

## Conservation Genetics Resources

### Characterisation of polymorphic microsatellite loci for the bryozoan *Fredericella sultana*, the primary host of the causative agent of salmonid proliferative kidney disease

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<b>Abstract:</b>	The freshwater bryozoan <i>Fredericella sultana</i> is the most common primary host for the myxozoan parasite <i>Tetracapsuloides bryosalmonae</i> , causing proliferative kidney disease (PKD) in salmonid fish. An Illumina next-generation sequencing library containing genomic DNA from both <i>T. bryosalmonae</i> and <i>F. sultana</i> yielded 10653 microsatellite motifs. Twenty-four loci were tested in both species and 12 novel polymorphic tri- and tetranucleotide microsatellite markers were developed for <i>F. sultana</i> . These markers provide a valuable resource for population genetic studies of <i>F. sultana</i> , whilst the apparent lack of microsatellites in the PKD agent suggests a low frequency of tri- and tetranucleotide repeats in the <i>T. bryosalmonae</i> genome.
<b>Suggested Reviewers:</b>	

1 **Characterisation of polymorphic microsatellite loci for the bryozoan**  
2 ***Fredericella sultana*, the primary host of the causative agent of salmonid**  
3 **proliferative kidney disease**

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24 **Key words:** Phylactolaemata, Myxozoa, *Tetracapsuloides bryosalmonae*, PKD, population  
25 genetics

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27

28 **Abstract.** The freshwater bryozoan *Fredericella sultana* is the most common primary host for  
29 the myxozoan parasite *Tetracapsuloides bryosalmonae*, causing proliferative kidney disease  
30 (PKD) in salmonid fish. An Illumina next-generation sequencing library containing genomic  
31 DNA from both *T. bryosalmonae* and *F. sultana* yielded 10653 microsatellite motifs. Twenty-  
32 four loci were tested in both species and 12 novel polymorphic tri- and tetranucleotide  
33 microsatellite markers were developed for *F. sultana*. These markers provide a valuable resource  
34 for population genetic studies of *F. sultana*, whilst the apparent lack of microsatellites in the  
35 PKD agent suggests a low frequency of tri- and tetranucleotide repeats in the *T. bryosalmonae*  
36 genome.

37

38 **Main text.** *Fredericella sultana* Blumenbach, 1779 (Bryozoa: Phylactolaemata) is a common  
39 freshwater bryozoan across Europe and also occurring in Asia, Australia and New Zealand. It is  
40 the most common host of the myxozoan parasite *Tetracapsuloides bryosalmonae* (Okamura &  
41 Wood 2002), which causes Proliferative Kidney Disease (PKD) in farmed and wild salmonids.  
42 As no direct transmission between fish is possible, *F. sultana* plays a key role in the spread and  
43 occurrence of PKD. Since bryozoan colonies can grow rapidly, reach high densities and disperse  
44 via colony fragments, understanding the population genetic parameters of both host and parasite  
45 is important for assessment of potential parasite dispersal and the spatial distribution of PKD  
46 (Okamura et al. 2010).

47

48 Here, we used Illumina MiSeq paired end sequencing to generate novel genomic sequences and  
49 to develop novel microsatellite markers for the *F. sultana* and *T. bryosalmonae* host-parasite  
50 system. Approximately 1000 *T. bryosalmonae* sacs were collected by dissection from *F. sultana*  
51 (River Itchen, Hampshire, UK). Genomic DNA (gDNA) from parasite sacs without any visible  
52 host material was extracted using a Qiagen Blood and Tissue kit. A Nextera library (40ng of  
53 gDNA) was prepared and sequenced on a 50% of a paired end (2x150bp) MiSeq run in-house at  
54 the Natural History Museum, London. The paired reads were quality controlled separately using  
55 PRINSEQ v.0.20.4 (Schmieder and Edwards 2011) (right-end-trimmed until the first base of  
56 quality score >25 was encountered, reads with average quality score <25 and those containing  
57 any ambiguous bases discarded). Post-cleaning, paired end reads were joined and 5,775,223  
58 contigs were searched for microsatellite motifs.

59

60 A total of 10653 microsatellite motifs (di-, tri-, tetra- and pentanucleotides) were identified from  
61 the raw reads using msatcommander v.1.0.8 software and primers for 865 microsatellites (repeat  
62 number 6-47, potential duplicates removed) were designed using Primer3 software (Electronic

63 supplementary material, Table 1). Twenty-four microsatellite loci were tested in a panel of 17 *F.*  
64 *sultana* individuals from seven populations consisting of 10 *T. bryosalmonae* infected and 7  
65 parasite-free specimens. Also, 6 *T. bryosalmonae*-infected brown trout (*Salmo trutta*) kidney  
66 samples collected from five rivers (Estonia) were screened.

67

68 PCR amplifications were performed in 6.1 µl total reaction volume, which included ca 10 to 100  
69 ng of DNA, 0.6 µM of forward and 1.2 µM of reverse primers, 0.5 µM of FAM, VIC, NED,  
70 PET-labeled universal M13 primer and 3.0 µl of 2×QIAGEN multiplex Master Mix.

71 Amplification conditions were: initial denaturation at 95°C for 15min, 15 cycles of 30s at 94°C,  
72 1min 30s at 58°C, 60s at 72°C, followed by 25 cycles of 30s at 94°C, 1min 30s at 52°C, 60s at  
73 72°C and a final extension of 10min at 60°C. Fragment analyses were carried out on ABI  
74 PRISM 3130xl (Applied Biosystems, USA) with LIZ600 size standard. Genotyping was  
75 performed using the software GeneMarker v. 1.6 (Soft Genetics, USA).

76

77 Of 24 screened microsatellite loci (22 tri-, 2 tetranucleotide repeats), 12 primer pairs were  
78 polymorphic in *F. sultana* (Electronic supplementary material, Table 2). These loci did not  
79 amplify in PKD infected fish kidney nor in gDNA extractions from single parasite sacs,  
80 indicating that they belong to *F. sultana*. No loci amplified from material expected to contain no  
81 *F. sultana*, suggesting all 24 loci originated from *F. sultana*. The number of alleles of *F. sultana*  
82 microsatellites ranged from 7 to 16 (mean 10.7). The expected and observed heterozygosity  
83 ranged from 0.82 to 0.97 and from 0.45 to 1.00, respectively.

84

85 Interestingly, none of the tested microsatellite markers amplified in *T. bryosalmonae*, despite the  
86 fact that the gDNA extraction for the MiSeq library was purified parasite material, with only  
87 residual host carry-over. To check the proportional representation of *F. sultana* and *T.*

88 *bryosalmonae* in the genomic library, blastn searches with 300bp sections of the small subunit  
89 rRNA gene of *F. sultana* and *T. bryosalmonae* were conducted against the joined MiSeq reads.

90 For *F. sultana* and *T. bryosalmonae*, 81 and 495 ssu rDNA matches to the respective queries  
91 were found. Despite potential copy number and genome size differences between the two  
92 species, these results confirm that *T. bryosalmonae* should have been significantly  
93 overrepresented in the MiSeq library. Therefore, it is likely that the frequency of tri- and  
94 tetranucleotide simple repeats in the genome of myxozoan parasite *T. bryosalmonae* is much  
95 lower compared to its bryozoan host *F. sultana*.

96

97 This study reports the development of twelve novel microsatellite markers for *F. sultana* that  
98 will complement the relatively small number of existing microsatellite loci in this species  
99 (Hartikainen and Jokela 2012). Our work also revealed that trinucleotide microsatellite motifs  
100 are likely rare in the genome of *T. bryosalmonae*.

101

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106

## 107 **References**

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**Characterisation of polymorphic microsatellite loci for the bryozoan *Fredericella sultana*, the***Journal Name*: Conservation Genetics Resources: Microsatellite Letters*Authors*: Dmitry Filippenko, Hanna Hartikainen, Beth Okamura, Anti Vasemägi*Corresponding Author*: Anti Vasemägi, Division of Genetic and Physiology, Department of Biology, U  
Itäinen Pitkätatu 4, FI-20014 Turku, Finland, e-mail: antvas@utu.fi**Electronic Supplementary Material Table 1****Table 1** Information on 865 primer pairs for microsatellite amplification in *Fredericella sultana* and *Te*

File name	Sequence	records_id	msats_id
M00328:4:000000000-A3DTF:1:1105:21563:21567:1	GTCGTGAATGTAGTCTG	1017247	1969
M00328:4:000000000-A3DTF:1:1107:20673:17734:1	GGTATATAATATAACAAT	1390522	2652
M00328:4:000000000-A3DTF:1:1108:23202:12612:1	GAGTTTGCTGCCATCCTC	1540471	2919
M00328:4:000000000-A3DTF:1:2107:10147:12262:1	TGCCATGACCATTGTGTC	4243710	7931
M00328:4:000000000-A3DTF:1:2108:5850:11303:1	GTCCTAGATAGATGAAG	4433214	8276
M00328:4:000000000-A3DTF:1:1101:16828:13095:1	GAGAGAGAGAGAGAGA	82664	158
M00328:4:000000000-A3DTF:1:1105:3137:16391:1	GTCTGAACCCCTCCCCC	961636	1838
M00328:4:000000000-A3DTF:1:1109:11895:15557:1	CGATTGCTATGGCTCTG	1782991	3392
M00328:4:000000000-A3DTF:1:1113:13109:14153:1	GACGGAGACAGACGGA	2606396	4911
M00328:4:000000000-A3DTF:1:2102:16874:22636:1	GAGGGGGAGGGGTGGC	3362186	6313
M00328:4:000000000-A3DTF:1:2109:5148:12938:1	GTCACCCTGTTGCCTGAC	4647938	8653
M00328:4:000000000-A3DTF:1:2114:10294:19917:1	TTTCTAAAGAGCGCACCC	5718405	10535
M00328:4:000000000-A3DTF:1:1103:21176:19532:1	GGCCTAACCATTCTTGAT	583282	1172
M00328:4:000000000-A3DTF:1:1106:9400:17523:1	CACCTTCACTGGCCGCC/	1181536	2263
M00328:4:000000000-A3DTF:1:1107:13217:22886:1	CGTACACTCTGTGCTTCA	1447035	2754
M00328:4:000000000-A3DTF:1:2111:12076:14107:1	ACCAGCAACTTCCAGCC	5052582	9379
M00328:4:000000000-A3DTF:1:1101:12480:5856:1	GCTGAGGAATCAGCAAC	11994	12
M00328:4:000000000-A3DTF:1:1103:17834:9894:1	GGCAGAGACAGCAATAC	479341	949
M00328:4:000000000-A3DTF:1:1110:26386:19202:1	GGGCGGCGCTTCTTCCA	2031030	3864
M00328:4:000000000-A3DTF:1:1114:19193:14433:1	GAGACGGACAGAGAGA	2822743	5325
M00328:4:000000000-A3DTF:1:2105:3102:12871:1	CATTGTGTTGACACACA/	3858154	7166
M00328:4:000000000-A3DTF:1:2109:8355:7290:1	CACACACACAGAGAGA	4592615	8546
M00328:4:000000000-A3DTF:1:2113:7805:13474:1	ACCCTGGCAGTACTGTG	5446426	10034
M00328:4:000000000-A3DTF:1:2114:21404:18282:1	GCCTGAAAGACAGACAC	5700394	10505
M00328:4:000000000-A3DTF:1:1101:6792:9852:1	GTGAAGTGCAAGCAGCT	46421	71
M00328:4:000000000-A3DTF:1:1101:9407:24490:1	CATATAGGTAGACAGAG	208264	441
M00328:4:000000000-A3DTF:1:1105:18146:13864:1	CCCTTGACTTCTGAGCC	933439	1792
M00328:4:000000000-A3DTF:1:2105:10486:14177:1	CTCTTTCTCTCTCCGTC	3872361	7201
M00328:4:000000000-A3DTF:1:2107:13284:22248:1	ATGCAAACCAATGCCGA	4349623	8140
M00328:4:000000000-A3DTF:1:1101:20283:6311:1	GTTGTGCACTCATCTCTT	14552	17
M00328:4:000000000-A3DTF:1:1106:12299:10116:1	ACTGCATGCATGGACAA	1101622	2116
M00328:4:000000000-A3DTF:1:1107:19791:8728:1	GTCTTTAGATTTAGTGCC	1291283	2453

M00328:4:000000000-A3DTF:1:1113:11009:8254:1	CTGCTGCAGCTTCCGTCC	2547069	4795
M00328:4:000000000-A3DTF:1:2102:20943:15017:1	GGCTCGAACACTACCGG	3284772	6164
M00328:4:000000000-A3DTF:1:2105:4021:10525:1	CCATGGAGGAATGCACT	3833302	7122
M00328:4:000000000-A3DTF:1:1110:14632:12699:1	CATACGCACATACATACC	1954515	3721
M00328:4:000000000-A3DTF:1:1111:21934:21060:1	GTGTGTGTGTGTGTTGT	2266882	4287
M00328:4:000000000-A3DTF:1:1114:11129:25851:1	GTAGTCAGTAGTTCTTG	2950758	5584
M00328:4:000000000-A3DTF:1:2109:20696:12200:1	GAGTATCATGCCCTGGC	4640030	8635
M00328:4:000000000-A3DTF:1:1104:17550:24294:1	CGCACAAAAAGAGTAGA	833852	1627
M00328:4:000000000-A3DTF:1:1112:13049:23162:1	TCGTATGTGTGCCAAGA	2501111	4716
M00328:4:000000000-A3DTF:1:2101:16369:21013:1	GCCCAATAACCCACAGC	3139249	5884
M00328:4:000000000-A3DTF:1:2105:13263:12202:1	GATAGACACAGGCAGAC	3850815	7148
M00328:4:000000000-A3DTF:1:2106:22705:11367:1	GACTACTTTATAATCCAA	4040522	7538
M00328:4:000000000-A3DTF:1:2106:10235:20831:1	CTCGATCTGGACGCGCA	4139357	7721
M00328:4:000000000-A3DTF:1:2113:4690:8451:1	GAGTGAGAGAGAGAGTA	5395770	9938
M00328:4:000000000-A3DTF:1:1102:4916:9594:1	TGACTGGATACATTTAG	266089	543
M00328:4:000000000-A3DTF:1:2102:10969:25213:1	GTATGCTGCAAAGCATA	3379738	6338
M00328:4:000000000-A3DTF:1:2106:14030:9193:1	AGCAAATAGCGGTGAAC	4018678	7495
M00328:4:000000000-A3DTF:1:2113:5280:23182:1	CGTTAATCGTGCTCTCT	5551743	10231
M00328:4:000000000-A3DTF:1:1107:8946:12305:1	ACATTTGGCTACAAGTC	1327340	2520
M00328:4:000000000-A3DTF:1:1109:25562:20326:1	GGTTGACACGACGCGAC	1837077	3498
M00328:4:000000000-A3DTF:1:1113:18257:19678:1	TAACTATACTTCACGTTC	2674272	5042
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M00328:4:000000000-A3DTF:1:1101:6812:8128:1	ATGCCACTGTTTCTGATT	29293	46
M00328:4:000000000-A3DTF:1:1114:7474:7840:1	ACTCAGGGGAACATATG	2756980	5201
M00328:4:000000000-A3DTF:1:2106:18996:11773:1	GTAAAGCGCCTAGTTCG	4044558	7551
M00328:4:000000000-A3DTF:1:2113:22354:6991:1	GCGCACGGCTACGCTGC	5384248	9906
M00328:4:000000000-A3DTF:1:1101:13778:23784:1	GCTGTACATTATAATTAT	202361	423
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M00328:4:000000000-A3DTF:1:1106:10673:13337:1	CTGCAGGAGTGCCGGTC	1134892	2183
M00328:4:000000000-A3DTF:1:1113:13417:10847:1	CTCTCTACCAATATATTA	2570236	4841
M00328:4:000000000-A3DTF:1:2103:12019:25337:1	CCTCTAGGCTAGCGACA/	3579070	6682
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M00328:4:000000000-A3DTF:1:2114:9360:9232:1	CCTTCGGTCCCTGTCTCT	5602482	10314
M00328:4:000000000-A3DTF:1:2114:21401:16304:1	AGCTCTCGCTTTGTCGTC	5677881	10453
M00328:4:000000000-A3DTF:1:1106:11447:8131:1	GTGTCGAGGGAGCTGG/	1083354	2082
M00328:4:000000000-A3DTF:1:1114:19808:16133:1	CTTTTAAAGCGCCTAGTT	2843459	5375
M00328:4:000000000-A3DTF:1:1114:17884:15679:1	CCCACACACAGTTCAAC/	2837668	5354
M00328:4:000000000-A3DTF:1:2105:21302:21227:1	GTCACTCGCTCACTCATT	3947011	7350
M00328:4:000000000-A3DTF:1:2106:9468:16502:1	TACACACACACAGACAA	4095350	7661
M00328:4:000000000-A3DTF:1:1103:19696:16256:1	CTTTTAAAGTGCCTTGAT	547885	1090
M00328:4:000000000-A3DTF:1:1105:10576:13901:1	ATGGTGAGGTGGGCTAT	933837	1793
M00328:4:000000000-A3DTF:1:1109:20397:16150:1	GTTGGGCACCAGCTATA	1789868	3409
M00328:4:000000000-A3DTF:1:2107:7123:13411:1	CACGAAGACCGAGTGAC	4256235	7954
M00328:4:000000000-A3DTF:1:2110:17325:23775:1	GTCTACATGCAGAACATC	4954477	9188
M00328:4:000000000-A3DTF:1:2111:20832:17116:1	TTATTTACTTGCTCAGCC	5086903	9447
M00328:4:000000000-A3DTF:1:1101:10330:17367:1	ATCCTTTACTGCCCCCTG	133611	275
M00328:4:000000000-A3DTF:1:1103:15900:20237:1	ATAGAACCCCGCAAGGA	590450	1187
M00328:4:000000000-A3DTF:1:1104:9802:9754:1	TGGATAGATGGACAGAC	684687	1376



M00328:4:000000000-A3DTF:1:1106:6494:20890:1	GTGTGCTTCTGCTTTTGC	1217401	2320
M00328:4:000000000-A3DTF:1:1108:20329:11052:1	CTCTCTCTCTCTCTCTC	1523822	2879
M00328:4:000000000-A3DTF:1:1111:14177:22863:1	GAACTCGCCCGACACCA	2286836	4321
M00328:4:000000000-A3DTF:1:1112:4874:17901:1	TTTTAAGCTTTCATGATA	2440202	4593
M00328:4:000000000-A3DTF:1:1113:18125:20785:1	GTAGAGGAGAAAGAAA	2687362	5067
M00328:4:000000000-A3DTF:1:2101:19488:14585:1	GCTTCTCACCCCTCCCTC	3068608	5758
M00328:4:000000000-A3DTF:1:1102:7449:21041:1	GATAAGCTTAATGCTAG	390591	791
M00328:4:000000000-A3DTF:1:2106:23381:8020:1	AGAGACAGCAGACAGAC	4007771	7467
M00328:4:000000000-A3DTF:1:2106:13280:9723:1	CTGTAATCCATCAAATGC	4023870	7505
M00328:4:000000000-A3DTF:1:1112:5707:13468:1	GCAGACTCCAAGGGAGT	2387125	4489
M00328:4:000000000-A3DTF:1:2105:11446:24544:1	CACGACAGGAAGGCACC	3974077	7409
M00328:4:000000000-A3DTF:1:2108:14608:10733:1	GGCTTAGAATGAGCTGC	4427382	8265
M00328:4:000000000-A3DTF:1:1102:11907:3685:1	GCCAGTGCGCATGCGAC	225238	465
M00328:4:000000000-A3DTF:1:1104:6903:18295:1	ATGCACAGACGCATGCA	775915	1534
M00328:4:000000000-A3DTF:1:1111:19877:15642:1	ACTAGGCACTGTTGCTC	2201530	4166
M00328:4:000000000-A3DTF:1:2110:22669:14499:1	ACCATGGCGCTTGAGGT	4859198	9033
M00328:4:000000000-A3DTF:1:1105:14828:26796:1	CCCCCACACACACACA	1057380	2044
M00328:4:000000000-A3DTF:1:1106:10893:13059:1	GAAAAGCAACAGACATA	1131869	2176
M00328:4:000000000-A3DTF:1:1108:4356:20319:1	GCATGCATACATACACA	1629981	3111
M00328:4:000000000-A3DTF:1:2103:13763:13515:1	CTTGTGAACTGGCTGCC	3469330	6480
M00328:4:000000000-A3DTF:1:2104:12494:4170:1	CATGGGAGAGAGGGAG	3584855	6692
M00328:4:000000000-A3DTF:1:2105:8587:17988:1	ACTATTGACTTACCAAGT	3914385	7292
M00328:4:000000000-A3DTF:1:2114:12197:15419:1	GCTCTCGCCTTTGCTACC	5667741	10436
M00328:4:000000000-A3DTF:1:1106:14110:18386:1	AGCCAGCAGTAGCTCGG	1191151	2275
M00328:4:000000000-A3DTF:1:1107:13829:23787:1	CTGCAATTTAGTGTCTCA	1455706	2772
M00328:4:000000000-A3DTF:1:1112:9429:11257:1	ACCTACTATTTTCATATGC	2363288	4441
M00328:4:000000000-A3DTF:1:1112:11489:18771:1	AGCATGTAAGTCTCGGG	2450794	4610
M00328:4:000000000-A3DTF:1:2107:13721:16078:1	ATGTCGTGCCCCGCCGG	4285562	8019
M00328:4:000000000-A3DTF:1:1111:9147:24577:1	GCGCCTAGTTCGAGATT	2303664	4349
M00328:4:000000000-A3DTF:1:2101:5538:6724:1	CTATAATCATGCTCTTTT	2983165	5620
M00328:4:000000000-A3DTF:1:2102:3885:8623:1	GGCCTGCCAACTGCCGG	3215945	6013
M00328:4:000000000-A3DTF:1:2102:17737:21846:1	CACATACACACACATC	3355175	6300
M00328:4:000000000-A3DTF:1:1105:15501:12427:1	AATTACTGGAGGAGCTA	917450	1766
M00328:4:000000000-A3DTF:1:1105:4891:20717:1	ATAAGAACGAGCGTAAT	1008891	1949
M00328:4:000000000-A3DTF:1:2102:21053:17403:1	AGGTAATGTGGGTGGG	3311211	6223
M00328:4:000000000-A3DTF:1:2102:13139:22215:1	CTCCGGATGTTTGAGCT	3358555	6305
M00328:4:000000000-A3DTF:1:2103:9506:19535:1	CTCTCCCCCTCTCGCT	3533373	6602
M00328:4:000000000-A3DTF:1:2104:20547:19636:1	CTTTCAGCACTTGTAATA	3731573	6943
M00328:4:000000000-A3DTF:1:1107:10158:9731:1	GAGAGAGAGAGAGAGA	1300658	2466
M00328:4:000000000-A3DTF:1:2101:19481:12050:1	GTCCCCGTACTGCGACA	3039188	5701
M00328:4:000000000-A3DTF:1:2106:21703:20229:1	GCAGTTGAGCCGTCTAG	4133603	7708
M00328:4:000000000-A3DTF:1:2107:11677:16833:1	GTGTATCATTGAGCCCG	4294075	8040
M00328:4:000000000-A3DTF:1:2109:17784:4530:1	CGGTGAGATAGGGACA	4578287	8525
M00328:4:000000000-A3DTF:1:2112:16527:13746:1	GAGAGAGAAAGAGAGC	5248688	9691
M00328:4:000000000-A3DTF:1:2113:16740:8057:1	AGAGAGGAGACAATGA	5392397	9930
M00328:4:000000000-A3DTF:1:1101:18822:8144:1	CCATTATTGTTGTAGACC	29450	47
M00328:4:000000000-A3DTF:1:2101:9219:18078:1	GTTTTTGTGATGTTATTA	3108661	5832

M00328:4:000000000-A3DTF:1:2107:11158:10266:1	GAATACCGGTGTGGACC	4222796	7873
M00328:4:000000000-A3DTF:1:2111:4958:10118:1	CCCCTGACACGACTTCA1	5009802	9295
M00328:4:000000000-A3DTF:1:1101:12529:9092:1	GCATGCAGTTTGTTC	38760	59
M00328:4:000000000-A3DTF:1:1104:16702:13431:1	GGTCACAGCTGCAGCCA	722255	1437
M00328:4:000000000-A3DTF:1:1111:12949:14409:1	GGGTAAGCGAGACGAC	2186415	4134
M00328:4:000000000-A3DTF:1:2102:16614:18572:1	GACTGAGAGGGGTGAA	3323848	6238
M00328:4:000000000-A3DTF:1:2114:17981:20138:1	CTATAAACACGATGATA	5720895	10541
M00328:4:000000000-A3DTF:1:1104:17725:5210:1	GCCGAGCGGCCTTCGTG	649876	1316
M00328:4:000000000-A3DTF:1:1104:10288:12875:1	TATATGAACTGAGCGAA	716247	1424
M00328:4:000000000-A3DTF:1:1104:9294:14688:1	TGTGCACTCTGAAGGCC	736185	1456
M00328:4:000000000-A3DTF:1:1110:13226:20915:1	GCCTCAATCTCTCATTCC	2050586	3896
M00328:4:000000000-A3DTF:1:1114:20112:14736:1	ATGTCACCGAGCCTGTG	2826335	5330
M00328:4:000000000-A3DTF:1:2105:14069:15260:1	GGTTATGTCACTGCGTTC	3884458	7221
M00328:4:000000000-A3DTF:1:2112:16337:14484:1	CTCCCATCTTCTCTACGT	5257187	9702
M00328:4:000000000-A3DTF:1:1104:19531:12118:1	TCCCAGGGCCACATCGA	708235	1409
M00328:4:000000000-A3DTF:1:1104:17380:12722:1	GGCAGTGGGTCCGCAG	714637	1420
M00328:4:000000000-A3DTF:1:1104:20111:14107:1	GTTAAAAGCAGATGACC	729749	1444
M00328:4:000000000-A3DTF:1:2103:13302:22795:1	GGCCAACTGACGTGTAC	3562991	6654
M00328:4:000000000-A3DTF:1:2107:14528:9713:1	GGCTCTAAGTGCCTAT	4217301	7862
M00328:4:000000000-A3DTF:1:2109:10237:26154:1	CCATTGATCGCTGCCAA	4775928	8875
M00328:4:000000000-A3DTF:1:2111:23034:17132:1	ATGGGCTGCAATCGAGC	5087069	9448
M00328:4:000000000-A3DTF:1:2112:17483:12955:1	GAATAGGCTCTTTAAC	5239968	9678
M00328:4:000000000-A3DTF:1:2114:20027:9059:1	CAGCATGGCCAGGCACC	5600859	10307
M00328:4:000000000-A3DTF:1:2114:15530:13336:1	TGGTAGGACTGCTGTTA	5644640	10402
M00328:4:000000000-A3DTF:1:1105:5453:23488:1	CTCCGTAACTGCTATCGC	1035549	1995
M00328:4:000000000-A3DTF:1:1110:11231:7607:1	CACTCTTCTCTCGTTG	1906810	3618
M00328:4:000000000-A3DTF:1:2102:14294:13483:1	GTTTTGTTGTCTAAAGC	3267629	6120
M00328:4:000000000-A3DTF:1:2104:8877:21026:1	TCGCTAGCCGGCGGCTG	3744691	6959
M00328:4:000000000-A3DTF:1:2105:10121:18791:1	GTTTATGCGTGCATGTG	3922865	7306
M00328:4:000000000-A3DTF:1:2113:12861:6190:1	CTCTTCTCCTGTCTGACT	5379361	9899
M00328:4:000000000-A3DTF:1:1101:10836:7487:1	TACATGGTGTGTGTGTC	23651	34
M00328:4:000000000-A3DTF:1:2104:26779:12761:1	ATCTAATTCGACCGCCG	3658604	6813
M00328:4:000000000-A3DTF:1:2107:9332:17215:1	GTCTTCATGTTTGACAAC	4298356	8047
M00328:4:000000000-A3DTF:1:2107:21634:18425:1	CTTCTCCGCCTCTCTCT	4311581	8071
M00328:4:000000000-A3DTF:1:1101:20453:12526:1	AACATGTGCATTGTGCA	75946	133
M00328:4:000000000-A3DTF:1:1114:6737:12095:1	AACCACGGCAGCAGGCA	2795869	5271
M00328:4:000000000-A3DTF:1:2106:21369:11957:1	GCTCTCTCTTCCCTCTG	4046390	7553
M00328:4:000000000-A3DTF:1:1101:5856:16394:1	CAGTTAGTGCATATCTA	122077	251
M00328:4:000000000-A3DTF:1:1107:9332:7855:1	CCTCAGTACAGCCTGGA	1283831	2436
M00328:4:000000000-A3DTF:1:1108:17748:18853:1	TGTGGAGGCAGCTCAA	1613241	3085
M00328:4:000000000-A3DTF:1:2102:13922:4037:1	GTTCAAAGTTTGTACA	3181718	5946
M00328:4:000000000-A3DTF:1:2104:9364:9338:1	GCGGATGCCGAGCCCCA	3623298	6761
M00328:4:000000000-A3DTF:1:2113:18142:8067:1	CGCATACGAAGCGCAAT	5392479	9931
M00328:4:000000000-A3DTF:1:1106:8788:10564:1	AGTATGAGCAGTTTCAT	1106131	2128
M00328:4:000000000-A3DTF:1:1109:10845:21063:1	TTATATGCCCTGTCCATG	1845029	3515
M00328:4:000000000-A3DTF:1:2111:22636:22468:1	GAGAGAGAGAGAGAGA	5143490	9552
M00328:4:000000000-A3DTF:1:2112:6752:25496:1	GTGCTTGAATGGGCTCA	5369794	9881

M00328:4:000000000-A3DTF:1:2113:15559:10661:1	CACAAGGAGGCCCTTCC	5416642	9972
M00328:4:000000000-A3DTF:1:2113:19595:25787:1	GCCCAAACGCCGGTAA	5571798	10270
M00328:4:000000000-A3DTF:1:1111:10377:18907:1	AATACATGTCTAACGTTG	2241547	4245
M00328:4:000000000-A3DTF:1:2104:6768:17545:1	GTTGGACATCCCTTGACG	3710303	6907
M00328:4:000000000-A3DTF:1:2110:20575:16954:1	CGTATGAACTATTATTAC	4885864	9074
M00328:4:000000000-A3DTF:1:2111:20168:11081:1	TACATGCACAAGCAAAC	5019697	9312
M00328:4:000000000-A3DTF:1:2111:22198:11604:1	CTCTCTGTCTCAAGTTGC	5025023	9322
M00328:4:000000000-A3DTF:1:2108:10107:19651:1	AGTGAGCAGCTGGATTG	4523573	8430
M00328:4:000000000-A3DTF:1:2109:13643:11008:1	GAGTGAAGGGAGGGA	4627637	8617
M00328:4:000000000-A3DTF:1:2114:16731:22204:1	GACCTCGCCCGCGATG	5742096	10586
M00328:4:000000000-A3DTF:1:1103:3448:17677:1	TGCCAATTCCATTCTGT	563452	1128
M00328:4:000000000-A3DTF:1:2105:6134:12366:1	GTTGCATATCATGCACCT	3852698	7150
M00328:4:000000000-A3DTF:1:2105:19250:25364:1	GACAGAGGCAGCAACA	3978623	7420
M00328:4:000000000-A3DTF:1:2108:21990:17574:1	ATACGAGTCTGCAAGCC	4501422	8398
M00328:4:000000000-A3DTF:1:2110:15022:21648:1	AAGGAGGTGCGCCTGCT	4934915	9157
M00328:4:000000000-A3DTF:1:2112:18537:13130:1	GAGTAAACGCATGGTGT	5241861	9681
M00328:4:000000000-A3DTF:1:1103:3737:16448:1	ACAAACATGCAGGTACG	550010	1095
M00328:4:000000000-A3DTF:1:1105:8476:25500:1	CTTCTAAGGCGCCTGGA	1051535	2029
M00328:4:000000000-A3DTF:1:1112:12932:20290:1	GCCCAGTGATGAAAAAA	2469228	4646
M00328:4:000000000-A3DTF:1:2112:15818:15996:1	GCAGTGACCCGGTTTCT	5274492	9732
M00328:4:000000000-A3DTF:1:1101:8057:23066:1	CTGTGGAGTGATAGCTT	195972	410
M00328:4:000000000-A3DTF:1:2106:14371:11450:1	GTATTTCGTGCATGTGTG	4041343	7542
M00328:4:000000000-A3DTF:1:2101:8426:18186:1	GAGTACCTACCGTCCGA	3109873	5834
M00328:4:000000000-A3DTF:1:1102:4107:14648:1	GGTAATACCTGTACGTC	320590	646
M00328:4:000000000-A3DTF:1:1105:4180:11748:1	GTGGTGTTCGAATGGA	910228	1747
M00328:4:000000000-A3DTF:1:1105:24090:12234:1	GTCTGTGTGCCCATCAG	915306	1759
M00328:4:000000000-A3DTF:1:1109:15913:25792:1	GCCGGATGCTCGGCAGC	1888474	3582
M00328:4:000000000-A3DTF:1:1114:23566:12958:1	GCGGTATATAATTGATT	2805383	5285
M00328:4:000000000-A3DTF:1:2107:22097:21998:1	GGGATACGCTAAGCTAT	4347295	8135
M00328:4:000000000-A3DTF:1:2114:10251:9920:1	GTTCTAGGCGCTCTACA	5609071	10322
M00328:4:000000000-A3DTF:1:1106:23124:9763:1	CTTGTAAGTGGCTTGCCG	1098248	2113
M00328:4:000000000-A3DTF:1:1106:19108:22020:1	CCTCCCTCCCGTCTTTC	1228415	2341
M00328:4:000000000-A3DTF:1:2108:10425:14267:1	GTGTAAGGCGACCATC	4464827	8336
M00328:4:000000000-A3DTF:1:1101:3524:16056:1	GCTGTATCAAACCTTCC	118051	239
M00328:4:000000000-A3DTF:1:1112:16777:21805:1	CCCACGTGTTCTCTCAG	2486210	4681
M00328:4:000000000-A3DTF:1:1113:12526:17930:1	CTATGGAAGAGCCCACT	2652954	4996
M00328:4:000000000-A3DTF:1:2101:12339:18957:1	AGTGAGACCTGGAGACA	3118256	5857
M00328:4:000000000-A3DTF:1:2104:21355:20695:1	CCGATTATGGCACCAAG	3741656	6956
M00328:4:000000000-A3DTF:1:2107:23133:15982:1	GCTGTCTAGCTCGGTAT	4284540	8017
M00328:4:000000000-A3DTF:1:2108:14776:13518:1	ATAGTATACTGCTCACAC	4456732	8318
M00328:4:000000000-A3DTF:1:2111:22050:21144:1	GCCGCTGGCTGTTTCGT	5130282	9536
M00328:4:000000000-A3DTF:1:1107:3951:9077:1	GTCCGAGGCACTTCATA	1294421	2459
M00328:4:000000000-A3DTF:1:2101:4021:8617:1	CGTCCAGCCTGCTCATGC	3001385	5648
M00328:4:000000000-A3DTF:1:2102:16510:6813:1	GCCTCCTGCAGGCTAGC	3199191	5989
M00328:4:000000000-A3DTF:1:2102:12862:18980:1	ACAATAACCAACATAGT	3328053	6248
M00328:4:000000000-A3DTF:1:1106:13038:19112:1	GATATGCGGATAACTGA	1198925	2296
M00328:4:000000000-A3DTF:1:1113:19931:18736:1	GCTGCCGTTGCTCCAAG	2662834	5013

M00328:4:000000000-A3DTF:1:2101:10853:19839:1	GACTTCCTCTCTGTCTCT	3127383	5867
M00328:4:000000000-A3DTF:1:1111:5085:18805:1	AGCCAAGCACGCGCACA	2240342	4243
M00328:4:000000000-A3DTF:1:2102:10991:24397:1	CGCACACACACTTGCATC	3375283	6332
M00328:4:000000000-A3DTF:1:2112:21492:19624:1	CAGCAGGACATGCAGAC	5315351	9791
M00328:4:000000000-A3DTF:1:2113:21110:11137:1	TCGTGAGCATGTCCCTA/	5421452	9984
M00328:4:000000000-A3DTF:1:1102:18419:5300:1	GTCTTCGACATAGAAGT	231655	478
M00328:4:000000000-A3DTF:1:1106:7362:22431:1	TCTCATTTCAGTACACTC	1232457	2346
M00328:4:000000000-A3DTF:1:2101:11858:23359:1	CACACACTCAGTAAGCTC	3160804	5925
M00328:4:000000000-A3DTF:1:1103:19209:9376:1	GTTCACTGCAATGTGCTC	474415	943
M00328:4:000000000-A3DTF:1:1108:19718:17150:1	CCGTCACCCGAGCACCG	1593274	3034
M00328:4:000000000-A3DTF:1:1109:14038:22214:1	GCATCATCCTGGGCATC/	1856870	3533
M00328:4:000000000-A3DTF:1:1113:12699:6362:1	CTCTTGCACTAGCTCCTC	2536293	4774
M00328:4:000000000-A3DTF:1:1113:3909:19518:1	GGGTTGCAGTTGCTGT	2672375	5035
M00328:4:000000000-A3DTF:1:2102:15815:16853:1	TTGCTCGATTACTCCCCT	3305203	6212
M00328:4:000000000-A3DTF:1:2103:8993:17989:1	CATGCGCACTACAACC/	3517847	6573
M00328:4:000000000-A3DTF:1:2104:8877:21026:1	TCGCTAGCCGGCGGCTG	3744691	6960
M00328:4:000000000-A3DTF:1:2109:9751:21981:1	CGTCTGTTCAATCGGGT	4744684	8838
M00328:4:000000000-A3DTF:1:1102:8452:6729:1	CCACAAGACTATAAATA	240587	493
M00328:4:000000000-A3DTF:1:1108:16872:6638:1	CAAGTAAATGTGTGTGT	1486259	2824
M00328:4:000000000-A3DTF:1:1114:13552:8780:1	ATGTGTGAGTGCTCGCT	2764007	5217
M00328:4:000000000-A3DTF:1:2101:14972:19765:1	CCCTATATGCATCCGCGC	3126608	5864
M00328:4:000000000-A3DTF:1:2103:19936:17422:1	CAGCAGAGGAAGGAAG	3511943	6560
M00328:4:000000000-A3DTF:1:2114:21801:13999:1	GCTTACGGCTGTGAGAA	5651936	10408
M00328:4:000000000-A3DTF:1:1110:17435:18589:1	GCCCTGGAGGAGAGTA/	2023645	3843
M00328:4:000000000-A3DTF:1:1112:18812:22024:1	GCCCCAGGCTTTGCCTG/	2488722	4688
M00328:4:000000000-A3DTF:1:1112:11815:23881:1	CATGTAGACAGGCACTG	2508370	4727
M00328:4:000000000-A3DTF:1:1113:5165:18583:1	GTTCTCTGAGGCTGCTG	2660960	5010
M00328:4:000000000-A3DTF:1:2107:15763:10866:1	GTCATATACAGCCGAAA	4229096	7892
M00328:4:000000000-A3DTF:1:2112:16407:21538:1	GCTCAATATGGAGCAAA	5335027	9827
M00328:4:000000000-A3DTF:1:1101:8932:25422:1	ATGAGAACTAACGCAAG	215080	448
M00328:4:000000000-A3DTF:1:1111:4290:16932:1	GACAAGAACAGTGTGCC	2217260	4200
M00328:4:000000000-A3DTF:1:1112:10297:8003:1	GTCTTACACAGCGAGAG	2334031	4409
M00328:4:000000000-A3DTF:1:1112:3995:21868:1	ATGTAGGTGAGAGCAG/	2486965	4684
M00328:4:000000000-A3DTF:1:2101:14631:13843:1	GCAGGAAACCAGGCTGC	3059916	5736
M00328:4:000000000-A3DTF:1:1102:10138:8550:1	GTTTACGCTGCTGTTGG	256045	520
M00328:4:000000000-A3DTF:1:1102:4641:15033:1	TACGAGTAGTCCCTGTC/	324952	655
M00328:4:000000000-A3DTF:1:1113:22965:12198:1	GCCCAAAGGCCATCGCA	2584073	4872
M00328:4:000000000-A3DTF:1:1113:15676:27499:1	GCGCAGCAAGGGGCCG	2746501	5183
M00328:4:000000000-A3DTF:1:2105:15573:10521:1	TTTCTAATGAGGTAAATC	3833268	7121
M00328:4:000000000-A3DTF:1:1101:15992:12069:1	CAGCAGCCTTCGGCAGC	70594	123
M00328:4:000000000-A3DTF:1:1105:13645:9569:1	GCCTAGCAGCTGGCTTT	888111	1714
M00328:4:000000000-A3DTF:1:1106:7199:22759:1	ATATTAATCTAGAGCGA/	1235679	2353
M00328:4:000000000-A3DTF:1:1107:6982:23800:1	CACACACACACACAC/	1455818	2774
M00328:4:000000000-A3DTF:1:1110:14545:18550:1	TAAGTATAGATACCCG	2023198	3841
M00328:4:000000000-A3DTF:1:2103:9228:9616:1	TGCATGCACCATCTCTTA	3428337	6402
M00328:4:000000000-A3DTF:1:2114:8813:15553:1	TGCAGAACCCGATCATG	5669296	10439
M00328:4:000000000-A3DTF:1:1107:7160:25187:1	CTCTCTCTCTCTCTCTC	1467603	2800

M00328:4:000000000-A3DTF:1:1108:20892:12147:1	GCCCTAAACCGGTCGGT	1535281	2906
M00328:4:000000000-A3DTF:1:2105:10438:15635:1	CATGTGCACGTCACTGC	3888588	7228
M00328:4:000000000-A3DTF:1:2107:8407:10707:1	GCCCTATGTTGCTGACCC	4227467	7889
M00328:4:000000000-A3DTF:1:2113:4641:13554:1	ATACGTACGCAATGCGG	5447296	10036
M00328:4:000000000-A3DTF:1:1104:16384:19323:1	CCTCAGGGCATAACCAGG	786957	1547
M00328:4:000000000-A3DTF:1:1105:3817:9879:1	GCTTAGTTCTATGTGAAC	891224	1719
M00328:4:000000000-A3DTF:1:1108:13723:24754:1	ATCTCGAACTAGGCGCT	1673869	3200
M00328:4:000000000-A3DTF:1:1101:21976:19402:1	CCAATATAATTAGCCAGC	157206	322
M00328:4:000000000-A3DTF:1:1105:15116:13180:1	GTAACATCTTCTCCCTT	925770	1780
M00328:4:000000000-A3DTF:1:1114:23968:16330:1	GCATGGTCACTCGATGC	2845944	5380
M00328:4:000000000-A3DTF:1:2109:14319:9841:1	ATGCCTTACTGGCTGGG	4615812	8600
M00328:4:000000000-A3DTF:1:2110:12097:25296:1	GAGAGAGAGAGAGAGT	4965145	9218
M00328:4:000000000-A3DTF:1:2111:20588:9884:1	CTCTGTCTCTCTCTCTC	5007416	9290
M00328:4:000000000-A3DTF:1:2111:8280:18759:1	AGCCAGAGGAACAGGT/	5104806	9482
M00328:4:000000000-A3DTF:1:2114:20453:19415:1	GGCTCTCAGCGTCTGGC	5712917	10526
M00328:4:000000000-A3DTF:1:1102:11117:16469:1	GATAGAGGCAGACTGAC	341182	686
M00328:4:000000000-A3DTF:1:1103:13604:15526:1	CAGCATAACCATGCCAG	539708	1075
M00328:4:000000000-A3DTF:1:1105:6727:13179:1	ATCTAGGATACTACTAG	925755	1779
M00328:4:000000000-A3DTF:1:1105:21923:18790:1	ATGTCGTCCTGAGAAAG	988382	1899
M00328:4:000000000-A3DTF:1:1112:4400:14658:1	CGTGTGTATACACGAGC	2400913	4530
M00328:4:000000000-A3DTF:1:2104:8380:11715:1	CTCTTTAATGTTCTGCT	3647483	6796
M00328:4:000000000-A3DTF:1:2106:15107:22585:1	AGCGCAAGTCGCAGTGC	4155177	7754
M00328:4:000000000-A3DTF:1:2110:7378:18448:1	ACTTATGGCCGCGAGTG	4902059	9100
M00328:4:000000000-A3DTF:1:1103:16097:23453:1	GTCTTAATGTTATTCTCT	620934	1271
M00328:4:000000000-A3DTF:1:1106:22340:11362:1	CGTACACACACACACAT	1114086	2142
M00328:4:000000000-A3DTF:1:1106:10506:23537:1	GTGCATGCACATGCACA	1242830	2370
M00328:4:000000000-A3DTF:1:1111:11560:17371:1	GTACATGTGTGCTTGAA	2222770	4210
M00328:4:000000000-A3DTF:1:1112:9890:14472:1	CCTTCACCCTAGCTGAAC	2398714	4527
M00328:4:000000000-A3DTF:1:1113:6263:22072:1	CTCTCGCCCCGTCTGTCA	2702069	5089
M00328:4:000000000-A3DTF:1:1114:26174:23537:1	GTCAGACTATTCACTT	2930114	5548
M00328:4:000000000-A3DTF:1:2101:12078:23139:1	CACATACAGTATACAAG	3158951	5922
M00328:4:000000000-A3DTF:1:2105:14718:13290:1	GTATTACTTCTGCACGTC	3862778	7179
M00328:4:000000000-A3DTF:1:2105:14052:25494:1	GGTCGAGACAGTCCCGA	3979305	7421
M00328:4:000000000-A3DTF:1:2110:15991:24666:1	GACAGAGACCGGGTCA	4961106	9201
M00328:4:000000000-A3DTF:1:2111:9745:16008:1	GCAGACAATAATGCAGA	5074369	9429
M00328:4:000000000-A3DTF:1:2113:19774:20596:1	ACCATGCATGCCTCAGC	5525953	10180
M00328:4:000000000-A3DTF:1:2114:6806:16069:1	TGCTCCACCCGCACTTCA	5675196	10449
M00328:4:000000000-A3DTF:1:1105:11704:21387:1	CCCCACGTGCTGCATAT	1015537	1966
M00328:4:000000000-A3DTF:1:1111:22681:13722:1	GGATTGGCAGCGTTGAC	2178194	4114
M00328:4:000000000-A3DTF:1:1111:22836:22376:1	ATGCAGGGCTTGAATCC	2281421	4312
M00328:4:000000000-A3DTF:1:1111:16132:25604:1	GGCTAACCCCTGAGCTAG	2312165	4366
M00328:4:000000000-A3DTF:1:2102:12405:22675:1	GCCTAGGATAAGCTGCC	3362535	6315
M00328:4:000000000-A3DTF:1:2105:20229:9789:1	GTGTATGGTGTGTGTGT	3825794	7098
M00328:4:000000000-A3DTF:1:2110:7488:19127:1	GAGTTTATCTGTCTCTC	4909362	9120
M00328:4:000000000-A3DTF:1:2113:17298:8911:1	CCCCCCCCCGCAGGG	5399824	9944
M00328:4:000000000-A3DTF:1:2113:10494:14462:1	GAGGGAGACAATGACA	5457460	10050
M00328:4:000000000-A3DTF:1:2113:17349:25163:1	TGCTAGGGCTTCTGGTG	5567678	10264

M00328:4:000000000-A3DTF:1:2102:3865:10366:1	GTCGTAGCATCCTAAAAA	3233691	6054
M00328:4:000000000-A3DTF:1:2103:12915:7906:1	CCCTCGTCCTCACGTACA	3411692	6375
M00328:4:000000000-A3DTF:1:2108:22665:19828:1	CTGCACGCGTTCCATGAC	4525442	8432
M00328:4:000000000-A3DTF:1:2107:19047:21533:1	ACACTAACTAAAGCAGA	4342777	8127
M00328:4:000000000-A3DTF:1:1104:17822:23265:1	GGGTAACCTCGAGGGGTC	825310	1613
M00328:4:000000000-A3DTF:1:2104:13140:5347:1	AGCATGGGTTGTGCGATA	3590296	6701
M00328:4:000000000-A3DTF:1:1108:12142:25768:1	CTACTGTAGTGTGCCCA	1681464	3213
M00328:4:000000000-A3DTF:1:2108:14316:4124:1	CCATTACGACTGCCTACT	4377981	8187
M00328:4:000000000-A3DTF:1:2111:13221:9264:1	GTGTCTCCCTCCGCTGTC	5001305	9275
M00328:4:000000000-A3DTF:1:1110:15337:23445:1	CTCTCTCTCTCTCTCAT	2077666	3948
M00328:4:000000000-A3DTF:1:2109:24096:16590:1	TTCTTTACCTTTACCTTTA	4688411	8713
M00328:4:000000000-A3DTF:1:2111:16353:10380:1	GGTTAGGTCTGCCTATG	5012498	9298
M00328:4:000000000-A3DTF:1:1110:14961:22115:1	AGCCTGCTCCAGGCTAC	2063821	3918
M00328:4:000000000-A3DTF:1:2110:13493:18699:1	ACATAGCAGGCAACATC	4904790	9110
M00328:4:000000000-A3DTF:1:2112:20587:19071:1	CAGCCAGACAGAGAGAC	5309257	9784
M00328:4:000000000-A3DTF:1:1102:15774:22483:1	GAAACAGATAGATAGAT	404482	832
M00328:4:000000000-A3DTF:1:1105:3118:17759:1	CTCTGATGATTCAATGTA	976942	1879
M00328:4:000000000-A3DTF:1:1108:15066:13405:1	CTGCAGCATAAAATGTG	1549477	2939
M00328:4:000000000-A3DTF:1:1112:11858:21989:1	CTACCGGAACGCTTAAAI	2488327	4686
M00328:4:000000000-A3DTF:1:1102:19861:6641:1	GCCCCGCGACGGTCATGG	239914	491
M00328:4:000000000-A3DTF:1:1109:9753:8094:1	CATATATATATATATATT	1706962	3251
M00328:4:000000000-A3DTF:1:1109:14024:12366:1	GAGAGAGAGAGAGAGA	1747492	3307
M00328:4:000000000-A3DTF:1:1111:14853:18017:1	GTCTTGCGGTGATCTGG	2230708	4229
M00328:4:000000000-A3DTF:1:1112:3901:17622:1	ACCGTAACCTCCACCTCA	2436811	4580
M00328:4:000000000-A3DTF:1:1113:12774:10704:1	ATATAAAACCGGTGACTI	2568814	4838
M00328:4:000000000-A3DTF:1:1114:21530:12567:1	TTGTTGTTGTTGTTGTTG	2801115	5279
M00328:4:000000000-A3DTF:1:2104:7762:24072:1	GTGCCTAGAGAGCAGTT	3769527	7008
M00328:4:000000000-A3DTF:1:2106:21080:9130:1	AGCACATTCTTGTGCTTC	4018100	7494
M00328:4:000000000-A3DTF:1:2113:4060:15599:1	GATAAAGGTAGAGGTAC	5470543	10079
M00328:4:000000000-A3DTF:1:1102:12719:8250:1	AATCTAGGGACTGTGAG	253303	507
M00328:4:000000000-A3DTF:1:2108:16825:13864:1	CACATACGCTATATGGTC	4460437	8327
M00328:4:000000000-A3DTF:1:2113:10282:10734:1	GCCTACTCTGGCATCTCT	5417390	9974
M00328:4:000000000-A3DTF:1:1105:20654:17053:1	CCCGGTATGATGTTCGTI	969047	1861
M00328:4:000000000-A3DTF:1:1109:19444:12311:1	AAATAGTTACCCATCCGC	1746912	3304
M00328:4:000000000-A3DTF:1:2103:11834:18448:1	CTACACGACCTAGTCTGC	3522498	6581
M00328:4:000000000-A3DTF:1:2112:12894:16611:1	CAGTGGCGCCGCTCACA	5281423	9745
M00328:4:000000000-A3DTF:1:1104:23847:12188:1	GAAGGATATTGTTGACG	708948	1411
M00328:4:000000000-A3DTF:1:2106:15941:19502:1	ACTTCCAAGTCAACCTT	4126310	7699
M00328:4:000000000-A3DTF:1:2108:7572:21553:1	CCACAGCCGTTTGTGCG	4542238	8469
M00328:4:000000000-A3DTF:1:1106:10238:24545:1	CTGCGAGTGCATATCGA	1251331	2383
M00328:4:000000000-A3DTF:1:1108:9704:22084:1	GGCCAGAAGCAAGCATC	1649051	3152
M00328:4:000000000-A3DTF:1:1110:13223:8486:1	CCGTTATCCCCAGCGGG	1913460	3633
M00328:4:000000000-A3DTF:1:1110:12489:21814:1	CTTTAAAAGCAGTTCCT	2060377	3908
M00328:4:000000000-A3DTF:1:1114:21448:17123:1	TGCATTGTGTTGCGTCAI	2855686	5406
M00328:4:000000000-A3DTF:1:2102:5297:18778:1	CTCCCTGTTTGTGTGCTC	3325969	6246
M00328:4:000000000-A3DTF:1:2106:18056:8037:1	GCTATCGTCCGGCCACTC	4007944	7469
M00328:4:000000000-A3DTF:1:1111:19076:17838:1	GCTTCCCGAGACGCGTTI	2228361	4221

M00328:4:000000000-A3DTF:1:2114:9567:9121:1	CTCCAGGTATGCACCGA	5601467	10311
M00328:4:000000000-A3DTF:1:1105:4707:11992:1	GTGCAGCAAACAGTACC	912724	1750
M00328:4:000000000-A3DTF:1:1106:13921:5873:1	GCTTGTGTCTCTCCACGT	1067562	2055
M00328:4:000000000-A3DTF:1:1110:8112:8272:1	CTCCTGAGATGGGCCGC	1911700	3630
M00328:4:000000000-A3DTF:1:1114:16791:25230:1	CTCTGAAATAGTGCTAG	2945860	5576
M00328:4:000000000-A3DTF:1:2104:20718:19898:1	GGTATATATATATATA	3734076	6947
M00328:4:000000000-A3DTF:1:2106:25310:13981:1	TGCATACCGTTTAGCTTT	4068193	7602
M00328:4:000000000-A3DTF:1:1105:13244:26087:1	GAATAGTACAAGTCAGA	1055114	2041
M00328:4:000000000-A3DTF:1:1108:11433:10611:1	GATCTGATACCGACAAA	1519350	2871
M00328:4:000000000-A3DTF:1:2102:21324:13218:1	CTGACTGCCTGTCCGCTT	3264599	6113
M00328:4:000000000-A3DTF:1:1101:15405:13042:1	CATCAGCATAGTGAACC	82044	155
M00328:4:000000000-A3DTF:1:1111:13933:5847:1	TCTCCTCTCTCTCCCC	2108422	3999
M00328:4:000000000-A3DTF:1:1111:9229:9872:1	GTGTGTGTGTGTGCGTG	2137006	4044
M00328:4:000000000-A3DTF:1:1114:4379:15968:1	TCTTTATATTTCTTTGATT	2841319	5366
M00328:4:000000000-A3DTF:1:1108:21495:17695:1	TGGCAAACGAAATGTGT	1599611	3057
M00328:4:000000000-A3DTF:1:1111:6221:8576:1	ATCTTGAGGTGCATCAT	2125142	4022
M00328:4:000000000-A3DTF:1:1113:7620:16937:1	GAGAGAGAGAGAGAGA	2640624	4974
M00328:4:000000000-A3DTF:1:2103:9489:15729:1	GCCTAATACAGTGCTTA	3493697	6525
M00328:4:000000000-A3DTF:1:2107:11283:20999:1	AAGCATGACTGCATCTT	4337856	8121
M00328:4:000000000-A3DTF:1:2114:15489:11606:1	CCTGTATACAGAGCAAC	5626060	10358
M00328:4:000000000-A3DTF:1:1101:23335:9232:1	GTGCAAAGACGATGAGC	40132	61
M00328:4:000000000-A3DTF:1:1103:20797:11008:1	CGCGTTGCCTTACTGAA	490403	968
M00328:4:000000000-A3DTF:1:2110:8135:8029:1	GTCCCTGTGCCCTAAA	4795043	8906
M00328:4:000000000-A3DTF:1:1105:4499:21034:1	CAGGAGGTTGAAGCTGC	1012118	1960
M00328:4:000000000-A3DTF:1:1105:24822:23211:1	CTAGTAACCTCTCAAAA	1033171	1990
M00328:4:000000000-A3DTF:1:2114:19635:12008:1	GGTCCATTTAGCGCCAC	5630370	10377
M00328:4:000000000-A3DTF:1:1102:26643:16078:1	TCTCTGGATTGCTCGCCC	336753	677
M00328:4:000000000-A3DTF:1:1104:16892:20840:1	ATACTTAAGTGATACAT	802693	1581
M00328:4:000000000-A3DTF:1:1108:11050:11797:1	GATAAGTGGCCTTCCTT	1531646	2892
M00328:4:000000000-A3DTF:1:1112:25217:19493:1	GTGCTAGGTTCCACAC	2459644	4628
M00328:4:000000000-A3DTF:1:2112:3079:15734:1	CTCTCTCTTTCTCTCTT	5271356	9728
M00328:4:000000000-A3DTF:1:2113:13043:16342:1	GGCTACAGCAGTTCACT	5478879	10091
M00328:4:000000000-A3DTF:1:1101:11257:27547:1	AACTAGGCCCGTTGAG	222793	461
M00328:4:000000000-A3DTF:1:1105:24552:15406:1	GTGATGCTACGAGCAAC	950738	1821
M00328:4:000000000-A3DTF:1:2109:22311:8427:1	CCGTTGCTGCGCTGGCT	4602482	8566
M00328:4:000000000-A3DTF:1:2113:16410:11984:1	CTTTCAGCACTTGTAAC	5430329	9997
M00328:4:000000000-A3DTF:1:1103:3635:16404:1	TTCCAGGGCCTTCTGTTC	549536	1093
M00328:4:000000000-A3DTF:1:2113:7194:8256:1	GTGTGTGTGTGTGTGTG	5394069	9934
M00328:4:000000000-A3DTF:1:1104:20265:12068:1	CTCACTTACTCTCGGT	707741	1406
M00328:4:000000000-A3DTF:1:1112:17833:19428:1	GTGCCTGTAGTACTTAG	2458846	4625
M00328:4:000000000-A3DTF:1:1114:2761:16386:1	GGGTGTAGGACAGGCA	2846616	5385
M00328:4:000000000-A3DTF:1:2101:22641:16233:1	TCCCACCATAGATTGGA	3087800	5792
M00328:4:000000000-A3DTF:1:1106:20334:7502:1	CTCCCTGGTTTGACTGTC	1078260	2071
M00328:4:000000000-A3DTF:1:1106:16641:26409:1	GCTCAGGTTGCGCACAGA	1263488	2403
M00328:4:000000000-A3DTF:1:1114:6737:12095:1	AACCACGGCAGCAGGCA	2795869	5270
M00328:4:000000000-A3DTF:1:1101:9046:16247:1	CTCTCTCTCTGCTCTCT	120363	244
M00328:4:000000000-A3DTF:1:1114:21172:22955:1	GGACAGACCTGTGCGTG	2924019	5536

M00328:4:000000000-A3DTF:1:2104:6882:8816:1	AGCATACACAGATTCAC	3618203	6748
M00328:4:000000000-A3DTF:1:2114:14769:16898:1	TACGCATACAGAACTAA	5684686	10469
M00328:4:000000000-A3DTF:1:2114:20552:23204:1	GATATCAGTTAGCGTAC	5751762	10611
M00328:4:000000000-A3DTF:1:1101:14147:23478:1	CATGCTCATCCATGCTGC	199681	417
M00328:4:000000000-A3DTF:1:1102:19882:22333:1	CACACACACACACACAC	403016	826
M00328:4:000000000-A3DTF:1:1109:4652:22530:1	CCTCCAATGTCTGCAAGC	1860072	3538
M00328:4:000000000-A3DTF:1:2101:4400:9109:1	GTTCTTGCATGTTGTGGC	3006483	5658
M00328:4:000000000-A3DTF:1:1103:3534:16043:1	GCACCACCTGTTCTTGT	545429	1085
M00328:4:000000000-A3DTF:1:1108:20822:13579:1	CATTTACAGTATATTTAA	1551409	2944
M00328:4:000000000-A3DTF:1:2114:13654:18630:1	GAGAGAGAGAGAGAGA	5704188	10514
M00328:4:000000000-A3DTF:1:2106:13560:23315:1	CTCCTCTCATGTAGCCAC	4161039	7765
M00328:4:000000000-A3DTF:1:2111:18528:19133:1	AGTATGGTTTATTGTGGC	5108866	9493
M00328:4:000000000-A3DTF:1:2113:14440:16883:1	ACCCTGCGCCAGGTTGG	5485051	10103
M00328:4:000000000-A3DTF:1:1103:17806:21673:1	GTACTAAGGGCACGTTA	604213	1229
M00328:4:000000000-A3DTF:1:2107:7751:10358:1	GGAGAGGAGAGGAGAG	4223796	7882
M00328:4:000000000-A3DTF:1:1103:6182:17971:1	CTCTCTCTCTCTCTCTC	566674	1132
M00328:4:000000000-A3DTF:1:1108:23016:16318:1	CTTATGGCCCCGTTTCG	1583416	3001
M00328:4:000000000-A3DTF:1:1111:14075:27418:1	CTCCAGGTGCTGACTTCC	2321062	4384
M00328:4:000000000-A3DTF:1:1113:16965:15580:1	GTCTCTGTGTCTCCGTGT	2623803	4943
M00328:4:000000000-A3DTF:1:2101:12339:18957:1	AGTGAGACCTGGAGACA	3118256	5856
M00328:4:000000000-A3DTF:1:2107:12706:10064:1	GATCTACACACAACCTCC	4220798	7868
M00328:4:000000000-A3DTF:1:2110:17715:21056:1	CCTCAATGGACTGTGCA	4929288	9141
M00328:4:000000000-A3DTF:1:2113:14428:10642:1	CTCTTATTTCCACAATG	5416449	9971
M00328:4:000000000-A3DTF:1:1101:7713:16499:1	CTACTCACTTCTCGTTA	123354	252
M00328:4:000000000-A3DTF:1:1110:8207:10791:1	CATCTGGGCAGGGGCAC	1934530	3676
M00328:4:000000000-A3DTF:1:1112:9255:25365:1	CTCTTAATATGTGCACGC	2521711	4750
M00328:4:000000000-A3DTF:1:2113:16590:17924:1	GAGCATATCCTATGGAA	5496856	10120
M00328:4:000000000-A3DTF:1:1102:14832:22388:1	ATGTAAATGTTCACAAA	403548	828
M00328:4:000000000-A3DTF:1:2102:18606:4231:1	CCGTTGAACCACGAAGC	3182499	5950
M00328:4:000000000-A3DTF:1:2108:8939:24820:1	TCTCTCACTAGGCACTC	4569588	8512
M00328:4:000000000-A3DTF:1:2114:21092:8294:1	CATATATGATGAGTGGA	5594005	10296
M00328:4:000000000-A3DTF:1:2114:23729:21266:1	CTCTCTCTCTCTTTTAC	5732595	10567
M00328:4:000000000-A3DTF:1:1101:16434:21098:1	GTGTGTGTGTGTGTGTG	175902	366
M00328:4:000000000-A3DTF:1:1104:16748:4139:1	GCCCAGGCATGACTACA	645744	1308
M00328:4:000000000-A3DTF:1:1106:3445:19528:1	GTATAAACGAATGGCGA	1203337	2304
M00328:4:000000000-A3DTF:1:1108:8727:13149:1	TTCCTAAACAGCCCAAT	1546473	2933
M00328:4:000000000-A3DTF:1:1108:10507:19117:1	CTTGCTGATGCTGCTGCC	1616368	3093
M00328:4:000000000-A3DTF:1:1109:13737:18020:1	GTTTATTGACAAGCGGT	1811317	3453
M00328:4:000000000-A3DTF:1:1111:10898:18863:1	CTATAAATGTCACTTCCA	2241024	4244
M00328:4:000000000-A3DTF:1:2108:10255:18523:1	GTATGGGGCTTAATGGT	4511612	8407
M00328:4:000000000-A3DTF:1:2109:24729:9883:1	CACGCGGACACAGTCGC	4616197	8601
M00328:4:000000000-A3DTF:1:2112:22448:11241:1	GAGGAACAGAAACAGA	5221479	9645
M00328:4:000000000-A3DTF:1:1105:17013:15610:1	GAGCTACCTCAAGCCAT	953020	1828
M00328:4:000000000-A3DTF:1:1111:17784:20418:1	CCAGAGTTTCATAGGGC	2259493	4272
M00328:4:000000000-A3DTF:1:2111:5557:23061:1	GGTAACGAGAGAGCTAC	5149195	9561
M00328:4:000000000-A3DTF:1:2112:21569:22323:1	CCTGAGTGCCATGAGTT	5343185	9840
M00328:4:000000000-A3DTF:1:1102:15799:11069:1	GTCTCTGTCTCTCTGT	281023	573



M00328:4:000000000-A3DTF:1:1105:20029:14128:1	GTGGAGTGATTAGCCCT	936343	1798
M00328:4:000000000-A3DTF:1:1108:15295:12205:1	GAGAGAGAGAGAGAGA	1535931	2908
M00328:4:000000000-A3DTF:1:1109:10180:6110:1	AACATCAGAAATGGGCC	1693728	3230
M00328:4:000000000-A3DTF:1:2114:8567:15979:1	TCTTAGGTCAAGTTGCC	5674170	10448
M00328:4:000000000-A3DTF:1:2114:20981:18257:1	CCACGACGCTGCCACA	5700147	10504
M00328:4:000000000-A3DTF:1:2101:18355:11997:1	GCCCTTGCTACTTTAATG	3038628	5700
M00328:4:000000000-A3DTF:1:2109:22007:13445:1	GTTACGTGTCGTCTGTCC	4653437	8665
M00328:4:000000000-A3DTF:1:1101:6573:8089:1	GGAGAGAGAGGGAGTG	28952	44
M00328:4:000000000-A3DTF:1:1107:9332:7855:1	CCTCAGTACAGCCTGGA	1283831	2437
M00328:4:000000000-A3DTF:1:1111:22302:14949:1	CATCTCGGCATTGTTACC	2192955	4144
M00328:4:000000000-A3DTF:1:1111:12613:26364:1	CACACACACACACACA	2317304	4379
M00328:4:000000000-A3DTF:1:1112:18756:10531:1	GAGAGAGAGAGAGAGA	2356123	4431
M00328:4:000000000-A3DTF:1:2108:11424:16133:1	GGATACGACACGAACTC	4485517	8357
M00328:4:000000000-A3DTF:1:2110:18912:15131:1	AGCATGCATTTTCGTGGA	4866039	9041
M00328:4:000000000-A3DTF:1:2113:14119:10990:1	GAGTGGCTCTGTCGATT	5419937	9981
M00328:4:000000000-A3DTF:1:1102:17425:21940:1	CCATGGGACATTTTCGTCC	399271	815
M00328:4:000000000-A3DTF:1:2107:6482:21751:1	GAGAGAGAGAGAGATGA	4344900	8131
M00328:4:000000000-A3DTF:1:2110:5284:10828:1	GGGGAAAATAAGTGC	4821023	8956
M00328:4:000000000-A3DTF:1:1101:12000:22733:1	GTGTGTGTGTGTGTGTG	192741	403
M00328:4:000000000-A3DTF:1:1102:7325:12272:1	GTTTCAGTGTCATTCTCG	293897	598
M00328:4:000000000-A3DTF:1:1103:23187:10459:1	CTGTCCGTCTCCGTTTGT	484971	961
M00328:4:000000000-A3DTF:1:2104:12680:17647:1	GGCTGTTGTGCTTATAAC	3711332	6908
M00328:4:000000000-A3DTF:1:2106:18035:8267:1	ATTTAATGTAATTATTTT	4010011	7476
M00328:4:000000000-A3DTF:1:1105:12548:26009:1	CTTCTTACTTCTGCGC	1054730	2039
M00328:4:000000000-A3DTF:1:1113:17290:12744:1	GTGTAAGGCTGCCTCT	2590062	4889
M00328:4:000000000-A3DTF:1:2110:5468:12459:1	GAACAGCCAGGCAGCTC	4837366	8993
M00328:4:000000000-A3DTF:1:1101:9780:13320:1	GATCATTGCAGTGCGAA	85451	166
M00328:4:000000000-A3DTF:1:1111:11215:10270:1	GCATTAGGCAAACTGG	2140844	4048
M00328:4:000000000-A3DTF:1:2101:17034:17150:1	GAGTAGACCGTGCTAGA	3098363	5814
M00328:4:000000000-A3DTF:1:2102:17592:9452:1	CAACAGTGCTGCTTACTA	3224178	6033
M00328:4:000000000-A3DTF:1:2110:5609:17179:1	AGGGTGCTCTCAAATTC	4888412	9078
M00328:4:000000000-A3DTF:1:2113:20339:12286:1	TAATGCAACCATGCAGA	5433560	10001
M00328:4:000000000-A3DTF:1:2114:11205:10389:1	CATCCACACGTGCCTAGC	5613748	10335
M00328:4:000000000-A3DTF:1:1108:16224:14963:1	TTTACCAGTATGTCTTA	1567355	2972
M00328:4:000000000-A3DTF:1:2111:13084:17155:1	GCATCTTCCAGCGTCGC	5087343	9449
M00328:4:000000000-A3DTF:1:1102:12953:19851:1	CGTTGATACCAATACGTA	378419	764
M00328:4:000000000-A3DTF:1:1112:5276:12806:1	GGACATCATGTGGTGAT	2379639	4483
M00328:4:000000000-A3DTF:1:2114:8991:10363:1	CGTATATCTGTTTCTCTT	5613505	10334
M00328:4:000000000-A3DTF:1:1102:10771:4808:1	TATCCAAGCCACGGTTAT	229387	472
M00328:4:000000000-A3DTF:1:1109:10180:6110:1	AACATCAGAAATGGGCC	1693728	3229
M00328:4:000000000-A3DTF:1:2107:15955:14140:1	CTTTCACTCTCTCTCTCTC	4264307	7968
M00328:4:000000000-A3DTF:1:1113:16990:5128:1	GTATGGGCGTTCAGGG	2534474	4772
M00328:4:000000000-A3DTF:1:2114:24030:18775:1	ATTTATATTTGCGTTTTT	5705863	10517
M00328:4:000000000-A3DTF:1:1104:5186:12841:1	CTGTCACCTCGCTGAACC	715895	1423
M00328:4:000000000-A3DTF:1:1107:6839:8582:1	GGATCCGTGTGTGCATT	1290044	2448
M00328:4:000000000-A3DTF:1:1107:19220:22202:1	GGGACAGGGACAGGGA	1440086	2742
M00328:4:000000000-A3DTF:1:1111:12290:17017:1	CTATTATTCTACATCGTG	2218343	4205

M00328:4:000000000-A3DTF:1:2106:17736:14987:1	GTGCACACTTGCGCGTG	4078963	7630
M00328:4:000000000-A3DTF:1:1109:20403:15335:1	GTGTAAAGCAGCGCGCA	1780372	3382
M00328:4:000000000-A3DTF:1:2103:11361:15004:1	GAGCCATATCGTAGTCA	3485825	6514
M00328:4:000000000-A3DTF:1:2106:15404:22291:1	GAGAGAGAGAGAGAGA	4152578	7749
M00328:4:000000000-A3DTF:1:1110:9825:15383:1	GTGACCCGAGTTGAAGA	1985368	3773
M00328:4:000000000-A3DTF:1:1111:12991:19393:1	AATACATAGGGTGACCG	2247357	4252
M00328:4:000000000-A3DTF:1:1110:16585:17632:1	ATACAAATTCGCCAGGC	2012383	3813
M00328:4:000000000-A3DTF:1:2104:10510:22813:1	GAATTTACTGACCAAT	3760257	6994
M00328:4:000000000-A3DTF:1:2105:10909:25357:1	CTCTGGCCGAGGCCTAC	3978578	7419
M00328:4:000000000-A3DTF:1:2108:14607:12321:1	CTCTCTCTCTCTCTCTC	4443779	8302
M00328:4:000000000-A3DTF:1:1113:9974:21675:1	TACTTGAATCTAACCGTC	2697509	5082
M00328:4:000000000-A3DTF:1:2112:10432:21148:1	TGCATGCTCACATGTATC	5331254	9814
M00328:4:000000000-A3DTF:1:2113:14119:10990:1	GAGTGGCTCTGTCGATT	5419937	9980
M00328:4:000000000-A3DTF:1:2112:8887:14192:1	TATCCATACAGATCGGCT	5253766	9697
M00328:4:000000000-A3DTF:1:2114:19473:17536:1	GTTTCGAGATTGAGTTCTC	5691880	10489
M00328:4:000000000-A3DTF:1:1102:19282:4550:1	CGCTCGTACTGCACAGT	228249	470
M00328:4:000000000-A3DTF:1:1110:9944:22980:1	GAGTGAGAGAGAGAGA	2072975	3937
M00328:4:000000000-A3DTF:1:1105:17329:22069:1	TGCTAATACAGTCCGCC	1022285	1980
M00328:4:000000000-A3DTF:1:1113:8348:10860:1	CTTGATAGGTGTTACTTC	2570358	4842
M00328:4:000000000-A3DTF:1:2107:6457:5990:1	CGTACACTCGCACGCA	4185339	7800
M00328:4:000000000-A3DTF:1:2110:19455:8544:1	GATATGAACTCGTTTAA	4799500	8914
M00328:4:000000000-A3DTF:1:1110:12576:14211:1	GTGCAGAGTGACGTAA	1971452	3749
M00328:4:000000000-A3DTF:1:2107:15873:6852:1	GTGTGCCACCAGCTGCG	4191431	7811
M00328:4:000000000-A3DTF:1:1101:15772:14844:1	GTCTATGTGTGCGATCTC	103604	203
M00328:4:000000000-A3DTF:1:1101:20949:22472:1	TGCTTACCTGAGCACAA	190068	397
M00328:4:000000000-A3DTF:1:1109:18013:16334:1	CACACACACACACACA	1791981	3420
M00328:4:000000000-A3DTF:1:1109:14434:18318:1	GCATACATAAGCCGGAT	1814781	3456
M00328:4:000000000-A3DTF:1:2109:16848:22999:1	GTGGCTTACCGCATTTAA	4754055	8854
M00328:4:000000000-A3DTF:1:2110:11458:8408:1	CTTGATGACAGCAAGCC	4798267	8910
M00328:4:000000000-A3DTF:1:1102:7306:4834:1	GGAGAAAGCGCTGGTTT	229496	474
M00328:4:000000000-A3DTF:1:1104:16911:23554:1	GCGTAAAGATCTTCATCT	827729	1617
M00328:4:000000000-A3DTF:1:1107:18893:17289:1	CGCTGCGCATGCGGCTT	1385394	2644
M00328:4:000000000-A3DTF:1:2104:12419:24762:1	AGCATGCACATGTGGCA	3773278	7014
M00328:4:000000000-A3DTF:1:2105:19296:15960:1	GGAGTAGAGGGTGGACA	3892187	7235
M00328:4:000000000-A3DTF:1:1109:16857:6419:1	CTCTCTCTCACTCTCTCTC	1695326	3232
M00328:4:000000000-A3DTF:1:1114:7169:6949:1	GTGCATTCTGTTTCATCT	2751844	5190
M00328:4:000000000-A3DTF:1:2108:8097:15033:1	GCCACAAGCATACTGGT	4473286	8345
M00328:4:000000000-A3DTF:1:1101:22481:19333:1	GCACTGCACTGGGCAGT	156432	319
M00328:4:000000000-A3DTF:1:2110:11209:24934:1	ATATGAACTCGTTTAAA	4962890	9206
M00328:4:000000000-A3DTF:1:1102:5768:14638:1	GTTAAAAACACACCTGT	320461	643
M00328:4:000000000-A3DTF:1:2104:5899:17748:1	TGACTATCCTATCTGTGT	3712450	6911
M00328:4:000000000-A3DTF:1:2106:15053:5591:1	ACGTA CTGGTGC GTGTC	3989577	7439
M00328:4:000000000-A3DTF:1:2108:11632:9868:1	ATGTGAAGCTTCTCAGG	4418529	8255
M00328:4:000000000-A3DTF:1:2109:20273:7004:1	GCCAGGTGCCGTCCTGA	4590377	8541
M00328:4:000000000-A3DTF:1:2110:14884:10826:1	GTATATAATGCATTCTA	4820984	8955
M00328:4:000000000-A3DTF:1:2113:15202:19914:1	GTGTGTGTGTGTGTGTG	5518872	10162
M00328:4:000000000-A3DTF:1:1110:21452:18381:1	GGGAGGCTGCTGGTG	2021271	3830

M00328:4:000000000-A3DTF:1:1105:9593:7115:1	GCTCCACCATAGTCCAA(	866289	1668
M00328:4:000000000-A3DTF:1:1106:20631:11542:1	TCGATGGAGAGGCAGG/	1115908	2147
M00328:4:000000000-A3DTF:1:1112:19509:25315:1	GTGCGCGTGAGACGCC(	2521321	4749
M00328:4:000000000-A3DTF:1:2101:16182:3258:1	GAGAGAGAGAGAGAGA	2961575	5593
M00328:4:000000000-A3DTF:1:1107:8191:13489:1	CTCCCAGCTGACATCAG(	1340660	2545
M00328:4:000000000-A3DTF:1:1110:10136:12857:1	GCTATTATACTACACTGA	1956240	3726
M00328:4:000000000-A3DTF:1:1112:5952:14390:1	GAGTCACCCGCTCCTCC(	2397799	4524
M00328:4:000000000-A3DTF:1:2110:5135:19494:1	GCGTCATAGTTATACCTC	4913101	9126
M00328:4:000000000-A3DTF:1:2113:14353:20050:1	TGGCCACCTTGTGCGGTG,	5520272	10166
M00328:4:000000000-A3DTF:1:1101:7301:15839:1	CTTACTGTTTCATGTGTTT	115456	232
M00328:4:000000000-A3DTF:1:1110:8965:12585:1	CACACATGCACACGCAC,	1953293	3719
M00328:4:000000000-A3DTF:1:1114:4189:17060:1	GCACATATGTATGTCAC(	2854892	5404
M00328:4:000000000-A3DTF:1:2105:20878:14481:1	AGCTCGCGCTTTCCGTT(	3875719	7208
M00328:4:000000000-A3DTF:1:2105:20344:20171:1	CCTATGTGTGCCACCT(	3936957	7335
M00328:4:000000000-A3DTF:1:1108:14000:13726:1	GAGAGACAGAGAGACA(	1553077	2946
M00328:4:000000000-A3DTF:1:2102:23504:14358:1	GATATATCCGGCAGGGT	3277388	6143
M00328:4:000000000-A3DTF:1:2112:19224:11301:1	CAGTATGACACTGTATT(	5222085	9650
M00328:4:000000000-A3DTF:1:1111:9871:20978:1	GATGAATCTGGGCTCTA(	2265913	4284
M00328:4:000000000-A3DTF:1:2101:12389:12564:1	TCCGTTCACTCCGTTTTG	3045164	5713
M00328:4:000000000-A3DTF:1:2107:12578:11236:1	GTTTAACCACGGTGCCA(	4232941	7902
M00328:4:000000000-A3DTF:1:1106:19643:15074:1	GAGAGGAACAGAGCAA,	1154161	2219
M00328:4:000000000-A3DTF:1:1109:16596:11561:1	AATTCTTACTTTCCTTGG	1739196	3298
M00328:4:000000000-A3DTF:1:1101:18173:21253:1	GTTAGAATTTGTGCGGC	177542	367
M00328:4:000000000-A3DTF:1:1104:10324:20341:1	GCCAGGCACGAACCTCT	797724	1568
M00328:4:000000000-A3DTF:1:1113:21320:12224:1	GGCCAACCGAGATGTAT	2584352	4873
M00328:4:000000000-A3DTF:1:1113:18086:21955:1	GAGAGAGACAGAGAGA	2700724	5085
M00328:4:000000000-A3DTF:1:2101:19154:4847:1	GCTCTTGTGCTGCTCCTC	2969280	5605
M00328:4:000000000-A3DTF:1:2109:8227:17877:1	CACTGAGAAGCCGTTCA	4702807	8749
M00328:4:000000000-A3DTF:1:1106:8198:8239:1	TGCTAATACAGTCCGCC(	1084296	2088
M00328:4:000000000-A3DTF:1:1108:25100:13273:1	ATTATGGCTTGCCTCTCG	1547966	2937
M00328:4:000000000-A3DTF:1:1113:13105:25664:1	TTATAAGTCTGTCTGTTT	2737515	5159
M00328:4:000000000-A3DTF:1:2113:17349:25163:1	TGCTAGGGCTTCTGGTG	5567678	10263
M00328:4:000000000-A3DTF:1:1104:13714:16272:1	ATATGGATGCTTATCATT	753773	1485
M00328:4:000000000-A3DTF:1:1108:15570:7411:1	CTACCGTGCCACTAGGC(	1491235	2831
M00328:4:000000000-A3DTF:1:2105:18498:22493:1	AGGTAGGCAAAGATTAC	3958612	7379
M00328:4:000000000-A3DTF:1:2114:9740:10314:1	ATTTTAATGAGTTCTTAA	5612993	10331
M00328:4:000000000-A3DTF:1:2104:15323:10303:1	GTTGAACTCCATGATGG	3632994	6786
M00328:4:000000000-A3DTF:1:2104:8246:22617:1	GTTGAGCCCCGTTCAGAI	3758542	6992
M00328:4:000000000-A3DTF:1:2105:4453:12784:1	CCTCCATACATTCCATGG	3857188	7163
M00328:4:000000000-A3DTF:1:2113:16914:23495:1	CACAAGAGACGCACGTC	5554568	10238
M00328:4:000000000-A3DTF:1:2114:24204:20003:1	ATCTACCTATGGCCGAT(	5719378	10536
M00328:4:000000000-A3DTF:1:2114:17227:20466:1	GTGCTATGCGCCTCTGCC	5724251	10555
M00328:4:000000000-A3DTF:1:1102:11684:21941:1	GTCTAGGCAGGAAGTAA	399284	816
M00328:4:000000000-A3DTF:1:2102:8574:20310:1	CACTAGCAGTAGTGCCT	3341093	6271
M00328:4:000000000-A3DTF:1:2105:21363:6940:1	CTGCTGCTTCAATCTACT	3798755	7047
M00328:4:000000000-A3DTF:1:2107:9150:20863:1	TCTTACCCTGCAACCTT	4336560	8115
M00328:4:000000000-A3DTF:1:1102:16454:6575:1	TTGTATAGGTTTGTGATC	239412	489

M00328:4:000000000-A3DTF:1:2102:15846:6736:1	TATTGTCAGTGTGTATTA	3198571	5985
M00328:4:000000000-A3DTF:1:2107:11938:14411:1	ATCTATTAGAGCCACAA	4267308	7976
M00328:4:000000000-A3DTF:1:2111:6222:20721:1	CTGCTGGTCTGTCTCAG	5125891	9529
M00328:4:000000000-A3DTF:1:1110:13707:25745:1	TCCCAGGTCAAGCGGAG	2097706	3979
M00328:4:000000000-A3DTF:1:2103:15573:16936:1	CCTTGCGGTTTGAACTA	3506812	6552
M00328:4:000000000-A3DTF:1:2105:8379:16803:1	GCCGTGTAGTCTGCTGC	3901451	7262
M00328:4:000000000-A3DTF:1:1105:16201:25088:1	CAAGAGTACCGTGTGTG	1048667	2023
M00328:4:000000000-A3DTF:1:2102:14243:2844:1	ATTGTTGGCATGGTAGG	3178262	5942
M00328:4:000000000-A3DTF:1:2103:17675:6551:1	GACCCTAACATGTGGTA	3400086	6359
M00328:4:000000000-A3DTF:1:2107:5997:20165:1	GCCCCGGATCATGCAGA	4329733	8103
M00328:4:000000000-A3DTF:1:1101:23958:22095:1	CTTGTAAGCGCCTAGT	186210	391
M00328:4:000000000-A3DTF:1:1102:12816:25382:1	GAGATAATCATTAAATA	428080	876
M00328:4:000000000-A3DTF:1:1109:16756:16237:1	CTTTTGGTGACCGTGCC	1790905	3414
M00328:4:000000000-A3DTF:1:1111:16750:21628:1	GGCAATGGATTGCCTAC	2273108	4299
M00328:4:000000000-A3DTF:1:1112:4874:17901:1	TTTTAAGCTTTCATGATA	2440202	4592
M00328:4:000000000-A3DTF:1:1114:3183:16140:1	AGCCTAGCCCACGCAGC	2843551	5376
M00328:4:000000000-A3DTF:1:2112:16876:15381:1	GCTTACGCTCAGGTGCC	5267288	9721
M00328:4:000000000-A3DTF:1:2107:15916:24122:1	ATACCTACTTGTTCCGTT	4365304	8160
M00328:4:000000000-A3DTF:1:2111:20369:19910:1	CAGCTCTTGCGTCTGGC	5117342	9515
M00328:4:000000000-A3DTF:1:1111:23266:20276:1	GTTATGAACATGCATGC	2257817	4271
M00328:4:000000000-A3DTF:1:1104:15232:15380:1	AGCTTCGTGGAAGAAGA	743859	1472
M00328:4:000000000-A3DTF:1:1110:13178:13995:1	AGCCTGGAGGGTCCAGC	1968930	3743
M00328:4:000000000-A3DTF:1:1105:19835:22282:1	ACGACACTCTGGATCCG	1024337	1983
M00328:4:000000000-A3DTF:1:2101:19736:9157:1	GAGTGGGCCAGCAGAG	3007012	5660
M00328:4:000000000-A3DTF:1:2106:18546:13411:1	GGTAAACAACCCACATG	4061983	7590
M00328:4:000000000-A3DTF:1:1114:24542:14559:1	GACAACACCAGAGTAGC	2824249	5326
M00328:4:000000000-A3DTF:1:1112:12689:22049:1	GTTCAACGGTCTGGGAC	2489008	4690
M00328:4:000000000-A3DTF:1:2105:20702:13395:1	TTATTATTGATTTTAAAA	3863957	7180
M00328:4:000000000-A3DTF:1:2113:7194:8256:1	GTGTGTGTGTGTGTGTG	5394069	9935
M00328:4:000000000-A3DTF:1:1106:25380:11496:1	GCCCAATGCAAGCCAAG	1115429	2145
M00328:4:000000000-A3DTF:1:2101:20626:16688:1	CTCTATGTCTCTCCCTC	3092936	5806
M00328:4:000000000-A3DTF:1:2110:9766:12727:1	CGTGCATGCCTGCTGCC	4840162	9003
M00328:4:000000000-A3DTF:1:2110:19614:18657:1	ACGCTCACCAGTGTCCG	4904341	9109
M00328:4:000000000-A3DTF:1:2108:19908:18913:1	GCTCAAACACTAGTGCAG	4515823	8412
M00328:4:000000000-A3DTF:1:2109:19171:11232:1	TGTTTGCACAAGCCACTC	4629928	8622
M00328:4:000000000-A3DTF:1:1109:19168:24299:1	GTTAAAAGCAGATGACC	1876817	3565
M00328:4:000000000-A3DTF:1:2108:18314:20717:1	TCGTAGGTTTGAGCATT	4534385	8453
M00328:4:000000000-A3DTF:1:2111:8528:16694:1	GCATTCTCCCGTTTCCCA	5082069	9443
M00328:4:000000000-A3DTF:1:2112:10747:20031:1	GAAAGACAGCCTGCGAC	5319747	9797
M00328:4:000000000-A3DTF:1:2113:11128:9309:1	CCCTTTAACAGACCTAAC	5403506	9954
M00328:4:000000000-A3DTF:1:1110:11921:20605:1	GTTTCAAGAGAACCAAA	2047038	3887
M00328:4:000000000-A3DTF:1:2101:18134:23833:1	ATGGAAGATCACCGGTT	3164628	5931
M00328:4:000000000-A3DTF:1:2109:7083:19342:1	CGTATATATTGTCACACT	4718335	8777
M00328:4:000000000-A3DTF:1:1108:24874:10512:1	ACTCAGCTTTGGTGTTCC	1518320	2869
M00328:4:000000000-A3DTF:1:1109:11961:21479:1	GCACAAATGTGTGAGCA	1849169	3520
M00328:4:000000000-A3DTF:1:2108:13704:22370:1	GCATTACAGCAGTGGCC	4550154	8487
M00328:4:000000000-A3DTF:1:1103:16849:20403:1	CAACAAGCCAAATCCCC	592178	1197

M00328:4:000000000-A3DTF:1:2102:21351:12045:1	TAATTTACCCAATCTCGA	3251671	6086
M00328:4:000000000-A3DTF:1:2107:3987:20323:1	ACATAGAAAAAAGAAAC	4331266	8105
M00328:4:000000000-A3DTF:1:2114:15181:20319:1	CTTTCAGCTTTTGTATTT	5722760	10550
M00328:4:000000000-A3DTF:1:2107:18088:16745:1	AGCGTTAAGTGTGCACA	4293081	8039
M00328:4:000000000-A3DTF:1:2107:13106:25888:1	ACACACCACTGACAGGA	4375737	8178
M00328:4:000000000-A3DTF:1:1102:5371:21223:1	ATTGATACCAGATAGAA	392437	796
M00328:4:000000000-A3DTF:1:1104:19518:13347:1	GTGTAAAGTTGTGTATG	721322	1434
M00328:4:000000000-A3DTF:1:1106:16304:15556:1	GGTTGATACATTATTCA	1159507	2223
M00328:4:000000000-A3DTF:1:2107:13771:8652:1	CCTTCAGCCTGATCTATT	4207098	7846
M00328:4:000000000-A3DTF:1:1102:17526:22256:1	GTCCTACGACTTGAGTA	402347	823
M00328:4:000000000-A3DTF:1:2108:6137:14114:1	CTGCTGGGCAACAGGTG	4463177	8331
M00328:4:000000000-A3DTF:1:2109:4331:21687:1	ATGCTCTCTCTCTCTCT	4741678	8832
M00328:4:000000000-A3DTF:1:2112:7140:17639:1	GTAGGAGTTGAGCTTCA	5293088	9760
M00328:4:000000000-A3DTF:1:1114:5312:23171:1	GGGTCGAGGCAAAGGG	2926342	5540
M00328:4:000000000-A3DTF:1:2111:5159:15652:1	GCCATAACTCTAGCACA	5070326	9422
M00328:4:000000000-A3DTF:1:1108:14734:24051:1	AAGTACATTGCTGCACT	1668129	3181
M00328:4:000000000-A3DTF:1:1112:8560:21812:1	CCGTAACGATGCCATGG	2486303	4683
M00328:4:000000000-A3DTF:1:1114:6706:20695:1	CGCTAGGGTCTTGCGAT	2898757	5487
M00328:4:000000000-A3DTF:1:1109:18773:20339:1	GTTTTAGACTTAAAT	1837203	3499
M00328:4:000000000-A3DTF:1:1111:23894:21559:1	TCTCAATGTTGTCCCTCA	2272305	4297
M00328:4:000000000-A3DTF:1:2104:16665:4286:1	CTCTTTTCTCCGTCTCT	3585261	6694
M00328:4:000000000-A3DTF:1:2105:13273:16071:1	ATTACACGCCAATAGCA	3893468	7239
M00328:4:000000000-A3DTF:1:2108:13082:14929:1	TCCTTTAATTATGTTACT	4472115	8343
M00328:4:000000000-A3DTF:1:1104:12037:20884:1	ATTCAGAGTACATTCTG	803138	1583
M00328:4:000000000-A3DTF:1:1108:9944:24177:1	CCTATTGGTTAATGCGG	1669184	3186
M00328:4:000000000-A3DTF:1:2102:7038:19669:1	CCGTATACACAGTGAAA	3334986	6257
M00328:4:000000000-A3DTF:1:1110:19082:9318:1	CTCCCGCTTGAAGTTA	1920362	3647
M00328:4:000000000-A3DTF:1:2107:8911:22852:1	CTTCTTCTCTCTCTCAC	4355040	8145
M00328:4:000000000-A3DTF:1:2109:22494:21637:1	GCTTTAGCTGACGTGCT	4741160	8829
M00328:4:000000000-A3DTF:1:2110:16354:19254:1	TCTTTGTCCAGGGCAGT	4910701	9123
M00328:4:000000000-A3DTF:1:2114:20464:20770:1	ACATAAAGAGGGCTGCA	5727478	10561
M00328:4:000000000-A3DTF:1:1112:11218:15614:1	GTGTAGGGAGAAGCAG	2412408	4543
M00328:4:000000000-A3DTF:1:2108:18911:21410:1	GCCCCTGCCCGTTGAC	4540912	8468
M00328:4:000000000-A3DTF:1:2108:18747:21800:1	ATGCAGAACACAAAGGC	4544718	8474
M00328:4:000000000-A3DTF:1:2109:19783:4695:1	CCTTAAACTCTTCACTT	4578628	8526
M00328:4:000000000-A3DTF:1:1101:23180:10276:1	GTTCCGTTGAGCTTTTGC	50828	78
M00328:4:000000000-A3DTF:1:1111:9432:8604:1	AGTCTCTCTCTCTCCC	2125371	4024
M00328:4:000000000-A3DTF:1:1114:5928:18200:1	CTATGGGTCAGGATGGC	2868831	5430
M00328:4:000000000-A3DTF:1:1101:18729:14038:1	GGGCTAGTAATAAATGA	94047	184
M00328:4:000000000-A3DTF:1:2114:18287:9357:1	GCTTAGCCCCGAGACCA	5603694	10315
M00328:4:000000000-A3DTF:1:2114:15230:23636:1	CACGTAAGGTCTCCAA	5755696	10622
M00328:4:000000000-A3DTF:1:1103:19495:22288:1	CGAAGCGCCTAGAACGA	610309	1241
M00328:4:000000000-A3DTF:1:2107:9707:16291:1	CCGTCGGCTTGCTAGTT	4287998	8029
M00328:4:000000000-A3DTF:1:2108:11851:8722:1	CATATAGACAGGGAGAC	4407464	8235
M00328:4:000000000-A3DTF:1:2108:19493:24776:1	CAGCAAGAGTGGTCTCA	4569308	8510
M00328:4:000000000-A3DTF:1:1103:19639:18050:1	CAGTTCTGCTGCTGCTG	567495	1135
M00328:4:000000000-A3DTF:1:1105:6233:23260:1	GCTGAGTGTCGTTCAAC	1033596	1993

M00328:4:000000000-A3DTF:1:1102:8814:8423:1	GGTATGCGCTCTGAAAG	254888	511
M00328:4:000000000-A3DTF:1:1110:9235:8122:1	GCCCCAGAGGGCATTTA	1910589	3628
M00328:4:000000000-A3DTF:1:1114:13824:13155:1	CATTTGCACCACATTAGT	2807663	5288
M00328:4:000000000-A3DTF:1:2108:22398:16772:1	ATACACCACCAACCAGA	4492547	8373
M00328:4:000000000-A3DTF:1:2109:15631:7154:1	GTGCTTGCACGGAGCTC	4591523	8542
M00328:4:000000000-A3DTF:1:1105:5296:10027:1	GTCCAAAGGTTGTACAA	892707	1721
M00328:4:000000000-A3DTF:1:1109:21464:16194:1	GTCATGCAGTTTCATGCT	1790398	3411
M00328:4:000000000-A3DTF:1:2103:5260:23780:1	ATATAAGTCAAGTAAGA	3570546	6667
M00328:4:000000000-A3DTF:1:2106:11237:14214:1	CCCTTACAGCCAGCATGC	4070690	7613
M00328:4:000000000-A3DTF:1:1102:22096:16164:1	GCATTGGCAAAAAGTCCT	337740	681
M00328:4:000000000-A3DTF:1:1112:5025:22492:1	GAGAAAGAGTCTAGAGA	2493903	4704
M00328:4:000000000-A3DTF:1:1104:6144:24841:1	CTTCTCAAGGATTGTTGA	837954	1631
M00328:4:000000000-A3DTF:1:1105:18528:8562:1	TAATAATGATATTATTAT	878465	1694
M00328:4:000000000-A3DTF:1:1105:10964:18219:1	GCGAGAGTCAGCATGAC	982148	1888
M00328:4:000000000-A3DTF:1:2107:16207:7395:1	ATTCTATGTTGCATGTGT	4195755	7820
M00328:4:000000000-A3DTF:1:2114:12088:11571:1	CATTTGTATAGCGGCAA	5625697	10357
M00328:4:000000000-A3DTF:1:1110:15341:15774:1	GTTTTGGCTCTTCTGGGT	1989980	3782
M00328:4:000000000-A3DTF:1:1114:4250:15315:1	GGTATATTTTCTAGCCTC	2833354	5343
M00328:4:000000000-A3DTF:1:2109:17642:7724:1	GACAGACACATAGGCAE	4596210	8553
M00328:4:000000000-A3DTF:1:2113:22917:24015:1	GCTGGGCATTGCAATAC	5559113	10252
M00328:4:000000000-A3DTF:1:2111:15432:15439:1	CCTGTATCCAAGTTTTCA	5067919	9417
M00328:4:000000000-A3DTF:1:1101:11220:12124:1	CCGCCACAGTACGTCAG	71203	124
M00328:4:000000000-A3DTF:1:1103:9765:19394:1	ATGTACCCACGCCTCGTT	581859	1167
M00328:4:000000000-A3DTF:1:1112:12557:14860:1	GAGAGAGAGAGAGAGA	2403232	4533
M00328:4:000000000-A3DTF:1:1104:15978:20877:1	ACCCCGCCAATGTAGC	803054	1582
M00328:4:000000000-A3DTF:1:1111:6415:6549:1	ATCCAAAACCTTCTTGAC	2111012	4001
M00328:4:000000000-A3DTF:1:2108:11783:17910:1	GAGGTTATGCAGAAGGT	4505105	8400
M00328:4:000000000-A3DTF:1:2109:6749:16643:1	GCATAAATCCGCCTACA	4688982	8716
M00328:4:000000000-A3DTF:1:1101:17209:26938:1	GCTCTAATCCCATGCAGC	221768	457
M00328:4:000000000-A3DTF:1:1105:17683:24537:1	GTAAGAACACGATGCTG	1044501	2015
M00328:4:000000000-A3DTF:1:1108:12533:14664:1	GGGCACGAGCGAGCTCC	1563933	2959
M00328:4:000000000-A3DTF:1:1111:23483:12105:1	ATCCAGCGGCTCACCTG	2159816	4083
M00328:4:000000000-A3DTF:1:1102:4857:17038:1	GGCTGCAGGTATGCACA	347637	699
M00328:4:000000000-A3DTF:1:1106:5553:12703:1	GCATCTGGCTCTGCCTTT	1128076	2167
M00328:4:000000000-A3DTF:1:2113:18399:14988:1	GTCGCCGTTGTATCCA	5463381	10066
M00328:4:000000000-A3DTF:1:2113:4029:9795:1	TAAGTGGGTTTGCAAAA	5408157	9963
M00328:4:000000000-A3DTF:1:2101:18807:20733:1	GAGAGAGAGAGAGAGA	3136426	5881
M00328:4:000000000-A3DTF:1:1109:12717:12514:1	CTCTCTCTCTCTTCTT	1749094	3309
M00328:4:000000000-A3DTF:1:2109:9126:22363:1	GCAGAGAAACGATTAAT	4748177	8844
M00328:4:000000000-A3DTF:1:2106:16411:12925:1	GAAGGTAGTAGTGGGCC	4056752	7575
M00328:4:000000000-A3DTF:1:1114:16019:15718:1	TTATATCGACTGTCCTCT	2838173	5356
M00328:4:000000000-A3DTF:1:1102:20784:7831:1	GCTATTGCTAACTCATT	249606	505
M00328:4:000000000-A3DTF:1:1102:20312:9233:1	GAGCTGGAGAGTGAGAG	262475	532
M00328:4:000000000-A3DTF:1:1102:22811:13371:1	GTGTGAGACTAGGGAAC	306076	624
M00328:4:000000000-A3DTF:1:1113:15376:22737:1	GGGTTAAGAGAGAGAG	2709432	5106
M00328:4:000000000-A3DTF:1:2107:16661:6762:1	GTGCCGCAGCAATCCGC	4190766	7809
M00328:4:000000000-A3DTF:1:1104:13490:4882:1	CTCTCCACCCTCTGTGCA	648489	1314

M00328:4:000000000-A3DTF:1:2104:14049:8905:1	AGAGAGAGAAGACATG	3619063	6750
M00328:4:000000000-A3DTF:1:2103:10169:13264:1	CATTTGACCTAAGCTAG/	3466577	6471
M00328:4:000000000-A3DTF:1:2102:18171:24114:1	GACCACGTATAAGACCC	3373621	6329
M00328:4:000000000-A3DTF:1:2110:13699:24126:1	CTATTATTATGGCCAAAT	4957373	9194
M00328:4:000000000-A3DTF:1:2114:13701:15088:1	GTACCTGACTGCTTACCC	5664042	10430
M00328:4:000000000-A3DTF:1:1110:19870:22597:1	GGCTTCACTTCACTTTCC	2068908	3929
M00328:4:000000000-A3DTF:1:2108:18116:12877:1	GAGTAGGGGGAAAAAG	4449731	8313
M00328:4:000000000-A3DTF:1:2108:20205:15430:1	CTTCCTAACCCCTCAGACA	4477710	8350
M00328:4:000000000-A3DTF:1:1114:20743:18633:1	ATTGTTGCCTGACTGCTT	2874087	5440
M00328:4:000000000-A3DTF:1:2102:14898:14232:1	GCATAGGGAAGAACTTA	3275992	6138
M00328:4:000000000-A3DTF:1:2111:18113:21160:1	GCACACCGACCGTCTGA	5130431	9537
M00328:4:000000000-A3DTF:1:1106:9903:6621:1	GCCCACAAATGATGGGA	1071846	2064
M00328:4:000000000-A3DTF:1:2106:11755:18385:1	GCCTGATCCCTCACTGCT	4115132	7684
M00328:4:000000000-A3DTF:1:1104:8527:9606:1	GTTTCGGCCTATGCTGCT	683216	1371
M00328:4:000000000-A3DTF:1:2112:23913:16202:1	GTTGATACGTTGATACG	5276898	9736
M00328:4:000000000-A3DTF:1:1102:14607:13558:1	GTGATAGCCTTCAGGTC	308141	627
M00328:4:000000000-A3DTF:1:1105:4949:14332:1	GGTCCCATCCTGCATCC	938668	1803
M00328:4:000000000-A3DTF:1:1105:16511:26310:1	TCAGTACACCGTGCATG	1056214	2042
M00328:4:000000000-A3DTF:1:1106:15163:5368:1	CTCTTTGTCTCCCGCTC	1065130	2051
M00328:4:000000000-A3DTF:1:2103:16045:15751:1	CCTCGGCGTCAACTCGT	3493945	6526
M00328:4:000000000-A3DTF:1:2114:21406:9836:1	CACACACACACATGCAA	5608271	10319
M00328:4:000000000-A3DTF:1:2106:18069:8024:1	GCTATCGTCCGGCCACT	4007814	7468
M00328:4:000000000-A3DTF:1:2102:17592:9452:1	CAACAGTGCTGCTTACT/	3224178	6034
M00328:4:000000000-A3DTF:1:1102:7325:12272:1	GTTTCAGTGTCATTCTG	293897	599
M00328:4:000000000-A3DTF:1:1108:10747:24407:1	TGCTAATACAGTCCGCC	1671036	3194
M00328:4:000000000-A3DTF:1:1110:20631:20840:1	CACAAAAGATCAGTCTT	2049719	3893
M00328:4:000000000-A3DTF:1:1112:23317:17377:1	GTGTAGCTCATCGGCTT	2433892	4574
M00328:4:000000000-A3DTF:1:1103:19495:22288:1	CGAAGCGCCTAGAACGA	610309	1242
M00328:4:000000000-A3DTF:1:2103:6980:16771:1	GTAGGAATCTCTCTAT	3505052	6546
M00328:4:000000000-A3DTF:1:2106:21452:12741:1	CTACTGACACGAGGTCG	4054745	7570
M00328:4:000000000-A3DTF:1:1102:9595:10588:1	TTCAAAGGTGGTCAGT	276129	559
M00328:4:000000000-A3DTF:1:2108:25806:16681:1	GCTCCCACCTGCCTGTCC	4491564	8370
M00328:4:000000000-A3DTF:1:2109:19317:16561:1	GATATAGAGAGGGGGA/	4688075	8712
M00328:4:000000000-A3DTF:1:1105:4591:20525:1	TACTGGAACAGGTGGAA	1006930	1942
M00328:4:000000000-A3DTF:1:1114:10371:19474:1	CGCTCAAGCAACTCGTT	2884413	5460
M00328:4:000000000-A3DTF:1:2108:15394:20735:1	GTGCAACAGTGATACAA	4534570	8454
M00328:4:000000000-A3DTF:1:2107:16110:7528:1	CAACCAACCCCAATCCA/	4196889	7823
M00328:4:000000000-A3DTF:1:1101:12039:10404:1	AGTCAAGAAAGCTACAG	52250	88
M00328:4:000000000-A3DTF:1:1105:7750:12378:1	GTTGTAGCCCCCGTCAG	916924	1764
M00328:4:000000000-A3DTF:1:1108:10609:11669:1	ACACAGGAGTGCCAAA	1530273	2891
M00328:4:000000000-A3DTF:1:1107:9588:15018:1	GTCGCCGACAGTACGGC	1358311	2573
M00328:4:000000000-A3DTF:1:1114:6691:21589:1	GAAGGAAGCTATAGTAA	2908858	5510
M00328:4:000000000-A3DTF:1:1114:4860:16025:1	AGCTTCGCTACTCGTCA	2842048	5368
M00328:4:000000000-A3DTF:1:2110:8474:24405:1	TGACCGTGCTGACCGAA	4959296	9196
M00328:4:000000000-A3DTF:1:2102:4563:20335:1	ATCCGATGGCTTCACGT	3341327	6272
M00328:4:000000000-A3DTF:1:2110:11200:12257:1	TTATAATTGTAGTCGCTC	4835231	8984
M00328:4:000000000-A3DTF:1:1103:7671:20687:1	CAGCATATGCAGGTTAC	594930	1204

M00328:4:000000000-A3DTF:1:2102:17979:17318:1	GAGTGACATCCGCCCA	3310314	6222
M00328:4:000000000-A3DTF:1:2106:18531:13421:1	GGTAAACAACCCACATG	4062100	7591
M00328:4:000000000-A3DTF:1:1106:19389:18582:1	GTCAAAGATTTATCGTTC	1193207	2281
M00328:4:000000000-A3DTF:1:2106:22369:4513:1	CTATTATTATGGCCAAAT	3984826	7427
M00328:4:000000000-A3DTF:1:2102:10780:20048:1	GCATGAAAGATTGATAA	3338640	6263
M00328:4:000000000-A3DTF:1:1110:21845:10541:1	GCATTAACCACCGTGTC/	1932057	3673
M00328:4:000000000-A3DTF:1:1103:12902:7529:1	ACATTTCCACATGCATAT	457718	910
M00328:4:000000000-A3DTF:1:2104:6682:21702:1	CTACTAATGAATTATTAA	3750496	6978
M00328:4:000000000-A3DTF:1:2108:25546:17547:1	GTTGATATGCATACATA(	4501133	8394
M00328:4:000000000-A3DTF:1:1111:16352:22980:1	TTTCACACGTTGTCAGTC	2288134	4324
M00328:4:000000000-A3DTF:1:2107:10864:15246:1	CACCTTATCTCAAGGCTA	4276503	7996
M00328:4:000000000-A3DTF:1:2112:14770:11692:1	GGTGAGATCCGTCAGTG	5226229	9661
M00328:4:000000000-A3DTF:1:2101:20578:15241:1	GCCTACGCGATTACCTAC	3076257	5773
M00328:4:000000000-A3DTF:1:2107:11379:18181:1	TCTCAGGGGCAGTGCTG	4308968	8068
M00328:4:000000000-A3DTF:1:2107:13008:20250:1	GATCTACTGTCTACGTA/	4330566	8104
M00328:4:000000000-A3DTF:1:2103:4074:13746:1	GCCGGAAGCTTAGATAC	3471889	6486
M00328:4:000000000-A3DTF:1:1102:4996:20096:1	CATCAGGACGGCCCCTG	381071	775
M00328:4:000000000-A3DTF:1:1104:12959:17717:1	CTCTGCGATGGCGCCGG	769551	1520
M00328:4:000000000-A3DTF:1:1110:10735:10967:1	CGGTTAAAAGAATGTCA	1936250	3680
M00328:4:000000000-A3DTF:1:1114:12201:17033:1	AAAATATGTTGCTAGGT	2854549	5401
M00328:4:000000000-A3DTF:1:2108:14726:3714:1	GTTCGAAGGTGTAGCTC	4377464	8185
M00328:4:000000000-A3DTF:1:1112:3802:15105:1	ACCTAGACCCGTAGGCA	2406187	4538
M00328:4:000000000-A3DTF:1:1108:3258:17286:1	CTCCTCCGACACTGGCTC	1594842	3037
M00328:4:000000000-A3DTF:1:2105:15962:25788:1	GTCTTGCAAAACCTCAC	3980645	7426
M00328:4:000000000-A3DTF:1:2109:14186:15359:1	GTGCCAAACGACTAAGA	4674583	8692
M00328:4:000000000-A3DTF:1:1113:14112:25151:1	ATGTGTGGTTTTAGCTTC	2733262	5155
M00328:4:000000000-A3DTF:1:2105:11796:9195:1	GTCTACCTGCGAGAAGA	3819642	7088
M00328:4:000000000-A3DTF:1:2113:17764:17523:1	CTTGCTCAATACGTGTG1	5492385	10113
M00328:4:000000000-A3DTF:1:1102:9698:22524:1	GTCTAGGATACGGTTCA/	404880	834
M00328:4:000000000-A3DTF:1:2103:15665:22482:1	GGTGTAGACATGCCCAT	3560302	6643
M00328:4:000000000-A3DTF:1:1101:4883:18177:1	CCTTTGTGCTTACACGTC	143161	295
M00328:4:000000000-A3DTF:1:2108:11111:6722:1	CTCGAAGGCCGGACATA	4390207	8212
M00328:4:000000000-A3DTF:1:2106:19769:13860:1	CCAGTGTGCTTTGTCCG/	4066837	7599
M00328:4:000000000-A3DTF:1:1111:4837:17704:1	ATCATACTCTAGTTGGAC	2226704	4217



**primary host of the causative agent of salmonid proliferative kidney disease**

University of Turku,

**Paracapsuloides bryosalmonae host-parasite system**

primer	left	left_sequence	left_tm	left_gc	left_self_ei	left_self_ar	left_hairpir
	0 2;21	CGTGAATGTAGTCTGGCACAC	60.014	52.381	0	0	0
	0 62;20	TCTCTTCTTCTTGCACGCG	59.596	50	1.24	1.24	0
	0 37;20	TGGTGCAGGGATTTAACGTG	59.224	50	0	0	0
	0 0;20	TGCCATGACCATTGTGTAC	59.509	50	0	5.2	0
	0 13;21	GAAGAAACGAGGAGAGTGTGC	59.68	52.381	0	0	0
	0 65;22	AGAGAAAGACTGAGAAACACCC	58.425	45.455	0	0	0
	0 25;20	GCGTGACGTCGTTTATGGAC	60.358	55	0	1.95	0
	0 71;20	GCGCGATGGTCAGCTATTAG	59.668	55	0	9.76	0
	0 163;19	GGAGACGGCCACATAACAAG	58.675	57.895	0	0	0
	0 17;19	GGGCTTGGGAGGAAAGGAG	60.463	63.158	0	0	0
	0 35;20	TGGCAGTTTGAGAGGGTTCC	60.659	55	0	0	0
	0 120;20	TGGAAGGTCGTTGTGGGAC	60.94	55	0	0	0
	0 90;20	GAGAACTCAACTTCCTGGCG	59.309	55	0	0	0
	0 19;20	TCAGGCAGCGTATCGATTTC	58.888	50	0	0	0
	0 51;20	CCGTCTCTCCCTCGACATTG	60.644	60	0	0	0
	0 2;19	CAGCAACTTCCAGCCCTTG	59.785	57.895	0	0	0
	0 120;22	GCATTTCCACATCTCTAGCAGG	59.882	50	0	0	0
	0 116;20	AGGAGATGGGAGGAAGGGAC	60.819	60	0	0	0
	0 54;20	CGGAAGAACTACAGCAGAGG	58.458	55	0	0	0
	0 17;19	GAGCAGGCAGAGACAAAGC	59.568	57.895	0	0	0
	0 29;21	TCGTACCTTGCTAACTCCTCG	60.012	52.381	0	0	0
	0 224;20	GTGTAAGAGAGAGCGCACAC	59.391	55	2.61	2.61	0
	0 31;18	AAACAGGCGGGCAAGGTG	61.664	61.111	0	0	0
	0 72;20	AGAGAGCTGACATACGCACG	60.641	55	0	0	0
	0 28;22	CTATGACCTAGCTCTCTGTGTG	58.191	50	0	0	0
	0 17;20	AGGGAGTTAGAGCCTGAGTG	58.911	55	0	0	0
	0 2;20	CTTGACTTCCTGAGCGTCAC	59.315	55	0	0	0
	0 132;18	CCTACCAGGCGAGCTCTC	59.616	66.667	0	0.84	0
	0 30;20	CTGTGCAGCTTGAGATTGCC	60.573	55	0	0	0
	0 6;20	CACTCATCTTGCACGTCC	59.384	55	0	0	0
	0 64;20	CTTGACGGCTTGACTGCTTG	60.5	55	0	0	0
	0 18;19	TCGAAGTTGACAGCTCCGC	61.11	57.895	0	0	0

0 109;20	TTTCTGTGGCGTTCATGTCC	59.514	50	0	0	0
0 0;19	GGCTCGAACACTACCGGTC	60.89	63.158	0	7.34	0
0 26;20	CTTGACGGCTTGACTGCTTG	60.5	55	0	0	0
0 18;19	CGCACACACACTGGTATGC	60.231	57.895	0	0	0
0 75;22	AGAGGAGAATGTGCATAAACGC	59.818	45.455	0	0	0
0 19;20	AGGATTTATGTCTGCCCTGC	58.41	50	0	0	0
0 25;20	CGAACTTTGGCTCTCGACTC	59.391	55	0	0	0
0 16;20	AGTGACAGACAGGTGACAGG	59.719	55	0	0	0
0 0;22	TCGTATGTGTGCCAAGAAGTTG	59.949	45.455	0	0	0
0 3;19	CAATAACCCACAGCCACGC	60.232	57.895	0	0	0
0 4;21	GACACAGGCAGAGGGATAATG	58.916	52.381	0	0	0
0 28;20	TCAGACTTGTCTGGGAGCTTC	60.152	55	0	0	0
0 34;19	CAACCGAGTGACAAGCGAG	59.58	57.895	0	0	0
0 185;20	GAGTGAGTGAATGCGAGACC	59.104	55	0	0	0
0 41;20	GTTACAGGTGCGTGTGCATCG	60.015	55	0	0	0
0 11;21	AGCATATTCGTGACGTAGCAC	59.281	47.619	0	7.55	0
0 125;19	ACAATCGCGCACAAGTACG	59.943	52.632	0	0	0
0 44;20	AGACTGAGTTCTTGCAGGGC	60.726	55	0	0	0
0 16;20	CGCAAGGTGAACAGAAGAGG	59.591	55	0	0	0
0 98;20	CTGCTCAATCTCTCTGCAGC	59.45	55	0	6.16	0
0 115;20	CAAGCTGTTGTGGCCACTAG	59.87	55	18.86	24.03	0
0 67;20	TTCTGTTGGCCTGATACCGG	60.511	55	0	0	0
0 1;18	TGCAGAGCGGACAAGAAG	58.055	55.556	0	0	0
0 305;20	GAGCGAATGAGTGAGCAACC	60.013	55	0	0	0
0 14;19	GGGTAGGAGGGTGGAGAGG	60.852	68.421	0	0	0
0 51;20	GCGCCTAGTTCGAGATTGAG	59.251	55	0	2.73	0
0 36;20	CGTCCACTATTCCGACATGC	59.526	55	0	0	0
0 5;20	GCGCCTAGTTCGAGATTGAG	59.251	55	0	2.73	0
0 29;20	ACGGAACCAGAGCAGAGTAG	59.579	55	0	0	0
0 15;20	TATGCAGCCACAGTAATGCC	59.077	50	0	0	0
0 35;20	GGTGTGAAGTAAGTCCGGAC	58.669	55	23.6	23.6	0
0 59;20	CTTACCGGGTAAATGGCGTC	59.45	55	0	0	0
0 91;20	CTGCAGCCTCTTACCATTG	59.94	55	0	0	0
0 54;20	AGTGCGAGTCTGAGCTAGTG	59.94	55	0	0	0
0 5;20	AAGGTGCGTGCATAATTGTG	58.107	45	0	0	0
0 93;21	GCGCTTCTTATCCACCTTCC	60.08	52.381	0	0	0
0 64;20	CTGGATTTCGATGCACTACCC	58.877	55	0	0	0
0 69;20	AGAGTCGGGAAAGAAGGCAG	60.152	55	0	0	0
0 43;20	GCGCCTAGTTCGAGATTGAG	59.251	55	0	2.73	0
0 3;20	TAAAGTTGTGACAGACGCCG	59.244	50	0	0	0
0 3;21	CATAGACAGAAAGACAGGCGC	59.814	52.381	0	0	0
0 112;20	AGATGAGGCACGACAGACAG	60.223	55	0	0	0
0 91;20	AAACACATACATGCTCGCGC	60.637	50	0	0	0
0 78;20	TTGCTTGTCAACCACGTTCC	60.011	50	0	0	0
0 44;22	ACAGCCTCATTTATATAGCGGC	59.162	45.455	0	0	0
0 24;18	GAGAGGGAGGCGAGGAAC	59.533	66.667	0	0	0
0 5;21	GTCTGTCTCTCTGCCAGAATG	58.861	52.381	0	0	0

0 51;20	TGAACTGGCAAATTGTCCGG	59.796	50	4.1	4.1	0
0 10;20	TATTATTAGGGTGGCCGCGG	60.439	55	20.7	20.7	0
0 0;18	CTGTGGACGTACGTGTGC	59.181	61.111	2.41	11.07	0
0 5;20	AGATTGAGTTCTCGCAGGGC	60.865	55	0	0	0
0 114;20	AACCTCCTGAGCAGAAGAGC	60.151	55	0	0	0
0 34;20	AATCTTGAAGGACCACACGC	59.227	50	0	0	0
0 34;21	GCCCTAACGGTAACTTTGGTC	59.674	52.381	0	0	0
0 77;20	GCGCCTAGTTCGAGATTGAG	59.251	55	0	2.73	0
0 16;21	CGTGGCGAGCTATACAAGTAG	59.086	52.381	0	0	0
0 8;20	GCGCCTAGTTCGAGATTGAG	59.251	55	0	2.73	0
0 252;20	CCTGCGATGCCCTTAAACTG	60.011	55	0	0	0
0 56;22	GCATTGACTGGAGTTAGTTTGG	58.329	45.455	0	0	0
0 2;21	TCCGGATTGTGCGGTA AATTG	60.012	47.619	0	6.19	0
0 129;20	ACACATTCAAAGAGCTGCG	59.87	50	0	0	0
0 6;21	AGGCATGGATAGAATTGTGCG	59.534	47.619	0	0	0
0 42;21	TCTGTTTCGTATCCCAAGTGG	58.432	47.619	0	0	0
0 4;18	TGTACCGTCGCGTCGTTC	60.842	61.111	2.24	10	0
0 33;19	GTGAGTGTGCATGCTGAGG	59.569	57.895	0	17.41	0
0 13;20	GCGCCTGATTATACTGCAGG	59.591	55	2.77	16.97	0
0 36;20	CTTGACCAGTGCGTTTCGTG	60.771	55	0	0	0
0 23;20	TCATTGACGTTTCGCCAGAC	59.594	50	0	0	0
0 22;20	TATCCGTTGTTGTTTCGCCC	59.588	50	0	0	0
0 1;20	CTCTAGGCTAGCGACAGGTG	60.082	60	0	0	0
0 6;18	GCCCACTACGGTTGCCTG	61.487	66.667	0	0	0
0 59;21	ACGCCGTGTATGTGCATATTG	60.147	47.619	0	0	0
0 79;20	GCGCCTAGTTCGAGATTGAG	59.251	55	0	2.73	0
0 329;20	TGCCATTCATTAAGCTCGCG	60.083	50	0	0	0
0 40;20	TACTCGCGCTTGTTCATG	60.568	50	0	4.1	0
0 79;20	AAAGTGCTTATCCGACGTGC	59.663	50	0	0	0
0 3;20	GTAGGACTTGCGGCAGAGAG	60.925	60	4.66	12.25	0
0 52;18	GCTTGCCATCGGTGTCAC	59.857	61.111	0	0	0
0 67;20	GCCCTCTATTTGTCAGCAG	59.656	55	0	0	0
0 5;19	TCGCTTTGTCGTGTGCATG	60.158	52.632	0	0	0
0 9;20	GAGCTGGAGACTCGAGGAAC	60.293	60	0	11.22	0
0 35;20	AGGCCACTATGCAAGCAAAC	59.866	50	0	2.76	0
0 46;19	CACCAGCGAACACACTCTC	59.209	57.895	0	0	0
0 22;22	CACTCAACCTCTTCCTCTCTTG	58.837	50	0	0	0
0 38;20	CACACACATTCGTCGACTG	59.946	55	1.55	1.55	0
0 7;22	AGTGCCTTGATTTGAGATTGGG	59.678	45.455	0	0	0
0 21;20	ATTAGAGATTCAGTGCGCGC	59.525	50	24.02	24.02	0
0 194;20	AGGTCAAATTGCAGCCGAAC	60.152	50	0	0	0
0 3;18	GAAGACCGAGTGAGTGCG	58.564	61.111	0	0	0
0 53;20	TGTGCATTTGAAACCCACAC	58.157	45	0.62	7.59	0
0 31;20	TCGATTTGTTGTCAGCCGTG	59.873	50	0	0	0
0 154;20	ATTGGATTGTTGACGCTGC	60.292	50	0	0	0
0 33;20	CCCGCTTAGAAACGGTGTTG	60.222	55	0	0	0
0 65;22	GACAGATGAATAGATGGACGGG	58.84	50	0	0	0

0 85;20	GCGCCTAGTTCGAGATTGAG	59.251	55	0	2.73	0
0 43;21	CATGTCTAGCTCGTATTGGCG	59.684	52.381	0	0	0
0 43;20	AAGCACTTCTCTGTAGCGAC	58.388	50	0	0	0
0 136;20	TGCCTATATGTGTACACGCC	58.23	50	0.21	13.88	0
0 95;20	GGGTATGCACATAGGGAGGG	60.078	60	0	0	0
0 143;20	TCAGTCGCTCCTTTCCTCTG	59.866	55	0	0	0
0 187;20	CGTCTGAAAGAGGCCTGAAG	59.025	55	0	0	0
0 19;20	ACAGCAAACGGAGAGACAGC	61.351	55	0	0	0
0 35;22	GCCATTAGTGAAGTACTAGAGAGCG	59.373	50	0	0	0
0 8;20	CAAGGGAGTGGGACGAAAGG	61.081	60	0	0	0
0 20;19	CCTCCATCGCTTCCCAAGG	60.909	63.158	0	0	0
0 19;20	ATCAACCAAATCAAGGCCGG	59.576	50	0	0	0
0 110;20	CTGCAGGGAAGTTACACGAG	59.027	55	0	2.22	0
0 2;18	GCACAGACGCATGCAAGC	61.221	61.111	0	4.41	0
0 60;20	TAGCTGCGGAGACCACTAAG	59.652	55	0	0	0
0 8;20	GCTTGAGGTATGCGTGCAAG	60.638	55	5.37	5.37	0
0 80;20	AAGCTGTGCCTACCTCATCC	60.224	55	0	0	0
0 23;21	CACGAAATGACAGCCGGATAC	60.148	52.381	0	0	0
0 6;21	ATACATACACAGGGCACATCC	58.276	47.619	0	0	0
0 26;20	CAGGCTCTGGTTCATGTAC	58.723	55	0	0	0
0 31;20	ATGGACGGATGGATGAGCTC	60.079	55	3.53	3.53	0
0 48;21	CCTTTCTAATCGGTGCTACGC	59.882	52.381	0	0	0
0 8;22	CTTTGCTACGTGACGATTGAAC	59.012	45.455	0	0	0
0 93;20	ATGCTGCCTCTGAAGACGAG	60.578	55	0	0	0
0 9;22	AGTGCTCATTACCATCTCGC	58.972	45.455	0	0	0
0 38;20	ATCTCCCATGAAACTGGCCC	60.518	55	0	0	0
0 2;21	CATGTACTGCTCGGGTCTAAC	58.937	52.381	0	0	0
0 96;20	ACAATCCGTTAAAGCTGCCG	59.941	50	0	0	0
0 0;20	GCGCCTAGTTCGAGATTGAG	59.251	55	0	2.73	0
0 32;20	GCGCCTAGTTCGAGATTGAG	59.251	55	0	2.73	0
0 25;20	ATCTGGCAAACGTTACAGCTG	59.87	50	6.96	11.52	0
0 90;19	TTCCACTCACAGACCCGTG	60.007	57.895	0	0	0
0 62;21	CGTCCATAGCACTGAAGACAC	59.48	52.381	0	0	0
0 242;20	AATAGACGAGTGAGACGCCG	60.362	55	0	0	0
0 0;20	AGGTAATGTGGGTGGGAGAG	59.193	55	0	0	0
0 37;20	CTTTGCACCGATCCTTCAGC	60.292	55	0	0	0
0 61;20	TTTCTTGCTCTCTGTTGCC	59.148	50	0	0	0
0 23;20	AGATCGACGTTGGGTTCTCG	60.573	55	0	0	0
0 99;18	AAAGGGAGGGCGAGCAAG	60.403	61.111	0	0	0
0 32;20	GTGAAGCCCAGTTGACGAAG	59.872	55	0	0	0
0 12;20	TCTAGCCGAGCCCAGACTAG	60.944	60	0	0	0
0 55;20	ATTGTTTGTGAGGACGTGCG	60.153	50	0	0	0
0 31;20	GGAGGAATACAGGACGGGAG	59.72	60	0	0	0
0 71;20	ACACATGTAGAGAGACCGGC	59.938	55	0	0	0
0 59;20	GGGTGACGATGAGAGTGAGG	60.294	60	0	0	0
0 5;20	ATTGTTGTAGACGGAGGGCG	60.861	55	0	0	0
0 65;20	TCGTCCCGTAATTCTCCAGC	60.294	55	0	0	0

0 21;20	CATCCGCTCACTGTGACAAG	59.664	55	0.81	6.61	0
0 175;20	AGATTGGGTTCTCACAGGGC	60.442	55	0	0	0
0 96;20	TTTGCAAGCCTGTACGATGC	60.223	50	1.1	1.1	0
0 37;20	TCCTTCTCATCTGGCCCATC	59.639	55	0	0	0
0 3;20	TAAGCGAGACGACCTTGACC	60.223	55	0	0	0
0 72;20	AGCGAGTGAGTGGAGTTAGC	60.223	55	0	0	0
0 51;20	CGCTACCACTATCTCTCGCC	60.502	60	0	0	0
0 181;21	GCGAGCAAGAACGTTATGAAG	58.703	47.619	0	4.2	0
0 35;20	TCAGCCATTATCGATCCGGC	60.791	55	15.44	15.44	0
0 76;20	GGCTTTGTGGAGTTGGGAAC	60.081	55	0	0	0
0 74;20	TCGTCGCCTGCTTCTTTCTC	61.132	55	0	0	0
0 27;20	CAACTGATCAGACCCACCCG	61.146	60	0.7	25.48	0
0 7;20	TCACTGCGTTGGTCCTCTTC	60.72	55	0	0	0
0 66;20	GCTCATAACCGGTAGAAACGC	59.528	55	2.67	8.11	0
0 5;19	GGGCCACATCGACTCACTC	60.898	63.158	0	0	0
0 23;19	CTCTCGTGGCACTGGTACG	60.887	63.158	0	0	0
0 118;22	AATCATTTGCGCAAGCTAACTG	58.393	40.909	0	0	0
0 181;20	AAATGGTTCTCACAGCGCAC	60.152	50	0	9.33	0
0 107;20	CGTAGTGGACAAGTTTGGGC	59.871	55	0	0	0
0 0;20	CCATTGATCGCTGCCAAATC	58.61	50	0	0	0
0 7;19	GCAATCGAGGAACCGCAAG	60.304	57.895	0	0	0
0 30;22	GCGGTTGATTTAGAGGATTTTCG	58.547	45.455	0	0	0
0 29;21	CCACTAACCACAAGTGTAGGC	59.332	52.381	0	0	0
0 131;22	AATCATTTGCGCAAGCTAACTG	58.393	40.909	0	0	0
0 46;21	TTCGAACCTAAGCCGTAGTTC	58.527	47.619	0	0	0
0 36;18	CTCGTTCGCTTGCTCTCG	59.341	61.111	0	0	0
0 106;20	CACACTTAAGCTGAGCGACG	60.016	55	0	0	0
0 12;20	GGCTGCAGAAAGTCACTACG	59.665	55	0	0	0
0 12;20	ATGTGCGTGCATGTTCTCTC	59.661	50	0	3.2	0
0 6;20	TCCTGTCTGACTCATTCGGC	60.223	55	0	0	0
0 89;20	TTGCGCTGTATCTTGTGTGC	60.222	50	0	7.66	0
0 14;20	CCGACCTGATGAGCCAAAGG	61.501	60	2.25	2.25	0
0 82;21	GGCATTGCACGAAATTGTCTC	59.484	47.619	0	8.53	0
0 52;20	TTGACTCGCCATCTTTCCTC	58.366	50	0	0	0
0 36;20	TTTGTACACACCTGAGCACG	59.166	50	0	0	0
0 69;19	CTGCATGCCTGGCTTTCTC	59.935	57.895	0	4.42	0
0 21;19	GGCTGTTTGTGCTGTCTG	60.158	57.895	0	0	0
0 25;20	TAGCCCAGTGAGTCGAGAAC	59.58	55	0	0	0
0 3;20	CAGTACAGCCTGGAACCTTG	58.939	55	0	0	0
0 173;20	CCATGCATGCTTCTCTGTCC	59.727	55	0	17.79	0
0 12;21	GTACACCAAAGAGAGTGCGTG	59.948	52.381	0	0	0
0 34;20	CCGCGCTCTTTCCTATTTTCG	60.153	55	0	3.47	0
0 140;20	GAGTTTCAGCGGGCGTATTG	60.361	55	0	0	0
0 109;20	CCATGTCGAAGCCATGAACC	60.011	55	0	9.61	0
0 24;20	AAGGGAATGCTTTGCTTGGG	59.789	50	0	0	0
0 78;20	GAAGAGACAGAAACACGGCC	59.592	55	0	0	0
0 25;20	ATTGCCGACAGAGGATGATG	58.504	50	0	0	0

0 171;20	TTGACAAATGACAGCGGCAG	60.152	50	0	0	0
0 83;22	GTTTGCACGGCCGAATAAATAC	59.637	45.455	7.26	20.01	0
0 70;20	CAGAGACCAAGCTGCAATCG	60.013	55	0	0	0
0 3;20	GGACATCCCTTGACGACTCC	60.579	60	0	0	0
0 94;20	CCGAGGTATGCTGCATCTTC	59.237	55	7.1	10.78	0
0 21;20	CCAGAGCCATTGAAGGTTGC	60.223	55	0	0	0
0 19;20	CGAATGCCTCACTATGTCCG	59.245	55	0	0	0
0 1;20	GTGAGCAGCTGGATTGTACG	59.735	55	0	0	0
0 0;18	GAGTGAAGGGAGGGAGG	58.706	66.667	0	0	0
0 17;21	CGTGACATGTGGGAAGTATG	60.348	52.381	0	22.97	0
0 351;20	AGAGTGAAGAAGGTGGGCTC	59.788	55	0	0	0
0 8;20	TCATGCACCTTCGCTGAAAG	59.587	50	0	0	0
0 0;18	GACAGAGGCAGCAACACC	59.075	61.111	0	0	0
0 24;20	TGACTAACCCTAGCCAGCG	60.223	55	0	0	0
0 36;18	TTTGTGACCCGACGCAGC	61.703	61.111	0	0	0
0 5;20	AACGCATGGTGTGACAAAGG	60.081	50	0	0	0
0 83;20	GCAGAGAACAACCAGCAGAC	59.872	55	0	0	0
0 32;20	CGCAGACCGTTATACAAGCG	60.153	55	0	0	0
0 27;20	AAGAGCTCGGAAGGCATAG	60.007	55	0	5.28	0
0 54;20	TGGGTTTATGAGGGCGAAGG	60.514	55	0	0	0
0 36;20	CTGGCCAGCTCTGATGATTC	59.156	55	0	17.84	0
0 9;19	CATGTGTGCCTGTATGCC	59.637	57.895	0	0	0
0 33;22	TCCCACATTACATAGAACGGTG	58.633	45.455	0	0	0
0 101;20	AGTAAAGGCAAGGGTACGCC	60.798	55	0	0.03	0
0 58;21	CGGACTGCTTCTATTGCTCAC	59.814	52.381	0	0	0
0 2;20	CTGTGTGCCATCAGTTGAC	59.87	55	0	0	0
0 7;19	GCTCGGCAGGCAATGATTG	60.671	57.895	0	0	0
0 37;21	CCAGTTCTGTTACTTCACGGG	59.337	52.381	0	0	0
0 18;20	GCTGGATGTTGCCTGGATG	60.294	55	0	0	0
0 7;19	GCGCTCTACAAATGCTGGG	60.012	57.895	0	0	0
0 106;20	AGCATGCTGAGTAGGGAAGG	59.933	55	0	16.97	0
0 1;20	CTCCCTCCCGTCTTTCATC	60.295	60	0	0	0
0 8;18	GCGACCATGCTTCTCGAG	59.022	61.111	2.6	2.6	0
0 79;22	TCTGTCAAGACGATCAAGAACG	59.182	45.455	0	0	0
0 12;20	TCTCAGCTTACGGTTCCTCG	59.94	55	0	0	0
0 123;20	AGATCAACTACCGAGACCGC	60.01	55	0	0	0
0 159;20	GACAGGGAGAGAATCGGGAC	60.009	60	0	0	0
0 0;20	CCGATTATGGCACCAAGACG	59.803	55	2.7	2.7	0
0 7;22	AGCTCGGTATTCAAGTAGTGTC	58.385	45.455	0	0	0
0 26;20	CACAGCTGCTTCGCTCTATG	59.806	55	0	12.01	0
0 116;20	ACGCGTAGAACCAGAAATGC	59.663	50	0	8.95	0
0 89;19	TTGAAGCCGCATACCCGTG	61.488	57.895	0	0	0
0 32;20	GTATGTCCGTCCCGTTATCG	58.692	55	0	0	0
0 93;18	CGAGACTCCGCATCTCCG	60.393	66.667	0	0	0
0 113;20	CCGATGTAACGTCAACCCAG	59.383	55	0	0	0
0 17;20	GTGTTTCGTGCATGAGTGCC	60.222	55	0	1.2	0
0 114;20	GACAGACAGGAATGTGCGTG	59.944	55	0	0	0

0 25;19	CGTCTCTGTCGTCTGTCCG	60.59	63.158	0	0	0
0 99;19	ACGCGCGTGTAATTTGTG	58.651	47.368	0	32.31	0
0 6;21	CACACTTGCATGCATATACGC	59.091	47.619	0	3.96	0
0 60;22	CCTGCAGTGAATGATAGCTTCG	60.207	50	0	10.84	0
0 95;20	ACAAGAATGGCGTCAACTGG	59.513	50	0	0.25	0
0 125;20	GTGTGACCCAGATTTTCAGCC	59.583	55	0	0	0
0 187;20	CTTTCTGCTGTGTCTGCCTG	59.871	55	0	0	0
0 74;20	CGTGACCAGCCAGTTTCTTC	59.872	55	0	0	0
0 87;21	AGCACTCCAAGGTTAGGTAGC	60.215	52.381	0	0	0
0 117;20	GGGTCTTGTGGCAAATGGTC	60.152	55	0	0	0
0 1;20	CATCATCCTGGGCATCACAG	59.15	55	0	0	0
0 10;21	AGCTCCTCATTGTGTTTCTC	58.7	47.619	0	0	0
0 8;20	GGTTGCTGTACGAGTGACAC	59.597	55	0	0.96	0
0 204;20	GTCATCGGCAGCGACTTATG	59.876	55	0	0	0
0 1;19	ATGCGCACTCACAACCATG	59.863	52.632	0	10.99	0
0 212;20	TGTGAGAGACAGTCGCTAGC	59.941	55	0.76	0.76	0
0 75;20	CCCGTTGTTCTGTGATTCC	59.585	55	0	0	0
0 25;20	TGATGACAGGTGAGGCATCG	60.579	55	0	3.84	0
0 38;20	TGTGTGCATGCGGGTATTC	59.94	50	0	0	0
0 69;21	GGTCCTATTTCCACAGCAACG	60.012	52.381	0	0	0
0 81;20	ACCGGGACAGCTCATCATAC	60.008	55	0	4.15	0
0 4;20	AGAGGAAGGAAGTGCTGTGCG	60.152	55	0	0	0
0 159;20	ATAGTCGATCGAGATGGCGG	59.941	55	0	11.43	0
0 67;20	AGGAGTGCAGAGGAGAATGG	59.568	55	0	0	0
0 154;20	GTCCATCTGCCGAATTCCAC	59.729	55	0	0	0
0 17;21	ACAGATCAGACACATGCATGC	59.74	47.619	6.51	22.71	0
0 133;20	CCCACTGTCCTGACTTCTCC	60.152	60	0	0	0
0 20;20	TATGTGACCGGATGCAAACC	59.009	50	0.4	0.4	0
0 63;20	TTGCCCTTCATGGTTTCTGC	59.792	50	0	0	0
0 57;20	AGCGCCTAGTTCGAGATTGG	60.647	55	0	2.73	0
0 249;20	ACACATGCTGCCACTTGAAC	60.081	50	0	0	0
0 42;20	TGACCTAGACTCGCCATTGC	60.579	55	0	0	0
0 11;19	AGCAGAGGAGTGGAGGGAC	61.079	63.158	0	0	0
0 4;20	GAAACCAGGCTGCACAAACC	60.998	55	0	0	0
0 10;20	CTGTTGGTGGTGTACGCTTG	60.153	55	0	3.49	0
0 137;20	TCAGTCGCTCATCTGCTAGC	60.364	55	4.81	4.81	0
0 48;20	TATTGCTTGCTTTCCGGGTGC	60.223	50	0	0	0
0 37;20	GGTTCCTTAATTGGCCACGC	58.749	50	0	0	0
0 42;20	GCGCCTAGTTCGAGATTGAG	59.251	55	0	2.73	0
0 9;20	TCGGCAGCTCAAATTCTCTG	59.018	50	0	0	0
0 157;19	GGTTCGGGTCAACTGCTTG	59.79	57.895	0	0	0
0 78;20	CCGTTGCAGAGTTCATGAGC	60.292	55	0	0	0
0 98;20	CTGCGCATTCACTACGTCTG	60.084	55	0	10.11	0
0 63;20	TGTGTGCACGTTGGTATTTCG	59.874	50	0	0	0
0 37;21	CTTACGTCCTTGATTGCCAC	60.012	52.381	0	0	0
0 3;20	AGAACCCGATCATGGAGCAG	60.296	55	0	0	0
0 149;20	TACTACTCCGCTTCGTCCG	60.082	55	4.12	4.12	0

0 33;20	AGCATTGTGAACCGTGAGTC	59.234	50	0	0	0
0 31;20	ACCATGTTCTTTCGCAGCAC	60.152	50	0	0	0
0 168;20	CTCCCTTCCAACCTCCAGTCC	60.151	60	0	0	0
0 41;20	ATGACGAGACCAATGTGAGG	58.074	50	0	0	0
0 28;20	TCAGCGCGTTGGAGAAATTC	59.943	50	0	19.23	0
0 124;20	CATCTTTGCCGAACCTCCAC	59.941	55	0	0	0
0 98;20	ATAGACGCGGATTCAACG	60.153	50	0	14.76	0
0 68;20	ACACATAAAGACGGAGAGCG	58.462	50	0	0	0
0 8;20	TTCTCCCTTCTGCCGACTC	60.152	55	0	0	0
0 64;20	CAAACCTTGGGCGTAGATGC	60.293	55	0	0	0
0 141;20	CCGGCAGCCTTATGTTTACG	60.083	55	0	7.41	0
0 72;22	AGAGACGTAGATGTACCGAGAG	59.038	50	0	0	0
0 158;21	CCTTTCGGTTCCTTCTCCTTG	59.33	52.381	0	0	0
0 33;20	GGAGTCCAAGCAATTCCGTG	59.941	55	0	0.31	0
0 31;20	CAGTATGTAGCATGGCCGTG	59.521	55	17.37	17.37	0
0 62;20	AGACTGAAAGACGGACCGAG	59.868	55	0	5	0
0 45;21	GTGAGCCAGACAGTCATTGAG	59.405	52.381	0	0	0
0 208;20	GCAACATAGCCGCACGTTAG	60.702	55	0	0	0
0 44;20	TAGTGAAGAGGGTCGTGCAG	59.866	55	0	0	0
0 24;20	TGCTGACATCCACCTAGCAC	60.51	55	0	0	0
0 12;20	TCCTGCTGATACCGACATTG	58.15	50	0	0	0
0 189;20	CGAGGTTTGAAGTGCAGAAC	60.499	55	0	0	0
0 6;20	GGCCGCGAGTGATATATATGC	59.457	55	0	0	0
0 63;20	AATTCCACCGCCATGTTCTG	59.58	50	0	0	0
0 15;20	ATTCACACAAATACGCGGGC	60.293	50	0	0	0
0 7;20	CACATGCACACACAAGCTGG	61.059	55	0	0	0
0 22;20	GCGTGCGTAGTAAAGATGGG	59.806	55	0	0	0
0 32;20	GCTTGCACGCTCGTAGTTAC	60.358	55	0	4.02	0
0 16;20	CATCCTCCCTCGTCTACCAC	59.723	60	0	0	0
0 13;20	GACTTGTTATAGACGCGGC	60.084	55	0	0	0
0 48;22	TCTCACTTCTCACATAACTGC	58.569	45.455	0	0	0
0 45;20	CCATTCATGTCCTCTCACGC	59.449	55	0	0	0
0 14;21	CGACACTGGATTGATTAGCCC	59.539	52.381	0	0	0
0 59;20	AGAGATGGAAAGACGGAGGC	59.935	55	0	0	0
0 142;20	CTTCCGAGGCTACTGAGGTC	60.01	60	0	0	0
0 78;20	AAAGTTTGCCGTCTAGCTGC	59.87	50	0	0	0
0 30;20	TTGACTGCAGACAAGCCAGC	61.923	55	0.43	21.13	0
0 1;20	CCCACGTGCTGCATATTTGG	60.644	55	8.32	8.32	0
0 0;18	GGATTGGCAGCGTTGACC	59.855	61.111	2.13	2.13	0
0 57;20	TAACATCCAGGTCTGTCCG	59.573	55	0	3.83	0
0 1;20	GCTAACCTGAGCTAGCTGG	60.651	60	11.31	15.05	0
0 159;20	CCTGTAGGCTAGTGGGTGTC	59.936	60	0	1.4	0
0 193;20	TAGGAGACGGGTGTATGGTG	58.993	55	0	0	0
0 190;20	AACGTATGCTGCAAGGGTTG	59.869	50	0	0.4	0
0 13;18	AGGGTGACGGATGTGCTG	60.085	61.111	0	0	0
0 32;18	TGACACACAGGCGCAGAG	60.708	61.111	0	0	0
0 191;20	TATCCTCTCGTCTGCAGCG	60.363	55	16.32	16.32	0



0 199;20	GCTCACACAGACGATCAAC	59.665	55	0	0	0
0 5;19	GTCCTCACGTACACACCCG	60.816	63.158	0	0	0
0 2;18	GCACGCGTTCCATGACTG	60.24	61.111	0	0	0
0 126;20	CAGCCGAGAGAGCATTGAAG	59.452	55	0	0	0
0 39;20	ATATGTAGGTGGGAGCAGGG	59.044	55	0	0	0
0 125;20	GTAGTATCCCTGCCGTGGTC	60.365	60	0	0	0
0 0;19	CTACTGTAGTGTGCCCAGC	58.299	57.895	0	3.06	0
0 2;20	ATTACGACTGCCTACTCGCC	60.364	55	0	0	0
0 10;20	CCGCTGTCTTCATCTCAGTC	58.82	55	0	0	0
0 27;22	CGTCTCACTCTCGCGTTAATTC	60.206	50	0	0	0
0 107;20	TCAGTTTCACCCGTTTGCAC	60.011	50	0	0	0
0 87;20	ATTCGTGACTTCCCGCCTAG	60.294	55	0	0	0
0 36;20	ATGAGTGTGACGATTGCAGC	59.94	50	0	0	0
0 29;21	GCACACAACGACATAATTGCC	59.486	47.619	0	0	0
0 21;20	AAAGAGACGCAAACAGGGAG	58.868	50	0	0	0
0 61;20	AGAAGGCGAGAGATGACTGC	60.294	55	0	0	0
0 17;20	ACGAATTTAGCTGGTCTGCC	59.013	50	0	0	0
0 71;22	TCCAAGTATAAAGAACCACGGC	59.161	45.455	0	0	0
0 23;22	TGTAGGACTAGTTCTGCAAAGG	58.23	45.455	0	14.05	0
0 36;20	AATTCCTGTGTGTTCCGCCAG	59.513	50	0	0	0
0 204;20	TGATCTATACGTCGGCAGCG	60.501	55	0	0	0
0 147;20	TTTGCTTCTTCGGAGTGACG	59.242	50	0	0	0
0 76;20	TATGCTGCTGTGTACCGTCG	60.921	55	0	0	0
0 0;20	ACCGTAACCTCCACCTCAAG	59.79	55	0	0	0
0 68;20	GAAAGACCTGTGCACACGAG	59.874	55	1.27	7.5	0
0 135;20	TTGTCATCCTCGCTCTCCAC	60.223	55	0	0	0
0 66;22	ACGAGCACAATGTCTACAAAGC	60.271	45.455	0	0	0
0 10;20	TGTCGTTGTTGTAGCAAGC	59.876	50	0	0	0
0 9;22	AGAGGTAGGTAGAAACGCAGAG	59.748	50	0	0	0
0 95;20	GTGCACCGTTTGAGTCTGTC	60.153	55	0	1.78	0
0 26;20	TAGAGCGGTCAGGAATTCGG	60.009	55	0	15.29	0
0 17;20	TTTCCTCCTGCCCTTCTCTG	59.786	55	0	0	0
0 1;20	CCGGTATGATGTTGTTGGC	60.083	55	0	0	0
0 1;20	AATAGTTACCCATCCGCCGC	61.007	55	0	0	0
0 0;20	CTACACGACCTAGTCTGGCC	60.01	60	0	0	0
0 117;21	GGCAGACAGAGGAACGAAATG	60.013	52.381	0	0	0
0 2;22	AGGATATTGTTGACGGCCTTAG	58.694	45.455	0	0	0
0 35;20	ATTCCTCGACTGCAACCTCG	60.859	55	0	0	0
0 2;20	ACAGCCGTTTGTGCGTTAC	60.707	50	0	0	0
0 5;20	AGTGCATATCGACTCTCCCG	59.797	55	0	0	0
0 13;19	CATGCTGCCAAGACGTTCC	60.231	57.895	0	0	0
0 38;20	CTCTAATCGGATTGGCGAGC	59.315	55	0	7.95	0
0 117;20	CACTGCCAGATATCCAACGC	59.802	55	0	0	0
0 18;20	GCTCATGCGTCTTGACTC	60.014	55	0	0	0
0 114;18	CCCTCTGTGCTCTGCTGG	60.479	66.667	0	0	0
0 4;20	TCGTCCGGCCACTCATTAAG	60.578	55	0	0	0
0 59;20	CATCTCTTAACAGCTCGCGC	60.153	55	0	0	0

0 34;20	TCGTCAACCTGAACCTAGCC	60.152	55	0	0	0
0 41;20	CTTACAAATCGACCGGCCAC	60.013	55	0	0	0
0 115;20	ACCCGTGTTTCCGTTTCTTC	59.445	50	0	0	0
0 42;21	GGTGCAGAAGAGAAAGATCGC	60.081	52.381	0	0	0
0 44;20	GGTGCTGTCGTTTCTTCTCG	59.946	55	0	0	0
0 185;20	ACACTATCCTCTTCGTCGGC	60.01	55	0	0	0
0 135;20	CGGTTTCTCGCAGGTCATTC	60.014	55	0	0	0
0 104;20	GTATGCAGCCAATGAGCTCG	60.153	55	0	6.65	0
0 22;20	CATTGGCAGTGGAGGACAAG	59.582	55	0	0	0
0 5;18	TGCCTGTCCGCTTGTCTG	60.712	61.111	0	0	0
0 2;22	TCAGCATAGTGAACCTTTTCGAC	59.17	45.455	0	0	0
0 17;22	CCTAGTTGTCAATTTGCTACGG	58.149	45.455	0	0	0
0 27;19	ACAGGAGAGTGAAGGAGCC	59.087	57.895	0	0	0
0 16;20	ATTTCCATTGAACCGGCTGC	60.223	50	0	0	0
0 178;20	GCACACCAATCGCTATCTCG	59.876	55	0	0	0
0 16;20	TATCGTTTCGCTTTCTTGGGC	59.378	50	0	0	0
0 194;20	GAGACCAGGCCTGATCTCTC	59.72	60	17.02	21.33	0
0 101;20	TCCGTCTGCATGTCTCTGAG	59.939	55	0	0	0
0 88;20	TTCTCACAGGGCGCTATACC	60.008	55	0	0	0
0 46;20	CAGAGGGCAAGAATAGGCAC	59.081	55	0	0	0
0 26;20	GAAGAACGGAGGAAGAGGGC	60.863	60	0	0	0
0 1;20	GCGTTGCCTTACTGAACTCG	60.291	55	0	0	0
0 59;20	AGATTGAGTTCTCGCAGGGC	60.865	55	0	0	0
0 46;20	TCTGACAACCCACGAGTCTG	60.081	55	0	0	0
0 35;22	AAGGACACAACCTGAGAAGCTAG	58.5	45.455	0	0	0
0 2;20	TCCATTTAGCGCCACAGGAG	60.867	55	0	0	0
0 27;20	TCACCCAGGATCATGCTTTC	58.339	50	0	0	0
0 101;21	AGTGAGTTGCAGTTAAGCCAC	59.535	47.619	0	0	0
0 8;20	GCCTTCCTTTAGTGCAGAGC	59.657	55	0	0	0
0 6;20	GGTTCACACTTGCTTGTC	60.081	55	0	0	0
0 78;20	TTCCACAGGTTCCCAGAGTC	59.714	55	0	0	0
0 4;20	ACAGCAGTTCACTCCAGAGG	60.079	55	0	0	0
0 92;20	GGTAGCACCGACTTACAACG	59.39	55	0	0	0
0 9;21	CGAGCAACCTTCCTGATAAGC	59.811	52.381	0	0	0
0 60;18	CATATGTGTGTGCGCCCG	60.012	61.111	0	0	0
0 30;20	GATTGAGTTCTCGCAGGGTG	59.379	55	0	0	0
0 31;20	GAAACTGACCGGCATGTGAC	60.222	55	0	0	0
0 139;20	CTGAATCGCCTCTGTCCCTG	60.931	60	0	0	0
0 116;21	TGTCTTCCCTCTGTTATCCGG	59.662	52.381	0	0	0
0 29;20	CGTACCTGTGCTCGTGTAAC	59.395	55	0	0	0
0 19;20	ATCAGTAGTCCGAGCCGATG	59.797	55	0	0	0
0 47;20	TCTTAGCCAACCTCTGAGCC	59.862	55	0	0	0
0 2;21	CCCTGGTTTGACTGTGTGTTT	60.079	52.381	0	0	0
0 275;20	TTGTGTGGAAGAGACGGGAG	60.08	55	0	0	0
0 15;21	CAAAGTAGTGCATGGCTGAAC	58.537	47.619	0	0	0
0 172;20	TCTCCTGCACACTGTTCTCC	60.08	55	0	0	0
0 3;18	CAGACCTGTGCGTGAGAG	58.159	61.111	0	0	0

0 64;19	ACCGATATCTGGTTCCCGC	60.007	57.895	0	11.5	0
0 34;20	TATACGAACCTGGAGTCCGG	59.074	55	12.14	12.14	0
0 59;22	CGGTAACCTTTATCATTGCGGG	59.95	50	0	0	0
0 28;20	GTCCATGCCTGCCTTTTCATC	60.01	55	0	0	0
0 175;20	ACCAGCCAGTTCAATGCATG	59.865	50	0	0	0
0 93;20	AAGCCACCACACTAGATCGC	60.863	55	0	0	0
0 45;20	AGCCTTTGTATGGCACTTGG	59.213	50	0	3.3	0
0 27;21	TCCCAAATAGCAACACATGGC	59.94	47.619	0	0	0
0 55;20	TGTGCCCAGCCCTAAACTAC	60.441	55	0	0	0
0 162;19	CCGGGACATGGGAGAAGAG	59.931	63.158	0	0	0
0 1;20	TCCTCTCATGTAGCCAGCAC	59.936	55	0	0	0
0 71;20	GCGTTAAGGCAGAAGTGTTG	58.416	50	0	11.43	0
0 8;20	CCAGGTTGGCACGCTCTATC	61.561	60	0	0	0
0 7;19	GGGCACGTAAACAGGTCG	59.867	57.895	0	0	0
0 180;20	GTTAGTAGCCGGCCTCAGAG	60.987	60	0	1.05	0
0 130;20	TCTTATACACCTCTCCGCGC	60.081	55	0	0	0
0 236;20	CAAACAACTCAATGCCGCG	59.948	50	0	0	0
0 79;20	TACCATCCCTGCGACATCAG	60.008	55	0	0	0
0 5;19	TGTGTCTCCGTGTCGTCTC	59.79	57.895	0	0	0
0 108;21	ACAGAGAATGAGCGAACGAAC	59.413	47.619	0	0	0
0 36;20	ATGAAAGGGTGACGGAGACC	60.151	55	0	0	0
0 56;20	TCTTCCCTTGTCCTGCAC	60.659	55	0	0	0
0 123;20	CAGCACCTCAAACCTTAGCCG	59.942	55	0	0	0
0 122;20	GGTGTTGCGAACGGAGATAC	59.737	55	0	0	0
0 45;20	TCGTTTGCCTTGACATCGC	59.944	50	0	0	0
0 237;20	CATTCTGCGAGTCTCCAAGG	59.095	55	0	0	0
0 115;20	GCACTGTACGAAGACTGAGC	59.391	55	0	0	0
0 98;20	CTTCAATCGGTCACCAACGG	59.943	55	0	0	0
0 38;20	GTGATATGCTCCTCGGACCC	60.437	60	0	0	0
0 103;20	CGGAGTAGGAGAGGCACAAG	60.294	60	0	0	0
0 111;20	TCAAGGGCACATAGGTCTCG	59.936	55	0	0	0
0 78;19	AGTCAGATTCTGCCGGGTG	60.157	57.895	0	3.04	0
0 169;20	ATGCTCTCTTCTCGTCGGG	60.294	55	0	0	0
0 91;20	CTTTGCTTGCTACTCCCGTG	59.942	55	0	0	0
0 211;20	ACCGTCTTTATCCTCCCGTG	59.937	55	0	0	0
0 77;20	GCAGCATTCTCAGGGTCAC	59.94	55	0	0	0
0 63;20	CGTAATGACTTCGCGGACAC	60.085	55	0	0	0
0 2;20	TTATTGACAAGCGGTGCCAC	59.869	50	0	0	0
0 43;20	CTCCCTGCCTTCCTTTCC	60.513	60	0	0	0
0 5;20	GGGCTTAATGGTGGTTGCAG	60.223	55	0	0	0
0 61;20	TCAGGCGATTGACTTGCAG	59.587	50	0	0	19.18
0 35;20	AGGCAGTCAGAGAGGCAAG	60.44	55	0	0	0
0 36;20	GTCCGCCTACAGAGATAGCG	60.502	60	0	0	0
0 152;20	ATCTGCGCCAACAATGTGTC	60.223	50	0	0	0
0 181;20	CCGCGATCTCCACTATCCTC	60.223	60	0	5.89	0
0 84;20	GAAGAGTGACAGAGGCACAC	58.954	55	0	0	0
0 138;20	TCTCTCACACTGCTGGTC	60.08	55	0	0	0

0 61;20	ACGAATTTAGCTGGCTTGCC	59.939	50	1.52	1.52	0
0 169;20	AGCCCACTAGACTACGCATG	60.009	55	0	0	0
0 16;20	CAGTGTGTAGGCAGCAGAAC	59.591	55	0	0	0
0 119;20	TCGCAGATCAGGATGACAGG	60.009	55	0	0	0
0 258;20	GGCAGCATCTTTCTACAGCG	60.083	55	0	0	0
0 44;20	ATCCACATCTGCACCTAGGC	60.296	55	0	5.96	0
0 148;20	GTGTATGCAGGCCACATGTC	60.011	55	4.44	9.01	0
0 31;20	ATGGGAAAGAGGAAGGGAGC	59.856	55	0	0	0
0 108;20	GCACTCTCGCTCAATTCGTG	60.359	55	0	0	0
0 0;20	CATCTCGGCATTGTTACCCG	59.803	55	0	0	0
0 48;20	CGTTGCATGAATATACGCG	58.861	50	1.24	1.24	0
0 61;20	AGAGACACTGACGCTGAGAG	59.585	55	0	0	0
0 28;20	TGGGAAAGAAATGGCTGCAC	59.792	50	0	0	0
0 3;20	ATGCATTTCTGGACCTAGC	59.084	50	0	0	0
0 188;20	ACACTATCCTCTTCGTCGGC	60.01	55	0	0	0
0 184;20	CGTTGCTCCTCAGTCAATG	60.013	55	0	0	0
0 163;20	TTCGTAAATGACACAGCGGC	59.944	50	0	0	0
0 56;20	GGGCGATAGGTACTCCAG	60.081	60	0	0	0
0 123;20	TATTTGTGCACGAGGGCATG	59.656	50	0	0	0
0 51;20	TAGCAGACATAGGGCTCGAC	59.437	55	0	0	0
0 9;20	TCCGTTTGTCTGTCTGCC	59.444	50	0	0	0
0 74;20	TTCTCAACTGGCCCTCTC	60.079	55	0	0	0
0 53;20	ATGACCGCGATTCTTTGAG	59.091	50	0	3.57	0
0 0;20	CTTCTTACTTCTGCGCGC	60.635	55	24.02	24.02	0
0 6;20	AAGCTGCCTTTTACTGAC	58.865	50	0	0	0
0 5;20	GCCAGGCAGCTGTAAGAAAG	59.94	55	0	6.2	0
0 22;22	AGTTTAAACGTTCAAAGCATCGG	58.605	40.909	0	2.57	0
0 35;20	TTTGACGACACACTGCGAAG	59.806	50	0	0	0
0 7;20	CCGTGCTAGAAGGGAAAGTG	59.02	55	0	0	0
0 27;20	CGCCTTAACTTTGACACCG	60.222	55	0	0	0
0 187;20	TTAGCGGATACTGGCCCTTC	60.007	55	0	0	0
0 169;20	CCAATAGCAGGCCAGTTTTG	59.937	55	7.83	7.83	0
0 61;20	CTCAAAGCTAAGCGACTCG	59.46	55	0	0	0
0 56;20	AGCATGTGACCAAGTTCTG	58.947	50	0	0	0
0 0;18	GCATCTTCCAGCGTCGG	59.63	61.111	0	0	0
0 140;20	CGCAGAGTTACAGCAGGTTG	59.944	55	0	0	0
0 31;20	CCATCATGGGACTCAAACCG	59.369	55	0	0	0
0 142;20	CTGCAACCTGGATTATGGGC	59.722	55	0	0	0
0 7;20	GCCACGGTTATTACGAGCAC	60.084	55	0	0	0
0 7;20	GAAATGGGCCAGTGTGTAGG	59.293	55	0	0	0
0 103;20	CACAGGGAGCTCACATTTGC	60.223	55	0	5.28	0
0 239;20	AATGGCCCTTAAACGTGTGC	60.152	50	0	0	0
0 18;20	TACGGAATGTACAGCGCTTC	58.822	50	0	0	0
0 3;20	TCACCTCGCTGAACCCTATG	59.936	55	0	0	0
0 1;22	GATCCGTGTGTGCATTTATTCG	59.131	45.455	0	0	0
0 3;18	ACAGGGACAGGGACGGAG	61.049	66.667	0	0	0
0 16;20	TGAACGTTGTAAGTCCACG	59.805	50	0	0	0

0 160;19	CGTGCATGTGTTACGTCCG	60.301	57.895	0	2.66	0
0 39;20	CCGGAGTTATTCACGAGCAC	59.457	55	0	0	0
0 65;20	GGACCATCTGTGTTTGCTGG	59.868	55	0	0	0
0 85;22	ACACAGAGAGCTAGCTAACGAG	60.077	50	5.84	7.37	0
0 16;20	AAGTGGTTCAAATCCGGCAG	59.508	50	0	0	0
0 11;22	TGACCGTGACTGATATTGTTGG	59.165	45.455	0	0	0
0 102;20	TTCGTCTCGTTGAAATCGCC	59.668	50	0	0	0
0 174;20	ACTTGACCTGGGAGTTCGAG	59.792	55	0	0	0
0 45;21	TGCCCTCCCTAATCACGTAAC	60.284	52.381	0	0	0
0 186;20	ACACATATCTCCGAGCCCAC	60.008	55	0	0	0
0 40;20	CAAGGCGAGTTGTGAGGAAG	59.591	55	0	0	0
0 44;20	GGGTGGATCGGTCAGCTATG	60.722	60	0	0.99	0
0 2;20	GTGGCTCTGTCGATTTCTGC	60.013	55	0	0	0
0 14;19	GGCTGCATCTGACGTATGC	59.794	57.895	8.73	8.73	0
0 5;20	AGATTGAGTTCTCGAGGGC	60.865	55	0	0	0
0 9;21	TGCACAGTTCAATCCATGCAG	60.215	47.619	0	0	0
0 158;22	TGAACTAGGCGGTTAACATGAG	58.903	45.455	0	0	0
0 5;20	ATACAGTCCGCTTCTCCTG	59.647	55	0	0	0
0 178;20	CTGGATCGCGAAGAACAAGG	59.735	55	0	0.54	0
0 272;20	CACACGTCCACATTCATGCG	60.909	55	0	0	0
0 56;20	TTCGTCTCGTTGAAATCGCC	59.668	50	0	0	0
0 67;20	ACCCTACTTGTTGCCAGAG	60.078	55	0	0	0
0 18;20	GTGCCCCGACTTGTCTGAAC	60.153	55	9.88	9.88	0
0 68;20	CCAACACCTGTAAATCGCCC	59.94	55	0	0	0
0 1;20	GCTTCACCTGAGCACAATG	60.152	55	0	0	0
0 123;20	GCTTGAGGTGAAAGAGCGAC	59.944	55	0	0	0
0 21;22	TCTATTCGAGAAGCAACGAGAG	58.469	45.455	0	0	0
0 75;20	GAGACGGGTGAGGAGCTTAC	60.294	60	0	0	0
0 236;20	TACCGGCAGCATAGAAGTGG	60.295	55	0	0	0
0 59;20	CACAGACGGCCAATGATGAC	60.012	55	0	0	0
0 168;20	TGTAGCGATGCATGCAAGTG	60.012	50	6.99	12.04	0
0 81;20	TCTTCGGTGAGAGACTGGTG	59.508	55	0	0	0
0 36;20	ATGCAAACACCGACACATG	60.152	50	0	0	0
0 6;21	GAGGGTGGACAGCAAATTAGC	60.011	52.381	0	1.17	0
0 141;20	TTTATAAGCGCGAGGGAGGG	60.366	55	0	0	0
0 5;20	TTCCTGTTTCATCTGTCTGCG	58.663	50	0	0	0
0 170;20	CCTTCGGTGTGCTGTCTTTC	59.872	55	0	0	0
0 31;20	TGCAGCTGAACAGAACTTGC	60.082	50	7.69	7.69	0
0 55;20	TTCGTCTCGTTGAAATCGCC	59.668	50	0	0	0
0 144;20	GCACCTAGTTCGAGATTGCG	59.807	55	0	0	0
0 19;20	TCTCCTTCCCTCCGTCTCCAG	60.805	60	0	0	0
0 29;20	GCTAGCCTTGCTCAAATGG	60.01	55	0	0	0
0 125;20	GTTTCAAGCTACGCCACTCC	59.943	55	0	0	0
0 14;20	TGATGTCAGTTGGGAGCGAG	60.508	55	0	0	0
0 63;20	GCCTCTAGCGAAAGGAATGG	59.161	55	0	0	0
0 89;20	TCTTCGAGACCCAGCTCAAG	59.866	55	0	0	0
0 21;20	TATGCTGCTGTGTACCGTCG	60.921	55	0	0	0

0 89;20	AAGTGGCACCGATATCAGTG	58.437	50	0.46	12.18	0
0 39;20	GGGTGCTAGGCGAGAAAGAC	61.21	60	0	0	0
0 60;20	CACCACTCTTCTGCTTCTG	58.944	55	0	0	0
0 164;20	TAGCACCCACAGATATCCGC	60.08	55	0	0	0
0 83;20	TTCGTCTCGTTGAAATCGCC	59.668	50	0	0	0
0 28;20	ACTGTCTCCAACACCACCG	59.793	55	0	0	0
0 189;20	TTCGTCTCGTTGAAATCGCC	59.668	50	0	0	0
0 83;22	CGAAGTATCTGCGGAGAATGAG	59.441	50	0	0	0
0 18;20	CCGTCTTATCCACCGCTTTG	59.733	55	0	0	0
0 72;20	CTTGCTTTACCTTCTCGCC	59.659	55	0	0	0
0 143;20	CAGATAGCCCTACCCTTCCG	59.792	60	0	0	0
0 7;20	TGTATGTCACCGCCCAACAG	61.078	55	0	0	0
0 56;20	TCGATTCTACTTCCGGCTG	60.009	55	0	0	0
0 56;20	ATGTGTGGGAGCGAGGAAAG	60.797	55	0	0	0
0 45;20	ACAGTGAGACAAGAGACCGG	59.794	55	0	0	0
0 54;20	GAAGGGCAAATGTCACCGAC	60.223	55	0	0	0
0 42;20	AGACACCCTAGGAGCTTTGC	60.151	55	0	0.38	0
0 158;20	GTTTCCAGAGACATGGCAGC	59.94	55	0	0	0
0 65;20	ACTACAAGGCTGGTCTCCAC	59.789	55	0	0	0
0 82;20	GACACGGCAGTTGTAAGAGG	59.311	55	0	0	0
0 111;20	TGAATATGGAGCGTGCGAAC	59.453	50	0	0	0
0 19;20	TCTTCGATCGTTAACCTGCC	58.456	50	0	0	0
0 19;21	GCTGGCACTGTGAGATCAATG	60.349	52.381	0	0	0
0 90;20	GAAACTCCACGATCAGCAGC	60.013	55	0	0	0
0 53;20	AGATAGGCATGGTGGGTTCC	59.931	55	0	0	0
0 96;20	GAGTGTTTTCGCGTCAGGTTG	60.431	55	0	0	0
0 181;20	TTCGTGATGCAGCAGGTTTC	59.871	50	0	18.17	0
0 59;20	CTTCGTCTTTACAGCCGTGG	59.666	55	0	0	0
0 0;20	TGCTAATACAGTCCGCCTCC	60.008	55	0	0	0
0 2;20	TATGGCTTGCCTCTCGAATG	58.508	50	0	10.56	0
0 8;20	CTGTCTGTTTACCTCTGGC	59.231	55	0	0	0
0 3;19	TAGGGCTTCTGGTGCTTCG	60.157	57.895	0	0	0
0 109;20	ATTGACCACTACACCGTTGC	59.23	50	0	0	0
0 18;20	CCTAGGTCCATTGTTGCCAG	59.003	55	0	0	0
0 4;21	AGGCAAAGATTACATCGCCAG	59.466	47.619	0	1.66	0
0 96;20	ACAGCACTATCTCTGAGCCG	60.01	55	0	0	0
0 174;20	TACACCTCTGGCTCTTGACG	59.866	55	0	0	0
0 76;20	TTCCTTCTTCACTCCCACC	59.711	55	0	0	0
0 12;22	CCATGGGTGTACTTTCCTTGTC	59.683	50	0	8.1	0
0 11;20	CACGTGCTCACAGACACATG	60.222	55	0	0	0
0 12;20	CCGATCCTTTAACGCGATGG	59.875	55	0	4.6	0
0 49;20	TCTACCATGCAGCCGTCTAC	60.009	55	0	0	0
0 2;21	CTAGGCAGGAAGTAACAACGC	59.745	52.381	0	0	0
0 28;20	TCGGGATCTAATTCTTGCGC	58.88	50	0	0	0
0 18;21	GTTTGTACTGCGACATGTGTG	58.829	47.619	0	0	0
0 1;20	CTTACCCTGCAACCTTGTC	59.797	55	0	0	0
0 51;20	TCCAGCGTTCTAACCAGCTG	60.791	55	8.24	8.24	0

0 59;20	GCCAATCTCGAACTAGGCAC	59.451	55	0	3.86	0
0 71;20	ACCTTTCGGCTCAGCAAATG	59.868	50	0	0	0
0 26;20	TGTCTTGCTCCTCCGATCTC	59.65	55	0	0	0
0 236;20	GCTATTTCCATTCGCCACCC	60.081	55	0	0	0
0 134;20	GAACCCTCACGCAATCAGAG	59.379	55	0	0	0
0 2;20	CGTG TAGTCTGCTGCCTAAC	59.106	55	0	0	0
0 63;20	TCGCAACTTACCGTGCATTC	59.944	50	0	0	0
0 7;20	GCATGGTAGGTTGGCAGTTC	59.939	55	0	0	0
0 61;20	TCCATGCACCCATTGTTGTG	59.792	50	0	0	0
0 26;20	CGGTCAGCTGTCCTCGTATG	60.988	60	0	11.35	0
0 8;20	GCGCCTAGTTCGAGATTGAG	59.251	55	0	2.73	0
0 68;20	TTGCTTATGTGTCTGGCTGG	58.932	50	0	0	0
0 133;20	TTCGTCTCGTTGAAATCGCC	59.668	50	0	0	0
0 60;20	CGCCAAGAATCGTTG GACTG	60.291	55	0	4.83	0
0 10;22	TCATGATAATTCCCAGGGTGTG	58.608	45.455	0	0	0
0 23;20	AGAGTTGTGTGCATTTCCGC	60.152	50	0	0	0
0 13;20	TGCCCAACACGACAATCAAG	59.798	50	0	0	0
0 163;20	GGGCGCTAGACAAGTAAACC	59.378	55	0	0	0
0 9;19	CGTCCTGGCAGAGTTCCAG	60.825	63.158	0	2.94	0
0 4;21	TGAACATGCATGCAACTAAGC	58.528	42.857	6	16.58	0
0 153;20	GAAATGATGGCGTGGGAAGG	60.01	55	0	0	0
0 18;20	GATTGCACTTCACGACCCAG	59.942	55	0	0	0
0 74;20	GCTTGAATCAGAGCAGCGAG	60.083	55	0	6.78	0
0 0;18	GAGTGGGCCAGCAGAGTG	60.792	66.667	0	5.51	0
0 230;20	TGAAATACCAACAGGCACGC	59.869	50	0	0	0
0 114;20	AGGTGGCAGACTACTTCCTG	59.497	55	0	0	0
0 200;20	ATCTGAGCCACCACATCTCC	59.933	55	0	0	0
0 15;18	AAACCTGGCGCCAAGAAG	58.981	55.556	13.86	22.17	0
0 139;20	CTGAATCGCCTCTGTCCCTG	60.931	60	0	0	0
0 43;21	TGTGCCGCTACATAAATGAGG	59.195	47.619	0	0	0
0 88;20	GCGCCTAGTTCGAGATTGAG	59.251	55	0	2.73	0
0 42;20	GGTAGCATGTCCCATTGCAC	60.01	55	0	0	0
0 199;20	GAGGCCAAAGAGTCCAATGC	59.939	55	0	0	0
0 77;20	CGCACGCTAGTTACCATTGG	60.083	55	0	0	0
0 16;20	TCAAACACGCCAGTTCACAC	60.012	50	0	0	0
0 50;20	AAGCTGCCTCTTTCACTGAC	58.865	50	0	0	0
0 50;20	GGAATGTCAGCCTCTACGTC	58.532	55	0	0	0
0 8;20	CCGTTTCCCATGCTATCGG	59.8	55	0	0	0
0 6;20	CAGCCTGCGACTAATGAACG	60.084	55	0	0	0
0 10;21	GACCTAACCTAACGCATAGC	58.999	52.381	0	0	0
0 21;21	TCTCTAGCGTATCACCCAC	59.188	52.381	0	0	0
0 143;20	TAAATGCGACGTCCAATGGC	60.012	50	2.08	4.15	0
0 112;21	CGTCTGAGTTCTTTTCGCAC	60.016	52.381	0	0	0
0 14;20	TTCCCTGCGAGCAAAGAAAC	59.798	50	0	2.57	0
0 24;22	AGCAAGACATATAGAGCTGCAC	59.034	45.455	0	0	0
0 22;19	GAGACTGCGCCTAGACTCC	60.01	63.158	0	8.55	0
0 43;20	GTGGTCTGTGTATGCTTGCC	59.941	55	0	0	0

0 7;21	CCCAATCTCGATCTAGGCATG	58.786	52.381	0	0	0
0 49;20	GTCCGTGTGAGAGTGGAAAG	58.957	55	0	0	0
0 24;20	CGCACAGCCTTTACAAGTG	59.944	55	0	0	0
0 97;20	CTTACCTCGTCACCATTGCG	59.736	55	0	0	0
0 105;20	AGCCTGGGTAGCTTTCACTG	60.441	55	0	0	0
0 25;20	CTGCGTTGCGTTCATTAGGG	60.637	55	0	0	0
0 102;20	ATCGCGCATTATGAGTGTGC	60.153	50	0	4.94	0
0 19;20	AAACGCAATGTGATGTACGC	58.489	45	0	0	0
0 88;20	TGTCTCGTGCATTTCCGTTG	59.873	50	0	0	0
0 61;20	TGGGTCATGAGGAGAAGGTC	59.2	55	0	0	0
0 111;20	GACGAAGGAAACACACACGG	60.153	55	0	0	0
0 89;20	TGCTCGCGATGTATCTCCTC	60.152	55	0	6.12	0
0 82;20	AACAACAACAGCTGCAGAGG	59.725	50	4.26	11.55	0
0 47;18	CACTGGCCTGGCACTGAG	61.105	66.667	7.78	15.63	0
0 30;20	CTTAATTCAGGCGAGCAGGG	59.445	55	0	0	0
0 13;21	CACTTGCCTTGCTACCTACTG	59.402	52.381	0	0	0
0 0;19	CCGTAACGATGCCATGGAG	59.13	57.895	0	2.48	0
0 78;20	AGATCGCTCTTATGGCCTCC	59.791	55	0	0	0
0 43;20	GCGCCTAGTTGAGATTGAG	59.251	55	0	2.73	0
0 1;20	CTCAATGTTGTCCCTCAGCC	59.296	55	0	0	0
0 40;20	TCCTTCTGTCTCACTCCACC	59.134	55	0	0	0
0 144;20	CGGCGGTCGTAACCTCAAATG	60.359	55	0	0	0
0 47;20	TCTTCAGGGTGAGCTGGAAG	59.788	55	4.6	4.6	0
0 101;20	AGGAACCGGATGCAGATTCC	60.585	55	4.31	5.32	0
0 31;20	CTGCTCGACAAACACAAGGG	60.152	55	0	0	0
0 121;20	ATAGGCGCCAGAGAAATGTG	58.795	50	0	13.73	0
0 53;20	ACCTCCTCCCATAGAAAGGC	59.266	55	0	0	0
0 41;20	TCTCTCTCCGACACCTCAG	60.801	60	0	0	0
0 9;21	GACGTGCTGAATGTAACTGC	58.894	47.619	0	1.47	0
0 0;19	TCTTTGTCCAGGGCAGTCC	60.004	57.895	0	0	0
0 3;20	TAAAGAGGGGCTGCAGAAGGG	60.151	55	0	17.14	0
0 0;20	GTGTAGGGGAGAAGCAGGTCC	60.223	60	0	0	0
0 11;19	GTTGACAACCTGCCAAGCCC	60.38	57.895	0	7.46	0
0 76;20	ACTGATAACCGGACGCTCAG	60.294	55	15.54	15.54	0
0 9;20	TCTTCACTTGGGAGGACTGC	60.079	55	0	0	0
0 128;20	GCGCCTAGTTGAGATTGAG	59.251	55	0	2.73	0
0 47;20	CGATACAGCGTTGCAGATGG	60.153	55	0	0	0
0 16;19	GGCAAGGAAATGTCTGCCC	59.858	57.895	0	0	0
0 80;21	GTGGGACCAAATACTAAGGCC	59.114	52.381	0	0	0
0 132;20	GATCGACAGAAGCATCGCAG	59.877	55	0	0	0
0 21;20	CAGCTCCCCTACTGTCTG	60.223	60	0	0	0
0 7;20	CCTAGAACGAGTTAGGGCC	60.008	60	0	0	0
0 1;21	CGTCGGCTTGCTAGTTCTTTC	60.346	52.381	0	0	0
0 86;22	AGTGATGTTTGAGAGTAAGCG	59.168	45.455	0	0	0
0 9;20	TGGTCTCACGTCAAACACTC	58.526	50	0	0	0
0 63;18	CTGCTCTGCTGGACTGCC	61.177	66.667	0	0	0
0 5;22	GTGTCGTTCAACATAAACACGG	59.198	45.455	0	0	0



0 86;20	GGTGTTCGGAACGGAGATAC	59.737	55	0	0	0
0 3;20	CCAGAGGGCATTAGAAGCG	59.445	55	0	0	0
0 5;21	GCACCACATTAGTTGGATGC	58.868	47.619	0	0	0
0 51;20	ATCACTGTCTTCACGAGCTG	58.384	50	0	0	0
0 125;20	GATGTATTGCTAAGCCGCGG	60.222	55	20.7	20.7	0
0 14;20	CAAGGTCTGTGCAAGGGTTG	60.081	55	0	0	0
0 59;20	TTAAACTTCTCACGGGCTGC	59.23	50	0	0	0
0 52;20	AACGGCAGGCTTTGAAGTTC	60.081	50	0	0	0
0 117;20	ATACGCCCTTTGTACGACCC	60.579	55	0	0	0
0 36;22	ACCACACTCAATAAACGCCTTC	59.947	45.455	0	0	0
0 108;20	GGTGCCATCCAACAGTTCAC	60.152	55	0	0	0
0 77;20	TTCTGCCAACGTTGCACTTG	60.643	50	9.78	17.86	0
0 68;21	CTGGTGCAACGTATTCAGGAG	59.745	52.381	0	0	0
0 14;20	GAGGCATGATCTTGGTGAGC	59.443	55	0	7.05	0
0 6;21	TGTTGCATGTGTTGTTGAAGG	58.589	42.857	0	0	0
0 146;20	ATTTAATGGAGGCTTCGCGG	59.442	50	0	3.95	0
0 3;20	TTGGCTCTTCTGGGTTCTG	60.369	55	0	0	0
0 140;20	GACTAGTGCGTTTCGAGTGC	60.016	55	0	0	0
0 1;20	ACAGACACATAGGCAGGCAG	60.511	55	0	0	0
0 54;20	TCAGGATCTGCAAGACCCTG	59.861	55	3.54	3.54	0
0 179;20	TCGAAACTGCAGCACCTTTG	60.082	50	0	0	0
0 49;20	AGCAAGGTGAAAGCATGCAG	60.152	50	0	18.98	0
0 30;20	TTCTGCAAACATGAGCCTGC	60.152	50	2.87	2.87	0
0 38;21	GTATGCGAGAAAGAGATGGCC	59.609	52.381	0	0	0
0 112;20	CAGTCGAAGCCAGAGGTAGG	60.294	60	0	0	0
0 68;20	TCTTCCAAGCCACTCTCGAG	59.866	55	2.6	2.6	0
0 6;20	ATGCAGAAGGTCAGAGGAGG	59.568	55	0	0	0
0 52;20	AGATTGAGTTCTCGCAGGGC	60.865	55	0	0	0
0 0;20	GCTCTAATCCCATGCAGCAG	59.513	55	0	0	0
0 3;21	AGAACACGATGCTGACAGAAG	59.068	47.619	0	0	0
0 36;20	CATCAACAGTTGCGACACCC	60.501	55	0	3.9	0
0 3;18	CAGCGGCTCACCTGACAC	61.472	66.667	0	0	0
0 97;20	CCGGACCGCGATTTAGATTC	59.597	55	0	0	0
0 161;20	ATCTGTCATCTGCCCTCCTG	59.641	55	0	0	0
0 2;20	CGCCGGTTGTATCCAGTTTG	60.292	55	0	0	0
0 31;20	CTGAGCATGAGACGGAAAGC	59.734	55	0	0	0
0 62;20	TATCAGGAGCTTTCCCGACG	60.009	55	0	0	0
0 25;20	ACTTCTCTCCTTCGTGCAG	60.152	55	0	0	0
0 24;21	CACAGTTATTGAGCCGTGTCC	60.013	52.381	0	0	0
0 79;20	CCAGAGCAGGCCGTAATTTG	60.011	55	0	0	0
0 49;20	AGCAGCAATAGGAGTGGAGG	59.933	55	0	0	0
0 90;20	CTTTCGCACTTGTCTACGCC	60.291	55	0	0	0
0 71;18	AGAGGGAGGCAGTGGGAC	61.058	66.667	0	0	0
0 143;20	GTGGGAGACAGTCATTGAGC	59.017	55	0	0	0
0 119;19	CTTGATTGACACGCGCAAC	59.015	52.632	0	0	0
0 145;20	GTCAGCCTCACCATTAACGC	60.013	55	0	0	0
0 8;18	CCTCTGTGCACCCTCTCC	59.767	66.667	0	12.6	0

0 135;20	GAGACACGAGACTTGGAGGG	60.223	60	0	0	0
0 3;20	TTGACCTAAGCTAGACGCC	59.937	55	0	0	0
0 14;20	CCCAGAGCTCAATTACCGTG	59.091	55	0	0	0
0 16;20	ATTGCCTCCCTCCTAACC	59.933	55	0	0	0
0 18;20	CTTCCATACTGTGCTGGCTG	59.372	55	0	0	0
0 15;20	TCCGTAGAAGGCCAGGATTC	59.645	55	0	0	0
0 25;20	GGAACAAGCCGAGAAAGACG	59.944	55	0	0	0
0 35;21	CTTCACTGGTAGGACTGCTG	59.061	52.381	0	0	0
0 13;20	TGCTTGTCTGTCTCCGTCTG	60.435	55	0	0	0
0 56;20	TGTGATGAATGCGGCAGATG	59.728	50	0	0	0
0 23;20	CAGTGGCAAGTGATGTGGAC	59.87	55	0	0	0
0 4;21	ACAAATGATGGGATGCGACTG	59.738	47.619	0	0	0
0 14;20	TGCTGGCTTCTGTCTGGTTC	61.011	55	0	0	0
0 50;20	ATGTGACGAAATTGGGCAGC	60.223	50	0	0	0
0 16;20	GTTACCCGGCTACTGTTTGG	59.871	55	0	0	0
0 43;20	GGGTCTTAGCCTTGGACTCC	60.224	60	0	0	0
0 7;20	ATCCTGCATCCTGGGTAGTG	59.639	55	0	0	0
0 71;20	TTTGACAGCACACCCATTGC	60.365	50	0	0	0
0 47;20	GCCCACCCTATCTCTGTAGC	60.08	60	0	0	0
0 30;20	CCACAGCTAAATGTTCCGCC	60.293	55	0	0	0
0 11;20	ATGCAACCTACTCCGAGCTC	60.295	55	0	0	0
0 4;20	TCGTCCGGCCACTCATTAAAG	60.578	55	0	0	0
0 27;20	CGCCTTAACCTTTGACACCG	60.222	55	0	0	0
0 51;20	TAGCAGACATAGGGCTCGAC	59.437	55	0	0	0
0 5;20	ATACAGTCCGCCTTCTCCTG	59.647	55	0	0	0
0 76;20	AGGTCCGGCATCTTAGAACG	60.294	55	0	0	0
0 6;20	CTCATCGGCTTCATGGTCAG	59.165	55	0	0	0
0 7;20	CCTAGAACGAGGTTAGGGCC	60.008	60	0	0	0
0 66;20	TTCTCTTGCCGTTTCGTAGG	59.94	55	0	0	0
0 119;20	TGTGTTGACGAATGCCACTG	59.801	50	0	0	0
0 64;21	CTTCTCTCTACCATCCTCCC	59.17	57.143	0	0	0
0 46;20	AGTACCCGTTCTCTGACAC	60.081	55	0	0	0
0 15;19	AGCGAGGGAAAGTACGAGC	60.232	57.895	0	0	0
0 3;19	TGGAACAGGTGGAAGCTTC	58.031	52.632	14.61	14.61	0
0 2;20	CTCAAGCAACTCGTTCAGGC	60.222	55	0	0	0
0 74;20	CACACAGCTTGCCACTAAGG	59.87	55	0	0	0
0 10;22	CAATCCAAGAACATGAGGTCCC	59.748	50	0	0	0
0 32;22	ACGGAAATCATCAAGGAACAGC	60.012	45.455	0	0	0
0 78;20	TAGAGAGCGTGCGGTACTAC	59.449	55	0	7.27	0
0 8;20	GTGTCCAAATTCCTCCTGCC	59.579	55	0	0	0
0 38;20	GCATGCGACTTATACAGCCC	59.872	55	0	0.41	0
0 33;20	CTCCGGTATTGTTTCGGTGC	60.013	55	0	0	0
0 51;20	GTCCACATGCCATCTTCTGC	60.011	55	0	0	0
0 2;20	ACCGTGCTGACCGAATATTG	59.093	50	0	0	0
0 1;20	TCCGATGGCTTCACGTGATG	61.208	55	19.27	19.27	0
0 7;20	TGTAGTCGCTGAAGGTCCTG	59.866	55	0	0	0
0 47;20	ACACGTGCATGTACAACCAC	59.801	50	11.4	14.04	0

0 13;20	CCCATCATTGACTTGGACGC	60.011	55	0	0	0
0 79;20	GGGCAGCTATAGGGTCGTAC	60.152	60	0	0	0
0 16;20	TCGAAACTGCAGCACCTTTG	60.082	50	0	0	0
0 16;20	ATTGCCTCCCTTCCTAACC	59.933	55	0	0	0
0 69;20	GCCTCACTAACACATTGCCC	59.939	55	0	0	0
0 63;20	CACGATGTATTGCAGGCAGG	60.082	55	0	0	0
0 68;20	CGGCAAGATGTTCCGTGATC	60.083	55	0	1.47	0
0 64;22	ACAGTGAGCTACCTTCATTTGG	59.089	45.455	0	0	0
0 40;20	GTACAAATGCCAGCTCCACC	59.939	55	0	0	0
0 82;20	AAGCCCACAAGTGACATTGC	60.08	50	0	0	0
0 88;19	TCTGCCATTGGACCGAGTG	60.458	57.895	0	0	0
0 8;21	CCGTGAGTGATCGATTGTGTG	60.082	52.381	0	10.62	0
0 10;20	TTACCTAGTGCAGCCGTCAG	60.223	55	0	0	0
0 9;20	CAGTGCTGACGTCACAATGG	60.222	55	11.04	21.64	0
0 42;20	TTAGTGAGCACCGAGGTAGC	59.938	55	4.62	4.62	0
0 44;20	CGTTACCCGTGATGCATCTC	59.526	55	0	3.68	0
0 69;20	TGCGTCGTCTCGTTGAAATC	59.671	50	0	0	0
0 12;20	GCCGTTATTTCAGTGACAGC	60.013	55	0	0	0
0 9;20	GAATGTCAAGACGCTCCTGC	60.013	55	0	0	0
0 62;20	AATTGGCCTCTGTAAGACGC	59.013	50	0	1.15	0
0 4;20	GAAGGTGTAGCTCGGCATTG	59.732	55	0	0	0
0 19;20	TTCTTGAAAGTGGAGCGCAC	59.8	50	0	0	0
0 10;20	ACTGGCTGTCTGATCGTACC	59.938	55	0	0	0
0 11;20	CCTCACGTTTGCCCTGATTC	59.941	55	0	0	0
0 29;20	TGTGTTACAAGCATTCCGGGC	59.869	50	0	0	0
0 91;20	GATTTGGTTCTCGCAGGGTG	59.941	55	0	0	0
0 65;20	TGTCTACCTGCGAGAAGTGG	59.866	55	0	0	0
0 12;18	GTGTGTTTCGTGTGCCACC	60.012	61.111	0	0	0
0 68;20	CTTTGGTCGGTCATGTCGTG	59.944	55	0	0	0
0 23;20	AAACATGGACCACACGATGC	59.869	50	0	0	0
0 15;20	GTGTTGGTTTGCACGTTAGC	59.256	50	0	0	0
0 30;20	GGAAACACGCTTAGCTCAGG	59.662	55	0	0	0
0 0;20	CCAGTGTGCTTTGTCCGAAG	60.152	55	0	0	0
0 6;20	CTCTAGTTGGACCACGGACC	60.223	60	0	0	0

left_end_st	left_penalt	right	right_sequ	right_tm	right_gc	right_self_	right_self_	right_hairp
3.82	1.014463	62;20	GAGCCCGA	58.745	55	0	0	0
6.01	0.404065	120;22	GAGGAATC	59.16	50	0	0	0
4.49	0.775601	96;21	TCAAGAGC	59.466	52.381	4.82	9.69	0
3.67	0.49125	60;20	GTGCGTGC	61.999	55	0	0	0
4.57	1.319642	71;22	GACACTTC	58.37	50	0	0	0
4.61	3.575367	127;19	CACGCGGC	59.722	57.895	0	10.4	0
4.02	0.357601	88;18	TGTGACCC	60.086	61.111	0	0	0
1.73	0.331687	130;22	GACGCAGA	58.731	50	0	1.06	0
3.16	2.324853	223;21	CATGCGTA	59.819	52.381	0	0	0
3.69	1.462568	78;20	CTAATGCC	59.088	55	0	0	0
3.62	0.659045	96;20	ATACAGCC	59.648	55	0	0	0
4.46	0.939967	181;20	CAGGGCGC	59.381	55	0	18.31	0
5.69	0.690975	150;22	TGGGAGAT	58.768	45.455	0	0	0
2.17	1.111791	81;20	TAGGTAGC	59.202	55	0	0	0
2.82	0.644299	111;22	GAGAAAGA	59.697	45.455	0	0	0
3.61	1.214964	64;20	GTATGCGC	60.909	55	0	0	0
4.85	2.117702	185;18	TCTCTCGT	60.164	61.111	0	0	0
4.46	0.81934	181;18	TCACAGTC	60.397	61.111	0	0	0
3.69	1.541882	117;20	TACGATCG	60.292	55	0	18.1	0
3.51	1.431549	81;20	GTCCTGCG	60.432	60	0	0	0
4.63	1.011689	93;20	TAGGGAAC	58.625	55	0	0	0
3.82	0.609339	288;20	CTCCGTCC	59.717	60	0	0	0
4	3.663533	95;20	GAACCAAA	59.872	55	0	0	0
5.34	0.641401	138;18	TCTCTCTC	61.808	66.667	0	0	0
3.82	3.809466	93;20	AATCGGTT	60.578	55	0	11.39	0
3.51	1.089288	82;20	TCCGTTCC	60.152	55	0	0	0
3.67	0.68548	67;20	ATACAGCT	59.156	55	0	0.76	0
3.2	2.3839	197;20	AAAGAAAC	59.87	50	0	0	0
4.52	0.572944	97;18	ACTCAGTG	60.398	61.111	0	0	0
4.79	0.615817	70;22	GAGACTAC	59.883	54.545	0	13.97	0
4.01	0.499985	129;21	CACACTTG	59.091	47.619	0	3.96	0
5.54	2.109834	84;20	GATTGAGT	60.013	55	0	0	0

4.02	0.485658	175;20	TCACAGAC	59.098	50	0	0	0
4.79	1.88975	68;18	TATGTCGG	60.242	61.111	0	5.88	0
4.01	0.499985	92;20	CACACTTG	59.395	50	11.85	19.52	0
3.14	1.23092	85;20	CTAGACGG	59.384	55	0	0	0
4.84	2.181697	142;21	GCATGCAC	59.078	47.619	0	10.99	0
4.85	1.590332	87;20	TCTACAGA	60.438	55	0	11.09	0
3.36	0.609339	93;20	TACGAGCG	60.014	55	6.97	6.97	0
4	0.281089	85;20	AGGATCTA	59.725	55	0	0	0
3.16	2.051185	69;20	CACTCCAA	59.31	55	0	0	0
5.34	1.231549	72;20	AAGCTGGT	60.224	55	0	0	0
1.9	2.084178	73;20	AAAGCGCC	59.939	50	0	0	0
3.86	0.151836	98;19	CGCAGGTC	61.529	63.158	0	0	0
5.03	1.420339	105;18	CTCGCCGC	60.925	66.667	0	0	0
3.85	0.89633	254;20	TCCTTCAG	60.152	55	0	0	0
3.84	0.015223	111;20	AGAGATTG	60.652	55	0	0	0
4.4	1.719377	83;18	TACGCGCG	61.82	61.111	11.29	29.43	0
3.67	1.057292	195;20	ACCTAACA	59.664	50	0	1.36	0
5.19	0.726381	114;20	CAAAGGTC	59.944	55	0	0	0
3.69	0.40926	88;19	GGCAGGAC	58.04	57.895	0	0	0
5.25	0.549812	169;20	TCCTCTGA	58.906	55	0	14.17	0
2.57	0.130117	186;20	ACTGAAGA	59.861	55	0	0	0
5.28	0.511474	138;20	AGGGCACT	59.227	50	0	0	0
2.85	3.94549	72;20	GCTCACTC	60.222	55	0	0	0
3.77	0.013327	376;20	CTACTTCTA	59.503	60	0	0	0
3.69	1.852112	83;22	CCTTCAAC	59.745	50	0	0	0
3.02	0.749254	123;20	CGCGTGTC	60.833	55	0	0	0
4.06	0.473511	108;20	AGATGGAC	60.865	55	0	0	0
3.02	0.749254	77;20	TGTAAAGC	60.293	55	0	1.21	0
2.57	0.421098	101;20	CCTGAAGC	59.449	55	0	0	0
4.4	0.922779	86;22	GCATCAAT	59.315	45.455	0	0	0
4.79	1.331089	107;21	CTAGTCCT	59.603	52.381	0	0	0
5.19	0.550275	132;20	GAACCAA	59.013	55	0	0	0
2.82	0.060217	163;21	GTGAACGC	59.945	52.381	0	0	0
2.74	0.059907	127;20	ACCTGTGA	59.236	50	0	0	0
3.33	1.892609	78;20	AACCACCT	60.441	55	0	0	0
3.13	1.079639	167;20	TTGAACCC	60.151	55	0	0	0
3.69	1.123353	138;20	GTGTGCCG	60.428	55	0	0	0
4.85	0.151551	142;21	TCTCGCTC	59.113	52.381	0	0	0
3.02	0.749254	117;20	AGTTCAGA	60.718	55	2.57	11.08	0
6.46	0.755704	77;20	GATTGAGT	59.379	55	0	0	0
6.53	1.186364	78;20	GCTCGTGA	59.944	55	0	0	0
3.51	0.223002	185;22	TCTTGTCAC	59.95	45.455	0	0	0
6.86	0.637123	168;18	GTTCTGTA	58.454	61.111	0	15.92	0
3.62	0.01106	151;22	TGGTCCAG	59.276	50	0	0	0
6.53	2.837973	119;20	GCGCCTAG	59.251	55	0	2.73	0
3.62	2.466606	100;20	CGCTCTCC	61.564	60	0	0	0
2.67	2.139254	80;21	AGAATCAC	59.335	47.619	0	0	0

5.14	0.204298	127;20	CTGGCATG	60.647	60	1.8	6.41	0
6.46	0.43877	87;20	TTTCTATGC	60.859	55	0	0	0
4.57	2.818976	77;20	AATGAGCA	59.375	50	0	0	0
5.19	0.864643	81;22	ACGTAACT	58.026	40.909	0	0	0
4.09	0.151468	192;20	CATGCATA	58.971	50	0	0	0
5.34	0.772532	113;19	CCTGCCCT	61.429	63.158	0	0.03	0
4.02	1.326375	110;22	ACACACAG	58.364	45.455	0	16.14	0
3.02	0.749254	154;21	TCTTGTGT	59.683	47.619	2.94	14.28	0
2.57	1.914127	94;20	TCATGCTG	59.795	50	0	6.84	0
3.02	0.749254	87;20	CACCAGAC	58.444	55	0	0	0
3.16	0.011278	331;20	GCGCCTAG	59.732	55	0	0	0
3.28	3.671413	135;20	CGGAGAGC	59.937	60	0	0	0
2.32	1.011898	81;20	GATTTAGT	59.446	55	0	0	0
5.18	0.130117	206;22	CCATGTTC	60.59	50	0	0	0
5.34	1.466463	85;20	TTTGCCGA	59.796	50	0	0	0
4	2.567786	123;19	GAGACGAT	59.71	63.158	0.63	9.79	0
3.95	2.84182	84;20	GTCCCTAA	59.514	55	0	0	0
3.86	1.431141	113;20	GCATGCAC	58.633	50	0	10.99	0
4.85	0.40926	94;20	ACGCCTGG	60.859	55	0	0	0
4.35	0.770995	117;20	TCTCGTCA	59.525	50	0	0	0
3.51	0.40628	104;20	TGTGCAAT	58.15	50	0	0	0
6.13	0.412271	103;20	TAGATCGT	59.364	55	0	0	0
4	0.081593	81;21	CGTCTGTC	60.082	52.381	0	0	0
4.85	3.486545	87;20	AGATTGAG	60.865	55	0	0	0
1.9	1.147319	141;20	CATATACA	60.291	55	0	0	0
3.02	0.749254	161;20	ATTGTAGG	60.801	55	0	14.1	0
5.87	0.082617	411;20	GTTCCCTT	59.588	55	0	0	0
4.06	0.56761	122;20	TCGAAGCA	59.159	50	1.56	17.4	0
5.34	0.336871	161;20	TTGGGCTA	58.954	45	1.5	1.5	0
3.2	0.925135	86;20	TTAGCGGG	60.01	55	0	0	0
3.67	2.142857	137;18	GTAAGGCC	61.627	66.667	0	11.13	0
4.24	0.343836	150;20	ACCAGCCT	60.224	55	0	0	0
4.06	1.158404	89;20	AGTACGTC	59.294	55	0	0	0
3.62	0.293233	94;20	AATGAATG	59.316	45	0	9.03	0
2.93	0.13415	120;20	CATGCCAC	60.223	55	0	0	0
3.2	1.791175	132;20	TTGCCCTT	59.795	50	0	0	0
3.02	3.163218	109;19	GGGATGAA	60.233	63.158	0	0	0
3.51	0.054019	124;20	CCTTGAGC	59.735	55	0	0	0
4.12	2.321603	94;20	AGGCACAC	58.931	50	0	0	0
6.86	0.47516	108;20	CCCTTTCTT	60.223	55	18.69	18.69	0
3.95	0.152057	281;20	CACTGCCT	59.942	55	0	0	0
5.34	3.435708	90;20	TCCCGACT	59.936	55	0	0	0
3.82	1.843103	140;20	GAACACGT	58.374	50	0	0	0
4.94	0.126574	118;20	CTCGACTA	59.457	55	0	0	0
5.25	0.292129	241;21	GTTGGTGG	59.063	52.381	0	0	0
3.33	0.222207	121;20	GACTGGCA	60.014	55	0	0	0
5.28	3.160062	153;20	TCGGCTGA	59.301	50	0	0	0

3.02	0.749254	175;18	CTGAGGGC	60.164	66.667	0	0	0
5.69	1.316342	132;20	AGCGTGAA	59.868	50	0	0	0
5.19	1.612087	132;20	CGCTCATG	60.084	55	0	0	0
5.68	1.769767	225;20	AGGCGGTA	59.064	55	0	0	0
4.3	0.078325	183;21	CCCACATA	59.207	52.381	0	5.15	0
3.35	0.134354	231;21	GTGGAGCA	58.934	52.381	0	0	0
3.02	0.975485	277;20	TACCAAGA	60.366	55	3.21	3.21	0
4.4	1.351112	109;20	TTCGCCAA	60.152	50	0	0	0
5.03	2.627263	124;21	TCTTGATG	59.405	47.619	0	0.42	0
3.11	1.080783	99;20	CAGTACCT	59.311	55	0	0	0
3.61	1.908858	111;20	GCGCCTAG	59.251	55	0	2.73	0
6.13	0.424231	110;20	GGAAGTGT	59.662	55	0	1.28	0
4.18	0.972552	202;20	AGAGACCA	60.86	55	0	0	0
4.01	3.220511	94;20	TTGGTCTG	60.006	55	0	0	0
2.18	0.348242	152;20	GGAATTAA	60.083	55	0	6.23	0
4.01	0.638256	100;20	TAGCCACC	60.509	55	0	0	0
3.51	0.223778	173;20	TAGGCCTC	59.648	55	0	4.02	0
2.24	1.147513	114;22	TCTGCCTC	58.078	45.455	0	0	0
3.51	2.724142	99;20	TGAACGTG	59.804	50	0	0	0
2.9	1.276545	119;20	TTGCTTAC	60.013	50	0	0	0
4.09	0.079415	124;20	AGGCCAAG	60.009	55	0	2.76	0
4.42	1.118416	141;20	CTTCGGTT	59.591	55	0	0	0
3.18	2.988451	101;20	CCTTCACCT	59.219	55	0	0	0
4.18	0.578175	187;20	ATCCTCGG	60.006	55	0	0	0
5.03	3.028214	102;21	GCCAGTTA	60.281	52.381	0	7.28	0
5.8	0.517537	131;21	ACAAACAT	59.087	42.857	0	0	0
2.34	2.063464	97;19	CGGAAGAC	59.725	57.895	0	0	0
5.69	0.058523	190;20	TTTGCCTC	60.223	50	0	3.42	0
3.02	0.749254	95;20	CACGCTTC	60.153	55	0	0	0
3.02	0.749254	127;20	CTTGTGGG	59.871	55	0	0	0
4.24	0.130117	121;19	ACCAGCAG	61.05	57.895	0	0	0
4.94	1.007333	185;20	AATGAAAG	60.499	50	0	4.44	0
3.67	1.520203	158;20	TTGAGTAG	60.223	55	10.04	10.04	0
6.46	0.361758	338;20	AAAGCCTT	60.081	50	0	0	0
3.2	0.80675	96;20	TTTGGGTC	61.168	55	0	6.93	0
4.26	0.292403	133;20	CGCGATAT	59.598	55	0	8.56	0
5.36	0.852038	157;20	CACCAGGA	59.653	55	0	0	0
4.04	0.572944	119;20	TCATTCCA	59.942	50	0	0	0
4.01	2.402655	196;20	TTCTAGCC	59.936	55	0	0	0
3.79	0.12755	129;20	ACAGTGCT	59.652	50	0	0	0
2.57	0.944384	109;20	TAGCTCAA	60.295	55	0	0	0
5.34	0.152528	152;20	TAGCGAGA	59.943	55	1.06	10.28	0
4.3	0.280187	126;22	GCTTGCAA	59.12	45.455	0	0	0
6.13	0.062408	170;18	AGTTTCTG	60.716	61.111	0	0	0
3.86	0.293865	156;20	CTGCCTCT	60.007	60	0	0	0
6.13	0.861164	103;20	AATGCTAG	60.007	55	0	0	0
4.85	0.294006	161;22	AGAGAAGC	59.687	45.455	3.41	3.41	0

3.16	0.335891	118;21	CATTAAGG	59.266	52.381	0	0	0
5.19	0.442453	273;20	AGCTGTCC	59.646	55	0	0	0
3.91	0.222526	194;21	GAGTATGC	60.013	52.381	0	0	0
3.51	0.361194	136;20	TTTGCAAC	59.73	50	0	0	0
4.02	0.222725	102;20	TCAACACG	59.875	50	0	0	0
3.09	0.222926	171;20	ACAGGGAC	59.573	55	0	0	0
5.54	0.501577	150;20	GTGTGTGT	58.877	55	0	0	0
3.02	2.297222	281;20	AGATTGAG	60.865	55	0	0	0
6.13	0.791283	135;20	TGCTTTGT	60.92	50	0	0	0
3.62	0.080615	177;19	GGGTCACA	58.389	57.895	0	0	0
2.87	1.132308	174;20	AGAGCAAC	60.44	55	0	0	0
5.28	1.146259	127;20	GCAGAACA	60.292	55	0	0	0
2.87	0.720133	107;20	TGCCAGAC	60.439	55	0	0	0
4.84	0.472279	166;20	AGTGTGAC	60.571	55	8.17	10.06	0
3.51	1.897746	106;20	CATCGAAC	59.946	55	0	0.37	0
3.67	1.886509	125;19	TGCCTTGC	61.044	57.895	0	0	0
3.16	3.606994	219;20	ATCGCTCG	60.294	55	0	0	0
5.34	0.152255	282;20	GAAACTCT	59.94	55	0	0	0
5.36	0.128729	208;20	TGTCTGCT	61.14	55	0	0	0
2.17	1.390382	101;20	CCAATCTC	59.525	55	0	0	0
4.01	1.303562	108;20	CAGGTTGC	60.152	55	0	2.38	0
3.46	3.453262	129;22	ACAGTGAC	59.089	45.455	0	0	0
3.93	1.668204	131;19	CACTGACG	59.575	57.895	0.49	10.12	0
3.16	3.606994	232;20	ATCGTTCG	58.083	50	0	0	0
3.01	2.472987	149;19	GTTTCCTT	59.283	57.895	0	0	0
4.04	2.659415	139;19	GCGAGCA	58.836	57.895	0	0	0
5.12	0.015846	208;20	TCGCCACT	59.801	50	0	0.06	0
3.51	0.334915	113;21	CACCTGCT	60.081	52.381	0	0	0
3.2	0.339172	114;20	GAGCTACA	59.455	55	0	0	0
5.54	0.223155	108;20	ACCGAAAT	60.224	55	0	0	0
4.57	0.22228	192;20	GCATGCAC	60.014	55	0	10.99	0
3.11	1.501084	117;20	GTGCCAAG	60.011	55	0	7.6	0
3.36	1.515584	185;20	GAAGGTGA	60.012	55	0	0	0
3.71	1.634018	155;20	GCGCGTGA	60.563	55	0	6.36	0
5.34	0.833664	140;20	CATTCGGA	59.879	55	0	0	0
2.87	1.064515	173;20	CCAAGCAA	60.152	55	0	0	0
3.51	1.158323	125;20	AGTGACAC	59.794	55	0	0	0
3.01	0.419544	129;21	GACAGACA	58.874	52.381	0	0	0
3.61	1.060696	108;20	CACGAATT	60.359	55	0	0	0
4.02	0.273093	278;20	AGAAACGT	59.587	50	0	0	0
5.34	1.05199	117;20	CCTGACTT	60.084	55	0	0	0
3.46	0.152892	139;20	GCAGAAAC	60.222	55	0	0	0
1.9	0.360534	245;20	GCACCGTC	58.985	55	11.75	11.75	0
3.62	0.011278	213;22	CTTCGACT	58.663	50	0	0	0
4.12	0.211383	128;22	GGTGGTTE	60.078	50	0	0	0
6.13	0.408139	184;20	TCCGAGTC	59.795	55	0	0	0
3.07	1.496193	131;20	CTGCAGCT	59.727	55	0	0	0



4.85	0.152275	276;21	GGACCTGA	59.943	52.381	0	0	0
1.89	2.363219	189;20	TGCCTTTG`	60.01	50	1.62	19.5	0
3.34	0.013007	177;20	TGTCTCTTI	60.079	55	0	0	0
3.85	0.578933	110;20	GTGTAGCA	60.014	55	0	0	0
2.87	0.762843	201;20	AGGGAGAC	60.079	55	0	0	0
4.17	0.222977	128;20	GCATGCTG	60.926	55	0	8.14	0
4.79	0.754525	124;22	GTGTGCAT	60.012	50	0	2.32	0
3.67	0.265367	109;20	AAACGACC	59.802	50	0	0	0
4.3	3.294247	108;20	CATGGTCT	60.082	55	0	0	0
2.39	1.347816	124;21	GCATGTCCG	59.816	52.381	0	0	0
4.7	0.211899	460;20	GCCAAGAC	59.872	55	0	0	0
2.62	0.412649	117;20	AGAAGAGC	60.223	55	0	0	0
4.16	2.925347	109;20	GTTCTCGC`	60.903	55	0	0	0
5.18	0.223053	133;20	TGCGTTCG	60.292	50	2.77	11.91	0
5.25	3.702883	145;20	TGCCTCCA^	59.495	55	0	0	0
3.11	0.081334	114;20	CCTCTGCC`	59.088	55	0	0	0
3.51	0.128335	193;20	CTCGTTCTI	60.223	60	0	0	0
4.68	0.153154	142;20	CCGTCAGA	59.594	55	0	0	0
2.23	0.007372	137;20	CGAGTTAA	59.806	55	0	0	0
3.46	0.513614	163;21	CAAGCATG	59.148	47.619	0	18.98	0
2.52	0.844082	146;21	ACCGATGT	58.707	47.619	0	0	0
5.36	1.363417	120;20	GCACAGCA	59.594	55	0	0	0
4.94	3.367159	145;20	CCAGCTAC	60.013	55	1.51	9.03	0
5.68	0.797963	216;18	CCCTCGTG`	61.867	66.667	0	0	0
3.51	1.186364	171;20	CAAGAGTC	59.943	55	0	0	0
3.18	0.130117	115;20	AGCAGCAA^	58.928	50	0	0	0
2.67	1.670596	120;20	CCTTTCGG`	60.295	60	0	0	0
5.28	1.663031	150;20	CCACTGTA^	59.386	55	0	0	0
3.51	0.294006	131;20	GCACTCTG`	59.872	55	0	0	0
4.45	1.011513	120;20	ACGTGTGC	60.083	50	0	0	0
3.46	0.066747	220;20	GCAACAAC	60.083	55	0	0	0
2.92	0.295294	113;22	GGTGAGAC	58.049	50	0	0	0
4.04	2.978486	122;20	TTGACCCG`	59.504	55	0	0	0
3.95	2.817961	194;20	GCGCCTAG	59.251	55	0	2.73	0
4.63	0.060217	127;20	TCTCTAGG^	60.223	55	3.04	10.21	0
5.68	0.010401	237;21	AGTGAGTT	59.535	47.619	0	0	0
4.46	0.008844	274;20	TGCTCCAT^	60.434	55	0	0	0
4.18	0.197222	117;18	CTGTCTGC^	58.194	61.111	0	0	0
3.67	3.615383	122;20	CTCCGACG	60.293	60	0	7.52	0
2.23	0.19437	141;20	GCGCCTAG	59.251	55	0	2.73	0
3.56	0.336871	231;20	GATGACCT	59.521	55	0	0	0
4.94	2.488477	205;20	GCACATAC	60.083	55	0	1.39	0
2.92	1.308333	147;21	ACAAAGTG	60.079	47.619	0	6.57	0
4.63	2.393179	211;18	ATTCTCGG^	60.48	61.111	0	0	0
4.45	0.616823	229;20	CTGGCCAG	59.156	55	0	17.84	0
4.02	0.222061	134;20	GCACAGCC	59.801	55	0	0	0
5.34	0.0561	229;22	GCCGAGAA^	59.628	50	0	0	0

4.79	1.590329	141;21	GCTGTGGA	58.934	52.381	0	0	0
3.33	2.348564	215;22	TCCTATTTG	59.547	45.455	0	0	0
4.42	1.908909	122;22	TGGACAAC	60.207	45.455	7.84	11.1	0
3.79	2.20656	178;20	GCTCATTG	59.732	55	0	0	0
4	0.487369	211;22	ACTGCATA	59.751	45.455	0	0	0
4.85	0.416844	244;20	ACTTTCAA	58.942	50	0	0	0
4.85	0.128927	306;20	CCACCGCT	59.806	55	0	0	0
2.87	0.12755	193;20	GCATTATC	59.333	50	0	10.99	0
3.58	1.215163	207;20	TCCGTCTT	59.866	55	0	0	0
4.02	0.151857	235;22	GAGGACAC	58.907	50	0	0	0
3.66	0.850037	121;20	AAGGGATT	59.937	55	0	2.69	0
3.71	2.300238	130;20	GAGCAATG	59.653	55	0	0	0
3.67	0.402963	128;20	CTGGCCAA	60.292	55	3.52	3.52	0
1.9	0.123682	324;20	AATGCTTG	59.872	50	0	3.15	0
3.66	1.137491	122;19	GCAAACGC	58.917	52.632	0	0	0
3.42	0.05929	331;21	CCGTCCGT	59.748	52.381	0	0	0
3.01	0.415312	193;22	TGAATGCG	58.022	40.909	0	0	0
3.84	0.579441	146;20	TTTCACCT	60.079	55	0	0	0
2.17	0.059907	159;20	CACAATCC	60.915	55	0	8.4	0
4.1	1.012417	190;20	ATAGAAGC	60.297	55	0	0	0
2.39	0.007828	204;18	CTGCAAGC	58.428	61.111	0	0	0
4.35	0.151755	125;20	TTCTACCT	60.152	55	3.53	3.53	0
6.13	0.05929	281;19	GTGCGAGT	59.572	57.895	0	0	0
3.16	0.431801	189;20	CGCCAAAT	60.291	55	0	0	0
4.02	0.271064	276;20	TGCAATGA	60.434	50	0	0	0
4.06	1.259938	139;20	TCTAAGTG	60.787	55	8.32	9.08	0
3.71	0.151551	255;20	AGTACCCT	58.501	50	0	4.19	0
3.27	0.99113	143;19	ACATGCGC	59.936	52.632	0	1.46	0
4.26	0.207808	183;22	CTCAATAC	58.301	45.455	0	0	0
3.16	0.647234	180;20	GTTGGTGT	59.799	55	0	0	0
3.18	0.081074	372;20	ACAGAGAT	59.368	55	0	0	0
3.56	0.57868	165;20	CGGAATTG	60.014	55	0	0	0
4.46	2.078915	134;20	TAAGCTAC	59.937	55	0	3.71	0
3.27	0.998141	127;20	AAAGGAG	59.789	55	0	0	0
4.01	0.152528	134;20	AATCGCCT	59.436	50	0	3.6	0
3.42	0.363682	261;20	CGGGTCTA	58.877	55	0	0	0
5.01	0.222775	172;20	CTGTGAGA	59.304	55	0	0	0
5.34	1.250736	163;18	GTGTCACC	59.162	61.111	0	0	0
3.02	0.749254	166;20	TGAAGCTC	60.787	55	0	0	0
3.35	0.982139	134;20	GACATAAA	59.874	55	0	0	0
4.01	1.210474	283;19	GTATGTGC	60.303	57.895	0	0	0
4.26	0.29172	203;20	ACGACATT	60.223	55	0	0	0
3.51	0.08442	222;21	GTTGGCCG	59.812	52.381	0	0	0
3.34	0.125797	188;20	GCGTTCAT	60.083	55	0	0	0
4.61	1.012417	162;20	AGATAGAT	59.788	55	0	0	0
4.24	0.295512	128;20	TGATAGGC	59.43	55	0	0	0
4.79	0.082363	276;19	GGATACGC	58.133	57.895	0	0	0

3.36	0.766453	159;20	CCTTTATG1	59.94	55	0	0	0
4.4	0.152255	157;20	TCCATAGT0	60.224	55	0	0	0
3.85	0.151344	296;18	GGTCAGGC	59.363	66.667	0	0	0
3.86	1.926074	167;20	TCACTTTCT	59.864	55	0	0	0
2.17	0.057003	155;20	TAAACGCA	59.944	50	0	0	0
4.02	0.059136	251;20	TCAGCAAC	59.866	55	0	0	0
4.1	0.153154	225;20	ACTATGGC	59.938	55	0	0	0
5.03	1.53751	196;20	TTGGTGTC0	59.303	50	0	0	0
3.36	0.151633	136;20	TTACGGCC	61.084	55	6.15	17.2	0
3.91	0.292817	192;20	TCCCTACT0	59.577	55	0	0	0
3.18	0.082806	269;20	GCAGCTAT	61.891	60	0	0	0
3.2	2.96209	200;20	CTACATGC0	59.539	50	0	29.38	0
3.61	1.67029	288;18	GAAGTTTG	60.087	61.111	0	0	0
4.94	0.059136	161;20	CTGCAGCG	59.665	55	0	0	0
4.94	0.478901	159;20	ATTGCTGC	59.73	50	0	0	0
4.63	0.131718	191;20	TCTCTCTG/	59.65	55	0	0	0
3.02	1.594747	174;20	ACACACAC	59.939	50	0	0	0
2.34	0.702223	337;20	CTGGTTTC	59.872	55	0	0	0
4.41	0.133538	173;20	TGCCTATC/	59.437	55	0	0	0
4.4	0.510203	155;18	CACCAGTA	58.251	61.111	6.62	6.62	0
2.82	1.849621	141;20	GAGCAAAC	58.755	50	0	0	0
3.62	0.498606	320;18	CTATCGCA/	60.772	66.667	0	0	0
3.14	0.542928	135;20	CTGCTACG	60.083	55	0	0	0
3.02	0.42032	191;22	ACGGATGC	60.078	45.455	0	0	0
6.13	0.29254	145;20	TAGGAGCA	59.86	55	0	0	0
4.85	1.059373	137;20	GCATGTCA	59.521	55	0	0	0
4	0.194134	152;20	CACACCCA	59.098	55	0	0	0
2.5	0.35803	160;22	CATTAGTC0	59.502	50	0	0	0
4.16	0.277204	146;20	GAAATCCA	60.012	55	0	0	0
6.53	0.083991	142;21	ATCTTGCA`	58.33	42.857	0.63	8.53	0
4.4	3.430532	178;20	ACGATTTG	59.798	50	0	0	0
5.34	0.550739	175;20	CGGGCAAC	58.939	55	0	0	0
5.19	1.461325	142;22	CCTATAAA`	58.534	45.455	0	0	0
4.7	0.064639	188;21	TTGACCCA.	58.439	47.619	0	0	0
3.85	0.009959	272;20	GCTTCGGA	60.571	55	0	1.11	0
5.25	0.129521	208;20	GCGCCTAG	59.807	55	0	1.07	0
4.85	1.922674	162;18	CAGCTTGT0	59.764	66.667	0	0	0
3.28	0.643717	132;20	CATGCCGT	60.012	55	0	0	0
4.02	2.145128	131;20	CCAGGCCG	59.587	55	0	0	0
4.79	0.426998	188;20	ACGCGTAT	58.246	50	0	8.95	0
4.85	0.651405	132;20	ACCCTAAC0	60.224	55	0	0	0
3.67	0.063998	290;21	ACCCAAAT	59.806	47.619	0	0	0
4.17	1.007203	323;22	GCTTGCAC	59.244	45.455	0	0	0
3.77	0.131316	321;21	GCGCTAGT	59.881	52.381	0	0	0
4.41	2.084735	145;20	GTAGCGCA	60.153	55	0	0	0
3.35	2.707825	164;20	TTGTCAGC0	60.439	55	0	0	0
5.18	0.363226	323;20	AGTGTCAG	59.935	55	0	0	0

3.18	0.334915	332;20	CCTTTGAG	60.152	55	0	0	0
5.28	1.816036	138;20	CTACAGCT	59.939	55	0	0	0
3.51	2.240277	135;20	TTTAGACT	61.073	55	0	0	0
3.02	0.547963	260;20	GCATCCGA	60.571	55	0	0	0
4.45	0.955827	174;20	CTTCACTT	59.872	55	0	0	0
4.02	0.365182	260;20	GGATGACA	59.17	55	0	0	0
4.85	2.700972	136;20	CCAGGTCA	59.376	55	0	0	0
5.54	0.364026	137;21	AGTATCCT	58.506	47.619	0	0	0
3.51	1.180008	147;20	ATCAGTCT	60.223	55	0	0.08	0
2.17	2.206037	166;19	CCACCCAG	60.232	57.895	0	0	0
4.57	0.01106	246;19	GGTGCGTA	60.013	57.895	0	0	0
3.02	0.29429	225;20	GTGGCAGT	60.222	55	0	0	0
5.25	0.060217	175;20	AAGGTAAA	58.49	50	0	0	0
4.52	1.513919	168;20	CCACCTTC	60.294	60	0	0	0
4.3	1.131739	159;21	GGCTAGTG	60.147	57.143	0	0	0
4.4	0.294148	201;20	CTGTGGCA	59.803	55	0	0	0
4.85	0.987367	157;20	GGCTATCG	61.623	60	0	1.12	0
5.68	2.839175	211;20	TGGGTGTC	59.718	50	0	0	0
3.11	3.769959	163;20	CAACGTGC	60.222	55	0	0	0
4.85	0.487369	177;20	CCGATCGT	60.501	60	0	12.2	0
5.18	0.50058	345;20	TTTCCCAA	59.793	50	0	0	0
4.35	0.758072	288;20	GCAGCCCA	59.939	55	0	0	0
5.12	0.920938	217;20	ACCGGAAC	60.368	55	0	7.06	0
3.02	0.209843	141;20	TATGCTGC	60.921	55	0	0	0
4.18	0.125604	209;20	GCTAGTCT	60.291	55	0	0	0
4.02	0.223155	276;20	TCTCCTTCT	59.504	55	0	0	0
3.51	2.270737	207;20	GAGTCAGT	60.925	60	0	0	0
4.01	0.124064	151;20	GGTTCAT	60.719	60	1.86	3.71	0
3.35	2.251691	150;20	TCTCCTTCT	59.711	55	0	0	0
3.51	0.152701	237;20	TGCCTGTT	59.869	50	0	0	0
4.3	0.009403	168;20	GTTGGTTA	60.565	55	0	7.03	0
3.35	0.214238	159;20	TCACTTGC	59.31	50	0	0	0
4.52	0.082806	144;20	GGAGCTCC	59.32	55	0	0	0
6.53	1.007025	144;20	GACAGTCA	60.013	55	0	1.96	0
5.36	0.010401	144;19	GCAGACCA	60.457	63.158	0	0	0
2.32	1.013036	260;20	ACCTACTC	59.579	55	0	0	0
2.18	3.306254	146;20	CAAAGCGA	59.872	55	0	0	0
4.63	0.858578	180;19	CTCTGCCT	60.158	63.158	0	0	0
2.5	0.707403	145;21	CTGCCTCA	59.338	52.381	0	0	0
5.14	0.203306	148;22	AGACGATC	60.077	50	0	0	0
3.62	1.231359	159;19	GATGATAA	59.788	57.895	0	0	0
5.03	0.68548	183;20	GAAGTTGC	60.013	55	0	0	0
4.84	0.198183	260;22	ATAATTGC	58.069	40.909	0	0	0
3.51	0.014385	162;21	AATGCAAT	60.685	47.619	8.44	17.25	23.29
4.85	2.47898	261;18	CCAGCCGG	59.541	61.111	0	28.46	0
1.85	0.57767	149;20	CTTGTTGG	59.94	55	0	3.4	0
6.86	0.153004	203;22	GGAGAAGT	59.16	50	0	0	0

3.93	0.151715	178;22	AAGGATGC	58.264	45.455	0	0	0
5.01	0.013113	188;20	GCCGACAT	60.015	55	0	0	0
2.87	0.554944	262;20	GTGCCATG	59.942	55	0	0	0
4.58	1.080635	189;20	TGCTCTCA	60.715	55	0	0	0
4.04	0.054167	190;21	GTTACTGA	59.344	52.381	0	0	0
5.54	0.010401	332;20	GAGGCAGC	59.043	50	0	0	0
2.67	0.013752	281;21	TTAACCGT	58.572	47.619	0	0	0
5.03	0.152567	253;19	AGCTGCTC	60.457	57.895	0	0	0
3.16	0.417998	168;22	TCATTTGG	59.617	45.455	0	0	0
3.51	2.711517	153;20	AAACGTTT	60.366	50	0	3.58	0
4.2	2.829636	151;20	AAGCTCGC	60.011	55	0	0	0
4.02	3.851482	166;20	TTAGCCTC	59.864	55	0	0	0
4.7	1.912963	176;20	TCGTTGTA	59.026	50	0	0.07	0
5.25	0.223129	166;19	GTGCGTAT	59.939	57.895	6.01	6.01	0
4.04	0.123682	327;21	AGGGCCTA	59.723	52.381	0	0	0
5.36	0.621891	165;21	GCAGACCA	59.398	52.381	0	0	0
3.2	0.279587	344;20	CTCCAGCC	60.081	60	0	7.34	0
3.35	0.061308	252;20	TTATTGTC	60.222	50	21.13	21.13	0
2.73	0.008281	239;20	GCACTCCA	59.522	55	0	0	0
5.01	0.919225	197;20	TGTGCATT	60.507	50	0	0	0
5.19	0.863334	179;19	TTTCGCCT	61.053	57.895	0	0	0
4.18	0.290579	153;20	TGATGGAC	60.007	55	0	0	0
5.19	0.864643	212;19	GGCTTGCC	60.45	57.895	0	3.94	0
3.51	0.080615	199;20	TCCGAGCA	58.154	50	0	0.9	0
3.42	3.499676	188;20	ACTTCGTG	58.96	50	0	0	0
3.69	0.866835	155;20	CTGGATGT	58.885	55	0	0	0
2.62	1.661293	181;20	GACCCAAG	59.935	60	0	0	0
5.01	1.46527	255;20	TCTGCTAG	59.862	55	1.07	5.72	0
4.09	0.342829	162;20	TCAACCCA	60.079	55	0	0	0
3.18	0.081269	160;20	AGTCACGT	58.295	50	0	4.18	0
3.36	0.285961	231;21	GAGAGAA/	59.124	52.381	18.82	18.82	0
3.69	0.079415	158;20	GACCACAC	59.037	55	0	0	0
4.1	0.610329	247;20	TAGAGTGC	60.152	55	0	3.47	0
3.09	1.188598	164;20	CCATGCCA	59.869	55	0	0	0
6.13	2.012356	215;20	CCAAGCCA	59.733	55	0	0	0
4.61	0.620872	185;20	ATGAGCCC	60.295	55	0	0	0
3.67	0.222304	187;20	ATGCATAG	60.08	55	0	0	0
4.45	0.931284	295;20	TACCTGCA	59.58	50	11.09	26.47	0
5.14	1.338114	271;22	TGCGTGTA	59.025	50	0	0	0
2.5	0.605405	186;20	AACCTCCT	60.224	55	0	0	0
3.84	0.203306	178;18	GCCTTAGC	58.397	61.111	0	0	0
4.7	0.138497	204;20	TATACACC	60.009	55	0	0	0
3.18	1.07907	160;20	GAGAAGGT	60.152	60	0	0	0
4.3	0.079952	433;20	ACAGTAGC	60.152	55	0.82	0.82	0
3.18	2.462986	173;20	CCAAGCAA	60.152	55	0	0	0
3.71	0.079684	333;18	ATCGCCCA	60.477	61.111	0	0	0
3.2	3.840788	163;20	GACGTCGT	60.085	55	0	0	0

6.13	1.007214	225;20	GGCTGGAT	59.939	55	0	0	0
5.14	0.925639	195;20	TCCAGGGT	59.863	55	0	0	0
6.13	2.049967	220;20	CATGCGAG	59.737	55	0	0	0
2.92	0.009737	190;20	CTCACAAT	60.427	55	23.16	23.16	0
4.06	0.134764	337;20	GCGACTGT	60.359	55	0	0	0
4.58	0.862899	255;20	GCCTTATG	59.944	55	0	0	0
3.61	0.786813	207;20	GGATTAAG	60.014	55	12.31	12.31	0
4.4	1.059547	190;20	CAATATTG	60.081	55	0	0	0
2.73	0.441101	219;19	TGTCCCTC	60.082	57.895	0	0	0
2.85	1.06906	323;22	AGCAAGTC	59.946	50	0	0	0
4.4	0.064478	165;20	ACTTGCGT	60.854	55	0	0	0
3.33	1.584024	235;20	ATGCAACC	59.507	50	0	0	0
2.08	1.560939	173;19	GCAATACG	60.086	57.895	0	0	0
4.79	1.133282	172;20	TCCACTCG	61.062	55	0	0	0
3.35	0.986924	345;20	GGTTCAGA	59.03	55	0	0	0
6.86	0.081464	296;20	AGAGACAT	59.938	55	0	0	0
6.46	0.05241	402;20	GGGCGATT	60.084	55	0	0	0
2.9	0.007941	245;20	CTAGCGTG	60.571	60	0	9.22	0
3.36	1.209692	171;20	GCCGGCAC	60.362	55	0	21.49	0
3.95	1.586802	274;20	TGCTCCAT	60.434	55	0	0	0
3.85	0.151427	202;20	CGCTATCA	59.878	55	0	0	0
4.57	0.659045	222;20	ACCACGAT	59.8	50	0	0	0
5.52	0.057608	289;20	TGCGGTCA	60.51	55	0	0	0
2.24	0.263407	289;20	AGGCCAAG	59.939	50	0	2.76	0
4.58	0.0564	212;20	TGTTTGTC	60.72	55	0	0	0
3.61	0.905235	404;20	ATCATTG	59.937	50	0	0	0
4.26	0.609339	282;20	CTCTGGGT	59.797	55	0	0	0
4.44	0.057003	266;20	ACTAGCGA	58.091	50	0	0	0
4.46	0.436967	206;20	ATGGCATG	60.008	50	0.28	8.66	0
3.16	0.293865	271;20	GGGCATGT	59.799	55	0	2.44	0
4.04	0.063838	279;20	CAGATTCT	59.938	55	0	0	0
4.61	1.157406	246;20	GCATGTGA	59.941	55	0	0	0
5.14	0.293865	338;20	AGACCGGT	60.505	55	0	7.04	0
4.94	0.057608	259;21	TGCGAGAA	58.609	47.619	0	1.14	0
4.94	0.063359	380;20	ATCAGAGC	59.859	55	0	0	0
3.67	0.059753	247;19	TGAGAGGC	60.77	63.158	0	0	0
3.67	0.084846	231;21	CCAAGTGC	60.012	52.381	0	0	0
5.01	0.130515	173;18	GTGGGAG	59.851	66.667	0	0	0
3.13	0.513399	212;20	AGAAAGAC	59.503	55	0	0	0
4.41	0.223129	174;20	ACTGTTTC	60.004	55	0	0	0
4.41	0.412649	231;19	AGGCGGAC	60.749	57.895	0	0	0
2.77	0.439764	204;20	TCTGCCTA	59.934	55	0	0	0
4.26	0.501577	206;20	TTATGTCA	59.945	50	12.42	19	0
3.67	0.222625	322;20	CCTACAAA	59.306	55	0	0	0
3.71	0.222675	351;20	TTGCACAC	60.152	50	0	0	0
3.82	1.045706	254;20	TCTGTGCC	59.934	55	0	0	0
4.02	0.08035	309;20	TTTGAGCA	58.929	50	0	0	0

4.52	0.060683	232;20	GCGCCTAG	59.251	55	0	2.73	0
4.06	0.008956	342;18	CACTTGCT	59.862	61.111	0	0	0
3.01	0.40926	187;20	CAACGGAT	60.083	55	0	0	0
4	0.008619	290;20	TGTGATCC	59.869	50	0	0	0
5.18	0.082932	429;20	CTCTGCAG	59.735	55	0	0	0
3.93	0.296243	216;20	GTCGGCAC	60.222	55	0	0	0
3.06	0.011278	320;20	GGCAAGCA	60.152	55	0	0	0
4.7	0.143614	204;20	GACATTGA	59.732	55	0	0	0
4.35	0.358784	281;20	GGTTAGTC	59.018	55	0	0	0
5.28	0.197222	173;20	TGAAGACA	60.293	55	1.69	1.69	0
6.01	1.139111	221;20	CATGTAGA	59.941	55	0	0	0
3.2	0.41493	234;20	TCCCTATCC	61.238	60	0	0	0
4.57	0.207808	201;20	AGCACACG	59.587	50	0	0	0
3.42	0.916398	176;20	GCAGTGCC	59.87	55	4.99	4.99	0
5.54	0.010401	361;20	GTCGTA	59.597	55	0	0	0
2.82	0.013007	360;18	GGGTTGCC	59.078	61.111	0	0	0
6.53	0.0564	337;20	CCGCTGAT	60.083	55	0	0	0
3.86	0.080549	229;21	CCCACAGG	59.398	52.381	0	0	0
4.06	0.344172	298;20	TACACACG	61.129	55	0	0	0
4.2	0.563498	226;20	TAATGCCT	60.433	55	15.07	20.34	0
4.85	0.556356	184;20	GCAGACAA	60.291	55	0	0	0
3.2	0.079009	249;20	CTGAACGG	59.736	55	0	0	0
3.02	0.909394	228;20	AGCATGTC	58.947	50	0	0	0
6.86	0.634593	177;19	AGGAGAGC	59.248	57.895	0	0	0
3.51	1.135124	181;21	AGGCTATA	58.119	52.381	0	0	0
2.62	0.059753	181;20	GTGTGTGT	60.502	55	0	0	0
4.18	3.395169	199;20	TCCGTACC	60.504	55	0	0	0
3.79	0.193898	212;20	GCTACCCT	59.654	55	0	0	0
3.16	0.979912	184;20	AGCTGCGT	59.944	50	0	0	0
4.94	0.222207	203;21	CGGTAGTA	60.014	52.381	0	0	0
3.46	0.007144	364;20	TTTGCCGA	59.872	50	0	13.79	0
2.93	0.062724	347;19	ACATGCGC	59.936	52.632	0	1.46	0
4.18	0.54021	236;22	TGCCTCAG	58.833	45.455	0	0	0
3.02	1.052761	234;20	ATGACCGC	59.091	50	0	3.57	0
4.79	2.37025	179;19	GTCAAAGA	59.941	57.895	0	0	0
3.77	0.0561	319;20	TGTGGATT	58.663	50	0	0	0
4.44	0.630655	210;20	AACAGAGC	59.789	55	0	0	0
5.36	0.277798	323;18	GAGACAGC	60.551	66.667	0	0	0
4.4	0.08362	187;20	AGAGCATE	60.01	55	0	7.21	0
3.18	0.70731	187;20	CAACGGAT	60.083	55	0	0	0
3.68	0.222725	283;20	GTGAATGT	59.729	55	0	0	0
4.57	0.151937	420;20	GGAACCCC	59.102	55	0	0	0
3.86	1.178289	199;20	AATCACCG	60.508	55	0	0	0
2.23	0.063838	185;20	TGGAAGCC	60.223	55	9.15	9.15	0
3.34	2.869056	183;20	CCAAATGC	60.223	55	0	0	0
4.63	3.048914	185;20	ATCACTGA	59.859	55	0	0	0
4.94	0.195316	199;20	GAGTCGAA	60.506	60	0	0	0

4.79	1.301401	343;20	CATGCACA	60.565	55	0	0	0
4.4	0.542928	223;20	TCCGCGGC	60.365	55	0	20.15	0
4.85	0.13212	249;20	AAATGCTC	59.732	50	0	0	0
4.18	2.077301	269;20	CAATCTGT	60.291	55	0	0	0
4.85	0.491684	201;20	GGCCCGTA	60.013	55	0	0	0
3.77	2.83498	196;20	CATAGCCC	59.799	55	0	0	0
5.54	0.332329	287;21	CAAATAGG	58.916	52.381	0	0	0
4.04	0.208315	360;20	AAATGACC	59.376	50	0	1.96	0
2.5	1.283789	231;20	GTGTGAC	59.597	55	0	11.96	0
4.61	0.007828	372;20	CAGCTGGT	60.293	55	0	2.22	0
3.46	0.40926	227;20	CTGCCTGG	59.591	55	0	0	0
2.23	0.721509	231;20	CTACTCGC	60.996	60	0	0	0
4.26	0.013327	189;20	TGCCGACG	60.011	55	0	0	0
3.14	1.206339	202;20	AGTGCTTT	59.869	50	0	0	0
5.19	0.864643	191;22	AGGTTTCT	59.616	45.455	0	0	0
4.41	1.214599	198;20	ATGACTGT	60.507	50	4.49	8.87	0
2.9	3.096716	347;20	GCGCCTAG	59.251	55	0	2.73	0
3.86	0.353069	195;20	TGTATAGT	59.443	55	0	0	0
3.61	0.265367	368;20	GTGGATGC	60.565	55	0	0	0
4.73	0.908625	463;19	AGGAACTC	60.082	57.895	0	0	0
5.54	0.332329	246;20	ACCTCGTC	59.866	55	0	0	0
3.35	0.078325	256;22	AGCATCTT	59.616	45.455	0	0	0
3.18	0.152509	207;22	TTGGAAGT	58.23	45.455	0	0	0
6.13	0.060062	259;21	GCCTCTGT	59.945	52.381	0	0	0
3.16	0.152373	193;20	CTGCCGAC	60.434	60	0	0	0
5.19	0.05625	315;20	TTGTGCCC	60.079	55	0	0	0
3.2	3.530557	213;20	AATCCGGA	60.009	55	4.15	4.15	0
2.34	0.293654	267;20	TGCTCCAC	59.86	55	0	0	0
4	0.294934	428;20	TGCCTGTT	59.869	50	0	0	0
3.06	0.012362	252;20	TTCGTCTC	59.668	50	0	0	0
3.16	0.01247	361;20	TGCCTGTT	59.869	50	0	0	0
4.17	0.492119	274;20	TTTGCATT	60.223	50	0	0	0
3.21	0.152077	229;20	AACGGGA/	58.934	50	0	0	0
3.09	1.010955	199;20	CATCACGC	60.013	55	0	0	0
4.3	0.366235	335;20	AACACCAA	59.442	50	0	0	0
5.18	1.336888	199;20	CCGCATCA	59.801	55	0	0	0
2.62	0.12755	364;20	GCGCCTAG	59.251	55	0	2.73	0
4.01	0.081722	227;19	GCGCACAC	60.302	57.895	0	0	0
5.54	0.332329	250;20	AACGGCAT	60.012	50	0	15.82	0
4.85	0.192725	340;20	TTAGAGGT	60.578	55	0	0	0
3.86	0.805198	215;20	CGTGTTCC	60.289	55	0	0	0
3.16	0.009737	225;20	ATTTGCTG	59.652	50	7.75	7.75	0
3.85	0.057154	321;20	CTTCTCTG	59.032	55	0	0	0
5.03	0.508107	210;20	AGATTGAG	60.865	55	0	0	0
3.16	0.839498	259;20	CAGCAAGT	59.944	55	0	0	0
3.02	0.134354	285;20	CCCTAGGC	61.531	65	4.99	4.99	0
5.12	0.920938	218;20	TCTACACC	60.152	55	0	0	0



3.66	1.56296	287;20	CCACAACA	60.082	55	0	0	0
3.01	1.209627	237;20	TCCACGCT	60.081	55	0.07	0.07	0
3.02	1.055923	256;22	TCAGTGGC	59.751	45.455	0	0	0
5.54	0.079952	362;20	CCTACATA	60.006	60	0	0	0
5.54	0.332329	282;20	TGTAATGC	59.306	50	0	0	0
4.94	0.207303	227;20	CAGGACGC	60.994	60	0	0	0
5.54	0.332329	388;20	CCTGCTTC	59.515	55	0	0	0
2.9	2.558976	282;20	ATCTACTA	60.152	55	0	0	0
2.77	0.267061	217;20	GGGCGAA	59.941	55	0	0	0
5.54	0.341494	270;22	AGAACAAC	59.945	45.455	0	0	0
4.3	0.208315	343;20	ACTGGGCC	60.151	55	0	0	0
3.16	1.077907	206;21	GCCCAATT	60.214	47.619	0	0	0
4.85	0.009403	256;20	CGCTTGAA	60.152	55	0	0	0
2.62	0.796774	256;20	CTCACTCA	59.664	55	0	0	0
5.28	0.205795	246;20	ACATGCCC	60.08	50	0	0	0
4.79	0.222551	255;20	ACAGTTGA	59.87	50	0	0	0
3.68	0.151344	243;20	CTTAGTGC	59.662	55	0	0	0
5.25	0.059753	362;18	GGCTTAGA	59.238	61.111	0	1.3	0
4.02	0.210869	267;20	GGGAAGG	60.513	60	0	0	0
3.69	0.688769	284;20	TGCCCAAG	60.079	55	0	0	0
3.95	0.547043	314;20	CAAGGGAC	59.091	55	0	0	0
4.85	1.544077	222;20	GCGGGTCC	59.872	55	0	0	0
2.82	1.348611	224;20	TTCCACAC	59.722	50	0	0	0
5.25	0.013327	295;20	CGTGTGTC	58.973	55	11.43	11.43	0
3.62	0.069392	257;21	ACCCTTGC	59.802	47.619	0	7.22	0
3.77	0.431397	301;20	TCATTCAA	59.437	50	0	0	0
2.78	0.129322	386;20	GCGCCTAG	59.251	55	0	2.73	0
4.94	0.333619	265;19	CTCTCCCT	59.254	63.158	0	0	0
4.3	0.008281	206;20	AAGCTGCC	58.865	50	0	0	0
2.67	1.491872	208;20	GCTCACAG	59.374	55	0	0	0
4.85	0.768876	212;22	TCGAATGA	60.015	45.455	0	0	0
3.79	1.157477	209;20	TCTCTTAT	60.011	55	0	0	0
4.17	0.770091	316;20	CTTGCGGA	59.594	55	0	0	0
4.85	0.997201	224;21	CGTTTCTG	60.214	52.381	0	0	0
4.85	1.534433	211;20	TTAGTGAG	59.938	55	4.62	4.62	0
5.52	0.009626	303;20	TGAAGAGC	60.437	55	0	0	0
4.35	0.133538	382;20	GAACGACC	59.946	55	0	0	0
4.61	0.289059	284;20	AGCGAGAA	59.521	50	0	0	0
3.18	2.316547	220;20	CCTCTCAC	58.729	55	0	0	0
3.21	0.221892	219;20	CTTGACGG	60.5	55	0	0	0
3.51	0.124832	220;20	GGTAGAAC	60.223	60	0	0	0
2.59	0.009403	256;21	GCACACTA	60.282	52.381	0	0	0
4.84	1.254594	213;19	TCGGGCAC	60.748	57.895	0	0	0
6.09	1.120029	238;20	TGCAGGTC	59.934	55	0	0	14.36
3.82	2.171186	228;20	GTGTGCAG	59.658	55	0	0	0
3.18	0.203059	211;20	CTAGTGCA	59.372	55	0	0	0
4.24	0.791283	262;20	GGACCACA	60.082	55	8.17	12.11	0

5.01	0.549349	271;20	GCGTAACA	59.948	55	0	1.21	0
2.32	0.13212	283;20	CACATGGC	60.292	55	0	0	0
2.75	0.349612	238;20	TTGAAGCT	60.503	55	11.9	23.21	0
4.61	0.081269	449;20	ATTTACAA	59.73	50	0	7.55	0
3.35	0.620872	347;20	CAGCGTTA	60.361	55	0	0	0
2.34	0.893619	216;19	TGGGCGTC	61.191	57.895	0	3.61	0
2.67	0.0564	277;20	ACGTTCGC	59.172	50	0	0	0
3.01	0.060683	221;20	AAAGAGTC	58.507	50	0	9.02	0
3.33	0.207555	275;20	GGGAGGA	60.151	60	0	0	0
2.39	0.988436	239;21	ACCTCTCA	60.352	52.381	0	0	0
3.02	0.749254	223;20	TAGTGATC	60.222	55	0	7.28	0
4.85	1.067925	283;20	TATGTCTG	59.938	55	0	0	0
5.54	0.332329	347;21	CCCTTAGG	59.192	52.381	0	0	0
3.51	0.291449	274;21	ACAGCCGC	59.739	47.619	0	0	0
3.82	3.392274	225;20	AGGCGGTA	59.064	55	0	0	0
5.54	0.152255	239;20	GCGATGCA	60.013	55	0	0	0
3.02	0.201828	229;20	TCCTCGTA	60.295	55	0	0	0
3.27	0.622401	382;20	TAACACCG	59.661	50	0	0	0
3.86	1.824899	227;21	TCGCATGT	60.015	47.619	0	0	0
3.09	2.471981	224;20	AAGTGCCT	60.575	55	0	0	0
3.46	0.01018	374;20	AGACGCAC	61.004	55	0	0	0
4.45	0.057608	239;20	TGTGCATG	59.871	50	0	0	0
5.03	0.083309	296;20	TACCAATC	60.927	55	0	0	0
3.51	2.792008	222;20	ACACATCA	61.011	55	0	0	0
5.34	0.130515	451;21	CATACTCA	59.407	52.381	0	0	0
3.86	0.50272	337;20	GCCTGTGA	60.011	55	0	0	0
3.71	0.066747	426;20	GTCAGGTC	60.936	60	0	0	0
2.85	3.018888	241;20	TATAACAA	59.297	50	0	0	0
4.45	0.931284	364;21	ACCGTGTC	59.526	52.381	0	0	0
3.86	1.804827	270;20	AGACGTGC	59.94	50	0	0	0
3.02	0.749254	315;20	CACGGTCG	60.153	55	0	0	0
4.57	0.01018	269;20	AGGGAGCT	60.009	55	0	0	0
3.56	0.061308	426;20	CTATCCGT	60.082	60	0	0	0
3.16	0.083433	305;20	GCATGTGT	60.015	55	0	0	0
3.82	0.012147	244;20	CTATCGGA	58.806	55	0	0	0
3.51	1.135124	279;20	ATGGTGTG	60.081	50	9.49	9.49	0
4.34	1.468499	279;20	CCACCAAG	59.871	55	0	0	0
4.18	0.199633	237;20	AAAGACGA	60.009	55	0	8.33	0
3.95	0.083806	235;20	AGAGATGC	60.006	55	0	0	0
2.97	2.001472	241;20	CCTTCCTA	60.223	60	0	0	0
4.61	1.812133	253;20	TGTTACGC	59.667	50	0	14.18	0
4.4	0.012147	375;20	GAAGTCGC	59.874	55	0	0	0
5.34	1.016362	343;21	AGCTATAC	59.804	52.381	0	0	0
2.78	0.202074	247;20	GAGAGCAC	60.648	60	0	0	0
4.57	2.966121	257;20	ATGAATAC	60.007	55	0	0	0
3.85	1.010142	255;20	TAAAGCCA	59.013	50	0	0	0
4.52	0.059136	277;20	CATCGGCA	60.781	55	0	13.44	0

4.06	2.214322	241;20	ACCTCAGC	58.496	50	0	0	0
2.62	1.042596	283;20	ATGACAGC	59.027	50	0	0	0
3.16	0.0561	259;20	CGCCAAGC	59.942	55	0	0	0
4.85	0.264245	333;20	ATGCAGCT	60.368	55	0	0	0
3.66	0.440765	341;20	TGATAGTT	60.579	55	0	0	0
3.53	0.637123	262;20	GCAGAAGC	60.013	55	0	0	0
4.57	0.152644	339;20	GTTTGCAG	60.222	55	0	0	0
4.42	1.510674	256;20	TTTCTGCA	59.944	50	0	0	0
4.1	0.126574	325;20	ATCGCTCA	59.104	50	6.63	6.63	0
3.85	0.80023	301;18	GGCGGTGC	59.148	61.111	0	0	0
4.94	0.152778	349;20	GCCTCCTG	59.298	55	0	0	0
3.71	0.152236	327;20	ATGGCCCT	59.933	55	0	0	0
3.69	0.274846	320;20	TTCTTAGG	59.862	55	0	2.93	0
3.35	3.104925	286;20	CCAACACT	60.222	55	0	0	0
4.45	0.555414	269;20	CAATGGTC	59.944	55	0	0	0
2.74	1.59759	254;20	TTGTCATA	60.01	55	0	14.33	0
3.86	1.870206	239;22	ACATGTAC	59.294	45.455	0	0	23.71
4.3	0.209332	318;21	CAGGTAGA	59.945	57.143	2.6	2.6	0
3.02	0.749254	285;20	GCAGGTTT	60.222	55	0	0	0
4.85	0.703881	243;20	TTCCACTG	60.152	55	0	0	0
4.61	0.86626	282;20	TGGGACCT	59.933	55	0	0	0
2.32	0.359001	386;20	ACCGATTC	60.081	55	0	0	0
3.46	0.211641	287;22	AATTTCCC	58.15	40.909	0	0	0
3.01	0.584849	344;20	CTCGGCTT	59.032	55	0	0	0
3.95	0.152451	274;20	ACGACAGT	60.436	55	0	8	0
3.21	1.205426	364;20	TTGTGAAG	60.082	50	0	13.64	0
4.35	0.733903	300;18	CGAAAGCA	59.859	61.111	0	0	0
3.35	0.801158	286;20	GCATAATG	59.265	50	0	0	0
4.4	2.106259	254;20	CTCTCCTC	60.58	60	0	0	0
3.85	1.004432	245;20	TAACCTCC	60.079	55	0	0	0
3.95	0.151155	249;20	ATTAATCC	60.006	55	0	0	0
4.46	0.223438	247;20	CAGCTCCT	60.863	60	0	0	0
5.19	1.380061	258;20	GGCGCTGC	59.521	55	0	5.51	0
3.35	0.293583	323;20	TGTCTCTC	59.512	55	0	0	0
4.4	0.079009	255;21	AGGCATTA	59.242	52.381	0	0	0
3.02	0.749254	377;20	GAGCAAGC	59.944	55	0	0	0
3.51	0.152835	299;18	CGCCCACT	59.856	61.111	0	0	0
5.36	1.142033	267;19	CCGAAATG	59.566	57.895	0	0	0
5.19	1.886313	329;22	GTGTTAGA	58.646	50	0	0	0
5.18	0.12254	383;20	ATAGTACC	59.724	55	0	0	0
3.51	0.223257	271;21	CACACTGA	59.744	52.381	0	0	0
5.8	0.008168	259;20	CCTATTTG	60.637	55	0	0	0
2.62	1.345667	253;20	TTAAGCAC	59.151	50	0	0	0
4.68	2.832004	338;20	CGGGTCTG	59.872	55	0	0	0
3.51	1.473754	261;20	CGACCTAC	60.152	60	0	0	0
4.85	3.177255	316;20	GGTGTAC	59.939	55	0	2.22	0
4.94	2.80206	258;20	GAGTCTCA	59.937	60	0	0	0

2.24	0.263407	340;20	GGCCCGTA	60.009	60	0	0	0
4.68	0.555414	258;20	GCACCGAA	59.53	55	0	0	0
3.91	2.132043	260;20	TGCCAATC	58.949	45	8.53	8.53	0
4.24	1.615515	307;20	ATATTGCA	59.938	50	0	0	0
6.46	0.222061	381;20	CTTCATTAC	59.736	55	0	0	0
3.77	0.081074	271;20	TGTTCTGT	60.152	50	0	8.59	0
5.25	0.770091	316;20	TGTTGAAA	59.869	50	0	0	0
3.01	0.081269	309;20	CGTGTA	60.085	55	0	0	0
4.46	0.579441	375;19	GATCTGAC	60.233	63.158	0	0	0
3.46	2.052692	294;20	CTGCCGAG	59.734	55	0	0	0
3.18	0.152057	366;20	CTTAGTGC	59.665	55	0	0	0
3.16	0.642556	336;20	AGGCTATG	60.08	55	0	0	0
3.69	1.255388	326;21	TGTTGCAT	58.589	42.857	0	0	0
4.26	0.5573	272;21	AGCCTTCC	59.04	47.619	0	0	0
3.46	2.410655	264;21	CTGGTGCA	59.745	52.381	0	0	0
6.46	0.558247	405;20	TTGCACGC	60.082	50	0	0	0
3.86	0.369469	265;18	CCATTGCA	59.143	61.111	0	0	0
4.4	0.016155	400;20	TTCGCCTA	59.798	55	0	0	0
4.85	0.511049	261;20	AGCAGGCC	59.933	55	0	0	0
4.45	0.139128	314;20	TCGAGAGT	60.01	55	0	0	0
2.77	0.081979	439;21	CTTCACTT	59.061	52.381	0	0	0
4.41	0.151917	312;20	CGTGCACA	61.484	60	0	15.73	0
4.85	0.151997	293;20	CAGCCATT	60.009	55	0	3.83	0
5.36	1.390721	303;20	CACCCGCC	60.081	60	0	0	0
3.18	0.293865	378;20	TCAGTGCT	60.293	55	0	0	0
4.04	0.134354	334;20	GCGTGAGA	59.11	55	0	0	0
4.3	0.431801	272;20	ATACAGAC	60.082	50	4.59	14.02	0
5.19	0.864643	318;20	CCTCAAAT	59.866	55	0	0	0
4.24	0.486512	267;20	CAGGCTGC	59.94	55	0	0	0
2.85	1.932113	270;20	GTGCGAAA	60.014	55	0	0	0
4.61	0.501178	303;20	ATGAGTGT	60.86	55	0	0	0
3.67	3.472109	270;20	AGAGTGAC	59.939	55	0	2.73	0
2.52	0.402963	365;20	ACGACAGC	60.999	55	0	0	0
3.86	0.359051	430;19	GTCGGGCC	60.38	63.158	0	0	0
2.93	0.291856	270;20	GCTCCGAA	60.292	55	0	0	0
3.51	0.266495	302;20	CCACACGG	59.941	55	0	0	0
5.12	0.009403	336;20	CTCGCGTC	60.222	55	0	0	0
4.41	0.151755	300;20	TCATGCCC	59.72	55	0	0	0
4.02	1.013446	300;20	CAGCCGCT	60.082	55	0	0	0
2.32	0.011278	356;22	TCTAACAT	60.075	50	0	0	0
4.3	0.066747	329;20	TGGGACCA	60.442	55	0	0	0
5.68	0.290579	372;20	CAGATGTT	60.011	55	0	0	0
4.46	3.057782	354;20	TGATCCGG	59.293	50	0	0	0
4.26	0.982883	426;20	ATCGCTAT	60.504	55	7.75	6.93	0
4.17	1.984925	402;20	CGGGTTCC	60.222	55	0	0	0
4.84	0.012685	432;20	CTTCCCTC	59.935	60	0	0	0
3.71	2.233409	296;20	ACACTCTT	59.866	55	0	0	0

4.3	0.222926	424;20	TTACAAGT	59.869	50	0	0	0
6.13	0.063359	292;21	TCTGGGTT	60.215	52.381	0	0	0
4.94	0.909394	305;20	TCGTGCTG	60.291	50	0	0	0
2.85	0.067239	306;21	AGGCATTA	59.242	52.381	0	0	0
4.85	0.62754	309;22	CGAGGAG	60.143	50	1.31	1.31	0
2.52	0.355165	309;20	TACGACCT	60.785	55	0	0	0
4.18	0.055651	319;20	GGGTGTAT	60.014	55	0	0	0
4.41	1.938925	329;20	TCGAAACT	60.082	50	0	0	0
3.51	0.43519	308;20	AGAAATTT	59.942	50	3.07	20.17	0
2.9	0.271642	351;20	GCCTCATA	59.802	55	0	0	0
4.02	0.130117	321;19	CACTGTCTG	60.23	57.895	0	0	0
3.51	1.261566	302;20	TATTGCAT	59.177	50	0	0	0
3.62	1.01074	312;20	TGCTAAGG	59.86	55	0	0	0
5.25	0.222876	349;20	ATAACGTG	59.73	50	0	0	0
3.28	0.128729	318;20	CGAACTCT	59.738	55	0	0	0
3.85	0.223699	347;20	ACGTCCAT	60.01	55	0	0	0
2.74	0.361194	311;20	GACCATTC	60.571	55	0	0	0
3.56	0.365299	373;22	ACATGTGT	60.207	45.455	0	1.77	0
3.58	0.079617	351;20	ACATCAAC	60.854	55	0	0	0
6.13	0.292817	333;22	TGAAAGAC	59.939	50	12.72	12.72	0
4.09	0.294575	318;20	GTCTTGCC	60.012	55	0	0	0
1.85	0.57767	313;20	GCTTCAAC	59.797	55	0	0	0
4.94	0.222207	340;18	TCTCCTCT	61.57	66.667	0	0	0
4.2	0.563498	365;19	AGCGCACA	59.2	52.632	0	9.33	0
3.86	0.353069	318;21	TCGCCTCA	59.666	52.381	0	0	0
3.95	0.29429	390;20	TGAGGACC	59.292	55	3.54	3.54	0
3.51	0.834955	320;20	GTGTTCTT	60.015	55	0	0	0
5.8	0.008168	324;19	CTTCTCCT	60.305	63.158	18.69	18.69	0
3.18	0.060217	382;20	GAGAGACC	59.727	60	0	0	0
3.66	0.19939	435;20	CGCACGGT	60.561	55	0	0	0
4.3	1.82961	382;20	CTTTCTCA	59.589	55	0	14.09	0
3.67	0.080549	364;20	CCAAATCG	59.661	55	0	0	0
5.03	1.231935	333;20	CGTGTGTG	60.015	55	0	0	0
3.86	2.96866	322;20	AGCTGCTG	58.733	50	0	0	0
4.85	0.222158	322;20	TGTGTTTG	60.012	50	0	0	0
2.69	0.130117	398;20	CACTCACC	59.594	55	0	0	0
4.46	2.252205	334;21	TCTACAGC	59.945	52.381	0	0	0
4.4	2.011767	357;21	CCAAACGA	59.553	52.381	0	0	0
2.73	0.550739	407;20	CAGGGTCT	59.866	55	0	0	0
4.85	0.420709	337;20	ATGTGGCT	59.938	50	0	0	0
5.19	0.12755	369;21	CTAGTCCT	59.603	52.381	0	0	0
5.01	0.013113	365;20	ATCTGTGC	60.224	55	14.15	18.73	0
4.26	0.010841	385;20	AGAACAG	59.658	55	0	0	0
1.9	0.906618	334;22	CCTTTGGG	58.283	50	0	1.1	0
3.07	1.208326	336;20	GCTCTTCC	60.011	55	0	0	0
3.86	0.133538	344;20	GAGAAAG	59.519	55	0	1.59	0
4.16	0.198665	385;20	CTGACCGC	60.084	55	7.4	7.4	0

5.19	0.011278	351;20	TGTACCTT	60.079	55	0	0	0
3.67	0.151897	417;20	ACGCCACA	60.153	50	12.31	12.31	0
2.77	0.081979	355;20	ATTCGCCT	59.933	55	0	0	0
2.85	0.067239	355;20	TCGAAACT	60.082	50	0	0	0
5.36	0.060683	407;22	GCTGGGCC	58.275	45.455	0	0	0
4.85	0.082363	404;20	GTTCGTGA	59.872	55	0	0	0
2.92	0.083183	411;20	AAGACCCA	60.724	55	0	0	0
3.28	2.911437	406;21	GGTTGATC	58.051	47.619	0	0	0
4.61	0.060683	386;20	GCGCCTAG	59.251	55	0	2.73	0
3.56	0.080417	431;20	GCTCATCA	59.804	55	2.68	2.68	0
3.51	1.45785	439;18	CTCGCATG	60.016	61.111	11.89	11.89	0
3.82	1.081552	356;21	CCCATGGC	59.806	52.381	0	2.67	0
3.51	0.223053	368;18	CGGCAAGC	59.856	61.111	0	4.1	0
3.16	0.222134	366;20	TCTACGTG	60.153	50	0	0	0
3.58	0.061778	401;20	GTCGACGC	60.015	55	0	0	0
2.75	0.473511	404;20	CTGAGGAA	59.872	55	0	0	0
2.17	0.329133	430;20	CAAATCAA	60.924	55	0	10.19	0
4.4	0.012685	373;20	ACGGAAGC	59.936	55	0	0	0
4.85	0.013327	370;20	GCACGACC	60.574	60	0	0	0
5.19	0.987367	425;20	AGTACATG	59.938	55	0	0	0
2.82	0.268198	369;20	GCCGAACT	59.022	55	0	0	0
5.34	0.199633	385;20	GATTCCAG	59.379	55	0	0	0
3.34	0.062408	377;20	TGTTTACT	58.563	50	0	0	0
2.52	0.059136	380;20	GGTTTATG	60.083	55	0	0	0
6.13	0.130515	398;20	CTGCCTAC	60.224	60	0	0	0
4.61	0.059136	464;20	CTTAAACA	60.222	55	0	0	0
4	0.133538	440;20	GGGTAGGC	58.874	55	0	0	0
4.61	2.011532	387;20	ATACCATC	60.08	55	0	0	0
4.35	0.055502	445;20	AAGCACCT	60.224	55	4.17	5.19	0
3.91	0.131316	426;20	CTAGCTGC	59.942	55	0	0	0
3.09	0.744043	422;20	TCACAAGC	59.526	50	0	12.34	0
3.86	0.338183	452;20	AGAATCGT	60.013	55	0	5.85	0
3.79	0.152451	441;21	ACACACTA	59.815	47.619	0	0	0
4.46	0.223078	467;20	ACTAGATG	60.081	55	3.83	15.89	0

right_end_	right_pena	pair_product_size	pair_compl	pair_compl	pair_penal	duplicate
3.16	1.255278	80	0	0	2.269741	0
4.61	2.84038	80	0	6.8	3.244444	0
3.2	1.533554	80	0	0	2.309155	0
4.57	1.999122	80	0	0	2.490372	0
4.3	3.630256	80	2.62	5.28	4.949898	0
1.89	1.277945	81	0	0	4.853312	0
5.18	2.085708	81	0	0	2.44331	0
5.28	3.269262	81	0	0	3.600949	0
4.35	1.181111	81	0	0	3.505963	0
3.2	0.912185	81	0	0	2.374753	0
5.28	0.351681	81	0	0	1.010726	0
2.34	0.618842	81	0	0	1.558809	0
1.85	3.232346	82	0	0	3.923321	0
4	0.797645	82	0	0	1.909436	0
4.01	2.303358	82	0	0	2.947658	0
3.67	0.909074	82	0	0	2.124038	0
3.51	2.164425	83	0	0	4.282127	0
3.95	2.396839	83	0	0	3.216179	0
4.63	0.292334	83	0	0	1.834216	0
4.79	0.431709	84	3.75	8.56	1.863258	0
3.85	1.374666	84	0	0	2.386355	0
4.3	0.283208	84	0	0	0.892547	0
4.18	0.12755	84	0	0	3.791083	0
4.17	3.808307	84	3.26	10.57	4.449709	0
5.34	0.577922	85	0	0	4.387389	0
2.62	0.15151	85	0	0	1.240798	0
4.18	0.844082	85	0	0	1.529563	0
6.13	0.129521	85	11.72	11.72	2.513421	0
4.85	2.398038	85	2.54	5.37	2.970982	0
3.34	2.116825	86	0	0	2.732642	0
4.42	1.908909	86	0	0	2.408894	0
6.53	0.013327	86	0	0	2.123161	0

1.78	0.901792	86	0	0	1.38745	0
3.51	2.241869	86	0	0	4.131618	0
3.95	0.604916	86	0	0	1.104901	0
4.01	0.615817	87	0	0	1.846736	0
3.16	1.922049	88	7.42	11	4.103745	0
4.85	0.437783	88	0	4.61	2.028116	0
4.18	0.014069	88	0	0	0.623408	0
5.25	0.275433	89	4.69	1.91	0.556522	0
4.35	0.690422	89	0	0	2.741607	0
4.7	0.223778	89	0.41	0	1.455327	0
3.01	0.060683	89	0	0	2.144862	0
3.58	2.528684	89	0	0	2.680521	0
3.36	2.925247	89	0	0	4.345586	0
3.51	0.152037	89	7.24	25.58	1.048367	0
4.85	0.652309	90	0	0	0.667532	0
3.16	3.820093	90	0	0	5.53947	0
6.86	0.335565	90	15.46	9.37	1.392857	0
2.74	0.0561	90	0	0	0.782481	0
1.78	2.959873	91	0	0	3.369133	0
5.19	1.094322	91	0	0	1.644134	0
4.4	0.139339	91	0	0	0.269456	0
3.79	0.772532	91	0	0	1.284006	0
4.1	0.222158	91	0	0	4.167648	0
6.13	0.496937	91	0	0	0.510264	0
3.51	2.254792	91	10.04	10.04	4.106904	0
2.34	0.83297	92	0	0	1.582224	0
6.53	0.864643	92	0	0	1.338153	0
4.63	0.293303	92	0	1.98	1.042558	0
2.23	0.550739	92	0	0	0.971838	0
4.85	2.685223	93	0	0	3.608002	0
4.17	1.397396	93	0	0	2.728486	0
4.45	0.987367	93	0	0	1.537642	0
4.46	1.05484	93	2.71	4.4	1.115057	0
4.44	0.764043	93	0	0	0.823951	0
3.51	0.440765	93	0	0	2.333374	0
4.63	0.151448	94	0	0	1.231087	0
2.39	0.428323	94	0	0	1.551676	0
3.18	1.886976	94	0	0	2.038527	0
3.51	0.718082	94	0	0	1.467336	0
4.61	0.620872	94	0	0	1.376576	0
2.62	0.05625	95	0.12	3.75	1.242614	0
3.02	2.050371	95	0	0	2.273373	0
4.94	3.545909	95	0	0	4.183032	0
4.7	2.724241	95	0	0	2.7353	0
3.02	0.749254	95	0	0	3.587227	0
3.71	1.564441	96	13.8	12.67	4.031046	0
5.19	1.665092	96	1.59	3.21	3.804347	0



3.71	0.647234	96	0	0	0.851531	0
4.61	0.859438	97	18.67	18.67	1.298207	0
2.39	0.625477	97	29.71	29.71	3.444453	0
1.85	3.974288	98	0	0	4.838931	0
3.51	1.028794	98	0	0	1.180262	0
2.9	2.4292	98	0	0	3.201732	0
5.01	3.635627	98	0	0	4.962002	0
3.67	1.316939	98	0	0	2.066193	0
2.78	0.205294	98	0	12.9	2.119421	0
3.51	1.556249	99	0	0	2.305503	0
3.02	0.268198	99	0	0	0.279476	0
3.46	0.063042	99	0	0	3.734455	0
5.8	0.554005	99	0	0	1.565903	0
4.85	2.590377	99	0	0	2.720494	0
4.85	0.203554	99	0	0	1.670016	0
3.71	1.290026	100	0	0	3.857812	0
3.32	0.486085	100	0	0	3.327904	0
4.35	1.366901	100	34.44	30.91	2.798042	0
3.02	0.858578	101	0	0	1.267839	0
6.09	0.474747	101	0	0	1.245742	0
5.28	1.849621	101	0	0	2.255901	0
3.69	0.636429	101	0	0	1.0487	0
5.34	1.081733	101	0.01	0	1.163326	0
5.19	0.864643	101	0	0	4.351187	0
6.86	0.290778	102	8.54	6.71	1.438097	0
3.85	0.800757	102	0	0	1.550011	0
3.13	0.411893	102	0	0	0.49451	0
3.86	0.840804	102	0.09	0	1.408414	0
6.09	1.045706	102	0	0	1.382576	0
4.79	0.009848	103	0	0	0.934983	0
3.69	3.626624	103	0	0	5.769481	0
4	0.223857	103	0	0	0.567693	0
3.58	0.706164	104	0	0	1.864568	0
5.34	0.684389	105	0	0	0.977623	0
5.28	0.222526	105	0	0	0.356675	0
4.26	0.205294	106	0	0	1.996469	0
3.51	1.232692	106	3.26	5.53	4.39591	0
5.34	0.265367	106	0	0	0.319386	0
1.89	1.068733	107	6.24	10.01	3.390336	0
6.13	0.222551	107	0	0	0.697711	0
2.67	0.057608	107	0	0	0.209666	0
3.61	0.063838	107	0	0	3.499546	0
6.09	1.625966	107	0	0	3.469069	0
3.32	0.542928	107	0	0	0.669502	0
2.87	1.936872	108	0	0	2.229001	0
5.03	0.013752	108	0	0	0.235958	0
4.52	0.699349	108	0	0	3.859411	0

3.86	2.164106	108	0	2.68	2.913361	0
2.77	0.13212	109	0	0	1.448462	0
5.69	0.083806	109	0	0	1.695893	0
4	0.935766	109	9.32	9.32	2.705532	0
3.51	1.793474	109	0	0	1.871799	0
3.11	2.06649	109	5.39	9.23	2.200844	0
3.42	0.365532	110	0	0	1.341017	0
2.01	0.152137	110	0	0	1.503249	0
3.21	1.595219	110	0	0	4.222482	0
4.2	0.688769	111	4.22	0	1.769552	0
3.02	0.749254	111	0	0	2.658112	0
5.03	0.338183	111	0	0	0.762414	0
6.09	0.8603	112	0	0	1.832852	0
4.17	0.005644	112	0	0	3.226155	0
5.36	0.082995	112	0	0	0.431237	0
4.35	0.509362	112	0	0	1.147618	0
4.02	0.351681	113	0	0	0.575459	0
2.67	3.922171	113	0	0	5.069684	0
4.4	0.196267	113	0	6.54	2.920409	0
4.06	0.01322	113	0	0	1.289765	0
5.34	0.008506	113	0	0	0.087922	0
4	0.40926	113	0	0	1.527677	0
4.01	0.781174	113	0	0	3.769625	0
4.61	0.005527	114	0	0	0.583702	0
3.02	1.281008	114	0	0	4.309222	0
3.82	1.912818	114	0	0	2.430355	0
4.42	1.274946	114	4.36	0	3.33841	0
4.4	0.222526	114	0	0	0.281049	0
3.66	0.152644	115	0	0	0.901898	0
2.93	0.128729	115	0	0	0.877984	0
5.52	2.049564	115	0.38	0.38	2.179681	0
5.18	0.499196	115	0	0	1.506529	0
3.46	0.222725	116	0	5.63	1.742928	0
3.46	0.080615	116	0	0	0.442373	0
3.77	1.168294	116	0	0	1.975044	0
3.16	0.401866	116	0	0	0.694269	0
4.85	0.346878	116	0	0	1.198916	0
6.46	0.05837	116	0	0	0.631314	0
3.86	0.063838	117	0	0	2.466493	0
4.11	0.3479	117	0	0	0.47545	0
4.45	0.294934	117	0	0	1.239318	0
5.12	0.057154	117	0	0	0.209682	0
3.51	2.879952	117	0	0	3.160138	0
6.13	2.715638	117	0	0	2.778046	0
2.39	0.007372	117	10.62	12.2	0.301237	0
4.61	0.006685	118	0	0	0.867849	0
4.4	2.313038	118	0	0	2.607044	0

5.28	1.734243	118	0	0	2.070134	0
3.14	0.354465	118	0	0	0.796918	0
4.57	1.013036	119	0	0	1.235562	0
3.66	0.269627	119	0	0	0.630821	0
3.34	0.12464	119	6.38	0	0.347365	0
4.3	0.427395	119	0	0	0.650321	0
3.51	1.123353	119	0	0	1.62493	0
5.19	0.864643	120	0	2.35	3.161865	0
3.95	0.920474	120	0	0	1.711758	0
3.14	2.611411	120	0	0	2.692026	0
3.46	0.439764	120	4.89	4.89	1.572072	0
4.85	0.29172	120	0	0	1.437979	0
1.85	0.439431	120	0	0	1.159564	0
5.19	0.571475	120	0	0	1.043754	0
5.34	0.054019	121	0	0	1.951765	0
3.67	2.043809	121	7.14	0.4	3.930317	0
4.12	0.29429	121	0	0	3.901284	0
4.06	0.059753	121	0	0	0.212008	0
3.46	1.140143	121	0	0	1.268873	0
4.79	0.47516	121	0	0	1.865542	0
3.46	0.151977	121	0	0	1.455539	0
3.28	2.911437	121	0	0	6.364699	0
4.85	1.425492	121	0	0	3.093696	0
4.12	1.916596	121	0	0	5.52359	0
3.51	1.716568	122	0	0	4.189555	0
3.86	2.163702	122	16.7	16.7	4.823117	0
4.4	0.198665	122	4.7	8.99	0.214511	0
3.02	1.080697	122	10.11	10.11	1.415611	0
3.51	0.544751	122	1.73	0	0.883923	0
3.53	0.223673	122	12.21	13.6	0.446827	0
4.16	0.013752	123	0	0	0.236032	0
4.12	0.011278	123	0	0	1.512362	0
5.03	0.012255	123	0	0	1.527839	0
3.01	0.563354	123	0	0	2.197372	0
5.87	0.121031	124	0	0	0.954695	0
4.79	0.152451	124	7.3	0	1.216966	0
3.35	0.205795	124	1.53	9.71	1.364117	0
4.68	2.125698	125	0	0	2.545242	0
4.4	0.358784	125	0	0	1.41948	0
5.25	0.413028	125	0	0	0.686121	0
4.06	0.083806	125	0	0	1.135796	0
4.94	0.222304	125	0.75	12.4	0.375196	0
3.69	1.014558	125	0	0	1.375093	0
3.36	3.33665	126	0	0	3.347928	0
4.35	2.077855	126	0	0	2.289238	0
3.91	0.204795	126	0	0	0.612935	0
4.61	0.273093	126	0	0	1.769285	0

3.02	1.057318	126	0	0	1.209593	0
3.66	0.010291	126	0	0	2.37351	0
4.02	0.079009	127	0	0	0.092016	0
4.4	0.013752	127	0	0	0.592685	0
4	0.078737	127	0	0	0.84158	0
5.36	0.926075	127	0	0	1.149051	0
3.18	2.012168	127	0	0	2.766693	0
2.93	0.197942	128	0	0	0.46331	0
5.18	0.082363	128	0	0	3.37661	0
3.35	1.184157	128	0	0	2.531973	0
4	0.12755	129	0	0	0.339449	0
4.09	0.22318	129	0	0	0.63583	0
2.9	0.903284	129	0	0	3.828631	0
3.09	0.291856	129	0	0	0.514909	0
3.46	0.505423	129	0	0	4.208305	0
4.4	0.912185	129	0.87	0.87	0.993519	0
4.3	0.22318	130	0	0	0.351516	0
3.66	0.40554	130	0	0	0.558694	0
4.85	0.194134	130	0	2.23	0.201506	0
2.75	1.851687	130	0	0	2.365301	0
4.45	2.292917	131	0	0	3.137	0
4.35	0.40554	131	13.86	11.68	1.768957	0
2.82	0.013433	132	0	0	3.380593	0
4.06	3.866833	133	0	0	4.664797	0
4.63	0.056701	133	12.56	12.83	1.243065	0
3.85	1.071977	133	0	0	1.202094	0
3.35	0.294575	133	0	1.27	1.965171	0
5.34	0.613812	133	0	0	2.276843	0
4.26	0.128335	133	0	0	0.422341	0
3.86	0.082553	133	0	0	1.094067	0
4.79	0.083183	134	0	0	0.149931	0
3.69	3.95122	134	0	0	4.246514	0
3.61	0.496496	134	0	0	3.474982	0
3.02	0.749254	135	0.15	0.15	3.567215	0
2.77	0.223155	135	0	0	0.283372	0
5.01	1.46527	135	0	0	1.475671	0
5.03	0.433596	135	0	5.63	0.442439	0
5.36	3.805541	135	2.46	8.67	4.002764	0
2.62	0.292955	135	0	0	3.908339	0
3.02	0.749254	135	0	0	0.943624	0
5.01	0.479319	135	0	0	0.81619	0
4.7	0.082553	136	0	0	2.57103	0
4.7	1.078815	136	0	0	2.387148	0
3.66	2.480242	136	0	0	4.873421	0
2.52	0.844082	136	0	0	1.460905	0
3.91	0.199148	137	0	0	0.421209	0
3.93	2.372398	137	0	0	2.428498	0

4.79	2.06649	137	0	0	3.656819	0
3.01	2.453204	138	0	2.24	4.801768	0
3.21	2.2069	138	0	0	4.115809	0
4.61	0.268198	138	0	0	2.474758	0
4.79	2.248633	138	0	0	2.736002	0
3.85	1.058305	139	0	0	1.475149	0
4.26	0.194134	139	0	0	0.323061	0
5.34	0.66678	139	0	0	0.79433	0
3.35	0.134354	140	0	0	1.349517	0
2.59	3.092972	140	10.16	10.07	3.244829	0
5.14	0.063359	140	0	0	0.913397	0
2.77	0.347218	140	16.94	23.22	2.647456	0
4.57	0.292129	140	0	0	0.695092	0
3.35	0.128139	140	0	0	0.251821	0
2.32	2.083017	140	0	0	3.220508	0
3.06	1.251971	140	0	0	1.311261	0
3.51	3.978031	140	0.23	4.52	4.393343	0
4.7	0.079009	141	19.2	25.16	0.65845	0
3.67	0.914958	141	21.43	31.95	0.974865	0
3.91	0.296985	141	0	0	1.309402	0
4.3	3.571693	141	0.1	12.43	3.579521	0
4.57	0.151917	141	0	0	0.303673	0
3.62	1.428304	141	0	0	1.487594	0
4.94	0.29118	142	0	0	0.722981	0
4.01	0.433913	142	0	0	0.704977	0
4.18	0.787421	142	0	0	2.047359	0
3.18	1.499448	142	0	0	1.650999	0
3.66	1.063691	142	0	16.32	2.054821	0
3.46	3.698519	142	0	0	3.906327	0
3.02	0.200606	143	0	0	0.847839	0
3.69	0.631699	143	0	0	0.712773	0
5.01	0.013752	143	0.7	0.7	0.592432	0
5.19	0.063359	143	0	0	2.142275	0
4.61	0.210869	143	0	0	1.209009	0
4	0.564461	144	0	0	0.716989	0
4.85	1.123353	144	0	0	1.487035	0
4.79	0.69598	144	0	0	0.918755	0
3.07	2.837751	144	0	0	4.088487	0
4.41	0.787421	144	0	0	1.536676	0
3.69	0.125604	145	0	0	1.107742	0
2.77	1.303248	145	0	0	2.513722	0
3.51	0.222825	145	0	0	0.514545	0
3.06	1.187701	145	0	0	1.272122	0
4.94	0.083433	145	1.52	3.83	0.209231	0
4.94	0.211641	145	0	0	1.224058	0
2.9	0.5698	145	0	0	0.865312	0
3.16	2.866589	146	0	0	2.948951	0

4.11	0.060062	146	0	0	0.826515	0
3.13	0.223568	146	0	0	0.375823	0
3.51	2.636647	146	4.72	6.98	2.78799	0
5.14	0.135586	146	0	0	2.06166	0
5.68	0.0564	147	0	8.92	0.113403	0
3.18	0.133538	147	0	0	0.192674	0
4.02	0.062408	147	0	0	0.215562	0
1.73	0.6971	148	0	0	2.23461	0
3.16	1.083679	148	0	0	1.235312	0
2.87	0.423444	148	0	0	0.716261	0
3.66	1.891105	148	0	0	1.973911	0
3.18	0.461004	148	0	0	3.423094	0
4.94	2.087066	148	0	0	3.757356	0
3.01	0.334915	148	0	0	0.394051	0
4.85	0.270201	148	0	0	0.749102	0
4.85	0.349612	149	9.95	9.95	0.48133	0
3.61	0.060528	149	0	0	1.655274	0
3.62	0.12755	149	0	0	0.829773	0
3.85	0.563498	149	0	1.95	0.697036	0
3.18	3.749359	149	3.71	3.71	4.259562	0
2.67	1.245324	149	8.94	8.94	3.094945	0
5.87	2.772446	149	6.29	9.48	3.271051	0
4.01	0.082932	149	0	0	0.62586	0
3.67	2.078463	150	0	0	2.498783	0
3.66	0.140397	150	0	0	0.432938	0
6.13	0.479319	150	0.58	2	1.538692	0
2.34	0.902479	150	2.04	2.04	1.096613	0
4.79	2.497664	150	0	0	2.855694	0
5.68	0.011605	150	0	0	0.288809	0
2.32	2.669847	150	0	0	2.753838	0
3.18	0.202074	150	0	0	3.632606	0
1.73	1.060696	150	0	0	1.611435	0
5.69	3.465578	150	0	0	4.926903	0
3.79	2.561326	150	0	6.26	2.625966	0
3.67	0.571231	150	0	0	0.58119	0
3.02	0.192725	150	0	0	0.322246	0
4.3	2.236409	150	6.41	2.69	4.159083	0
3.69	0.011714	151	0	0	0.65543	0
2.97	0.413028	151	0	0	2.558156	0
4.61	1.753637	151	0	0	2.180635	0
4.85	0.224204	151	3.21	3.21	0.87561	0
4.35	1.194303	152	0	0	1.258301	0
3.21	2.755732	152	0	0	3.762935	0
2.85	1.11914	152	0	0	1.250456	0
3.67	0.153079	152	14.03	14.03	2.237814	0
4.26	0.4391	152	0	0	3.146925	0
2.57	0.065122	152	0	0	0.428348	0

6.13	0.152255	153	0	0	0.48717	0
3.77	0.061151	153	0	0	1.877187	0
5.34	1.072775	153	0	0	3.313051	0
4.01	0.571231	154	0	0	1.119194	0
3.67	0.12755	155	0	1.92	1.083377	0
3.82	0.830451	155	0	0	1.195633	0
5.54	0.623936	156	0	0	3.324908	0
2.62	2.494389	156	0	0	2.858416	0
3.51	0.223002	157	0	0	1.40301	0
3.68	1.23187	158	0	0	3.437908	0
5.34	1.012751	158	0	0	1.023811	0
3.18	0.221654	158	0	0	0.515944	0
5.36	1.510391	159	0	0	1.570608	0
3.51	0.293865	159	0	0	1.807784	0
4.61	1.146748	159	0	0	2.278487	0
5.03	0.196744	160	37.85	37.85	0.490892	0
4.26	1.623462	160	0	0	2.610829	0
2.77	0.282298	160	0	0.75	3.121472	0
3.51	0.222378	160	0	0	3.992336	0
4.79	0.500779	161	0	0	0.988148	0
4.85	0.206799	161	0	0	0.707379	0
3.71	0.061308	161	0	0	0.81938	0
3.02	0.367898	161	0	0	1.288836	0
5.12	0.920938	161	0	0	1.130781	0
4.34	0.290845	161	0	0	0.416449	0
4	0.496496	161	0	0	0.719651	0
4.46	0.925135	161	0.43	12.66	3.195872	0
4.04	0.719447	161	0	0	0.843512	0
4.61	0.289059	161	2.4	0	2.540749	0
4.4	0.130515	162	4.3	7.96	0.283217	0
4.4	0.564762	162	0	0	0.574166	0
4.26	0.690422	162	0	0	0.90466	0
4.35	0.680054	163	0	0	0.76286	0
6.53	0.013327	163	0	0	1.020352	0
3.51	1.456926	163	0	0.2	1.467327	0
4.3	0.421098	163	0	0	1.434135	0
4.02	0.12755	164	0	0	3.433804	0
4.45	1.157512	164	0	0	2.01609	0
3.51	1.662004	164	0	0	2.369407	0
4.7	2.07668	165	0	0	2.279986	0
4.85	1.211521	165	0	0	2.44288	0
2.18	0.013327	165	0.89	0.89	0.698807	0
4.49	3.931304	165	0	0	4.129487	0
5.18	1.684966	165	0	0	1.699351	0
3.77	2.459312	165	0	0	4.938292	0
3.07	0.060217	165	0	0	0.637888	0
3.86	2.84038	166	0	0	2.993384	0

3.86	3.736314	166	0	0	3.888028	0
4.04	0.014805	167	0	0	0.027919	0
3.36	0.058217	167	0	0	0.613161	0
3.69	0.714698	167	4.22	4.22	1.795333	0
3.51	1.656399	167	0	1.77	1.710566	0
2.32	0.957395	167	0	0	0.967796	0
5.36	2.428335	167	0	0	2.442086	0
4.79	1.456926	168	0	0.35	1.609493	0
4.85	2.38289	168	0	0	2.800889	0
4.52	0.366118	168	0	0	3.077635	0
4.18	0.01106	169	0	0	2.840696	0
5.14	0.135586	169	4.06	0	3.987068	0
5.01	0.974017	169	0	0	2.886979	0
4.57	1.061091	169	0	0	1.28422	0
4.12	1.277071	170	1.44	6.54	1.400753	0
3.61	1.602376	170	0	0	2.224266	0
4.79	0.080549	170	0	0	0.360136	0
5.52	0.222427	171	0	0	0.283735	0
5.28	0.477649	171	0	0	0.48593	0
6.13	0.507069	171	5.74	5.74	1.426295	0
4.3	2.053054	172	5.18	12.61	2.916388	0
1.73	0.0068	172	0	0	0.297379	0
3.95	1.450099	172	3.63	3.63	2.314741	0
3.34	1.845705	173	0	0	1.92632	0
3.51	1.039501	173	0	0	4.539177	0
2.34	1.115073	173	0	0	1.981908	0
4.85	0.064639	174	0	0	1.725932	0
3.34	0.13766	174	0	0	1.60293	0
4.35	0.0786	174	0	0	0.421429	0
4.46	1.705045	174	0	0	1.786314	0
5.73	1.875814	174	0	0	2.161775	0
2.5	0.963122	174	0	0	1.042537	0
4.17	0.151572	175	0	0	0.7619	0
1.89	0.131316	175	0	0	1.319914	0
3.95	0.267061	175	0	0	2.279417	0
4.18	0.29479	175	0	9.41	0.915662	0
6.13	0.079684	176	0	0	0.301988	0
3.82	0.419932	176	0	0	1.351216	0
4.3	2.974953	177	0	0	4.313067	0
5.25	0.223778	177	0	0	0.829183	0
4.35	3.603227	177	0	0	3.806533	0
4.85	0.009403	177	0	0	0.1479	0
4.61	0.151551	178	0	0	1.230621	0
4.35	0.151551	178	0	0	0.231503	0
4.79	0.152451	178	0	0	2.615437	0
3.77	2.476692	179	0	0	2.556376	0
3.91	0.084603	180	0	0	3.925391	0



4.09	0.061308	181	0	0	1.068522	0
4.16	0.136827	181	1.82	9.85	1.062466	0
3.79	0.262572	181	0	0	2.312538	0
5.03	0.427416	182	0	0	0.437152	0
2.67	0.358784	182	0	0	0.493548	0
4.73	0.0561	182	0	0	0.918999	0
4.49	0.014175	182	0	0	0.800988	0
4.3	0.081074	183	0	0	1.140621	0
3.68	1.082329	183	0	0	1.52343	0
3.2	2.054497	183	0	0	3.123558	0
4.79	0.854312	184	0	0	0.91879	0
3.51	0.493426	184	0	0	2.077451	0
3.02	1.086268	184	0	0	2.647206	0
3.46	1.061578	185	0	0	2.19486	0
3.51	0.970362	185	0	0	1.957286	0
5.34	0.062408	186	0	0	0.143872	0
4.35	0.084237	186	0	0	0.136646	0
5.14	0.570501	186	0	0	0.578443	0
2.67	0.362432	186	0	0	1.572124	0
5.03	0.433596	186	8.38	7.59	2.020397	0
3.51	0.121784	186	0	0	0.273211	0
3.32	0.199633	186	0	0	0.858677	0
2.85	0.510203	186	0	0	0.567812	0
3.09	0.060683	187	0	0	0.32409	0
3.2	0.720133	187	0	0	0.776533	0
3.86	0.062724	187	0	0	0.967959	0
5.01	0.203059	187	4.6	2.8	0.812398	0
3.18	1.908539	188	0.05	0	1.965542	0
4.01	0.008281	188	0	0	0.445248	0
4.04	0.200606	188	0	3.25	0.49447	0
3.61	0.061778	188	0	0	0.125616	0
2.73	0.059136	188	0	0	1.216543	0
5.19	0.504809	189	3.6	3.6	0.798674	0
3.51	2.390512	189	2.39	0	2.448121	0
3.85	0.141463	189	0	0	0.204822	0
3.46	1.770225	189	0	0	1.829978	0
1.75	1.012417	189	0	0	1.097263	0
3.69	2.148594	189	0	0	2.279109	0
3.36	0.496937	189	2.43	10.04	1.010335	0
3.46	0.004354	189	0	0	0.227484	0
3.51	1.749146	189	0	0	2.161795	0
3.01	0.066095	189	5.84	11.28	0.505858	0
3.67	0.054907	190	0	0	0.556484	0
5.01	0.694305	190	0	0	0.91693	0
5.25	0.152196	190	0	0	0.374871	0
3.85	0.066095	190	11.23	10.7	1.1118	0
4.45	1.071164	191	0	0	1.151515	0

3.02	0.749254	191	0	3.4	0.809938	0
4.85	2.138408	191	0	0	2.147364	0
5.19	0.083183	191	0	0	0.492444	0
3.6	0.131115	191	0	8.38	0.139734	0
5.68	0.265367	191	1.21	0	0.3483	0
3.18	0.222304	192	0	0	0.518548	0
4.17	0.152176	192	0	0	0.163455	0
2.34	0.268198	193	0	0	0.411812	0
5.19	0.982139	193	0	0	1.340923	0
3.69	0.293303	193	0	0	0.490526	0
4.16	0.058523	193	0	0	1.197634	0
5.18	1.238411	193	0	0	1.653341	0
3.07	0.412649	193	0	0	0.620458	0
4.35	0.129521	193	0	0	1.045919	0
4.4	0.402963	193	0	0	0.413364	0
3.66	2.92225	194	0	0	2.935256	0
4.85	0.083183	194	14.11	13.1	0.139583	0
2.34	1.602376	194	0	0	1.682924	0
4.63	1.129328	195	25.45	25.45	1.473501	0
5.03	0.433121	195	0	6.42	0.996619	0
5.18	0.291046	195	17.27	21.81	0.847401	0
4.35	0.264245	195	13	13.47	0.343254	0
3.02	1.052761	195	0	0	1.962155	0
3.01	1.752168	196	15.16	15.16	2.386762	0
3.18	2.881115	196	0	0	4.016239	0
3.86	0.501978	196	0	0	0.56173	0
2.85	0.504402	197	0	0	3.899571	0
3.07	0.34586	197	0	0	0.539759	0
3.07	0.0561	197	0	0	1.036012	0
3.33	1.014463	197	0	0	1.23667	0
3.21	0.127746	197	0	0	0.13489	0
3.66	1.063691	197	0	0	1.126415	0
2.74	3.167183	197	0	0	3.707393	0
3.02	0.909394	198	0	0	1.962155	0
3.34	1.059018	198	0	0	3.429268	0
5.34	1.336888	199	0	0	1.392987	0
4.63	0.210869	199	0	0	0.841524	0
4.7	2.55105	199	0	0	2.828848	0
4.35	0.009626	200	0	1.02	0.093246	0
5.19	0.083183	200	0	0	0.790494	0
3.51	0.271064	200	0	0	0.493789	0
4.35	0.89769	201	0	0	1.049627	0
3.2	0.508316	201	0	0	1.686605	0
3.36	0.223155	202	1.61	2.43	0.286993	0
3.34	0.223129	202	0.37	0	3.092185	0
3.97	0.141463	202	0	4.88	3.190376	0
3.67	0.505627	203	0	0	0.700943	0

2.5	0.564527	203	32.83	32.83	1.865928	0
3.35	0.365066	204	0	0	0.907994	0
6.86	0.268198	204	0	0	0.400318	0
4.63	0.290778	204	0	0	2.36808	0
4.35	0.013113	205	0	0	0.504798	0
5.19	0.200606	205	0	0	3.035585	0
4.41	2.084178	206	0	0	2.416507	0
2.87	0.623936	206	0	0	0.832251	0
3.32	0.402963	206	0	0	1.686753	0
4.06	0.292609	206	0	0	0.300437	0
4.35	0.40926	207	0	0	0.818521	0
3.51	0.995564	207	0	0	1.717073	0
2.74	0.010511	207	0.39	5.03	0.023838	0
4.06	0.131316	208	0	0	1.337654	0
2.62	2.38423	208	0	0	3.248872	0
4.85	0.506656	209	0	0	1.721255	0
3.02	0.749254	209	20.67	22.05	3.845971	0
6.13	0.556828	210	10.4	16.01	0.909897	0
4.35	0.565471	210	0	0	0.830838	0
4.85	1.081779	210	0	0	1.990404	0
3.01	0.133742	210	0	0	0.466071	0
4.61	2.38423	211	1.12	2.09	2.462555	0
4.16	3.769959	211	0	0	3.922468	0
4.09	1.055419	212	0	0	1.115481	0
2.57	0.433754	212	0	0	0.586127	0
2.73	0.07928	212	0	0	0.13553	0
4.79	0.008956	212	0	0	3.539512	0
3.61	0.140397	212	6.52	9.55	0.434051	0
4.52	0.130515	212	0	0	0.425449	0
5.54	0.332329	213	0.05	0	0.344691	0
4.52	0.130515	213	0	0	0.142986	0
4.18	0.22285	213	1.94	1.94	0.714969	0
2.74	1.065506	213	0	0	1.217583	0
3.06	0.013433	213	0	0	1.024388	0
5.52	0.558247	214	0	0	0.924482	0
2.9	0.198906	214	5.02	1.25	1.535794	0
3.02	0.749254	214	0	0	0.876804	0
4.35	1.301705	215	0	0	1.383428	0
2.34	0.011714	215	0	0	0.344043	0
6.13	0.57767	216	0	0	0.770396	0
5.03	0.289008	216	0	0	1.094206	0
4.85	0.348242	216	0.78	1.79	0.357978	0
4.01	0.968181	216	11.02	11.02	1.025334	0
5.19	0.864643	216	0	0	1.37275	0
4.63	0.0561	216	0	0	0.895598	0
3.86	1.531232	216	0	0	1.665586	0
3.85	0.151917	217	0	0	1.072855	0

4.79	0.082171	218	0	0	1.645132	0
4.02	0.081269	218	0	0	1.290896	0
2.74	2.249393	218	2.37	0	3.305316	0
3.46	0.005527	218	0	0	0.085479	0
3.77	0.693748	219	0	0	1.026077	0
3.02	0.993515	219	0.83	0.83	1.200818	0
3.66	0.484806	219	0	0	0.817135	0
6.86	0.15249	219	0	0	2.711466	0
3.21	0.059136	219	0	0	0.326197	0
4.85	2.055059	220	0	0	2.396552	0
3.66	0.151281	220	0	6.48	0.359596	0
4.52	1.214353	220	0	0	2.292259	0
5.69	0.152451	220	0	0	0.161854	0
4.06	0.335891	220	4.44	4.44	1.132665	0
4.4	0.080417	221	0	0	0.286211	0
5.69	0.130117	221	0	0	0.352667	0
4.79	0.338183	221	0	0	0.489527	0
4.85	2.76154	222	0	0	2.821293	0
3.11	0.513399	222	0	0	0.724267	0
3.18	0.0786	222	0	0	0.767369	0
1.9	0.909394	223	0	0	1.456437	0
2.52	0.12755	223	0	0	1.671627	0
2.77	0.278393	225	0	0	1.627004	0
3.51	1.027279	225	0	0	1.040606	0
3.62	1.197575	225	0	0	1.266967	0
6.53	0.562538	225	0	0	0.993935	0
3.02	0.749254	225	0	0	0.878577	0
3.35	1.745831	225	0	0	2.079449	0
3.51	1.135124	226	0	0	1.143405	0
3.69	0.625992	226	0	0	2.117863	0
4.18	2.015116	226	0	1.31	2.783992	0
4.79	0.010511	226	0	0	1.167988	0
3.51	0.40554	227	0	0	1.175631	0
3.77	1.21411	227	0	0	2.211311	0
3.58	0.061778	227	0	0	1.596211	0
4.63	0.436804	227	0	0	0.44643	0
5.18	0.054167	228	0	0	0.187705	0
4.26	0.479319	228	0	0	0.768378	0
4.26	1.270937	228	0	0	3.587483	0
4.01	0.499985	228	0	0	0.721878	0
5.01	0.223438	228	0	0	0.34827	0
4	1.281778	228	0	0	1.291181	0
3.18	1.747644	230	0	0	3.002239	0
4.3	0.066095	230	0	0	1.186123	0
4.01	0.342495	230	0	0	2.51368	0
3.66	0.62754	230	0	0	0.830599	0
3.07	0.082363	231	0	0	0.873646	0

4.18	0.052119	232	0	0	0.601468	0
3.51	0.292334	232	0	0	0.424454	0
3.86	0.503387	232	0	0	0.852999	0
4.85	0.269913	233	0	0	0.351183	0
5.54	0.360534	233	0	0	0.981406	0
2.39	2.19123	233	0	0	3.084849	0
5.01	0.827896	234	0	0	0.884296	0
3.51	1.49295	234	0	0	1.553633	0
4	0.151344	234	0	0	0.358899	0
3.51	1.352393	234	0	0	2.340828	0
5.54	0.222231	235	0	2.3	0.971485	0
4.35	0.06225	235	0	0	1.130175	0
3.06	1.807858	235	0	0	2.140187	0
4.06	1.26075	235	0	0	1.5522	0
4	0.935766	235	0	0	4.32804	0
3.01	0.013327	236	7.32	7.32	0.165582	0
3.02	0.294504	236	0	0	0.496332	0
5.52	0.338512	239	0	0	0.960914	0
4.26	1.014866	239	0	0	2.839765	0
6.13	0.575417	240	0	0	3.047399	0
2.62	1.003867	241	6.41	5.51	1.014047	0
3.95	0.129125	241	0	0	0.186733	0
3.35	0.927488	242	0	0	1.010797	0
5.01	1.01074	242	0	0	3.802747	0
4.42	1.592863	242	0	0	1.723378	0
3.06	0.010841	243	0	0	0.513561	0
4.85	0.936083	246	0.25	0.33	1.00283	0
6.13	0.702743	246	0	0.17	3.721631	0
2.08	1.473713	246	0	0	2.404997	0
3.07	0.059598	247	0	0	1.864425	0
3.77	0.152778	247	0	0	0.902032	0
3.06	0.008506	247	0	0	0.018686	0
3.86	0.081851	247	0	0	0.143159	0
5.19	0.014805	248	0	0	0.098238	0
4.46	1.193915	248	0	0	1.206062	0
4.4	0.081074	249	16.47	24.39	1.216198	0
3.67	0.128729	249	0	0	1.597228	0
4.7	0.009291	249	0	0	0.208924	0
4.24	0.005876	249	0	0.93	0.089682	0
3.67	0.223335	251	0	0	2.224807	0
4.41	0.333296	252	3.49	0	2.145429	0
4.01	0.125604	252	0	0.56	0.137751	0
4.4	1.195699	252	0	0	2.21206	0
3.86	0.648418	253	0	14.99	0.850492	0
3.71	0.006685	253	0	0	2.972806	0
2.9	0.986617	253	0	0	1.996759	0
2.39	0.780967	254	33.92	33.92	0.840103	0

3.62	1.503808	254	0	0	3.71813	0
4.09	0.972552	254	0	0	2.015148	0
3.16	0.057608	255	0	0	0.113708	0
3.35	0.368018	256	0	0	0.632263	0
4.7	0.57868	256	0	0	1.019446	0
3.51	0.013327	257	3.81	8.04	0.650449	0
3.61	0.222304	257	0	0	0.374948	0
5.19	0.055502	257	0	0	1.566176	0
4.49	0.895651	257	0	0	1.022224	0
3.51	2.852118	258	0	0	3.652347	0
2.34	0.702176	258	0	0	0.854954	0
2.57	0.066747	258	0	0	0.218983	0
4.46	0.138497	258	9.79	21.65	0.413343	0
5.68	0.222304	259	0	0	3.32723	0
4.63	0.055502	259	0	0	0.610915	0
5.14	0.009848	261	0	0	1.607438	0
3.16	2.705605	261	0	0	4.575811	0
6.46	1.054985	261	0	0	1.264317	0
5.03	0.222304	262	0	1.84	0.971559	0
3.97	0.151715	262	0	0	0.855595	0
4.52	0.067075	262	0	0	0.933334	0
2.75	0.080549	262	0	0	0.43955	0
3.33	3.849936	262	0	0	4.061577	0
3.35	0.968181	263	0	0	1.553029	0
5.01	0.436318	263	0	0	0.588769	0
3.79	0.081979	263	0	0	1.287405	0
5.28	2.140617	265	0	0	2.87452	0
3.01	0.73492	265	0	0	1.536078	0
6.13	0.57995	265	0	0	2.686208	0
3.32	0.0786	265	0	0	1.083032	0
5.19	0.005527	266	15.01	15.01	0.156682	0
2.77	0.862899	267	0	0	1.086337	0
2.18	0.479319	267	0	0	1.85938	0
4.79	0.487798	267	7.96	10.5	0.781381	0
3.18	1.757778	267	4.04	0	1.836787	0
3.01	0.05625	269	0	0	0.805504	0
2.9	2.143535	270	3.65	3.65	2.296369	0
3.51	1.433595	270	0	0	2.575628	0
3.71	3.35445	271	0	0	5.240762	0
6.46	0.276022	271	0	0	0.398562	0
4.7	1.25645	271	0	0	1.479707	0
5.34	0.637123	272	0	0	0.64529	0
5.01	0.849372	272	0	0	2.195039	0
4.01	0.12755	272	0	0	2.959554	0
4.4	0.152295	272	0	0	1.626048	0
4.45	0.061151	273	0	0	3.238406	0
2.57	0.063042	273	0	0	2.865102	0

3.69	0.009291	274	0	0	0.272698	0
3.58	0.46983	275	0	0	1.025244	0
4.06	1.051186	275	0	0	3.183229	0
4.45	0.062093	276	0	0	1.677607	0
4.94	0.264245	276	0	0	0.486306	0
2.82	0.151816	277	2.36	2.36	0.23289	0
5.25	0.130515	277	0	0	0.900607	0
3.95	0.084846	277	0	0	0.166115	0
4.7	1.232826	277	4.59	4.59	1.812267	0
3.01	0.266495	278	11.61	1.32	2.319187	0
5.19	0.334915	278	0	0	0.486972	0
3.35	0.080085	279	0	0	0.722641	0
3.46	2.410655	279	2.64	0	3.666042	0
3.06	1.959868	279	0	0	2.517169	0
3.69	1.255388	279	2.64	3.77	3.666042	0
3.02	0.081979	279	0	0	0.640226	0
4.85	2.857242	280	0	0	3.226711	0
3.02	0.20232	280	7.34	8.23	0.218475	0
4	0.066747	280	12.39	12.39	0.577797	0
3.91	0.010069	280	0	0	0.149198	0
4.41	1.938925	281	0.29	9.71	2.020904	0
3.2	1.484454	283	0	0	1.636371	0
4.01	0.009403	283	1.87	0	0.1614	0
2.59	0.080549	285	9.92	7.75	1.471269	0
2.24	0.293303	286	0	0	0.587168	0
3.16	0.889578	286	0.66	2.53	1.023932	0
5.34	0.082363	286	0	2.31	0.514164	0
3.62	0.13415	286	0	0	0.998792	0
4.85	0.059753	287	0	0	0.546265	0
5.28	0.014175	287	0	0	1.946287	0
6.53	0.8603	287	0	0	1.361478	0
2.18	0.061464	287	19.29	23.38	3.533573	0
4.17	0.998658	288	0	0	1.401622	0
3.85	1.379799	288	0.79	1.53	1.73885	0
4.41	0.29172	288	0	3.95	0.583576	0
2.87	0.059136	291	0	0	0.325631	0
2.77	0.221821	294	0	0	0.231224	0
2.08	0.279887	295	0	0	0.431642	0
3.07	0.082363	296	0	0	1.095809	0
4.94	2.07535	299	0	0	2.086628	0
4.01	0.442283	300	0	0	0.50903	0
3.35	0.010511	302	0	0	0.30109	0
4	0.706737	303	0	0.47	3.764519	0
4.85	0.504198	303	0	0	1.487081	0
4.85	0.222207	303	0	0	2.207132	0
4.85	0.064639	307	0	0	0.077324	0
4.61	0.133742	308	0	0	2.36715	0

4.84	0.130515	309	0	0	0.353442	0
2.9	1.214869	310	0	0	1.278228	0
4.84	0.29118	311	0	0	1.200574	0
3.18	1.757778	311	0	0	1.825017	0
2.62	2.142863	313	0	0	2.770403	0
5.19	0.784747	314	0	2.25	1.139912	0
4.68	0.014175	314	0	0	0.069826	0
2.77	0.081979	314	0.29	0	2.020904	0
5.69	0.057608	315	0	0	0.492798	0
4.35	0.198183	315	0	0	0.469825	0
3.18	1.230337	317	0.74	0.74	1.360453	0
5.12	0.823454	318	0	0	2.085021	0
5.19	0.139762	318	0	0	1.150501	0
3.01	0.269913	319	0	0	0.492789	0
4.85	0.26174	322	0	0	0.390469	0
5.54	0.009737	324	0	2.7	0.233436	0
5.01	0.571231	324	0	0	0.932425	0
3.11	2.207094	324	3.65	5.11	2.572393	0
5.03	0.854312	324	6.73	6.1	0.933929	0
3.01	2.060967	325	0	0	2.353784	0
5.19	0.011605	327	0	0	0.30618	0
4.17	0.203059	329	0	0	0.78073	0
3.35	3.569507	331	0	0	3.791713	0
3.66	1.799573	333	0	0	2.363071	0
4.3	1.333928	334	0	0	1.686998	0
3.36	0.707884	334	1.28	5.5	1.002174	0
2.85	0.015119	334	0	0	0.850073	0
6.13	1.305234	336	0	0	1.313402	0
3.18	0.273384	336	0	0	0.333601	0
3.67	0.561493	336	0	0	0.760883	0
3.51	0.410762	338	0	0	2.240372	0
3.86	0.339172	338	0	0	0.419721	0
3.18	0.015223	338	0	0	1.247158	0
2.69	1.267222	339	0	0	4.235882	0
3.95	0.012147	340	0	0	0.234305	0
5.03	0.40554	344	0	0	0.535657	0
3.82	1.055419	345	0	0	3.307623	0
4.02	1.447137	346	0	0	3.458905	0
4.02	0.13415	349	0	0	0.684889	0
3.16	0.062093	349	7.98	4.45	0.482802	0
4.17	1.397396	352	0	0	1.524946	0
4.4	0.223516	352	0	0	0.236629	0
6.46	0.341827	354	0	0	0.352667	0
3.02	3.716825	354	0	0	4.623443	0
3.06	0.010841	355	6.56	13.98	1.219167	0
5.36	0.480998	357	0	0	0.614536	0
4.85	0.083806	358	0	0	0.282471	0



4.85	0.0786	358	0	0	0.089878	0
4.49	0.152606	358	0	0	0.304503	0
2.85	0.067239	359	0	0	0.149218	0
2.77	0.081979	359	0	0	0.149218	0
2.85	3.724688	360	0	0	3.785371	0
2.77	0.12755	361	0	0	0.209913	0
4.94	0.723586	363	0	0	0.806769	0
3.33	2.948915	363	0	0	5.860352	0
3.02	0.749254	366	0	0	0.809938	0
3.42	0.196029	369	0	0	0.276445	0
3.67	2.016136	369	0	0	3.473986	0
4.02	1.194303	369	0	0	2.275855	0
4.41	2.143535	376	0	0	2.366587	0
4.01	0.152528	377	0	0	0.374662	0
2.82	0.014805	379	0	0	0.076583	0
4.57	0.12755	380	0	0	0.601061	0
3.51	0.924198	381	0	0	1.253331	0
3.18	0.063998	381	0	0	0.076683	0
2.43	0.573929	381	0	0	0.587256	0
4.04	0.061778	383	0	0	1.049145	0
4.3	0.977694	385	2.26	0.93	1.245892	0
5.34	0.620872	386	1.46	1.46	0.820505	0
4	1.437435	387	0	0	1.499844	0
6.13	0.082806	389	0	0	0.141942	0
4	0.223516	389	0	0	0.354031	0
4.79	0.222207	393	7.95	7.95	0.281343	0
4.42	1.125858	395	0	0	1.259396	0
3.18	0.079684	395	0	0	2.091216	0
3.09	0.224043	397	0	0	0.279545	0
3.61	0.057608	423	0	0	0.188924	0
4.34	0.474334	427	8.75	10.33	1.218377	0
4.94	0.012578	442	0	0	0.350761	0
5.34	1.184596	462	0	0	1.337047	0
4.2	0.081204	481	0	0	0.304282	0

**Characterisation of polymorphic microsatellite loci for the bryozoan *Fredericella sultana*, the primary host of the causativ***Journal Name* : Conservation Genetics Resources: Microsatellite Letters*Authors* : Dmitry Filippenko, Hanna Hartikainen, Beth Okamura, Anti Vasemägi*Corresponding Author* : Anti Vasemägi, Division of Genetic and Physiology, Department of Biology, University of Turku, Itäinen Pitkäkatu 4, FI-20014 Turku, Finland, e-mail: antvas@utu.fi**Electronic Supplementary Material Table 2****Table 2** Sequence and developed primer information for 24 microsatellite loci that were tested in *Fredericella sultana* and *Tetrac*

Sequence name	Start, bp	End, bp	Total length, bp	Sequence	Primer sequence (5' Forward*)
Fs004TKU	117	156	303	AATTACTGGAGGAGCTACTACAATGCTGCTCCTCCTTTTG ACATTGCAGTTCCAAGGAACTGCGTCCATAGCACTGAAGA CACCAGAGAGGGCTGGAAAGGCAGTGCCACAGTGGGCA GCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC AGGGAAGACGTCGCCTACTCAAGCAGTGGGAAATGAGTC CAACAGAGTGAGACCCGCAGAGCAAAGCTTCTGTCACC AGCAGTCGTTAGGTGGAAACAGACAAAGCTGTTTGGCAG CCATCATAACTGATTGAATAAGATGAGATC	CGTCCATAGCAC TGAAGACAC
Fs005TKU	39	90	154	GCAGTTGAGCCGTCTAGCCGAGCCCAGACTAGTGGCTGC AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC CAGCAGCAGCAGCAGTGCAAGGCCAGCACCGGCTGGGC GGTACATTGAGCTAGGGCACTCATGCAGCAGTGCTGGCG	TCTAGCCGAGCC CAGACTAG

Fs009TKU	83	137	204	GCCCTAAACCGGTTCGGTCTGTCAAATTTTAGAAAGCATTG TGAACCGTGAGTCAAAAGGTTTGCCCACCCCTGGTCTAG GGCTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA GCAGCAGCAGCAGCAGCAGCAGCCAACGATTATGGTAATTTG ACAGGGTTTCGGCACACATAAAGGGTTCGTATATGTGCTTAG TTCACAGC	AGCATTGTGAAC CGTGAGTC
Fs010TKU	173	230	366	GCAGACAATAATGCAGACAGGCAGCTGAATGAAGATCTGA ACTCCCTAAGGGTTCATGAATCAATACAGGATGCAACTCGA ATGGGCTTGAACACATGCCCGGGTGGGCTTTGAAGCCAT CATGCTGCAACTGTTTCTACTAGCTTCCGAGGCTACTGAG GTCAGTCCACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTACAGTGT GCATGCTGCCCGATGCCTGCCTGTACCAGCTGTGAGACA CAAAGGCATCCGAAGCCGGTAGCCTGACGCATGGCTGTG CTATCATCAGTCAAGTTGGCCTCGGCCGTGCGAAAAGAGT CAGCGCCCAAC	CTTCCGAGGCTA CTGAGGTC
Fs012TKU	106	136	215	TGCATTGTGTTTCGTGCATGCTCATGCGTCTTGACACTCGC TAAGTTCAAACAGCTGGTAGCAGCATGGTTAGTAGGGGAC ATCGAGACGTACAATGCCTGTTACTTGCTGCTGCTGCTGC TGCTGCTGCTGCTGCTGCTGCGGCCCTGCCGCTGTCCCTGC CGCCAGCGAAATCCGGATTGCATTTTTGCCATCTGGTCTT GTGACCTCCTGTGTAC	GCTCATGCGTCT TGACACTC
Fs014TKU	62	101	194	ACCCTGCGCCAGGTTGGCACGCTCTATCTCAATTTATGCG AAGGGCCACGAAAAGTGCATAGGATGATGATGATGATGAT GATGATGATGATGATGATGATAATAATGATGATCGTAATTG TTTATCTCCTAGATTTGCGTATTTAGGTAAGTACGCTCCAA TCTATCTGTCTCTTCAGAGCGCCGTATTGCAT	CCAGGTTGGCAC GCTCTATC

Fs015TKU	218	257	313	GCCCAGGCATGACTACATTTACGAGAAAGTTTTAAACATC CCTTACGCTTTGGGCTTTTGCTTGATCTCTGAAAATCG TAAAACCTTTGCTTTGCTTGCTACTCCCGTGCACGCTATT GCATAATTAATTTAAATATAATCACTCTCAGACTCTTGTTAA GAGCCCAGGACGAACTCGCATAGCTGAGCACGCTCTTAA TGTGGCTCATTATTATTAGTAGTAGTAGTAGTAGTAGTAGT AGTAGTAGTAGTAGTATCTACGAAGCTACTTTCTCGCATTT TCTTAGATTCTCATCCCGTTACCTGTGGAC	CTTTGCTTGCTAC TCCCGTG
Fs016TKU	140	212	264	GCATTAGGCAAACTGGTGAGTTAACGATTTCTTTTTTGAC GACACACTGCGAAGCACAAGCCTTGCTTATGTGGAGTGAA TGGGTTACTCAGCCGATGAAATCAGAGGATATCAGTAGCA ACTGCGGCAGCAGAATAGGAGCAGCAGCAGCAGCAGCAG CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA GCAGCAGCAGCAGCCATGAAGTGGCAAGGGTAGCCAGTG GCGACTGCAGCAGTGGTGGTGACCGTG	TTTGACGACACA CTGCGAAG
Fs021TKU	41	77	345	GTTAGAATTTGTGCGGCTCGCTGGCACTGTGAGATCAATG CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA GACCGTTGCTCTTTTGCTAGCCCGCGCTCCCCTGGGAAG GCTCGCGCCGGGCAATTACGTTAGTGACAGAGCGCACGA GCTGATACAAGGAAAACCTAGTTACTGCATTGCAACCTTA ATTGATAAGCCTTTTAAGCGCATCGTATCAAAGGGAAAGC GTGGGAAAATTGTGAAAGGTCAAAGTAGTGACGACGAGG CTCGCTGATCGGCGAAGTCGAGGAGGCGTGGCTGCCGC GCGTGACGGGCCTTTGAACGGATGGGGTGGAC	GCTGGCACTGTG AGATCAATG

Fs024TKU	90	126	336	<p>GTTTCAAGAGAACCAAAAAAATCTCTCTAGCGTATCACCC  ACGTAGTGAAGCCAAGCTTAGAGATACATACAGATACACA  TGATACACATGATGATGATGATGATGATGATGATGATGAT  GATGATGCTGATGATGAGGATGGTGATAATTTATCTCATT  ACACAAGGAAACCGCAAGGACTAAATGTTACTCTGCACAG  TTTGAGTACATCTAGAGCCTAAGCGGCTATCATCGCAGAT  ACGTCGACTCCCCTGCATTGTCTCGCGTAACAAAACGAAC  TGGAAAGAATGGCAAGGCAGAGGAGCAGTCGTGCTAGTT  CGTAGCGGAGTAGCAC</p>	<p>TCTCTCTAGCGT  ATCACCCAC</p>
Fs025TKU	83	143	429	<p>GCACAAATGTGTGAGCACAGGGAGAGCAAGACATATAGA  GCTGCACTGATAGATATATAGATGAGATAGATAGGTATATA  AATAGATAGATAGATAGATAGATAGATAGATAGATAGATAG  ATAGATAGATAGATAGATAGATAGACAGATAGCTAGAGAG  GTAGAGTACCTATATAGACAGAGAAATAAAGAGAGGGAGA  GAGAGTGGAGTTATGCTGTGCCATTGAGTTTGCATGACGG  CAAGCAAGCACATTTAGAGGACGGCCAGGTATTCATTGCA  TCCAGTCACCCTTCAGAATGAGGAACTATCTGCCTCAGTG  GCTGGCGAGCGATCAAATCAGTTTCTTGCTTGTCCTACTAGA  CTAGACTTTTGCAGGACAACCGAGCACGAAGCCTGTGCA  GTTGTTCTAAATATGGCCTCCAGACTGG</p>	<p>AGCAAGACATAT  AGAGCTGCAC</p>
Fs030TKU	158	197	359	<p>GCTGGGCATTGCAATACGTCAGAGCAGAGCCGTGCCGAG  TCCATCGGTTTCATTCTCAGGATCTGCAAGACCCTGCCGAG  CAGTCTGCAGGTCCGAGGAAAACAACCCTGCTGCTTGA  CTGGAGAGCAGCCAGCAATCTCTGCCCTATGTGGCGGGG  CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA  GCGAAAGACTGAGTGTCTGATGCTCCACTGGAGGCATAC  AGCTCGGCTGGGTCTGTTTGGAAACCCTGCAATCAATTATT  TCATGCATCACCGTCATCAGCATAATCACTTATGGCACCG  GCATCACTGCCTACTCTCGAACTATCTGGTCAGGGTAACT  TGGGT</p>	<p>TCAGGATCTGCA  AGACCCTG</p>



Fs008TKU	65	98	272	AAGGAGGTGCGCCTGCTGCCGTGCGACCGTTTCTTTTTTG TGACCCGACGCAGCTGCCAAGGCGACGGCGGCGGCGGC GGCGGCGGCGGCGGCGGCGGTGCGGGCTGCAGGCGGC ACCGGAACCAAAGACGGGCACCGCAGCGCGGAAGAGG TACTGGAGGCAGGCGTGCGAGTCACTACGCCGGCGGCT GGCTTATCAGTCCGGAGCCGGTGCATCTGAGTATAAAAA AGGCGGATAATCGGAACGACGGAGAGACAGACTGGAGAG C	TTTGTGACCCGA CGCAGC
Fs013TKU	72	144	379	TCCCACCATAGATTGGAACAGATCTCGAGCTTCCGTATT TGACCTTTCTTAGCCAACTCCTGAGCCTAAATAGTAGTAG TAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG AGTAGTAGTAGTAGTAGTAGTAGTACGTTTACTGTTTTGT TTATGATACGGCGCCACCGAGATCTACACTATCCTCTTC GTCGGCAGCGTCAGAGGTGTATAAGAGTCAGTCGCACCA TAGATAGGGACAGATCATGAGGTTTCCGTATTTGACGTTT CTTAGTCACCTCCTGAGCAGTAATAGTAGTAGTAGTAGTA GTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG TAGTAGTAGTAGTAGTAGT	TCTTAGCCAACT CCTGAGCC
Fs020TKU	212	245	350	GTGCGCGTGAGACGCCGCACGCGTGCGCGTCGGGGGCG GGGCCACCCCCCGCCCCAGCCGCACCACTCTTCCTGCTT CTGCCATTGTTGATTACATGCCGCCCGGTGTGGACGTCC GCTCACCGTTCCGACGCGGTCCCCACCTGGCAGCGCTGC TGGGGCCAGCCGCACTTGCCACGGCACTGGCGACGCAG CGGCGGCAGCAGCAGCAGGAGCAGCAGCAGCAGCAGCA GCAGCAGCAGCAGCATTGCTGCTGCAGTATTCATTGCTG CCACTGATTTTCGCCGGCGGCTTCGCGGTTGCTGTGGCG GCGGCACCGTGGACACCTCCGCGCTGGCGGCTCTGTGC TG	CACCACTCTTCC TGCTTCTG

Fs023TKU	257	293	426	<p>GTTGAACTCCATGATGGTTTGCAGAGATGCGCTCGCCATT TACACCTCTGGC  TTCTCTCCTATATATATGTGCGAGCATTTTTCTGCTTTCTT TCTTGACG  CTAGTATCGAATATGCGATTGAATGCGATCGCGCCTCCGT  AAGGCGACGAACTCTTAGCCACCGTGTCTGTAACCGTCTT  ATCCACCGCTTTGTACACCTCTGGCTCTTGACGCTTCAGC  TTTTCAACGTAATCCTCATCGTCGTCGTCCTCATCGTCGC  TAGGTGGTTTAGTCTCCTTCTTCTTCTTCTTCTTCTTCTT  TTCTTCTTCTTATCCTTGTCCCTCCTTATCCTCCTTCTTCTT  CCTATCGTTATCGATCTTGATCGCCTCTGTCTCCGCCTTC  TTCTTCTCAGCGTCCAATCAGCGTTTCTCTGGTCGTTTCG  TTAGATCCTGCGCATTCTTATCC</p>
Fs026TKU	245	272	327	<p>GTCCTACGACTTGAGTAGGTTGGTTGGTTCGAACGAAATTG TGGGTCATGAGG  ACGACAGGCACGGCCCTCGTTGGGTCATGAGGAGAAGG AGAAGGTC  TCATCCATGGCGATGGGATCCGCACTCCTGTGGTGGCAA  TGCCGTCTTCGACACGGGACGATAGCCGCGGCAGCGTG  GAGCGGCTGTCTCTTGCGGCGGGATCGACTACGCGAAG  ACGACGATGGGCGACGTCCACCCCTCGTTCTTCTTCCCG  TCGCCC GCCCGCGTCGTCGTCGTCGTCGTCGTCGTCGTC  GCCGAGCCATCGCGATCGTCGCGTTTTTCTGTCCATTTC  ACCGCCGCCTCCGT</p>
Fs027TKU	169	196	389	<p>CTCCCGCTTGGAAGTTATTAGAGCCGTTGACGGCCGAGA ACCTCCTCCCAT  GCTCCATAGCGCGAACCTCCTCCCATAGAAAGGCAAAAAC AGAAAGGC  TCTTTTGGGAAGCTGCCAGGGTGACGCTAGAATCGCGCC  GCCATTCCACCAGCAGCGGTTCGACGCGCGTCGCAGTCGA  CAGTATCAGCAACGGCGGCGGGCGGGCGGGCGGGCGGGCG  GTGGGGCCTTGGTAGCGCCTGGCCTTTCGCGCGCCAAA  GCCAGAGCTGGCCGCGCTGGGCGGGCGCTCGCAAGCC  GAGAGCATGCGCGACGCGCGAGCACCGACCCGTTGCTCT  GCTTTCGCCCACGGGGCCCTCGGCGTATGCCGAGCTCCG  ACCGCATGACTGGCCGCGGTAGACGAGGTGGCCTCGG  C</p>



Fs029TKU	78	147	359	ATACACCACCAACCAGAAAAGGCAGCAGGAATACATTGTC	ATCACTGTCTTCA
				TGCTGGTTGTTATCACTGTCTTCACGAGCTGTTACTGAGC	CGAGCTG
				TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	
				TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTATGGCACTTATA	
				AAAAGTAAAGGCGAGCGAATTTAACAGTGCCATTTATATG	
				GTGGCCAGAAAGCCTATCACTGCCACCTGCAGGGTGGGG	
				GGCAATGAAGATTTGTCTGGTGCAGAGCTTGAACACAAAA	
				CCTGAGTCGTTAAGAGCAAGCACCTAGCTCCCAGGCGTT	
				TGTGCAATATTTCCGGTGTGCTGCAAGTCAACCCCCTCCCA	
				CT	

- \* Forward primer sequences are presented without the M13-tail.
- \*\* The GTTT "tail" (Browstein et al. 1996) was added to the reverse primer
- \*\*\* Number of alleles
- \*\*\*\* Observed heterozygosity
- \*\*\*\*\* Expected heterozygosity

**e agent of salmonid proliferative kidney disease**

*apsuloides bryosalmonae* host-parasite system (n = 17)

- 3')

Reverse**	Motif/Repeat	$N_A^{***}$	Allele size range, bp	$H_O^{****}$	$H_E^{*****}$
GTTTGAGTAGGC GACGTCTTCC	(AGC) <sub>13</sub>	7	133 - 170	1.0000	0.8636
GTTTAGCTCAATG TACCGCCCAG	(AGC) <sub>17</sub>	16	88 - 244	0.6429	0.9444

GTTTCCTTTATGT GTGCCGAACCC	(AGC) <sub>18</sub>	10	154 - 200	0.6154	0.9046
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GTTTGCTTCGGAT GCCTTTGTGTC	(AGC) <sub>19</sub>	15	139 - 230	0.9167	0.9457
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GTTTAATGCAATC CGGATTTGCTG	(AGC) <sub>10</sub>	11	173 - 237	0.9231	0.9169
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GTTTGCAATACGG CGCTCTGAAG	(ATC) <sub>13</sub>	8	188 - 201	0.7500	0.8225
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GTTTGCGAGAAA GTAGCTTCGTAG	(ACT) <sub>13</sub>	8	227 - 387	0.4545	0.9221
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GTTTGCTACCCTT GCCACTTCATG	(AGC) <sub>24</sub>	12	168 - 204	0.8667	0.8667
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GTTTCCCACGCTT TCCCTTTG	(AGC) <sub>12</sub>	10	239 - 407	0.5000	0.9233
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GTTTGTTACGCGA GACAATGCAG	(ATC) <sub>12</sub>	8	268 - 284	0.6667	0.8506
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GTTTATGAATACC TGGCCGTCCTC	(AGAT) <sub>15</sub>	9	255 - 302	0.7000	0.8895
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GTTTCGAGAGTAG GCAGTGATGC	(AGC) <sub>13</sub>	11	299 - 363	1.0000	0.967
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GTTTGAACCAAAC  
CAGCTCACGAG

GTTTCTCGCCGC  
AGACAGAGTC

GTTTGTCCCTAAC  
ACCAGCAACAC

GTTTGCTTTGTGG  
TGTTGCGAAC

GTTTAGAAACGTT  
GATCCAGCAGC

GTTTGCCTCCAGT  
AACCTCTTCC

GTTTATACACCTC  
TGACGCTGCC

GTTTCAGTGGCA  
GCAATGAATACTG

GTTTGAACGACCA  
GAGAAACGCTG

GTTTGGCGGTGG  
AAATGGACAG

GTTTCGAAAGCAG  
AGCAACGGG



GTTTATATTGCAC  
AAACGCCTGGG