AGG	274
TTAAAACCCCTAACCTTACT	6272	+	AGG	10403
TAGGTTATTAATTGAAATTT	6291	+	CGG	1
TCGGTTGATTCTATATCTAA	6310	+	CGG	401
GAATGACGGTATGAATATAT	6337	-	CGG	1369
GTTTTAAACCCAAAGAATGA	6351	-	CGG	3600
ATATTCATACCGTCATTCTT	6358	+	TGG	12611
TATTCATACCGTCATTCTTT	6359	+	GGG	3306
TCCTGCCGTTAAATATAGAG	6373	-	CGG	338
TAAAACCGCTCTATATTTAA	6384	+	CGG	706
ACCGCTCTATATTTAACGGC	6388	+	AGG	992
TTTAAAAGAATAGCATCATT	6436	+	TGG	1448
TTAAAAGAATAGCATCATTT	6437	+	GGG	569
TAAAAGAATAGCATCATTTG	6438	+	GGG	876
TAATTATTTCAACAAATGAA	6470	+	TGG	80
TTATTTCAACAAATGAATGG	6473	+	TGG	145
TATTTCAACAAATGAATGGT	6474	+	GGG	359
AAAACTAATAGCATCATCTA	6502	-	TGG	6725
AACTTTGAAGCTTCTAGAGC	6577	+	AGG	2676
GAACCACAATTTTCTCTTCT	6585	-	AGG	2804
GGACCTAGAAGAGAAAATTG	6598	+	TGG	9
GGTTCTTGTAAATTATTTTC	6619	+	AGG	4593
TGGGAAATTCCACCTTTATG	6700	-	TGG	216

AAATAACTTTATCCACATAA	6704	+	AGG	5790
TAACTTTATCCACATAAAGG	6707	+	TGG	131
AAACTTGGGAACTTGTCTTT	6719	-	GGG	6
AAAACTTGGGAACTTGTCTT	6720	-	TGG	141
AGAAACATTCTCTAAAACTT	6733	-	GGG	270
TAGAAACATTCTCTAAAACT	6734	-	TGG	71
GTTTTAGAGAATGTTTCTAC	6754	+	AGG	1746
TTATTGAAGGCGCATCAAAA	6761	-	GGG	122
ATTATTGAAGGCGCATCAAA	6762	-	AGG	89
GGTATTGATAAAATTATTGA	6774	-	AGG	4
ATGGATCCTATTTTAGGTAA	6795	-	AGG	19
ATAATTATGGATCCTATTTT	6801	-	AGG	230
TCAATACCTTTACCTAAAAT	6805	+	AGG	2687
AGATTGGGGGTGAATAATTA	6814	-	TGG	33
TCGCTATTGCGTTAGATTGG	6827	-	GGG	207
ATCGCTATTGCGTTAGATTG	6828	-	GGG	22
TATCGCTATTGCGTTAGATT	6829	-	GGG	1844
TTATCGCTATTGCGTTAGAT	6830	-	TGG	29
CCATTTCGTTATCTCCTTTC	6863	-	TGG	6046
ATAATAAAATTATACCAGAA	6865	+	AGG	618
CCAGAAAGGAGATAACGAAA	6879	+	TGG	1736
TTTAGAACGATAAAAGAAAG	6907	+	TGG	119
AATTTAAGTGCTAAAGCTAA	6970	+	AGG	882
ATTTAAGTGCTAAAGCTAAA	6971	+	GGG	6999
GCCAATTGTCAGGACGACTT	6992	-	AGG	893
GTGTATATTTGCCAATTGTC	7002	-	AGG	524
TCCTAAGTCGTCCTGACAAT	7007	+	TGG	179
GTAGTTAAACATATGAATGA	7048	+	TGG	1105
GGACAAAAATCAATCAATAG	7069	+	TGG	15414
TAGTGGCGTTCAAGAACTTA	7086	+	TGG	6731
ATACAAAAAAGAGCTGAAAA	7129	+	CGG	503
GCTGAAAACGGTGTGTTTAA	7141	+	AGG	544
TCCGAAAATGGCATTTCGGT	7173	-	TGG	57
GTTTTCCGAAAATGGCATTT	7177	-	CGG	1545
GATAATCCGTTTTCCGAAAA	7185	-	TGG	25
ACCAACCGAAATGCCATTTT	7188	+	CGG	2625
ATTTTCGGAAAACGGATTAT	7203	+	CGG	4
GAAAACGGATTATCGGCAAA	7210	+	CGG	3
AAAACGGATTATCGGCAAAC	7211	+	GGG	102
GCAAACGGGTTTTCGGAAAA	7225	+	CGG	1
GTTTTCGGAAAACGGAAAAA	7233	+	CGG	2
TATTAGTAGTACGCCCTTTT	7244	-	CGG	317
GGAAAAACGGAAAACCGAAA	7246	+	AGG	103

AATAACAATACTAATAATGA	7312	+	TGG	1207
TAATGATGGAAGTATATTGT	7326	+	CGG	3
AATGATGGAAGTATATTGTC	7327	+	GGG	688
TAGGGAATGGAATACACAGT	7338	-	CGG	265
GATAATTTCTTTATAGGGAA	7351	-	TGG	4
TATTCGATAATTTCTTTATA	7356	-	GGG	873
GTATTCGATAATTTCTTTAT	7357	-	AGG	541
GAATACTTAAATAAAAAAGC	7390	+	AGG	1
AAGATTTTATTAAAGCAAGA	7445	+	TGG	1749
CAAGATGGAATCAAGATTTT	7460	+	AGG	1117
ATGGAATCAAGATTTTAGGT	7464	+	TGG	742
GAATCAAGATTTTAGGTTGG	7467	+	AGG	9
TTGATATCAAAACAGCTGAA	7505	+	TGG	149
AACAGCTGAATGGTTAAACA	7515	+	CGG	6454
CAAAAAGTGTTTCTGGTCTA	7535	-	AGG	62
TTACTGCCAAAAAGTGTTTC	7542	-	TGG	31
CTTAGACCAGAAACACTTTT	7552	+	TGG	8467
ACTTTTTGGCAGTAAATTTG	7566	+	AGG	13
CTTTTTGGCAGTAAATTTGA	7567	+	GGG	32
TTTTTGGCAGTAAATTTGAG	7568	+	GGG	207
TCCAATTGATCCGTGCCAGT	7596	-	TGG	9158
AATCAAAAAATACAACCAAC	7597	+	TGG	686
AAAAATACAACCAACTGGCA	7602	+	CGG	34
ACCAACTGGCACGGATCAAT	7611	+	TGG	15870
TGAAGTACGACGAAAGTTAT	7640	+	TGG	363
GAAGTACGACGAAAGTTATT	7641	+	GGG	1187
CGACGAAAGTTATTGGGATT	7647	+	AGG	48
GACGAAAGTTATTGGGATTA	7648	+	GGG	42
ACGAAAGTTATTGGGATTAG	7649	+	GGG	32
CGAAAGTTATTGGGATTAGG	7650	+	GGG	216
TTTATCTTTTCGCTGAATAG	7668	-	TGG	3500
AATCCTTTTTCGACATGAGT	7713	-	AGG	6141
CAACCTACTCATGTCGAAAA	7726	+	AGG	256
GGATTGAAATGTGAGAGATG	7747	+	TGG	1713
CCATTCGGGTGTTTTTTAGT	7782	-	AGG	1810
CTTTATACTCGTAACCATTC	7796	-	GGG	5898
TCTTTATACTCGTAACCATT	7797	-	CGG	7939
AATGGTTACGAGTATAAAGA	7816	+	CGG	27
TTGCAAATGTGAAATCTATG	7839	+	AGG	676
ACTGTTGCATCTCTTAAAGA	7905	-	CGG	543
TGTACTTGTTTTTCATTTTG	7941	-	TGG	9521
ACAGCAATAGAGTACGTACA	7990	+	AGG	56
CCTTGCAATATTAATGATTT	8013	-	TGG	99

CCAAAATCATTAATATTGCA	8029	+	AGG	1309
TTAATATTGCAAGGTTCATA	8038	+	CGG	7009
TTGCAAGGTTCATACGGAAC	8044	+	TGG	14
TTGCGATAGCGTATGCTAGG	8057	-	TGG	30
CTTTTGCGATAGCGTATGCT	8060	-	AGG	184
GCAAAAGCAGTCAAAGCTAA	8092	+	AGG	3
CAAAAGCAGTCAAAGCTAAA	8093	+	GGG	8413
AGTCAAAGCTAAAGGGCATA	8100	+	CGG	905
TTGATACGATCCATCAACAT	8124	-	TGG	5946
TATGCACATACCAATGTTGA	8130	+	TGG	720
TTTACTTGTACTAGATGATA	8229	+	TGG	2984
TTACTTGTACTAGATGATAT	8230	+	GGG	481
AGCATTGTTGATAACAGAGT	8290	+	AGG	1375
AACTAAATCAAAATATGAAC	8351	+	TGG	2653
GCGAGAAAAGTAAGAGTAAT	8404	+	CGG	1375
GAGTAATCGGAGACGATTTC	8417	+	AGG	40
AGTAATCGGAGACGATTTCA	8418	+	GGG	324
ATTTCAGGGAGCGAGATGCA	8432	+	TGG	605
TTTAGTTTTTAAAAATTCTT	8442	-	TGG	2337
CGCTCAGAAACTCATAGATG	8501	+	AGG	30
GAAACTCATAGATGAGGCAC	8507	+	AGG	22
AGGCACAGGGCGATGAAAAT	8521	+	AGG	122
CTGCAAGTTTTTGGATAAAT	8536	-	AGG	4
CTTAATATTCGACGATAGCG	8572	-	GGG	2057
TCCTTAATATTCGACGATAG	8574	-	CGG	13
CCCGCTATCGTCGAATATTA	8589	+	AGG	63
TATAAGTAATATTTTTCTTT	8609	-	CGG	639
TATCTTCCGTGCCATCTTCT	8632	-	CGG	7828
TATTACTTATACCGAGAAGA	8637	+	TGG	1429
AGATGGCACGGAAGATATTA	8654	+	AGG	58
AATGAAGTTTATTCGCTCAC	8700	+	AGG	6895
TTTCTTTTCGTCGCTGAAAT	8709	-	GGG	160
TTTTCTTTTCGTCGCTGAAA	8710	-	TGG	4
CAGCGACGAAAAGAAAATCA	8732	+	TGG	12
GAGCGCCTTTGAATCGTTTT	8749	-	AGG	3
AGTGACCTAAAACGATTCAA	8760	+	AGG	6
AAACGATTCAAAGGCGCTCA	8769	+	CGG	4
AACGATTCAAAGGCGCTCAC	8770	+	GGG	427
CTTTTATATGAGCAAGAGCT	8793	+	AGG	351
TTTTATATGAGCAAGAGCTA	8794	+	GGG	1088
CAACGATATTTGATATTTAG	8824	+	AGG	34
CGATATTTGATATTTAGAGG	8827	+	TGG	518
TGATATTTAGAGGTGGCACA	8834	+	TGG	307

TAAATTTAACGAAACGTTCG	8867	+	AGG	1420
CGAAACGTTCGAGGCACCTA	8876	+	TGG	260
CGTGGACGAGGCGAGCCCAT	8876	-	AGG	153
GAAACGTTCGAGGCACCTAT	8877	+	GGG	2077
GTATTACGAAAGCGTGGACG	8888	-	AGG	91
CTACCTGTATTACGAAAGCG	8894	-	TGG	161
CGTCCACGCTTTCGTAATAC	8907	+	AGG	306
TTATGATTTGTATAAGCTGT	8936	-	TGG	293
AATCATAAAGCGTATATACA	8967	+	AGG	265
GCGCGCTCTAGATTTAACTT	8981	-	AGG	151
TTCGACCATGATTTAAGTAA	9032	-	TGG	1462
ACTTTCCATTACTTAAATCA	9043	+	TGG	20484
GAAGAAAAAGAAAAGTGAAA	9068	+	TGG	85
AAAAAGAAAAGTGAAATGGT	9072	+	TGG	7409
TTAATTAAGTTATCGATATC	9098	-	CGG	173
ACAGTATTAGACGCATGTAA	9138	+	TGG	408
ACGCATGTAATGGTCATGTG	9148	+	TGG	83
AGCTAGTTATTTCTGTAATT	9166	-	TGG	1432
ATAACTAGCTCAAAGCGTTA	9195	+	TGG	1156
TCAACTCGCATGATTATTTT	9209	-	TGG	209
AAAAATAATCATGCGAGTTG	9227	+	AGG	2525
TAAACGCAACGATTGATATA	9279	+	AGG	1
TACTGATATTCAACTTCTGT	9289	-	AGG	11770
ATATCAGTATTTTGATGATG	9319	+	TGG	188
GGATATCGAAAAAGAAGCGC	9340	+	TGG	10089
TCATACTCTAGTAATTCGTC	9367	-	TGG	1653
AATTAGAAATGTAAATGTAG	9415	+	AGG	3111
TAGAAATGTAAATGTAGAGG	9418	+	TGG	899
ATGAGTGTCGTGAAGATTAA	9446	+	CGG	217
TCATGTTCGGTAAATTTATA	9457	-	TGG	1470
TATCAATTCATTTTCATGTT	9470	-	CGG	410
AATGAATTGATAAAAAAGAA	9497	+	CGG	1
ATGAATTGATAAAAAAGAAC	9498	+	GGG	272
AAAAAGAACGGGTTAACTCC	9509	+	TGG	67
ACTCTTTTTGCAACCATTCC	9511	-	AGG	409
GAACGGGTTAACTCCTGGAA	9514	+	TGG	70
ATGGTTGCAAAAAGAGTACG	9533	+	TGG	15
GTTGCAAAAAGAGTACGTGG	9536	+	TGG	36
AAAAAGAGTACGTGGTGGCT	9541	+	GGG	58
CATGCCATAAGGTGCGTTTA	9560	-	AGG	11
TCAGCTAAGCGCATGCCATA	9571	-	AGG	5268
GAAGCCTTAAACGCACCTTA	9572	+	TGG	609
GCTCTCTCGTTGCATAATTC	9614	-	TGG	137

GCAAAGAACGTGAAATAGCT	9651	+	AGG	2787
AGCTAGGCAACGACGTAAAG	9667	+	AGG	1220
AAGAGGTTGAACTACGTAAG	9684	+	AGG	285
TGTGGTACATTAAACAAATG	9694	-	TGG	2563
GGATCACGTGAATGTTTTTG	9712	-	TGG	3
TAAGTGACATCGAACCAGTA	9733	-	CGG	449
AACATTCACGTGATCCGTAC	9735	+	TGG	2709
CACTCCATTTCTTGAACATT	9759	-	TGG	324
ATAACCAAATGTTCAAGAAA	9771	+	TGG	447
TCGCCGTATGTGTAATGTGC	9849	-	TGG	2042
CAACCAGCACATTACACATA	9862	+	CGG	5183
AGATTTTATTGAACAAGTAA	9900	+	CGG	4940
ATTGCAAATGCTAATTGTGG	9915	-	TGG	889
CCTATTGCAAATGCTAATTG	9918	-	TGG	4104
CCACAATTAGCATTTGCAAT	9934	+	AGG	3966
TCCTCATGACCATTCTTTAA	9969	-	CGG	5313
TCTAGAGCACCGTTAAAGAA	9976	+	TGG	1773
ACCGTTAAAGAATGGTCATG	9984	+	AGG	8
AAAGAATGGTCATGAGGATA	9990	+	TGG	46
TAGATAGAGTGTTTGACTTG	10031	+	TGG	21
AGATAGAGTGTTTGACTTGT	10032	+	GGG	926
TTTACGCGCGTTATCTGTCA	10047	-	TGG	2426
ATCTCTTAGAGCCGAAAAAT	10081	-	TGG	968
GAATACTTAAACCAATTTTT	10086	+	CGG	518
CTCTAAGAGATATCTGTATC	10109	+	AGG	286
AATAAGCGCCATTCACTACA	10138	-	TGG	3974
GCACATATCCATGTAGTGAA	10146	+	TGG	301
AATGGCGCTTATTACTTTCA	10164	+	CGG	5
ATGGCGCTTATTACTTTCAC	10165	+	GGG	633
CATATCGTACCAGATTGGCA	10188	+	AGG	3196
GAAAAAGACATTTGATACAG	10214	+	CGG	30
TTTGATACAGCGGAAGAGCT	10224	+	CGG	122
GGAATATATATAAAGCAACA	10245	+	TGG	719
ATATATAAAGCAACATGGTT	10250	+	TGG	2824
GCAACATGGTTTGGAATACG	10259	+	AGG	37
AGCAACTAACTTTATTTTAG	10288	+	AGG	243
TAACTTTATTTTAGAGGAGA	10294	+	TGG	225
TATTAGACGAGTTAATTAAA	10350	+	TGG	448
ATTAGACGAGTTAATTAAAT	10351	+	GGG	10629
TAAATGGGCGCGAGAAAATC	10366	+	CGG	3
ATTTTCCCTTGTGATAGCTC	10369	-	CGG	939
GAAAATCCGGAGCTATCACA	10379	+	AGG	191
AAAATCCGGAGCTATCACAA	10380	+	GGG	986

TTTTCAACAGGATTTAGTGA	10412	+	TGG	274
GTCGAACACTTATTTGTATT	10435	-	TGG	1764
ACTATGAAGGGGATATCAAT	10471	-	TGG	522
TTTCAATATCAACTATGAAG	10482	-	GGG	134
TTTTCAATATCAACTATGAA	10483	-	GGG	129
TTTTTCAATATCAACTATGA	10484	-	AGG	83
CTTATCAAATACCGTGTCTT	10514	-	TGG	373
AAAAGAAGTAACCAAAGACA	10519	+	CGG	1218
GTTGTTTGAAATGTACGAGA	10552	+	TGG	207
TTTGAAATGTACGAGATGGA	10556	+	AGG	1061
GAAATGTACGAGATGGAAGG	10559	+	AGG	110
ACTAGTGTTTGCATATAATA	10577	-	CGG	335
AGTATAAAAGAATGTTTATA	10613	+	TGG	3338
AAGATATAGAATGCTTTGGT	10630	-	AGG	2385
GTTTAAGATATAGAATGCTT	10634	-	TGG	14243
ATATGACGATGACGTTAATC	10677	+	TGG	441
ATGACGTTAATCTGGAAAGA	10685	+	TGG	1
TGACGTTAATCTGGAAAGAT	10686	+	GGG	69
GACGTTAATCTGGAAAGATG	10687	+	GGG	1450
AATCTGGAAAGATGGGGAGT	10693	+	TGG	23
GATACAAAGACTTACTTTAT	10714	-	AGG	1794
TTTTGTGCAAAGTACGAATG	10797	+	AGG	10
CAGTTTTAATACCGTATTCG	10810	-	TGG	290
TGAGGAAGAAGCCACGAATA	10815	+	CGG	170
CTATGCTTGCAGTTTGGAAC	10847	-	GGG	1331
TCTATGCTTGCAGTTTGGAA	10848	-	CGG	26
CGACCTCTATGCTTGCAGTT	10853	-	TGG	544
GTTCCAAACTGCAAGCATAG	10866	+	AGG	2090
AAGCATAGAGGTCGAAAAAG	10878	+	TGG	3
CATAGAGGTCGAAAAAGTGG	10881	+	AGG	1126
TCGTCCCACACTCGATATTT	10901	-	CGG	293
TGATGCCGAAATATCGAGTG	10912	+	TGG	1062
CGAGTGTGGGACGAATATAC	10926	+	AGG	294
GGAAGAATACACGATGTTGT	10947	+	AGG	14542
AGTTCACTATGAAAACTACG	10991	+	CGG	2333
GTAGAACTTATGCAAAGTAC	11052	+	AGG	96
AAACAACAACGAAATATATG	11087	+	CGG	1020
AACAACAACGAAATATATGC	11088	+	GGG	3400
CCTATTACAGATTCATCGTC	11132	-	TGG	6742
ATATCTATTGATGTTGTAAA	11190	+	TGG	5662
ATTAAAAGATTTTATGTTTG	11219	+	AGG	148
TTAAAAGATTTTATGTTTGA	11220	+	GGG	301
ATACTCAAAGTAATCATTTT	11235	-	CGG	64

CTCACAGTCATATCTAAGGA	11271	-	AGG	2
TAACCTCACAGTCATATCTA	11275	-	AGG	116
CTTCCTTAGATATGACTGTG	11288	+	AGG	17
AGATATGACTGTGAGGTTAA	11295	+	AGG	167
ATTTGAATCATCACATTTAT	11324	+	TGG	4288
TGAATCATCACATTTATTGG	11327	+	AGG	156
AACAGAATGAACTATGAAAC	11351	+	AGG	1266
ACAGAATGAACTATGAAACA	11352	+	GGG	726
CAGAATGAACTATGAAACAG	11353	+	GGG	1102
TAGCGTCCATTACACCTAGT	11361	-	TGG	1430
TATGAAACAGGGGTCCAACT	11363	+	AGG	95
AGGGGTCCAACTAGGTGTAA	11371	+	TGG	19
AACTAGGTGTAATGGACGCT	11379	+	AGG	84
AAGCAACGTGATGAGCTTAT	11438	+	TGG	259
AGCAACGTGATGAGCTTATT	11439	+	GGG	323
GCAACGTGATGAGCTTATTG	11440	+	GGG	1579
GATGAGCTTATTGGGGATAT	11447	+	AGG	45
AAGAGAACGCAACAAAGAGC	11476	+	TGG	4166
TGGAGAAGAAAGCAAGTGCA	11496	+	TGG	35
GGAGAAGAAAGCAAGTGCAT	11497	+	GGG	743
AAAGATTTAATAAACGAATT	11543	+	TGG	9
ATAAACGAATTTGGCAAAGA	11552	+	TGG	371
GATGGTGAAAGAGTTAAATT	11570	+	TGG	1389
TGAAAGAGTTAAATTTGGAA	11575	+	TGG	361
ATTAAACAATAAAACTTTTA	11599	+	TGG	1466
AAACAATAAAACTTTTATGG	11602	+	AGG	2999
CGGATTGTTCTATTTGTTCA	11626	-	CGG	610
ATACGCACTAGCACTTATAA	11646	-	CGG	109
ATAAGTGCTAGTGCGTATAA	11667	+	CGG	109
GTATAACGGCAATGACACAG	11681	+	AGG	1982
TATAACGGCAATGACACAGA	11682	+	GGG	1256
GGGATTACTAAAAGAGATTG	11702	+	AGG	32
AGCGTTTGATGAAATACTTG	11744	+	AGG	1373
GCGTTTGATGAAATACTTGA	11745	+	GGG	4729
ATTCAACATTCAGTTAAAGA	11781	+	AGG	2363
ATTGAACTTGATGAAGCAGT	11805	+	AGG	6
TTGAACTTGATGAAGCAGTA	11806	+	GGG	26
TGAAGCAGTAGGGATTATGA	11816	+	CGG	145
GAAGCAGTAGGGATTATGAC	11817	+	GGG	1
TCAAGTTGTCTATAAATATG	11840	+	AGG	156
AGTTGTCTATAAATATGAGG	11843	+	AGG	179
CTATAAATATGAGGAGGCAC	11849	+	AGG	379
AGAGTTATTACAAATACAAA	11907	+	AGG	162

CTATCTCGTAAGTTCAGCGT	11931	-	TGG	2133
ATGTAGTTGAATTCTTTGAA	11981	+	TGG	813
CTTTGAATGGTTTAATACAT	11994	+	TGG	3593
CATTGGAAACGTTTAAGAAC	12011	+	TGG	8762
AAGAACTGGAAGAAGAAACC	12025	+	AGG	220
TGTACGTCTAACGGCTTACC	12027	-	TGG	74
TCATCAAGTTGTACGTCTAA	12036	-	CGG	162
TGATGAATTAGCTGACATGT	12069	+	TGG	1704
TTAGCTGACATGTTGGCGTT	12076	+	TGG	29
TTGAGTATTGCGAATCAAGT	12100	+	AGG	3557
AATTCTTTGAATATTATCTG	12222	-	TGG	533
ATAACAATTGCTTGTTGGTC	12249	-	GGG	74
TCACTATAACAATTGCTTGT	12254	-	TGG	13341
TTTTGTATGCGTCAATGAGT	12308	-	TGG	9713
CATACAAAAAGAAAATGAAA	12338	+	AGG	41
AGGAATCATGAAAGACAAGA	12358	+	TGG	2314
CAAGATGGAACAGCAGACGC	12373	+	AGG	1575
GGAACAGCAGACGCAGGAAA	12379	+	AGG	33
AGACATATTAGATCGAGTCA	12412	+	AGG	18
CATATTAGATCGAGTCAAGG	12415	+	AGG	9707
AGATCGAGTCAAGGAGGTTT	12421	+	TGG	20
ACAACATTCAAAGATTCAAC	12466	+	AGG	896
CTAAAGCTAAGAGTAATCAA	12509	+	AGG	7
TCAAAGGTTTACAGTCGTTG	12525	+	AGG	1529
AGAAGCGAAAGAGAAGTACG	12561	+	AGG	393
AGAGATGCAGTTATTAAAGT	12595	+	GGG	1
GTCAGTTGTATGAAAATATA	12617	+	AGG	91
TCAGTTGTATGAAAATATAA	12618	+	GGG	162
TATGAAAATATAAGGGAGTG	12625	+	TGG	1
ATGAAAATATAAGGGAGTGT	12626	+	GGG	532
GTTAAAATTAAAACTATTTC	12660	+	AGG	4010
AAAATTAAAACTATTTCAGG	12663	+	TGG	15
CTTTCAACATATTTTTCAAA	12695	-	AGG	2
GAAAGAATGACGAGTTTTAA	12729	+	TGG	20
GTATCTGTTTTAATATACGT	12767	-	TGG	869
TGAATCAATCACACTTATTG	12809	+	AGG	5605
ATCACACTTATTGAGGAGCA	12816	+	TGG	16
TCACACTTATTGAGGAGCAT	12817	+	GGG	65
CTGAGAATTTTATTACATGA	12851	+	CGG	1651
TTAACGATAGAAAAAGATTA	12956	+	TGG	477
AGAGAACTTGTATTGAACAA	12980	+	AGG	102
TTGAACAAAGGTTATATAGT	12992	+	TGG	140
TGAACAAAGGTTATATAGTT	12993	+	GGG	829

TATAGTTGGGATCAATGTTG	13006	+	AGG	1109
AGTTGGGATCAATGTTGAGG	13009	+	AGG	503
TTTTTCGGGAATTTCATTTT	13034	-	AGG	281
TTATTTCAGTGTACTTTTTC	13048	-	GGG	1554
ATTATTTCAGTGTACTTTTT	13049	-	CGG	80
TCAATCTTAGCTTTTTCTTC	13094	-	AGG	520
TCATTCATATTAGCCATCAT	13166	-	AGG	129
TGAATTTTACAGTCCTATGA	13169	+	TGG	4255
ATATGAATGAACATGAATTA	13195	+	AGG	1005
TATGAATGAACATGAATTAA	13196	+	GGG	886
TCTCCAGTATCAATTAAACT	13220	-	AGG	258
ATGCCTAGTTTAATTGATAC	13233	+	TGG	1890
AGTTTAATTGATACTGGAGA	13239	+	TGG	1190
GATTAAAAAACTTAAAAATA	13269	+	TGG	359
AAAAACTTAAAAATATGGAT	13274	+	TGG	551
GCTGGAATACTGCGATTATT	13312	+	CGG	249
TAACTAGCCACTGTGTATAT	13350	-	AGG	133
CATATCGCCTATATACACAG	13359	+	TGG	75
CTTGATGTACTTCTTTGTGT	13373	-	TGG	8380
CAACACAAAGAAGTACATCA	13390	+	AGG	9
AACACAAAGAAGTACATCAA	13391	+	GGG	162
ATAGCGCAGACATACAAGCT	13526	+	AGG	204
ATACAAGCTAGGTTAAAAGT	13537	+	AGG	43
AAAGTAAAAGTTAAGACGAT	13564	+	TGG	103
TTCTTTACTTCGTATAAGAT	13599	-	CGG	259
GATCTTATACGAAGTAAAGA	13617	+	AGG	2398
GCAAGTATATATTATGATGA	13718	+	CGG	138
GACGGCTAATGATGATGTAG	13736	+	AGG	183
CTCAACTTTGCGAAGTCACT	13745	-	CGG	2565
GCGATCAGTCTGATTTGATG	13783	+	AGG	1149
CGATCAGTCTGATTTGATGA	13784	+	GGG	16
TCAGTCTGATTTGATGAGGG	13787	+	CGG	37
GTCTGATTTGATGAGGGCGG	13790	+	AGG	15
GAGTCAATTGTTAATATGAT	13836	+	AGG	829
TGTATTAGCTGATGTAATAC	13880	+	CGG	118
ATTGAATTGCTATCATATTC	13883	-	CGG	913
AGCAATTCAATTGCACAGTA	13911	+	TGG	356
GAGTTTTCCCCTTGTGGTTT	13934	-	CGG	106
TTACTTGAGTTTTCCCCTTG	13940	-	TGG	4
GCAACGTTGCCGAAACCACA	13941	+	AGG	595
CAACGTTGCCGAAACCACAA	13942	+	GGG	25
AACGTTGCCGAAACCACAAG	13943	+	GGG	71
AAGTTGAAGATGTTGTTGTG	13978	+	AGG	439

GGCTTGAGAGAGCAAATAAA	13999	+	AGG	73
GTATGCTCAGATGTTAAAAG	14021	+	AGG	1867
AAATCAATCGCAACAGAGAT	14054	+	TGG	22
AATCAATCGCAACAGAGATT	14055	+	GGG	187
TTCTTAGAGTTATTGAAGAA	14094	+	AGG	21
TATTGAAGAAAGGTTATAAC	14104	+	AGG	388
ATTGAAGAAAGGTTATAACA	14105	+	GGG	290
TTTCTGTTCAATTTAGAGTT	14132	-	AGG	375
TCTTTTCTGCTAATTCATCA	14170	-	CGG	7371
GTAAGAATTATCTTAAGACG	14303	+	TGG	37
TAAGAATTATCTTAAGACGT	14304	+	GGG	190
AAGAATTATCTTAAGACGTG	14305	+	GGG	2562
ATCGATGAGAACATCTAATG	14318	-	TGG	4
AAACTACCCACCATATAGGC	14399	-	AGG	58
AATTAAACTACCCACCATAT	14403	-	AGG	177
TCACTTACTACCTGCCTATA	14405	+	TGG	34
CTTACTACCTGCCTATATGG	14408	+	TGG	384
TTACTACCTGCCTATATGGT	14409	+	GGG	38
CGTTCAATAAATGTGAAAGG	14452	-	AGG	896
CTACGTTCAATAAATGTGAA	14455	-	AGG	75
AATGCCCCTACATCTTGTGC	14480	-	AGG	412
GTAGCTCCTGCACAAGATGT	14490	+	AGG	63
TAGCTCCTGCACAAGATGTA	14491	+	GGG	117
AGCTCCTGCACAAGATGTAG	14492	+	GGG	222
AGCACAAACTTTTCTTGCTT	14575	-	CGG	980
AAGCAAGAAAAGTTTGTGCT	14594	+	AGG	806
TTTGTGCTAGGACTCATAGA	14606	+	GGG	13
CGTCAATATATGCTTTCCGT	14619	-	TGG	5994
TCATAGAGGGCAAGAGCCAA	14619	+	CGG	180
CGGAAAGCATATATTGACGC	14639	+	AGG	301
GGAAAGCATATATTGACGCA	14640	+	GGG	11
GACGCAGGGTATTCGACTAA	14654	+	AGG	159
TATTCGACTAAAGGTAAGAG	14663	+	TGG	58
ATTCGACTAAAGGTAAGAGT	14664	+	GGG	110
TTCGACTAAAGGTAAGAGTG	14665	+	GGG	9
CGAGTACACTTTTTAAAAAT	14706	+	CGG	2
TACACTTTTTAAAAATCGGA	14710	+	AGG	7
ACGCAATTTTTCGTACCTTC	14720	-	CGG	3387
AAAATCGGAAGGTTTCCGGA	14721	+	AGG	44
AAGTAGCTGAACAATCAAAA	14763	+	TGG	20
CATATTCTTCAAAGGCCTTT	14775	-	TGG	3074
ATCAAAATGGACACGCCAAA	14776	+	AGG	54
TAGCCACTCATATTCTTCAA	14783	-	AGG	1

AGGCCTTTGAAGAATATGAG	14796	+	TGG	82
TAAGAATGACATTGAAATAG	14833	+	AGG	3316
AAGAATGACATTGAAATAGA	14834	+	GGG	739
TCATACCATCTAAACTAGCG	14868	-	AGG	1628
GCATTCCTCGCTAGTTTAGA	14879	+	TGG	162
GGTATGAATAGAATGACGTT	14900	+	AGG	7156
AAGATTGAACAAATAGATAA	14978	+	AGG	4152
CAAATAGATAAAGGTGACAG	14987	+	TGG	148
ACAACTTCACGACGCAATAA	15028	+	CGG	1378
TAAACTTAAATCTTTATATA	15068	+	CGG	10
AGCAAACGCAAAAACAAGAT	15112	+	TGG	1215
TGGTTTATGTTAATTAATCA	15132	+	CGG	535
AATCACGGAGCAAAGCGTAC	15147	+	AGG	6051
CGAAAGATAGCAGACGAAGA	15219	+	AGG	410
GCACCAGCAAGTATATATTG	15236	-	AGG	175
ACACCTCAATATATACTTGC	15249	+	TGG	18831
ATACTTGCTGGTGCAACATT	15261	+	AGG	15
ATAGAGTTAACTAACAAATA	15306	+	TGG	323
TATAATTCATTCATGTTATT	15351	+	TGG	8006
CATGTTATTTGGCGTTCAAG	15362	+	TGG	219
GGCGTTCAAGTGGTTCAGAC	15372	+	AGG	136
ACAGGTCACAGTAAAGTAAG	15390	+	TGG	11
AGTGGTATAGGAGCTATACG	15408	+	TGG	53
ATACGTGGTATGACATCGTT	15423	+	TGG	205
AGCGTCGTTAGCGCATGAAG	15461	+	AGG	40
GAGATTAAGTCACGTTGTAG	15492	+	TGG	162
AAGTCACGTTGTAGTGGAAC	15498	+	TGG	144
TGGAACTGGTGCAAGAATAT	15512	+	TGG	1133
ATGCTCGGGATGGTCAGGGT	15525	-	TGG	208
ACCAATGCTCGGGATGGTCA	15529	-	GGG	58
AACCAATGCTCGGGATGGTC	15530	-	AGG	35
TCAACAACCAATGCTCGGGA	15535	-	TGG	165
TCTTTCAACAACCAATGCTC	15539	-	GGG	1296
ATCTTTCAACAACCAATGCT	15540	-	CGG	1268
ACCCTGACCATCCCGAGCAT	15544	+	TGG	23
GAAAATACAGATCCTAAAGC	15585	+	AGG	1166
TATTGTCATCGAGCTTAAAT	15604	-	TGG	1219
TAGATATAAAGAGTCTATTA	15656	+	AGG	126
CGTTCATAGAACATACCTGA	15671	-	TGG	624
ATTAAGGCTTCAACACCATC	15672	+	AGG	1031
TTCTATGAACGTAATATCAA	15699	+	CGG	335
AACGTAATATCAACGGTATG	15706	+	TGG	13
ACGTAATATCAACGGTATGT	15707	+	GGG	1685

ATCAACGGTATGTGGGTGTC	15714	+	TGG	29
GGTATGTGGGTGTCTGGTGA	15720	+	CGG	113
ATTCTCATTCAAATCAAAGT	15738	-	CGG	967
TACGATTAAAGCAGATGAAC	15776	+	TGG	1244
CCAGCAAAGTATTCTTTGAT	15791	-	AGG	75
CCTATCAAAGAATACTTTGC	15807	+	TGG	309
AATACTTTGCTGGTGTCGAC	15817	+	TGG	145
ATACTTTGCTGGTGTCGACT	15818	+	GGG	29
TACTTTGCTGGTGTCGACTG	15819	+	GGG	5
GACTGGGGTTACGAGCACTA	15834	+	TGG	69
TATGGATCTATTGTGTTAAT	15852	+	AGG	2
TCTATTGTGTTAATAGGACG	15858	+	AGG	42
TTAATAGGACGAGGTATAGA	15867	+	TGG	626
TGGTAACTTTTATTTTATTG	15887	+	AGG	7
AATCATCAATAAACTTAAAT	15904	-	TGG	1726
AATTTAAGTTTATTGATGAT	15922	+	TGG	1243
ATTTAAGTTTATTGATGATT	15923	+	GGG	220
TAAGTTTATTGATGATTGGG	15926	+	TGG	242
AAAGATATTGTAAGTAGATA	15957	+	TGG	51
CGCTGATAAAAGTAAACTAT	16058	+	CGG	199
GCTGATAAAAGTAAACTATC	16059	+	GGG	16
AAGTAAACTATCGGGTGTAG	16067	+	AGG	146
ACTTGTTCTTTATGATAATA	16121	+	TGG	760
TTCTTTATGATAATATGGAT	16126	+	AGG	64
TATGGATAGGTTTAAGCAAG	16139	+	AGG	308
AAGAGGTATTTAAATATGTT	16156	+	TGG	3851
TTATAGGCTCTCCGTTTGTA	16165	-	GGG	100
TTTATAGGCTCTCCGTTTGT	16166	-	AGG	749
TATGTTTGGCACCCTACAAA	16170	+	CGG	234
ACGTCATCAAATTCTTTTAT	16181	-	AGG	2986
AAAAGAATTTGATGACGTGT	16202	+	TGG	457
AGGTTTAGTATGTGTGTATA	16224	-	TGG	173
ATACTAAACCTGAACGATTA	16252	+	AGG	590
CTAAACCTGAACGATTAAGG	16255	+	AGG	307
TAAACCTGAACGATTAAGGA	16256	+	GGG	826
AACCTGAACGATTAAGGAGG	16258	+	GGG	1
ATAGATGATATTGAAGCACA	16301	+	AGG	21
ATTAGAGCCTCAATATGCTT	16315	-	AGG	12629
AATATTGCCTAAGCATATTG	16324	+	AGG	26
TAAAGACGATAGAGAGAGAA	16363	+	TGG	173
ATTGGTCGACGTTTGAATAT	16411	-	TGG	3665
AAATCTTCTTTTTCTTCAAT	16429	-	TGG	3083
GAAAAAGAAGATTTTGAAAC	16454	+	TGG	526

AAAGAAGATTTTGAAACTGG	16457	+	TGG	5
TTGAAACTGGTGGAAATGTA	16467	+	AGG	65
ACACGTGTTGGTTATTTACA	16550	+	TGG	35
TCATCTAAATCATAAGTAAC	16561	-	AGG	184
ACTATTTCTAATGGCAAAGT	16622	-	TGG	2422
ATCATCAACACTATTTCTAA	16631	-	TGG	3914
TAGAAATAGTGTTGATGATG	16651	+	AGG	984
GATGATGAGGATTCTGAAAT	16664	+	AGG	42
GGATTCTGAAATAGGTAAAA	16672	+	TGG	330
GGTAAAATGGCAGCAATTTG	16685	+	CGG	330
ATGGCAGCAATTTGCGGATA	16691	+	TGG	5
CAATTTGCGGATATGGTGCT	16698	+	AGG	142
TTAGCATATATTGATACGAA	16721	+	TGG	17
TTGATACGAATGGTGATGTT	16731	+	AGG	126
GCCAACAAAAATAACATTAT	16754	-	AGG	1062
AAGTAGCGCAATGAGTATGT	16792	-	AGG	1574
TATGAAAAAGATGATGATAA	16832	+	TGG	2415
TATTATGTATTTCGAGGAGA	16895	+	AGG	3
ATTGACGCTTTGCAAGAAGT	16919	+	TGG	111
TTGTTAGGTACACCAAACAA	16954	-	TGG	40
TTTGATTACAATCCATTGTT	16958	+	TGG	957
CCTATCATCTCTTTGTTGTT	16969	-	AGG	620
CCTAACAACAAAGAGATGAT	16985	+	AGG	102
GATGATAGGAGATGCTGAAA	16999	+	AGG	4
TACCCATACCGCGTAACACA	17082	-	AGG	2994
TTAGCATACCTTGTGTTACG	17090	+	CGG	527
ATACCTTGTGTTACGCGGTA	17095	+	TGG	125
TACCTTGTGTTACGCGGTAT	17096	+	GGG	61
ATTCAAGAAACACAAAAGAG	17135	+	TGG	272
TGAGTTGTTCGACAAAGATA	17164	+	TGG	161
TCTTTTCGATTCGATCTAAA	17217	-	TGG	1840
TTTAATTCTGACGAGTTTAA	17285	+	CGG	270
TTAAGTTTCATTCCAATGAT	17299	-	AGG	22
AACGGAAATGTACCTATCAT	17303	+	TGG	289
TGGAATGAAACTTAAACTTA	17323	+	TGG	269
GTAAGATGACAGCTATGTTG	17376	+	AGG	3138
TTATCTGCATTAAAGCGTAA	17417	+	AGG	1069
TATCTGCATTAAAGCGTAAA	17418	+	GGG	362
AAAGCGTAAAGGGTACAACT	17428	+	TGG	90
TACGAGTGAACTTAAATATC	17454	-	AGG	2367
GATTCTTCTAACTTATTAAC	17482	-	TGG	2349
GTTCTGAAACTTGTCCCTTC	17520	-	AGG	2075
ACAAGTGCTAATTAACCTGA	17521	+	AGG	92

CAAGTGCTAATTAACCTGAA	17522	+	GGG	24
GACAAGTTTCAGAACGAACA	17544	+	AGG	380
GTTTCAGAACGAACAAGGTT	17549	+	AGG	869
TGATTACGAATTAGACGAAA	17596	+	TGG	822
GCGTCACCTTCATCTATGTC	17635	-	AGG	472
AAATTACCTGACATAGATGA	17645	+	AGG	1215
TCATTCTGATTGGTTATTTT	17669	-	GGG	1800
ATCATTCTGATTGGTTATTT	17670	-	TGG	13
CTCATCAATATCATTCTGAT	17679	-	TGG	578
TGATATTGATGAGTATATCG	17705	+	AGG	662
GATATTGATGAGTATATCGA	17706	+	GGG	18
TTAGCAAATAGTTGTTCTAT	17735	-	TGG	128
ATGATGATGTGTATGTTACA	17827	+	TGG	987
CTGAATTCAATAAATACAAC	17851	+	AGG	2037
TAAATACAACAGGCTCAATA	17861	+	AGG	3439
AATAAGGAGTTAACTCGTAT	17877	+	AGG	5323
CATATAAATAAAGGCTCATA	17962	-	AGG	1856
GAGCCTTTATTTATATGAAA	17984	+	TGG	76
GTTTGATGTTCCGAGTAAAG	18026	+	AGG	1233
ATTAAACGAATGAACTCAAT	18056	-	AGG	7023
TCACGATGTTTTTGTAGTGT	18080	-	TGG	1346
ATACGTATGCACATTACACA	18135	+	AGG	14115
ATTACACAAGGTATTATGAG	18147	+	TGG	44
ACAAGGTATTATGAGTGGAG	18152	+	AGG	134
CAAGGTATTATGAGTGGAGA	18153	+	GGG	8
AAAGCAATACGTGATGATGT	18192	+	CGG	575
TAAAGCTCAATCATTGCGTG	18221	+	TGG	66
GGCAGAGCAATGTCACAAGC	18258	+	TGG	70
AGCTGGACTTGATAGCGCAA	18275	+	TGG	157
GCAATGGTTGCTAAAGATAA	18291	+	CGG	25
GTTTGAAGATGAAGAAACGT	18313	+	TGG	4972
GATACTCATCGTCATTTAGA	18363	+	TGG	6
ATACTCATCGTCATTTAGAT	18364	+	GGG	1
TACTCATCGTCATTTAGATG	18365	+	GGG	34
TCATTTAGATGGGGAATCAG	18374	+	TGG	50
GATCAGAATTTTAAATCAAG	18402	+	TGG	615
ATCAGAATTTTAAATCAAGT	18403	+	GGG	2922
TTTAAATCAAGTGGGTGTGT	18411	+	TGG	4
TTAAATCAAGTGGGTGTGTT	18412	+	GGG	63
ATCAAGTGGGTGTGTTGGGC	18416	+	AGG	85
TTTACACCAATAAATAGCTT	18425	-	GGG	233
GTTTACACCAATAAATAGCT	18426	-	TGG	129
CAGGCGCCCAAGCTATTTAT	18435	+	TGG	76

TTACGTGCTCTCATTACAGT	18512	-	TGG	3043
ATGAGAGCACGTAAAGACGA	18537	+	TGG	321
ACTCACGATAAGTCATGAAT	18559	-	GGG	1819
CATTCATGACTTATCGTGAG	18577	+	TGG	482
ATTCATGACTTATCGTGAGT	18578	+	GGG	906
TGGGAGAAATATAAGCGAAA	18597	+	AGG	1287
GAGAAATATAAGCGAAAAGG	18600	+	TGG	242
CGAAAAGGTGGTAATTGATA	18612	+	TGG	380
ATAAAAGTAAATGTTGATAC	18643	+	TGG	3233
CTCTATTATCTCTTCGTACA	18682	-	AGG	3420
AAATGAAGCTGATTTAGATA	18759	+	TGG	666
AGCAGTTTAACGACATGCTA	18841	-	AGG	24
GCTTTTTATTATGCACTTTT	18877	+	CGG	1028
TATGCACTTTTCGGACTGTT	18886	+	AGG	50
ATGCACTTTTCGGACTGTTA	18887	+	GGG	121
CGGACTGTTAGGGTACGCGA	18897	+	AGG	5
GGACTGTTAGGGTACGCGAA	18898	+	GGG	2
AGGGTACGCGAAGGGCAAAA	18906	+	AGG	4
AGAAGTAAAAGATTATCTAA	18990	+	AGG	84
TTATCTAAAGGGACTTAAGA	19002	+	CGG	360
GTGTCTGTTGATGACGTTAA	19024	+	AGG	104
GAATGATAACGATCTAATTC	19068	-	AGG	8451
TTAGATCGTTATCATTCGAA	19090	+	AGG	396
ATGGAAAGAGAAAAATCTTG	19122	+	AGG	343
ATCTAATCGAACAAGAAGTA	19145	+	CGG	159
TTTTGTTCTTCTGATTGCTC	19161	-	AGG	2121
GTTAGAAAAACGCGACGCAG	19224	+	AGG	940
AAGTTAAGAAGTAACGCGCT	19258	+	AGG	260
TAACGCGCTAGGTAAAGCGC	19269	+	AGG	26
AATCTATCAACTAAGGATGT	19287	-	TGG	195
GCCTAAAAATCTATCAACTA	19294	-	AGG	1770
TCCTTAGTTGATAGATTTTT	19309	+	AGG	576
TTTTTGAACATACTTGTCAA	19363	-	AGG	168
TTTGACAAGTATGTTCAAAA	19381	+	AGG	8
GAGTCTAAATTTAAATCGAG	19408	+	TGG	4418
CAATGGACTTTACATTTGAA	19451	-	GGG	10
TCAATGGACTTTACATTTGA	19452	-	AGG	441
TTCTTTCGCCATTTCTTCAA	19468	-	TGG	1360
TGTAAAGTCCATTGAAGAAA	19476	+	TGG	101
CAATATTAGAAAATAAAGTG	19509	+	AGG	7
TAAAGTGAGGTAATAAAATA	19522	+	TGG	105
ACATTGCCTGGCGTGTATGT	19534	-	TGG	103
GCAACTCCAACATACACGCC	19544	+	AGG	260

TCCGATAAAATAACATTGCC	19546	-	TGG	2337
GCCAGGCAATGTTATTTTAT	19561	+	CGG	153
ATTAAAGTACCTTGTTCTGC	19588	-	TGG	2180
GGCGTTATTCCAGCAGAACA	19595	+	AGG	171
TTTAATCATGAAAGACATTA	19621	+	TGG	305
TTTTTCTTTTGTGCTGTCAT	19663	-	TGG	873
AAATTTACTTACTTAGCAAA	19700	+	AGG	3
ACTTACTTAGCAAAAGGTGT	19706	+	AGG	143
CAAAAGGTGTAGGCGCCTAC	19716	+	TGG	37
AAAAGGTGTAGGCGCCTACT	19717	+	GGG	70
ATTTCTGCTTGTGCATATTC	19753	-	AGG	1812
TGAATATGCACAAGCAGAAA	19771	+	TGG	539
GAAATGGAAGCTAAGAAAAT	19787	+	TGG	1
TTAAGAAACTCTTTTGATAA	19804	-	CGG	256
TGCAAAAGATTTCTTTAATG	19849	+	AGG	352
TAAAATGCCTCTGCAATTAG	19861	-	AGG	189
GGTTAAACCTCTAATTGCAG	19870	+	AGG	24
TAGTACCAAAGATAACAGCT	19896	-	TGG	1175
TTTGACCAAGCTGTTATCTT	19907	+	TGG	1688
CCACTAGTTGAAGTGTTGTA	19924	-	AGG	22
CCTTACAACACTTCAACTAG	19940	+	TGG	232
AGTGGTAAACCGCTTGTTGA	19958	+	AGG	283
GTTGAAGGCGCAGAAGAGAA	19973	+	AGG	70
TAGTAGCCATTAATGCCGAA	20016	-	AGG	9
TAATTTATACGTAGACCTTT	20017	+	CGG	1141
GATGAAGAGTTAGATCCAAA	20060	+	CGG	1
TTCCCGTTAGCATCAAATAA	20128	-	TGG	93
AGACCATTATTTGATGCTAA	20141	+	CGG	1
GACCATTATTTGATGCTAAC	20142	+	GGG	2738
TCCGCTCCAGTATAAGATAG	20167	-	TGG	30
GGATTACCACTATCTTATAC	20177	+	TGG	2347
ACCACTATCTTATACTGGAG	20182	+	CGG	9
AAAGAAATCGTTAGCACTAA	20218	+	TGG	1
AAGAAATCGTTAGCACTAAT	20219	+	GGG	721
CGTTAGCACTAATGGGTGAT	20226	+	TGG	6
GTTAGCACTAATGGGTGATT	20227	+	GGG	39
GATTGGGATTACGCACGTTA	20243	+	CGG	2103
GCACGTTACGGTATCTTACA	20255	+	AGG	104
TGCTTGTAACGTCGTTAACG	20288	-	TGG	1535
TTACAAGCATCAGATGCTTC	20318	+	TGG	38
GTTCAAATAATGATACTGGT	20325	-	TGG	1459
TCACGTTCAAATAATGATAC	20329	-	TGG	12
TTAAGCGTTGCGAACGCTTC	20401	-	TGG	13

CATATCTCCTCCTATTCAGT	20425	-	TGG	388
AACGCTTAAACCAACTGAAT	20431	+	AGG	533
GCTTAAACCAACTGAATAGG	20434	+	AGG	20
CTGAATAGGAGGAGATATGA	20445	+	TGG	105
TTTACCTTAATATCTTCTGC	20457	-	AGG	431
TAATCCTGCAGAAGATATTA	20469	+	AGG	5
GACTATTACTGTTACAAAGA	20508	+	AGG	15
GACTCTTATTACAGTCTTGT	20536	+	CGG	1728
CAGTCTTGTCGGTTACAAAG	20547	+	AGG	163
CGCTCTTATCAGACGTAGTA	20564	-	CGG	1169
AAACTTTTACTCAAGAAAAA	20634	+	TGG	4
TTTACTCAAGAAAAATGGAG	20639	+	TGG	252
TGAAGAAGAAATATTTAAGA	20675	+	TGG	134
ATATTTAAGATGGAAGTTGA	20685	+	CGG	37
ACGGAATACTAGAAGATGTT	20704	+	AGG	655
AACAATGATTTTATGAAAGA	20736	+	TGG	471
ACATACTTTTTGATTGAGTA	20756	-	AGG	441
CAGGTCGTTGATAATACTCT	20788	-	AGG	1085
TTTAAATTCTTTTTAACTTC	20807	-	AGG	46
GAATTTAAAGTCAAGAAGTA	20837	+	TGG	114
AATTTAAAGTCAAGAAGTAT	20838	+	GGG	2034
ATTTAAAGTCAAGAAGTATG	20839	+	GGG	2854
GTGTCGTACACTTATAACGA	20865	+	TGG	42
ATACTCCACTAATGTAATCA	20875	-	GGG	71
AATACTCCACTAATGTAATC	20876	-	AGG	938
GGTGTCCCTGATTACATTAG	20886	+	TGG	19
ACATTAGTGGAGTATTAAAC	20899	+	AGG	227
CTCTACCTTATTGATTTAAA	20927	-	CGG	29
TTCATCCGTTTAAATCAATA	20938	+	AGG	1198
CGTTTAAATCAATAAGGTAG	20944	+	AGG	385
GTGTGAGGGAATTCGTCGTA	20968	-	TGG	48
TTCCAATAGAAATAGTGTGA	20982	-	GGG	5
TTCCCTCACACTATTTCTAT	20996	+	TGG	1532
ATTGGAAGTATCAAAAAAGT	21014	+	AGG	115
ACAAAGCGTTCTTGTATAAT	21028	-	TGG	91
GTAAGCGATAAAACAATTAA	21065	+	AGG	14
TAAAACAATTAAAGGATTTA	21073	+	TGG	463
TTTAGTTGTTCAGATGTAGT	21085	-	AGG	2785
GTAAGTCGTAAGGTACATAT	21141	-	AGG	212
TTAGCTATTGGTAAGTCGTA	21151	-	AGG	59
AATAAATTGTTTTTAGCTAT	21163	-	TGG	1021
AAACAATTTATTTGAGTATG	21190	+	AGG	40
AACAATTTATTTGAGTATGA	21191	+	GGG	156

GGTAGAATCTTTAGTATTGT	21212	+	AGG	61
TGTAGGCGATTCTGTAGATC	21229	+	AGG	6
GGCGATTCTGTAGATCAGGG	21233	+	CGG	15
TAAACTACTACGACTTAAGC	21268	+	AGG	486
CGTACTTAACTTTTGCCATA	21277	-	TGG	281
CGACTTAAGCAGGTGCCATA	21278	+	TGG	4230
CATATGGCAAAAGTTAAGTA	21294	+	CGG	1
TAAGTACGGTGCTGATAGCA	21308	+	TGG	142
TGATAGCATGGTTGTTGAAT	21320	+	TGG	16
TCGATAAGAAAATAGAAGAG	21349	+	TGG	13
CGATAAGAAAATAGAAGAGT	21350	+	GGG	140
ATAGAAGAGTGGGTTAAAAA	21360	+	AGG	12
TCTAAAAAACCTAAGTCAAC	21416	-	AGG	5245
GCATTAGCTCCTGTTGACTT	21423	+	AGG	382
ATTGACTTTAAATATTTCGA	21462	+	TGG	40
GACTTTAAATATTTCGATGG	21465	+	TGG	73
ACTTTAAATATTTCGATGGT	21466	+	GGG	454
TGCGCCGACACTTATAACAC	21477	-	TGG	27
TTATCCAGTGTTATAAGTGT	21489	+	CGG	150
TATGCAATATACGTTGAATA	21519	+	CGG	138
ATATACGTTGAATACGGTAC	21525	+	TGG	15
GGTACTGGTATATATGCTAC	21540	+	TGG	124
GGTATATATGCTACTGGTCC	21546	+	TGG	225
TTTGTAGCACGACTACCACC	21548	-	AGG	1109
ATATATGCTACTGGTCCTGG	21549	+	TGG	77
TGGAGTTTTAAAGGTGATGA	21594	+	CGG	68
TTAAAGGTGATGACGGCGAA	21601	+	TGG	5
GGCGAATGGTACACAACATA	21615	+	TGG	459
GCAGGGTTCCAAAATGGCTG	21629	-	TGG	19
TCAATTGCAGGGTTCCAAAA	21635	-	TGG	9
GTCAAGCGCCACAGCCATTT	21637	+	TGG	30
TGCGTCCTGCGTCAATTGCA	21646	-	GGG	1300
TTGCGTCCTGCGTCAATTGC	21647	-	AGG	423
TGGAACCCTGCAATTGACGC	21657	+	AGG	140
TCGAGCAGTATTTTTCATAG	21691	+	AGG	93
AGCAGTATTTTTCATAGAGG	21694	+	TGG	70
CATAGAGGTGGTTAAATATG	21706	+	TGG	1
TATATTTGATTTGTAAGTTC	21725	-	AGG	1983
CAACTAGTTTGTTAATGTTA	21766	-	GGG	30
TCAACTAGTTTGTTAATGTT	21767	-	AGG	47
TTAACAAACTAGTTGATGAT	21790	+	AGG	45
TAACAAACTAGTTGATGATA	21791	+	GGG	2
ATTCACCCACAACAATATAT	21829	-	GGG	8722

GATTCACCCACAACAATATA	21830	-	TGG	280
TGTTTACCCATATATTGTTG	21839	+	TGG	3
GTTTACCCATATATTGTTGT	21840	+	GGG	3591
GCAACAATGAGAGAAACAGT	21894	+	CGG	95
ACAGTTCGCTACACAATACG	21938	+	AGG	363
AAGCTCATTTTAAGCGCGAT	21963	+	AGG	70
TCGTAATTATCTATTTCTAT	21986	-	AGG	494
ATACTGCTTGACTATCGATA	22021	-	CGG	118
TAGTAAACCTGTCTATATCA	22045	-	GGG	179
TTAGTAAACCTGTCTATATC	22046	-	AGG	47
CAGTATTCCCTGATATAGAC	22054	+	AGG	162
ATAGACAGGTTTACTAAGCA	22068	+	TGG	225
TTACTAAGCATGGCACGATA	22078	+	CGG	135
AGACATAAAAAGAAAAACGA	22116	+	AGG	15
AAACGAAGGAGTGTATTAAA	22130	+	TGG	36
GGATCTAAGTCAGTTTCAGC	22166	-	TGG	6933
TTATTAGCTGACTTACAAGA	22218	+	AGG	697
TTAGCTGACTTACAAGAAGG	22221	+	TGG	6
GATTTAGCTGAAATAGTACG	22260	+	AGG	510
AATAGTACGAGGCGGTAAAA	22271	+	CGG	3
AATGATTCTGACATTGCATT	22286	-	GGG	3506
AAATGATTCTGACATTGCAT	22287	-	TGG	44
GAATCATTTAAATTAACAAT	22317	+	TGG	536
TTAACAATTGGTAATGTGCC	22329	+	TGG	43
GCTTCAATTCCTTTATCTCC	22331	-	AGG	108
GGTAATGTGCCTGGAGATAA	22338	+	AGG	4
GTGAAACACGCTGTACAAAC	22371	+	AGG	3135
AAACACGCTGTACAAACAGG	22374	+	TGG	5
CAGGTGGACAGTTGCGTATA	22390	+	TGG	3
GAGCGTAATAAACGTGCAGA	22419	+	CGG	178
GGTAAACATCACGGAATGTT	22440	+	TGG	1151
AATGACATTTCAAATGATTC	22457	-	TGG	985
AACTATCATTAAAAGTTAAA	22519	+	TGG	1429
GCAGCTTCAAACCACTCTTT	22556	-	CGG	86
AAGATAACTTGCCGAAAGAG	22561	+	TGG	46
AAAGAGTGGTTTGAAGCTGC	22575	+	AGG	318
AATTTTTCGTATTCAACTGT	22586	-	AGG	1583
ACAGTTGAATACGAAAAATT	22605	+	CGG	126
GAAAAATTCGGCGAAAAAGT	22617	+	CGG	1
TGTTGTATCTGATTCACACA	22667	+	CGG	3938
ATCTATTAGTTTACATAGAA	22678	-	TGG	69
CTATGTAAACTAATAGATCA	22699	+	AGG	14
TATGTAAACTAATAGATCAA	22700	+	GGG	8

ATGTAAACTAATAGATCAAG	22701	+	GGG	5
TGTAAACTAATAGATCAAGG	22702	+	GGG	93
AATTTTTTTATAAAAAAATA	22717	-	GGG	1
TTTATAAAAAAATTGAAAAG	22742	+	AGG	96
TTAATTTTTAATGTTGTAAT	22772	-	TGG	712
ACAACATTAAAAATTAATGA	22794	+	CGG	220
CTGAGAATTTTTCAGCTTTT	22846	-	CGG	1153
TTCTCAGAAGATAGCGAAGA	22878	+	TGG	2
TCTCAGAAGATAGCGAAGAT	22879	+	GGG	51
GATAGCGAAGATGGGAGAAA	22887	+	AGG	2
GGGAGAAAAGGAGCAATGCC	22899	+	AGG	50
TTAAATATAACATTGAATCC	22901	-	TGG	524
GGATTCAATGTTATATTTAA	22920	+	CGG	52
CTAATTGTTCTCGAGTTGGT	22993	-	GGG	494
TCTAATTGTTCTCGAGTTGG	22994	-	TGG	3
TTTTCTAATTGTTCTCGAGT	22997	-	TGG	2580
TGATTTCATCACTGAAAACG	23045	+	AGG	11
TCCAAAGCCCCTTGTAATAA	23060	-	CGG	148
GATACTTTGCCGTTATTACA	23067	+	AGG	406
ATACTTTGCCGTTATTACAA	23068	+	GGG	4
TACTTTGCCGTTATTACAAG	23069	+	GGG	1
GCCGTTATTACAAGGGGCTT	23075	+	TGG	114
ACAATAGTGGTTTTTTCAAG	23107	+	AGG	3
CAATAGTGGTTTTTTCAAGA	23108	+	GGG	3
AGAGGGAGAGTCGCTCGTAC	23125	+	TGG	124
TCCTCGCTTTTGGCCATATT	23150	-	CGG	39
ATTGAACAAAGCACCGAATA	23153	+	TGG	39
CATTTCTTTGTCCTCGCTTT	23160	-	TGG	17
ACCGAATATGGCCAAAAGCG	23165	+	AGG	98
GACAAAGAAATGACGAAAGC	23187	+	AGG	758
AATGATGAAAGAGAATTACA	23216	+	AGG	50
AGAGAATTACAAGGAAATCA	23225	+	TGG	50
GAGAATTACAAGGAAATCAT	23226	+	GGG	501
TATTTTTGAGTAATCGTGTA	23240	-	AGG	98
TACACGATTACTCAAAAATA	23259	+	AGG	5
CAACTGACAGCTAGATATTT	23282	+	AGG	492
GTGCTAACAATTCATGTTCA	23295	-	GGG	21
AGTGCTAACAATTCATGTTC	23296	-	AGG	277
AGCCAATCACGCCATTCAGC	23323	-	AGG	74
TAGCACTAACACCTGCTGAA	23328	+	TGG	203
CACCTGCTGAATGGCGTGAT	23337	+	TGG	10
TGGCGTGATTGGCTTATTGG	23348	+	TGG	17
TGATTGGCTTATTGGTGGTC	23353	+	AGG	21

GGCTTATTGGTGGTCAGGAT	23358	+	AGG	48
TTAATAATTGTCTTTGATCT	23367	-	AGG	284
ATTGAACAAGCGCAAGCTAA	23405	+	CGG	494
GCTTAGTACAAGCTTCTAAG	23427	+	AGG	43
CGTTACGAAATAAGAGAACC	23483	+	TGG	195
TGTACACGAGCATAGCTACC	23485	-	AGG	13101
GCTAACCTCCTTTCGATTCA	23571	-	AGG	4
AGAAAATTCCTTGAATCGAA	23579	+	AGG	85
AAATTCCTTGAATCGAAAGG	23582	+	AGG	4
GCCATAAAATGAGTATCCAA	23593	-	AGG	931
ATCGAAAGGAGGTTAGCCTT	23593	+	TGG	97
GCCTTTGGATACTCATTTTA	23608	+	TGG	361
TCATTTTATGGCAAAGATTA	23620	+	TGG	78
GAGCTTTCCTTACGTTGCTT	23643	-	TGG	81
GAGATTTCCAAAGCAACGTA	23652	+	AGG	979
ACATCTGTTTCAATTTCGTT	23689	-	TGG	1222
TAGCGCGTTGTAAAGCTCTT	23733	-	TGG	144
TTTACAACGCGCTAAATCAA	23758	+	TGG	386
CTAAATCAATGGCTCAACGA	23769	+	TGG	1204
CTAAAGCTACTGTCGAAGCT	23937	+	TGG	34
GAGAAAACATGTTGTTAAGT	23959	+	TGG	40
CTTTAACCGCCATTTTAGCG	23979	-	GGG	90
CCTTTAACCGCCATTTTAGC	23980	-	GGG	576
CCCTTTAACCGCCATTTTAG	23981	-	CGG	2
AGATGCAAACCCCGCTAAAA	23986	+	TGG	10
TGCAAACCCCGCTAAAATGG	23989	+	CGG	141
AAGATTTAATAGATCTTAGC	24027	+	AGG	7112
ATTTCCTAATTTCCATCTGC	24053	-	TGG	3656
TTGATATTGATTCCAGCAGA	24057	+	TGG	30
GATTCCAGCAGATGGAAATT	24065	+	AGG	2
AAAGAATTCAATGAAGTCGA	24101	+	AGG	3
GGAGCAGTTAAACGTTCTTT	24122	+	CGG	42
ATTATGAGAAAAGAAGTAAA	24158	+	TGG	3
TAAATGGAACAAGTGATATT	24174	+	TGG	673
AAATGGAACAAGTGATATTT	24175	+	GGG	2
AATGGAACAAGTGATATTTG	24176	+	GGG	13
AACAACTCATTGAAAGATTA	24206	+	CGG	256
GAAAGATTACGGCGAGAAAA	24217	+	TGG	87
AGTTCGGATTTTAGTAGCTA	24227	-	AGG	129
CGAAGATAGTACCGAAAGTT	24243	-	CGG	19
GCTACTAAAATCCGAACTTT	24248	+	CGG	61
CGGTACTATCTTCGCGCAAC	24268	+	AGG	335
ATCTTCGCGCAACAGGTCAA	24275	+	AGG	57

GGTACTAATCCGGCAATCAC	24313	-	TGG	68
GCATTGATACCAGTGATTGC	24320	+	CGG	575
CATTATTGCAGGTACTAATC	24323	-	CGG	28
TTAAGTACTGCCATTATTGC	24334	-	AGG	256
CGGATTAGTACCTGCAATAA	24340	+	TGG	54
AATAATGGCAGTACTTAATG	24355	+	CGG	1
ATGGCAGTACTTAATGCGGT	24359	+	TGG	12
CTTAATGCGGTTGGTGTATT	24368	+	AGG	32
GCGGTTGGTGTATTAGGTGG	24374	+	TGG	2
GTTGGCGCATTCTCTGTCGC	24410	+	AGG	8
GCATTCTCTGTCGCAGGTCT	24416	+	TGG	93
GTCGCAGGTCTTGGAGTTGT	24425	+	TGG	20
GGTCTTGGAGTTGTTGGCTT	24431	+	TGG	17
AGTTGTTGGCTTTGGTGCAA	24439	+	TGG	107
GGCTATTAGCGCTCTTAAAA	24460	+	TGG	84
GCTCTTAAAATGGTTGAAGA	24470	+	TGG	7
AATGGTTGAAGATGGAACAT	24478	+	TGG	17
GCGATCAGTTAAAAACTACA	24537	+	TGG	518
ATCTTTAATGCGATGTCAGC	24590	+	AGG	3099
GCGATGTCAGCAGGTATCAG	24599	+	AGG	73
ATAGATACTTCAGATAAGAA	24634	-	TGG	323
AGCAAACGCACGCAAGTTTG	24682	+	AGG	65
ACGCACGCAAGTTTGAGGAT	24687	+	TGG	6
CGCACGCAAGTTTGAGGATT	24688	+	GGG	36
TTTGAAGCATTGAATAGCAT	24740	+	AGG	49
AGCATAGGTGGCGCAATCTT	24755	+	CGG	3
GGAGATTTATTGAACGCTGC	24776	+	AGG	6
TTGAACGCTGCAGGAAGATT	24785	+	TGG	109
TGAGACACAAATTTGAACAA	24826	-	CGG	27
TTGTTCAAATTTGTGTCTCA	24845	+	AGG	235
AGCCCAATTTTGGAAAGCTA	24866	-	TGG	80
CCACACTATTAGCCCAATTT	24876	-	TGG	38
TGTCCATAGCTTTCCAAAAT	24879	+	TGG	3
GTCCATAGCTTTCCAAAATT	24880	+	GGG	22
CCAAAATTGGGCTAATAGTG	24892	+	TGG	12
AATTGGGCTAATAGTGTGGC	24896	+	TGG	12
ACCACTAACTTACCTAAGAT	24953	+	TGG	594
CCTAAGATTGGTCAGATATT	24965	+	TGG	16
ATATTTGGCAATGTGTTCGC	24980	+	TGG	1064
GGCAATGTGTTCGCTGGTAT	24986	+	TGG	493
ACAGTTCTAACATTTTTGAC	25035	+	TGG	180
TAACTTCTCAATTTAGAGCA	25068	+	TGG	57
AGAGCATGGTCAGAACAAGT	25082	+	AGG	39

GAACAAGTAGGACAATCACA	25094	+	AGG	3
ATCAGTTACGTTCAAGAGAA	25130	+	TGG	15
CCGATTAACTGCATAATAGT	25138	-	AGG	3611
CCTACTATTATGCAGTTAAT	25154	+	CGG	179
TAATATCGTAAAAGCGTTAG	25177	+	TGG	178
GTAAAAGCGTTAGTGGCATT	25184	+	TGG	1430
AGTGGCATTTGGTACTGCAA	25195	+	TGG	7
TCTAGTAATTTACTAGCTAT	25204	-	AGG	47
GATTTCGTTACTAATTTAGC	25241	+	TGG	4
TGGGTGTGCTTCGAATAGTT	25256	-	TGG	40
CGATAATTTGAGCGACTGCT	25275	-	GGG	135
CCGATAATTTGAGCGACTGC	25276	-	TGG	411
CCAGCAGTCGCTCAAATTAT	25292	+	CGG	4
GCTCAAATTATCGGTGTTAT	25301	+	CGG	52
ATCGGTGTTATCGGTATTTT	25310	+	AGG	46
GTATTTTAGGTGGCGTATTT	25323	+	TGG	5
TATTTTAGGTGGCGTATTTT	25324	+	GGG	24
TGGCGTATTTTGGGCTTTAA	25333	+	TGG	267
ACACTGCTAACAGCTGCAAT	25342	-	CGG	1200
CTGGATTTAACTAGAATAAC	25430	+	TGG	5
TGGATTTAACTAGAATAACT	25431	+	GGG	432
GGATTTAACTAGAATAACTG	25432	+	GGG	41
TTTAACTAGAATAACTGGGG	25435	+	TGG	7
GGGGTGGTAAGTAAAGCGTT	25451	+	CGG	3
AAAGCGTTCGGTTTATTGAC	25463	+	TGG	2
GTGCTTTCACAAGTATTTCT	25485	+	TGG	1559
ACTGCAACTACTGCTAATAT	25492	-	TGG	998
GCAGTCATTGGTGTATTCAT	25526	+	TGG	109
TTGGTATTCTTGTTTATTTA	25545	+	TGG	7
GAAAAACAATAACAGAAGCT	25587	+	TGG	3060
ACAATAACAGAAGCTTGGAA	25592	+	CGG	138
GGTATTAAAACAGCAGTTTC	25613	+	CGG	59
TACTACACCTTGAATCGCAC	25616	-	CGG	120
GCAGTTTCCGGTGCGATTCA	25625	+	AGG	1
CGATTCAAGGTGTAGTAGAT	25638	+	TGG	184
TAGATTGGTTAACTCAATTG	25653	+	TGG	249
AGATTGGTTAACTCAATTGT	25654	+	GGG	16
GATTGGTTAACTCAATTGTG	25655	+	GGG	65
TGTCCTAATACTTGTAATAT	25693	-	AGG	293
ATGCCTATATTACAAGTATT	25706	+	AGG	23
CATGCAAGTTTTAGGTGTTT	25738	+	TGG	103
GTTTTAGGTGTTTTGGTAAT	25745	+	AGG	11
AATGTTATGAATATCATACA	25778	+	AGG	5

TGAATATCATACAAGGTTTG	25785	+	TGG	82
ATATCACTGTTCCTATGGCT	25812	-	TGG	206
TACGGATATCACTGTTCCTA	25817	-	TGG	71
ACAATTGCGTTCCAAGCCAT	25817	+	AGG	23
TACTATGATTTGGACAGCTA	25835	-	CGG	3
TGAATAAACCTACTATGATT	25845	-	TGG	60
GTAGCTGTCCAAATCATAGT	25853	+	AGG	41
GCTTTAATTCAGTTGCTTAC	25886	+	TGG	1274
TTGCTTACTGGCGACTTCTC	25898	+	AGG	7
CTGGCGACTTCTCAGGTGCT	25905	+	TGG	11
TGGCGACTTCTCAGGTGCTT	25906	+	GGG	16
CCAAATCGTATCAAGTACAT	25934	-	TGG	2239
CCAATGTACTTGATACGATT	25950	+	TGG	500
GGCAATACATGCAATCAGTT	25971	+	TGG	937
TCAGTTTGGGAGTCAATTAT	25985	+	CGG	18
TCAATTATCGGCTTTTTAAC	25997	+	TGG	28
AATCGAACGCTTTCAATGTT	26027	+	TGG	52
TTTCAATGTTTGGTACAAGT	26037	+	TGG	36
GTACAAGTTGGTCACAGATA	26049	+	TGG	13
CTAATTTTGTTAGCAGTATT	26082	+	TGG	27
TTTGGAGCACTGTTACAAGT	26100	+	TGG	987
GTTGGTTCAGTCGTGTTGCT	26118	+	TGG	790
CAGTCGTGTTGCTTGGAGTG	26125	+	TGG	22
TTGGAGTGTGGCTGAAAAAA	26137	+	TGG	1
TGGAGTGTGGCTGAAAAAAT	26138	+	GGG	18
CTGAATGGGTTTCTAACATT	26193	+	TGG	240
TTCGCGAGTAAAGTAGCTGA	26231	+	TGG	128
TCGCGAGTAAAGTAGCTGAT	26232	+	GGG	289
AAAAGAGTTGTCTCAAATGT	26258	+	AGG	6
GTTGTCTCAAATGTAGGTGA	26264	+	CGG	237
GACGGTATGAGTGATGCACT	26282	+	TGG	422
TTCAGTGATTTCTTAAATGC	26321	+	CGG	703
TTTGCCGATTAATTCCGCTC	26324	-	CGG	67
TGATTTCTTAAATGCCGGAG	26326	+	CGG	58
AATGCCGGAGCGGAATTAAT	26336	+	CGG	40
ATTAATCGGCAAAGTAGCTG	26350	+	AGG	126
TTAATCGGCAAAGTAGCTGA	26351	+	GGG	34
GACTACTTTGTGCGCAGCAT	26363	-	TGG	83
TGCGCACAAAGTAGTCAGCG	26386	+	CGG	78
CACAAAGTAGTCAGCGCGGT	26390	+	AGG	258
GCGATGCGATTTCATCAGCT	26412	+	TGG	12
CGATGCGATTTCATCAGCTT	26413	+	GGG	3
TCTGTAACTTCATTCGTAAG	26438	+	TGG	34

ACTTCATTCGTAAGTGGACA	26444	+	CGG	9
CACGGTGGAGGTAGTAGCTT	26462	+	AGG	21
GGAGGTAGTAGCTTAGGTAA	26468	+	AGG	6
TAGCTTAGGTAAAGGTTTAG	26476	+	CGG	102
AAAGTAATTGCTACAGACTT	26510	+	TGG	65
AGAGGATAGCTCTTTATTAA	26522	-	AGG	172
TATACTATCTGTCAAAGTAG	26540	-	AGG	322
CTGTCTATAGAAGTACTTAC	26569	-	AGG	642
CTAATCGTTACATTCACAAT	26638	-	AGG	1452
GAATGTAACGATTAGAAATG	26662	+	AGG	34
AATGTAACGATTAGAAATGA	26663	+	GGG	22
TGCGTGATTTAATTAAATCA	26673	-	AGG	1
GAAGTTTCAACTTATTATAA	26736	+	GGG	11
GTTTCAACTTATTATAAGGG	26739	+	AGG	9
CGCACGATATAGAAGTAATA	26777	+	AGG	157
TCCAAGTGATTATAAGTGAA	26814	-	AGG	43
TCCTTTCACTTATAATCACT	26829	+	TGG	2318
GTAGTTGAATATAACGTTAC	26854	+	AGG	663
GAATATAACGTTACAGGCGC	26860	+	AGG	22
TCGTAACTATTCTGATATAG	26889	+	AGG	54
CGTAACTATTCTGATATAGA	26890	+	GGG	141
TCTGATATAGAGGGTATTGA	26899	+	TGG	38
AAAAAGTAGAGCTTAAGATA	26954	+	AGG	397
TGTGAAGCATAAGCAATTTT	26970	-	AGG	279
AACGTCCAGCAAATAGTGCT	27008	-	TGG	187
GACGTCCAAGCACTATTTGC	27019	+	TGG	252
TTGCTGGACGTTTTTATTTA	27035	+	AGG	1
TGCTGGACGTTTTTATTTAA	27036	+	GGG	3
TCATACTTAATTGAATTGTC	27063	-	TGG	239
TCAAATGCTTGTTTGTCTTT	27102	-	TGG	62
TTTGAGCTTGATTATGTTGA	27136	+	TGG	48
GATGGACGACAACTTTTTGT	27154	+	AGG	2505
TTTGACACAACACAAACATC	27196	+	AGG	496
TTGACACAACACAAACATCA	27197	+	GGG	1092
TGACACAACACAAACATCAG	27198	+	GGG	238
ACTTTCAAAGTATGGTAGTT	27229	-	CGG	78
TAACCGACACTTTCAAAGTA	27237	-	TGG	190
CTACCATACTTTGAAAGTGT	27250	+	CGG	218
CAGGTACCGACCATTTTTCA	27287	-	GGG	619
TCAGGTACCGACCATTTTTC	27288	-	AGG	7
GTAATAACGACCCTGAAAAA	27293	+	TGG	4
TAACGACCCTGAAAAATGGT	27297	+	CGG	422
TCGTTTGTAGGCAATCTATC	27306	-	AGG	98

CTCTTATCACCTTCGTTTGT	27318	-	AGG	26
GATAGATTGCCTACAAACGA	27325	+	AGG	40
CTACAAACGAAGGTGATAAG	27335	+	AGG	80
ACATTTTACAACACTAACTC	27367	+	AGG	1618
AACTGATTAAACTGTGTTAA	27399	-	AGG	59
AGATGTTAAAGCTAATGATA	27465	+	AGG	450
GTTAAAGCTAATGATAAGGA	27469	+	TGG	1
TTCACTTTCTATACAGATAA	27493	+	AGG	15
AGGAAATATCTCAGTTATTA	27513	+	AGG	354
AAGGAAGTTGATTTAAAAGC	27532	+	CGG	55
GTCGAAGATTATTTTATCTC	27535	-	CGG	1098
GGAGATAAAATAATCTTCGA	27553	+	CGG	58
TATATTTAAATAACCTCTAT	27568	-	AGG	1203
GACGGTAAACATACCTATAG	27571	+	AGG	272
TAATAAAACTTTAGAACAAC	27615	+	CGG	205
TTCCAGCCTGGATATAAAAC	27618	-	CGG	9
GAACAACCGGTTTTATATCC	27628	+	AGG	300
GACTTGAATCGATTCCAGCC	27630	-	TGG	18
AACCGGTTTTATATCCAGGC	27632	+	TGG	47
CACAAATTATATTTTAGATA	27700	+	AGG	148
CTTTTTAATAAAATTGGCAT	27712	-	AGG	156
TGTAGACTTTTTAATAAAAT	27718	-	TGG	2
AATTTTATTAAAAAGTCTAC	27736	+	AGG	132
ATTTTATTAAAAAGTCTACA	27737	+	GGG	31
TTAAAAAGTCTACAGGGTGT	27743	+	AGG	2
TAAAAAGTCTACAGGGTGTA	27744	+	GGG	18
CGCTATTAATGTTAGTACAA	27769	+	AGG	1626
GCTAAATGAAGATAGTTCTT	27802	+	TGG	588
GCGAGTACGTTTGACGCAAT	27845	+	AGG	58
TGGACGATCACTCATGTTGA	27884	+	AGG	23
ATACTTGATAAGTCTACTAT	27938	+	TGG	1156
CTACTATTGGCGAAAAAATA	27951	+	AGG	1
TAAGGCTTGATATCAAAGCT	27969	+	AGG	5
GGTAAATCCTAGAATTGTTA	27993	-	AGG	417
TTGATGACCTTAACAATTCT	28002	+	AGG	5
TAAAACTTTCGTTATACTCT	28014	-	TGG	337
GAGTATAACGAAAGTTTTAC	28034	+	AGG	7
TTCTTCAATACTGTCTTTAA	28064	+	AGG	596
CAATACTGTCTTTAAAGGAA	28069	+	CGG	22
AATACTGTCTTTAAAGGAAC	28070	+	GGG	10
AATTTAGATGCATCTACTTT	28096	-	TGG	213
AGTAGATGCATCTAAATTCG	28117	+	AGG	2
GTAGATGCATCTAAATTCGA	28118	+	GGG	6

GCATCTAAATTCGAGGGATT	28124	+	AGG	23
AAATTCGAGGGATTAGGCAA	28130	+	AGG	1
CGATTAGAAATCTTTAAAAA	28160	+	AGG	2
ACCAGCTTTAATGTAATAAT	28247	-	TGG	26
GCCAATTATTACATTAAAGC	28262	+	TGG	6
ATCACCATAACCTTTAATAA	28319	-	AGG	43
AAATGTTATACCTTTATTAA	28325	+	AGG	27
TATACCTTTATTAAAGGTTA	28331	+	TGG	1
CAACAGACTTTTGCAGAAGC	28367	+	GGG	191
TTACCTATCAATTGTGCTAA	28396	-	TGG	33
CATCCATTAGCACAATTGAT	28409	+	AGG	1493
ATACGTCCATCAACAAGCGG	28429	-	TGG	525
TTAATACGTCCATCAACAAG	28432	-	CGG	813
GAAGCGCCACCGCTTGTTGA	28439	+	TGG	205
AGATAGTTTAAAAAAAGCAA	28477	+	TGG	145
ACGTAACGCTACAAAGTCTA	28520	-	AGG	379
CTATTTTAGGGTTAGCTTCT	28551	-	GGG	49
TAACAACATCACCTATTTTA	28563	-	GGG	234
CTAACAACATCACCTATTTT	28564	-	AGG	311
CCAGAAGCTAACCCTAAAAT	28568	+	AGG	2
AATAGGTGATGTTGTTAGAG	28585	+	TGG	52
AGGTGATGTTGTTAGAGTGG	28588	+	TGG	19
CACTAAGTCGTTATATCCTA	28601	-	TGG	94
AGAGTGGTGGATTCTGCCAT	28601	+	AGG	3
ACTAAGCAAGATGTAGTATT	28685	+	AGG	681
TAGTATTAGGAGACTTTACA	28698	+	AGG	217
TTTTAGTTCTTTAGATGGGT	28772	-	CGG	3
ATGCTTTTAGTTCTTTAGAT	28776	-	GGG	115
AATGCTTTTAGTTCTTTAGA	28777	-	TGG	14
TTTATCTATAAATAATGAAT	28837	+	TGG	1
AAAACAGTTACAACTGCTAA	28907	+	TGG	260
ATCAAATCAATTGGAACGAT	28973	+	TGG	172
ATTGGCGACTCTGTAGCTAG	28991	+	AGG	2
TTGGCGACTCTGTAGCTAGA	28992	+	GGG	4
ACTAATTTCACAGAAATGTT	29027	+	AGG	143
AAAACGACTAATCTTGCAAG	29066	+	AGG	160
ACGACTAATCTTGCAAGAGG	29069	+	TGG	83
TGCAAGAGGTGGCGCAACAA	29080	+	TGG	159
TCTACCGCTTCTTTACCTAT	29095	-	TGG	255
ACAATGGCAACAGTTCCAAT	29096	+	AGG	20
AGTTCCAATAGGTAAAGAAG	29107	+	CGG	3
AGACAAGCAGAGCAAATAAG	29147	+	AGG	5
CAGTGCCTTGTAATATGATT	29157	-	AGG	150

GGAGACCTAATCATATTACA	29168	+	AGG	58
TACAAGGCACTGATGATGAT	29184	+	TGG	304
ACTGATGATGATTGGTTACA	29192	+	CGG	16
ATGATTGGTTACACGGTTAT	29199	+	TGG	51
TGATTGGTTACACGGTTATT	29200	+	GGG	100
TGGTTACACGGTTATTGGGC	29204	+	AGG	26
TCCGTTTTATCAGTGCCTAT	29215	-	CGG	739
TATTGGGCAGGCGTACCGAT	29216	+	AGG	54
ACCGATAGGCACTGATAAAA	29230	+	CGG	17
AACTTCAATTGCAGAACAAA	29258	-	AGG	585
ATCACTAGTATTTTTGAATC	29296	-	TGG	16
GTATTGTTGTACCACTCATA	29337	-	GGG	155
CGTATTGTTGTACCACTCAT	29338	-	AGG	92
ACAAGACAATGCCCTATGAG	29342	+	TGG	65
TGTTTTTGTCCGTGTCTTTA	29361	-	CGG	122
AACAATACGCCGTAAAGACA	29368	+	CGG	512
GACACGGACAAAAACAAACT	29384	+	AGG	3
ACACGGACAAAAACAAACTA	29385	+	GGG	3
CAAACTAGGGTTAACACTTG	29398	+	AGG	10
GTGTGATATGCGTCAAACAC	29449	-	TGG	359
TTCCTAAAAGCTGGATTGTA	29485	-	TGG	109
AGCCATACAATCCAGCTTTT	29499	+	AGG	18
AGCTTTTAGGAAAGCGAGCA	29512	+	TGG	50
TTTTAGGAAAGCGAGCATGG	29515	+	AGG	2
AGGAAAGCGAGCATGGAGGA	29519	+	CGG	38
CCTCGTGACCTTTTTCGTTA	29532	-	GGG	12
ACCTCGTGACCTTTTTCGTT	29533	-	AGG	116
GGCTTACACCCTAACGAAAA	29540	+	AGG	10
CCCTAACGAAAAAGGTCACG	29548	+	AGG	10
TATTATGTACGAGTTAATCA	29572	+	AGG	22
ATTACAGTTTTTACGACTAA	29598	+	AGG	9
ACAGTTTTTACGACTAAAGG	29601	+	AGG	9
GTAATTAATCCGTAAGCCAT	29611	-	TGG	522
CGACTAAAGGAGGCAACCAA	29611	+	TGG	81
AGGAGGCAACCAATGGCTTA	29618	+	CGG	406
ACAAGTTTACATTCAATGAC	29648	+	AGG	671
GTTTACATTCAATGACAGGT	29652	+	CGG	76
AACTATCGCTTGTTAGATGA	29699	+	AGG	21
CGTATATTTCTTCTTTTTGA	29736	-	TGG	289
GATTATTTAACGTATTTAAA	29819	+	TGG	13
CTAGAATCATATTGCTAAAA	29826	-	CGG	11
CGTTTTAGCAATATGATTCT	29843	+	AGG	275
CATTGATACCGTCGCCGTTA	29850	-	TGG	121

AATATGATTCTAGGCCATAA	29852	+	CGG	149
ATTCTAGGCCATAACGGCGA	29858	+	CGG	24
GACGCGCGTATTGATAATAC	29897	+	AGG	71
CGTATTGATAATACAGGTTA	29903	+	TGG	74
ACTAGATGCTTTCACTAAAA	29968	+	AGG	144
CTTGCTCTTTTGGTTCGAAT	30024	-	CGG	67
AATTCCGGTTCTTGCTCTTT	30034	-	TGG	17
CGAACCAAAAGAGCAAGAAC	30046	+	CGG	20
GATAAATCAGTGATAAATTC	30049	-	CGG	6
TGCATTACTGCATTTGTATA	30073	-	TGG	60
ATGCAGTAATGCAATCATTT	30099	+	TGG	65
TGCAGTAATGCAATCATTTT	30100	+	GGG	708
TATAAATAATTTTCGTTCTA	30111	-	GGG	274
ATATAAATAATTTTCGTTCT	30112	-	AGG	27
TATATGACGCAAGCTCGTCC	30146	+	AGG	5246
GATAACATGTAATGATTACC	30148	-	TGG	360
CTATCAATAAATTGTCCGTT	30181	-	GGG	26
TTATCTAGATTGAAGCCCAA	30182	+	CGG	109
TCTATCAATAAATTGTCCGT	30182	-	TGG	67
GATAGATTGCTTGTTAAAAA	30215	+	CGG	7
AGATTGCTTGTTAAAAACGG	30218	+	CGG	11
AATGCGTATAGATACATTGA	30254	+	TGG	3
GATACATTGATGGAGAATTA	30264	+	TGG	20
ATGGATTTATTCAGCTGTAT	30283	+	TGG	178
TTATTTCTCCAGTTCTATAT	30321	-	TGG	554
GTACGTTTCCAATATAGAAC	30329	+	TGG	2
AGAACTGGAGAAATAACTTA	30344	+	TGG	480
TATCTGTCGTTAAATATATT	30373	-	CGG	695
TACGTCAGCGATTTATAATC	30412	+	CGG	214
AAAATCATTAAATTTTCTAC	30415	-	CGG	5
TTCTTAAGTTGTCTTTCAGT	30454	-	GGG	1622
ATTCTTAAGTTGTCTTTCAG	30455	-	TGG	100
GAATTCGTTGAACTTTGTTG	30490	+	AGG	44
AGTGCTGACGATATTGATAA	30518	+	AGG	5
AGACAAAGTATTGTATCAAA	30544	+	TGG	32
GTATCTGAAGTGTATTCCAT	30556	-	AGG	72
GTATCAAATGGATATACCTA	30556	+	TGG	12
TCATAAGTGATACCTTGCAT	30583	-	AGG	90
TCAGATACACAACCTATGCA	30587	+	AGG	343
CAAGGTATCACTTATGATGC	30605	+	AGG	84
ATGATGCAGGTATCTTATAT	30618	+	TGG	70
GGTATCTTATATTGGTATAC	30626	+	AGG	3
ACCTTGTAAGTAGTTAGGGT	30647	-	TGG	174

CGAAACCTTGTAAGTAGTTA	30651	-	GGG	20
TCGAAACCTTGTAAGTAGTT	30652	-	AGG	24
GCCAACCCTAACTACTTACA	30662	+	AGG	192
TTTAAACGACGTATCGATAT	30713	+	TGG	2622
AAACGACGTATCGATATTGG	30716	+	CGG	46
AGGAGACTTCCAAGAAGCTG	30757	+	AGG	104
GGAGACTTCCAAGAAGCTGA	30758	+	GGG	16
ATGTATTACGATCTAGAAAC	30788	+	AGG	15
GGACGCAAAGCGCTTTTAAT	30809	+	AGG	157
GACGCAAAGCGCTTTTAATA	30810	+	GGG	396
ACGCAAAGCGCTTTTAATAG	30811	+	GGG	22
CTTTTAATAGGGGTAACTAT	30821	+	TGG	158
ATAGGGGTAACTATTGGACC	30827	+	TGG	44
GAGTGATGTCTGTTGTTACC	30829	-	AGG	1062
GTTAACACCTCTTTGGCCGA	30860	-	TGG	20
CATCACTCAATTTATTCCAT	30860	+	CGG	4
AGAATTGGTTAACACCTCTT	30867	-	TGG	416
ATTTATTCCATCGGCCAAAG	30869	+	AGG	5
GTGCAATGTTTTTTAAGAAT	30882	-	TGG	15
GAATCAGTCATCGATACTTG	30904	-	AGG	6
CAAGTATCGATGACTGATTC	30923	+	AGG	629
GTATCGATGACTGATTCAGG	30926	+	CGG	43
GCTGGGTTCTGTATTGGTAA	30943	-	CGG	4
AGATATGCTGGGTTCTGTAT	30949	-	TGG	135
TAATATCACTTAGATATGCT	30960	-	GGG	424
GTAATATCACTTAGATATGC	30961	-	TGG	49
AGCATATCTAAGTGATATTA	30979	+	CGG	22
CTAAGTGATATTACGGAAGT	30986	+	TGG	16
CTCTAAACGCTTTCGGTAAC	31038	-	GGG	11
TCTCTAAACGCTTTCGGTAA	31039	-	CGG	2
CCTGCATCTCTAAACGCTTT	31045	-	CGG	311
CCGAAAGCGTTTAGAGATGC	31061	+	AGG	1399
TGGTTCTTTGATGTACTGCC	31085	+	TGG	417
AGAGCACCATTATAGTGTCC	31087	-	AGG	210
GTACTGCCTGGACACTATAA	31097	+	TGG	9
ATTTCTACCTGTGCTGTTTC	31124	-	TGG	51
GTACTTACCAGAAACAGCAC	31133	+	AGG	28
ATTTTCAATAAGAAAAACAA	31190	+	CGG	2
ATAAGAAAAACAACGGAGCA	31197	+	TGG	30
TCCCAATAACCGGCGTTTTG	31213	-	CGG	1
AATTTCTGTCCGCAAAACGC	31220	+	CGG	19
AGGGATATGTTCCCAATAAC	31223	-	CGG	31
GTCCGCAAAACGCCGGTTAT	31227	+	TGG	21

ATAATTTTGTAATATTCTTA	31242	-	GGG	145
GATAATTTTGTAATATTCTT	31243	-	AGG	10
TTATCAGATTTAAAAATCGT	31277	+	TGG	187
GCAATACCTTTAAAGTCTTT	31333	-	AGG	301
GATTTTCCTAAAGACTTTAA	31343	+	AGG	396
AAAGACTTTAAAGGTATTGC	31352	+	AGG	86
ACTTTAAAGGTATTGCAGGT	31356	+	TGG	50
AGAAGTAAAATCGAATACAC	31384	+	CGG	47
GAAGTAAAATCGAATACACC	31385	+	GGG	850
AATACTTGTGTTGTGTTACC	31387	-	CGG	241
CTAAAAATTGATGTGCAGAC	31425	-	GGG	177
ACTAAAAATTGATGTGCAGA	31426	-	CGG	259
CAATTTTTAGTTAGAAACTT	31454	+	TGG	9
TTAGTTAGAAACTTTGGTAC	31460	+	TGG	144
AACTTTGGTACTGGTGGCGT	31469	+	TGG	33
GTACTGGTGGCGTTGGTAAA	31476	+	TGG	12
TGGTAAATGGAGTTTATTCG	31489	+	AGG	4
GGTAAATGGAGTTTATTCGA	31490	+	GGG	6
GAGTTTATTCGAGGGAAAGG	31498	+	TGG	207
CTGATGTTTGTGTCAATAAT	31578	-	TGG	130
AGTTTCTATGAATCAGATAG	31615	+	AGG	26
TATGAATCAGATAGAGGAAC	31621	+	TGG	13
TGTTCAGAACTTATAGATAA	31662	-	CGG	340
TCTATCTACGTTATAATCAT	31711	-	CGG	11
GATGATTATAACGTAGATAG	31729	+	AGG	414
ACGATAGTAGACGCAATTAA	31774	+	TGG	7
CGATAGTAGACGCAATTAAT	31775	+	GGG	1271
GAATGTTTTAAAAATTCATT	31800	-	CGG	1410
AATGAATTTTTAAAACATTC	31819	+	AGG	116
ATTTTTAAAACATTCAGGCA	31824	+	AGG	1410
TTCAGGCAAGGTGCATGCTC	31836	+	AGG	403
CAGGCATTCTTTACACAAAA	31855	+	CGG	3
AGGCATTCTTTACACAAAAC	31856	+	GGG	16
ATTGAAAATGATTTAGTTAG	31918	+	TGG	52
TTGAAAATGATTTAGTTAGT	31919	+	GGG	707
GATTTAGTTAGTGGGTTTGA	31927	+	TGG	26
CAGCCATATTTTGCTTTAAT	32000	-	TGG	785
TAACCAATTAAAGCAAAATA	32013	+	TGG	2
GTGAATGATAGTGCGACAAA	32062	+	AGG	140
GAAGTTGAACAACAAATCAA	32221	+	TGG	368
TTGTTGAATTACCTTTAACA	32234	-	AGG	754
AATGGCGCTGACCTTGTTAA	32239	+	AGG	20
AAGGTAATTCAACAACAAAT	32258	+	TGG	126

TCTAAACTTACAGATGATTA	32287	+	CGG	387
TGCGCTTAAAACGCTATCTA	32320	-	TGG	35
TAAGCGCAGTTAACACATCT	32351	+	AGG	381
GTGCCTATATCCGTCTTTTC	32388	-	TGG	35
AACAGATGCGCCAGAAAAGA	32394	+	CGG	15
GCGCCAGAAAAGACGGATAT	32401	+	AGG	8
ATAGGCACGTTAGAGAAGCC	32419	+	TGG	7
TCATCAACACCATCTTGTCC	32421	-	AGG	1094
TTAGAGAAGCCTGGACAAGA	32428	+	TGG	11
GGACAAGATGGTGTTGATGA	32440	+	CGG	9
ACTTATACATCAAGCAAATC	32482	+	TGG	635
ATAATACTGCTCGTGCAACA	32531	+	TGG	2040
ACTCATCGTTTGAATCGTCT	32540	-	GGG	4389
TACTCATCGTTTGAATCGTC	32541	-	TGG	872
TACACAAAATACAAAATCTA	32578	+	CGG	1619
AATACAAAATCTACGGCACA	32585	+	TGG	3043
CATCATTCTTTTTATAAAAC	32594	-	GGG	514
CCGTTTTATAAAAAGAATGA	32611	+	TGG	1
CAGTATGTAGATGATAAATT	32692	+	CGG	3
ATAAATTCGGAACAACGAGC	32705	+	TGG	602
GCAACAACATAAGATGACAG	32727	+	AGG	33
CATAAGATGACAGAGGCGAA	32734	+	TGG	58
GTTAACTTAAATAATGCGCA	32770	+	AGG	23
AATAATGCGCAAGGCGATTT	32779	+	GGG	9
TTACTATGCAACAAGAGTGC	32820	+	CGG	12
TCAACGCTACCTGGTAAATC	32823	-	CGG	29
ACAAGAGTGCCGGATTTACC	32830	+	AGG	642
TCATAACTTTCAACGCTACC	32832	-	TGG	1109
AGGTAGCGTTGAAAGTTATG	32850	+	AGG	3
GGTAGCGTTGAAAGTTATGA	32851	+	GGG	5
AAGTTATGAGGGTTATTTAT	32862	+	CGG	66
TAAATCTTTTTAGAGTTATA	32910	-	AGG	436
TACACACGATCAATCACAAA	32947	+	CGG	3122
ACGGCAGACTTGAGCAACAG	32966	+	TGG	7
ACCGTTGATTTATGTTCATT	32979	-	AGG	129
TCCTAATGAACATAAATCAA	32994	+	CGG	69
TCAACGGTATTGTTCGACGG	33010	+	TGG	15
TTGTTCGACGGTGGCGCAAA	33019	+	TGG	4
GACGGTGGCGCAAATGGTGT	33025	+	AGG	38
AAAATAGAATAGTTTGTGTA	33054	-	CGG	292
TATTCTATTTTGTTGGTAAG	33082	+	TGG	3
TTGGTAAGTGGAACTTATCC	33094	+	AGG	563
AATCCCTCAATAACGCCACC	33096	-	TGG	368

GTAAGTGGAACTTATCCAGG	33097	+	TGG	33
TTATCCAGGTGGCGTTATTG	33108	+	AGG	2
TATCCAGGTGGCGTTATTGA	33109	+	GGG	7
GGTGGCGTTATTGAGGGATT	33115	+	CGG	1
TTGAATCGCGTTAGGTAATG	33127	-	CGG	9
TTACTCAATTGAATCGCGTT	33135	-	AGG	473
GCGAATGTAGTTGACTCAGA	33175	+	CGG	181
GTAGTTGACTCAGACGGCAA	33181	+	CGG	38
GTTGACTCAGACGGCAACGG	33184	+	TGG	110
TAAAGTAGTGCTACTTGTTT	33214	-	TGG	63
TTAGGTAAAACATCAGGTTC	33280	+	TGG	67
TTTAGTTATAGTAACTTTGT	33295	-	TGG	955
AGTTACTATAACTAAAATTA	33318	+	TGG	9
GTTACTATAACTAAAATTAT	33319	+	GGG	15
TTACTATAACTAAAATTATG	33320	+	GGG	560
AACGATAAAAACGAAGTTAT	33366	+	CGG	74
ATCGGATTCGTTAATACTGG	33384	+	CGG	46
AACTCTTCTTTAAATTTAAT	33428	-	AGG	705
TTAGTGAAAACAAACTTTCT	33455	-	AGG	592
AGAAAGTTTGTTTTCACTAA	33474	+	CGG	262
CTTTGTTGGTTTGATGCATT	33521	-	CGG	1407
TTAAATCTGACGCACTTTGT	33535	-	TGG	108
TGCGTCAGATTTAAGTGATG	33560	+	AGG	8
TGATGAGGAACTTCGCGGAA	33575	+	TGG	66
TGTTTTGTTAGTTTTCAGTT	33669	-	CGG	31
AACTAACAAAACAAATACTG	33695	+	AGG	158
ACTAACAAAACAAATACTGA	33696	+	GGG	1289
CTAACAAAACAAATACTGAG	33697	+	GGG	456
TAACAAAACAAATACTGAGG	33698	+	GGG	67
GTTTTAATGTCTTTAAAAGT	33731	-	TGG	317
ACATTAAAACTTTTTATGTG	33760	+	TGG	12
CATTAAAACTTTTTATGTGT	33761	+	GGG	133
ATAAAAATGAGCAAATTAAG	33790	+	TGG	25
AATTAAGTGGTACGTAGACA	33803	+	TGG	13
ATTAAGTGGTACGTAGACAT	33804	+	GGG	509
GAAGAATATGCATTGATCAC	33840	+	TGG	6
GACTTTTCATCTTTTGCCTC	33857	-	TGG	53
CACTGGTGAAAAATATCCAG	33857	+	AGG	6
GGCAAAAGATGAAAAGTCAC	33878	+	AGG	993
AGTCACAGGTGTAATGCTTG	33892	+	AGG	133
TTTTTAATTTAACACAAAGT	33916	+	AGG	104
AAAGTAGGTGGCGTAATGTT	33931	+	TGG	2
CCATTCATGTTCGTGCCGTT	33943	-	TGG	633

TAATGTTTGGATTTACCAAA	33944	+	CGG	160
CCAAACGGCACGAACATGAA	33959	+	TGG	12
ACTCTCAATGAGATTAAATT	34024	+	AGG	340
CGTCTATCTGTCTTTCCCTC	34085	-	TGG	1275
ATATACGCGATATGAAAATG	34151	+	TGG	12
GATATGAAAATGTGGATTCT	34159	+	CGG	129
ATGTGGATTCTCGGTTTGAT	34168	+	AGG	15
TGTGGATTCTCGGTTTGATA	34169	+	GGG	153
GCTTTACTAAGAACTATTTT	34216	+	TGG	39
GAACTATTTTTGGTATTTAA	34226	+	AGG	3
CTATTTTTGGTATTTAAAGG	34229	+	AGG	1
TCCTAAAATCCCTTTAAGCA	34242	-	TGG	2583
GAGGTGATTACCATGCTTAA	34248	+	AGG	1
AGGTGATTACCATGCTTAAA	34249	+	GGG	8
ACCATGCTTAAAGGGATTTT	34257	+	AGG	10
GGATTTTAGGATATAGCTTC	34270	+	TGG	22
GATTTTAGGATATAGCTTCT	34271	+	GGG	117
ATAGCTTCTGGGCGTGCTTC	34282	+	TGG	18
TTCTGGGCGTGCTTCTGGTT	34287	+	TGG	50
ACAGTTAAGAGTCAGTGCTT	34322	+	CGG	196
AAGAGTCAGTGCTTCGGCAC	34328	+	TGG	41
TTTTTATTTTGATTGAAATG	34352	+	AGG	1
ATTGAAATGAGGTGCATACA	34363	+	TGG	19
TTGAAATGAGGTGCATACAT	34364	+	GGG	96
CTGTAGGCTTTCTAGTCTTT	34380	-	GGG	30
GCTGTAGGCTTTCTAGTCTT	34381	-	TGG	28
AAAGCCTACAGCTAGTGAAG	34408	+	TGG	9
GCCTACAGCTAGTGAAGTGG	34411	+	TGG	11
CAGCTAGTGAAGTGGTGGAG	34416	+	TGG	2
AGCTAGTGAAGTGGTGGAGT	34417	+	GGG	27
GAGTGGGCAAAGTCGAATAT	34433	+	TGG	26
CAAAGTCGAATATTGGTAAG	34440	+	AGG	87
GATTAATATAGATAATTATC	34462	+	GGG	1
ATTAATATAGATAATTATCG	34463	+	GGG	1229
ATTATCGGGGCAGTCAATGT	34476	+	TGG	33
TTATCGGGGCAGTCAATGTT	34477	+	GGG	18
ACTTTATTTTTAAAAGATAT	34509	+	TGG	9
GATATTGGGGTTTTGTAACA	34524	+	TGG	5
ATATTGGGGTTTTGTAACAT	34525	+	GGG	4
TATTGGGGTTTTGTAACATG	34526	+	GGG	31
TGTAACATGGGGCAATGCTA	34537	+	AGG	25
ATGGGGCAATGCTAAGGATA	34543	+	TGG	34
CGATAGAATCGGAAACCCTT	34564	-	AGG	3380

GGCTAATTACAGATATCCTA	34564	+	AGG	312
GCTAATTACAGATATCCTAA	34565	+	GGG	338
CAGATGAATAACGATAGAAT	34575	-	CGG	668
CGATTCTATCGTTATTCATC	34592	+	TGG	151
TTATTCATCTGGATTTGTAC	34603	+	CGG	14
ACTGCGATGTCTCCAGGTTC	34606	-	CGG	23
TCTGGATTTGTACCGGAACC	34610	+	TGG	24
AACCTGGAGACATCGCAGTT	34626	+	TGG	15
GACATCGCAGTTTGGCACCC	34634	+	TGG	114
CCGAACCTATTCCGTTGCCA	34635	-	GGG	209
TCCGAACCTATTCCGTTGCC	34636	-	AGG	77
GCAGTTTGGCACCCTGGCAA	34640	+	CGG	27
TGGCACCCTGGCAACGGAAT	34646	+	AGG	7
CCCTGGCAACGGAATAGGTT	34651	+	CGG	128
GGCAACGGAATAGGTTCGGA	34655	+	CGG	2
AGATGGTCCTACTACTATTG	34667	-	CGG	798
GGACACACCGCAATAGTAGT	34676	+	AGG	96
TAAAAATAACTTTTATTAGA	34684	-	TGG	5
TATTAGAATTAACCCAGTTT	34716	-	TGG	291
TTTATAGCGTTGACCAAAAC	34719	+	TGG	179
TTATAGCGTTGACCAAAACT	34720	+	GGG	353
ACTGGGTTAATTCTAATAGT	34737	+	TGG	41
TAATAGTTGGACAGGTTCTC	34750	+	CGG	7
AATAGTTGGACAGGTTCTCC	34751	+	GGG	360
GGGTGTCTTACTAAACTTCC	34753	-	CGG	316
AGCCTGTAACACTTACATAA	34773	-	GGG	158
AAGCCTGTAACACTTACATA	34774	-	AGG	62
CTAGTATCTTTTGAATATGG	34804	-	AGG	12
TTGCTAGTATCTTTTGAATA	34807	-	TGG	74
GAACTTGTATCAGTACTACT	34831	-	AGG	1400
GCCAGTAATTGTTGAGTCAT	34865	-	TGG	492
GCCAATGACTCAACAATTAC	34880	+	TGG	583
GTTTTAACTTCTTTAAATTG	34900	-	CGG	1
CATTGATCATATAGTTGTAA	34987	+	TGG	439
ATTGATCATATAGTTGTAAT	34988	+	GGG	862
GATGAACGCTCAGATATTCA	35012	+	AGG	672
TCTCTATCGACATATAAATG	35104	-	CGG	23
GCATTTATATGTCGATAGAG	35122	+	AGG	18
ATGTCGATAGAGAGGCTACA	35130	+	TGG	18
GTGACGCGGGTCATCAAAAT	35150	-	TGG	26
CTAGCCAATTAGGGTGACGC	35163	-	GGG	28
ACTAGCCAATTAGGGTGACG	35164	-	CGG	65
CTTCAATAACTAGCCAATTA	35172	-	GGG	6

ACTTCAATAACTAGCCAATT	35173	-	AGG	5
ATGACCCGCGTCACCCTAAT	35175	+	TGG	130
TGGCTAGTTATTGAAGTATG	35195	+	TGG	3
CAAATACAAGCGTTAATACG	35255	+	TGG	3161
AAGCGTTAATACGTGGTGTT	35262	+	TGG	103
CGTGGTGTTTGGTTATTGTC	35273	+	AGG	21
GTGGTGTTTGGTTATTGTCA	35274	+	GGG	21
CTTATCTGAAACGACGTTAA	35308	+	AGG	473
TCATACTACGCCAAATATTA	35319	-	GGG	152
TTCATACTACGCCAAATATT	35320	-	AGG	1459
TAAAGGTAGACCCTAATATT	35325	+	TGG	94
AATTACGACTTGATTAAGCA	35369	+	AGG	399
CTTGATTAAGCAAGGTATAC	35377	+	CGG	512
TGCTCATACTTTGCGTTATC	35380	-	CGG	696
TGATGGAGTAGGGCCTCGTG	35525	-	TGG	24
GTTGACAGTGCGTCCACACG	35528	+	AGG	15
GTTTTTCGTCTGATGGAGTA	35535	-	GGG	118
GGTTTTTCGTCTGATGGAGT	35536	-	AGG	26
ATGCTTGGTTTTTCGTCTGA	35542	-	TGG	610
CTTGTTTCAGTAACGATGCT	35557	-	TGG	103
AGTGCTTGCTGGAATGTGAA	35581	-	TGG	1
TTTGTCTATCCAGTGCTTGC	35592	-	TGG	1257
ATTCACATTCCAGCAAGCAC	35599	+	TGG	738
CACTGGATAGACAAATGTCT	35616	+	AGG	104
ACTGGATAGACAAATGTCTA	35617	+	GGG	53
CTGGATAGACAAATGTCTAG	35618	+	GGG	971
CCCATGTATGAGATTTTTTC	35628	-	GGG	23
CCCCATGTATGAGATTTTTT	35629	-	CGG	1
ACCCGAAAAAATCTCATACA	35643	+	TGG	1
CCCGAAAAAATCTCATACAT	35644	+	GGG	8
CCGAAAAAATCTCATACATG	35645	+	GGG	346
AAAAATCTCATACATGGGGC	35649	+	TGG	5
AAAATCTCATACATGGGGCT	35650	+	GGG	36
AACACGAGCACAAACGAGCT	35680	+	CGG	171
CAATGAATGTTAAGCGAATA	35703	+	TGG	28
AATGAATGTTAAGCGAATAT	35704	+	GGG	225
TGCTATCAAATGCTTAATTT	35741	+	AGG	411
CTTAATTTAGGCAAGTATCA	35753	+	AGG	6
GCGCTTAACAAAATACTTAA	35789	+	AGG	43
AACAAAATACTTAAAGGAAA	35795	+	AGG	37
AAAGGAAAAGGAACGCTCGA	35807	+	CGG	7
AAAGGAACGCTCGACGGACA	35813	+	AGG	51
CGGACAAGGCAAAGCATTCG	35827	+	CGG	2123

GCGCACGCTTTCTTAGAAAG	35891	+	TGG	5
AACTTCGCTAATGGTAGATA	35924	+	CGG	33
TACGGTGCATATAATTACTT	35942	+	CGG	835
GCATATAATTACTTCGGTAT	35948	+	TGG	1905
CAAACGTCATTGCATAATCA	35970	-	GGG	1093
GCAAACGTCATTGCATAATC	35971	-	AGG	65
ATGACGTTTGCTAAAAATAA	35999	+	AGG	59
CGTTTGCTAAAAATAAAGGT	36003	+	TGG	26
CCGCCCATGATTGCTTTTGC	36016	-	TGG	459
ATCTCCAGCAAAAGCAATCA	36028	+	TGG	2
CCAGCAAAAGCAATCATGGG	36032	+	CGG	229
CGGTGCTAGCTTCGTAAGAA	36052	+	AGG	5
AGAAAGGATTACATCAATAA	36068	+	AGG	93
TCTTAGGATTCCATCTAATT	36090	-	CGG	82
ACACATTGTACCGAATTAGA	36096	+	TGG	401
CGATTGTACTTGCTTGATGT	36132	-	TGG	2220
GCTAAGTTATATAAACAAAT	36170	+	CGG	5
TATAAACAAATCGGCTTAAA	36179	+	AGG	61
TAAAAGGTATCTACTTCACA	36195	+	AGG	1077
AAAAGGTATCTACTTCACAA	36196	+	GGG	42
AGGGATAAATATAAATAAAG	36215	+	AGG	159
GAAACGAGAATAAAAAATGA	36266	+	TGG	116
AAAAATGATGGTGTTGACTT	36278	+	AGG	246
GGTGTTGACTTAGGTGACAT	36287	+	TGG	250
AATACAGCATCTATAAGAAT	36335	+	AGG	5
ATAGGTATCAATGACAAACA	36353	+	AGG	22
CGTATCGATCTAAAAGCACA	36377	+	TGG	158
TCCATAAACAAATGTAATCT	36391	-	AGG	93
ACCTAGATTACATTTGTTTA	36406	+	TGG	176
ACAACATCGTCGATAATAAG	36439	-	GGG	363
TTACAACATCGTCGATAATA	36441	-	AGG	52
ATTATCGACGATGTTGTAAA	36461	+	AGG	6
AACCTTTTTAGGTATCTTGT	36476	-	AGG	15
GCGTGTTTGATAACCTTTTT	36487	-	AGG	80
TACCTACAAGATACCTAAAA	36490	+	AGG	5
AAAAAGGTTATCAAACACGC	36506	+	TGG	365
TCTTTCAATATCGTTGATAG	36590	+	TGG	1562
AAAAGAAATCGATGTTAAAT	36631	+	TGG	998
AGTAGATTTAAAGGTGCGAA	36764	+	AGG	67
AAAGGTGCGAAAGGTGATAA	36773	+	AGG	16
GAAAGGTGATAAAGGCGAAC	36781	+	CGG	19
AAAGGTGATAAAGGCGAACC	36782	+	GGG	45
CCTTTTGCACCAGGTTGTCC	36784	-	CGG	492

AAAGGCGAACCGGGACAACC	36791	+	TGG	117
CCTGCTTCACCTTTTGCACC	36793	-	AGG	650
CCGGGACAACCTGGTGCAAA	36800	+	AGG	17
CCTGGTGCAAAAGGTGAAGC	36809	+	AGG	28
AAAGGTGAAGCAGGTAAAAA	36818	+	AGG	2
GCAGGTAAAAAAGGAGAACA	36827	+	AGG	21
AAAGGAGAACAAGGCGCACC	36836	+	CGG	1107
ACTACAGTACCGTTTTTACC	36838	-	GGG	1494
TACTACAGTACCGTTTTTAC	36839	-	CGG	4
CAAGGCGCACCCGGTAAAAA	36845	+	CGG	10
ATTTGCCACATTTTAGTGTC	36871	-	AGG	34
TCAATCCTGACACTAAAATG	36882	+	TGG	21
ACTAAAATGTGGCAAATTGA	36893	+	TGG	939
TTGATTTTGTCCAATAACTC	36925	-	AGG	1013
CAAAGCAGAACCTGAGTTAT	36931	+	TGG	147
ATCAATATCGCAAATGTTGA	36959	+	AGG	17
TCAATATCGCAAATGTTGAA	36960	+	GGG	40
CAACGACTCTAAAACGTATA	37030	+	CGG	466
CTTAATGTGTTCATAGATTC	37069	-	AGG	1355
GAAAGTGTATTGCAACAGAT	37145	+	TGG	380
AGTTAGTACAGAAGATTTTG	37174	+	AGG	144
TCGTCATGATTATGATTTTT	37213	-	TGG	288
AGCTTTTACTAAACAACAAG	37273	+	CGG	1137
CCTGTCCAAATTTTAACCGT	37312	-	CGG	1725
AAAAAGCGCATCTCAACCGA	37312	+	CGG	195
CTCAACCGACGGTTAAAATT	37323	+	TGG	13
CCGACGGTTAAAATTTGGAC	37328	+	AGG	7
TAATTAAGTAAAGTGTATTA	37371	-	GGG	401
TTAATTAAGTAAAGTGTATT	37372	-	AGG	152
TAATACACTTTACTTAATTA	37390	+	AGG	109
AATACACTTTACTTAATTAA	37391	+	GGG	190
ATACACTTTACTTAATTAAG	37392	+	GGG	19
TAATTAAGGGGTGATTTTTA	37404	+	TGG	718
GTAAAGAAACTTATTTACGA	37444	+	AGG	167
GAATATACAAAAGTATATGC	37471	+	TGG	54
ATGAAGGCTTTTTCCATACT	37484	-	TGG	433
GGTTTTATTACAAAAGATGA	37500	-	AGG	35
GGATATTTATTTTTAGGTAA	37521	-	GGG	2
CGGATATTTATTTTTAGGTA	37522	-	AGG	14
CTATCCGGATATTTATTTTT	37527	-	AGG	1864
CTTACCTAAAAATAAATATC	37539	+	CGG	1
GTTGATTCTTCTATGCTATC	37542	-	CGG	1258
TAGAAGAATCAACAGCAAAA	37568	+	TGG	705

ACAGCAAAATGGACAATAAA	37579	+	TGG	85
GTCACCTGATAACTTTTATT	37593	-	AGG	1669
TGAACCTAATAAAAGTTATC	37605	+	AGG	1709
ACAATAGAAAATGTACGTAG	37630	+	CGG	885
ATGTACGTAGCGGTATAATG	37640	+	AGG	35
AGGGTTTCGCAAACTAATTT	37660	+	AGG	2880
AATTTAGGTTCAAGTGATTT	37675	+	AGG	82
TCAAGTGATTTAGGAATATC	37684	+	AGG	249
GGAATATCAGGAGTCAATAG	37696	+	CGG	66
GTGACATACAACATCCCTGA	37734	-	AGG	1202
ATCAACTTTAGTAATCCTTC	37735	+	AGG	34
TCAACTTTAGTAATCCTTCA	37736	+	GGG	56
AATTATTCAATGGTCAATGT	37782	-	CGG	1653
AGTCGTTTAAAATTATTCAA	37792	-	TGG	91
TTTTAGTCGTTTTTTTATTT	37834	+	TGG	8
GGAAAAAAGGAGCAAACAAA	37855	+	TGG	3566
AATCAATTCTTAGCGAATAA	37925	+	AGG	3
CTTTCTTCATCTACTGGTAT	37939	-	CGG	327
GAAACACTTTCTTCATCTAC	37945	-	TGG	953
CATTTCCCTTCTTGAGATGT	38017	-	TGG	183
GATAATCCAACATCTCAAGA	38027	+	AGG	465
ATAATCCAACATCTCAAGAA	38028	+	GGG	521
CAACATCTCAAGAAGGGAAA	38034	+	TGG	15
AACATCTCAAGAAGGGAAAT	38035	+	GGG	49
AGTAAATATAGAAAAGCAAC	38090	+	AGG	13
GGTGTCATTACTTCTTTAAT	38104	-	AGG	32
TTTGTGTCGTTCATATTCGT	38125	-	AGG	983
ATGAACGACACAAATGATTT	38150	+	AGG	52
TGAACGACACAAATGATTTA	38151	+	GGG	686
CGACACAAATGATTTAGGGT	38155	+	AGG	1884
CACAAATGATTTAGGGTAGG	38158	+	TGG	57
CAAAAAATCAAGCAGAAAAA	38198	+	TGG	349
AAATGGTTTGACAATTCATT	38215	+	AGG	559
AATGGTTTGACAATTCATTA	38216	+	GGG	127
GAAATCCATACCAACCATCT	38234	-	GGG	749
TGAAATCCATACCAACCATC	38235	-	TGG	812
GGGAAACAATTCAACCCAGA	38236	+	TGG	14
AACAATTCAACCCAGATGGT	38240	+	TGG	166
TTCAACCCAGATGGTTGGTA	38245	+	TGG	4
CGCTAACATAAAGAACATAT	38272	-	TGG	1867
ATGTTCTTTATGTTAGCGAC	38293	+	AGG	14
TTATGTTAGCGACAGGCGAA	38300	+	AGG	219
GCGACAGGCGAAAGGCTGCA	38308	+	AGG	11

TCTTTGCTTTATTATCAAAC	38333	-	GGG	238
ATCTTTGCTTTATTATCAAA	38334	-	CGG	129
AAAGCAAAGATTGAAAAATA	38362	+	TGG	11
ACGACAATATCCAACTTTTG	38400	-	CGG	195
CAGCTTTTTACCGCAAAAGT	38406	+	TGG	124
CTCCGCCACCATACTTTGAC	38426	-	GGG	71
GCTCCGCCACCATACTTTGA	38427	-	CGG	5
GTCGTTTTCCCGTCAAAGTA	38434	+	TGG	426
GTTTTCCCGTCAAAGTATGG	38437	+	TGG	471
TTCCCGTCAAAGTATGGTGG	38440	+	CGG	3
TCAAAGTATGGTGGCGGAGC	38446	+	TGG	154
TTAAATACTTTCACATCATT	38497	+	TGG	32
TCACATCATTTGGTCAAAAC	38507	+	TGG	645
TCATTTGGTCAAAACTGGAA	38512	+	CGG	1608
GGTCAAAACTGGAACGGTAA	38518	+	AGG	167
AAAACTGGAACGGTAAAGGT	38522	+	TGG	10
AACGGTAAAGGTTGGACTAA	38530	+	TGG	151
ACTAATGGCGTTGCGCAACC	38545	+	TGG	285
ACAGTTTCAGGACCCCAACC	38547	-	AGG	69
ATGGCGTTGCGCAACCTGGT	38549	+	TGG	322
TGGCGTTGCGCAACCTGGTT	38550	+	GGG	52
GGCGTTGCGCAACCTGGTTG	38551	+	GGG	28
ACATGTCTTGTCACAGTTTC	38559	-	AGG	19
TTTAACCTAATAAAATACAT	38598	-	TGG	2688
ACAATCCAATGTATTTTATT	38609	+	AGG	375
TGCCAACGCTTAAGTTGTTA	38624	-	GGG	736
TTGCCAACGCTTAAGTTGTT	38625	-	AGG	290
TTCCCTAACAACTTAAGCGT	38638	+	TGG	1257
AGCGTTGGCAATAAAGCTAA	38653	+	AGG	115
GCAAGCGACTACAAAAAAAG	38685	+	AGG	37
GCTACAAGCATAATTTTTTT	38703	-	AGG	95
AAAAAAATTATGCTTGTAGC	38722	+	CGG	691
AGGATCGTTATAACCATGAC	38725	-	CGG	31
ATTATGCTTGTAGCCGGTCA	38728	+	TGG	13
GTTCCGTTTCCTACTGCTCC	38745	-	AGG	896
TATAACGATCCTGGAGCAGT	38752	+	AGG	241
GATCCTGGAGCAGTAGGAAA	38758	+	CGG	4
CTTAAATACTTAGCGATATT	38802	-	AGG	517
GCTAAGTATTTAAGACATGC	38827	+	AGG	7419
GGACATGAAGTTGCATTATA	38848	+	CGG	122
CATGAAGTTGCATTATACGG	38851	+	TGG	272
ATGTATCAAGATACTGCATA	38893	+	CGG	556
ACTGCATACGGTGTTAATGT	38905	+	AGG	99

GTAGGCAATAAAAAAGATTA	38923	+	TGG	6
AAAAAGATTATGGCTTATAT	38933	+	TGG	319
AAAAGATTATGGCTTATATT	38934	+	GGG	78
CTTATATTGGGTTAAATCAC	38946	+	AGG	18
TTATATTGGGTTAAATCACA	38947	+	GGG	813
GAAATACATTTAGACGCAGC	38986	+	AGG	239
GCAGCAGGAGAAAGCGCAAG	39001	+	TGG	6
GCAGGAGAAAGCGCAAGTGG	39004	+	TGG	41
CAGGAGAAAGCGCAAGTGGT	39005	+	GGG	248
GATGTTATTAAAAATAACTT	39082	+	AGG	3
AATAACTTAGGACAAATAAG	39094	+	AGG	3
ACATTTAGTAAATCATTACG	39108	-	AGG	858
AATTATCGTTTATCTGAATT	39172	+	AGG	429
TATTACTAATAAAAATGATA	39198	+	TGG	670
CTAATAAAAATGATATGGAT	39203	+	TGG	1483
TTGTATTCTAAATTAATAGC	39244	+	CGG	376
AGGCTTACCATGAATCGCAC	39247	-	CGG	44
TTAATAGCCGGTGCGATTCA	39256	+	TGG	9
CCAGCTACCAAACCACCTAT	39267	-	AGG	160
GCGATTCATGGTAAGCCTAT	39268	+	AGG	104
ATTCATGGTAAGCCTATAGG	39271	+	TGG	3
TGGTAAGCCTATAGGTGGTT	39276	+	TGG	208
CCTATAGGTGGTTTGGTAGC	39283	+	TGG	26
GTATAACCTGCTGGCACTGG	39324	-	TGG	6
AGTGTATAACCTGCTGGCAC	39327	-	TGG	2603
TTATCGAGTGTATAACCTGC	39333	-	TGG	1510
AAAAATCCACCAGTGCCAGC	39334	+	AGG	6206
TGCCTTGTTCTTTTTTATAA	39365	-	GGG	299
TTGCCTTGTTCTTTTTTATA	39366	-	AGG	26
TACACAGTAGCTAATGTTAA	39406	+	AGG	28
AAAGGTAATAATGTAAGAGA	39424	+	CGG	21
TCAACTAATTCAAGAATTAC	39451	+	AGG	23
CAACTAATTCAAGAATTACA	39452	+	GGG	768
AACTAATTCAAGAATTACAG	39453	+	GGG	193
ATACGTAATTGTTGTGTTGT	39466	-	TGG	60
AACACAACAATTACGTATGA	39487	+	CGG	362
GACGGTGCATATTGTATTAA	39505	+	TGG	37
CAACGTCGTTATATAGCGAC	39562	+	AGG	61
TCGTTATATAGCGACAGGAG	39567	+	AGG	174
AGCGACAGGAGAGGTAGACA	39576	+	AGG	204
ACAGGAGAGGTAGACAAGGC	39580	+	AGG	49
GGTAATAGAATAAGTAGTTT	39601	+	TGG	149
AATTTTGCTACATTAATTAT	39660	+	AGG	127

ATTTTGCTACATTAATTATA	39661	+	GGG	57
ACAGTTATTAAATAACTATT	39690	+	TGG	108
TTATTAAATAACTATTTGGA	39694	+	TGG	20
AGAAATGTTAAAAAGTGTAT	39712	-	AGG	3115
AAGATTTAAATGTAGATAAC	39754	+	AGG	5218
TTTAAATGTAGATAACAGGC	39758	+	AGG	1884
TAGATAACAGGCAGGTACTT	39766	+	CGG	2174
TAGCTATAACATAAAAAAAT	39779	-	AGG	2
ATAACAAAAAACTAGCCCGA	39803	-	AGG	2228
TTTATGTTATAGCTAGCCTT	39803	+	CGG	6
TTATGTTATAGCTAGCCTTC	39804	+	GGG	790
GTGACATGCTTGGGTGAACA	39861	-	AGG	3092
AAACATCCAGTGACATGCTT	39870	-	GGG	96
AAAACATCCAGTGACATGCT	39871	-	TGG	855
TGTTCACCCAAGCATGTCAC	39880	+	TGG	426
CTAAAGTCATATATACTACG	39928	-	GGG	3992
GCTAAAGTCATATATACTAC	39929	-	GGG	1062
TGCTAAAGTCATATATACTA	39930	-	CGG	2591
TATAATTGCTTTTATATAGT	40003	+	AGG	276
GTAGGAGTGAACTATATAGC	40021	+	CGG	9
TAGGAGTGAACTATATAGCC	40022	+	GGG	1088
TCAGATACATGGCCTCTGCC	40024	-	CGG	89
TGAACTATATAGCCGGGCAG	40028	+	AGG	6
GGGACCAACAGTCAGATACA	40035	-	TGG	9
GAGGCCATGTATCTGACTGT	40047	+	TGG	78
ACAAGGAAGATGTCTCCTGT	40055	-	GGG	35
TATCTGACTGTTGGTCCCAC	40056	+	AGG	24
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ACCACAGATCCTATTAATTT	40194	+	AGG	337
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AGATGAAAAAACGACTATAA	165	-	AGG	2311
AAAGCAATTATGAAAAGAGT	194	-	AGG	889
TACACACATAAGTTTATTGG	234	-	CGG	1151
GCATACACACATAAGTTTAT	237	-	TGG	2032
AAGTTACTACTCACACACTA	259	-	AGG	7383
ATTTAATGATTCTGCAGCTG	308	+	AGG	2683
GAAATCCTATGCAAGGCAGT	331	-	AGG	3288
TGCCAAGGAAATCCTATGCA	338	-	AGG	3547
TGCCTTGCATAGGATTTCCT	352	+	TGG	741
TTTATATTCACAACTTGCCA	353	-	AGG	3895
AACCAAGCTATGTTGATAGA	376	-	GGG	194
AACCCTCTATCAACATAGCT	390	+	TGG	1489
AAATAAAAAGATGCAACAAT	399	-	GGG	7227
AAAATAAAAAGATGCAACAA	400	-	TGG	295
ATTTGCTATCCTTGAATTGA	461	+	TGG	778
GGTATGACTTTGGCCGAACT	479	-	AGG	10688
GGCGATTTTTCTTCCTAGTT	482	+	CGG	42
AGAAAAACAAGGTATGACTT	489	-	TGG	1455
AAACAATCAAGAGAAAAACA	500	-	AGG	683
TAATAGAACTATCAAGTAAA	556	-	AGG	193
TCTATTATAAGGAAAACTTT	588	+	CGG	633
TTATCATGATGTTACAAAAG	637	-	AGG	2449
GATTACTTACGTAATGCGAA	676	+	AGG	2713
TTCAAAAGTTTAGTATCTAT	698	-	AGG	18997
TAAACTTTTGAAATCTAAAA	725	+	TGG	172
GACACCAATTTCTTCAGAAA	756	-	GGG	1398
TGACACCAATTTCTTCAGAA	757	-	AGG	52
AAAACCCTTTCTGAAGAAAT	768	+	TGG	1243
ACTTTATCTAACATGATACA	804	+	CGG	8729
CTTTATCTAACATGATACAC	805	+	GGG	15515
CCATTTATTACCGGGTAGGA	821	-	TGG	5111
AATACCATTTATTACCGGGT	825	-	AGG	2420
GAGAACAAAACCATCCTACC	827	+	CGG	17109
AAATAAATACCATTTATTAC	830	-	CGG	1454
CCATCCTACCCGGTAATAAA	837	+	TGG	5575

AAAATATCTCTTCCTTCTTG	869	-	AGG	4648
TTAGAATTGACACCTCAAGA	873	+	AGG	17740
AAAAAGAAAGTTTTAACTTA	927	+	AGG	1245
AAGAAAGTTTTAACTTAAGG	930	+	AGG	4158
ACTTAAGGAGGAACAACAAA	942	+	TGG	6
TTGATTTCGTGCCACTGTGC	993	-	GGG	19034
GTTGATTTCGTGCCACTGTG	994	-	CGG	1685
AGCAATTCACACCCGCACAG	998	+	TGG	33743
GAAATCAACAGAATTATTGA	1024	+	CGG	1
GTCGTCGAGTTGTAGCTCGG	1048	-	CGG	990
TTGGTCGTCGAGTTGTAGCT	1051	-	CGG	4235
TTTTAATAACCTCAACATCT	1070	-	TGG	14436
ACTCGACGACCAAGATGTTG	1077	+	AGG	8119
AGTTATTCAAAAATCACGAA	1154	+	AGG	854
GTGAATTGCTAGTAGTGTGT	1181	-	TGG	15299
GAAACAATCTTTATAAACGC	1308	+	AGG	1174
GAATTAGCTATCATAACTTC	1365	+	TGG	3986
TTATCTAATTGTTTATCGAT	1389	+	TGG	8679
ATTGGAGCATGCAAATAACT	1407	+	TGG	9048
TCTGATGAATATTCATCTCT	1424	-	CGG	31754
AACACCTATTAACGTAGTAT	1449	-	TGG	17762
GATTCCAATACTACGTTAAT	1461	+	AGG	13894
GTTGTAGCTTTTCTAGCTTT	1646	-	AGG	66
ATTTAAGGTGGTTATTCTTA	1698	-	TGG	2577
TTGTTATCAAATATTTAAGG	1710	-	TGG	3345
ATGTTGTTATCAAATATTTA	1713	-	AGG	6379
TTACAAACAAAATCGAACAT	1802	+	CGG	616
AATATTCAAGAAAAAGAAAA	1835	+	TGG	17
AAGAGAGTTATATAAAGCTT	1876	+	TGG	10403
TTAAAAAGCGTTTTAGCGCT	1902	+	TGG	9
TAAAAAGCGTTTTAGCGCTT	1903	+	GGG	707
TGAAGCATTTCAAAGAAAAT	1938	+	AGG	222
GAAGCATTTCAAAGAAAATA	1939	+	GGG	147
TACAAGTGTACTTACAAGTA	1966	+	CGG	7930
ACAAGTACGGTTGTTAATAA	1979	+	CGG	2643
AAACATGTTGCGATGATGTC	2048	+	AGG	59970
ATGATGTCAGGTACAGAAAA	2060	+	AGG	389
TGTTCCATGCTTTTTCAATT	2091	-	TGG	10306
TCATCCAAATTGAAAAAGCA	2103	+	TGG	2077
GCACGTTGCATAATCATTTC	2116	-	TGG	4932
GCATCTGCAAATACAATTTT	2197	-	TGG	793
ACTAAGACATCAATTTTAGT	2246	+	TGG	5823
GCAAAGATCATTAAACAAAA	2276	+	CGG	1511

AAACAAAACGGTATAAACAT	2288	+	CGG	86
AACAAAACGGTATAAACATC	2289	+	GGG	7615
GGCAACGCAGATTGTTTGAG	2310	+	TGG	1310
TTTGAGTGGTTACGTCAAAA	2324	+	CGG	325
CCACACCCTTGCGTTTAATA	2334	-	AGG	6202
CGGATTCCTTATTAAACGCA	2344	+	AGG	2051
GGATTCCTTATTAAACGCAA	2345	+	GGG	3912
CCTTATTAAACGCAAGGGTG	2350	+	TGG	1082
CGTTCCATTGAATACTGTGT	2368	-	AGG	43714
CATGCCTACACAGTATTCAA	2380	+	TGG	4208
AGAAACATCAATCACACATT	2425	+	CGG	3750
ACATCAATCACACATTCGGA	2429	+	CGG	2290
TGTCCTTTACCTGTTACTTT	2458	-	TGG	11332
AGTAAGACGCCAAAAGTAAC	2465	+	AGG	14780
ACGCCAAAAGTAACAGGTAA	2471	+	AGG	1661
TACTTTGTTAACAAGTTTTT	2501	+	AGG	13
AGAAAAACAAACAACTTAAT	2524	+	AGG	14250
AACTGCCATTGTGATGAGGA	2564	-	GGG	321
CAACTGCCATTGTGATGAGG	2565	-	AGG	148
TCACAACTGCCATTGTGATG	2568	-	AGG	162
AACAACCCTCCTCATCACAA	2575	+	TGG	1995
AATGGCAGTTGTGACGTGGA	2593	+	AGG	184
CAGTTGTGACGTGGAAGGTT	2598	+	TGG	2770
AACGCCCTGCTACTAATCAC	2629	-	AGG	4601
GAAAACCTGTGATTAGTAGC	2640	+	AGG	2775
ATTTTCAGCATCTTTCGGTA	2681	-	TGG	5510
GTAGAATTTTCAGCATCTTT	2686	-	CGG	8306
TTTGTTCGGCGAACTTCAAA	2724	-	AGG	6245
TTATTTGCTAATAGTTTGTT	2738	-	CGG	4527
GTTGGTGGTACTATGATTTT	2793	-	TGG	83
TATGTGTTTTCTGGTGTTGG	2808	-	TGG	1510
CTATATGTGTTTTCTGGTGT	2811	-	TGG	8989
TCGCCTCTATATGTGTTTTC	2817	-	TGG	58
ACACCAGAAAACACATATAG	2830	+	AGG	6468
ACACAAATCCATCAATTGTT	2890	+	TGG	8805
GTAGAAGTACAGTATACAAC	2918	+	TGG	20869
TATTACCGCAAAGATAATTT	2947	+	AGG	2461
ATATTAATCAGAGTGCCTGT	2982	-	TGG	8273
TACATTGATTATTCACCAAC	2983	+	AGG	4359
TCTGATTAATATTTCTAAAT	3009	+	TGG	5548
TGATCAGAAAGCATAAAAAA	3041	+	TGG	12
AAAGCATAAAAAATGGTATT	3048	+	AGG	3245
GCATAAAAAATGGTATTAGG	3051	+	AGG	793

TGAAGCATAATACTGCTACT	3088	-	AGG	23247
GCTGTAGTGAAGTATAGAAA	3134	-	CGG	3260
TTCTATACTTCACTACAGCA	3154	+	TGG	3397
CACTACAGCATGGTCAATTG	3164	+	CGG	6
ACTACAGCATGGTCAATTGC	3165	+	GGG	815
ATAAAAAAACTGCTACTTGT	3239	+	TGG	29511
GTTCAATATAAAACGAAAAA	3300	+	CGG	285
CAATATAAAACGAAAAACGG	3303	+	AGG	1542
GTCAAGATGTATTACGAAAT	3328	+	AGG	4400
CGCAAAAATATTCATGTTAA	3361	+	CGG	4107
TTTAAGCTATTCATTTTAAA	3391	+	AGG	33
ATTCATTTTAAAAGGTCATA	3399	+	TGG	532
TTCATTTTAAAAGGTCATAT	3400	+	GGG	3338
ACGACATAAGCATGTTTAAT	3441	-	TGG	12864
AGATGAGAATGACTTAGATA	3480	+	TGG	861
CAATCCATTCATCTATTGCT	3503	-	TGG	34893
TTAACCAAGCAATAGATGAA	3515	+	TGG	829
TGAAGAGAACACAGACGAAC	3540	+	AGG	17221
TAATTAACTTAGTCATGAAA	3569	+	TGG	2324
TAACTTAGTCATGAAATGGT	3573	+	AGG	3643
CTTAGTCATGAAATGGTAGG	3576	+	AGG	5
TAACTTATATCATTCGTCAT	3617	+	AGG	8856
AACTTATATCATTCGTCATA	3618	+	GGG	10766
GGTTTGTTAGTTATATAAAT	3630	-	TGG	3579
ATATCTGAATTGTTATCAGT	3651	-	TGG	16568
CCTAGCTCTATTTCTATTTG	3682	-	TGG	1170
CCACAAATAGAAATAGAGCT	3698	+	AGG	1977
CACAAATAGAAATAGAGCTA	3699	+	GGG	898
AATAGAGCTAGGGAGTTTAA	3709	+	CGG	2603
AGCTAGGGAGTTTAACGGTA	3714	+	TGG	3049
GGAAGAAGCGAGTATCAATA	3735	+	TGG	214
GACAGAAACTATTGAGTACG	3786	+	AGG	10174
GAGGAGGTAGAACATGACTG	3805	+	AGG	5
AGTATGCTTACTTTTTCTTG	3823	-	TGG	35193
ATATCGCTGAGAAAAATAAA	3882	+	AGG	164
TTCTATAAATTTGCAGTATA	3908	+	CGG	979
TTTGCAGTATACGGAAAAAT	3917	+	TGG	3094
GTATACGGAAAAATTGGCTC	3923	+	AGG	418
TTTATCTCTTGTAGCAAACG	3935	-	TGG	2193
TTCGTCATTGACATTAACGA	3980	+	AGG	2625
GTCATTGACATTAACGAAGG	3983	+	TGG	330
CATTAACGAAGGTGGAACAA	3991	+	CGG	6822
GGAACAACGGTTACTGACGA	4004	+	AGG	1414

CTCATCTCCTGTAAAATTTG	4066	-	AGG	2391
TTTTTTACCTCAAATTTTAC	4075	+	AGG	3672
TTACAGGAGATGAGAGAAAA	4091	+	CGG	907
TCTCCCCAATCATTAAACGT	4186	-	TGG	2075
AAAAACCAACGTTTAATGAT	4197	+	TGG	2718
AAAACCAACGTTTAATGATT	4198	+	GGG	287
AAACCAACGTTTAATGATTG	4199	+	GGG	10
GTCAGTATGTACAGATTAAT	4241	+	AGG	17749
CATGACCTGTAATAACAAAG	4272	-	TGG	2096
AAATTCCACTTTGTTATTAC	4283	+	AGG	5223
TTTGTTATTACAGGTCATGA	4292	+	AGG	4
AACAAAGATAAAGATGATGA	4319	+	AGG	2
GCGCTTCAATAGTGATAGTA	4338	-	GGG	21139
TGCGCTTCAATAGTGATAGT	4339	-	AGG	5612
CTCAAAGTGATGTGTTAGCT	4404	+	AGG	5169
TCAAAGTGATGTGTTAGCTA	4405	+	GGG	4257
ATTGAAGAATTTGATGATAA	4433	+	CGG	21
TTATTGTTAATTGTTATTGA	4510	-	AGG	474
TCTACTACGTCCGTAATGCT	4546	-	AGG	8864
ATTTGCAAATCCTAGCATTA	4552	+	CGG	2761
GTAGTAGAAGCAATTAGAAA	4577	+	TGG	2570
GAAACTAAAAATTAATTAAA	4599	+	AGG	6
CTAAAAATTAATTAAAAGGA	4603	+	CGG	155
TATTTAATTATGAAAATCAC	4626	+	AGG	1763
AATCAAGAAAAGTTTTATAA	4674	+	CGG	105
AAGTTTTATAACGGCTCAGC	4683	+	AGG	1106
AGTTTTATAACGGCTCAGCA	4684	+	GGG	6794
GGCTCAGCAGGGTTTCAAGC	4695	+	TGG	322
ATCGTATTTGAAAATGATGA	4779	+	AGG	2
TGGAAATCATATTTATACGG	4814	-	CGG	4
TCTTGGAAATCATATTTATA	4817	-	CGG	9147
ATTGAATTAGTTACTCGATT	4866	+	AGG	10361
TTGGTATCAAAATCTAAGCT	4889	-	AGG	973
AAACTTACCAATAAGATCAT	4908	-	TGG	67
TTTGATACCAATGATCTTAT	4917	+	TGG	9152
TATTGGTAAGTTTTGTCACT	4934	+	TGG	7715
TTTGTCACTTGGTATTGAAA	4945	+	TGG	3
TGGAAATTCAATGAAGATGA	4965	+	AGG	2564
AGATGAAGGTAAGTATTTTA	4979	+	CGG	1
ACATCATCGCCCTTTTTGTA	5003	-	AGG	9686
ATTTATTAAACCTTACAAAA	5009	+	AGG	1628
TTTATTAAACCTTACAAAAA	5010	+	GGG	3048
TGCTTATCTGTCTTCGGAAT	5036	-	AGG	1461

GCTTTTTGCTTATCTGTCTT	5042	-	CGG	466
CAAAAAGCTGAAGAAAATAA	5073	+	CGG	179
AAAAAGCTGAAGAAAATAAC	5074	+	GGG	1441
AAAAGCTGAAGAAAATAACG	5075	+	GGG	89
AATTGGCCACTGCTTTCAAA	5117	-	TGG	1416
AGCAATCCATTTGAAAGCAG	5127	+	TGG	3213
CTTGGTCGTCATATCCAAAT	5134	-	TGG	1102
TTTGAAAGCAGTGGCCAATT	5136	+	TGG	570
CACCTTAAAACGCTAAATCT	5152	-	TGG	6942
AGATTTAGCGTTTTAAGGTG	5171	+	TGG	446
AAGTACCGTCGTTATCTTTC	5203	-	TGG	2819
AGATACCAGAAAGATAACGA	5214	+	CGG	5638
TTCAACACCAGTAGCAACGA	5229	-	CGG	113
ACTTATTCCGTCGTTGCTAC	5238	+	TGG	20037
CACATTGACTTACTAGAAAA	5280	+	CGG	323
ACCTCTACTTCTGCTTTTAG	5291	-	TGG	230
TCCACTAAAAGCAGAAGTAG	5306	+	AGG	909
AAAAGCAGAAGTAGAGGTTC	5312	+	CGG	2451
ATAGATAGTTTTTTATTGTC	5315	-	CGG	147
GTAGAGATATAGAACTTCAC	5383	+	TGG	3081
TAGAGATATAGAACTTCACT	5384	+	GGG	17408
AGAGATATAGAACTTCACTG	5385	+	GGG	545
AATTTTCTAGTTGATTCTAC	5396	-	TGG	1297
AAAATTATTACAAACAGAAT	5429	+	TGG	468
ACTGTTCTATGAAAGTTGCA	5488	+	AGG	46
CTGTTCTATGAAAGTTGCAA	5489	+	GGG	1895
TTACTCGTTTCTACACTCAT	5540	-	AGG	166
AAGATAAAGCGTTATTATAT	5590	+	TGG	5
TTCCGCATATTACACAGTTG	5608	-	CGG	46
AACCGCAACTGTGTAATATG	5622	+	CGG	123
TAATGTGCCAGGTCTGCGTG	5633	-	AGG	17
CGGAAAGCCTCACGCAGACC	5642	+	TGG	4910
CGACTGCTTCATAATGTGCC	5644	-	AGG	284
CTGGCACATTATGAAGCAGT	5661	+	CGG	1888
CTAATACATGTTTGTCATAG	5695	-	TGG	763
CACAACGAGCAACATGCGAT	5751	+	TGG	8348
TTATCCACGAGTCATGCAAG	5782	-	TGG	73
AATACCACTTGCATGACTCG	5794	+	TGG	6033
CGTGGATAAAAGTTGATGAG	5812	+	AGG	328
AGGCTCAATAAAATGTTGAA	5832	+	AGG	73
AATGTTGAAAGGAGAGAAAA	5843	+	AGG	7
CTTCCGCCAAGATGACGATT	5883	-	AGG	597
AGCACTCCTAATCGTCATCT	5893	+	TGG	10862

ACTCCTAATCGTCATCTTGG	5896	+	CGG	6879
TGCTATGCATGCTGTAAAAG	5932	+	TGG	1744
AAAAACCTGTATTAACTAAA	5956	-	CGG	176
AATCTCCGTTTAGTTAATAC	5967	+	AGG	3839
TTTTACAAAAGCTTTACCAT	5991	+	AGG	6392
TCAATTAGTTTGTCCGCCTA	5991	-	TGG	2258
TGGGTAATAGACATCAAAAA	6015	-	AGG	6
TTTTTTGATGTCTATTACCC	6033	+	AGG	2353
TTTTTGATGTCTATTACCCA	6034	+	GGG	439
AAAGTTACATTACAGCCCCT	6034	-	GGG	258
TTTTGATGTCTATTACCCAG	6035	+	GGG	2311
TAAAGTTACATTACAGCCCC	6035	-	TGG	81
GAAACAATAAGTAAACTTTC	6075	-	TGG	763
AAAGTTTACTTATTGTTTCT	6095	+	AGG	541
GTTAAAAGAATGTTAAAGTC	6108	-	AGG	1200
GAAAAACAAAGATTTGTTTC	6141	-	GGG	2402
AGAAAAACAAAGATTTGTTT	6142	-	CGG	405
TTAAAGTGATTTAAAAACTG	6190	+	AGG	101
ATGTCTTACTTAACAAAAAA	6219	-	AGG	9
TAATAACCTAGTAAGGTTAG	6262	-	GGG	30
TTAATAACCTAGTAAGGTTA	6263	-	GGG	11
ATTAATAACCTAGTAAGGTT	6264	-	AGG	869
TTTCAATTAATAACCTAGTA	6269	-	AGG	658
TTAAAACCCCTAACCTTACT	6272	+	AGG	8348
TAGGTTATTAATTGAAATTT	6291	+	CGG	54
TCGGTTGATTCTATATCTAA	6310	+	CGG	1180
GAATGACGGTATGAATATAT	6337	-	CGG	910
GTTTTAAACCCAAAGAATGA	6351	-	CGG	1163
ATATTCATACCGTCATTCTT	6358	+	TGG	3900
TATTCATACCGTCATTCTTT	6359	+	GGG	8568
TCCTGCCGTTAAATATAGAG	6373	-	CGG	147
TAAAACCGCTCTATATTTAA	6384	+	CGG	1539
ACCGCTCTATATTTAACGGC	6388	+	AGG	1432
TTTAAAAGAATAGCATCATT	6436	+	TGG	1273
TTAAAAGAATAGCATCATTT	6437	+	GGG	1251
TAAAAGAATAGCATCATTTG	6438	+	GGG	2623
TAATTATTTCAACAAATGAA	6470	+	TGG	1962
TTATTTCAACAAATGAATGG	6473	+	TGG	148
TATTTCAACAAATGAATGGT	6474	+	GGG	468
AAAACTAATAGCATCATCTA	6502	-	TGG	1974
AACTTTGAAGCTTCTAGAGC	6577	+	AGG	981
GAACCACAATTTTCTCTTCT	6585	-	AGG	1479
GGACCTAGAAGAGAAAATTG	6598	+	TGG	22

GGTTCTTGTAAATTATTTTC	6619	+	AGG	2976
TGGGAAATTCCACCTTTATG	6700	-	TGG	223
AAATAACTTTATCCACATAA	6704	+	AGG	3047
TAACTTTATCCACATAAAGG	6707	+	TGG	29
AAACTTGGGAACTTGTCTTT	6719	-	GGG	45
AAAACTTGGGAACTTGTCTT	6720	-	TGG	15
AGAAACATTCTCTAAAACTT	6733	-	GGG	80
TAGAAACATTCTCTAAAACT	6734	-	TGG	567
GTTTTAGAGAATGTTTCTAC	6754	+	AGG	1086
TTATTGAAGGCGCATCAAAA	6761	-	GGG	99
ATTATTGAAGGCGCATCAAA	6762	-	AGG	10
GGTATTGATAAAATTATTGA	6774	-	AGG	2
ATGGATCCTATTTTAGGTAA	6795	-	AGG	44
ATAATTATGGATCCTATTTT	6801	-	AGG	433
TCAATACCTTTACCTAAAAT	6805	+	AGG	1125
AGATTGGGGGTGAATAATTA	6814	-	TGG	19
TCGCTATTGCGTTAGATTGG	6827	-	GGG	231
ATCGCTATTGCGTTAGATTG	6828	-	GGG	37
TATCGCTATTGCGTTAGATT	6829	-	GGG	2111
TTATCGCTATTGCGTTAGAT	6830	-	TGG	22
CCATTTCGTTATCTCCTTTC	6863	-	TGG	6835
ATAATAAAATTATACCAGAA	6865	+	AGG	663
CCAGAAAGGAGATAACGAAA	6879	+	TGG	637
TTTAGAACGATAAAAGAAAG	6907	+	TGG	67
AATTTAAGTGCTAAAGCTAA	6970	+	AGG	1712
ATTTAAGTGCTAAAGCTAAA	6971	+	GGG	2581
GCCAATTGTCAGGACGACTT	6992	-	AGG	219
GTGTATATTTGCCAATTGTC	7002	-	AGG	232
TCCTAAGTCGTCCTGACAAT	7007	+	TGG	1097
GTAGTTAAACATATGAATGA	7048	+	TGG	740
GGACAAAAATCAATCAATAG	7069	+	TGG	6461
TAGTGGCGTTCAAGAACTTA	7086	+	TGG	4239
ATACAAAAAAGAGCTGAAAA	7129	+	CGG	852
GCTGAAAACGGTGTGTTTAA	7141	+	AGG	467
TCCGAAAATGGCATTTCGGT	7173	-	TGG	89
GTTTTCCGAAAATGGCATTT	7177	-	CGG	393
GATAATCCGTTTTCCGAAAA	7185	-	TGG	56
ACCAACCGAAATGCCATTTT	7188	+	CGG	1869
GAAATGCCATTTTCGGAAAA	7195	+	CGG	1
ATTTTCGGAAAACGGATTAT	7203	+	CGG	16
GAAAACGGATTATCGGCAAA	7210	+	CGG	9
AAAACGGATTATCGGCAAAC	7211	+	GGG	47
GCAAACGGGTTTTCGGAAAA	7225	+	CGG	2

GTTTTCGGAAAACGGAAAAA	7233	+	CGG	13
TATTAGTAGTACGCCCTTTT	7244	-	CGG	1842
GGAAAAACGGAAAACCGAAA	7246	+	AGG	56
AATAACAATACTAATAATGA	7312	+	TGG	984
TAATGATGGAAGTATATTGT	7326	+	CGG	14
AATGATGGAAGTATATTGTC	7327	+	GGG	255
TAGGGAATGGAATACACAGT	7338	-	CGG	266
GATAATTTCTTTATAGGGAA	7351	-	TGG	37
TATTCGATAATTTCTTTATA	7356	-	GGG	207
GTATTCGATAATTTCTTTAT	7357	-	AGG	32
GAATACTTAAATAAAAAAGC	7390	+	AGG	2
AAGATTTTATTAAAGCAAGA	7445	+	TGG	1273
CAAGATGGAATCAAGATTTT	7460	+	AGG	1568
ATGGAATCAAGATTTTAGGT	7464	+	TGG	1184
GAATCAAGATTTTAGGTTGG	7467	+	AGG	25
TAGGTTGGAGGATTTTAAAA	7479	+	AGG	2
TTGATATCAAAACAGCTGAA	7505	+	TGG	499
AACAGCTGAATGGTTAAACA	7515	+	CGG	2075
CAAAAAGTGTTTCTGGTCTA	7535	-	AGG	36
TTACTGCCAAAAAGTGTTTC	7542	-	TGG	96
CTTAGACCAGAAACACTTTT	7552	+	TGG	7091
ACTTTTTGGCAGTAAATTTG	7566	+	AGG	382
CTTTTTGGCAGTAAATTTGA	7567	+	GGG	297
TTTTTGGCAGTAAATTTGAG	7568	+	GGG	72
TCCAATTGATCCGTGCCAGT	7596	-	TGG	7773
AATCAAAAAATACAACCAAC	7597	+	TGG	980
AAAAATACAACCAACTGGCA	7602	+	CGG	807
ACCAACTGGCACGGATCAAT	7611	+	TGG	14919
TGAAGTACGACGAAAGTTAT	7640	+	TGG	1437
GAAGTACGACGAAAGTTATT	7641	+	GGG	1155
CGACGAAAGTTATTGGGATT	7647	+	AGG	510
GACGAAAGTTATTGGGATTA	7648	+	GGG	139
ACGAAAGTTATTGGGATTAG	7649	+	GGG	26
CGAAAGTTATTGGGATTAGG	7650	+	GGG	169
TTTATCTTTTCGCTGAATAG	7668	-	TGG	1063
AATCCTTTTTCGACATGAGT	7713	-	AGG	2100
CAACCTACTCATGTCGAAAA	7726	+	AGG	948
GGATTGAAATGTGAGAGATG	7747	+	TGG	780
CCATTCGGGTGTTTTTTAGT	7782	-	AGG	2050
CTTTATACTCGTAACCATTC	7796	-	GGG	3900
TCTTTATACTCGTAACCATT	7797	-	CGG	4095
AATGGTTACGAGTATAAAGA	7816	+	CGG	18
TTGCAAATGTGAAATCTATG	7839	+	AGG	1866

ACTGTTGCATCTCTTAAAGA	7905	-	CGG	456
TGTACTTGTTTTTCATTTTG	7941	-	TGG	5297
ACAGCAATAGAGTACGTACA	7990	+	AGG	114
CCTTGCAATATTAATGATTT	8013	-	TGG	48
CCAAAATCATTAATATTGCA	8029	+	AGG	1443
TTAATATTGCAAGGTTCATA	8038	+	CGG	4224
TTGCAAGGTTCATACGGAAC	8044	+	TGG	23
TTGCGATAGCGTATGCTAGG	8057	-	TGG	53
CTTTTGCGATAGCGTATGCT	8060	-	AGG	545
GCAAAAGCAGTCAAAGCTAA	8092	+	AGG	300
CAAAAGCAGTCAAAGCTAAA	8093	+	GGG	3154
AGTCAAAGCTAAAGGGCATA	8100	+	CGG	745
TTGATACGATCCATCAACAT	8124	-	TGG	6695
TATGCACATACCAATGTTGA	8130	+	TGG	965
TTTACTTGTACTAGATGATA	8229	+	TGG	1581
TTACTTGTACTAGATGATAT	8230	+	GGG	373
AGCATTGTTGATAACAGAGT	8290	+	AGG	3433
AACTAAATCAAAATATGAAC	8351	+	TGG	1228
GCGAGAAAAGTAAGAGTAAT	8404	+	CGG	964
GAGTAATCGGAGACGATTTC	8417	+	AGG	386
AGTAATCGGAGACGATTTCA	8418	+	GGG	716
ATTTCAGGGAGCGAGATGCA	8432	+	TGG	535
TTTAGTTTTTAAAAATTCTT	8442	-	TGG	3634
CGCTCAGAAACTCATAGATG	8501	+	AGG	430
GAAACTCATAGATGAGGCAC	8507	+	AGG	142
AGGCACAGGGCGATGAAAAT	8521	+	AGG	159
CTGCAAGTTTTTGGATAAAT	8536	-	AGG	14
CTTAATATTCGACGATAGCG	8572	-	GGG	1377
TCCTTAATATTCGACGATAG	8574	-	CGG	66
CCCGCTATCGTCGAATATTA	8589	+	AGG	45
TATAAGTAATATTTTTCTTT	8609	-	CGG	1979
TATCTTCCGTGCCATCTTCT	8632	-	CGG	3796
TATTACTTATACCGAGAAGA	8637	+	TGG	704
AGATGGCACGGAAGATATTA	8654	+	AGG	171
AATGAAGTTTATTCGCTCAC	8700	+	AGG	4333
TTTCTTTTCGTCGCTGAAAT	8709	-	GGG	17
TTTTCTTTTCGTCGCTGAAA	8710	-	TGG	2
CAGCGACGAAAAGAAAATCA	8732	+	TGG	168
GAGCGCCTTTGAATCGTTTT	8749	-	AGG	2
AGTGACCTAAAACGATTCAA	8760	+	AGG	8
AAACGATTCAAAGGCGCTCA	8769	+	CGG	4
AACGATTCAAAGGCGCTCAC	8770	+	GGG	313
CTTTTATATGAGCAAGAGCT	8793	+	AGG	1076

TTTTATATGAGCAAGAGCTA	8794	+	GGG	1735
CAACGATATTTGATATTTAG	8824	+	AGG	1234
CGATATTTGATATTTAGAGG	8827	+	TGG	196
TGATATTTAGAGGTGGCACA	8834	+	TGG	1020
TAAATTTAACGAAACGTTCG	8867	+	AGG	1993
CGAAACGTTCGAGGCACCTA	8876	+	TGG	1038
CGTGGACGAGGCGAGCCCAT	8876	-	AGG	278
GAAACGTTCGAGGCACCTAT	8877	+	GGG	1651
GTATTACGAAAGCGTGGACG	8888	-	AGG	158
CTACCTGTATTACGAAAGCG	8894	-	TGG	53
CGTCCACGCTTTCGTAATAC	8907	+	AGG	984
TTATGATTTGTATAAGCTGT	8936	-	TGG	261
AATCATAAAGCGTATATACA	8967	+	AGG	145
GCGCGCTCTAGATTTAACTT	8981	-	AGG	470
TTCGACCATGATTTAAGTAA	9032	-	TGG	811
ACTTTCCATTACTTAAATCA	9043	+	TGG	16235
GAAGAAAAAGAAAAGTGAAA	9068	+	TGG	1097
AAAAAGAAAAGTGAAATGGT	9072	+	TGG	1211
TTAATTAAGTTATCGATATC	9098	-	CGG	86
ACAGTATTAGACGCATGTAA	9138	+	TGG	715
ACGCATGTAATGGTCATGTG	9148	+	TGG	294
AGCTAGTTATTTCTGTAATT	9166	-	TGG	1824
ATAACTAGCTCAAAGCGTTA	9195	+	TGG	969
TCAACTCGCATGATTATTTT	9209	-	TGG	84
AAAAATAATCATGCGAGTTG	9227	+	AGG	4306
TAAACGCAACGATTGATATA	9279	+	AGG	4
TACTGATATTCAACTTCTGT	9289	-	AGG	8804
ATATCAGTATTTTGATGATG	9319	+	TGG	51
GGATATCGAAAAAGAAGCGC	9340	+	TGG	6677
TCATACTCTAGTAATTCGTC	9367	-	TGG	996
AATTAGAAATGTAAATGTAG	9415	+	AGG	750
TAGAAATGTAAATGTAGAGG	9418	+	TGG	283
ATGAGTGTCGTGAAGATTAA	9446	+	CGG	244
TCATGTTCGGTAAATTTATA	9457	-	TGG	1035
TATCAATTCATTTTCATGTT	9470	-	CGG	197
AATGAATTGATAAAAAAGAA	9497	+	CGG	131
ATGAATTGATAAAAAAGAAC	9498	+	GGG	1174
AAAAAGAACGGGTTAACTCC	9509	+	TGG	286
ACTCTTTTTGCAACCATTCC	9511	-	AGG	677
GAACGGGTTAACTCCTGGAA	9514	+	TGG	158
ATGGTTGCAAAAAGAGTACG	9533	+	TGG	51
GTTGCAAAAAGAGTACGTGG	9536	+	TGG	40
AAAAAGAGTACGTGGTGGCT	9541	+	GGG	301

CATGCCATAAGGTGCGTTTA	9560	-	AGG	24
TCAGCTAAGCGCATGCCATA	9571	-	AGG	1984
GAAGCCTTAAACGCACCTTA	9572	+	TGG	286
GCTCTCTCGTTGCATAATTC	9614	-	TGG	308
GCAAAGAACGTGAAATAGCT	9651	+	AGG	2836
AGCTAGGCAACGACGTAAAG	9667	+	AGG	764
AAGAGGTTGAACTACGTAAG	9684	+	AGG	895
TGTGGTACATTAAACAAATG	9694	-	TGG	406
GGATCACGTGAATGTTTTTG	9712	-	TGG	4
TAAGTGACATCGAACCAGTA	9733	-	CGG	293
AACATTCACGTGATCCGTAC	9735	+	TGG	839
CACTCCATTTCTTGAACATT	9759	-	TGG	1011
ATAACCAAATGTTCAAGAAA	9771	+	TGG	313
TCGCCGTATGTGTAATGTGC	9849	-	TGG	618
CAACCAGCACATTACACATA	9862	+	CGG	8028
AGATTTTATTGAACAAGTAA	9900	+	CGG	1718
ATTGCAAATGCTAATTGTGG	9915	-	TGG	389
CCTATTGCAAATGCTAATTG	9918	-	TGG	390
CCACAATTAGCATTTGCAAT	9934	+	AGG	4208
TCCTCATGACCATTCTTTAA	9969	-	CGG	1425
TCTAGAGCACCGTTAAAGAA	9976	+	TGG	760
ACCGTTAAAGAATGGTCATG	9984	+	AGG	130
AAAGAATGGTCATGAGGATA	9990	+	TGG	106
TAGATAGAGTGTTTGACTTG	10031	+	TGG	625
AGATAGAGTGTTTGACTTGT	10032	+	GGG	507
TTTACGCGCGTTATCTGTCA	10047	-	TGG	2041
ATCTCTTAGAGCCGAAAAAT	10081	-	TGG	216
GAATACTTAAACCAATTTTT	10086	+	CGG	319
CTCTAAGAGATATCTGTATC	10109	+	AGG	897
AATAAGCGCCATTCACTACA	10138	-	TGG	2484
GCACATATCCATGTAGTGAA	10146	+	TGG	255
AATGGCGCTTATTACTTTCA	10164	+	CGG	27
ATGGCGCTTATTACTTTCAC	10165	+	GGG	105
CATATCGTACCAGATTGGCA	10188	+	AGG	1996
GAAAAAGACATTTGATACAG	10214	+	CGG	6
TTTGATACAGCGGAAGAGCT	10224	+	CGG	332
GGAATATATATAAAGCAACA	10245	+	TGG	475
ATATATAAAGCAACATGGTT	10250	+	TGG	1199
GCAACATGGTTTGGAATACG	10259	+	AGG	176
AGCAACTAACTTTATTTTAG	10288	+	AGG	399
TAACTTTATTTTAGAGGAGA	10294	+	TGG	37
TATTAGACGAGTTAATTAAA	10350	+	TGG	178
ATTAGACGAGTTAATTAAAT	10351	+	GGG	7132

TAAATGGGCGCGAGAAAATC	10366	+	CGG	28
ATTTTCCCTTGTGATAGCTC	10369	-	CGG	751
GAAAATCCGGAGCTATCACA	10379	+	AGG	340
AAAATCCGGAGCTATCACAA	10380	+	GGG	1071
GGGAAAATATTTTTTTCAAC	10400	+	AGG	2
TTTTCAACAGGATTTAGTGA	10412	+	TGG	283
GTCGAACACTTATTTGTATT	10435	-	TGG	889
ACTATGAAGGGGATATCAAT	10471	-	TGG	1481
TTTCAATATCAACTATGAAG	10482	-	GGG	25
TTTTCAATATCAACTATGAA	10483	-	GGG	71
TTTTTCAATATCAACTATGA	10484	-	AGG	129
CTTATCAAATACCGTGTCTT	10514	-	TGG	1421
AAAAGAAGTAACCAAAGACA	10519	+	CGG	493
GTTGTTTGAAATGTACGAGA	10552	+	TGG	209
TTTGAAATGTACGAGATGGA	10556	+	AGG	353
GAAATGTACGAGATGGAAGG	10559	+	AGG	91
ACTAGTGTTTGCATATAATA	10577	-	CGG	169
AGTATAAAAGAATGTTTATA	10613	+	TGG	2789
AAGATATAGAATGCTTTGGT	10630	-	AGG	1213
GTTTAAGATATAGAATGCTT	10634	-	TGG	4653
ATATGACGATGACGTTAATC	10677	+	TGG	480
ATGACGTTAATCTGGAAAGA	10685	+	TGG	1
TGACGTTAATCTGGAAAGAT	10686	+	GGG	234
GACGTTAATCTGGAAAGATG	10687	+	GGG	372
AATCTGGAAAGATGGGGAGT	10693	+	TGG	58
GATACAAAGACTTACTTTAT	10714	-	AGG	2088
TTTTGTGCAAAGTACGAATG	10797	+	AGG	29
CAGTTTTAATACCGTATTCG	10810	-	TGG	2306
TGAGGAAGAAGCCACGAATA	10815	+	CGG	344
CTATGCTTGCAGTTTGGAAC	10847	-	GGG	648
TCTATGCTTGCAGTTTGGAA	10848	-	CGG	38
CGACCTCTATGCTTGCAGTT	10853	-	TGG	350
GTTCCAAACTGCAAGCATAG	10866	+	AGG	1785
AAGCATAGAGGTCGAAAAAG	10878	+	TGG	4
CATAGAGGTCGAAAAAGTGG	10881	+	AGG	503
TCGTCCCACACTCGATATTT	10901	-	CGG	196
TGATGCCGAAATATCGAGTG	10912	+	TGG	376
CGAGTGTGGGACGAATATAC	10926	+	AGG	1076
GGAAGAATACACGATGTTGT	10947	+	AGG	9865
AGTTCACTATGAAAACTACG	10991	+	CGG	2347
GTAGAACTTATGCAAAGTAC	11052	+	AGG	118
AAACAACAACGAAATATATG	11087	+	CGG	319
AACAACAACGAAATATATGC	11088	+	GGG	1793

CCTATTACAGATTCATCGTC	11132	-	TGG	9699
ATATCTATTGATGTTGTAAA	11190	+	TGG	1357
ATTAAAAGATTTTATGTTTG	11219	+	AGG	661
TTAAAAGATTTTATGTTTGA	11220	+	GGG	348
ATACTCAAAGTAATCATTTT	11235	-	CGG	44
TAACCTCACAGTCATATCTA	11275	-	AGG	313
CTTCCTTAGATATGACTGTG	11288	+	AGG	194
AGATATGACTGTGAGGTTAA	11295	+	AGG	214
ATTTGAATCATCACATTTAT	11324	+	TGG	1306
TGAATCATCACATTTATTGG	11327	+	AGG	47
AACAGAATGAACTATGAAAC	11351	+	AGG	371
ACAGAATGAACTATGAAACA	11352	+	GGG	249
CAGAATGAACTATGAAACAG	11353	+	GGG	580
TAGCGTCCATTACACCTAGT	11361	-	TGG	748
TATGAAACAGGGGTCCAACT	11363	+	AGG	283
AGGGGTCCAACTAGGTGTAA	11371	+	TGG	39
AACTAGGTGTAATGGACGCT	11379	+	AGG	381
AAGCAACGTGATGAGCTTAT	11438	+	TGG	673
AGCAACGTGATGAGCTTATT	11439	+	GGG	209
GCAACGTGATGAGCTTATTG	11440	+	GGG	711
GATGAGCTTATTGGGGATAT	11447	+	AGG	46
AAGAGAACGCAACAAAGAGC	11476	+	TGG	1824
TGGAGAAGAAAGCAAGTGCA	11496	+	TGG	322
GGAGAAGAAAGCAAGTGCAT	11497	+	GGG	287
AAAGATTTAATAAACGAATT	11543	+	TGG	40
ATAAACGAATTTGGCAAAGA	11552	+	TGG	36
GATGGTGAAAGAGTTAAATT	11570	+	TGG	254
TGAAAGAGTTAAATTTGGAA	11575	+	TGG	606
ATTAAACAATAAAACTTTTA	11599	+	TGG	2049
AAACAATAAAACTTTTATGG	11602	+	AGG	1929
CGGATTGTTCTATTTGTTCA	11626	-	CGG	589
ATACGCACTAGCACTTATAA	11646	-	CGG	127
ATAAGTGCTAGTGCGTATAA	11667	+	CGG	59
GTATAACGGCAATGACACAG	11681	+	AGG	689
TATAACGGCAATGACACAGA	11682	+	GGG	669
GGGATTACTAAAAGAGATTG	11702	+	AGG	14
AGCGTTTGATGAAATACTTG	11744	+	AGG	236
GCGTTTGATGAAATACTTGA	11745	+	GGG	2150
ATTCAACATTCAGTTAAAGA	11781	+	AGG	4154
ATTGAACTTGATGAAGCAGT	11805	+	AGG	4
TTGAACTTGATGAAGCAGTA	11806	+	GGG	65
TGAAGCAGTAGGGATTATGA	11816	+	CGG	36
GAAGCAGTAGGGATTATGAC	11817	+	GGG	1

TCAAGTTGTCTATAAATATG	11840	+	AGG	36
AGTTGTCTATAAATATGAGG	11843	+	AGG	468
CTATAAATATGAGGAGGCAC	11849	+	AGG	92
AGAGTTATTACAAATACAAA	11907	+	AGG	94
CTATCTCGTAAGTTCAGCGT	11931	-	TGG	1028
ATGTAGTTGAATTCTTTGAA	11981	+	TGG	55
CTTTGAATGGTTTAATACAT	11994	+	TGG	3679
CATTGGAAACGTTTAAGAAC	12011	+	TGG	3959
AAGAACTGGAAGAAGAAACC	12025	+	AGG	513
TGTACGTCTAACGGCTTACC	12027	-	TGG	1105
TCATCAAGTTGTACGTCTAA	12036	-	CGG	211
TGATGAATTAGCTGACATGT	12069	+	TGG	840
TTAGCTGACATGTTGGCGTT	12076	+	TGG	33
TTGAGTATTGCGAATCAAGT	12100	+	AGG	867
AATTCTTTGAATATTATCTG	12222	-	TGG	651
ATAACAATTGCTTGTTGGTC	12249	-	GGG	104
TCACTATAACAATTGCTTGT	12254	-	TGG	6540
TTTTGTATGCGTCAATGAGT	12308	-	TGG	2499
CATACAAAAAGAAAATGAAA	12338	+	AGG	4
AGGAATCATGAAAGACAAGA	12358	+	TGG	2235
CAAGATGGAACAGCAGACGC	12373	+	AGG	1068
GGAACAGCAGACGCAGGAAA	12379	+	AGG	63
AGACATATTAGATCGAGTCA	12412	+	AGG	20
CATATTAGATCGAGTCAAGG	12415	+	AGG	8304
AGATCGAGTCAAGGAGGTTT	12421	+	TGG	170
GATCGAGTCAAGGAGGTTTT	12422	+	GGG	3
ACAACATTCAAAGATTCAAC	12466	+	AGG	521
CTAAAGCTAAGAGTAATCAA	12509	+	AGG	6
TCAAAGGTTTACAGTCGTTG	12525	+	AGG	818
AGAAGCGAAAGAGAAGTACG	12561	+	AGG	321
GTCAGTTGTATGAAAATATA	12617	+	AGG	8
TCAGTTGTATGAAAATATAA	12618	+	GGG	91
ATGAAAATATAAGGGAGTGT	12626	+	GGG	433
GTTAAAATTAAAACTATTTC	12660	+	AGG	2481
AAAATTAAAACTATTTCAGG	12663	+	TGG	13
CTTTCAACATATTTTTCAAA	12695	-	AGG	1
GAAAGAATGACGAGTTTTAA	12729	+	TGG	7
GTATCTGTTTTAATATACGT	12767	-	TGG	552
TGAATCAATCACACTTATTG	12809	+	AGG	3455
ATCACACTTATTGAGGAGCA	12816	+	TGG	36
TCACACTTATTGAGGAGCAT	12817	+	GGG	61
CTGAGAATTTTATTACATGA	12851	+	CGG	1259
TTAACGATAGAAAAAGATTA	12956	+	TGG	117

AGAGAACTTGTATTGAACAA	12980	+	AGG	37
TTGAACAAAGGTTATATAGT	12992	+	TGG	145
TGAACAAAGGTTATATAGTT	12993	+	GGG	1109
TATAGTTGGGATCAATGTTG	13006	+	AGG	1283
AGTTGGGATCAATGTTGAGG	13009	+	AGG	158
TTTTTCGGGAATTTCATTTT	13034	-	AGG	360
TTATTTCAGTGTACTTTTTC	13048	-	GGG	671
ATTATTTCAGTGTACTTTTT	13049	-	CGG	75
TCAATCTTAGCTTTTTCTTC	13094	-	AGG	451
TCATTCATATTAGCCATCAT	13166	-	AGG	342
TGAATTTTACAGTCCTATGA	13169	+	TGG	3715
ATATGAATGAACATGAATTA	13195	+	AGG	299
TATGAATGAACATGAATTAA	13196	+	GGG	549
TCTCCAGTATCAATTAAACT	13220	-	AGG	114
ATGCCTAGTTTAATTGATAC	13233	+	TGG	677
AGTTTAATTGATACTGGAGA	13239	+	TGG	439
GATTAAAAAACTTAAAAATA	13269	+	TGG	136
AAAAACTTAAAAATATGGAT	13274	+	TGG	142
GCTGGAATACTGCGATTATT	13312	+	CGG	237
TAACTAGCCACTGTGTATAT	13350	-	AGG	133
CATATCGCCTATATACACAG	13359	+	TGG	97
CTTGATGTACTTCTTTGTGT	13373	-	TGG	3498
CAACACAAAGAAGTACATCA	13390	+	AGG	48
AACACAAAGAAGTACATCAA	13391	+	GGG	76
ATAGCGCAGACATACAAGCT	13526	+	AGG	398
ATACAAGCTAGGTTAAAAGT	13537	+	AGG	73
AAAGTAAAAGTTAAGACGAT	13564	+	TGG	159
TTCTTTACTTCGTATAAGAT	13599	-	CGG	185
GATCTTATACGAAGTAAAGA	13617	+	AGG	668
GCAAGTATATATTATGATGA	13718	+	CGG	70
GACGGCTAATGATGATGTAG	13736	+	AGG	130
CTCAACTTTGCGAAGTCACT	13745	-	CGG	4823
GCGATCAGTCTGATTTGATG	13783	+	AGG	255
CGATCAGTCTGATTTGATGA	13784	+	GGG	390
TCAGTCTGATTTGATGAGGG	13787	+	CGG	13
GTCTGATTTGATGAGGGCGG	13790	+	AGG	21
GAGTCAATTGTTAATATGAT	13836	+	AGG	231
TGTATTAGCTGATGTAATAC	13880	+	CGG	280
ATTGAATTGCTATCATATTC	13883	-	CGG	766
AGCAATTCAATTGCACAGTA	13911	+	TGG	1022
GAGTTTTCCCCTTGTGGTTT	13934	-	CGG	359
TTACTTGAGTTTTCCCCTTG	13940	-	TGG	23
GCAACGTTGCCGAAACCACA	13941	+	AGG	940

CAACGTTGCCGAAACCACAA	13942	+	GGG	337
AACGTTGCCGAAACCACAAG	13943	+	GGG	230
AAGTTGAAGATGTTGTTGTG	13978	+	AGG	408
GGCTTGAGAGAGCAAATAAA	13999	+	AGG	64
GTATGCTCAGATGTTAAAAG	14021	+	AGG	1629
AAATCAATCGCAACAGAGAT	14054	+	TGG	22
AATCAATCGCAACAGAGATT	14055	+	GGG	520
TTCTTAGAGTTATTGAAGAA	14094	+	AGG	49
TATTGAAGAAAGGTTATAAC	14104	+	AGG	549
ATTGAAGAAAGGTTATAACA	14105	+	GGG	145
TTTCTGTTCAATTTAGAGTT	14132	-	AGG	342
TCTTTTCTGCTAATTCATCA	14170	-	CGG	4195
GTAAGAATTATCTTAAGACG	14303	+	TGG	16
TAAGAATTATCTTAAGACGT	14304	+	GGG	80
AAGAATTATCTTAAGACGTG	14305	+	GGG	611
ATCGATGAGAACATCTAATG	14318	-	TGG	10
AAACTACCCACCATATAGGC	14399	-	AGG	51
AATTAAACTACCCACCATAT	14403	-	AGG	469
TCACTTACTACCTGCCTATA	14405	+	TGG	87
CTTACTACCTGCCTATATGG	14408	+	TGG	140
TTACTACCTGCCTATATGGT	14409	+	GGG	62
CGTTCAATAAATGTGAAAGG	14452	-	AGG	138
CTACGTTCAATAAATGTGAA	14455	-	AGG	40
AATGCCCCTACATCTTGTGC	14480	-	AGG	235
GTAGCTCCTGCACAAGATGT	14490	+	AGG	240
TAGCTCCTGCACAAGATGTA	14491	+	GGG	55
AGCTCCTGCACAAGATGTAG	14492	+	GGG	211
AGCACAAACTTTTCTTGCTT	14575	-	CGG	432
AAGCAAGAAAAGTTTGTGCT	14594	+	AGG	731
TTTGTGCTAGGACTCATAGA	14606	+	GGG	96
CGTCAATATATGCTTTCCGT	14619	-	TGG	4886
TCATAGAGGGCAAGAGCCAA	14619	+	CGG	384
CGGAAAGCATATATTGACGC	14639	+	AGG	135
GGAAAGCATATATTGACGCA	14640	+	GGG	48
GACGCAGGGTATTCGACTAA	14654	+	AGG	207
TATTCGACTAAAGGTAAGAG	14663	+	TGG	112
ATTCGACTAAAGGTAAGAGT	14664	+	GGG	293
TTCGACTAAAGGTAAGAGTG	14665	+	GGG	17
CGAGTACACTTTTTAAAAAT	14706	+	CGG	4
TACACTTTTTAAAAATCGGA	14710	+	AGG	7
ACGCAATTTTTCGTACCTTC	14720	-	CGG	986
AAAATCGGAAGGTTTCCGGA	14721	+	AGG	67
AAGTAGCTGAACAATCAAAA	14763	+	TGG	182

CATATTCTTCAAAGGCCTTT	14775	-	TGG	2686
ATCAAAATGGACACGCCAAA	14776	+	AGG	328
TAGCCACTCATATTCTTCAA	14783	-	AGG	4
AGGCCTTTGAAGAATATGAG	14796	+	TGG	84
TAAGAATGACATTGAAATAG	14833	+	AGG	306
AAGAATGACATTGAAATAGA	14834	+	GGG	178
TCATACCATCTAAACTAGCG	14868	-	AGG	873
GCATTCCTCGCTAGTTTAGA	14879	+	TGG	179
GGTATGAATAGAATGACGTT	14900	+	AGG	2424
AAGATTGAACAAATAGATAA	14978	+	AGG	1281
CAAATAGATAAAGGTGACAG	14987	+	TGG	472
ACAACTTCACGACGCAATAA	15028	+	CGG	726
TAAACTTAAATCTTTATATA	15068	+	CGG	5
AGCAAACGCAAAAACAAGAT	15112	+	TGG	772
TGGTTTATGTTAATTAATCA	15132	+	CGG	443
AATCACGGAGCAAAGCGTAC	15147	+	AGG	2815
CGAAAGATAGCAGACGAAGA	15219	+	AGG	648
GCACCAGCAAGTATATATTG	15236	-	AGG	104
ACACCTCAATATATACTTGC	15249	+	TGG	8625
ATACTTGCTGGTGCAACATT	15261	+	AGG	7
ATAGAGTTAACTAACAAATA	15306	+	TGG	149
TATAATTCATTCATGTTATT	15351	+	TGG	4405
CATGTTATTTGGCGTTCAAG	15362	+	TGG	55
GGCGTTCAAGTGGTTCAGAC	15372	+	AGG	237
ACAGGTCACAGTAAAGTAAG	15390	+	TGG	23
AGTGGTATAGGAGCTATACG	15408	+	TGG	103
ATACGTGGTATGACATCGTT	15423	+	TGG	61
AGCGTCGTTAGCGCATGAAG	15461	+	AGG	30
GAGATTAAGTCACGTTGTAG	15492	+	TGG	120
AAGTCACGTTGTAGTGGAAC	15498	+	TGG	193
TGGAACTGGTGCAAGAATAT	15512	+	TGG	918
ATGCTCGGGATGGTCAGGGT	15525	-	TGG	260
ACCAATGCTCGGGATGGTCA	15529	-	GGG	121
AACCAATGCTCGGGATGGTC	15530	-	AGG	297
TCAACAACCAATGCTCGGGA	15535	-	TGG	112
TCTTTCAACAACCAATGCTC	15539	-	GGG	1018
ATCTTTCAACAACCAATGCT	15540	-	CGG	789
ACCCTGACCATCCCGAGCAT	15544	+	TGG	76
GAAAATACAGATCCTAAAGC	15585	+	AGG	1052
TATTGTCATCGAGCTTAAAT	15604	-	TGG	1514
TAGATATAAAGAGTCTATTA	15656	+	AGG	337
CGTTCATAGAACATACCTGA	15671	-	TGG	1491
ATTAAGGCTTCAACACCATC	15672	+	AGG	667

TTCTATGAACGTAATATCAA	15699	+	CGG	93
AACGTAATATCAACGGTATG	15706	+	TGG	41
ACGTAATATCAACGGTATGT	15707	+	GGG	936
ATCAACGGTATGTGGGTGTC	15714	+	TGG	80
GGTATGTGGGTGTCTGGTGA	15720	+	CGG	77
ATTCTCATTCAAATCAAAGT	15738	-	CGG	3063
TACGATTAAAGCAGATGAAC	15776	+	TGG	377
CCAGCAAAGTATTCTTTGAT	15791	-	AGG	179
CCTATCAAAGAATACTTTGC	15807	+	TGG	396
AATACTTTGCTGGTGTCGAC	15817	+	TGG	262
ATACTTTGCTGGTGTCGACT	15818	+	GGG	58
TACTTTGCTGGTGTCGACTG	15819	+	GGG	67
GACTGGGGTTACGAGCACTA	15834	+	TGG	39
TATGGATCTATTGTGTTAAT	15852	+	AGG	4
TCTATTGTGTTAATAGGACG	15858	+	AGG	129
TTAATAGGACGAGGTATAGA	15867	+	TGG	301
TGGTAACTTTTATTTTATTG	15887	+	AGG	63
AATCATCAATAAACTTAAAT	15904	-	TGG	1503
AATTTAAGTTTATTGATGAT	15922	+	TGG	579
ATTTAAGTTTATTGATGATT	15923	+	GGG	365
TAAGTTTATTGATGATTGGG	15926	+	TGG	40
AAAGATATTGTAAGTAGATA	15957	+	TGG	45
CGCTGATAAAAGTAAACTAT	16058	+	CGG	1950
GCTGATAAAAGTAAACTATC	16059	+	GGG	26
AAGTAAACTATCGGGTGTAG	16067	+	AGG	69
ACTTGTTCTTTATGATAATA	16121	+	TGG	499
TTCTTTATGATAATATGGAT	16126	+	AGG	117
TATGGATAGGTTTAAGCAAG	16139	+	AGG	349
AAGAGGTATTTAAATATGTT	16156	+	TGG	1596
TTATAGGCTCTCCGTTTGTA	16165	-	GGG	369
TTTATAGGCTCTCCGTTTGT	16166	-	AGG	736
TATGTTTGGCACCCTACAAA	16170	+	CGG	941
ACGTCATCAAATTCTTTTAT	16181	-	AGG	1574
AAAAGAATTTGATGACGTGT	16202	+	TGG	248
AGGTTTAGTATGTGTGTATA	16224	-	TGG	298
ATACTAAACCTGAACGATTA	16252	+	AGG	282
CTAAACCTGAACGATTAAGG	16255	+	AGG	61
TAAACCTGAACGATTAAGGA	16256	+	GGG	134
AAACCTGAACGATTAAGGAG	16257	+	GGG	2
AACCTGAACGATTAAGGAGG	16258	+	GGG	4
ATAGATGATATTGAAGCACA	16301	+	AGG	33
ATTAGAGCCTCAATATGCTT	16315	-	AGG	10004
AATATTGCCTAAGCATATTG	16324	+	AGG	109

TAAAGACGATAGAGAGAGAA	16363	+	TGG	113
ATTGGTCGACGTTTGAATAT	16411	-	TGG	3122
AAATCTTCTTTTTCTTCAAT	16429	-	TGG	3934
GAAAAAGAAGATTTTGAAAC	16454	+	TGG	331
AAAGAAGATTTTGAAACTGG	16457	+	TGG	101
TTGAAACTGGTGGAAATGTA	16467	+	AGG	90
ACACGTGTTGGTTATTTACA	16550	+	TGG	57
TCATCTAAATCATAAGTAAC	16561	-	AGG	198
ACTATTTCTAATGGCAAAGT	16622	-	TGG	1421
ATCATCAACACTATTTCTAA	16631	-	TGG	921
TAGAAATAGTGTTGATGATG	16651	+	AGG	858
GATGATGAGGATTCTGAAAT	16664	+	AGG	77
GGATTCTGAAATAGGTAAAA	16672	+	TGG	272
GGTAAAATGGCAGCAATTTG	16685	+	CGG	497
ATGGCAGCAATTTGCGGATA	16691	+	TGG	4
CAATTTGCGGATATGGTGCT	16698	+	AGG	766
TTAGCATATATTGATACGAA	16721	+	TGG	29
TTGATACGAATGGTGATGTT	16731	+	AGG	233
GCCAACAAAAATAACATTAT	16754	-	AGG	1435
AAGTAGCGCAATGAGTATGT	16792	-	AGG	1687
TATGAAAAAGATGATGATAA	16832	+	TGG	1091
TATTATGTATTTCGAGGAGA	16895	+	AGG	29
ATTGACGCTTTGCAAGAAGT	16919	+	TGG	65
TTGTTAGGTACACCAAACAA	16954	-	TGG	64
TTTGATTACAATCCATTGTT	16958	+	TGG	883
CCTATCATCTCTTTGTTGTT	16969	-	AGG	2845
CCTAACAACAAAGAGATGAT	16985	+	AGG	112
GATGATAGGAGATGCTGAAA	16999	+	AGG	8
TACCCATACCGCGTAACACA	17082	-	AGG	2963
TTAGCATACCTTGTGTTACG	17090	+	CGG	127
ATACCTTGTGTTACGCGGTA	17095	+	TGG	35
TACCTTGTGTTACGCGGTAT	17096	+	GGG	163
ATTCAAGAAACACAAAAGAG	17135	+	TGG	349
TGAGTTGTTCGACAAAGATA	17164	+	TGG	270
TCTTTTCGATTCGATCTAAA	17217	-	TGG	1648
TTTAATTCTGACGAGTTTAA	17285	+	CGG	48
TTAAGTTTCATTCCAATGAT	17299	-	AGG	16
AACGGAAATGTACCTATCAT	17303	+	TGG	279
TGGAATGAAACTTAAACTTA	17323	+	TGG	630
GTAAGATGACAGCTATGTTG	17376	+	AGG	1686
TTATCTGCATTAAAGCGTAA	17417	+	AGG	814
TATCTGCATTAAAGCGTAAA	17418	+	GGG	588
AAAGCGTAAAGGGTACAACT	17428	+	TGG	129

TACGAGTGAACTTAAATATC	17454	-	AGG	1368
GATTCTTCTAACTTATTAAC	17482	-	TGG	1055
GTTCTGAAACTTGTCCCTTC	17520	-	AGG	2198
ACAAGTGCTAATTAACCTGA	17521	+	AGG	202
CAAGTGCTAATTAACCTGAA	17522	+	GGG	56
GACAAGTTTCAGAACGAACA	17544	+	AGG	900
GTTTCAGAACGAACAAGGTT	17549	+	AGG	1344
TGATTACGAATTAGACGAAA	17596	+	TGG	607
GCGTCACCTTCATCTATGTC	17635	-	AGG	689
AAATTACCTGACATAGATGA	17645	+	AGG	1017
TCATTCTGATTGGTTATTTT	17669	-	GGG	1827
ATCATTCTGATTGGTTATTT	17670	-	TGG	79
CTCATCAATATCATTCTGAT	17679	-	TGG	67
TGATATTGATGAGTATATCG	17705	+	AGG	456
GATATTGATGAGTATATCGA	17706	+	GGG	19
TTAGCAAATAGTTGTTCTAT	17735	-	TGG	76
ATGATGATGTGTATGTTACA	17827	+	TGG	854
CTGAATTCAATAAATACAAC	17851	+	AGG	1929
TAAATACAACAGGCTCAATA	17861	+	AGG	1070
AATAAGGAGTTAACTCGTAT	17877	+	AGG	4235
CATATAAATAAAGGCTCATA	17962	-	AGG	876
GAGCCTTTATTTATATGAAA	17984	+	TGG	7
GTTTGATGTTCCGAGTAAAG	18026	+	AGG	835
ATTAAACGAATGAACTCAAT	18056	-	AGG	6481
TCACGATGTTTTTGTAGTGT	18080	-	TGG	1021
ATACGTATGCACATTACACA	18135	+	AGG	7229
ATTACACAAGGTATTATGAG	18147	+	TGG	51
ACAAGGTATTATGAGTGGAG	18152	+	AGG	49
CAAGGTATTATGAGTGGAGA	18153	+	GGG	19
AAAGCAATACGTGATGATGT	18192	+	CGG	320
TAAAGCTCAATCATTGCGTG	18221	+	TGG	976
GGCAGAGCAATGTCACAAGC	18258	+	TGG	231
AGCTGGACTTGATAGCGCAA	18275	+	TGG	38
GCAATGGTTGCTAAAGATAA	18291	+	CGG	17
GTTTGAAGATGAAGAAACGT	18313	+	TGG	2284
GATACTCATCGTCATTTAGA	18363	+	TGG	25
ATACTCATCGTCATTTAGAT	18364	+	GGG	17
TACTCATCGTCATTTAGATG	18365	+	GGG	864
TCATTTAGATGGGGAATCAG	18374	+	TGG	165
GATCAGAATTTTAAATCAAG	18402	+	TGG	366
ATCAGAATTTTAAATCAAGT	18403	+	GGG	989
TTTAAATCAAGTGGGTGTGT	18411	+	TGG	42
TTAAATCAAGTGGGTGTGTT	18412	+	GGG	263

ATCAAGTGGGTGTGTTGGGC	18416	+	AGG	365
TTTACACCAATAAATAGCTT	18425	-	GGG	409
GTTTACACCAATAAATAGCT	18426	-	TGG	290
CAGGCGCCCAAGCTATTTAT	18435	+	TGG	173
TTACGTGCTCTCATTACAGT	18512	-	TGG	2337
ATGAGAGCACGTAAAGACGA	18537	+	TGG	547
ACTCACGATAAGTCATGAAT	18559	-	GGG	358
CATTCATGACTTATCGTGAG	18577	+	TGG	720
ATTCATGACTTATCGTGAGT	18578	+	GGG	423
TGGGAGAAATATAAGCGAAA	18597	+	AGG	177
GAGAAATATAAGCGAAAAGG	18600	+	TGG	254
CGAAAAGGTGGTAATTGATA	18612	+	TGG	84
ATAAAAGTAAATGTTGATAC	18643	+	TGG	2415
CTCTATTATCTCTTCGTACA	18682	-	AGG	2947
AAATGAAGCTGATTTAGATA	18759	+	TGG	96
AGCAGTTTAACGACATGCTA	18841	-	AGG	33
GCTTTTTATTATGCACTTTT	18877	+	CGG	820
TATGCACTTTTCGGACTGTT	18886	+	AGG	71
ATGCACTTTTCGGACTGTTA	18887	+	GGG	156
CGGACTGTTAGGGTACGCGA	18897	+	AGG	32
GGACTGTTAGGGTACGCGAA	18898	+	GGG	4
AGGGTACGCGAAGGGCAAAA	18906	+	AGG	1
AGAAGTAAAAGATTATCTAA	18990	+	AGG	52
GAAGTAAAAGATTATCTAAA	18991	+	GGG	1
TTATCTAAAGGGACTTAAGA	19002	+	CGG	219
GTGTCTGTTGATGACGTTAA	19024	+	AGG	104
GAATGATAACGATCTAATTC	19068	-	AGG	2867
TTAGATCGTTATCATTCGAA	19090	+	AGG	72
ATGGAAAGAGAAAAATCTTG	19122	+	AGG	798
ATCTAATCGAACAAGAAGTA	19145	+	CGG	277
TTTTGTTCTTCTGATTGCTC	19161	-	AGG	468
GTTAGAAAAACGCGACGCAG	19224	+	AGG	571
AAGTTAAGAAGTAACGCGCT	19258	+	AGG	358
TAACGCGCTAGGTAAAGCGC	19269	+	AGG	38
AATCTATCAACTAAGGATGT	19287	-	TGG	112
GCCTAAAAATCTATCAACTA	19294	-	AGG	761
TCCTTAGTTGATAGATTTTT	19309	+	AGG	372
TTTTTGAACATACTTGTCAA	19363	-	AGG	501
TTTGACAAGTATGTTCAAAA	19381	+	AGG	105
GAGTCTAAATTTAAATCGAG	19408	+	TGG	1249
CAATGGACTTTACATTTGAA	19451	-	GGG	10
TCAATGGACTTTACATTTGA	19452	-	AGG	16
TTCTTTCGCCATTTCTTCAA	19468	-	TGG	632

TGTAAAGTCCATTGAAGAAA	19476	+	TGG	172
CAATATTAGAAAATAAAGTG	19509	+	AGG	151
TAAAGTGAGGTAATAAAATA	19522	+	TGG	17
ACATTGCCTGGCGTGTATGT	19534	-	TGG	331
GCAACTCCAACATACACGCC	19544	+	AGG	496
TCCGATAAAATAACATTGCC	19546	-	TGG	1139
GCCAGGCAATGTTATTTTAT	19561	+	CGG	10
ATTAAAGTACCTTGTTCTGC	19588	-	TGG	1976
GGCGTTATTCCAGCAGAACA	19595	+	AGG	214
TTTAATCATGAAAGACATTA	19621	+	TGG	53
TTTTTCTTTTGTGCTGTCAT	19663	-	TGG	948
AAATTTACTTACTTAGCAAA	19700	+	AGG	9
ACTTACTTAGCAAAAGGTGT	19706	+	AGG	598
CAAAAGGTGTAGGCGCCTAC	19716	+	TGG	36
AAAAGGTGTAGGCGCCTACT	19717	+	GGG	146
ATTTCTGCTTGTGCATATTC	19753	-	AGG	1686
TGAATATGCACAAGCAGAAA	19771	+	TGG	268
GAAATGGAAGCTAAGAAAAT	19787	+	TGG	4
TTAAGAAACTCTTTTGATAA	19804	-	CGG	19
TGCAAAAGATTTCTTTAATG	19849	+	AGG	277
TAAAATGCCTCTGCAATTAG	19861	-	AGG	178
GGTTAAACCTCTAATTGCAG	19870	+	AGG	87
TAGTACCAAAGATAACAGCT	19896	-	TGG	458
TTTGACCAAGCTGTTATCTT	19907	+	TGG	1263
CCACTAGTTGAAGTGTTGTA	19924	-	AGG	59
CCTTACAACACTTCAACTAG	19940	+	TGG	358
AGTGGTAAACCGCTTGTTGA	19958	+	AGG	417
GTTGAAGGCGCAGAAGAGAA	19973	+	AGG	22
TAGTAGCCATTAATGCCGAA	20016	-	AGG	173
TAATTTATACGTAGACCTTT	20017	+	CGG	875
GATGAAGAGTTAGATCCAAA	20060	+	CGG	1
TTCCCGTTAGCATCAAATAA	20128	-	TGG	145
AGACCATTATTTGATGCTAA	20141	+	CGG	12
GACCATTATTTGATGCTAAC	20142	+	GGG	1924
TCCGCTCCAGTATAAGATAG	20167	-	TGG	53
GGATTACCACTATCTTATAC	20177	+	TGG	874
ACCACTATCTTATACTGGAG	20182	+	CGG	36
AAAGAAATCGTTAGCACTAA	20218	+	TGG	7
AAGAAATCGTTAGCACTAAT	20219	+	GGG	1868
CGTTAGCACTAATGGGTGAT	20226	+	TGG	91
GTTAGCACTAATGGGTGATT	20227	+	GGG	133
GATTGGGATTACGCACGTTA	20243	+	CGG	932
GCACGTTACGGTATCTTACA	20255	+	AGG	213

TGCTTGTAACGTCGTTAACG	20288	-	TGG	1476
TTACAAGCATCAGATGCTTC	20318	+	TGG	15
GTTCAAATAATGATACTGGT	20325	-	TGG	1334
TCACGTTCAAATAATGATAC	20329	-	TGG	10
TTAAGCGTTGCGAACGCTTC	20401	-	TGG	48
CATATCTCCTCCTATTCAGT	20425	-	TGG	1415
AACGCTTAAACCAACTGAAT	20431	+	AGG	305
GCTTAAACCAACTGAATAGG	20434	+	AGG	75
CTGAATAGGAGGAGATATGA	20445	+	TGG	83
TTTACCTTAATATCTTCTGC	20457	-	AGG	509
TAATCCTGCAGAAGATATTA	20469	+	AGG	15
GACTATTACTGTTACAAAGA	20508	+	AGG	105
GACTCTTATTACAGTCTTGT	20536	+	CGG	1291
CAGTCTTGTCGGTTACAAAG	20547	+	AGG	164
CGCTCTTATCAGACGTAGTA	20564	-	CGG	1503
AAACTTTTACTCAAGAAAAA	20634	+	TGG	27
TTTACTCAAGAAAAATGGAG	20639	+	TGG	146
TGAAGAAGAAATATTTAAGA	20675	+	TGG	361
ATATTTAAGATGGAAGTTGA	20685	+	CGG	46
ACGGAATACTAGAAGATGTT	20704	+	AGG	357
AACAATGATTTTATGAAAGA	20736	+	TGG	137
ACATACTTTTTGATTGAGTA	20756	-	AGG	120
CAGGTCGTTGATAATACTCT	20788	-	AGG	668
TTTAAATTCTTTTTAACTTC	20807	-	AGG	42
GAATTTAAAGTCAAGAAGTA	20837	+	TGG	116
AATTTAAAGTCAAGAAGTAT	20838	+	GGG	1227
ATTTAAAGTCAAGAAGTATG	20839	+	GGG	1497
GTGTCGTACACTTATAACGA	20865	+	TGG	97
ATACTCCACTAATGTAATCA	20875	-	GGG	49
AATACTCCACTAATGTAATC	20876	-	AGG	473
GGTGTCCCTGATTACATTAG	20886	+	TGG	40
ACATTAGTGGAGTATTAAAC	20899	+	AGG	346
CTCTACCTTATTGATTTAAA	20927	-	CGG	17
TTCATCCGTTTAAATCAATA	20938	+	AGG	813
CGTTTAAATCAATAAGGTAG	20944	+	AGG	857
GTGTGAGGGAATTCGTCGTA	20968	-	TGG	390
TTCCAATAGAAATAGTGTGA	20982	-	GGG	2
CTTCCAATAGAAATAGTGTG	20983	-	AGG	1
TTCCCTCACACTATTTCTAT	20996	+	TGG	933
ATTGGAAGTATCAAAAAAGT	21014	+	AGG	91
ACAAAGCGTTCTTGTATAAT	21028	-	TGG	111
GTAAGCGATAAAACAATTAA	21065	+	AGG	2
TAAAACAATTAAAGGATTTA	21073	+	TGG	176

TTTAGTTGTTCAGATGTAGT	21085	-	AGG	2536
GTAAGTCGTAAGGTACATAT	21141	-	AGG	324
TTAGCTATTGGTAAGTCGTA	21151	-	AGG	38
AATAAATTGTTTTTAGCTAT	21163	-	TGG	1577
AAACAATTTATTTGAGTATG	21190	+	AGG	3
AACAATTTATTTGAGTATGA	21191	+	GGG	75
GGTAGAATCTTTAGTATTGT	21212	+	AGG	129
TGTAGGCGATTCTGTAGATC	21229	+	AGG	212
GGCGATTCTGTAGATCAGGG	21233	+	CGG	31
TAAACTACTACGACTTAAGC	21268	+	AGG	388
CGTACTTAACTTTTGCCATA	21277	-	TGG	1343
CGACTTAAGCAGGTGCCATA	21278	+	TGG	3534
CATATGGCAAAAGTTAAGTA	21294	+	CGG	3
TAAGTACGGTGCTGATAGCA	21308	+	TGG	318
TGATAGCATGGTTGTTGAAT	21320	+	TGG	12
TCGATAAGAAAATAGAAGAG	21349	+	TGG	14
CGATAAGAAAATAGAAGAGT	21350	+	GGG	388
ATAGAAGAGTGGGTTAAAAA	21360	+	AGG	9
TCTAAAAAACCTAAGTCAAC	21416	-	AGG	2733
GCATTAGCTCCTGTTGACTT	21423	+	AGG	314
ATTGACTTTAAATATTTCGA	21462	+	TGG	51
GACTTTAAATATTTCGATGG	21465	+	TGG	332
ACTTTAAATATTTCGATGGT	21466	+	GGG	94
TGCGCCGACACTTATAACAC	21477	-	TGG	23
TTATCCAGTGTTATAAGTGT	21489	+	CGG	146
TATGCAATATACGTTGAATA	21519	+	CGG	47
ATATACGTTGAATACGGTAC	21525	+	TGG	35
GGTACTGGTATATATGCTAC	21540	+	TGG	58
GGTATATATGCTACTGGTCC	21546	+	TGG	319
TTTGTAGCACGACTACCACC	21548	-	AGG	918
ATATATGCTACTGGTCCTGG	21549	+	TGG	69
AAGATTCCGTGGAGTTTTAA	21585	+	AGG	2
TGGAGTTTTAAAGGTGATGA	21594	+	CGG	32
TTAAAGGTGATGACGGCGAA	21601	+	TGG	4
GGCGAATGGTACACAACATA	21615	+	TGG	1293
GCAGGGTTCCAAAATGGCTG	21629	-	TGG	17
TCAATTGCAGGGTTCCAAAA	21635	-	TGG	9
GTCAAGCGCCACAGCCATTT	21637	+	TGG	155
TGCGTCCTGCGTCAATTGCA	21646	-	GGG	587
TTGCGTCCTGCGTCAATTGC	21647	-	AGG	159
TGGAACCCTGCAATTGACGC	21657	+	AGG	244
TCGAGCAGTATTTTTCATAG	21691	+	AGG	17
AGCAGTATTTTTCATAGAGG	21694	+	TGG	238

CATAGAGGTGGTTAAATATG	21706	+	TGG	11
TATATTTGATTTGTAAGTTC	21725	-	AGG	1843
CAACTAGTTTGTTAATGTTA	21766	-	GGG	50
TCAACTAGTTTGTTAATGTT	21767	-	AGG	88
TTAACAAACTAGTTGATGAT	21790	+	AGG	142
TAACAAACTAGTTGATGATA	21791	+	GGG	4
ATTCACCCACAACAATATAT	21829	-	GGG	3648
GATTCACCCACAACAATATA	21830	-	TGG	170
TGTTTACCCATATATTGTTG	21839	+	TGG	111
GTTTACCCATATATTGTTGT	21840	+	GGG	1989
GCAACAATGAGAGAAACAGT	21894	+	CGG	54
ACAGTTCGCTACACAATACG	21938	+	AGG	309
AAGCTCATTTTAAGCGCGAT	21963	+	AGG	58
TCGTAATTATCTATTTCTAT	21986	-	AGG	342
ATACTGCTTGACTATCGATA	22021	-	CGG	37
TAGTAAACCTGTCTATATCA	22045	-	GGG	90
TTAGTAAACCTGTCTATATC	22046	-	AGG	29
CAGTATTCCCTGATATAGAC	22054	+	AGG	416
ATAGACAGGTTTACTAAGCA	22068	+	TGG	248
TTACTAAGCATGGCACGATA	22078	+	CGG	136
AGACATAAAAAGAAAAACGA	22116	+	AGG	38
AAACGAAGGAGTGTATTAAA	22130	+	TGG	35
GGATCTAAGTCAGTTTCAGC	22166	-	TGG	2923
TTATTAGCTGACTTACAAGA	22218	+	AGG	201
TTAGCTGACTTACAAGAAGG	22221	+	TGG	3
GATTTAGCTGAAATAGTACG	22260	+	AGG	251
AATAGTACGAGGCGGTAAAA	22271	+	CGG	3
AATGATTCTGACATTGCATT	22286	-	GGG	2358
AAATGATTCTGACATTGCAT	22287	-	TGG	52
GAATCATTTAAATTAACAAT	22317	+	TGG	146
TTAACAATTGGTAATGTGCC	22329	+	TGG	140
GCTTCAATTCCTTTATCTCC	22331	-	AGG	46
GGTAATGTGCCTGGAGATAA	22338	+	AGG	1
GTGAAACACGCTGTACAAAC	22371	+	AGG	1228
AAACACGCTGTACAAACAGG	22374	+	TGG	8
CAGGTGGACAGTTGCGTATA	22390	+	TGG	9
GAGCGTAATAAACGTGCAGA	22419	+	CGG	51
CGTGCAGACGGTAAACATCA	22431	+	CGG	9
GGTAAACATCACGGAATGTT	22440	+	TGG	1029
AATGACATTTCAAATGATTC	22457	-	TGG	301
AACTATCATTAAAAGTTAAA	22519	+	TGG	501
GCAGCTTCAAACCACTCTTT	22556	-	CGG	199
AAGATAACTTGCCGAAAGAG	22561	+	TGG	28

AAAGAGTGGTTTGAAGCTGC	22575	+	AGG	155
AATTTTTCGTATTCAACTGT	22586	-	AGG	911
ACAGTTGAATACGAAAAATT	22605	+	CGG	30
GAAAAATTCGGCGAAAAAGT	22617	+	CGG	100
TGTTGTATCTGATTCACACA	22667	+	CGG	2305
ATCTATTAGTTTACATAGAA	22678	-	TGG	129
CTATGTAAACTAATAGATCA	22699	+	AGG	51
TATGTAAACTAATAGATCAA	22700	+	GGG	15
ATGTAAACTAATAGATCAAG	22701	+	GGG	28
TGTAAACTAATAGATCAAGG	22702	+	GGG	8
TTTATAAAAAAATTGAAAAG	22742	+	AGG	13
TTAATTTTTAATGTTGTAAT	22772	-	TGG	165
ACAACATTAAAAATTAATGA	22794	+	CGG	127
CTGAGAATTTTTCAGCTTTT	22846	-	CGG	406
TTCTCAGAAGATAGCGAAGA	22878	+	TGG	4
TCTCAGAAGATAGCGAAGAT	22879	+	GGG	48
GATAGCGAAGATGGGAGAAA	22887	+	AGG	23
GGGAGAAAAGGAGCAATGCC	22899	+	AGG	178
TTAAATATAACATTGAATCC	22901	-	TGG	750
GGATTCAATGTTATATTTAA	22920	+	CGG	20
CTAATTGTTCTCGAGTTGGT	22993	-	GGG	519
TCTAATTGTTCTCGAGTTGG	22994	-	TGG	49
TTTTCTAATTGTTCTCGAGT	22997	-	TGG	1843
TGATTTCATCACTGAAAACG	23045	+	AGG	24
TCCAAAGCCCCTTGTAATAA	23060	-	CGG	193
GATACTTTGCCGTTATTACA	23067	+	AGG	380
ATACTTTGCCGTTATTACAA	23068	+	GGG	4
TACTTTGCCGTTATTACAAG	23069	+	GGG	1
GCCGTTATTACAAGGGGCTT	23075	+	TGG	127
ACAATAGTGGTTTTTTCAAG	23107	+	AGG	54
CAATAGTGGTTTTTTCAAGA	23108	+	GGG	18
AGAGGGAGAGTCGCTCGTAC	23125	+	TGG	148
TCCTCGCTTTTGGCCATATT	23150	-	CGG	83
ATTGAACAAAGCACCGAATA	23153	+	TGG	63
CATTTCTTTGTCCTCGCTTT	23160	-	TGG	19
ACCGAATATGGCCAAAAGCG	23165	+	AGG	190
GACAAAGAAATGACGAAAGC	23187	+	AGG	838
AATGATGAAAGAGAATTACA	23216	+	AGG	8
AGAGAATTACAAGGAAATCA	23225	+	TGG	64
GAGAATTACAAGGAAATCAT	23226	+	GGG	323
TATTTTTGAGTAATCGTGTA	23240	-	AGG	156
TACACGATTACTCAAAAATA	23259	+	AGG	11
CAACTGACAGCTAGATATTT	23282	+	AGG	459

GTGCTAACAATTCATGTTCA	23295	-	GGG	40
AGTGCTAACAATTCATGTTC	23296	-	AGG	49
AGCCAATCACGCCATTCAGC	23323	-	AGG	790
TAGCACTAACACCTGCTGAA	23328	+	TGG	276
CACCTGCTGAATGGCGTGAT	23337	+	TGG	28
TGGCGTGATTGGCTTATTGG	23348	+	TGG	17
TGATTGGCTTATTGGTGGTC	23353	+	AGG	13
GGCTTATTGGTGGTCAGGAT	23358	+	AGG	145
TTAATAATTGTCTTTGATCT	23367	-	AGG	170
ATTGAACAAGCGCAAGCTAA	23405	+	CGG	242
GCTTAGTACAAGCTTCTAAG	23427	+	AGG	63
CGTTACGAAATAAGAGAACC	23483	+	TGG	366
TGTACACGAGCATAGCTACC	23485	-	AGG	7169
GCTAACCTCCTTTCGATTCA	23571	-	AGG	5
AAATTCCTTGAATCGAAAGG	23582	+	AGG	5
GCCATAAAATGAGTATCCAA	23593	-	AGG	401
ATCGAAAGGAGGTTAGCCTT	23593	+	TGG	146
GCCTTTGGATACTCATTTTA	23608	+	TGG	140
TCATTTTATGGCAAAGATTA	23620	+	TGG	18
GAGCTTTCCTTACGTTGCTT	23643	-	TGG	119
GAGATTTCCAAAGCAACGTA	23652	+	AGG	860
ACATCTGTTTCAATTTCGTT	23689	-	TGG	2044
TAGCGCGTTGTAAAGCTCTT	23733	-	TGG	260
TTTACAACGCGCTAAATCAA	23758	+	TGG	554
CTAAATCAATGGCTCAACGA	23769	+	TGG	330
CTAAAGCTACTGTCGAAGCT	23937	+	TGG	254
GAGAAAACATGTTGTTAAGT	23959	+	TGG	302
CTTTAACCGCCATTTTAGCG	23979	-	GGG	66
CCTTTAACCGCCATTTTAGC	23980	-	GGG	62
CCCTTTAACCGCCATTTTAG	23981	-	CGG	1
AGATGCAAACCCCGCTAAAA	23986	+	TGG	42
TGCAAACCCCGCTAAAATGG	23989	+	CGG	79
CCCGCTAAAATGGCGGTTAA	23996	+	AGG	1
AAGATTTAATAGATCTTAGC	24027	+	AGG	3405
ATTTCCTAATTTCCATCTGC	24053	-	TGG	3857
TTGATATTGATTCCAGCAGA	24057	+	TGG	12
GATTCCAGCAGATGGAAATT	24065	+	AGG	22
AAAGAATTCAATGAAGTCGA	24101	+	AGG	5
GGAGCAGTTAAACGTTCTTT	24122	+	CGG	57
ATTATGAGAAAAGAAGTAAA	24158	+	TGG	150
TAAATGGAACAAGTGATATT	24174	+	TGG	438
AAATGGAACAAGTGATATTT	24175	+	GGG	2
AATGGAACAAGTGATATTTG	24176	+	GGG	50

AACAACTCATTGAAAGATTA	24206	+	CGG	199
GAAAGATTACGGCGAGAAAA	24217	+	TGG	5
AGTTCGGATTTTAGTAGCTA	24227	-	AGG	33
CGAAGATAGTACCGAAAGTT	24243	-	CGG	22
GCTACTAAAATCCGAACTTT	24248	+	CGG	120
CGGTACTATCTTCGCGCAAC	24268	+	AGG	470
ATCTTCGCGCAACAGGTCAA	24275	+	AGG	114
GGTACTAATCCGGCAATCAC	24313	-	TGG	95
GCATTGATACCAGTGATTGC	24320	+	CGG	110
CATTATTGCAGGTACTAATC	24323	-	CGG	46
TTAAGTACTGCCATTATTGC	24334	-	AGG	128
CGGATTAGTACCTGCAATAA	24340	+	TGG	222
AATAATGGCAGTACTTAATG	24355	+	CGG	2
ATGGCAGTACTTAATGCGGT	24359	+	TGG	12
CTTAATGCGGTTGGTGTATT	24368	+	AGG	44
GCGGTTGGTGTATTAGGTGG	24374	+	TGG	10
GTTGGCGCATTCTCTGTCGC	24410	+	AGG	106
GCATTCTCTGTCGCAGGTCT	24416	+	TGG	209
GTCGCAGGTCTTGGAGTTGT	24425	+	TGG	10
GGTCTTGGAGTTGTTGGCTT	24431	+	TGG	6
AGTTGTTGGCTTTGGTGCAA	24439	+	TGG	99
GGCTATTAGCGCTCTTAAAA	24460	+	TGG	105
GCTCTTAAAATGGTTGAAGA	24470	+	TGG	5
AATGGTTGAAGATGGAACAT	24478	+	TGG	25
GCGATCAGTTAAAAACTACA	24537	+	TGG	912
ATCTTTAATGCGATGTCAGC	24590	+	AGG	2873
GCGATGTCAGCAGGTATCAG	24599	+	AGG	80
ATAGATACTTCAGATAAGAA	24634	-	TGG	133
AGCAAACGCACGCAAGTTTG	24682	+	AGG	411
ACGCACGCAAGTTTGAGGAT	24687	+	TGG	65
CGCACGCAAGTTTGAGGATT	24688	+	GGG	74
TTTGAAGCATTGAATAGCAT	24740	+	AGG	77
AGCATAGGTGGCGCAATCTT	24755	+	CGG	8
GGAGATTTATTGAACGCTGC	24776	+	AGG	22
TTGAACGCTGCAGGAAGATT	24785	+	TGG	252
GCTGCAGGAAGATTTGGCGA	24791	+	CGG	2
TGAGACACAAATTTGAACAA	24826	-	CGG	49
TTGTTCAAATTTGTGTCTCA	24845	+	AGG	121
AGCCCAATTTTGGAAAGCTA	24866	-	TGG	89
CCACACTATTAGCCCAATTT	24876	-	TGG	131
TGTCCATAGCTTTCCAAAAT	24879	+	TGG	58
GTCCATAGCTTTCCAAAATT	24880	+	GGG	13
CCAAAATTGGGCTAATAGTG	24892	+	TGG	60

AATTGGGCTAATAGTGTGGC	24896	+	TGG	42
ACCACTAACTTACCTAAGAT	24953	+	TGG	525
CCTAAGATTGGTCAGATATT	24965	+	TGG	133
ATATTTGGCAATGTGTTCGC	24980	+	TGG	789
GGCAATGTGTTCGCTGGTAT	24986	+	TGG	391
ACAGTTCTAACATTTTTGAC	25035	+	TGG	242
TAACTTCTCAATTTAGAGCA	25068	+	TGG	9
AGAGCATGGTCAGAACAAGT	25082	+	AGG	339
GAACAAGTAGGACAATCACA	25094	+	AGG	21
ATCAGTTACGTTCAAGAGAA	25130	+	TGG	5
CCGATTAACTGCATAATAGT	25138	-	AGG	1275
CCTACTATTATGCAGTTAAT	25154	+	CGG	96
TAATATCGTAAAAGCGTTAG	25177	+	TGG	473
GTAAAAGCGTTAGTGGCATT	25184	+	TGG	1264
AGTGGCATTTGGTACTGCAA	25195	+	TGG	15
TCTAGTAATTTACTAGCTAT	25204	-	AGG	137
GATTTCGTTACTAATTTAGC	25241	+	TGG	1
TGGGTGTGCTTCGAATAGTT	25256	-	TGG	66
CGATAATTTGAGCGACTGCT	25275	-	GGG	162
CCGATAATTTGAGCGACTGC	25276	-	TGG	302
CCAGCAGTCGCTCAAATTAT	25292	+	CGG	10
GCTCAAATTATCGGTGTTAT	25301	+	CGG	18
ATCGGTGTTATCGGTATTTT	25310	+	AGG	93
GTATTTTAGGTGGCGTATTT	25323	+	TGG	15
TATTTTAGGTGGCGTATTTT	25324	+	GGG	105
TGGCGTATTTTGGGCTTTAA	25333	+	TGG	111
ACACTGCTAACAGCTGCAAT	25342	-	CGG	565
CTGGATTTAACTAGAATAAC	25430	+	TGG	3
TGGATTTAACTAGAATAACT	25431	+	GGG	655
GGATTTAACTAGAATAACTG	25432	+	GGG	128
TTTAACTAGAATAACTGGGG	25435	+	TGG	7
GGGGTGGTAAGTAAAGCGTT	25451	+	CGG	1
AAAGCGTTCGGTTTATTGAC	25463	+	TGG	2
GTGCTTTCACAAGTATTTCT	25485	+	TGG	883
ACTGCAACTACTGCTAATAT	25492	-	TGG	337
GCAGTCATTGGTGTATTCAT	25526	+	TGG	98
TTGGTATTCTTGTTTATTTA	25545	+	TGG	23
GAAAAACAATAACAGAAGCT	25587	+	TGG	705
ACAATAACAGAAGCTTGGAA	25592	+	CGG	132
GGTATTAAAACAGCAGTTTC	25613	+	CGG	327
TACTACACCTTGAATCGCAC	25616	-	CGG	89
GCAGTTTCCGGTGCGATTCA	25625	+	AGG	17
CGATTCAAGGTGTAGTAGAT	25638	+	TGG	226

TAGATTGGTTAACTCAATTG	25653	+	TGG	276
AGATTGGTTAACTCAATTGT	25654	+	GGG	34
GATTGGTTAACTCAATTGTG	25655	+	GGG	44
TGTCCTAATACTTGTAATAT	25693	-	AGG	173
ATGCCTATATTACAAGTATT	25706	+	AGG	78
CATGCAAGTTTTAGGTGTTT	25738	+	TGG	280
GTTTTAGGTGTTTTGGTAAT	25745	+	AGG	20
AATGTTATGAATATCATACA	25778	+	AGG	5
TGAATATCATACAAGGTTTG	25785	+	TGG	261
ATATCACTGTTCCTATGGCT	25812	-	TGG	208
ACAATTGCGTTCCAAGCCAT	25817	+	AGG	55
TACGGATATCACTGTTCCTA	25817	-	TGG	45
TACTATGATTTGGACAGCTA	25835	-	CGG	42
TGAATAAACCTACTATGATT	25845	-	TGG	181
GTAGCTGTCCAAATCATAGT	25853	+	AGG	45
GCTTTAATTCAGTTGCTTAC	25886	+	TGG	1161
TTGCTTACTGGCGACTTCTC	25898	+	AGG	20
CTGGCGACTTCTCAGGTGCT	25905	+	TGG	15
TGGCGACTTCTCAGGTGCTT	25906	+	GGG	53
TTGGGAGACTATTAAAACTA	25924	+	CGG	2
CCAAATCGTATCAAGTACAT	25934	-	TGG	1492
CCAATGTACTTGATACGATT	25950	+	TGG	81
GGCAATACATGCAATCAGTT	25971	+	TGG	278
TCAGTTTGGGAGTCAATTAT	25985	+	CGG	13
TCAATTATCGGCTTTTTAAC	25997	+	TGG	28
AATCGAACGCTTTCAATGTT	26027	+	TGG	201
TTTCAATGTTTGGTACAAGT	26037	+	TGG	19
GTACAAGTTGGTCACAGATA	26049	+	TGG	37
CTAATTTTGTTAGCAGTATT	26082	+	TGG	141
TTTGGAGCACTGTTACAAGT	26100	+	TGG	754
GTTGGTTCAGTCGTGTTGCT	26118	+	TGG	115
CAGTCGTGTTGCTTGGAGTG	26125	+	TGG	105
TGGAGTGTGGCTGAAAAAAT	26138	+	GGG	128
TTAAACTTTATTATCACAAA	26168	+	AGG	1
CTGAATGGGTTTCTAACATT	26193	+	TGG	1180
TTCGCGAGTAAAGTAGCTGA	26231	+	TGG	3
TCGCGAGTAAAGTAGCTGAT	26232	+	GGG	216
AAAAGAGTTGTCTCAAATGT	26258	+	AGG	14
GTTGTCTCAAATGTAGGTGA	26264	+	CGG	70
GACGGTATGAGTGATGCACT	26282	+	TGG	591
TTCAGTGATTTCTTAAATGC	26321	+	CGG	340
TTTGCCGATTAATTCCGCTC	26324	-	CGG	131
TGATTTCTTAAATGCCGGAG	26326	+	CGG	36

AATGCCGGAGCGGAATTAAT	26336	+	CGG	142
ATTAATCGGCAAAGTAGCTG	26350	+	AGG	373
TTAATCGGCAAAGTAGCTGA	26351	+	GGG	46
GACTACTTTGTGCGCAGCAT	26363	-	TGG	115
TGCGCACAAAGTAGTCAGCG	26386	+	CGG	34
CACAAAGTAGTCAGCGCGGT	26390	+	AGG	557
GCGATGCGATTTCATCAGCT	26412	+	TGG	31
CGATGCGATTTCATCAGCTT	26413	+	GGG	37
TCTGTAACTTCATTCGTAAG	26438	+	TGG	40
ACTTCATTCGTAAGTGGACA	26444	+	CGG	50
CACGGTGGAGGTAGTAGCTT	26462	+	AGG	33
GGAGGTAGTAGCTTAGGTAA	26468	+	AGG	3
TAGCTTAGGTAAAGGTTTAG	26476	+	CGG	65
AAAGTAATTGCTACAGACTT	26510	+	TGG	100
AGAGGATAGCTCTTTATTAA	26522	-	AGG	91
TATACTATCTGTCAAAGTAG	26540	-	AGG	179
CTGTCTATAGAAGTACTTAC	26569	-	AGG	276
CTAATCGTTACATTCACAAT	26638	-	AGG	766
GAATGTAACGATTAGAAATG	26662	+	AGG	22
AATGTAACGATTAGAAATGA	26663	+	GGG	14
GAAGTTTCAACTTATTATAA	26736	+	GGG	49
GTTTCAACTTATTATAAGGG	26739	+	AGG	8
CGCACGATATAGAAGTAATA	26777	+	AGG	135
GATATAGAAGTAATAAGGAA	26782	+	TGG	36
TCCAAGTGATTATAAGTGAA	26814	-	AGG	32
TCCTTTCACTTATAATCACT	26829	+	TGG	1071
GTAGTTGAATATAACGTTAC	26854	+	AGG	154
GAATATAACGTTACAGGCGC	26860	+	AGG	30
TCGTAACTATTCTGATATAG	26889	+	AGG	8
CGTAACTATTCTGATATAGA	26890	+	GGG	131
TCTGATATAGAGGGTATTGA	26899	+	TGG	142
AAAAAGTAGAGCTTAAGATA	26954	+	AGG	265
TGTGAAGCATAAGCAATTTT	26970	-	AGG	803
AACGTCCAGCAAATAGTGCT	27008	-	TGG	329
GACGTCCAAGCACTATTTGC	27019	+	TGG	211
TGCTGGACGTTTTTATTTAA	27036	+	GGG	11
TCATACTTAATTGAATTGTC	27063	-	TGG	73
TCAAATGCTTGTTTGTCTTT	27102	-	TGG	443
TTTGAGCTTGATTATGTTGA	27136	+	TGG	67
GATGGACGACAACTTTTTGT	27154	+	AGG	1319
TTTGACACAACACAAACATC	27196	+	AGG	149
TTGACACAACACAAACATCA	27197	+	GGG	1603
TGACACAACACAAACATCAG	27198	+	GGG	133

ACTTTCAAAGTATGGTAGTT	27229	-	CGG	145
TAACCGACACTTTCAAAGTA	27237	-	TGG	56
CTACCATACTTTGAAAGTGT	27250	+	CGG	117
CAGGTACCGACCATTTTTCA	27287	-	GGG	180
TCAGGTACCGACCATTTTTC	27288	-	AGG	12
GTAATAACGACCCTGAAAAA	27293	+	TGG	6
TAACGACCCTGAAAAATGGT	27297	+	CGG	179
TCGTTTGTAGGCAATCTATC	27306	-	AGG	158
CTCTTATCACCTTCGTTTGT	27318	-	AGG	387
GATAGATTGCCTACAAACGA	27325	+	AGG	83
CTACAAACGAAGGTGATAAG	27335	+	AGG	61
ACATTTTACAACACTAACTC	27367	+	AGG	603
TCAGGAGAAGTTTATTATAA	27385	+	CGG	3
AACTGATTAAACTGTGTTAA	27399	-	AGG	69
AGATGTTAAAGCTAATGATA	27465	+	AGG	187
GTTAAAGCTAATGATAAGGA	27469	+	TGG	3
TTCACTTTCTATACAGATAA	27493	+	AGG	9
AGGAAATATCTCAGTTATTA	27513	+	AGG	205
AAGGAAGTTGATTTAAAAGC	27532	+	CGG	16
GTCGAAGATTATTTTATCTC	27535	-	CGG	281
GGAGATAAAATAATCTTCGA	27553	+	CGG	6
TATATTTAAATAACCTCTAT	27568	-	AGG	722
GACGGTAAACATACCTATAG	27571	+	AGG	241
TAATAAAACTTTAGAACAAC	27615	+	CGG	185
TTCCAGCCTGGATATAAAAC	27618	-	CGG	6
GAACAACCGGTTTTATATCC	27628	+	AGG	397
GACTTGAATCGATTCCAGCC	27630	-	TGG	64
AACCGGTTTTATATCCAGGC	27632	+	TGG	83
CACAAATTATATTTTAGATA	27700	+	AGG	49
CTTTTTAATAAAATTGGCAT	27712	-	AGG	130
TGTAGACTTTTTAATAAAAT	27718	-	TGG	22
AATTTTATTAAAAAGTCTAC	27736	+	AGG	163
ATTTTATTAAAAAGTCTACA	27737	+	GGG	200
TTAAAAAGTCTACAGGGTGT	27743	+	AGG	11
TAAAAAGTCTACAGGGTGTA	27744	+	GGG	93
CGCTATTAATGTTAGTACAA	27769	+	AGG	803
GCTAAATGAAGATAGTTCTT	27802	+	TGG	541
GCGAGTACGTTTGACGCAAT	27845	+	AGG	86
TAGGTGCTATAACTAAAATG	27864	+	TGG	31
TGGACGATCACTCATGTTGA	27884	+	AGG	44
ATACTTGATAAGTCTACTAT	27938	+	TGG	302
TAAGGCTTGATATCAAAGCT	27969	+	AGG	42
GGTAAATCCTAGAATTGTTA	27993	-	AGG	287

TTGATGACCTTAACAATTCT	28002	+	AGG	86
TAAAACTTTCGTTATACTCT	28014	-	TGG	685
GAGTATAACGAAAGTTTTAC	28034	+	AGG	1
TTCTTCAATACTGTCTTTAA	28064	+	AGG	100
CAATACTGTCTTTAAAGGAA	28069	+	CGG	11
AATACTGTCTTTAAAGGAAC	28070	+	GGG	16
AATTTAGATGCATCTACTTT	28096	-	TGG	403
AGTAGATGCATCTAAATTCG	28117	+	AGG	9
GTAGATGCATCTAAATTCGA	28118	+	GGG	13
GCATCTAAATTCGAGGGATT	28124	+	AGG	54
AAATTCGAGGGATTAGGCAA	28130	+	AGG	1
CGATTAGAAATCTTTAAAAA	28160	+	AGG	102
ACCAGCTTTAATGTAATAAT	28247	-	TGG	36
GCCAATTATTACATTAAAGC	28262	+	TGG	10
ATCACCATAACCTTTAATAA	28319	-	AGG	71
AAATGTTATACCTTTATTAA	28325	+	AGG	19
TATACCTTTATTAAAGGTTA	28331	+	TGG	1
ACAACAGACTTTTGCAGAAG	28366	+	CGG	9
CAACAGACTTTTGCAGAAGC	28367	+	GGG	158
TTACCTATCAATTGTGCTAA	28396	-	TGG	17
CATCCATTAGCACAATTGAT	28409	+	AGG	287
ATACGTCCATCAACAAGCGG	28429	-	TGG	306
TTAATACGTCCATCAACAAG	28432	-	CGG	652
GAAGCGCCACCGCTTGTTGA	28439	+	TGG	237
AGATAGTTTAAAAAAAGCAA	28477	+	TGG	24
ACGTAACGCTACAAAGTCTA	28520	-	AGG	695
CTATTTTAGGGTTAGCTTCT	28551	-	GGG	174
CCTATTTTAGGGTTAGCTTC	28552	-	TGG	2
TAACAACATCACCTATTTTA	28563	-	GGG	369
CTAACAACATCACCTATTTT	28564	-	AGG	251
CCAGAAGCTAACCCTAAAAT	28568	+	AGG	2
AATAGGTGATGTTGTTAGAG	28585	+	TGG	30
AGGTGATGTTGTTAGAGTGG	28588	+	TGG	2
CACTAAGTCGTTATATCCTA	28601	-	TGG	177
AGAGTGGTGGATTCTGCCAT	28601	+	AGG	13
ACTAAGCAAGATGTAGTATT	28685	+	AGG	566
TAGTATTAGGAGACTTTACA	28698	+	AGG	368
TTTTAGTTCTTTAGATGGGT	28772	-	CGG	6
ATGCTTTTAGTTCTTTAGAT	28776	-	GGG	196
AATGCTTTTAGTTCTTTAGA	28777	-	TGG	21
TTTATCTATAAATAATGAAT	28837	+	TGG	1
AAAACAGTTACAACTGCTAA	28907	+	TGG	237
ATCAAATCAATTGGAACGAT	28973	+	TGG	202

ATTGGCGACTCTGTAGCTAG	28991	+	AGG	10
TTGGCGACTCTGTAGCTAGA	28992	+	GGG	20
ACTAATTTCACAGAAATGTT	29027	+	AGG	11
AAAACGACTAATCTTGCAAG	29066	+	AGG	10
ACGACTAATCTTGCAAGAGG	29069	+	TGG	37
TGCAAGAGGTGGCGCAACAA	29080	+	TGG	60
TCTACCGCTTCTTTACCTAT	29095	-	TGG	290
ACAATGGCAACAGTTCCAAT	29096	+	AGG	128
AGTTCCAATAGGTAAAGAAG	29107	+	CGG	4
AGACAAGCAGAGCAAATAAG	29147	+	AGG	7
CAGTGCCTTGTAATATGATT	29157	-	AGG	190
GGAGACCTAATCATATTACA	29168	+	AGG	51
TACAAGGCACTGATGATGAT	29184	+	TGG	201
ACTGATGATGATTGGTTACA	29192	+	CGG	44
ATGATTGGTTACACGGTTAT	29199	+	TGG	64
TGATTGGTTACACGGTTATT	29200	+	GGG	227
TGGTTACACGGTTATTGGGC	29204	+	AGG	117
TCCGTTTTATCAGTGCCTAT	29215	-	CGG	1724
TATTGGGCAGGCGTACCGAT	29216	+	AGG	137
ACCGATAGGCACTGATAAAA	29230	+	CGG	24
ACGGATACAAAAACGTTTTA	29249	+	CGG	1
AACTTCAATTGCAGAACAAA	29258	-	AGG	364
ATCACTAGTATTTTTGAATC	29296	-	TGG	22
GTATTGTTGTACCACTCATA	29337	-	GGG	186
CGTATTGTTGTACCACTCAT	29338	-	AGG	77
ACAAGACAATGCCCTATGAG	29342	+	TGG	211
TGTTTTTGTCCGTGTCTTTA	29361	-	CGG	475
AACAATACGCCGTAAAGACA	29368	+	CGG	492
GACACGGACAAAAACAAACT	29384	+	AGG	8
ACACGGACAAAAACAAACTA	29385	+	GGG	35
CAAACTAGGGTTAACACTTG	29398	+	AGG	85
GTGTGATATGCGTCAAACAC	29449	-	TGG	214
TTCCTAAAAGCTGGATTGTA	29485	-	TGG	178
AGCCATACAATCCAGCTTTT	29499	+	AGG	68
AGCTTTTAGGAAAGCGAGCA	29512	+	TGG	113
TTTTAGGAAAGCGAGCATGG	29515	+	AGG	18
AGGAAAGCGAGCATGGAGGA	29519	+	CGG	76
CCTCGTGACCTTTTTCGTTA	29532	-	GGG	8
ACCTCGTGACCTTTTTCGTT	29533	-	AGG	68
GGCTTACACCCTAACGAAAA	29540	+	AGG	9
CCCTAACGAAAAAGGTCACG	29548	+	AGG	11
TATTATGTACGAGTTAATCA	29572	+	AGG	44
ATTACAGTTTTTACGACTAA	29598	+	AGG	73

ACAGTTTTTACGACTAAAGG	29601	+	AGG	22
GTAATTAATCCGTAAGCCAT	29611	-	TGG	733
CGACTAAAGGAGGCAACCAA	29611	+	TGG	148
AGGAGGCAACCAATGGCTTA	29618	+	CGG	359
ACAAGTTTACATTCAATGAC	29648	+	AGG	383
GTTTACATTCAATGACAGGT	29652	+	CGG	108
AACTATCGCTTGTTAGATGA	29699	+	AGG	175
CGTATATTTCTTCTTTTTGA	29736	-	TGG	302
GATTATTTAACGTATTTAAA	29819	+	TGG	14
CTAGAATCATATTGCTAAAA	29826	-	CGG	9
CGTTTTAGCAATATGATTCT	29843	+	AGG	164
CATTGATACCGTCGCCGTTA	29850	-	TGG	298
AATATGATTCTAGGCCATAA	29852	+	CGG	97
ATTCTAGGCCATAACGGCGA	29858	+	CGG	50
GACGCGCGTATTGATAATAC	29897	+	AGG	28
CGTATTGATAATACAGGTTA	29903	+	TGG	195
ACTAGATGCTTTCACTAAAA	29968	+	AGG	155
CTTGCTCTTTTGGTTCGAAT	30024	-	CGG	94
AATTCCGGTTCTTGCTCTTT	30034	-	TGG	20
CGAACCAAAAGAGCAAGAAC	30046	+	CGG	6
GATAAATCAGTGATAAATTC	30049	-	CGG	35
TGCATTACTGCATTTGTATA	30073	-	TGG	91
ATGCAGTAATGCAATCATTT	30099	+	TGG	40
TGCAGTAATGCAATCATTTT	30100	+	GGG	792
TATAAATAATTTTCGTTCTA	30111	-	GGG	72
ATATAAATAATTTTCGTTCT	30112	-	AGG	278
TATATGACGCAAGCTCGTCC	30146	+	AGG	3016
GATAACATGTAATGATTACC	30148	-	TGG	365
CTATCAATAAATTGTCCGTT	30181	-	GGG	148
TCTATCAATAAATTGTCCGT	30182	-	TGG	111
TTATCTAGATTGAAGCCCAA	30182	+	CGG	108
GATAGATTGCTTGTTAAAAA	30215	+	CGG	54
AGATTGCTTGTTAAAAACGG	30218	+	CGG	15
AATGCGTATAGATACATTGA	30254	+	TGG	4
GATACATTGATGGAGAATTA	30264	+	TGG	20
ATGGATTTATTCAGCTGTAT	30283	+	TGG	211
TTATTTCTCCAGTTCTATAT	30321	-	TGG	505
GTACGTTTCCAATATAGAAC	30329	+	TGG	5
AGAACTGGAGAAATAACTTA	30344	+	TGG	150
TATCTGTCGTTAAATATATT	30373	-	CGG	330
TACGTCAGCGATTTATAATC	30412	+	CGG	209
AAAATCATTAAATTTTCTAC	30415	-	CGG	20
TTCTTAAGTTGTCTTTCAGT	30454	-	GGG	1049

ATTCTTAAGTTGTCTTTCAG	30455	-	TGG	254
GAATTCGTTGAACTTTGTTG	30490	+	AGG	28
AGTGCTGACGATATTGATAA	30518	+	AGG	18
AGACAAAGTATTGTATCAAA	30544	+	TGG	41
GTATCTGAAGTGTATTCCAT	30556	-	AGG	40
GTATCAAATGGATATACCTA	30556	+	TGG	20
TCATAAGTGATACCTTGCAT	30583	-	AGG	124
TCAGATACACAACCTATGCA	30587	+	AGG	365
CAAGGTATCACTTATGATGC	30605	+	AGG	49
ATGATGCAGGTATCTTATAT	30618	+	TGG	240
GGTATCTTATATTGGTATAC	30626	+	AGG	3
ACCTTGTAAGTAGTTAGGGT	30647	-	TGG	116
CGAAACCTTGTAAGTAGTTA	30651	-	GGG	31
TCGAAACCTTGTAAGTAGTT	30652	-	AGG	83
GCCAACCCTAACTACTTACA	30662	+	AGG	119
TTTAAACGACGTATCGATAT	30713	+	TGG	1456
AAACGACGTATCGATATTGG	30716	+	CGG	40
AGGAGACTTCCAAGAAGCTG	30757	+	AGG	20
GGAGACTTCCAAGAAGCTGA	30758	+	GGG	27
ATGTATTACGATCTAGAAAC	30788	+	AGG	5
GGACGCAAAGCGCTTTTAAT	30809	+	AGG	94
GACGCAAAGCGCTTTTAATA	30810	+	GGG	151
ACGCAAAGCGCTTTTAATAG	30811	+	GGG	54
CTTTTAATAGGGGTAACTAT	30821	+	TGG	98
ATAGGGGTAACTATTGGACC	30827	+	TGG	79
GAGTGATGTCTGTTGTTACC	30829	-	AGG	802
CATCACTCAATTTATTCCAT	30860	+	CGG	60
GTTAACACCTCTTTGGCCGA	30860	-	TGG	29
AGAATTGGTTAACACCTCTT	30867	-	TGG	258
ATTTATTCCATCGGCCAAAG	30869	+	AGG	17
GTGCAATGTTTTTTAAGAAT	30882	-	TGG	24
GAATCAGTCATCGATACTTG	30904	-	AGG	21
CAAGTATCGATGACTGATTC	30923	+	AGG	307
GTATCGATGACTGATTCAGG	30926	+	CGG	37
GCTGGGTTCTGTATTGGTAA	30943	-	CGG	10
AGATATGCTGGGTTCTGTAT	30949	-	TGG	240
TAATATCACTTAGATATGCT	30960	-	GGG	356
GTAATATCACTTAGATATGC	30961	-	TGG	59
AGCATATCTAAGTGATATTA	30979	+	CGG	12
CTAAGTGATATTACGGAAGT	30986	+	TGG	9
CTCTAAACGCTTTCGGTAAC	31038	-	GGG	57
TCTCTAAACGCTTTCGGTAA	31039	-	CGG	2
CCTGCATCTCTAAACGCTTT	31045	-	CGG	486

CCGAAAGCGTTTAGAGATGC	31061	+	AGG	832
TGGTTCTTTGATGTACTGCC	31085	+	TGG	300
AGAGCACCATTATAGTGTCC	31087	-	AGG	180
GTACTGCCTGGACACTATAA	31097	+	TGG	31
ATTTCTACCTGTGCTGTTTC	31124	-	TGG	291
GTACTTACCAGAAACAGCAC	31133	+	AGG	50
ATTTTCAATAAGAAAAACAA	31190	+	CGG	5
ATAAGAAAAACAACGGAGCA	31197	+	TGG	82
TCCCAATAACCGGCGTTTTG	31213	-	CGG	1
AATTTCTGTCCGCAAAACGC	31220	+	CGG	148
AGGGATATGTTCCCAATAAC	31223	-	CGG	27
GTCCGCAAAACGCCGGTTAT	31227	+	TGG	106
ATAATTTTGTAATATTCTTA	31242	-	GGG	94
GATAATTTTGTAATATTCTT	31243	-	AGG	100
TTATCAGATTTAAAAATCGT	31277	+	TGG	204
GCAATACCTTTAAAGTCTTT	31333	-	AGG	109
GATTTTCCTAAAGACTTTAA	31343	+	AGG	57
AAAGACTTTAAAGGTATTGC	31352	+	AGG	86
ACTTTAAAGGTATTGCAGGT	31356	+	TGG	75
AGAAGTAAAATCGAATACAC	31384	+	CGG	23
GAAGTAAAATCGAATACACC	31385	+	GGG	1105
AATACTTGTGTTGTGTTACC	31387	-	CGG	350
CTAAAAATTGATGTGCAGAC	31425	-	GGG	720
ACTAAAAATTGATGTGCAGA	31426	-	CGG	92
CAATTTTTAGTTAGAAACTT	31454	+	TGG	5
TTAGTTAGAAACTTTGGTAC	31460	+	TGG	39
AACTTTGGTACTGGTGGCGT	31469	+	TGG	78
GTACTGGTGGCGTTGGTAAA	31476	+	TGG	37
TGGTAAATGGAGTTTATTCG	31489	+	AGG	24
GGTAAATGGAGTTTATTCGA	31490	+	GGG	11
ATGGAGTTTATTCGAGGGAA	31495	+	AGG	2
GAGTTTATTCGAGGGAAAGG	31498	+	TGG	104
CTGATGTTTGTGTCAATAAT	31578	-	TGG	93
AGTTTCTATGAATCAGATAG	31615	+	AGG	72
TATGAATCAGATAGAGGAAC	31621	+	TGG	40
TGTTCAGAACTTATAGATAA	31662	-	CGG	251
TCTATCTACGTTATAATCAT	31711	-	CGG	60
GATGATTATAACGTAGATAG	31729	+	AGG	209
ACGATAGTAGACGCAATTAA	31774	+	TGG	103
CGATAGTAGACGCAATTAAT	31775	+	GGG	1262
GAATGTTTTAAAAATTCATT	31800	-	CGG	272
AATGAATTTTTAAAACATTC	31819	+	AGG	79
ATTTTTAAAACATTCAGGCA	31824	+	AGG	437

TTCAGGCAAGGTGCATGCTC	31836	+	AGG	260
CAGGCATTCTTTACACAAAA	31855	+	CGG	7
AGGCATTCTTTACACAAAAC	31856	+	GGG	69
ATTGAAAATGATTTAGTTAG	31918	+	TGG	63
TTGAAAATGATTTAGTTAGT	31919	+	GGG	66
GATTTAGTTAGTGGGTTTGA	31927	+	TGG	56
CAGCCATATTTTGCTTTAAT	32000	-	TGG	1003
TAACCAATTAAAGCAAAATA	32013	+	TGG	8
GTGAATGATAGTGCGACAAA	32062	+	AGG	78
GAAGTTGAACAACAAATCAA	32221	+	TGG	130
TTGTTGAATTACCTTTAACA	32234	-	AGG	361
AATGGCGCTGACCTTGTTAA	32239	+	AGG	72
AAGGTAATTCAACAACAAAT	32258	+	TGG	77
TCTAAACTTACAGATGATTA	32287	+	CGG	297
TGCGCTTAAAACGCTATCTA	32320	-	TGG	32
TAAGCGCAGTTAACACATCT	32351	+	AGG	176
GTGCCTATATCCGTCTTTTC	32388	-	TGG	85
AACAGATGCGCCAGAAAAGA	32394	+	CGG	43
GCGCCAGAAAAGACGGATAT	32401	+	AGG	40
ATAGGCACGTTAGAGAAGCC	32419	+	TGG	20
TCATCAACACCATCTTGTCC	32421	-	AGG	544
TTAGAGAAGCCTGGACAAGA	32428	+	TGG	29
GGACAAGATGGTGTTGATGA	32440	+	CGG	21
ACTTATACATCAAGCAAATC	32482	+	TGG	259
ATAATACTGCTCGTGCAACA	32531	+	TGG	1145
ACTCATCGTTTGAATCGTCT	32540	-	GGG	3005
TACTCATCGTTTGAATCGTC	32541	-	TGG	558
TACACAAAATACAAAATCTA	32578	+	CGG	1126
AATACAAAATCTACGGCACA	32585	+	TGG	1549
CATCATTCTTTTTATAAAAC	32594	-	GGG	207
CCATCATTCTTTTTATAAAA	32595	-	CGG	51
CCGTTTTATAAAAAGAATGA	32611	+	TGG	8
CAGTATGTAGATGATAAATT	32692	+	CGG	4
ATAAATTCGGAACAACGAGC	32705	+	TGG	345
GCAACAACATAAGATGACAG	32727	+	AGG	101
CATAAGATGACAGAGGCGAA	32734	+	TGG	51
GTTAACTTAAATAATGCGCA	32770	+	AGG	53
AATAATGCGCAAGGCGATTT	32779	+	GGG	34
TTACTATGCAACAAGAGTGC	32820	+	CGG	23
TCAACGCTACCTGGTAAATC	32823	-	CGG	35
ACAAGAGTGCCGGATTTACC	32830	+	AGG	296
TCATAACTTTCAACGCTACC	32832	-	TGG	1270
AGGTAGCGTTGAAAGTTATG	32850	+	AGG	82

GGTAGCGTTGAAAGTTATGA	32851	+	GGG	5
AAGTTATGAGGGTTATTTAT	32862	+	CGG	109
TAAATCTTTTTAGAGTTATA	32910	-	AGG	179
TACACACGATCAATCACAAA	32947	+	CGG	1749
ACGGCAGACTTGAGCAACAG	32966	+	TGG	17
ACCGTTGATTTATGTTCATT	32979	-	AGG	110
TCCTAATGAACATAAATCAA	32994	+	CGG	243
TCAACGGTATTGTTCGACGG	33010	+	TGG	32
TTGTTCGACGGTGGCGCAAA	33019	+	TGG	3
GACGGTGGCGCAAATGGTGT	33025	+	AGG	50
AAAATAGAATAGTTTGTGTA	33054	-	CGG	43
TATTCTATTTTGTTGGTAAG	33082	+	TGG	2
TTGGTAAGTGGAACTTATCC	33094	+	AGG	417
AATCCCTCAATAACGCCACC	33096	-	TGG	478
GTAAGTGGAACTTATCCAGG	33097	+	TGG	19
TTATCCAGGTGGCGTTATTG	33108	+	AGG	3
TATCCAGGTGGCGTTATTGA	33109	+	GGG	19
GGTGGCGTTATTGAGGGATT	33115	+	CGG	3
TTGAATCGCGTTAGGTAATG	33127	-	CGG	56
TTACTCAATTGAATCGCGTT	33135	-	AGG	258
GCGAATGTAGTTGACTCAGA	33175	+	CGG	157
GTAGTTGACTCAGACGGCAA	33181	+	CGG	48
GTTGACTCAGACGGCAACGG	33184	+	TGG	100
TAAAGTAGTGCTACTTGTTT	33214	-	TGG	208
TTAGGTAAAACATCAGGTTC	33280	+	TGG	100
TTTAGTTATAGTAACTTTGT	33295	-	TGG	550
AGTTACTATAACTAAAATTA	33318	+	TGG	12
GTTACTATAACTAAAATTAT	33319	+	GGG	18
TTACTATAACTAAAATTATG	33320	+	GGG	290
AACGATAAAAACGAAGTTAT	33366	+	CGG	52
ATCGGATTCGTTAATACTGG	33384	+	CGG	48
AACTCTTCTTTAAATTTAAT	33428	-	AGG	346
TTAGTGAAAACAAACTTTCT	33455	-	AGG	470
AGAAAGTTTGTTTTCACTAA	33474	+	CGG	196
CTTTGTTGGTTTGATGCATT	33521	-	CGG	1211
TTAAATCTGACGCACTTTGT	33535	-	TGG	208
TGCGTCAGATTTAAGTGATG	33560	+	AGG	13
TGATGAGGAACTTCGCGGAA	33575	+	TGG	130
TGTTTTGTTAGTTTTCAGTT	33669	-	CGG	76
AACTAACAAAACAAATACTG	33695	+	AGG	364
ACTAACAAAACAAATACTGA	33696	+	GGG	280
CTAACAAAACAAATACTGAG	33697	+	GGG	561
TAACAAAACAAATACTGAGG	33698	+	GGG	38

GTTTTAATGTCTTTAAAAGT	33731	-	TGG	185
ACATTAAAACTTTTTATGTG	33760	+	TGG	23
CATTAAAACTTTTTATGTGT	33761	+	GGG	189
ATAAAAATGAGCAAATTAAG	33790	+	TGG	80
AATTAAGTGGTACGTAGACA	33803	+	TGG	112
ATTAAGTGGTACGTAGACAT	33804	+	GGG	420
GAAGAATATGCATTGATCAC	33840	+	TGG	9
GACTTTTCATCTTTTGCCTC	33857	-	TGG	76
CACTGGTGAAAAATATCCAG	33857	+	AGG	20
GGCAAAAGATGAAAAGTCAC	33878	+	AGG	564
AGTCACAGGTGTAATGCTTG	33892	+	AGG	18
TTTTTAATTTAACACAAAGT	33916	+	AGG	56
AAAGTAGGTGGCGTAATGTT	33931	+	TGG	2
CCATTCATGTTCGTGCCGTT	33943	-	TGG	1689
TAATGTTTGGATTTACCAAA	33944	+	CGG	276
CCAAACGGCACGAACATGAA	33959	+	TGG	31
ACTCTCAATGAGATTAAATT	34024	+	AGG	226
CGTCTATCTGTCTTTCCCTC	34085	-	TGG	3608
ATATACGCGATATGAAAATG	34151	+	TGG	6
GATATGAAAATGTGGATTCT	34159	+	CGG	285
ATGTGGATTCTCGGTTTGAT	34168	+	AGG	15
TGTGGATTCTCGGTTTGATA	34169	+	GGG	177
GCTTTACTAAGAACTATTTT	34216	+	TGG	132
GAACTATTTTTGGTATTTAA	34226	+	AGG	8
CTATTTTTGGTATTTAAAGG	34229	+	AGG	8
TCCTAAAATCCCTTTAAGCA	34242	-	TGG	1140
GAGGTGATTACCATGCTTAA	34248	+	AGG	3
AGGTGATTACCATGCTTAAA	34249	+	GGG	13
ACCATGCTTAAAGGGATTTT	34257	+	AGG	22
GGATTTTAGGATATAGCTTC	34270	+	TGG	32
GATTTTAGGATATAGCTTCT	34271	+	GGG	136
ATAGCTTCTGGGCGTGCTTC	34282	+	TGG	40
TTCTGGGCGTGCTTCTGGTT	34287	+	TGG	89
ACAGTTAAGAGTCAGTGCTT	34322	+	CGG	210
AAGAGTCAGTGCTTCGGCAC	34328	+	TGG	131
ATTGAAATGAGGTGCATACA	34363	+	TGG	100
TTGAAATGAGGTGCATACAT	34364	+	GGG	388
CTGTAGGCTTTCTAGTCTTT	34380	-	GGG	87
GCTGTAGGCTTTCTAGTCTT	34381	-	TGG	31
AAAGCCTACAGCTAGTGAAG	34408	+	TGG	10
GCCTACAGCTAGTGAAGTGG	34411	+	TGG	22
CAGCTAGTGAAGTGGTGGAG	34416	+	TGG	3
AGCTAGTGAAGTGGTGGAGT	34417	+	GGG	48

GAGTGGGCAAAGTCGAATAT	34433	+	TGG	226
CAAAGTCGAATATTGGTAAG	34440	+	AGG	65
GATTAATATAGATAATTATC	34462	+	GGG	4
ATTAATATAGATAATTATCG	34463	+	GGG	493
ATTATCGGGGCAGTCAATGT	34476	+	TGG	128
TTATCGGGGCAGTCAATGTT	34477	+	GGG	64
ACTTTATTTTTAAAAGATAT	34509	+	TGG	4
CTTTATTTTTAAAAGATATT	34510	+	GGG	7
TTTATTTTTAAAAGATATTG	34511	+	GGG	2
GATATTGGGGTTTTGTAACA	34524	+	TGG	23
ATATTGGGGTTTTGTAACAT	34525	+	GGG	4
TATTGGGGTTTTGTAACATG	34526	+	GGG	85
TGTAACATGGGGCAATGCTA	34537	+	AGG	86
ATGGGGCAATGCTAAGGATA	34543	+	TGG	54
CGATAGAATCGGAAACCCTT	34564	-	AGG	1399
GGCTAATTACAGATATCCTA	34564	+	AGG	373
GCTAATTACAGATATCCTAA	34565	+	GGG	230
CAGATGAATAACGATAGAAT	34575	-	CGG	369
CGATTCTATCGTTATTCATC	34592	+	TGG	82
TTATTCATCTGGATTTGTAC	34603	+	CGG	29
ACTGCGATGTCTCCAGGTTC	34606	-	CGG	70
TCTGGATTTGTACCGGAACC	34610	+	TGG	35
AACCTGGAGACATCGCAGTT	34626	+	TGG	136
GACATCGCAGTTTGGCACCC	34634	+	TGG	510
CCGAACCTATTCCGTTGCCA	34635	-	GGG	181
TCCGAACCTATTCCGTTGCC	34636	-	AGG	155
GCAGTTTGGCACCCTGGCAA	34640	+	CGG	86
TGGCACCCTGGCAACGGAAT	34646	+	AGG	67
CCCTGGCAACGGAATAGGTT	34651	+	CGG	41
GGCAACGGAATAGGTTCGGA	34655	+	CGG	3
AGATGGTCCTACTACTATTG	34667	-	CGG	284
GGACACACCGCAATAGTAGT	34676	+	AGG	152
TAAAAATAACTTTTATTAGA	34684	-	TGG	58
TATTAGAATTAACCCAGTTT	34716	-	TGG	242
TTTATAGCGTTGACCAAAAC	34719	+	TGG	26
TTATAGCGTTGACCAAAACT	34720	+	GGG	273
ACTGGGTTAATTCTAATAGT	34737	+	TGG	70
TAATAGTTGGACAGGTTCTC	34750	+	CGG	15
AATAGTTGGACAGGTTCTCC	34751	+	GGG	472
GGGTGTCTTACTAAACTTCC	34753	-	CGG	125
AGCCTGTAACACTTACATAA	34773	-	GGG	604
AAGCCTGTAACACTTACATA	34774	-	AGG	141
CTAGTATCTTTTGAATATGG	34804	-	AGG	24

TTGCTAGTATCTTTTGAATA	34807	-	TGG	8
GAACTTGTATCAGTACTACT	34831	-	AGG	1129
GCCAGTAATTGTTGAGTCAT	34865	-	TGG	458
GCCAATGACTCAACAATTAC	34880	+	TGG	349
GTTTTAACTTCTTTAAATTG	34900	-	CGG	4
CATTGATCATATAGTTGTAA	34987	+	TGG	189
ATTGATCATATAGTTGTAAT	34988	+	GGG	979
GATGAACGCTCAGATATTCA	35012	+	AGG	559
TCTCTATCGACATATAAATG	35104	-	CGG	109
GCATTTATATGTCGATAGAG	35122	+	AGG	28
ATGTCGATAGAGAGGCTACA	35130	+	TGG	23
GTGACGCGGGTCATCAAAAT	35150	-	TGG	38
CTAGCCAATTAGGGTGACGC	35163	-	GGG	202
ACTAGCCAATTAGGGTGACG	35164	-	CGG	65
CTTCAATAACTAGCCAATTA	35172	-	GGG	68
ACTTCAATAACTAGCCAATT	35173	-	AGG	18
ATGACCCGCGTCACCCTAAT	35175	+	TGG	117
TGGCTAGTTATTGAAGTATG	35195	+	TGG	29
CAAATACAAGCGTTAATACG	35255	+	TGG	1534
AAGCGTTAATACGTGGTGTT	35262	+	TGG	983
CGTGGTGTTTGGTTATTGTC	35273	+	AGG	28
GTGGTGTTTGGTTATTGTCA	35274	+	GGG	43
CTTATCTGAAACGACGTTAA	35308	+	AGG	416
TCATACTACGCCAAATATTA	35319	-	GGG	242
TTCATACTACGCCAAATATT	35320	-	AGG	784
TAAAGGTAGACCCTAATATT	35325	+	TGG	260
AATTACGACTTGATTAAGCA	35369	+	AGG	69
CTTGATTAAGCAAGGTATAC	35377	+	CGG	711
TGCTCATACTTTGCGTTATC	35380	-	CGG	385
TGATGGAGTAGGGCCTCGTG	35525	-	TGG	81
GTTGACAGTGCGTCCACACG	35528	+	AGG	47
GTTTTTCGTCTGATGGAGTA	35535	-	GGG	109
GGTTTTTCGTCTGATGGAGT	35536	-	AGG	84
ATGCTTGGTTTTTCGTCTGA	35542	-	TGG	14
CTTGTTTCAGTAACGATGCT	35557	-	TGG	357
AGTGCTTGCTGGAATGTGAA	35581	-	TGG	8
TTTGTCTATCCAGTGCTTGC	35592	-	TGG	1320
ATTCACATTCCAGCAAGCAC	35599	+	TGG	813
CACTGGATAGACAAATGTCT	35616	+	AGG	337
ACTGGATAGACAAATGTCTA	35617	+	GGG	114
CTGGATAGACAAATGTCTAG	35618	+	GGG	895
CCCATGTATGAGATTTTTTC	35628	-	GGG	35
CCCCATGTATGAGATTTTTT	35629	-	CGG	1

ACCCGAAAAAATCTCATACA	35643	+	TGG	3
CCCGAAAAAATCTCATACAT	35644	+	GGG	5
CCGAAAAAATCTCATACATG	35645	+	GGG	19
AAAAATCTCATACATGGGGC	35649	+	TGG	6
AAAATCTCATACATGGGGCT	35650	+	GGG	95
AACACGAGCACAAACGAGCT	35680	+	CGG	837
CAATGAATGTTAAGCGAATA	35703	+	TGG	87
AATGAATGTTAAGCGAATAT	35704	+	GGG	351
TGCTATCAAATGCTTAATTT	35741	+	AGG	377
CTTAATTTAGGCAAGTATCA	35753	+	AGG	223
GCGCTTAACAAAATACTTAA	35789	+	AGG	32
AACAAAATACTTAAAGGAAA	35795	+	AGG	13
AAAGGAAAAGGAACGCTCGA	35807	+	CGG	11
AAAGGAACGCTCGACGGACA	35813	+	AGG	195
CGGACAAGGCAAAGCATTCG	35827	+	CGG	876
GCGCACGCTTTCTTAGAAAG	35891	+	TGG	6
AACTTCGCTAATGGTAGATA	35924	+	CGG	80
TACGGTGCATATAATTACTT	35942	+	CGG	730
GCATATAATTACTTCGGTAT	35948	+	TGG	1255
CAAACGTCATTGCATAATCA	35970	-	GGG	1795
GCAAACGTCATTGCATAATC	35971	-	AGG	24
ATGACGTTTGCTAAAAATAA	35999	+	AGG	4
CGTTTGCTAAAAATAAAGGT	36003	+	TGG	199
CCGCCCATGATTGCTTTTGC	36016	-	TGG	237
ATCTCCAGCAAAAGCAATCA	36028	+	TGG	19
TCTCCAGCAAAAGCAATCAT	36029	+	GGG	1
CCAGCAAAAGCAATCATGGG	36032	+	CGG	187
CGGTGCTAGCTTCGTAAGAA	36052	+	AGG	140
AGAAAGGATTACATCAATAA	36068	+	AGG	129
TCTTAGGATTCCATCTAATT	36090	-	CGG	143
ACACATTGTACCGAATTAGA	36096	+	TGG	252
CGATTGTACTTGCTTGATGT	36132	-	TGG	1993
GCTAAGTTATATAAACAAAT	36170	+	CGG	5
TATAAACAAATCGGCTTAAA	36179	+	AGG	173
TAAAAGGTATCTACTTCACA	36195	+	AGG	453
AAAAGGTATCTACTTCACAA	36196	+	GGG	83
AGGGATAAATATAAATAAAG	36215	+	AGG	153
GAAACGAGAATAAAAAATGA	36266	+	TGG	117
AAAAATGATGGTGTTGACTT	36278	+	AGG	184
GGTGTTGACTTAGGTGACAT	36287	+	TGG	372
AATACAGCATCTATAAGAAT	36335	+	AGG	6
ATAGGTATCAATGACAAACA	36353	+	AGG	11
CGTATCGATCTAAAAGCACA	36377	+	TGG	388

TCCATAAACAAATGTAATCT	36391	-	AGG	97
ACCTAGATTACATTTGTTTA	36406	+	TGG	151
ACAACATCGTCGATAATAAG	36439	-	GGG	523
TTACAACATCGTCGATAATA	36441	-	AGG	11
ATTATCGACGATGTTGTAAA	36461	+	AGG	179
AACCTTTTTAGGTATCTTGT	36476	-	AGG	12
GCGTGTTTGATAACCTTTTT	36487	-	AGG	119
TACCTACAAGATACCTAAAA	36490	+	AGG	25
AAAAAGGTTATCAAACACGC	36506	+	TGG	154
TCTTTCAATATCGTTGATAG	36590	+	TGG	298
AAAAGAAATCGATGTTAAAT	36631	+	TGG	658
AGTAGATTTAAAGGTGCGAA	36764	+	AGG	25
AAAGGTGCGAAAGGTGATAA	36773	+	AGG	17
GAAAGGTGATAAAGGCGAAC	36781	+	CGG	29
AAAGGTGATAAAGGCGAACC	36782	+	GGG	45
CCTTTTGCACCAGGTTGTCC	36784	-	CGG	942
AAAGGCGAACCGGGACAACC	36791	+	TGG	130
CCTGCTTCACCTTTTGCACC	36793	-	AGG	1277
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ACTACAGTACCGTTTTTACC	36838	-	GGG	1646
CAAGGCGCACCCGGTAAAAA	36845	+	CGG	51
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TCAATCCTGACACTAAAATG	36882	+	TGG	11
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CTTAATGTGTTCATAGATTC	37069	-	AGG	1938
GAAAGTGTATTGCAACAGAT	37145	+	TGG	302
AGTTAGTACAGAAGATTTTG	37174	+	AGG	31
TCGTCATGATTATGATTTTT	37213	-	TGG	278
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CCTGTCCAAATTTTAACCGT	37312	-	CGG	656
AAAAAGCGCATCTCAACCGA	37312	+	CGG	151
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TAATTAAGGGGTGATTTTTA	37404	+	TGG	1405
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GTAAAGAAACTTATTTACGA	37444	+	AGG	104
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CTATCCGGATATTTATTTTT	37527	-	AGG	774
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AGTCGTTTAAAATTATTCAA	37792	-	TGG	31
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CAACATCTCAAGAAGGGAAA	38034	+	TGG	12
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AACGGTAAAGGTTGGACTAA	38530	+	TGG	37
ACTAATGGCGTTGCGCAACC	38545	+	TGG	109
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ATGGCGTTGCGCAACCTGGT	38549	+	TGG	448
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GGCGTTGCGCAACCTGGTTG	38551	+	GGG	180
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ATTATGCTTGTAGCCGGTCA	38728	+	TGG	58
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TAGCTATAACATAAAAAAAT	39779	-	AGG	3
ATAACAAAAAACTAGCCCGA	39803	-	AGG	228
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AAACATCCAGTGACATGCTT	39870	-	GGG	52
AAAACATCCAGTGACATGCT	39871	-	TGG	967
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TGCTAAAGTCATATATACTA	39930	-	CGG	1677
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GGGACCAACAGTCAGATACA	40035	-	TGG	14
GAGGCCATGTATCTGACTGT	40047	+	TGG	87
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TAACCGTATCGATTAAGATA	40130	-	CGG	2249
TAACCGTATCTTAATCGATA	40143	+	CGG	995
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CTGTGGTTTTGTTGGTTGTA	40162	-	GGG	585
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TCCTAAATTAATAGGATCTG	40179	-	TGG	12
AACCACAATCCTAAATTAAT	40187	-	AGG	3207
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Spacer Sequence	Location	Strand	PAM	Reads Replicate 1	Reads Replicate 2
TTCAAAAGTTTAGTATCTAT	698	-	AGG	20913	18997
GAGAACAAAACCATCCTACC	827	+	CGG	21295	17109
TTAGAATTGACACCTCAAGA	873	+	AGG	13956	17740
TTGATTTCGTGCCACTGTGC	993	-	GGG	12816	19034
AGCAATTCACACCCGCACAG	998	+	TGG	29015	33743
TTTTAATAACCTCAACATCT	1070	-	TGG	27705	14436
GTGAATTGCTAGTAGTGTGT	1181	-	TGG	17596	15299
TCTGATGAATATTCATCTCT	1424	-	CGG	32678	31754
AAACATGTTGCGATGATGTC	2048	+	AGG	30908	59970
CGTTCCATTGAATACTGTGT	2368	-	AGG	52680	43714
AGTAAGACGCCAAAAGTAAC	2465	+	AGG	14924	14780
GTAGAAGTACAGTATACAAC	2918	+	TGG	13903	20869
TGAAGCATAATACTGCTACT	3088	-	AGG	23825	23247
ATAAAAAAACTGCTACTTGT	3239	+	TGG	38980	29511
CAATCCATTCATCTATTGCT	3503	-	TGG	34547	34893
TGAAGAGAACACAGACGAAC	3540	+	AGG	13776	17221
ATATCTGAATTGTTATCAGT	3651	-	TGG	12604	16568
AGTATGCTTACTTTTTCTTG	3823	-	TGG	15478	35193
GTCAGTATGTACAGATTAAT	4241	+	AGG	23623	17749
GCGCTTCAATAGTGATAGTA	4338	-	GGG	23891	21139

Normalized Reads Replicate 1	Normalized Reads Replicate 2
8327.881099	8380.610381
8479.999427	7547.71085
5557.49575	7826.079284
5103.530061	8396.933095
11554.22321	14885.87335
11032.56089	6368.505104
7007.000231	6749.221362
13012.88665	14008.41723
12308.04519	26456.03014
20977.99342	19284.624
5942.96837	6520.262222
5536.390328	9206.451442
9487.484684	10255.51664
15522.44084	13018.90788
13757.15145	15393.20093
5485.816957	7597.120144
5019.108372	7309.046312
6163.579766	15525.54725
9407.045149	7830.049674
9513.766908	9325.563134

Spacer Sequence	Location	Strand	Reads Replicate 1	Reads Replicate 2
CCTTGAATGAATTGAATGCC	1698	-	53	17
TAGCTAGCACTTAATTGTGT	4738	+	2	1
TACTTACTTCTATTTGACTC	7908	-	4	1
GATTCATCAACGGTTACACC	8733	+	2	1
TCGTTTTAACTTGTACTATA	14939	-	38	10
TATTGGGCAGGCGTACCGAT	15516	+	2	2
GCAGTAATGCAATCATTTTG	16415	+	4	3
GATACATTGATGGAGAATTA	16578	+	72	64
GTACGTTTCCAATATAGAAC	16643	+	1	2
TATCTGTCGTTAAATATATT	16706	-	4	4
TCATAAGTGATACCTTGCAT	16916	-	1	1
ATGATGCAGGTATCTTATAT	16932	+	2	1
GAGTGATGTCTGTTGTTACC	17162	-	1	2
AGATATGCTGGGTTCTGTAT	17282	-	4	2
CCGAAAGCGTTTAGAGATGC	17375	+	20	25
TGGTTCTTTGATGTACTGCC	17399	+	58	64
TATGAATCAGATAGAGGAAC	17935	+	14	15
TAAGCGCAGTTAACACATCT	18665	+	1	1
ATAAATTCGGAACAACGAGC	19019	+	2	2
ACAAGAGTGCCGGATTTACC	19144	+	1	3
TCATAACTTTCAACGCTACC	19165	-	3	1
CACAAACTATTCTATTTTGT	19389	+	2	3
TTGGTAAGTGGAACTTATCC	19408	+	167	147
TTTAGTTATAGTAACTTTGT	19628	-	27	27
CATTAAAACTTTTTATGTGT	20081	+	28	24
ATTGAAATGAGGTGCATACA	20683	+	70	64
TTGAAATGAGGTGCATACAT	20684	+	1	1
GGAACAAGTAACTTCGCTAA	22262	+	3	9
CGATTGTACTTGCTTGATGT	22519	-	26	17
ACTAAAATGTGGCAAATTGA	23261	+	3	1
ATCAATATCGCAAATGTTGA	23327	+	1	2
CAACGACTCTAAAACGTATA	23398	+	74	59
TAATTAAGGGGTGATTTTTA	23838	+	659	597
CTATCCGGATATTTATTTTT	23980	-	57	44
CAGAATCGAACAACCCGGCT	25088	+	2	1
AATTTAAATCCACTTCATGC	33574	-	8	10
AATGATTTTCAAAATTTCTT	34614	-	10	4
GCTGTAGTGAAGTATAGAAA	34894	-	2173	2038
ATAAAAAAACTGCTACTTGT	34980	+	689	730
CAATCCATTCATCTATTGCT	35263	-	3877	3510
TGAAGAGAACACAGACGAAC	35281	+	6386	6057
AATAGAGCTAGGGAGTTTAA	35450	+	72	84

AATAGTTTCTGTCACTGTTT	35520	-	12	17
CAGAAACTATTGAGTACGAG	35529	+	23	10
AGAAACTATTGAGTACGAGG	35530	+	10456	9904
CACAACGAGCAACATGCGAT	37179	+	1142	992
AATACCACTTGCATGACTCG	37222	+	2300	2268
AGCACTCCTAATCGTCATCT	37321	+	772	684
TGGGTAATAGACATCAAAAA	37462	-	81	77
AAAGTTACATTACAGCCCCT	37481	-	2	1
GAAAAACAAAGATTTGTTTC	37588	-	139	118
TTAAAACCCCTAACCTTACT	37700	+	2898	2633
TCGGTTGATTCTATATCTAA	37738	+	51	53
TATTCATACCGTCATTCTTT	37787	+	683	653
TAATTATTTCAACAAATGAA	37898	+	179	152
AAAACTAATAGCATCATCTA	37949	-	14	13
TAATTATGGATCCTATTTTA	38247	-	13	2
ATAATTATGGATCCTATTTT	38248	-	100	81
ATCGCTATTGCGTTAGATTG	38275	-	5	2
TATCGCTATTGCGTTAGATT	38276	-	1894	1736
CAAGATGGAATCAAGATTTT	38860	+	170	151
CTTAGACCAGAAACACTTTT	38952	+	1	1
CAAAAAGTGTTTCTGGTCTA	38954	-	13	3
CGACGAAAGTTATTGGGATT	39047	+	99	118
GGATTGAAATGTGAGAGATG	39147	+	83	76
TTAATATTGCAAGGTTCATA	39438	+	4	4
GCAAAAGCAGTCAAAGCTAA	39492	+	1	1
CAAAAGCAGTCAAAGCTAAA	39493	+	140	123
AGTCAAAGCTAAAGGGCATA	39500	+	41	45
TTGATACGATCCATCAACAT	39543	-	5	9
TTTACTTGTACTAGATGATA	39629	+	80	81
AGCATTGTTGATAACAGAGT	39690	+	10	6
GCGAGAAAAGTAAGAGTAAT	39804	+	6	8
AGTAATCGGAGACGATTTCA	39818	+	16	7
AATGAAGTTTATTCGCTCAC	40100	+	27	22
AACGATTCAAAGGCGCTCAC	40170	+	19	17
CGATATTTGATATTTAGAGG	40227	+	1083	1011
ATCATAAAGCGTATATACAA	40368	+	12	5
ACTTTCCATTACTTAAATCA	40443	+	5690	5185
ACGCATGTAATGGTCATGTG	40548	+	519	437
TACTGATATTCAACTTCTGT	40708	-	59	55
GGATATCGAAAAAGAAGCGC	40740	+	89	70
TCATACTCTAGTAATTCGTC	40786	-	4	1
ATGAATTGATAAAAAAGAAC	40898	+	5	1
ACTCTTTTTGCAACCATTCC	40930	-	1	1

AAGAGGTTGAACTACGTAAG	41084	+	32	25
AACATTCACGTGATCCGTAC	41135	+	17	21
CAACCAGCACATTACACATA	41262	+	12	14
TCGCCGTATGTGTAATGTGC	41268	-	1	1
TCCTCATGACCATTCTTTAA	41388	-	243	212
AGATAGAGTGTTTGACTTGT	41432	+	1	2
CATATCGTACCAGATTGGCA	41588	+	8	2
TTTTTCACACCTTGCCAATC	41600	-	152	139
TAACTTTATTTTAGAGGAGA	41694	+	12	22
ATTAGACGAGTTAATTAAAT	41751	+	124	126
GTCGAACACTTATTTGTATT	41854	-	2	1
ACTATGAAGGGGATATCAAT	41890	-	519	507
AGTTTTATCGAGTTTAAAGA	42330	+	4	1
GGAGAAGAAAGCAAGCGCAT	42628	+	3	2
ATTCAACATTCAGTTAAAGA	42912	+	585	529

Normalized Reads Replicate 1	Normalized Reads Replicate 2
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44.16961131	47.51835396
88.33922261	71.27753095
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88.33922261	95.03670793
22.08480565	23.75917698
44.16961131	23.75917698
22.08480565	47.51835396
88.33922261	47.51835396
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1280.918728	1520.587327
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22.08480565	23.75917698
44.16961131	47.51835396
22.08480565	71.27753095
66.25441696	23.75917698
44.16961131	71.27753095
3688.162544	3492.599016
596.2897527	641.4977785
618.3745583	570.2202476
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14553.88693	14184.22866
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1788.869258	1829.456628
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220.8480565	142.5550619
132.5088339	190.0734159
353.3568905	166.3142389
596.2897527	522.7018936
419.6113074	403.9060087
23917.84452	24020.52793
265.0176678	118.7958849
125662.5442	123191.3327
11462.01413	10382.76034
1303.003534	1306.754734
1965.547703	1663.142389
88.33922261	23.75917698
110.4240283	23.75917698
22.08480565	23.75917698

706.7137809	593.9794246
375.4416961	498.9427166
265.0176678	332.6284777
22.08480565	23.75917698
5366.607774	5036.94552
22.08480565	47.51835396
176.6784452	47.51835396
3356.890459	3302.525601
265.0176678	522.7018936
2738.515901	2993.6563
44.16961131	23.75917698
11462.01413	12045.90273
88.33922261	23.75917698
66.25441696	47.51835396
12919.61131	12568.60462

Spacer Sequence	Location	Strand	PAM	Reads Replicate 1	Reads Replicate 2
GCATACACACATAAGTTTAT	237	-	TGGCG	1	1
ATTTGCTATCCTTGAATTGA	461	+	TGGCG	1	1
ACAACCCTCCTCATCACAAT	2576	+	GGCAG	1	1
AAAAACCAACGTTTAATGAT	4197	+	TGGGG	1	1
AAAAACCAACGTTTAATGAT	4197	+	TGGGG	1	3
AAAAACCAACGTTTAATGAT	4197	+	TGGGG	5724	7180
AAAAACCAACGTTTAATGAT	4197	+	TGGGG	16747	20989
ATTGAAGAATTTGATGATAA	4433	+	CGGAG	3	1
TCTTGGAAATCATATTTATA	4817	-	CGGCG	30	33
TCTTGGAAATCATATTTATA	4817	-	CGGCG	41	44
TCTTGGAAATCATATTTATA	4817	-	CGGCG	368	395
ACTTATTCCGTCGTTGCTAC	5238	+	TGGTG	17	12
ACTTATTCCGTCGTTGCTAC	5238	+	TGGTG	30	52
CACAACGAGCAACATGCGAT	5751	+	TGGCG	1	1
TGCTATGCATGCTGTAAAAG	5932	+	TGGAG	78	98
TTTTACAAAAGCTTTACCAT	5991	+	AGGCG	1	1
TTTTACAAAAGCTTTACCAT	5991	+	AGGCG	248	291
TTTTACAAAAGCTTTACCAT	5991	+	AGGCG	662	742
ATAACCAAATGTTCAAGAAA	9771	+	TGGAG	1	5
AACCAGCACATTACACATAC	9863	+	GGCGA	1	1
AGATAGAGTGTTTGACTTGT	10032	+	GGGAG	1	1
GCACATATCCATGTAGTGAA	10146	+	TGGCG	1	1
TTTTTCAATATCAACTATGA	10484	-	AGGGG	16	12
ATTTGAATCATCACATTTAT	11324	+	TGGAG	4	3
ATTTGAATCATCACATTTAT	11324	+	TGGAG	16	20
AAGAGAACGCAACAAAGAGC	11476	+	TGGAG	1	1
ATTAAACAATAAAACTTTTA	11599	+	TGGAG	6	1
ATTAAACAATAAAACTTTTA	11599	+	TGGAG	1563	1977
ATTAAACAATAAAACTTTTA	11599	+	TGGAG	1892	2376
CAACGTTGCCGAAACCACAA	13942	+	GGGGA	1	4
TATTCGACTAAAGGTAAGAG	14663	+	TGGGG	6	7
CGTTCATAGAACATACCTGA	15671	-	TGGTG	1	1
CGTTCATAGAACATACCTGA	15671	-	TGGTG	102	125
TTAATAGGACGAGGTATAGA	15867	+	TGGTA	1	1
TATGTTTGGCACCCTACAAA	16170	+	CGGAG	6	4
CCTAACAACAAAGAGATGAT	16985	+	AGGAG	1	3
GATACTCATCGTCATTTAGA	18363	+	TGGGG	2	8
AAGAAATCGTTAGCACTAAT	20219	+	GGGTG	1	1
AACGCTTAAACCAACTGAAT	20431	+	AGGAG	1	1
CGCTCTTATCAGACGTAGTA	20564	-	CGGCG	19	26
TTTAGTTGTTCAGATGTAGT	21085	-	AGGCG	23	31
CTAAAAAACCTAAGTCAACA	21415	-	GGAGC	1	1

TTTTCTAATTGTTCTCGAGT	22997	-	TGGTG	19	13
TAGCACTAACACCTGCTGAA	23328	+	TGGCG	1	2
GAATGGCGTGATTGGCTTAT	23345	+	TGGTG	8	3
AGATGCAAACCCCGCTAAAA	23986	+	TGGCG	1	4
AACAACTCATTGAAAGATTA	24206	+	CGGCG	3	1
GCGATCAGTTAAAAACTACA	24537	+	TGGCG	3	1
GCTTTAATTCAGTTGCTTAC	25886	+	TGGCG	12	20
TTTGACACAACACAAACATC	27196	+	AGGGG	1	1
TTGACACAACACAAACATCA	27197	+	GGGGA	2	1
CATTTTACAACACTAACTCA	27368	+	GGAGA	1	1
AGCTTTTAGGAAAGCGAGCA	29512	+	TGGAG	1	1
GTACGTTTCCAATATAGAAC	30329	+	TGGAG	6	8
GGACGCAAAGCGCTTTTAAT	30809	+	AGGGG	2	4
GAAGTTGAACAACAAATCAA	32221	+	TGGCG	1	1
GTTATCGGATTCGTTAATAC	33381	+	TGGCG	2	4
TTAATTTAACACAAAGTAGG	33919	+	TGGCG	1	1
ACTTTATTTTTAAAAGATAT	34509	+	TGGGG	1	4
AACTTCGCTAATGGTAGATA	35924	+	CGGTG	1	1
CGACACAAATGATTTAGGGT	38155	+	AGGTG	1	1
CGACACAAATGATTTAGGGT	38155	+	AGGTG	10	10
CGCTAACATAAAGAACATAT	38272	-	TGGCG	12	9
TGCTAAAGTCATATATACTA	39930	-	CGGGG	7	7
TGCTAAAGTCATATATACTA	39930	-	CGGGG	7	9
CATTCCCGTATAACAGTTTA	39967	+	CCAGG	14	14

Normalized Reads Replicate 1	Normalized Reads Replicate 2
36.04772719	28.91844997
36.04772719	28.91844997
36.04772719	28.91844997
36.04772719	28.91844997
36.04772719	86.75534991
206337.1904	207634.4708
603691.2873	606969.3464
108.1431816	28.91844997
1081.431816	954.308849
1477.956815	1272.411799
13265.56361	11422.78774
612.8113622	347.0213997
1081.431816	1503.759398
36.04772719	28.91844997
2811.722721	2834.008097
36.04772719	28.91844997
8939.836343	8415.268942
23863.5954	21457.48988
36.04772719	144.5922499
36.04772719	28.91844997
36.04772719	28.91844997
36.04772719	28.91844997
576.7636351	347.0213997
144.1909088	86.75534991
576.7636351	578.3689994
36.04772719	28.91844997
216.2863631	28.91844997
56342.5976	57171.77559
68202.29984	68710.23713
36.04772719	115.6737999
216.2863631	202.4291498
36.04772719	28.91844997
3676.868173	3614.806246
36.04772719	28.91844997
216.2863631	115.6737999
36.04772719	86.75534991
72.09545438	231.3475998
36.04772719	28.91844997
36.04772719	28.91844997
684.9068166	751.8796992
829.0977254	896.4719491
36.04772719	28.91844997

684.9068166	375.9398496
36.04772719	57.83689994
288.3818175	86.75534991
36.04772719	115.6737999
108.1431816	28.91844997
108.1431816	28.91844997
432.5727263	578.3689994
36.04772719	28.91844997
72.09545438	28.91844997
36.04772719	28.91844997
36.04772719	28.91844997
216.2863631	231.3475998
72.09545438	115.6737999
36.04772719	28.91844997
72.09545438	115.6737999
36.04772719	28.91844997
36.04772719	115.6737999
36.04772719	28.91844997
36.04772719	28.91844997
360.4772719	289.1844997
432.5727263	260.2660497
252.3340903	202.4291498
252.3340903	260.2660497
504.6681807	404.8582996

Sample	Oligo	Number of Reads		
		Replicate 1	Replicate 2	Replicate 3
1	CACATCAATTAGTAAGACGCCAAAAGTAAC	37	41	29
	ATAATAATGAACATGTCTTGTCACAGTTTC	5	1	3

Percent Acquired			Percent Acquired	St. Dev.
Replicate 1	Replicate 2	Replicate 3		
88.095238	97.619048	90.625	92.11309524	4.933209659
11.904762	2.3809524	9.375	7.886904762	4.933209659

Sample	**Oligo**
A	TTAACCAAGCAATAGATGAATGGATTGAAGAGAACACAGACGAACAGGACAGACTAATTAACT TTCCATTCCCTATAAAGAAATTATCGAATACTTAAATAAAAAAGCAGGAAAGCATTTTAAACA
B	TTCCATTCCCTATAAATGAATGGATTGAAGAGAACACAGACGAACAGGAAAGCATTTTAAACA TTAACCAAGCAATAGAGAAATTATCGAATACTTAAATAAAAAAGCAGGACAGACTAATTAACT

Number of Reads			Percent Acquired			Percent Acquired
Replicate 1	Replicate 2	Replicate 3	Replicate 1	Replicate 2	Replicate 3	
284	278	268	98.269896	98.932384	96.750903	97.98439435
5	3	9	1.7301038	1.0676157	3.2490975	2.015605646
84	82	70	98.823529	98.795181	98.591549	98.73675314
1	1	1	1.1764706	1.2048193	1.4084507	1.263246857

St. Dev.
1.1184137
1.1184137
0.1265466
0.1265466

Sample	Oligo	Number of Reads		
		Replicate 1	Replicate 2	Replicate 3
1	AGAAATTATCTGAAGAGAACACAGACGAAC	158	90	140
	ATGAATGGATGAATACTTAAATAAAAAAGC	4	10	0
2	ATGAATGGATGAATACTTAAACAGACGAAC	5	14	8
	AGAAATTATCTGAAGAGAACATAAAAAAGC	1	3	1
3	AGAAATTATCGAATACTTAAACAGACGAAC	33	45	32
	ATGAATGGATTGAAGAGAACATAAAAAAGC	0	1	0
4	AGAAATTATCGAATAAGAACACAGACGAAC	49	52	72
	ATGAATGGATTGAAGCTTAAATAAAAAAGC	2	1	4

Percent Acquired			Percent Acquired	St. Dev.
Replicate 1	Replicate 2	Replicate 3		
97.530864	90	100	95.8436214	5.20913536
2.4691358	10	0	4.156378601	5.20913536
83.333333	82.352941	88.888889	84.8583878	3.524768995
16.666667	17.647059	11.111111	15.1416122	3.524768995
100	97.826087	100	99.27536232	1.255109281
0	2.173913	0	0.724637681	1.255109281
96.078431	98.113208	94.736842	96.30949367	1.700000953
3.9215686	1.8867925	5.2631579	3.690506325	1.700000953

Sample	Oligo	Number of Reads		
		Replicate 1	Replicate 2	Replicate 3
1	ATAATAATGAACATGTCTTGACAGACGAAC	199	120	186
	ATAATAATGAACATGTCTTGTCACAGTTTC	10	21	6
2	ATAATAATGATGAAGAGAACTCACAGTTTC	17	10	21
	ATAATAATGAACATGTCTTGTCACAGTTTC	15	8	17
3	ATGAATGGATACATGTCTTGTCACAGTTTC	42	31	47
	ATAATAATGAACATGTCTTGTCACAGTTTC	38	21	31

Percent Acquired			Percent Acquired	St. Dev.
Replicate 1	Replicate 2	Replicate 3		
95.215311	85.106383	96.875	92.39889799	6.369789897
4.784689	14.893617	3.125	7.601102005	6.369789897
53.125	55.555556	55.263158	54.64790448	1.326952391
46.875	44.444444	44.736842	45.35209552	1.326952391
52.5	59.615385	60.25641	57.45726496	4.305065082
47.5	40.384615	39.74359	42.54273504	4.305065082

Oligo	Number of Reads			P
	Replicate 1	Replicate 2	Replicate 3	Replicate 1
AGAAATTATCGAATACTTAAACCGATCAGT	73	12	34	94.8051948
AGAAATTATCGAATACTTAATTAATGACTA	4	2	1	5.19480519

ercent Acquired		Percent Acquired	St. Dev.
Replicate 2	Replicate 3		
85.7142857	97.1428571	92.55411255	6.03768082
14.2857143	2.85714286	7.445887446	6.03768082

Bin (kb)	Sum Normalized Reads Early Time Point	Sum Normalized Reads Late Time Point
1	81931.3392	102354.9272
2	73873.75101	74019.40905
3	73586.87689	81927.32451
4	109057.9906	131249.2337
5	44594.90213	43411.01355
6	37122.5188	31289.78714
7	20495.82662	21002.89533
8	23217.73956	24117.49172
9	16758.12268	15068.4221
10	14606.47516	15603.63283
11	8009.928594	10157.21521
12	28598.87474	24409.85354
13	21030.16403	19376.04331
14	8686.236614	14761.91374
15	18536.28394	15134.43928
16	39025.05328	33041.60026
17	39171.42323	31563.2869
18	42283.77826	37443.53173
19	10817.4455	12104.72211
20	8505.680062	9980.383466
21	21870.34775	26755.8213
22	17644.5912	14283.28916
23	13530.83471	9886.073204
24	28711.42471	17812.85072
25	15091.86983	15575.33975
26	11537.28873	8245.074647
27	6069.724708	6356.511652
28	9126.721279	8954.759367
29	8892.639333	6229.192798
30	3972.427456	3366.87635
31	13093.7412	10140.71091
32	10523.78906	8881.668914
33	8087.192134	6658.30449
34	3972.152497	3576.716683
35	6972.324163	4868.767271
36	2243.758861	2619.467524
37	16088.59699	9770.543133
38	11841.57693	9431.02619
39	10994.15263	10588.68465
40	11147.94648	9706.883706
41	11542.87957	6552.205445

Spacer	Location	PAM	Reads Sonication	Barcodes Sonication
AGTATGCTTACTTTTTCTTG	3823	TGG	44061	4852
TTGATTTCGTGCCACTGTGC	993	GGG	39319	6526
GTCAGTATGTACAGATTAAT	4241	AGG	35094	4111
TTCAAAAGTTTAGTATCTAT	698	AGG	27625	5785
AAACATGTTGCGATGATGTC	2048	AGG	24648	4609
CAATCCATTCATCTATTGCT	3503	TGG	22350	4201
ATAAAAAAACTGCTACTTGT	3239	TGG	20101	4663
TCTGATGAATATTCATCTCT	1424	CGG	19122	3176
TTTTAATAACCTCAACATCT	1070	TGG	16000	4491
CGTTCCATTGAATACTGTGT	2368	AGG	15253	3594
GAGAACAAAACCATCCTACC	827	CGG	15152	3299
AGTAAGACGCCAAAAGTAAC	2465	AGG	14789	1240
AGTGTATAACCTGCTGGCAC	39327	TGG	14730	1785
GTAGAAGTACAGTATACAAC	2918	TGG	14650	2434
ACTTTCCATTACTTAAATCA	9043	TGG	14293	3738
ATTTCCTAATTTCCATCTGC	24053	TGG	14049	3496
TTAGAATTGACACCTCAAGA	873	AGG	13663	1490
TGAAGAGAACACAGACGAAC	3540	AGG	13246	1840
TATATGACGCAAGCTCGTCC	30146	AGG	13111	2801
AGCAATTCACACCCGCACAG	998	TGG	12651	3690
GTGAATTGCTAGTAGTGTGT	1181	TGG	12033	3482
TCTAAAAAACCTAAGTCAAC	21416	AGG	11534	2703
GCTAAGTATTTAAGACATGC	38827	AGG	11424	2724
TCACTATAACAATTGCTTGT	12254	TGG	11418	1405
GGATATCGAAAAAGAAGCGC	9340	TGG	11240	2529
CTTTATCTAACATGATACAC	805	GGG	10637	2464
GAATGATAACGATCTAATTC	19068	AGG	10415	2541
TGAAGCATAATACTGCTACT	3088	AGG	10205	2367
TCCAATTGATCCGTGCCAGT	7596	TGG	10099	2496
CCTATTACAGATTCATCGTC	11132	TGG	9938	1670
TTTGTCTATCCAGTGCTTGC	35592	TGG	9798	1420
CCATTTCGTTATCTCCTTTC	6863	TGG	9569	1376
TAGAGATATAGAACTTCACT	5384	GGG	9521	3021
ATCTTTAATGCGATGTCAGC	24590	AGG	9396	2053
GGATCTAAGTCAGTTTCAGC	22166	TGG	9203	169
GCGCTTCAATAGTGATAGTA	4338	GGG	8628	1340
ATTAAAGTACCTTGTTCTGC	19588	TGG	8417	1830
CATATTAGATCGAGTCAAGG	12415	AGG	8093	1988
CAATGTTGACTGATGACTAT	17902	AGG	7997	1602
GGAAGAATACACGATGTTGT	10947	AGG	7888	971
ATAAAAGTAAATGTTGATAC	18643	TGG	7653	1857
TTACGTGCTCTCATTACAGT	18512	TGG	7613	2094
AAGATTTAATAGATCTTAGC	24027	AGG	7606	775
CTTGATGTACTTCTTTGTGT	13373	TGG	7462	298

ATACGTATGCACATTACACA	18135	AGG	7336	1474
GCTTTAATTCAGTTGCTTAC	25886	TGG	7230	1240
TACATTGATTATTCACCAAC	2983	AGG	7224	1549
CGTCAATATATGCTTTCCGT	14619	TGG	7213	731
TCATAACTTTCAACGCTACC	32832	TGG	7146	1438
AGAAACTATTGAGTACGAGG	3789	AGG	7075	1001
ACTTATTCCGTCGTTGCTAC	5238	TGG	7000	1291
CTAAATTCAGTGATGTATTC	15995	AGG	6990	1531
TTAATTATGCTCGTAAGAAT	1241	CGG	6736	846
ATATTAATCAGAGTGCCTGT	2982	TGG	6369	519
AACACCTATTAACGTAGTAT	1449	TGG	6367	1370
CGATTGTACTTGCTTGATGT	36132	TGG	6269	686
AGGCTTACCATGAATCGCAC	39247	CGG	6156	1340
AATGAAGTTTATTCGCTCAC	8700	AGG	6126	1583
TTGATACGATCCATCAACAT	8124	TGG	6029	1907
GTTCCGTTTCCTACTGCTCC	38745	AGG	5924	76
TCGCCGTATGTGTAATGTGC	9849	TGG	5909	736
AAAAATCCACCAGTGCCAGC	39334	AGG	5796	1603
AAGAGAACGCAACAAAGAGC	11476	TGG	5774	1036
ATTTCTGCTTGTGCATATTC	19753	AGG	5731	549
TTTTGTATGCGTCAATGAGT	12308	TGG	5515	503
TGGTTCTTTGATGTACTGCC	31085	TGG	5512	611
TGTCCTTTACCTGTTACTTT	2458	TGG	5366	966
CATTGGAAACGTTTAAGAAC	12011	TGG	5288	905
GAGTGATGTCTGTTGTTACC	30829	AGG	5223	1376
TGTTGTATCTGATTCACACA	22667	CGG	5213	315
TATCTTCCGTGCCATCTTCT	8632	CGG	5202	1495
ACGCAATTTTTCGTACCTTC	14720	CGG	5133	828
TACTGATATTCAACTTCTGT	9289	AGG	5005	437
TTTTGTTCTTCTGATTGCTC	19161	AGG	4972	1394
GAGTATAACGAAAGTTTTAC	28034	AGG	4857	1139
ATTAGAGCCTCAATATGCTT	16315	AGG	4793	949
GTGTATATTTGCCAATTGTC	7002	AGG	4620	631
ACCAACTGGCACGGATCAAT	7611	TGG	4605	96
TTTGATACCAATGATCTTAT	4917	TGG	4582	256
ATTCACATTCCAGCAAGCAC	35599	TGG	4582	705
AATCACGGAGCAAAGCGTAC	15147	AGG	4519	1056
AAATTCCACTTTGTTATTAC	4283	AGG	4411	734
ACTCATCGTTTGAATCGTCT	32540	GGG	4387	30
CGACTTAAGCAGGTGCCATA	21278	TGG	4315	501
GTGAAACACGCTGTACAAAC	22371	AGG	4179	558
TGCCAAACTGCGATGTCTCC	34612	AGG	4154	123
GACCATTATTTGATGCTAAC	20142	GGG	4151	922
TCCGATAAAATAACATTGCC	19546	TGG	4144	563
ACTTTATCTAACATGATACA	804	CGG	4139	312

GCAACTCCAACATACACGCC	19544	AGG	4134	878
CCGAAAGCGTTTAGAGATGC	31061	AGG	4090	716
TCAAAGTGATGTGTTAGCTA	4405	GGG	4079	598
CTCTATTATCTCTTCGTACA	18682	AGG	4035	1119
GGATTACCACTATCTTATAC	20177	TGG	4014	709
GAAGTAAAATCGAATACACC	31385	GGG	4001	275
CATATCGTACCAGATTGGCA	10188	AGG	3996	264
TTTTCTAATTGTTCTCGAGT	22997	TGG	3987	892
CCCTATAATGTTATTTTTGT	16769	TGG	3939	1055
GAAAAATCGCCATCAATTCA	454	AGG	3913	584
GATTCTTCTAACTTATTAAC	17482	TGG	3875	821
CACAACGAGCAACATGCGAT	5751	TGG	3873	461
ACAAGTTTACATTCAATGAC	29648	AGG	3853	737
CTTTATACTCGTAACCATTC	7796	GGG	3693	641
TATATTTGATTTGTAAGTTC	21725	AGG	3691	678
GATTGGGATTACGCACGTTA	20243	CGG	3654	776
TACTCATCGTTTGAATCGTC	32541	TGG	3652	24
GTTTAAGATATAGAATGCTT	10634	TGG	3633	714
TACCCATACCGCGTAACACA	17082	AGG	3620	429
ATATCTGAATTGTTATCAGT	3651	TGG	3615	1027
TACAAGTGTACTTACAAGTA	1966	CGG	3614	319
TGCGTCCTGCGTCAATTGCA	21646	GGG	3603	249
AATACAAAATCTACGGCACA	32585	TGG	3564	475
CGTGTAGTTAATACTCCGTT	20059	TGG	3494	653
GCATATAATTACTTCGGTAT	35948	TGG	3489	611
GCAATACATGCAATCAGTTT	25972	GGG	3468	912
ATTGGTCGACGTTTGAATAT	16411	TGG	3455	45
TTAAATATAACATTGAATCC	22901	TGG	3443	949
GAAAATACAGATCCTAAAGC	15585	AGG	3416	798
GTTGATTCTTCTATGCTATC	37542	CGG	3407	483
CATTATGAAGCAGTCGGCAG	5667	AGG	3373	829
CGGAAAGCCTCACGCAGACC	5642	TGG	3346	147
ACTACAGTACCGTTTTTACC	36838	GGG	3302	571
GTTCTGAAACTTGTCCCTTC	17520	AGG	3290	528
AACAATTGATGGATTTGTGT	2871	AGG	3275	581
GCATACACACATAAGTTTAT	237	TGG	3236	757
TCACGATGTTTTTGTAGTGT	18080	TGG	3233	728
GAAACACTTTCTTCATCTAC	37945	TGG	3217	241
ATGATGATGTGTATGTTACA	17827	TGG	3206	830
TCTACTACGTCCGTAATGCT	4546	AGG	3169	568
AATAAGGAGTTAACTCGTAT	17877	AGG	3159	491
AAGAGAGTTATATAAAGCTT	1876	TGG	3140	30
GAAACAATCTTTATAAACGC	1308	AGG	3111	114
AACAAAACGGTATAAACATC	2289	GGG	3102	279
GGACAAAAATCAATCAATAG	7069	TGG	3099	474

GTAAGATGACAGCTATGTTG	17376	AGG	3091	126
TTATCGAGTGTATAACCTGC	39333	TGG	3072	520
ATTGAATTAGTTACTCGATT	4866	AGG	3020	10
ATAATACTGCTCGTGCAACA	32531	TGG	3010	925
TAGGAGTGAACTATATAGCC	40022	GGG	3004	417
GAAAAACAAAGATTTGTTTC	6141	GGG	2990	372
AAAAATAATCATGCGAGTTG	9227	AGG	2969	850
CGTCTATCTGTCTTTCCCTC	34085	TGG	2944	505
TTCTATACTTCACTACAGCA	3154	TGG	2928	630
AATTTTTCGTATTCAACTGT	22586	AGG	2927	352
GAATTAGCTATCATAACTTC	1365	TGG	2927	696
ATTTTCAGCATCTTTCGGTA	2681	TGG	2917	624
AAGTAGCGCAATGAGTATGT	16792	AGG	2915	288
ATGCCTAGTTTAATTGATAC	13233	TGG	2899	766
TCGCCTCTATATGTGTTTTC	2817	TGG	2861	648
GACTCTTATTACAGTCTTGT	20536	CGG	2819	625
TCTTTTCTGCTAATTCATCA	14170	CGG	2818	569
ACATTTTACAACACTAACTC	27367	AGG	2808	197
TCATCAACACCATCTTGTCC	32421	AGG	2799	1024
ACTATTTCTAATGGCAAAGT	16622	TGG	2796	790
CGCTCTTATCAGACGTAGTA	20564	CGG	2788	512
CTTGATTAAGCAAGGTATAC	35377	CGG	2772	379
AACATTCACGTGATCCGTAC	9735	TGG	2762	448
GTTTACCCATATATTGTTGT	21840	GGG	2751	671
CGTTCATAGAACATACCTGA	15671	TGG	2748	425
AATGACATTTCAAATGATTC	22457	TGG	2737	167
GTTCAAATAATGATACTGGT	20325	TGG	2726	487
ATTAAACGAATGAACTCAAT	18056	AGG	2709	412
ACACAAATCCATCAATTGTT	2890	TGG	2691	53
ACGACATAAGCATGTTTAAT	3441	TGG	2678	502
GTTTTAGAGAATGTTTCTAC	6754	AGG	2658	481
GTGACATACAACATCCCTGA	37734	AGG	2629	198
ACTCGACGACCAAGATGTTG	1077	AGG	2627	662
CTAAAAATTGATGTGCAGAC	31425	GGG	2622	582
ACACCTCAATATATACTTGC	15249	TGG	2594	305
GTTTGAAGATGAAGAAACGT	18313	TGG	2545	680
CTATGCTTGCAGTTTGGAAC	10847	GGG	2543	302
AGCCAATCACGCCATTCAGC	23323	AGG	2521	671
TCCTAAAATCCCTTTAAGCA	34242	TGG	2517	474
ACGTAATATCAACGGTATGT	15707	GGG	2516	807
GACATCGCAGTTTGGCACCC	34634	TGG	2499	851
CCTTTTGCACCAGGTTGTCC	36784	CGG	2490	637
CAAGATGGAACAGCAGACGC	12373	AGG	2463	567
TGATGAATTAGCTGACATGT	12069	TGG	2452	558
TTTAGTTGTTCAGATGTAGT	21085	AGG	2423	649

GTTAAAATTAAAACTATTTC	12660	AGG	2365	96
TCTTTATACTCGTAACCATT	7797	CGG	2352	352
CCAAATCGTATCAAGTACAT	25934	TGG	2341	603
TTATCTAATTGTTTATCGAT	1389	TGG	2335	592
GGCTCAGCAGGGTTTCAAGC	4695	TGG	2325	300
CAAGATACTATCGAAGCTGT	31981	CGG	2283	491
CTGAATTCAATAAATACAAC	17851	AGG	2271	339
ATTCACCCACAACAATATAT	21829	GGG	2263	582
AATCAAAAAATACAACCAAC	7597	TGG	2261	522
GCGTCACCTTCATCTATGTC	17635	AGG	2260	279
CATTAACGAAGGTGGAACAA	3991	CGG	2258	445
CAACCAGCACATTACACATA	9862	CGG	2256	411
ATTCTCATTCAAATCAAAGT	15738	CGG	2249	182
CTTAATGTGTTCATAGATTC	37069	AGG	2230	506
AAAAAAATTATGCTTGTAGC	38722	CGG	2224	322
AACAACAACGAAATATATGC	11088	GGG	2211	68
TGTACTTGTTTTTCATTTTG	7941	TGG	2203	265
CAAACGTCATTGCATAATCA	35970	GGG	2195	317
TGCTCATACTTTGCGTTATC	35380	CGG	2187	348
AAGAGGTATTTAAATATGTT	16156	TGG	2148	378
CCGATAATTTGAGCGACTGC	25276	TGG	2122	356
AGTTTTATAACGGCTCAGCA	4684	GGG	2120	494
GCGATCAGTTAAAAACTACA	24537	TGG	2105	92
CCACAATTAGCATTTGCAAT	9934	AGG	2063	320
TTAAAACCCCTAACCTTACT	6272	AGG	2057	145
GGTATGAATAGAATGACGTT	14900	AGG	2051	326
CTTAGACCAGAAACACTTTT	7552	TGG	2046	175
AATCTCCGTTTAGTTAATAC	5967	AGG	2037	526
CCACACCCTTGCGTTTAATA	2334	AGG	2034	138
CTTTGTTGGTTTGATGCATT	33521	CGG	2034	453
ACTACAGCATGGTCAATTGC	3165	GGG	2011	558
AAGTTACTACTCACACACTA	259	AGG	1973	187
AGCACTCCTAATCGTCATCT	5893	TGG	1969	702
TTTAAAAATCGGAAGGTTTC	14717	CGG	1961	114
GGCAAAAGATGAAAAGTCAC	33878	AGG	1957	359
TTATTTCAGTGTACTTTTTC	13048	GGG	1946	99
CGTACTTAACTTTTGCCATA	21277	TGG	1937	110
TACGAGTGAACTTAAATATC	17454	AGG	1932	559
CTATCTCGTAAGTTCAGCGT	11931	TGG	1924	251
ATTTGCAAATCCTAGCATTA	4552	CGG	1924	492
AAGCTCATTTTAAGCGCGAT	21963	AGG	1915	310
CATGCCTACACAGTATTCAA	2380	TGG	1912	513
TTTTTCACACCTTGCCAATC	10181	TGG	1910	543
GACAGAAACTATTGAGTACG	3786	AGG	1901	181
CTTATCTGAAGTATCTATGC	24655	TGG	1900	222

TTTTTTACCTCAAATTTTAC	4075	AGG	1888	288
AAATTACCTGACATAGATGA	17645	AGG	1887	405
ACACTGCTAACAGCTGCAAT	25342	CGG	1886	315
TCATACTCTAGTAATTCGTC	9367	TGG	1866	170
AATAAGCGCCATTCACTACA	10138	TGG	1863	253
GATTACTTACGTAATGCGAA	676	AGG	1837	298
GATTCCAATACTACGTTAAT	1461	AGG	1836	366
ACATCATCGCCCTTTTTGTA	5003	AGG	1830	209
AGAGCACCATTATAGTGTCC	31087	AGG	1825	49
ATTGGAGCATGCAAATAACT	1407	TGG	1823	362
GAGTCTAAATTTAAATCGAG	19408	TGG	1819	286
GTAGAGATATAGAACTTCAC	5383	TGG	1818	239
ACAACTTCACGACGCAATAA	15028	CGG	1808	193
AAATCTTCTTTTTCTTCAAT	16429	TGG	1807	109
CTGAGAATTTTATTACATGA	12851	CGG	1807	375
AAAAGAATTTGATGACGTGT	16202	TGG	1801	269
GACAAAGAAATGACGAAAGC	23187	AGG	1789	219
AATGCCCCTACATCTTGTGC	14480	AGG	1785	379
AATACCACTTGCATGACTCG	5794	TGG	1778	442
GATGGACGACAACTTTTTGT	27154	AGG	1776	323
CCGCCCATGATTGCTTTTGC	36016	TGG	1764	267
AATAGAGCTAGGGAGTTTAA	3709	CGG	1745	394
AGATTTTATTGAACAAGTAA	9900	CGG	1729	44
AATTTTCTAGTTGATTCTAC	5396	TGG	1728	242
TTAATATTGCAAGGTTCATA	8038	CGG	1717	273
AAAACTAATAGCATCATCTA	6502	TGG	1714	248
GGATTCCTTATTAAACGCAA	2345	GGG	1712	340
CATATTCTTCAAAGGCCTTT	14775	TGG	1709	83
GACCAAGATTTAGCGTTTTA	5166	AGG	1705	317
TTCTTAAGTTGTCTTTCAGT	30454	GGG	1695	213
CGTCCACGCTTTCGTAATAC	8907	AGG	1676	369
CTCAACTTTGCGAAGTCACT	13745	CGG	1663	36
GGTATGTGGGTGTCTGGTGA	15720	CGG	1661	106
AATGATTCTGACATTGCATT	22286	GGG	1660	57
TCCGTTTTATCAGTGCCTAT	29215	CGG	1654	184
TGAATTTTACAGTCCTATGA	13169	TGG	1650	218
AATCCCTCAATAACGCCACC	33096	TGG	1650	247
AACTAAATCAAAATATGAAC	8351	TGG	1639	197
TGAACCTAATAAAAGTTATC	37605	AGG	1631	295
GGCAACGCAGATTGTTTGAG	2310	TGG	1629	269
GACGGTATGAGTGATGCACT	26282	TGG	1601	142
ACTTATTATTATGTATTTCG	16889	AGG	1600	49
CCATTCATGTTCGTGCCGTT	33943	TGG	1599	186
TCAGATACACAACCTATGCA	30587	AGG	1596	71
GCTAAAGTCATATATACTAC	39929	GGG	1596	372

CTAATCGTTACATTCACAAT	26638	AGG	1588	505
TCTTTCAACAACCAATGCTC	15539	GGG	1578	363
ACAACATTCAAAGATTCAAC	12466	AGG	1577	460
TGTTCACCCAAGCATGTCAC	39880	TGG	1573	137
AAATAAAAAGATGCAACAAT	399	GGG	1571	156
GCATTGATACCAGTGATTGC	24320	CGG	1569	16
CCTTAATATTCGACGATAGC	8573	GGG	1564	131
TGAATCAATCACACTTATTG	12809	AGG	1560	183
TTGCGTCCTGCGTCAATTGC	21647	AGG	1555	31
AACGCCCTGCTACTAATCAC	2629	AGG	1550	260
GTTAGAAAAACGCGACGCAG	19224	AGG	1548	88
AAATAACTTTATCCACATAA	6704	AGG	1548	207
ATATCACTGTTCCTATGGCT	25812	TGG	1547	294
ATAAATTCGGAACAACGAGC	32705	TGG	1533	41
AATCCTTTTTCGACATGAGT	7713	AGG	1531	108
TTTACGCGCGTTATCTGTCA	10047	TGG	1528	188
TGAAATCCATACCAACCATC	38235	TGG	1520	267
AAGATTTAAATGTAGATAAC	39754	AGG	1513	520
GTTTGATGTTCCGAGTAAAG	18026	AGG	1502	70
GAAAGAATGACGAGTTTTAA	12729	TGG	1502	233
TATGCACATACCAATGTTGA	8130	TGG	1500	329
ATATTTGGCAATGTGTTCGC	24980	TGG	1497	180
TGGAACTGGTGCAAGAATAT	15512	TGG	1491	123
AAGAAATCGTTAGCACTAAT	20219	GGG	1489	294
GCGTTTGATGAAATACTTGA	11745	GGG	1479	196
TCTTGGAAATCATATTTATA	4817	CGG	1474	3
GTCGAAGATTATTTTATCTC	27535	CGG	1473	384
TTTATAGGCTCTCCGTTTGT	16166	AGG	1463	286
ACTCCTAATCGTCATCTTGG	5896	CGG	1449	80
ATGAGAGCACGTAAAGACGA	18537	TGG	1443	214
GATACAAAGACTTACTTTAT	10714	AGG	1435	113
ATTGCAAATGCTAATTGTGG	9915	TGG	1435	256
AATTTAAGTTTATTGATGAT	15922	TGG	1432	268
TTCAGTGATTTCTTAAATGC	26321	CGG	1431	220
GCTTTTTATTATGCACTTTT	18877	CGG	1427	55
ATACGTCCATCAACAAGCGG	28429	TGG	1424	83
TTAAGTACTGCCATTATTGC	24334	AGG	1424	112
TAACTTAGTCATGAAATGGT	3573	AGG	1424	164
TGGAACCCTGCAATTGACGC	21657	AGG	1419	389
TAAACTACTACGACTTAAGC	21268	AGG	1412	325
TCCTCATGACCATTCTTTAA	9969	CGG	1410	172
GTCAAGATGTATTACGAAAT	3328	AGG	1408	37
ACTAATGGCGTTGCGCAACC	38545	TGG	1399	341
TTGAAAATGATTTAGTTAGT	31919	GGG	1395	315
TATGAAAAAGATGATGATAA	16832	TGG	1392	312

TATTTAATTATGAAAATCAC	4626	AGG	1391	292
AAGTCACGTTGTAGTGGAAC	15498	TGG	1389	267
GTGTGATATGCGTCAAACAC	29449	TGG	1387	308
ATTAAGGCTTCAACACCATC	15672	AGG	1383	423
ATCTTTCAACAACCAATGCT	15540	CGG	1379	130
ACTTATACATCAAGCAAATC	32482	TGG	1375	36
AACAACCCTCCTCATCACAA	2575	TGG	1373	79
ACTGCAACTACTGCTAATAT	25492	TGG	1372	24
TTCCCCCTCCTTAATCGTTC	16244	AGG	1360	201
ACTAAAATGTGGCAAATTGA	36893	TGG	1357	113
CAGTATTCCCTGATATAGAC	22054	AGG	1352	288
TTTAAACGACGTATCGATAT	30713	TGG	1349	404
GACAAGTTTCAGAACGAACA	17544	AGG	1342	334
AGGGAATGGAATACACAGTC	7337	GGG	1340	77
TGTAGGCGATTCTGTAGATC	21229	AGG	1336	435
AATTAAACTACCCACCATAT	14403	AGG	1335	319
CAGCCATATTTGCTTTAAT	32000	TGG	1334	122
GAAACAATAAGTAAACTTTC	6075	TGG	1330	299
TTTATATTCACAACTTGCCA	353	AGG	1327	133
CCATCCTACCCGGTAATAAA	837	TGG	1322	300
ACCGCTCTATATTTAACGGC	6388	AGG	1311	96
GGTAAACATCACGGAATGTT	22440	TGG	1310	298
ATATCTATTGATGTTGTAAA	11190	TGG	1300	394
CTTTGAATGGTTTAATACAT	11994	TGG	1300	527
CGAGTGTGGGACGAATATAC	10926	AGG	1295	321
CTAATACATGTTTGTCATAG	5695	TGG	1294	215
CTCAAAGTGATGTGTTAGCT	4404	AGG	1288	202
GATTTGATTACCTCTTTACT	18020	CGG	1286	76
ATATTCATACCGTCATTCTT	6358	TGG	1286	218
CTGTCTATAGAAGTACTTAC	26569	AGG	1281	10
GAAAAACAATAACAGAAGCT	25587	TGG	1281	504
GATGAACGCTCAGATATTCA	35012	AGG	1280	239
TCCTTTCACTTATAATCACT	26829	TGG	1275	241
CTAAATCAATGGCTCAACGA	23769	TGG	1271	12
TGCCAAGGAAATCCTATGCA	338	AGG	1270	7
ACACCAGAAAACACATATAG	2830	AGG	1270	287
AATACTTGTGTTGTGTTACC	31387	CGG	1266	168
TTTGTGTCGTTCATATTCGT	38125	AGG	1260	379
CCGATTAACTGCATAATAGT	25138	AGG	1258	190
GTATAACGGCAATGACACAG	11681	AGG	1245	65
AATTTCTGTCCGCAAAACGC	31220	CGG	1242	33
AGATGAGAATGACTTAGATA	3480	TGG	1241	270
TTTACCTTAATATCTTCTGC	20457	AGG	1233	368
ATTCAACATTCAGTTAAAGA	11781	AGG	1232	7
GATAACATGTAATGATTACC	30148	TGG	1232	272

GGCGTTCAAGTGGTTCAGAC	15372	AGG	1231	118
CGGACAAGGCAAAGCATTCG	35827	CGG	1225	263
ATCAAGTGGGTGTGTTGGGC	18416	AGG	1222	163
AATTATTCAATGGTCAATGT	37782	CGG	1221	169
ACAAGAGTGCCGGATTTACC	32830	AGG	1221	306
ACTAAGTAACACTGAATTAA	23899	TGG	1211	226
CGCAAAAATATTCATGTTAA	3361	CGG	1211	250
CAAAAAGAGTACGTGGTGGC	9540	TGG	1208	36
TCAGCTAAGCGCATGCCATA	9571	AGG	1197	327
AATTGGCCACTGCTTTCAAA	5117	TGG	1192	308
GATTTGGGATATTTAACTGC	32794	TGG	1192	340
TTGACACAACACAAACATCA	27197	GGG	1187	157
TTCCCTAACAACTTAAGCGT	38638	TGG	1187	172
CGTAGACCTTTCGGCATTAA	20026	TGG	1184	133
TATAATTCATTCATGTTATT	15351	TGG	1184	203
TGCCAACGCTTAAGTTGTTA	38624	GGG	1183	325
TTTTACAAAAGCTTTACCAT	5991	AGG	1183	434
TACGATTAAAGCAGATGAAC	15776	TGG	1182	45
TAGCGTCCATTACACCTAGT	11361	TGG	1180	150
GTAAAAGCGTTAGTGGCATT	25184	TGG	1179	239
TTCGTCATTGACATTAACGA	3980	AGG	1172	300
AGTGGTAAACCGCTTGTTGA	19958	AGG	1171	231
TACTACACCTTGAATCGCAC	25616	CGG	1170	122
GACGTCCAAGCACTATTTGC	27019	TGG	1166	239
ACAGTTCTAACATTTTTGAC	25035	TGG	1166	377
GTTTTCCCGTCAAAGTATGG	38437	TGG	1165	198
AGAAAAACAAACAACTTAAT	2524	AGG	1163	335
CGGTACTATCTTCGCGCAAC	24268	AGG	1152	92
GGTATGACTTTGGCCGAACT	479	AGG	1142	197
AACGGAAATGTACCTATCAT	17303	TGG	1139	218
GAGATTTCCAAAGCAACGTA	23652	AGG	1133	165
CCTATCAAAGAATACTTTGC	15807	TGG	1131	122
GAACTTGTATCAGTACTACT	34831	AGG	1128	254
CAACAGACTTTTGCAGAAGC	28367	GGG	1128	288
CCTTTAACCGCCATTTTAGC	23980	GGG	1127	186
ATAACTAGCTCAAAGCGTTA	9195	TGG	1126	207
AAAAGAAGTAACCAAAGACA	10519	CGG	1126	307
CTACACCTAAATTATCTTTG	2936	CGG	1124	205
TTTTTTGATGTCTATTACCC	6033	AGG	1119	185
GTTTTAAACCCAAAGAATGA	6351	CGG	1116	232
GGCAATGTGTTCGCTGGTAT	24986	TGG	1115	378
AGCAATCCATTTGAAAGCAG	5127	TGG	1113	359
TACTACAGTACCGTTTTTAC	36839	CGG	1110	325
AGAGGGAGAGTCGCTCGTAC	23125	TGG	1109	138
TACACACGATCAATCACAAA	32947	CGG	1105	25

GTTTACCATCATACAAGGAT	40369	GGG	1105	142
GTGCCTATATCCGTCTTTTC	32388	TGG	1103	175
CGCTATTAATGTTAGTACAA	27769	AGG	1102	80
TATTCATACCGTCATTCTTT	6359	GGG	1102	323
ATTCATGACTTATCGTGAGT	18578	GGG	1101	53
TTATGTTATAGCTAGCCTTC	39804	GGG	1094	170
ATTGAATTGCTATCATATTC	13883	CGG	1094	249
TGCTTATCTGTCTTCGGAAT	5036	AGG	1094	275
CACCTTAAAACGCTAAATCT	5152	TGG	1089	186
GGTTCTTGTAAATTATTTTC	6619	AGG	1085	197
AACGATTCAAAGGCGCTCAC	8770	GGG	1083	177
AAGCAAGAAAAGTTTGTGCT	14594	AGG	1083	311
ATCCTTGTATGATGGTAAAC	40350	CGG	1071	383
AATACTCCACTAATGTAATC	20876	AGG	1069	108
AATACTTTGCTGGTGTCGAC	15817	TGG	1066	123
CGGAAAGCATATATTGACGC	14639	AGG	1062	254
ATCATCAACACTATTTCTAA	16631	TGG	1060	128
AAAACAGTTACAACTGCTAA	28907	TGG	1060	316
CAAATAGATAAAGGTGACAG	14987	TGG	1053	158
TAAAGCTCAATCATTGCGTG	18221	TGG	1052	126
CCTGCTTCACCTTTTGCACC	36793	AGG	1050	242
TGGTTCGATATCTTTATTGC	13294	TGG	1049	56
GTAATTAATCCGTAAGCCAT	29611	TGG	1049	213
AATTTAAGTGCTAAAGCTAA	6970	AGG	1049	330
TAAAACTTTCGTTATACTCT	28014	TGG	1047	142
GAAGCGCCACCGCTTGTTGA	28439	TGG	1047	357
TTGAGTATTGCGAATCAAGT	12100	AGG	1036	258
TTGGTAAGTGGAACTTATCC	33094	AGG	1032	216
ATAGAGGTGGTTAAATATGT	21707	GGG	1029	265
AGTTCACTATGAAAACTACG	10991	CGG	1028	137
TCAAAGGTTTACAGTCGTTG	12525	AGG	1023	300
GTCGAACACTTATTTGTATT	10435	TGG	1022	183
AGATACCAGAAAGATAACGA	5214	CGG	1016	155
ATATGTATCGAGTGATGACA	40072	AGG	1016	249
TAAATACAACAGGCTCAATA	17861	AGG	1013	183
AATTTAAAGTCAAGAAGTAT	20838	GGG	1012	276
AAAAAGAAAAGTGAAATGGT	9072	TGG	1011	283
CATATCTCCTCCTATTCAGT	20425	TGG	1007	133
AATTAGAAATGTAAATGTAG	9415	AGG	1003	163
CCATTTATTACCGGGTAGGA	821	TGG	1001	324
CTATAAATATGAGGAGGCAC	11849	AGG	999	258
TTTGAAATGTACGAGATGGA	10556	AGG	998	403
AAGATATAGAATGCTTTGGT	10630	AGG	987	210
CGGATTCCTTATTAAACGCA	2344	AGG	987	285
ACATTTAGTAAATCATTACG	39108	AGG	983	112

ATTTGCTATCCTTGAATTGA	461	TGG	979	239
GGAAAAAAGGAGCAAACAAA	37855	TGG	977	52
GGTTAAACCTCTAATTGCAG	19870	AGG	976	162
ACAGTATTAGACGCATGTAA	9138	TGG	975	105
AAAAACCAACGTTTAATGAT	4197	TGG	962	236
AACAGCTGAATGGTTAAACA	7515	CGG	959	245
CTAATTGTTCTCGAGTTGGT	22993	GGG	958	229
GCTGAAAACGGTGTGTTTAA	7141	AGG	950	14
AAAAAGAGTACGTGGTGGCT	9541	GGG	946	160
GAAATCCATACCAACCATCT	38234	GGG	942	156
GCACGTTGCATAATCATTTC	2116	TGG	929	129
CAAGTATCGATGACTGATTC	30923	AGG	926	180
ACAATAGAAAATGTACGTAG	37630	CGG	926	266
TTGTTCAAATTTGTGTCTCA	24845	AGG	920	102
GTTAAAAGAATGTTAAAGTC	6108	AGG	920	316
TCTTTCAATATCGTTGATAG	36590	TGG	915	103
GTAGTTAAACATATGAATGA	7048	TGG	914	62
AACCAATGCTCGGGATGGTC	15530	AGG	914	194
AAAGGAGAACAAGGCGCACC	36836	CGG	913	131
ATTTAAAGTCAAGAAGTATG	20839	GGG	913	339
ACTAAGACATCAATTTTAGT	2246	TGG	912	66
GCCAACAAAAATAACATTAT	16754	AGG	908	163
GTTGACTCAGACGGCAACGG	33184	TGG	895	205
CGGATTGTTCTATTTGTTCA	11626	CGG	895	206
AAACAATAAAACTTTTATGG	11602	AGG	894	1
AGCATTGTTGATAACAGAGT	8290	AGG	894	180
GCAACGTGATGAGCTTATTG	11440	GGG	894	203
CCTGTCCAAATTTTAACCGT	37312	CGG	893	125
AACTTTGAAGCTTCTAGAGC	6577	AGG	891	88
GAACAACCGGTTTTATATCC	27628	AGG	890	220
GTTGTTTGAAATGTACGAGA	10552	TGG	883	132
CGATCAGTCTGATTTGATGA	13784	GGG	883	151
GTTAGAAACTTTGGTACTGG	31463	TGG	879	142
GAATATACAAAAGTATATGC	37471	TGG	877	70
ATATGACGATGACGTTAATC	10677	TGG	867	198
ACATCTGTTTCAATTTCGTT	23689	TGG	864	165
TATTGGTAAGTTTTGTCACT	4934	TGG	862	192
TTAAATCTGACGCACTTTGT	33535	TGG	862	230
AGCTAGGCAACGACGTAAAG	9667	AGG	859	241
TAGGGAATGGAATACACAGT	7338	CGG	855	42
GTAGTTGAATATAACGTTAC	26854	AGG	854	127
CTAAAGTCATATATACTACG	39928	GGG	851	110
CCATTCGGGTGTTTTTTAGT	7782	AGG	851	133
GTGCTTTCACAAGTATTTCT	25485	TGG	850	28
TTTACTTGTACTAGATGATA	8229	TGG	844	209

CAAAAGCAGTCAAAGCTAAA	8093	GGG	842	180
GTATTGTTGTACCACTCATA	29337	GGG	841	5
ATAACAAAAAACTAGCCCGA	39803	AGG	838	140
TCATCAAGTTGTACGTCTAA	12036	CGG	838	141
TTCATACTACGCCAAATATT	35320	AGG	838	313
TTTTATATGAGCAAGAGCTA	8794	GGG	834	157
TTCCCTCACACTATTTCTAT	20996	TGG	829	146
TTCTTTCGCCATTTCTTCAA	19468	TGG	826	150
AGTTTAATTGATACTGGAGA	13239	TGG	825	12
GTATCTGTTTTAATATACGT	12767	TGG	825	58
ACTCTTTTTGCAACCATTCC	9511	AGG	824	196
TTATTTGCTAATAGTTTGTT	2738	CGG	822	63
TTTAGTTATAGTAACTTTGT	33295	TGG	818	153
AGAAATGTTAAAAAGTGTAT	39712	AGG	814	48
ATGCTCGGGATGGTCAGGGT	15525	TGG	814	130
TTAATACGTCCATCAACAAG	28432	CGG	814	192
GGTGTTGACTTAGGTGACAT	36287	TGG	812	132
CTGGATAGACAAATGTCTAG	35618	GGG	812	189
TACACACATAAGTTTATTGG	234	CGG	811	47
CGATAGAATCGGAAACCCTT	34564	AGG	811	78
GCAAAGAACGTGAAATAGCT	9651	AGG	809	77
TCTTTTCGATTCGATCTAAA	17217	TGG	809	200
TAGTGGCGTTCAAGAACTTA	7086	TGG	804	102
CTGTTCTATGAAAGTTGCAA	5489	GGG	802	18
ATACTTGATAAGTCTACTAT	27938	TGG	801	195
TATGTTTGGCACCCTACAAA	16170	CGG	800	62
TGGAATGAAACTTAAACTTA	17323	TGG	799	111
TTATTTCTCCAGTTCTATAT	30321	TGG	798	15
TTTGACACAACACAAACATC	27196	AGG	796	56
AAGTTAAGAAGTAACGCGCT	19258	AGG	794	267
TCGTTATATAGCGACAGGAG	39567	AGG	792	38
TTCGACCATGATTTAAGTAA	9032	TGG	791	138
ATTTGAATCATCACATTTAT	11324	TGG	791	154
TCATTCTGATTGGTTATTTT	17669	GGG	788	162
AATACCATTTATTACCGGGT	825	AGG	788	235
ATTTAATGATTCTGCAGCTG	308	AGG	787	35
CAATATAAAACGAAAAACGG	3303	AGG	786	60
TATTGTCATCGAGCTTAAAT	15604	TGG	780	219
TTTATCTCTTGTAGCAAACG	3935	TGG	780	238
AACCAAGCTATGTTGATAGA	376	GGG	778	189
ATTTTTAAAACATTCAGGCA	31824	AGG	777	85
TTTGTAGCACGACTACCACC	21548	AGG	777	151
TATCGCTATTGCGTTAGATT	6829	GGG	775	96
TGTGAGGGAATTCGTCGTAT	20967	GGG	774	187
CATATAAATAAAGGCTCATA	17962	AGG	773	270

ATACGTAATTGTTGTGTTGT	39466	TGG	772	23
AATAAATTGTTTTTAGCTAT	21163	TGG	771	150
AAAATATCTCTTCCTTCTTG	869	AGG	767	113
GAAATCCTATGCAAGGCAGT	331	AGG	766	265
ACTGCATACGGTGTTAATGT	38905	AGG	765	145
CTTATCTGAAACGACGTTAA	35308	AGG	763	223
GTAGAATTTTCAGCATCTTT	2686	CGG	762	61
TTTGTTCGGCGAACTTCAAA	2724	AGG	762	101
ATTGATCATATAGTTGTAAT	34988	GGG	761	1
ATTCGAAAGGATTAGAATCA	19103	TGG	758	229
TAGTAGCCATTAATGCCGAA	20016	AGG	757	40
TATTAGAATTAACCCAGTTT	34716	TGG	753	110
GGGTGTCTTACTAAACTTCC	34753	CGG	751	185
GGTCATGGTTATAACGATCC	38743	TGG	750	227
GAAAACCTGTGATTAGTAGC	2640	AGG	746	221
CTATCCGGATATTTATTTTT	37527	AGG	745	6
AAAGAGTGGTTTGAAGCTGC	22575	AGG	744	63
AGACGTGAACTCTTCAAAGA	23552	AGG	744	250
TTTATCCTACTGCCTTGCAT	342	AGG	743	15
TGGGAAATTCCACCTTTATG	6700	TGG	740	216
CACTCACGATAAGTCATGAA	18560	TGG	738	154
TTTGACCAAGCTGTTATCTT	19907	TGG	734	174
TCTTCTGCGCCTTCAACAAG	19951	CGG	728	24
TCACAATGGCAGTTGTGACG	2589	TGG	728	138
GAAATACATTTAGACGCAGC	38986	AGG	726	152
TATAGTTGGGATCAATGTTG	13006	AGG	726	179
GTTGGTTCAGTCGTGTTGCT	26118	TGG	725	90
CATTCATGACTTATCGTGAG	18577	TGG	724	139
TGATATTTAGAGGTGGCACA	8834	TGG	718	93
TAATTAACTTAGTCATGAAA	3569	TGG	716	44
TATGTGTTTTCTGGTGTTGG	2808	TGG	713	80
GCCTAAAAATCTATCAACTA	19294	AGG	713	93
TCATCTAAATCATAAGTAAC	16561	AGG	713	297
TAAGAATTATCTTAAGACGT	14304	GGG	712	79
TTGATTTTGTCCAATAACTC	36925	AGG	709	118
ACAACATCGTCGATAATAAG	36439	GGG	705	115
TATAACGATCCTGGAGCAGT	38752	AGG	705	128
TATTTCAACAAATGAATGGT	6474	GGG	703	104
TAGATAACAGGCAGGTACTT	39766	CGG	702	141
TCTTTGCTTTATTATCAAAC	38333	GGG	700	147
ACGTAACGCTACAAAGTCTA	28520	AGG	698	159
GTTTCAGAACGAACAAGGTT	17549	AGG	697	123
ACTATAAGTGATGTTTATTC	37771	AGG	697	145
AGATAGAGTGTTTGACTTGT	10032	GGG	693	127
TTTGTTTCAAACGTATTAGA	4474	AGG	690	153

CAGGTACCGACCATTTTTCA	27287	GGG	690	201
TTCATCCGTTTAAATCAATA	20938	AGG	687	24
AACTATCGCTTGTTAGATGA	29699	AGG	687	194
ATTTAAGGTGGTTATTCTTA	1698	TGG	685	68
TATGGATAGGTTTAAGCAAG	16139	AGG	685	171
AAATCAACGGTATTGTTCGA	33007	CGG	683	171
ACAAGTACGGTTGTTAATAA	1979	CGG	682	74
TTAATAGGACGAGGTATAGA	15867	TGG	680	129
GAAGCCTTAAACGCACCTTA	9572	TGG	679	91
TCAATACCTTTACCTAAAAT	6805	AGG	677	145
TAGAAATAGTGTTGATGATG	16651	AGG	675	61
TCGTTTGTAGGCAATCTATC	27306	AGG	675	65
ACTCACGATAAGTCATGAAT	18559	GGG	672	80
GCAACGTTGCCGAAACCACA	13941	AGG	671	78
AGATGAAAAAACGACTATAA	165	AGG	671	170
GCCATAAAATGAGTATCCAA	23593	AGG	670	47
ATGTTGTTATCAAATATTTA	1713	AGG	667	175
CCTTACAACACTTCAACTAG	19940	TGG	661	175
AATAACAATACTAATAATGA	7312	TGG	660	61
TACTTACGTAATGCGAAAGG	679	TGG	658	58
ATTTAAGTGCTAAAGCTAAA	6971	GGG	657	252
TTTTTCTTTTGTGCTGTCAT	19663	TGG	656	58
TCAACAACCAATGCTCGGGA	15535	TGG	656	150
AGGTTTAGTATGTGTGTATA	16224	TGG	655	160
TTAGCATACCTTGTGTTACG	17090	CGG	655	191
CAAATACAAGCGTTAATACG	35255	TGG	654	107
TACACATGTAACAGAGAAAA	138	TGG	654	127
TTGTTGAATTACCTTTAACA	32234	AGG	654	185
TAATATCACTTAGATATGCT	30960	GGG	653	212
ACGGAATACTAGAAGATGTT	20704	AGG	651	129
ATGCACTTTTCGGACTGTTA	18887	GGG	649	212
GGTATATATGCTACTGGTCC	21546	TGG	645	32
AGCTAGGGAGTTTAACGGTA	3714	TGG	644	102
TTGCAAATGTGAAATCTATG	7839	AGG	643	156
TAATTTATACGTAGACCTTT	20017	CGG	642	44
AGCACAAACTTTTCTTGCTT	14575	CGG	642	134
CGATAGTAGACGCAATTAAT	31775	GGG	639	47
ACAAGTGCTAATTAACCTGA	17521	AGG	639	114
TCTCCCCAATCATTAAACGT	4186	TGG	637	48
AAGAGGTTGAACTACGTAAG	9684	AGG	636	49
ATGGCGCTTATTACTTTCAC	10165	GGG	636	74
CGCTAACATAAAGAACATAT	38272	TGG	634	250
CAACGATATTTGATATTTAG	8824	AGG	633	182
TGAATATGCACAAGCAGAAA	19771	TGG	631	145
CTCCGCCACCATACTTTGAC	38426	GGG	631	183

TTTATTAAACCTTACAAAAA	5010	GGG	630	210
GAGATTAAGTCACGTTGTAG	15492	TGG	629	78
TACTCATCGTCATTTAGATG	18365	GGG	628	55
TAAAAGGTATCTACTTCACA	36195	AGG	628	94
TTTGGAGCACTGTTACAAGT	26100	TGG	626	88
CGTTTAAATCAATAAGGTAG	20944	AGG	625	122
TAAGTTTATTGATGATTGGG	15926	TGG	624	33
CGTGTACGTTAGAGAATGAC	40347	CGG	623	166
CCTATCATCTCTTTGTTGTT	16969	AGG	621	42
GGTACTAATCCGGCAATCAC	24313	TGG	621	81
CGCGGGTCATCAAAATTGGT	35146	TGG	618	54
TTTATCTTTTCGCTGAATAG	7668	TGG	618	227
GATTTAGTTAGTGGGTTTGA	31927	TGG	615	48
TGGAAATTCAATGAAGATGA	4965	AGG	614	154
AGCAATTCAATTGCACAGTA	13911	TGG	611	19
AGCAAACGCAAAAACAAGAT	15112	TGG	611	123
ATCACCATAACCTTTAATAA	28319	AGG	610	46
GAAAGTGTATTGCAACAGAT	37145	TGG	610	129
ACTAACAAAACAAATACTGA	33696	GGG	608	194
TTATCTGCATTAAAGCGTAA	17417	AGG	607	30
AGCTTTTACTAAACAACAAG	37273	CGG	607	98
TACGTAATTGTTGTGTTGTT	39465	GGG	607	103
GTAGTAGAAGCAATTAGAAA	4577	TGG	606	127
TAACAACATCACCTATTTTA	28563	GGG	605	85
AAAAATACAACCAACTGGCA	7602	CGG	603	163
AGGAATCATGAAAGACAAGA	12358	TGG	603	194
GAAAATCCGGAGCTATCACA	10379	AGG	601	68
CGACACAAATGATTTAGGGT	38155	AGG	598	197
ATAGACAGGTTTACTAAGCA	22068	TGG	593	87
AACAATTCAACCCAGATGGT	38240	TGG	591	113
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TCTAAACTTACAGATGATTA	32287	CGG	589	72
TGTTTTTGTCCGTGTCTTTA	29361	CGG	587	90
AATGATGGAAGTATATTGTC	7327	GGG	586	124
TGATGAGGAACTTCGCGGAA	33575	TGG	586	204
TTTACAACGCGCTAAATCAA	23758	TGG	584	116
AAAGCAATACGTGATGATGT	18192	CGG	583	107
AGTTGTCTATAAATATGAGG	11843	AGG	581	193
TGGCGTATTTTGGGCTTTAA	25333	TGG	579	113
AAGAATGACATTGAAATAGA	14834	GGG	578	23
CCTATTGCAAATGCTAATTG	9918	TGG	578	60
ACCTTGTAAGTAGTTAGGGT	30647	TGG	576	56
TGCGCTTCAATAGTGATAGT	4339	AGG	576	96
TTATAGGCTCTCCGTTTGTA	16165	GGG	573	168
ATACTAAACCTGAACGATTA	16252	AGG	572	43

TACTTTGTTAACAAGTTTTT	2501	AGG	572	97
AAGAACTGGAAGAAGAAACC	12025	AGG	572	112
TAAGTACGGTGCTGATAGCA	21308	TGG	571	150
CACAAATAGAAATAGAGCTA	3699	GGG	569	78
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TGCTAAAGTCATATATACTA	39930	CGG	569	142
ACTGTTGCATCTCTTAAAGA	7905	CGG	568	53
TATATTTAAATAACCTCTAT	27568	AGG	567	38
TCAATTAGTTTGTCCGCCTA	5991	TGG	565	179
ATTCAAGAAACACAAAAGAG	17135	TGG	562	114
TGGTTTATGTTAATTAATCA	15132	CGG	559	68
CCAAAATCATTAATATTGCA	8029	AGG	558	68
AAGATTGAACAAATAGATAA	14978	AGG	555	6
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ATATATAAAGCAACATGGTT	10250	TGG	554	70
AGCTTTAGTTGCATTATATT	23906	TGG	552	91
ATGAATTGATAAAAAAGAAC	9498	GGG	551	122
TAGTACCAAAGATAACAGCT	19896	TGG	550	18
GGCGAATGGTACACAACATA	21615	TGG	550	168
GTTTTCCGAAAATGGCATTT	7177	CGG	550	186
AGAATTGGTTAACACCTCTT	30867	TGG	549	36
TTTTTGATGTCTATTACCCA	6034	GGG	549	52
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GGCTTTCTAGTCTTTGGGTT	34375	AGG	549	118
ATTAAAAGATTTTATGTTTG	11219	AGG	547	78
TTAACCAAGCAATAGATGAA	3515	TGG	547	150
ACCACTAACTTACCTAAGAT	24953	TGG	546	183
GAAACGTTCGAGGCACCTAT	8877	GGG	545	63
TAACCGTATCGATTAAGATA	40130	CGG	545	137
CGTATATTTCTTCTTTTTGA	29736	TGG	544	192
ACGCCAAAAGTAACAGGTAA	2471	AGG	542	44
AAAAAGCGCATCTCAACCGA	37312	CGG	541	165
AAGAAAGTTTTAACTTAAGG	930	AGG	540	114
TCAGATACATGGCCTCTGCC	40024	CGG	536	61
GACCGGTTTACCATCATACA	40364	AGG	536	63
TAAATTTAACGAAACGTTCG	8867	AGG	536	78
AAAAGAAATCGATGTTAAAT	36631	TGG	533	47
GTGAATGATAGTGCGACAAA	32062	AGG	530	105
ATTAGACGAGTTAATTAAAT	10351	GGG	525	43
TTTAAATGTAGATAACAGGC	39758	AGG	523	73
TAGTAAACCTGTCTATATCA	22045	GGG	521	35
TAACTTATATCATTCGTCAT	3617	AGG	521	84
GGTAAAATGGCAGCAATTTG	16685	CGG	517	30
AAGCAACGTGATGAGCTTAT	11438	TGG	516	136
GACGCGCGTATTGATAATAC	29897	AGG	516	141

TTACTCAATTGAATCGCGTT	33135	AGG	512	51
GACTACTTTGTGCGCAGCAT	26363	TGG	511	116
TGTTCCATGCTTTTTCAATT	2091	TGG	510	153
CTGGCACATTATGAAGCAGT	5661	CGG	510	161
AAGAATTATCTTAAGACGTG	14305	GGG	508	61
ACAGTTCGCTACACAATACG	21938	AGG	508	61
GAGTAATCGGAGACGATTTC	8417	AGG	506	6
TAAAAGAATAGCATCATTTG	6438	GGG	505	58
ATTTCAGGGAGCGAGATGCA	8432	TGG	504	39
TTTTGATGTCTATTACCCAG	6035	GGG	503	56
TCAATCTTAGCTTTTTCTTC	13094	AGG	502	9
AACTTATATCATTCGTCATA	3618	GGG	501	119
ATACGTGGTATGACATCGTT	15423	TGG	499	74
TATTGAAGAAAGGTTATAAC	14104	AGG	499	122
CATGACCTGTAATAACAAAG	4272	TGG	496	138
TTTAACCTAATAAAATACAT	38598	TGG	494	64
TTAGTTAGAAACTTTGGTAC	31460	TGG	494	124
ACATCAATCACACATTCGGA	2429	CGG	493	156
TAGCACTAACACCTGCTGAA	23328	TGG	492	105
AATCATCAATAAACTTAAAT	15904	TGG	491	152
TTGTTATCAAATATTTAAGG	1710	TGG	490	149
AGCTAGTTATTTCTGTAATT	9166	TGG	488	81
TAATATCGTAAAAGCGTTAG	25177	TGG	487	63
ACAGTTTCAGGACCCCAACC	38547	AGG	487	125
AGAGCATGGTCAGAACAAGT	25082	AGG	486	6
TCTGATATAGAGGGTATTGA	26899	TGG	486	167
GCGAGAAAAGTAAGAGTAAT	8404	CGG	485	49
TATTACTTATACCGAGAAGA	8637	TGG	484	106
AGGAAAGCGAGCATGGAGGA	29519	CGG	484	135
ACATACTTTTTGATTGAGTA	20756	AGG	483	37
TGCTATGCATGCTGTAAAAG	5932	TGG	483	110
CGATAATTTGAGCGACTGCT	25275	GGG	481	34
TCATCCAAATTGAAAAAGCA	2103	TGG	477	9
TGCCTTGCATAGGATTTCCT	352	TGG	476	81
AAATGAAGCTGATTTAGATA	18759	TGG	476	130
AATAGTTGGACAGGTTCTCC	34751	GGG	471	40
TACAAAAGCTTTACCATAGG	5994	CGG	469	96
GTGACATGCTTGGGTGAACA	39861	AGG	468	145
CCAGCAAAGTATTCTTTGAT	15791	AGG	466	105
TAACCTCACAGTCATATCTA	11275	AGG	465	42
TTCTTCAATACTGTCTTTAA	28064	AGG	464	109
TCATTTAGATGGGGAATCAG	18374	TGG	463	29
AGATGTTAAAGCTAATGATA	27465	AGG	463	73
TTATTAGCTGACTTACAAGA	22218	AGG	462	28
TAATTAAGGGGTGATTTTTA	37404	TGG	462	100

AGGAGGCAACCAATGGCTTA	29618	CGG	459	34
TAACTAGCCACTGTGTATAT	13350	AGG	459	99
GTTAGCACTAATGGGTGATT	20227	GGG	459	139
ATTTTCCCTTGTGATAGCTC	10369	CGG	458	15
CTTATCAAATACCGTGTCTT	10514	TGG	458	122
ATAACAATTGCTTGTTGGTC	12249	GGG	457	10
TTTGCCGATTAATTCCGCTC	26324	CGG	457	15
GACACCAATTTCTTCAGAAA	756	GGG	455	112
GAATGACGGTATGAATATAT	6337	CGG	455	173
AACAATACGCCGTAAAGACA	29368	CGG	454	31
ACATTGCCTGGCGTGTATGT	19534	TGG	454	172
GAGAAATATAAGCGAAAAGG	18600	TGG	453	71
TGGTAAGCCTATAGGTGGTT	39276	TGG	452	14
TAACCGTATCTTAATCGATA	40143	CGG	452	110
CAACGACTCTAAAACGTATA	37030	CGG	451	19
TCCAAAGCCCCTTGTAATAA	23060	CGG	449	113
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TCATGTTCGGTAAATTTATA	9457	TGG	448	116
AAAACTTGGGAACTTGTCTT	6720	TGG	448	156
AAACATCCAGTGACATGCTT	39870	GGG	448	161
TAAAACCGCTCTATATTTAA	6384	CGG	447	18
ACTTACTTAGCAAAAGGTGT	19706	AGG	446	44
AGAAAAACTTGTGTACTAAA	93	AGG	446	46
TTATCATGATGTTACAAAAG	637	AGG	445	118
ATTAAGTGGTACGTAGACAT	33804	GGG	445	156
TTTGATTACAATCCATTGTT	16958	TGG	443	65
AGAAACATCAATCACACATT	2425	CGG	441	119
TACACAAAATACAAAATCTA	32578	CGG	440	3
TCATCACCTTTAAAACTCCA	21575	CGG	439	38
ATTGAAGAAAGGTTATAACA	14105	GGG	438	56
TGATTACGAATTAGACGAAA	17596	TGG	437	13
TTATCTAGATTGAAGCCCAA	30182	CGG	437	88
TATAACGGCAATGACACAGA	11682	GGG	437	162
GACGGTAAACATACCTATAG	27571	AGG	436	92
ACAGGAGAGGTAGACAAGGC	39580	AGG	434	27
TGTAAAGTCCATTGAAGAAA	19476	TGG	434	101
GGCTAATTACAGATATCCTA	34564	AGG	433	48
TTAAAAGATTTTATGTTTGA	11220	GGG	428	15
GAAAGGTGATAAAGGCGAAC	36781	CGG	428	21
AAAGACTTTAAAGGTATTGC	31352	AGG	427	31
GCTTCAATTCCTTTATCTCC	22331	AGG	427	67
TAGTATTAGGAGACTTTACA	28698	AGG	427	69
AACGATGTGTACTTTGATTT	33262	AGG	426	33
CGCTGATAAAAGTAAACTAT	16058	CGG	426	37
ATTGAACAAGCGCAAGCTAA	23405	CGG	426	151

GCCAGTAATTGTTGAGTCAT	34865	TGG	424	125
TCAAAGTATGGTGGCGGAGC	38446	TGG	424	173
TTAGTGAAAACAAACTTTCT	33455	AGG	422	36
CCACAAATAGAAATAGAGCT	3698	AGG	418	66
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CAAAGTCGAATATTGGTAAG	34440	AGG	416	34
TACAAGGCACTGATGATGAT	29184	TGG	416	93
ACTTTAAATATTTCGATGGT	21466	GGG	416	107
TTACAAACAAAATCGAACAT	1802	CGG	414	8
AACTTTAGATGCTATCCAGA	34086	GGG	414	101
TCGGTTGATTCTATATCTAA	6310	CGG	414	157
TCATACTTAATTGAATTGTC	27063	TGG	413	9
ATCACTAGTATTTTTGAATC	29296	TGG	413	43
AATTTAGATGCATCTACTTT	28096	TGG	413	58
GGCAGAGCAATGTCACAAGC	18258	TGG	413	93
CAAAAGGTGTAGGCGCCTAC	19716	TGG	412	50
TCATTTGGTCAAAACTGGAA	38512	CGG	410	89
CCAACAAAAATAACATTATA	16753	GGG	409	11
GATACTTTGCCGTTATTACA	23067	AGG	409	57
ATTCAATCAATTGTTTTTCT	4834	TGG	408	42
CAGTTTTAATACCGTATTCG	10810	TGG	407	34
ATTGAAGAATTTGATGATAA	4433	CGG	407	39
CAGGAGAAAGCGCAAGTGGT	39005	GGG	407	67
GAGAAAACATGTTGTTAAGT	23959	TGG	407	134
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GGCAATACATGCAATCAGTT	25971	TGG	405	11
TAAGTGACATCGAACCAGTA	9733	CGG	405	20
TGTACGTCTAACGGCTTACC	12027	TGG	405	20
AATGAATGTTAAGCGAATAT	35704	GGG	403	105
CGTTACGAAATAAGAGAACC	23483	TGG	402	51
AGAAAAACAAGGTATGACTT	489	TGG	402	74
GAGAATTACAAGGAAATCAT	23226	GGG	401	21
AAAATCCGGAGCTATCACAA	10380	GGG	400	100
AGCCTGTAACACTTACATAA	34773	GGG	400	114
GGAGAAGAAAGCAAGTGCAT	11497	GGG	399	5
GACGTTAATCTGGAAAGATG	10687	GGG	398	61
AGGAAATATCTCAGTTATTA	27513	AGG	398	82
CTTATATTGGGTTAAATCAC	38946	AGG	397	35
TAACCGACACTTTCAAAGTA	27237	TGG	397	52
TGTTCAGAACTTATAGATAA	31662	CGG	397	108
GAACCACAATTTTCTCTTCT	6585	AGG	396	11
ACTTTAAAGGTATTGCAGGT	31356	TGG	396	68
TCACATCATTTGGTCAAAAC	38507	TGG	395	107
TTTTCAACAGGATTTAGTGA	10412	TGG	394	44
CTTGTTAAAAACGGCGGTCA	30224	CGG	394	174

TTTGAGCTTGATTATGTTGA	27136	TGG	393	46
GTTTTTCGTCTGATGGAGTA	35535	GGG	392	4
ACCTCTACTTCTGCTTTTAG	5291	TGG	392	95
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ACTTTCAAAGTATGGTAGTT	27229	CGG	386	113
ATTTGCCACATTTTAGTGTC	36871	AGG	385	149
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AGATATGCTGGGTTCTGTAT	30949	TGG	383	58
CACCCTTATGTAAGTGTTAC	34787	AGG	381	14
TTATGTTAGCGACAGGCGAA	38300	AGG	381	72
AACGTCCAGCAAATAGTGCT	27008	TGG	381	99
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CCTGCATCTCTAAACGCTTT	31045	CGG	376	65
AACACAACAATTACGTATGA	39487	CGG	372	77
TATCTAGACCCTCAGCTTCT	30750	TGG	370	28
TTACTATAACTAAAATTATG	33320	GGG	370	45
TAATTAAGTAAAGTGTATTA	37371	GGG	370	50
GCTAATTACAGATATCCTAA	34565	GGG	370	105
TGATGCCGAAATATCGAGTG	10912	TGG	369	37
GATCTTATACGAAGTAAAGA	13617	AGG	369	78
ATTCTTAAGTTGTCTTTCAG	30455	TGG	367	23
GCTGTAGTGAAGTATAGAAA	3134	CGG	366	36
TAAATGGAACAAGTGATATT	24174	TGG	366	63
AAACAATCAAGAGAAAAACA	500	AGG	366	95
TTACAAGCATCAGATGCTTC	20318	TGG	365	24
ATCAAATCAATTGGAACGAT	28973	TGG	365	81
ACTTGTTCTTTATGATAATA	16121	TGG	365	118
AGCGTTTGATGAAATACTTG	11744	AGG	364	6
TGATATTGATGAGTATATCG	17705	AGG	364	9
ATGAAAATATAAGGGAGTGT	12626	GGG	363	83
TACATACTCCAAACAATTGA	2882	TGG	362	31
TATACTATCTGTCAAAGTAG	26540	AGG	361	79
GGATTGAAATGTGAGAGATG	7747	TGG	361	96
TTTACTCAAGAAAAATGGAG	20639	TGG	359	88
TAAAGTAGTGCTACTTGTTT	33214	TGG	358	76
ACTAAGCAAGATGTAGTATT	28685	AGG	358	99
TTATCCAGTGTTATAAGTGT	21489	CGG	356	12
GAAACTCATAGATGAGGCAC	8507	AGG	356	36
CTTTTGCGATAGCGTATGCT	8060	AGG	356	54
TTAGGTAAAACATCAGGTTC	33280	TGG	355	131
GACTTTAAATATTTCGATGG	21465	TGG	354	161
AATAAATACCATTTATTACC	829	GGG	352	10
TGGACGATCACTCATGTTGA	27884	AGG	352	10
ATTTAAGTTTATTGATGATT	15923	GGG	352	38
TATTTTTGAGTAATCGTGTA	23240	AGG	352	54

GGATTCTGAAATAGGTAAAA	16672	TGG	352	108
ATAATAAAATTATACCAGAA	6865	AGG	351	55
TCCTAAGTCGTCCTGACAAT	7007	TGG	350	27
TTTAATTCTGACGAGTTTAA	17285	CGG	350	58
TAAATCTTTTTAGAGTTATA	32910	AGG	350	105
ATGGAATCAAGATTTTAGGT	7464	TGG	349	42
GCTCTCTCGTTGCATAATTC	9614	TGG	349	61
ATGACCCGCGTCACCCTAAT	35175	TGG	349	122
CCAAAAACACTGTTGTATCA	40303	AGG	348	43
GCACATATCCATGTAGTGAA	10146	TGG	346	64
TCTGATTAATATTTCTAAAT	3009	TGG	346	95
TATATTGGGTTAAATCACAG	38948	GGG	345	50
ACAAGACAATGCCCTATGAG	29342	TGG	345	67
ATCAATATCGCAAATGTTGA	36959	AGG	344	35
CAATTTGCGGATATGGTGCT	16698	AGG	343	101
TCATACCATCTAAACTAGCG	14868	AGG	342	32
ATCTAATCGAACAAGAAGTA	19145	CGG	342	81
GCGAATGTAGTTGACTCAGA	33175	CGG	342	87
AGTATAAAAGAATGTTTATA	10613	TGG	341	78
TGAACGACACAAATGATTTA	38151	GGG	339	56
TATCTGCATTAAAGCGTAAA	17418	GGG	337	2
AGATGGTCCTACTACTATTG	34667	CGG	337	71
CATTAAAACTTTTTATGTGT	33761	GGG	336	36
ATAATCCAACATCTCAAGAA	38028	GGG	336	53
ACTATGAAGGGGATATCAAT	10471	TGG	335	73
AAAGTTTACTTATTGTTTCT	6095	AGG	334	34
TTAATTTTTAATGTTGTAAT	22772	TGG	334	70
GAAGTACGACGAAAGTTATT	7641	GGG	333	19
ATGGCGTTGCGCAACCTGGT	38549	TGG	333	77
TTACCTATCAATTGTGCTAA	28396	TGG	332	69
ATTAATCGGCAAAGTAGCTG	26350	AGG	332	83
TAATAAAACTTTAGAACAAC	27615	CGG	332	88
GGCGTTATTCCAGCAGAACA	19595	AGG	329	48
AGACAAGCAGAGCAAATAAG	29147	AGG	329	48
AGCGACAGGAGAGGTAGACA	39576	AGG	329	50
CGTAACTATTCTGATATAGA	26890	GGG	327	20
TCCACTAAAAGCAGAAGTAG	5306	AGG	327	48
CTTGGTCGTCATATCCAAAT	5134	TGG	326	45
TCATTCATATTAGCCATCAT	13166	AGG	326	56
GGTTTGTTAGTTATATAAAT	3630	TGG	326	85
TATCTGACTGTTGGTCCCAC	40056	AGG	326	99
TATCTGTCGTTAAATATATT	30373	CGG	325	59
GTAAGTCGTAAGGTACATAT	21141	AGG	321	8
CGACTAAAGGAGGCAACCAA	29611	TGG	321	24
GGAACAACGGTTACTGACGA	4004	AGG	320	95

TTTACACCAATAAATAGCTT	18425	GGG	320	97
TTAATTAAGTAAAGTGTATT	37372	AGG	319	53
AAGTACCGTCGTTATCTTTC	5203	TGG	318	14
TTAATAATTGTCTTTGATCT	23367	AGG	317	5
CATTTCCCTTCTTGAGATGT	38017	TGG	317	85
AGCTGGACTTGATAGCGCAA	18275	TGG	316	83
CCTACTAAAAAACACCCGAA	7798	TGG	316	138
TTATTCATCTGGATTTGTAC	34603	CGG	315	80
GAATATAACGTTACAGGCGC	26860	AGG	314	105
AGAAAGTTTGTTTTCACTAA	33474	CGG	313	19
AAAATAGAATAGTTTGTGTA	33054	CGG	313	28
ACGTCATCAAATTCTTTTAT	16181	AGG	313	97
AACTGCCATTGTGATGAGGA	2564	GGG	313	124
TCGCGAGTAAAGTAGCTGAT	26232	GGG	312	36
TTTGCAGTATACGGAAAAAT	3917	TGG	312	80
CATGCAAGTTTTAGGTGTTT	25738	TGG	312	91
CATAGAGGTCGAAAAAGTGG	10881	AGG	311	8
GCAACAATGAGAGAAACAGT	21894	CGG	311	25
GTCTGATTTGATGAGGGCGG	13790	AGG	311	62
CTAGCCAATTAGGGTGACGC	35163	GGG	310	61
TGTTTACCCATATATTGTTG	21839	TGG	310	112
GTTATCGGATTCGTTAATAC	33381	TGG	308	31
CAGGTCGTTGATAATACTCT	20788	AGG	308	32
AAAGCATAAAAAATGGTATT	3048	AGG	308	73
TCCTGCCGTTAAATATAGAG	6373	CGG	308	138
ACAAGGTATTATGAGTGGAG	18152	AGG	307	70
GCACGTTACGGTATCTTACA	20255	AGG	306	34
AAACTACCCACCATATAGGC	14399	AGG	305	39
TAAGAATGACATTGAAATAG	14833	AGG	305	48
ATTTCTACCTGTGCTGTTTC	31124	TGG	304	14
TAATTATTTCAACAAATGAA	6470	TGG	304	100
TTCATTTTAAAAGGTCATAT	3400	GGG	304	113
TGGATTTAACTAGAATAACT	25431	GGG	303	39
CTTCCGCCAAGATGACGATT	5883	AGG	303	53
ACCAATCTTAGGTAAGTTAG	24938	TGG	303	63
TTATATTGGGTTAAATCACA	38947	GGG	302	10
AGTGGTATAGGAGCTATACG	15408	TGG	302	17
CAGATGAATAACGATAGAAT	34575	CGG	301	92
GTATGCTCAGATGTTAAAAG	14021	AGG	300	49
TGAACAAAGGTTATATAGTT	12993	GGG	300	50
TTTAAAAGAATAGCATCATT	6436	TGG	300	80
AACAGAATGAACTATGAAAC	11351	AGG	299	19
GAATCATTTAAATTAACAAT	22317	TGG	299	42
TACCTTGTGTTACGCGGTAT	17096	GGG	298	100
TTTCTGTTCAATTTAGAGTT	14132	AGG	297	130

CCGACGGTTAAAATTTGGAC	37328	AGG	296	51
AAAAGGTATCTACTTCACAA	36196	GGG	295	34
TCCGAACCTATTCCGTTGCC	34636	AGG	294	56
CTAATAAAAATGATATGGAT	39203	TGG	293	20
TGTACACGAGCATAGCTACC	23485	AGG	293	35
CTCATCAATATCATTCTGAT	17679	TGG	293	46
TGAGTTGTTCGACAAAGATA	17164	TGG	292	50
GAAGAATATGCATTGATCAC	33840	TGG	291	50
TTCCTAAAAGCTGGATTGTA	29485	TGG	291	72
TCATACTACGCCAAATATTA	35319	GGG	290	2
TGTATTAGCTGATGTAATAC	13880	CGG	290	129
TAACGACCCTGAAAAATGGT	27297	CGG	289	74
ACTAGTGTTTGCATATAATA	10577	CGG	288	10
CGAAAGATAGCAGACGAAGA	15219	AGG	287	31
CGTTCAATAAATGTGAAAGG	14452	AGG	287	32
AAAAGGTGTAGGCGCCTACT	19717	GGG	286	11
TTAAAAGAATAGCATCATTT	6437	GGG	286	18
GCAATACCTTTAAAGTCTTT	31333	AGG	286	25
CCAGCAAAAGCAATCATGGG	36032	CGG	286	85
GGAATATATATAAAGCAACA	10245	TGG	286	99
TTACAACATCGTCGATAATA	36441	AGG	285	96
ATCATAAAGCGTATATACAA	8968	GGG	285	114
CTTTTAATAGGGGTAACTAT	30821	TGG	284	5
ATTGACGCTTTGCAAGAAGT	16919	TGG	284	29
GCATTAGCTCCTGTTGACTT	21423	AGG	283	13
TGAAAGAGTTAAATTTGGAA	11575	TGG	283	64
GAAGTTGAACAACAAATCAA	32221	TGG	281	31
CAAAGCAGAACCTGAGTTAT	36931	TGG	281	44
TTTAGTTTTTAAAAATTCTT	8442	TGG	281	50
CTAACAAAACAAATACTGAG	33697	GGG	280	55
GTATCAGGATAACGAGCGAG	10124	TGG	279	39
AAAAAGGTTATCAAACACGC	36506	TGG	279	44
TCGCTATTGCGTTAGATTGG	6827	GGG	278	30
AAAAGCAGAAGTAGAGGTTC	5312	CGG	277	80
TGGCGTTGCGCAACCTGGTT	38550	GGG	276	12
CCGAACCTATTCCGTTGCCA	34635	GGG	276	63
ACGACAATATCCAACTTTTG	38400	CGG	276	80
GTTGATTTCGTGCCACTGTG	994	CGG	276	126
TGAAGTACGACGAAAGTTAT	7640	TGG	275	27
ACATTAGTGGAGTATTAAAC	20899	AGG	275	29
AACACGAGCACAAACGAGCT	35680	CGG	275	85
GGATCACGTGAATGTTTTTG	9712	TGG	275	98
AATACTGTCTTTAAAGGAAC	28070	GGG	275	106
TCTCCAGTATCAATTAAACT	13220	AGG	274	67
AGTAATCGGAGACGATTTCA	8418	GGG	273	32

CCAGAAAGGAGATAACGAAA	6879	TGG	273	37
AAACTTACCAATAAGATCAT	4908	TGG	273	47
GCGATCAGTCTGATTTGATG	13783	AGG	273	57
AACGCTTAAACCAACTGAAT	20431	AGG	272	37
TTGAACGCTGCAGGAAGATT	24785	TGG	272	68
CCAGACGATGAATCTGTAAT	11148	AGG	271	4
TGACACAACACAAACATCAG	27198	GGG	271	29
ATAGCGCAGACATACAAGCT	13526	AGG	269	27
TACGTCAGCGATTTATAATC	30412	CGG	269	27
AGATATGACTGTGAGGTTAA	11295	AGG	269	70
ATATACGTTGAATACGGTAC	21525	TGG	266	60
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TTTGAAGCATTGAATAGCAT	24740	AGG	263	75
TAGATAGAGTGTTTGACTTG	10031	TGG	262	3
AGGATCGTTATAACCATGAC	38725	CGG	262	33
GGCTTATTGGTGGTCAGGAT	23358	AGG	261	37
GGGAGAAAAGGAGCAATGCC	22899	AGG	260	36
AAAGCAATTATGAAAAGAGT	194	AGG	260	49
AAAAAGTAGAGCTTAAGATA	26954	AGG	260	54
TATGCAATATACGTTGAATA	21519	CGG	260	100
AGGGTTTCGCAAACTAATTT	37660	AGG	259	15
TCAATTATCGGCTTTTTAAC	25997	TGG	259	49
CATGTTATTTGGCGTTCAAG	15362	TGG	259	78
TTTCAATATCAACTATGAAG	10482	GGG	259	100
AAAGTTACATTACAGCCCCT	6034	GGG	258	45
AATAGGTGATGTTGTTAGAG	28585	TGG	257	6
AGTTGTTGGCTTTGGTGCAA	24439	TGG	257	31
CGAAACGTTCGAGGCACCTA	8876	TGG	257	84
CACAGTAAAGTAAGTGGTAT	15396	AGG	256	1
AAAAAGAACGGGTTAACTCC	9509	TGG	256	68
CAGTCTTGTCGGTTACAAAG	20547	AGG	255	47
TTACTTGTACTAGATGATAT	8230	GGG	254	3
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TGCAAACCCCGCTAAAATGG	23989	CGG	253	68
GTTGTCTCAAATGTAGGTGA	26264	CGG	252	19
GAGTCAATTGTTAATATGAT	13836	AGG	252	39
GCGTGTTTGATAACCTTTTT	36487	AGG	250	1
AGTTCGGATTTTAGTAGCTA	24227	AGG	250	65
TCAAATGCTTGTTTGTCTTT	27102	TGG	249	9
CTCTTATCACCTTCGTTTGT	27318	AGG	249	18
CTTTCTTCATCTACTGGTAT	37939	CGG	249	37
TCAACGCTACCTGGTAAATC	32823	CGG	249	79
TATTATGTACGAGTTAATCA	29572	AGG	248	82

GACGGCTAATGATGATGTAG	13736	AGG	247	39
GCCTTTGGATACTCATTTTA	23608	TGG	247	39
ACCAACCGAAATGCCATTTT	7188	CGG	247	42
CCTAACAACAAAGAGATGAT	16985	AGG	247	52
GGTAAATCCTAGAATTGTTA	27993	AGG	247	68
AACCCTCTATCAACATAGCT	390	TGG	247	101
CAAGTGCTAATTAACCTGAA	17522	GGG	246	25
TTGGTATCAAAATCTAAGCT	4889	AGG	246	36
CATTGATCATATAGTTGTAA	34987	TGG	246	65
GCTAAATGAAGATAGTTCTT	27802	TGG	244	11
CCGGGACAACCTGGTGCAAA	36800	AGG	243	14
CGATAAGAAAATAGAAGAGT	21350	GGG	243	68
GTAATATCACTTAGATATGC	30961	TGG	243	73
CATCATTCTTTTTATAAAAC	32594	GGG	241	47
GCAACAACATAAGATGACAG	32727	AGG	241	82
CATGAAGTTGCATTATACGG	38851	TGG	240	58
GTTTTAATGTCTTTAAAAGT	33731	TGG	240	87
GCTGATAAAAGTAAACTATC	16059	GGG	238	26
GCTTTTTGCTTATCTGTCTT	5042	CGG	236	2
TGCTTGTAACGTCGTTAACG	20288	TGG	235	31
TCTATCAATAAATTGTCCGT	30182	TGG	233	2
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GCATAAAAAATGGTATTAGG	3051	AGG	233	43
GCAGCTTCAAACCACTCTTT	22556	CGG	233	44
CGACCTCTATGCTTGCAGTT	10853	TGG	233	68
AATCTATCAACTAAGGATGT	19287	TGG	232	24
TTAATTAAGTTATCGATATC	9098	CGG	232	47
CAGTGCCTTGTAATATGATT	29157	AGG	232	48
GGACATGAAGTTGCATTATA	38848	CGG	231	5
TAAAAAGCGTTTTAGCGCTT	1903	GGG	231	10
AAACAACAACGAAATATATG	11087	CGG	231	33
AATAGGATCTGTGGTTTTGT	40170	TGG	231	51
GAATGTTTTAAAAATTCATT	31800	CGG	231	53
AATTATCGTTTATCTGAATT	39172	AGG	229	5
GAATTTAAAGTCAAGAAGTA	20837	TGG	229	33
TGAATAAACCTACTATGATT	25845	TGG	228	28
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AAAACCTGTGATTAGTAGCA	2641	GGG	227	31
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TGAATATCATACAAGGTTTG	25785	TGG	226	45
GTTTCAACTTATTATAAGGG	26739	AGG	225	35
ATTCGACTAAAGGTAAGAGT	14664	GGG	223	19
ATAGATAGTTTTTTATTGTC	5315	CGG	223	22
TTACTCGTTTCTACACTCAT	5540	AGG	222	61

AACTAGGTGTAATGGACGCT	11379	AGG	222	92
TACGGTGCATATAATTACTT	35942	CGG	220	42
ATCAGAATTTTAAATCAAGT	18403	GGG	220	58
GCCAATGACTCAACAATTAC	34880	TGG	219	38
CTCATCTCCTGTAAAATTTG	4066	AGG	219	58
CGACTGCTTCATAATGTGCC	5644	AGG	219	86
TATTACCGCAAAGATAATTT	2947	AGG	218	10
TTCAGGCAAGGTGCATGCTC	31836	AGG	218	35
TTATCCACGAGTCATGCAAG	5782	TGG	217	32
AATACACTTTACTTAATTAA	37391	GGG	217	57
GCGATTCATGGTAAGCCTAT	39268	AGG	217	69
ATGGATTTATTCAGCTGTAT	30283	TGG	216	7
ACAAGGAAGATGTCTCCTGT	40055	GGG	216	19
GATAAATCAGTGATAAATTC	30049	CGG	216	50
ATGTTCTTTATGTTAGCGAC	38293	AGG	216	60
AAGCGTTAATACGTGGTGTT	35262	TGG	215	37
AAATGGTTTGACAATTCATT	38215	AGG	215	38
AGGTGATTACCATGCTTAAA	34249	GGG	214	8
TGGTTACACGGTTATTGGGC	29204	AGG	214	17
CAGTTGTGACGTGGAAGGTT	2598	TGG	213	2
CATCCATTAGCACAATTGAT	28409	AGG	213	2
AACTAACAAAACAAATACTG	33695	AGG	213	62
GCGATGTCAGCAGGTATCAG	24599	AGG	212	2
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CTTTTTAATAAAATTGGCAT	27712	AGG	212	44
GAATGGCGTGATTGGCTTAT	23345	TGG	212	67
GCCAACCCTAACTACTTACA	30662	AGG	211	54
TATAATTGCTTTTATATAGT	40003	AGG	211	87
TAACGAAATAGTATTTGTTT	12907	TGG	210	15
ATACTTTGCTGGTGTCGACT	15818	GGG	210	25
AATTTTATTAAAAAGTCTAC	27736	AGG	210	29
GGAGATTTATTGAACGCTGC	24776	AGG	210	50
GTTCCAAACTGCAAGCATAG	10866	AGG	209	52
AAGTTGAAGATGTTGTTGTG	13978	AGG	209	57
AACAACTCATTGAAAGATTA	24206	CGG	209	70
GAGTTTTCCCCTTGTGGTTT	13934	CGG	208	21
AACTTCAATTGCAGAACAAA	29258	AGG	207	110
TCTAATTGTTCTCGAGTTGG	22994	TGG	205	47
GTAGAACTTATGCAAAGTAC	11052	AGG	205	56
GATGACATGAACGCTATAGA	26714	CGG	204	10
ACCCTGACCATCCCGAGCAT	15544	TGG	203	20
ATTAATAACCTAGTAAGGTT	6264	AGG	203	42
CAACTGACAGCTAGATATTT	23282	AGG	203	52
AAAGGCGAACCGGGACAACC	36791	TGG	202	13
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AAAACGACTAATCTTGCAAG	29066	AGG	201	55
AAAGGTAATAATGTAAGAGA	39424	CGG	201	56
GATTCACCCACAACAATATA	21830	TGG	200	9
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GACTATTACTGTTACAAAGA	20508	AGG	197	47
TTCTATGAACGTAATATCAA	15699	CGG	196	20
CACAAAGTAGTCAGCGCGGT	26390	AGG	196	93
AATGAATTTTTAAAACATTC	31819	AGG	195	38
GGCTATTAGCGCTCTTAAAA	24460	TGG	195	50
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CAAGATGGAATCAAGATTTT	7460	AGG	194	66
CGCTCAGAAACTCATAGATG	8501	AGG	193	10
ATGTAGTTGAATTCTTTGAA	11981	TGG	193	29
GCTTTGGAAATCTCTAATAT	23627	TGG	192	2
AGCTCCTGCACAAGATGTAG	14492	GGG	191	9
GTAAAGAAACTTATTTACGA	37444	AGG	191	14
GTATCGATGACTGATTCAGG	30926	CGG	191	38
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TAGATTGGTTAACTCAATTG	25653	TGG	190	33
TGAGGAAGAAGCCACGAATA	10815	CGG	190	37
TTCTATAAATTTGCAGTATA	3908	CGG	190	65
AGATAGTTTAAAAAAAGCAA	28477	TGG	189	16
CCAAATATCTGACCAATCTT	24949	AGG	189	17
CTTAAATACTTAGCGATATT	38802	AGG	189	53
GATAGATTGCCTACAAACGA	27325	AGG	188	25
GGACGCAAAGCGCTTTTAAT	30809	AGG	187	20
GTTAACACCTCTTTGGCCGA	30860	TGG	187	36
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ACAGTTAAGAGTCAGTGCTT	34322	CGG	186	37
GCAAGTATATATTATGATGA	13718	CGG	186	48
ACAGAATGAACTATGAAACA	11352	GGG	186	63
AGAAAGCAAGTGCATGGGAT	11502	AGG	186	68
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TTATTGTTAATTGTTATTGA	4510	AGG	185	57
GGGAAACAATTCAACCCAGA	38236	TGG	184	24
AAGATTTTATTAAAGCAAGA	7445	TGG	184	30
CTTAATATTCGACGATAGCG	8572	GGG	182	88
GGTAGAATCTTTAGTATTGT	21212	AGG	181	1
CGATTCAAGGTGTAGTAGAT	25638	TGG	181	11

CGTGGATAAAAGTTGATGAG	5812	AGG	181	15
CGTATTGATAATACAGGTTA	29903	TGG	180	3
TCCCAATAACCGGCGTTTTG	31213	CGG	180	24
CCACTAGTTGAAGTGTTGTA	19924	AGG	179	48
CCAATGTACTTGATACGATT	25950	TGG	178	21
ACGACTAATCTTGCAAGAGG	29069	TGG	178	36
AATGGTTTGACAATTCATTA	38216	GGG	178	42
ATATGAATGAACATGAATTA	13195	AGG	177	9
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GTAGTTGACTCAGACGGCAA	33181	CGG	177	38
CACTAAGTCGTTATATCCTA	28601	TGG	176	4
ATAGATACTTCAGATAAGAA	24634	TGG	176	23
TCGTCCCACACTCGATATTT	10901	CGG	176	25
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TCCTTAGTTGATAGATTTTT	19309	AGG	176	44
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ATAGCTTCTGGGCGTGCTTC	34282	TGG	175	29
ATTATCGGGGCAGTCAATGT	34476	TGG	175	29
TAGCGCGTTGTAAAGCTCTT	23733	TGG	175	58
GGTGGCGTTTTAGGTTTAGT	24392	TGG	174	69
TCCACCACTTCACTAGCTGT	34396	AGG	173	33
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GCTTAGTACAAGCTTCTAAG	23427	AGG	173	59
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AACGGTAAAGGTTGGACTAA	38530	TGG	171	34
ACCTAGATTACATTTGTTTA	36406	TGG	171	35
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CATAAGATGACAGAGGCGAA	32734	TGG	171	63
AGAAAAACAAAGATTTGTTT	6142	CGG	170	42
GAGCGTAATAAACGTGCAGA	22419	CGG	169	41
GTTGCAAAAAGAGTACGTGG	9536	TGG	168	37
TAGAAATGTAAATGTAGAGG	9418	TGG	168	66
CCTAGCTCTATTTCTATTTG	3682	TGG	166	21
GAGCTTTCCTTACGTTGCTT	23643	TGG	166	22
TCAACTCGCATGATTATTTT	9209	TGG	166	30
TAGAAGAATCAACAGCAAAA	37568	TGG	166	53
GATACTCATCGTCATTTAGA	18363	TGG	165	13
AACTAATTCAAGAATTACAG	39453	GGG	165	32
TACACAGTAGCTAATGTTAA	39406	AGG	164	3

TGAATCATCACATTTATTGG	11327	AGG	164	20
CAGAATGAACTATGAAACAG	11353	GGG	164	39
TGTGAAGCATAAGCAATTTT	26970	AGG	163	26
TGCATTACTGCATTTGTATA	30073	TGG	163	27
TGGAGAAGAAAGCAAGTGCA	11496	TGG	163	39
TAAAGTTACATTACAGCCCC	6035	TGG	163	45
TCTACCGCTTCTTTACCTAT	29095	TGG	163	53
AAGTTTTATAACGGCTCAGC	4683	AGG	162	16
TTGAAATGAGGTGCATACAT	34364	GGG	162	42
TTTAATCATGAAAGACATTA	19621	TGG	161	1
ACACATTGTACCGAATTAGA	36096	TGG	161	30
TAAAACAATTAAAGGATTTA	21073	TGG	161	36
TTATTAAATAACTATTTGGA	39694	TGG	161	47
AGCGTTGGCAATAAAGCTAA	38653	AGG	161	62
ACCAATGCTCGGGATGGTCA	15529	GGG	160	25
TCATAAGTGATACCTTGCAT	30583	AGG	160	27
ATCGAAAGGAGGTTAGCCTT	23593	TGG	159	1
AGCATATCTAAGTGATATTA	30979	CGG	159	7
TGTTTTGTTAGTTTTCAGTT	33669	CGG	159	43
GCATTCCTCGCTAGTTTAGA	14879	TGG	159	44
AGCAACTAACTTTATTTTAG	10288	AGG	158	25
ATTGAACTTGATGAAGCAGT	11805	AGG	157	13
AGTTGGGATCAATGTTGAGG	13009	AGG	157	20
GTCGCAGGTCTTGGAGTTGT	24425	TGG	157	23
AAAATTATTACAAACAGAAT	5429	TGG	156	25
GATTTAGCTGAAATAGTACG	22260	AGG	156	38
TTAGTAAACCTGTCTATATC	22046	AGG	154	8
AACTCTTCTTTAAATTTAAT	33428	AGG	154	14
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TATGAATGAACATGAATTAA	13196	GGG	153	39
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TGTCCTAATACTTGTAATAT	25693	AGG	152	26
CTACAAACGAAGGTGATAAG	27335	AGG	151	17
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TGTGGATTCTCGGTTTGATA	34169	GGG	150	30
GCCGTTATTACAAGGGGCTT	23075	TGG	148	12
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TCAACTTTAGTAATCCTTCA	37736	GGG	146	17
GACTTGAATCGATTCCAGCC	27630	TGG	146	40
GTACTTACCAGAAACAGCAC	31133	AGG	146	53
ACTAGATGCTTTCACTAAAA	29968	AGG	145	10
ACTGGGTTAATTCTAATAGT	34737	TGG	145	16
AAAACAAACAACTTAATAGG	2527	AGG	145	26
TAATGTTTGGATTTACCAAA	33944	CGG	145	32
TTAACAATTGGTAATGTGCC	22329	TGG	145	37
CAAGGTATCACTTATGATGC	30605	AGG	144	6
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AAAAAGCTGAAGAAAATAAC	5074	GGG	144	51
ATAGAGTTAACTAACAAATA	15306	TGG	144	54
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TGACGTTAATCTGGAAAGAT	10686	GGG	143	32
AGTTATTCAAAAATCACGAA	1154	AGG	143	41
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AACGATAAAAACGAAGTTAT	33366	CGG	140	5
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ATAAGTGCTAGTGCGTATAA	11667	CGG	140	29
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CGTGGTGTTTGGTTATTGTC	35273	AGG	140	48
GAGCGCCTTTGAATCGTTTT	8749	AGG	138	22
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AACCACAATCCTAAATTAAT	40187	AGG	134	43
TTACTATGCAACAAGAGTGC	32820	CGG	133	1
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TTGATACGAATGGTGATGTT	16731	AGG	133	30
TGTACGTAGCGGTATAATGA	37641	GGG	133	30
AATGGCGCTGACCTTGTTAA	32239	AGG	133	34
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GAAATTGTTGATACACGTGT	16538	TGG	132	33
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GCATTTATATGTCGATAGAG	35122	AGG	131	8
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CAGTCGTGTTGCTTGGAGTG	26125	TGG	129	45
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CGGATTAGTACCTGCAATAA	24340	TGG	126	13
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CGTGGACGAGGCGAGCCCAT	8876	AGG	123	18
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AAATGTTATACCTTTATTAA	28325	AGG	122	4
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CAACGTTGCCGAAACCACAA	13942	GGG	107	13
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TGGAGTTTTAAAGGTGATGA	21594	CGG	99	21
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TCAAGTGATTTAGGAATATC	37684	AGG	97	24
AAACGACGTATCGATATTGG	30716	CGG	97	37
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TTTTTAATTTAACACAAAGT	33916	AGG	65	7
TTAGAGAAGCCTGGACAAGA	32428	TGG	65	11
ACGCAAAGCGCTTTTAATAG	30811	GGG	65	12
GTGTCGTACACTTATAACGA	20865	TGG	65	17
TCTATTATAAGGAAAACTTT	588	CGG	64	2
ACTTAAGGAGGAACAACAAA	942	TGG	64	4
TCAAGTTGTCTATAAATATG	11840	AGG	64	5
AGGGATAAATATAAATAAAG	36215	AGG	64	6
TATTGGGGTTTTGTAACATG	34526	GGG	64	7
TCAACTAATTCAAGAATTAC	39451	AGG	64	7
GTGCAATGTTTTTTAAGAAT	30882	TGG	64	10
CAATACTGTCTTTAAAGGAA	28069	CGG	64	17
ACTAGCCAATTAGGGTGACG	35164	CGG	64	17
CCCGCTATCGTCGAATATTA	8589	AGG	64	27
GGCGATTTTTCTTCCTAGTT	482	CGG	64	29
GTATCTGAAGTGTATTCCAT	30556	AGG	63	5
TAATACACTTTACTTAATTA	37390	AGG	63	9
GTGGTGTTTGGTTATTGTCA	35274	GGG	63	11
TCGTCATGATTATGATTTTT	37213	TGG	63	27
TTAGCATATATTGATACGAA	16721	TGG	62	3
ATAGATGATATTGAAGCACA	16301	AGG	62	5

GAATGTTGTCAAAAGAATAC	25411	TGG	62	9
GTCGTGCTACAAAGATTCCG	21574	TGG	62	25
AGACAAAGTATTGTATCAAA	30544	TGG	62	30
CTAGTATCTTTTGAATATGG	34804	AGG	61	9
CGAAAGTTATTGGGATTAGG	7650	GGG	61	16
GATGAGCTTATTGGGGATAT	11447	AGG	60	4
CACGGTGGAGGTAGTAGCTT	26462	AGG	60	6
TGGAGTGTGGCTGAAAAAAT	26138	GGG	60	9
GAGCCTTTATTTATATGAAA	17984	TGG	60	12
GATAATCCGTTTTCCGAAAA	7185	TGG	59	2
ACAATCCAATGTATTTTATT	38609	AGG	59	23
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TTTTAGTTCTTTAGATGGGT	28772	CGG	58	1
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GCAGTCATTGGTGTATTCAT	25526	TGG	58	3
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GTCGTTTTCCCGTCAAAGTA	38434	TGG	58	20
GTACTGGTGGCGTTGGTAAA	31476	TGG	57	1
AAAAACCTGTATTAACTAAA	5956	CGG	57	3
TATTACTAATAAAAATGATA	39198	TGG	57	6
GTAGGCGATTCTGTAGATCA	21230	GGG	57	9
AGCCATACAATCCAGCTTTT	29499	AGG	57	10
AACTGATTAAACTGTGTTAA	27399	AGG	57	16
ACGGCAGACTTGAGCAACAG	32966	TGG	57	18
ATATACGCGATATGAAAATG	34151	TGG	57	25
TATAAATAATTTTCGTTCTA	30111	GGG	57	33
GGTATCTTATATTGGTATAC	30626	AGG	56	5
TCCGCAAAACGCCGGTTATT	31228	GGG	56	5
GACTGGGGTTACGAGCACTA	15834	TGG	56	11
GACGAAAGTTATTGGGATTA	7648	GGG	56	12
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AGATTTAGCGTTTTAAGGTG	5171	TGG	56	28
TTAGCTATTGGTAAGTCGTA	21151	AGG	55	1
GTATTCGATAATTTCTTTAT	7357	AGG	55	2
ACTGCGATGTCTCCAGGTTC	34606	CGG	55	11
GAAGAAAAAGAAAAGTGAAA	9068	TGG	55	14
GTGCTAACAATTCATGTTCA	23295	GGG	55	16
GTTGACAGTGCGTCCACACG	35528	AGG	55	23
CTTACTACCTGCCTATATGG	14408	TGG	54	1
TAATAACCTAGTAAGGTTAG	6262	GGG	54	3
AATCTGGAAAGATGGGGAGT	10693	TGG	54	10
GGAACAGCAGACGCAGGAAA	12379	AGG	54	12
ATTGACTTTAAATATTTCGA	21462	TGG	54	12
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TTAGCAGTAGTTGCAGTCAT	25514	TGG	53	21
TTTCAATTAATAACCTAGTA	6269	AGG	53	23
TCACACTTATTGAGGAGCAT	12817	GGG	52	7
AGAGGATAGCTCTTTATTAA	26522	AGG	52	9
AACCGCAACTGTGTAATATG	5622	CGG	52	10
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GCTTAAACCAACTGAATAGG	20434	AGG	51	9
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CAATATTAGAAAATAAAGTG	19509	AGG	51	14
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GGCGTTGCGCAACCTGGTTG	38551	GGG	50	14
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TCTTAGGATTCCATCTAATT	36090	CGG	49	2
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TGAAGAAGAAATATTTAAGA	20675	TGG	48	3
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CAAACTAGGGTTAACACTTG	29398	AGG	47	2
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GAAGCATTGAATAGCATAGG	24743	TGG	47	4
GTATAACCTGCTGGCACTGG	39324	TGG	47	5
CGCACGCAAGTTTGAGGATT	24688	GGG	47	9
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AATCGAACGCTTTCAATGTT	26027	TGG	47	16
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CTTGCTCTTTTGGTTCGAAT	30024	CGG	46	18
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TGATGGAGTAGGGCCTCGTG	35525	TGG	45	4
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ATCTCTTAGAGCCGAAAAAT	10081	TGG	45	11
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CAAGGCGCACCCGGTAAAAA	36845	CGG	41	3
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