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Short Communication

A genome-wide resource of intron spanning primers compatible for quantitative PCR and intron length polymorphism in rice

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Abstract

Whole genome sequence availability in rice has provided several advantages for genomics as well as other omics assisted applications. Genome-wide molecular markers are one of such availability that has exceptional importance in modern plant breeding. In the present study, a resource of intron-spanning primers (ISPs) was developed using whole genome sequence information of two rice subspecies, *japonica* (cv. Nipponbare) and *indica* (cv. 93-11). The ISPs were designed in a way that the PCR using a cDNA template will yield 60 to 100 base pair size amplicon ideal for the quantitative PCR analysis. Whereas, PCR using genomic DNA will amplify the introns, which are more prone to sequence variation. The sequence variation in the intron serves as an excellent marker resource. The application of ISPs was demonstrated by characterizing 12 diverse rice cultivars. A total of eight out of ten ISPs were found to be polymorphic. The resource will be helpful for the rice molecular biologist and breeder community.

Key words: Gene-specific marker, gene expression analysis, informative marker, rice genome, sequence variation

A molecular/DNA markers are segments of DNA having variability across the genotypes, which is helpful to associate with genomic location, gene or phenotype. During the past few decades, molecular markers have found to be useful for several applications in plant breeding and molecular biology like marker-assisted breeding, genetic mapping of QTLs and genes, genetic diagnosis, and diversity evaluation. More particularly, markers provide deeper insights into the diversity available for crops and greatly complemented breeding programs. Numerous marker technologies have been developed based on the DNA sequence variation and its efficient detection (genotyping). Most commonly used DNA markers techniques includes Restriction Fragment Length Polymorphism (RFLP), Amplified Fragment Length Polymorphism (AFLP), Random Amplified Polymorphic DNA (RAPD), Simple Sequence Repeats (SSRs), Inter Simple Sequence Repeats (ISSR), and Single Nucleotide Polymorphism (SNP). Each marker based application has specific requirements; for instance, genetic purity testing mostly needs ten to twenty informative markers, whereas applications like genome-wide association study prefer to have thousands of markers. In addition, the cost of genotyping and technological requirements are variable with the marker techniques.

Gene-specific markers have several advantages in studies like allele-mining, haplotype association, QTL/gene mapping, and marker-assisted breeding. In this regards, SNP markers are always a choice considering the high level of abundance in the genome. Besides providing abundant availability and lowest cost per genotype, SNP marker techniques have several limitations, like the requirement of high-end technology and prior sequence information, and not cost-efficient for smaller assays. Similarly, PCR-based marker techniques like RAPD, SSR, and ISSR are more convenient for less equipped labs but suffers from

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limited availability. In this regards, markers exploring the variation in the introns has unique advantages. Introns being higher polymorphic sequence compared to the flanking exonic regions, which is mostly conserved provide an opportunity to develop markers. Intron-Length Polymorphism (ILP) markers provide information about variation in the length of introns between different genotypes, and they are preferred due to their high specificity, robustness and reproducibility nature, co-dominant multi-allelic genetic inheritance pattern and distribution in the gene regions. Furthermore, since most of the genes (85%) in rice genome contain introns (Deshmukh et al. 2016), so a set of genome-wide ILP markers is likely to cover most of the genome.

In several whole genome sequenced plant species, efforts have been made towards the development of ILP markers (Wang et al. 2006; Zhao et al. 2008; Zhao et al. 2009; He et al. 2015; Gupta et al. 2011; Muthamilarasan et al. 2014; Choi et al. 2004; Shu et al. 2010). However, most of these studies have adopted conventional homology-based approaches for genome-wide ILP marker development. The homology-based approaches are not efficient to target all the annotated genes; thus they usually provide low-genomic coverage. In addition, previously published most of the ILP marker sets do not provide any additional information about the polymorphism. Recently, Badoni et al. (2016) have explored the whole genome sequenced lines to prioritize a subset of IPL markers based on the computationally predicted polymorphism. The IPL marker which showed polymorphism between two genotypes is more likely to show polymorphism with other genotypes. In this regard, publically available whole genome sequence information of cultivar Nipponbare (*japonica* rice) was explored to develop Intron Spanning Primer (ISP) sets. Subsequently, the predicted amplicons were compared with cultivar 93-11 (*indica* rice) that also have publically available high-quality whole genome sequence data. With the comparison, ISP pairs expected to provide polymorphism among these genotypes were identified. We have also shown polymorphism for randomly selected 10 markers among 12 diverse rice cultivars. Importantly, the primer sets are designed in a way that they produce 60 to 120 bp amplicon on the cDNA template, which can be used for gene expression analysis using Q-PCRs.

Genome-wide intron spanning marker designing in rice

Whole genome sequence data of cultivar Nipponbare in the form of pseudo molecules, and annotations in GFF3 format were retrieved from Rice Genome Annotation Project database (http://rice.plantbiology.msu.edu/). Similarly, whole genome sequence information and annotations for cultivar 93-11 were retrieved from BGI rice database (http://rise2.genomics.org.cn/page/rice/index.jsp). Introns along with exon sequence of 60 bp flanking to each side of each intron were extracted based on annotation information using GFF parser (https://biopython.org/wiki/GFF_Parsing). To identify ILP between Nipponbare and 93-11, in silico PCR was performed

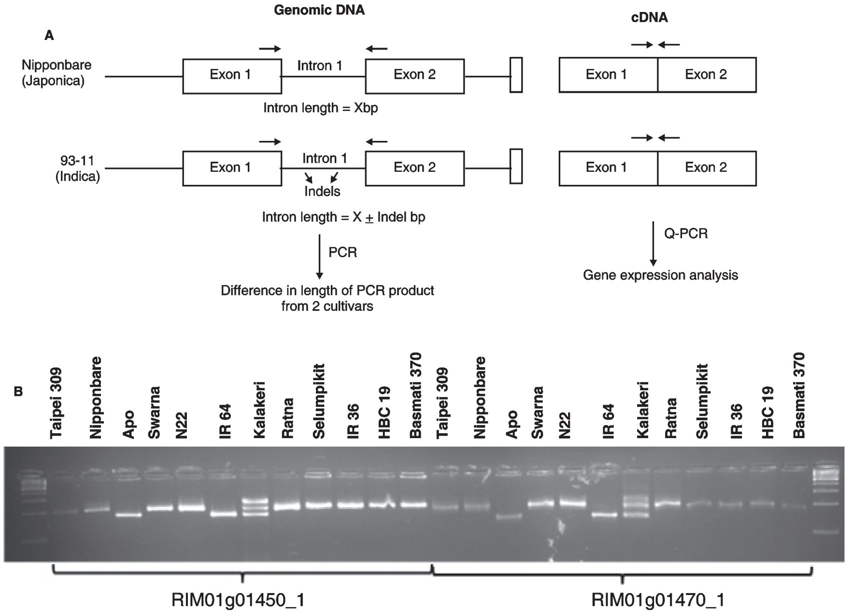

Fig. 1. A. Schematic depicting the use of primer pairs for identification of ILP markers using genomic DNA and for gene expression analysis using Q-PCR. Both forward and reverse primers are designed from the region spanning an intron, and based on the presence of InDels (Insertions/deletions), resulting PCR product would have different length in different accessions. B. Validation of two ILP markers (RIM01g01450_1 and RIM01g01470_1) using genomic DNA of different rice accessions

Table 1. Set of intron spanning primers used for the validation of length polymorphism

ID	Forward primer	Length	Reverse primer	Length	Poly-morphism
RIM01g01450_1	AGAGATGGCAAGGTCTGCCT	20	CGTCTTTCACTCTCGTGCTG	20	Yes
RIM01g01470_1	TGGATCTCAACAAGTGCGAG	20	ACCACTCCTTCTCCCCATTC	20	Yes
RIM01g01510_12	GCGGCAAAATCCAATAAAAA	20	AATTCGTGCTTTCGTCGTCT	20	Yes
RIM01g01640_1	GCCTCCCCGAGTTCAAGT	18	GCCAGAAGACAGGAACATCA	20	Yes
RIM01g29507_7	CAAGGACCCTGAGCGAAAG	19	GAGCACTTACCAAGAACCCA	20	No
RIM01g31920_2	AAAGGCATGTGAACCGTTTG	20	ACACTCAGACTCGGACCTGC	20	Yes
RIM01g32044_2	GGAGGGAGAAGCCAAAGATG	20	TGAACAGACGAGACAATCGC	20	No
RIM01g32720_8	CTACAGTTCGTTTGGTCGGC	20	CAGGTTCCACGTAGCAATGA	20	Yes
RIM01g33990_5	CAAAAGTGGCTTTTCTTGGG	20	AGACCCTTTGCCTCATTGTT	20	Yes
RIM06g29660_1	ATGAAGCGTGGGCTCATAGT	20	GGCGAATTCCTTCTTTGCTA	20	Yes

for all the primer sets using multithreaded e-PCR (me-PCR) and amplicon with these two genomes was compared in MS Excel.

A total of 84,634 genome-wide ISPs covering the entire set of 12 rice chromosomes were developed (Supplementary Table S1). Of the identified total ISPs, we found 35,326 ISPs produced amplicon polymorphic among Nipponbare and 93-11 cultivars. Based on the polymorphism among *indica* (93-11) and *japonica* (Nipponbare), the sorted sub-set is considered as informative ILP markers. Of the total ILP markers, 22938 of them are ^{3}10 and <20 bp in length, which could be visualized using 4% agarose gels or Polyacrylamide gel electrophoresis (PAGE). A total of 2134 ILPs were found to be ^{3}20 bp in length, which could be easily visualized by normal 2-3% agarose gel electrophoresis (Supplementary Table S2).

Validation of the intron-spanning primers

We randomly selected 10 ISPs (Table 1) to check polymorphism among 12 diverse rice cultivars belonging to both *japonica* and *indica* subspecies. Genomic DNA was extracted from *japonica* cultivars (Taipei 309, Nipponbare) and *indica* cultivars (Apo, Swarna, N22, IR64, Kalakeri, Selumpikit, IR36, HBC 19, and Basmati 370) and amplified using a set of the randomly selected 10 ISP primers. PCR products were evaluated for these ILPs on 2% agarose gel. A total 8 of these 10 ISPs showed polymorphism among the analyzed cultivars. Figure 1B shows the polymorphism of 2 selected ISPs (RIM01g01450_1 and RIM01g 01470_1) in 12 diverse rice cultivars. The polymorphism could easily be visualized in 2% agarose gel. In accordance with in-silico analysis, the marker RIM01g01450_1 has produced an amplicon of 200 bp size in *japonica* cultivars and167 bp in *indica* varieties (Fig. 1B). Similarly, as expected according to in-silico analysis, RIM01g01470_1 marker give amplicon of 175 bp in *japonica* cultivars whereas 133 bp amplicon in *indica* cultivars (Fig. 1B).

The utility of intron-spanning primers for gene expression analysis

The size of the amplicon is crucial if the ISPs are used for gene expression analysis in Quantitative-PCR. Usually, amplicon length of around 60 to 100bp is considered good for Q-PCR analysis, as too small amplicon size could cause confusion with primer dimers, whereas longer amplicon length may compromise the amplification efficiency, particularly when short cycling times are used. Longer amplicon also tends to create a secondary structure that could be problematic for the correct estimation of expression level. More importantly, intron ISP is helpful to eradicate the problems that arise with the DNA quantitation. As the same primer pair can be used for both Q-PCR and ILP analysis, the amplicon size with genomic DNA would depend upon the length of the intron. As depicted in Fig. 1A, the total amplicon length from genomic DNA would be 60-120 bp + length of the intron. If there is contamination of genomic DNA in the cDNA, it will produce two different amplicons and subsequent steps to remove the contamination can be performed.

The ISP resource provided in the present study can be utilized in mapping more particularly for

Quantitative Trait Locus (QTL) fine-mapping where identification of candidate is mostly the objective along with finding tightly linked markers. In addition, the set is useful for the allele mining of important genes in the most cost-efficient way. Furthermore, this high-density genetic database of molecular markers will expedite the molecular mapping of various QTLs associated with various agronomic traits and associated differentially expressed genes at the whole genome level for marker-assisted genetic enhancement in rice. Furthermore, given the utility of genic ISM and ILP markers in terms of their simplicity in discovery and designing, and their potential to find out functional allelic polymorphism among accessions in the gene regions, makes them an ideal tool for breeding programs.

Authors' contribution

Conceptualization of research (HS, RD); Designing of the experiments (HS, RD, JK, BPS); Contribution of experimental materials (HS, RD, JK); Execution of field/lab experiments and data collection (JK, BPS, RC, RK, RJG); Analysis of data and interpretation (HS, RD, HR, JK); Preparation of manuscript (HR, JK, HS, RD).

Declaration

The authors declare no conflict of interest.

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Sr.No.	**Mrker_na**	**Japonica_**	**Japonica_**	Japonica_	Indica_Pro	**Polymorp**	**FORWARD**	**Tm(°C)**	**Primer_siz**
127	RIM01g01	226584	226784	200	167	33	AGAGATG	61.33	20
129	RIM01g01	241056	241231	175	133	42	TGGATCTC	59.984	20
141	RIM01g01	265223	266304	1081	1054	27	GCGGCAA	59.913	20
155	RIM01g01	319215	320544	1329	1430	101	GCCTCCCC	60.199	18
242	RIM01g01	412811	413390	579	608	29	CTGTTCCG	59.751	20
267	RIM01g01	442158	444204	2046	1987	59	TGGAAAG	59.903	20
302	RIM01g02	537452	538871	1419	1398	21	ACGACCC	59.935	20
313	RIM01g02	548619	548836	217	237	20	CCGTCAAC	60.668	20
327	RIM01g02	590154	590898	744	715	29	ATTGCCGA	59.978	20
390	RIM01g02	961533	962762	1229	1325	96	GCATTCAG	59.002	20
402	RIM01g02	1010294	1010500	206	226	20	TGGTCTGG	60.326	20
440	RIM01g02	1124283	1124426	143	319	176	CAACCGTT	59.96	20
462	RIM01g03	1300840	1301916	1076	1104	28	ATCAGGG	60.06	20
498	RIM01g03	1457763	1457956	193	172	21	CCATGTGA	59.105	20
529	RIM01g03	1601455	1602310	855	702	153	TGGAATG	59.222	20
596	RIM01g04	2014615	2015191	576	535	41	TTATGTTC	59.871	20
633	RIM01g04	2132913	2133394	481	638	157	GAAATAA	58.405	25
642	RIM01g04	2245945	2246352	407	459	52	CGCTGGTT	59.993	20
735	RIM01g05	2606437	2606591	154	178	24	GGAGACT	60.012	22
775	RIM01g05	2728473	2729060	587	547	40	CATTACCT	59.813	20
796	RIM01g05	2769618	2770114	496	476	20	GTGGTTCG	60.319	19
815	RIM01g05	2790511	2791115	604	564	40	GAGATCG	60.981	18
847	RIM01g06	2878345	2878586	241	279	38	GGCTAATC	60.175	20
866	RIM01g06	3019480	3019947	467	492	25	GTACTCAG	60.397	20
935	RIM01g07	3322202	3322933	731	866	135	GTGACGG	59.988	19
951	RIM01g07	3396744	3397487	743	590	153	TTTTTAAG	61	20
952	RIM01g07	3397527	3397704	177	153	24	GTCACCAC	59.837	20
1041	RIM01g07	3766562	3768432	1870	1840	30	CACGTAGC	59.864	20
1050	RIM01g07	3772861	3773556	695	789	94	AACGTCGC	60.628	20
1052	RIM01g07	3779504	3780573	1069	1032	37	AGGAGAT	59.755	20
1065	RIM01g07	3843441	3844024	583	542	41	TTTGGGAG	60.913	20
1110	RIM01g08	3991479	3992495	1016	1039	23	GCAGATG	60.021	20
1117	RIM01g08	4060480	4061154	674	696	22	GGACCTCC	59.903	20
1130	RIM01g08	4117423	4119394	1971	1924	47	ACCAGACC	62.06	20
1163	RIM01g08	4263939	4264350	411	379	32	TTGCAGAC	60.287	20
1177	RIM01g08	3750079	3750253	174	195	21	CACTCAGC	60.766	19
1185	RIM01g08	4376230	4376998	768	808	40	CTGCATTT	60.152	19
1252	RIM01g08	4510922	4511578	656	632	24	GTTGGTTC	59.943	20
1356	RIM01g09	5009105	5011159	2054	2032	22	ATTGGAGC	59.974	20
1384	RIM01g09	5175286	5176233	947	794	153	GTGGCACT	61.296	19
1400	RIM01g10	5236259	5236854	595	575	20	CTCCACGT	60.415	18
1405	RIM01g10	5239561	5242946	3385	3420	35	GCTTCCAT	60.195	20
1496	RIM01g11	5900592	5905954	5362	5434	72	CCTCAAGG	60.241	20
1593	RIM01g11	6377486	6380674	3188	3168	20	GACTTCAT	59.676	20
1636	RIM01g11	6475288	6476127	839	797	42	GATGTTTC	59.602	19
1639	RIM01g11	6478422	6478657	235	255	20	GGACAGGT	60.51	20

1671	RIM01g12	6583620	6585683	2063	1888	175	TGACACG	60.16	20
1683	RIM01g12	6688740	6689854	1114	1182	68	TCTCCTCA	59.43	20
1688	RIM01g12	6692643	6692849	206	354	148	TTAGGAA	58.405	27
1700	RIM01g12	6839170	6839773	603	685	82	CCTCATTT	60.042	20
1720	RIM01g12	6903907	6904978	1071	1099	28	GAGCTCC	59.542	18
1762	RIM01g12	7043516	7045144	1628	1557	71	CTGACCA	60.261	20
1768	RIM01g12	7061337	7063602	2265	2212	53	GACATGG	60.113	19
1780	RIM01g12	7118394	7118872	478	335	143	GTATGGA	59.147	20
1782	RIM01g12	7120986	7121895	909	728	181	AAAGCCC	60.255	20
1828	RIM01g13	7281497	7282512	1015	984	31	TTGGGTAT	60.088	20
1869	RIM01g13	7343148	7343767	619	573	46	TCATGCAG	60.526	20
1882	RIM01g13	7385021	7385893	872	1059	187	GAGGAGC	60.065	19
1883	RIM01g13	7385874	7386541	667	724	57	TCGGAAG	59.734	20
1899	RIM01g13	7458031	7458525	494	442	52	GTCCCCTC	59.807	20
1928	RIM01g13	7558593	7558820	227	255	28	CAGTTGG	59.864	20
1973	RIM01g13	7757804	7758933	1129	1107	22	GCGCTGTA	60.419	20
2032	RIM01g14	7994138	7994368	230	199	31	GGTGGTG	59.362	21
2088	RIM01g14	8290735	8291685	950	1019	69	AGAAGGA	60.72	19
2116	RIM01g14	8353481	8353964	483	577	94	TCGTGTG	60.112	20
2122	RIM01g14	8383524	8384512	988	957	31	CCTTCAGT	59.73	20
2145	RIM01g15	8683631	8684664	1033	988	45	TGGGATC	60.218	20
2149	RIM01g15	8717977	8718683	706	743	37	ACCGTGAT	59.939	20
2309	RIM01g16	9265328	9266284	956	902	54	CATCACAG	60.261	20
2364	RIM01g16	9498475	9499024	549	521	28	CAGCATG	59.297	20
2475	RIM01g18	10149177	10150374	1197	1064	133	TGAGAGC	58.968	20
2488	RIM01g18	10185539	10187246	1707	1627	80	ATGCCCA	59.962	20
2492	RIM01g18	10194552	10195247	695	722	27	CTGACAC	59.691	20
2509	RIM01g18	10311585	10312664	1079	1200	121	TGCTGATG	60.192	21
2523	RIM01g18	10472433	10477055	4622	4710	88	GAGCGTA	59.895	20
2564	RIM01g19	10766868	10767571	703	619	84	AATTTTCT	59.474	20
2706	RIM01g20	11516757	11519461	2704	2735	31	TGAAGCG	60.538	20
2756	RIM01g21	11740916	11748270	7354	7421	67	ACCAGTA	60.182	20
2768	RIM01g21	11833121	11833281	160	182	22	TGATGTG	59.673	20
2777	RIM01g21	11845782	11847208	1426	1399	27	GTGGCGA	59.297	20
2779	RIM01g21	11848911	11850850	1939	1969	30	AGGCGTC	60.419	20
2795	RIM01g21	11956482	11958852	2370	2398	28	TGGTAGC	60.074	20
2804	RIM01g21	11961968	11962148	180	229	49	TGATCTTT	59.78	22
2831	RIM01g21	12125400	12125586	186	160	26	GGTCACC	59.165	20
2845	RIM01g21	12219765	12220744	979	949	30	TTTTTAGG	59.448	20
2877	RIM01g21	12344147	12345594	1447	1511	64	CGTCAAG	60.205	18
2879	RIM01g21	12346541	12348790	2249	2278	29	GAAGGAT	59.273	20
3013	RIM01g23	1918778	1919330	552	470	82	TATGGCT	60.288	20
3047	RIM01g23	13275522	13277085	1563	1586	23	TGTTCCT	60.724	20
3102	RIM01g24	13516831	13518680	1849	1823	26	CTTCCTG	60.269	20
3129	RIM01g24	2504894	2505823	929	960	31	CGAAGGA	60.187	20
3138	RIM01g24	13562822	13564387	1565	1639	74	CACGGTTG	60.415	20
3157	RIM01g24	13628246	13629070	824	765	59	CTTTGGAT	59.288	20

3173	RIM01g24	13761091	13761202	111	84	27	TGGAACA	59.773	20
3247	RIM01g24	14031193	14033996	2803	2828	25	AGAAGAT	59.105	20
3256	RIM01g24	14036881	14037071	190	289	99	TGTGATCC	59.631	20
3282	RIM01g25	14102530	14106528	3998	3886	112	ATCGTCAA	60.395	20
3309	RIM01g25	14252058	14252657	599	568	31	CCTCCTCC	59.622	19
3345	RIM01g25	14453141	14453338	197	221	24	ACGATTTC	60.026	19
3426	RIM01g26	14900412	14901431	1019	1043	24	TGATAATG	59.613	22
3543	RIM01g27	15455199	15456192	993	936	57	GGTTTGCC	60.088	20
3569	RIM01g27	15644950	15647980	3030	2994	36	TTCCTGGT	60.656	20
3589	RIM01g28	10181194	10181346	152	126	26	CCCTCAGC	59.844	20
3605	RIM01g28	3750083	3750240	157	178	21	CCATGTGA	59.105	20
3632	RIM01g28	15975573	15976608	1035	1009	26	CAATTGGT	59.996	22
3679	RIM01g28	16231475	16231975	500	413	87	CTTCCTTG	58.839	19
3710	RIM01g29	16385154	16386432	1278	1304	26	ATCAGATT	60.226	20
3720	RIM01g29	16423603	16423787	184	72	112	ATGGCGA	59.96	20
3743	RIM01g29	16482542	16489762	7220	7256	36	TGAAAGT	60.088	20
3756	RIM01g29	16524833	16525446	613	707	94	AACCATTG	59.374	20
3770	RIM01g29	16544211	16544511	300	278	22	CAAGGAC	60.918	19
3908	RIM01g31	17482691	17483982	1291	1344	53	AAAGGCA	60.924	20
3918	RIM01g32	17539321	17540042	721	547	174	GGAGGGA	61.095	20
4014	RIM01g32	17940687	17942326	1639	1513	126	CTACAGTT	60.689	20
4195	RIM01g33	18703977	18704364	387	420	33	CAAAAGT	59.719	20
4256	RIM01g34	18927192	18937559	10367	10339	28	ATTCATGC	59.04	20
4261	RIM01g34	18983194	18984917	1723	1692	31	TGATCCTC	60.187	20
4327	RIM01g35	19380152	19380920	768	793	25	CCTCATTC	59.075	20
4348	RIM01g35	19466530	19466987	457	575	118	CTACAATC	59.716	20
4350	RIM01g35	19480111	19482145	2034	1878	156	CCTTCCTT	58.787	20
4467	RIM01g36	20061509	20063095	1586	1489	97	GTCTCTTG	60.564	20
4587	RIM01g36	20595702	20597332	1630	1580	50	CAAATGCA	60.096	20
4600	RIM01g37	20652503	20653485	982	1026	44	TCTCCATC	60.072	20
4689	RIM01g37	21120685	21121325	640	547	93	TGGGTTAT	59.931	20
4783	RIM01g38	21359971	21360996	1025	986	39	TCGCTGAC	60.016	20
4807	RIM01g38	21423253	21423517	264	328	64	TCGTGTCA	60.776	20
4808	RIM01g38	21423690	21424437	747	620	127	TGTCAAGA	59.822	19
4810	RIM01g38	21424620	21424987	367	275	92	TGAAAGA	58.801	21
4900	RIM01g39	21993200	21994558	1358	1391	33	CGCGAGT	60.027	19
4952	RIM01g39	22217684	22218183	499	551	52	GATAGCA	59.845	20
4954	RIM01g39	3750083	3750240	157	178	21	CCATGTGA	59.105	20
4997	RIM01g39	22435114	22436875	1761	1646	115	CATCTTCC	59.596	19
5034	RIM01g39	22536815	22537058	243	218	25	GAAACCGT	59.966	20
5043	RIM01g40	22618210	22622405	4195	4087	108	TTTTGGTG	59.024	20
5051	RIM01g40	22646649	22647745	1096	1135	39	CAGGGCT	60.297	21
5197	RIM01g40	23096413	23102809	6396	6417	21	TGGAGAT	60.248	21
5232	RIM01g41	23226951	23227805	854	659	195	CTCCTCGC	60.291	20
5288	RIM01g41	23463168	23463360	192	224	32	GCGGTTGT	60.852	18
5365	RIM01g42	23856267	23856788	521	604	83	ATGACCTG	60.048	18
5394	RIM01g42	23933896	23935155	1259	1222	37	CAGAGCA	59.911	20

5407	RIM01g42	24140637	24141706	1069	1106	37	AAATCTTG	59.734	24
5430	RIM01g42	24236965	24237677	712	746	34	TTTCATGG	59.474	20
5437	RIM01g42	24268767	24270595	1828	1775	53	AGAGGGC	59.827	20
5467	RIM01g42	24376928	24378333	1405	1459	54	TACAGCCT	59.807	20
5493	RIM01g42	24485179	24485857	678	705	27	AAACACAT	59.927	20
5579	RIM01g43	24891189	24891446	257	363	106	CAGCGAT	62.854	18
5586	RIM01g43	24895530	24895852	322	386	64	TTATCCTT	59.382	20
5595	RIM01g43	24904065	24905096	1031	1102	71	GGTGGCT	60.4	18
5654	RIM01g43	25113486	25115491	2005	1892	113	CACCAGG	60.197	18
5940	RIM01g46	26299691	26301037	1346	1269	77	AATGCTCG	60.538	20
5943	RIM01g46	3750083	3750240	157	178	21	CCATGTGA	59.105	20
5972	RIM01g46	3750083	3750240	157	178	21	CCATGTGA	59.105	20
6171	RIM01g47	27185238	27187365	2127	2097	30	ATACCCGA	60.588	19
6296	RIM01g48	27857987	27859434	1447	1323	124	GATTTCTA	59.128	21
6312	RIM01g48	27943497	27944834	1337	1308	29	TTTGGAAG	60.118	21
6315	RIM01g48	27961086	27963664	2578	2549	29	CTCCGTCG	60.261	20
6327	RIM01g48	28009008	28010020	1012	968	44	CATTCCGC	60.57	20
6372	RIM01g49	28173731	28174387	656	624	32	TTGAAGG	60.088	20
6438	RIM01g49	28422344	28423227	883	916	33	CGTGCATT	59.585	20
6508	RIM01g49	28650766	28651683	917	883	34	CAACCAA	59.873	20
6511	RIM01g49	8776173	8777596	1423	1276	147	TGACCCA	59.935	20
6537	RIM01g50	28740857	28741091	234	206	28	AAACAGCT	59.74	20
6548	RIM01g50	28740857	28741091	234	206	28	AAACAGCT	59.74	20
6627	RIM01g50	29044592	29045213	621	706	85	AGCATTC	59.674	20
6697	RIM01g50	29246040	29247913	1873	1915	42	AGCTGAG	59.85	19
6751	RIM01g51	29424028	29424969	941	852	89	ATGGATTG	59.204	20
6844	RIM01g51	29568152	29568804	652	719	67	AGATCAG	60.53	20
6865	RIM01g51	29646372	29646539	167	187	20	CGTCTTCT	60.443	20
6901	RIM01g51	29853802	29854389	587	614	27	ATTGTCTC	61.071	19
6911	RIM01g51	29873772	29874720	948	971	23	AACAGCTG	60.549	19
6931	RIM01g52	29988212	29990205	1993	2013	20	CCTGCACT	59.989	20
7002	RIM01g52	30177542	30177760	218	198	20	ATGAGCA	60.296	20
7029	RIM01g52	30236996	30239441	2445	2416	29	CCAACCTT	61.049	20
7051	RIM01g52	30398349	30399555	1206	1165	41	GTCCTCGT	60.786	20
7110	RIM01g53	30635809	30636100	291	423	132	GGGGTTG	58.504	20
7133	RIM01g53	30754480	30755279	799	935	136	TGTTTCCC	58.869	21
7142	RIM01g53	30763695	30763991	296	142	154	CGTGATTG	60.235	20
7167	RIM01g53	30867809	30868429	620	663	43	ACGCTGCT	60.223	19
7254	RIM01g54	31104595	31105284	689	768	79	CTGACGAT	60.463	20
7335	RIM01g54	31363145	31363509	364	404	40	GCGCATAA	59.694	20
7375	RIM01g54	31511366	31512307	941	916	25	GCTAGCAA	59.985	20
7376	RIM01g54	31512262	31513019	757	806	49	ATGCCTA	57.449	20
7416	RIM01g54	31601923	31603172	1249	1276	27	TGGGACTT	60.012	20
7539	RIM01g55	32168657	32169513	856	967	111	TCATCAGA	60.234	21
7595	RIM01g56	32414965	32415601	636	662	26	CCACCGG	60.713	20
7706	RIM01g56	32671319	32671986	667	708	41	TGAGAGCT	59.391	21
7795	RIM01g57	32964730	32966379	1649	1696	47	GTGTATG	59.976	19

7814	RIM01g570	32972936	32974274	1338	1317	21	TACCACCA	59.429	20
7817	RIM01g570	32974667	32975046	379	417	38	TCTTCAAG	57.692	22
7919	RIM01g577	33395913	33396640	727	748	21	ACTCCTCCT	59.856	20
7920	RIM01g577	33408984	33409371	387	473	86	GTGTTCCT	59.505	18
7933	RIM01g578	33432131	33432875	744	722	22	TTCTTGTT	59.903	20
7945	RIM01g578	33467743	33468547	804	845	41	CAACGTCA	60.465	19
7947	RIM01g578	33473252	33474058	806	715	91	TCTACAGA	59.726	20
8009	RIM01g583	33709415	33710120	705	654	51	TGCAGTGT	60.757	20
8035	RIM01g586	33896930	33899974	3044	3090	46	CCTCTTCT	59.721	20
8062	RIM01g586	33925572	33926263	691	590	101	TTTCGTCT	59.844	20
8091	RIM01g591	34141244	34143067	1823	1849	26	GCGCTCTA	60.285	20
8133	RIM01g594	34397387	34398846	1459	1371	88	ATGGCTA	59.579	20
8135	RIM01g594	34400976	34401781	805	830	25	GCACATCA	59.963	20
8144	RIM01g595	26659368	26660769	1401	1267	134	GGAGGATT	59.81	20
8274	RIM01g605	34995856	35000779	4923	4807	116	CGGCGTCT	62.907	18
8281	RIM01g606	35062004	35062296	292	314	22	CGTGACCT	59.776	19
8368	RIM01g614	35539289	35542626	3337	3179	158	TTCTTCAT	60.158	20
8373	RIM01g614	35572284	35574079	1795	1752	43	CAAGCCT	59.67	20
8385	RIM01g616	35636266	35638340	2074	2117	43	CTACTTCCT	59.187	20
8395	RIM01g616	35682476	35684367	1891	1863	28	TACAACCT	59.591	20
8421	RIM01g618	35767075	35767599	524	407	117	CTATTCAA	60.786	20
8545	RIM01g625	36213298	36213506	208	250	42	GAGGAGG	59.807	20
8573	RIM01g626	36281435	36282073	638	660	22	ATTGCCAG	59.967	20
8654	RIM01g630	36499721	36500736	1015	1075	60	TATCAGG	60.088	20
8688	RIM01g631	11291249	11291852	603	436	167	AGGGGGA	60.89	20
8723	RIM01g636	876894	878015	1121	1039	82	TGTATTAA	59.64	20
8751	RIM01g637	37001667	37002871	1204	1250	46	GTCTACAT	59.957	20
8789	RIM01g642	37280174	37281063	889	788	101	CGAAGGAT	59.302	23
8798	RIM01g642	37299103	37299390	287	265	22	CTGACCAG	60.136	20
8834	RIM01g645	37469557	37470221	664	700	36	GGCCATTT	59.867	20
8897	RIM01g647	37582939	37583185	246	206	40	TTCAGGCT	59.888	20
8941	RIM01g650	37767358	37767884	526	476	50	CATGAAC	60.001	20
8971	RIM01g652	37839048	37840729	1681	1862	181	TGTCCCTG	60.626	20
8984	RIM01g653	37909610	37910128	518	465	53	TTGGTTCG	60.301	20
9026	RIM01g655	38032258	38033793	1535	1594	59	CCGTCCTA	60.125	20
9064	RIM01g656	38092806	38093000	194	235	41	ATAGCAA	60.812	19
9065	RIM01g656	38115307	38116320	1013	1064	51	ACTCAGCT	61.275	20
9069	RIM01g657	38164904	38165827	923	977	54	GCCTCTCG	59.925	19
9071	RIM01g657	38196812	38198816	2004	1982	22	GGTTCTTT	60.232	20
9083	RIM01g658	38255468	38256105	637	663	26	GGCACCT	60.073	20
9087	RIM01g659	38287044	38289517	2473	2537	64	GTCCTCTG	61.785	20
9108	RIM01g661	38382373	38383913	1540	1517	23	CATGGTCA	60.932	19
9408	RIM01g680	39543697	39545525	1828	1787	41	CTTCGTCC	59.958	19
9460	RIM01g682	39668740	39669224	484	387	97	TCCTGGTA	59.989	20
9483	RIM01g683	39729353	39729787	434	413	21	CTCGCGGA	60.042	19
9500	RIM01g684	39767754	39768262	508	560	52	TCAGGAT	59.787	20
9523	RIM01g685	39809487	39811068	1581	1708	127	GAAGTTGT	60.975	20

9568	RIM01g690	40129521	40129954	433	461	28	GTCGGCAT	62.145	20
9584	RIM01g691	40167893	40168489	596	641	45	ATTCTGAT	60.226	20
9592	RIM01g691	40176881	40177536	655	678	23	TGGGGGA	59.784	20
9603	RIM01g691	40204291	40205378	1087	1133	46	GTCGATG	59.944	18
9621	RIM01g692	40225374	40225676	302	265	37	ATTGGCAT	60.226	20
9635	RIM01g692	40241649	40242032	383	423	40	TTGTAGGA	59.272	20
9641	RIM01g698	3750083	3750240	157	178	21	CCATGTGA	59.105	20
9642	RIM01g698	19520339	19520572	233	257	24	ACCTCGAG	60.096	20
9653	RIM01g698	40361904	40362839	935	967	32	TGCTGACA	59.988	20
9679	RIM01g700	40493088	40494298	1210	1182	28	CGTCGACA	60.701	20
9709	RIM01g702	40657812	40658652	840	883	43	AGGGCAC	59.476	20
9778	RIM01g705	40846048	40846329	281	308	27	CCAAGACA	59.962	20
9872	RIM01g712	41192692	41193889	1197	1174	23	GTCATCAA	60.52	20
9879	RIM01g712	41197311	41197481	170	146	24	TTTTGTAG	60.152	21
9883	RIM01g712	41219463	41221781	2318	2347	29	GATGGTA	60.342	19
9893	RIM01g713	41252097	41269255	17158	17217	59	GAGGGAG	59.986	20
9964	RIM01g718	41619002	41619683	681	721	40	GAAAGTTT	59.441	23
9994	RIM01g719	41691681	41692879	1198	1260	62	GATGGAG	59.805	20
10036	RIM01g722	41893348	41893953	605	647	42	ATTTTACA	58.809	20
10153	RIM01g727	42218161	42219242	1081	965	116	GGCCTTG	60.088	20
10266	RIM01g733	42511130	42511421	291	336	45	CACTCTCT	60.275	20
10433	RIM01g741	42946436	42946909	473	451	22	TCGCAGAT	60.073	20
10450	RIM01g741	42959828	42960001	173	196	23	CTTGGCTG	60.309	20
10647	RIM02g015	290940	291705	765	713	52	CAAGCGTA	59.993	20
10958	RIM02g032	5175286	5176218	932	800	132	GTGGCACT	61.296	19
11053	RIM02g036	10120627	10120971	344	295	49	ATTTGCAA	60.786	20
11071	RIM02g036	1546549	1548025	1476	1329	147	GCTTCTCA	60.285	20
11116	RIM02g041	1784982	1787419	2437	2518	81	ATCAACCA	60.657	20
11211	RIM02g045	2016407	2017013	606	654	48	TCTGGGGT	60.943	20
11213	RIM02g045	2017745	2018069	324	353	29	ACTGTCCT	59.966	20
11227	RIM02g046	2097603	2099423	1820	1796	24	ACAAGTG	60.009	20
11248	RIM02g048	2255256	2255421	165	200	35	TTTTGCCT	57.243	24
11251	RIM02g048	2259459	2259886	427	392	35	ATCAATG	60.667	20
11334	RIM02g051	33435673	33436696	1023	1054	31	CTGTTGG	59.648	20
11336	RIM02g052	2498491	2499886	1395	1366	29	CCCCCTCT	60.455	20
11526	RIM02g063	3154861	3155375	514	356	158	TTCTATTT	59.926	20
11566	RIM02g065	3267687	3267891	204	265	61	AAGGTGG	60.188	19
11668	RIM02g071	3750083	3750240	157	178	21	CCATGTGA	59.105	20
11717	RIM02g073	3788602	3789569	967	935	32	GGAACAA	59.08	20
11749	RIM02g075	3879918	3882455	2537	2592	55	GCGTCCAT	59.397	20
11761	RIM02g075	3927873	3928081	208	245	37	ATGGAGG	59.879	19
11800	RIM02g077	4036781	4037502	721	688	33	TGATCCTC	61.046	20
11802	RIM02g077	4044744	4044899	155	176	21	CCTCGTCC	60.195	18
11906	RIM02g082	4386299	4386947	648	589	59	AGCAGAAT	60.776	20
11922	RIM02g083	4430024	4430329	305	334	29	GCATAGG	59.668	20
11964	RIM02g084	4482034	4482337	303	268	35	AGAGGCAT	59.154	19
12015	RIM02g091	4718808	4719557	749	721	28	AGGTGATT	59.009	20

12023	RIM02g09	4786114	4786475	361	389	28	GAGGTGC	60.012	20	
12049	RIM02g09	4947222	4948102	880	945	65	CAACATG	60.84	20	
12119	RIM02g10	5317054	5317259	205	322	117	AGCTGGA	60.298	20	
12120	RIM02g10	5317233	5317774	541	635	94	CGGCATTG	60.192	18	
12155	RIM02g10	35572018	35574080	2062	2019	43	GCCGAGG	62.223	19	
12242	RIM02g10	5624550	5625278	728	683	45	GCCTCGCT	59.101	20	
12245	RIM02g10	5625711	5626649	938	974	36	CAGGAAC	60.081	20	
12291	RIM02g11	17188312	17188425	113	148	35	CAAAAGC	60.132	20	
12353	RIM02g11	6167121	6167899	778	850	72	ACCAGCG	59.904	20	
12400	RIM02g12	6313021	6313745	724	746	22	TCATTAGT	58.872	20	
12494	RIM02g12	6776466	6777050	584	459	125	TGGGTCT	59.807	20	
12498	RIM02g12	6792707	6793190	483	519	36	AGGTCCAT	60.293	20	
12522	RIM02g13	6921100	6921444	344	321	23	AGAGAGG	60.088	20	
12539	RIM02g13	6988856	6989975	1119	990	129	GCACTAAT	60.34	20	
12574	RIM02g13	11177616	11177827	211	166	45	CCATGGA	59.522	20	
12716	RIM02g14	7677520	7687008	9488	9607	119	AGGAGCA	60.226	20	
12717	RIM02g14	7706938	7707116	178	146	32	CTCCCCCG	60.494	19	
12753	RIM02g14	7881067	7881771	704	642	62	GACATGGT	60.667	20	
12845	RIM02g14	8300105	8301266	1161	1074	87	GTCGCCAA	60.363	18	
12922	RIM02g15	3750083	3750240	157	178	21	CCATGTGA	59.105	20	
12944	RIM02g15	8779723	8781422	1699	1676	23	AGGCTTG	59.95	20	
12972	RIM02g15	9013024	9015239	2215	2147	68	CCAGAGCT	59.761	21	
12974	RIM02g15	9042346	9043316	970	946	24	CCAATCTT	61.364	18	
12983	RIM02g16	9116225	9117213	988	1050	62	TCAAGGA	59.803	20	
13015	RIM02g16	17120063	17120650	587	669	82	CAACATCG	60.263	20	
13032	RIM02g16	13094667	13095515	848	1023	175	TCTCCGCC	60.135	20	
13069	RIM02g16	9544722	9548161	3439	3463	24	CTCTCCAT	59.905	19	
13104	RIM02g17	3750083	3750240	157	178	21	CCATGTGA	59.105	20	
13186	RIM02g17	10207577	10208058	481	385	96	CTCCACGT	61.691	18	
13323	RIM02g18	10638807	10639289	482	445	37	ATCTGCGG	60.11	20	
13404	RIM02g18	11072726	11073574	848	934	86	AGATGCTG	59.723	20	
13463	RIM02g19	11289974	11290323	349	326	23	CAACTAGT	60.305	20	
13478	RIM02g19	11389707	11389920	213	258	45	CGCATTCA	60.233	20	
13597	RIM02g20	14081542	14081772	230	253	23	TAATGGC	60.088	20	
13639	RIM02g20	12256461	12257084	623	754	131	TGTTGTGT	59.525	21	
13670	RIM02g20	12372025	12373068	1043	1069	26	TGTTACTG	59.415	20	
13740	RIM02g21	34210591	34210917	326	364	38	TGGCAAA	59.916	20	
13768	RIM02g21	12789240	12789812	572	422	150	AAGACGA	60.096	20	
13787	RIM02g21	12847218	12847879	661	681	20	GAAGCTCT	60.483	20	
13792	RIM02g21	12860265	12863398	3133	3202	69	ACCGACCA	60.648	20	
13866	RIM02g22	13308426	13308858	432	464	32	TGCAGTTG	59.875	20	
13905	RIM02g22	13015732	13016772	1040	958	82	TGCGTGCA	59.694	20	
14018	RIM02g24	14427147	14427366	219	192	27	GAGGACG	60.05	20	
14027	RIM02g24	1429877	1431113	1236	1204	32	AGATGAA	59.923	20	
14042	RIM02g25	14563392	14563494	102	139	37	GGCAATC	60.051	20	
14051	RIM02g25	14639353	14640214	861	905	44	GCAATCAT	59.644	21	
14074	RIM02g25	12406429	12407257	828	802	26	TATGGGTT	59.933	20	

14091	RIM02g25	14654180	14656052	1872	1821	51	TCAAAGT	59.881	20
14110	RIM02g25	7263962	7264093	131	252	121	GTACATA	60.221	20
14198	RIM02g26	15378561	15379299	738	648	90	TCTGTCAT	59.988	20
14201	RIM02g26	15381578	15382680	1102	1053	49	GCTGTGG	61.141	18
14245	RIM02g26	15667059	15667270	211	232	21	GATCTTGA	59.537	20
14280	RIM02g26	15775152	15776385	1233	1268	35	TACCCGAA	59.966	20
14453	RIM02g27	16465343	16465996	653	725	72	TTTGGTCC	59.143	20
14481	RIM02g28	16612522	16613530	1008	1039	31	GCAAGCG	60.225	20
14484	RIM02g28	16614497	16615510	1013	908	105	TGTTTCTT	59.097	20
14490	RIM02g28	16617200	16624851	7651	7631	20	CGTAGACA	59.365	20
14532	RIM02g28	21583467	21584193	726	617	109	TCAAGTCA	60.139	21
14543	RIM02g28	16905313	16906676	1363	1341	22	GGATGAT	60.021	20
14558	RIM02g28	16954667	16954961	294	273	21	TCATTTTG	60.193	20
14584	RIM02g28	17071625	17072896	1271	1096	175	TCGCTTAA	60.089	20
14609	RIM02g29	26417581	26417681	100	185	85	GGGAGCT	62.299	18
14736	RIM02g29	17800824	17802395	1571	1602	31	GATGGCGT	61.014	20
14751	RIM02g30	17857340	17860340	3000	2956	44	CAGCTCAT	59.726	20
14759	RIM02g30	17869307	17869705	398	472	74	TGAACCAG	60.195	20
14797	RIM02g30	18033802	18039761	5959	6073	114	GTATGGG	60.057	20
14845	RIM02g30	18284762	18286435	1673	1644	29	GAGATGT	60.048	20
14970	RIM02g31	18767833	18768528	695	720	25	AAATTGGA	60.065	19
15037	RIM02g32	19107922	19109089	1167	1116	51	AGCAAGG	58.815	20
15038	RIM02g32	12479515	12480529	1014	937	77	CTCAAGC	60.95	19
15041	RIM02g32	3750083	3750240	157	178	21	CCATGTGA	59.105	20
15123	RIM02g32	19376246	19376581	335	271	64	GGTTTTAG	60.365	20
15137	RIM02g32	19433737	19434904	1167	1264	97	GAATTCAT	59.756	20
15144	RIM02g32	19463758	19464224	466	565	99	CGTGGCA	60.924	20
15180	RIM02g33	19644235	19645555	1320	1293	27	GAGTCCGA	60.873	20
15189	RIM02g33	19677775	19678494	719	609	110	AATCTCAT	59.108	21
15201	RIM02g33	19747490	19747683	193	273	80	CGAAAGA	60.397	20
15216	RIM02g33	19802074	19802226	152	87	65	CGATGATG	59.4	20
15219	RIM02g33	19815805	19816033	228	271	43	TTTTGCAA	59.849	20
15222	RIM02g33	11498617	11498961	344	398	54	AGATTGAA	60.081	20
15232	RIM02g33	19877006	19878423	1417	1467	50	TGAGATC	59.215	20
15234	RIM02g33	19878671	19879562	891	839	52	TTAACAA	59.013	20
15270	RIM02g33	20006495	20006788	293	263	30	CGAGCAG	60.005	20
15275	RIM02g33	20013579	20013932	353	506	153	GAAGCAG	59.871	19
15279	RIM02g33	20103507	20104949	1442	1384	58	AGCGTCCT	61.825	18
15343	RIM02g34	20408766	20409026	260	300	40	GCGTTGT	60.134	21
15351	RIM02g34	10454408	10456936	2528	2508	20	ATGACAGT	59.393	20
15390	RIM02g34	20557842	20559751	1909	1857	52	CTTCCCGG	62.228	19
15409	RIM02g34	20659524	20661581	2057	2078	21	AGCAAATT	61.091	20
15412	RIM02g34	20673732	20675980	2248	2273	25	TCAGGGTA	58.945	21
15486	RIM02g34	20908604	20909451	847	824	23	GATCACC	60.164	18
15520	RIM02g35	21026335	21032299	5964	5923	41	GAGGGCA	59.997	20
15567	RIM02g35	22527407	22527594	187	162	25	ATCCTCG	60.61	18
15574	RIM02g35	21239639	21240265	626	691	65	TTCGTAAG	59.43	20

15575	RIM02g35	21239639	21240265	626	691	65	TTCGTAAG	59.43	20
15576	RIM02g35	21239639	21240265	626	691	65	TTCGTAAG	59.43	20
15577	RIM02g35	21239639	21240265	626	691	65	TTCGTAAG	59.43	20
15578	RIM02g35	21239639	21240265	626	691	65	TTCGTAAG	59.43	20
15579	RIM02g35	21239639	21240265	626	691	65	TTCGTAAG	59.43	20
15593	RIM02g35	2196564	2198428	1864	1699	165	CGACTGGT	60.277	20
15647	RIM02g36	21836711	21837322	611	491	120	GGGCCTG	60.34	20
15669	RIM02g36	22007568	22010043	2475	2568	93	TTGTTATG	60.011	20
15702	RIM02g36	22104548	22106584	2036	2057	21	TTCTTCCT	60.38	20
15705	RIM02g36	36068046	36068614	568	507	61	TCCATGGA	60.934	20
15706	RIM02g36	36068625	36069440	815	782	33	AACCAAT	59.973	20
15941	RIM02g38	23289681	23290139	458	485	27	CGGCCAA	60.424	20
15960	RIM02g38	23378909	23379632	723	775	52	GATCCGA	59.077	18
15994	RIM02g38	23449206	23450951	1745	1690	55	GAGAGAC	60.941	19
16058	RIM02g39	23637695	23642972	5277	5162	115	CGGATTCT	60.187	20
16059	RIM02g39	23643183	23643583	400	375	25	AGGGACA	60.737	20
16155	RIM02g39	23413348	23414078	730	751	21	ATATGCTT	60.103	20
16188	RIM02g40	24217903	24219520	1617	1638	21	GTCGACAT	59.521	19
16258	RIM02g40	24554384	24555425	1041	1091	50	GCTACGG	60.769	18
16294	RIM02g40	24740197	24740702	505	525	20	TGATGTTG	59.967	20
16325	RIM02g40	10766745	10766934	189	167	22	AACAATG	60.701	20
16326	RIM02g40	10766868	10767571	703	619	84	AATTTTCT	59.474	20
16339	RIM02g41	24811153	24813565	2412	2379	33	CTGGGTTA	60.517	20
16397	RIM02g41	25184741	25184932	191	225	34	CTCCTCCT	60.727	18
16440	RIM02g42	25396379	25396705	326	476	150	TGGATTCA	58.117	20
16503	RIM02g42	25649229	25652950	3721	3700	21	AATTCGAG	60.019	19
16557	RIM02g43	25892262	25892526	264	244	20	GCTGAGA	59.694	20
16563	RIM02g43	25931945	25932451	506	540	34	CAGGGCA	61.536	18
16598	RIM02g43	26154091	26154990	899	817	82	CTTCATCT	59.577	20
16617	RIM02g43	26360112	26362077	1965	2013	48	TCTCCGTC	62.612	18
16649	RIM02g43	26437058	26437925	867	839	28	GCTGGCG	59.967	20
16652	RIM02g43	26467020	26467257	237	279	42	GTCCCAA	59.153	20
16670	RIM02g43	26538270	26539019	749	787	38	CTCCTCAC	60.767	19
16676	RIM02g44	26633103	26633338	235	202	33	CATCTATG	60.615	20
16677	RIM02g44	26633453	26633846	393	414	21	CAAGCTC	60.647	20
16700	RIM02g44	26815859	26816652	793	772	21	CGAGAAG	59.462	21
16712	RIM02g44	26938496	26939846	1350	1378	28	AGACAGA	59.981	20
16782	RIM02g44	27033098	27034671	1573	1624	51	GCCTGTTA	58.9	20
16786	RIM02g44	27040664	27041216	552	483	69	CGCTGCCA	60.834	20
16815	RIM02g45	27312849	27318013	5164	5295	131	GGAAGGC	61.388	19
16820	RIM02g45	27342832	27343949	1117	1159	42	CTTCATCA	60.073	20
16839	RIM02g45	27543441	27543869	428	390	38	ACCGACT	59.933	20
16894	RIM02g45	27782641	27784990	2349	2450	101	ACGGACA	59.535	20
16964	RIM02g46	28099549	28100655	1106	1146	40	GAAGAGG	59.927	20
16968	RIM02g46	28109180	28109763	583	555	28	GACACCTG	59.847	20
16988	RIM02g46	28209208	28209418	210	160	50	GCACTGA	59.323	20
17003	RIM02g46	28256931	28258199	1268	1417	149	TGGGTCC	60.18	19

17122	RIM02g470	28693248	28694255	1007	958	49	ATTTGCCT	60.11	20
17148	RIM02g471	28758670	28759058	388	241	147	TCCAATTG	60.692	20
17359	RIM02g480	29433106	29434475	1369	1306	63	GCTGCTC	62.127	18
17444	RIM02g487	29828053	29828251	198	172	26	GCCCACTT	60.111	20
17544	RIM02g492	30105114	30105467	353	172	181	TCTGATGA	61.159	20
17545	RIM02g492	30105266	30105768	502	321	181	ACCAAAC	59.569	20
17634	RIM02g496	30358966	30359252	286	216	70	ACGAAGA	59.585	18
17699	RIM02g500	30568852	30570363	1511	1477	34	GGCATCA	60.633	20
17717	RIM02g501	30632087	30632476	389	409	20	CGCAGAT	60.027	21
17724	RIM02g501	30647891	30648107	216	277	61	TCAAGCG	59.523	20
17790	RIM02g505	30889753	30890228	475	433	42	GCAACGA	60.02	20
17881	RIM02g512	31341355	31341517	162	183	21	GGACACC	59.399	20
17934	RIM02g515	31559801	31561288	1487	1516	29	GTGACTTG	60.012	20
18062	RIM02g522	32003707	32004321	614	592	22	AATGAAT	59.871	20
18079	RIM02g523	32033463	32035751	2288	2193	95	GAAGCTA	60.352	20
18114	RIM02g525	32117503	32118012	509	484	25	AAGTGGA	59.934	20
18123	RIM02g526	32173648	32179921	6273	6462	189	GTTTTCGA	60.257	20
18124	RIM02g526	32185655	32186439	784	812	28	ACGGTCTT	60.801	18
18253	RIM02g536	32823246	32824032	786	734	52	AGGGGCC	59.42	20
18286	RIM02g537	32932252	32932907	655	632	23	GCCTAGC	59.034	20
18339	RIM02g539	33052844	33054571	1727	1770	43	GCCTCCAA	60.158	18
18360	RIM02g540	33068854	33069798	944	922	22	CTGGAGG	59.708	20
18426	RIM02g541	33211782	33211991	209	154	55	TAATCTGT	60.036	20
18453	RIM02g544	33353933	33354094	161	247	86	AAGTTCAA	59.187	20
18502	RIM02g545	33394689	33395756	1067	1104	37	CTCAAGG	60.353	20
18505	RIM02g545	33407540	33408167	627	657	30	CCTCTTAA	59.724	20
18518	RIM02g545	33429301	33430354	1053	1248	195	GGGACAC	59.927	20
18609	RIM02g550	33710760	33711454	694	647	47	TCCGACAA	59.83	20
18611	RIM02g550	33711786	33712236	450	352	98	TGGTCCT	59.605	20
18696	RIM02g555	33997382	33998270	888	943	55	AAAAATG	57.409	25
18757	RIM02g559	34234347	34235421	1074	1104	30	AGAGGGT	60.111	20
18777	RIM02g559	34250668	34250875	207	243	36	TTGCCTTG	59.078	20
18799	RIM02g560	34293818	34294297	479	425	54	CTCGCTT	61.08	20
18826	RIM02g561	34346356	34347260	904	804	100	CTGCAGG	59.77	20
18838	RIM02g562	18319925	18320106	181	347	166	GCACTAG	59.985	20
18839	RIM02g562	7995040	7995530	490	656	166	AAGGAAT	60.074	20
18841	RIM02g562	7995976	7996433	457	531	74	TGGGTGT	59.924	20
18875	RIM02g563	34496632	34497386	754	793	39	TGCGCTC	59.115	21
18897	RIM02g565	34593382	34596293	2911	2952	41	CATTGAG	59.751	20
18914	RIM02g565	34627944	34628456	512	576	64	TAGAAGC	60.154	20
18975	RIM02g567	34759609	34760264	655	547	108	AAGGAGC	60.204	20
18992	RIM02g567	34789066	34789821	755	781	26	GAGATGG	59.739	19
19019	RIM02g568	34833486	34834486	1000	1025	25	CAACGTGT	60.001	20
19047	RIM02g570	34921791	34922295	504	532	28	CAGCTGG	59.869	20
19070	RIM02g571	34976416	34977323	907	887	20	CAAGCAA	59.366	21
19090	RIM02g571	34997229	34998497	1268	1236	32	GCCAAGA	59.992	20
19174	RIM02g575	35263542	35263923	381	360	21	GCAACCAT	59.25	20

19197	RIM02g57	35298837	35299587	750	666	84	TCGACTGA	60.737	20
19249	RIM02g57	35463922	35464059	137	161	24	CGGATCG	59.474	20
19271	RIM02g58	35544860	35545412	552	526	26	CTGGTGCT	60.508	20
19304	RIM02g58	35579676	35582523	2847	2904	57	CCACGGA	58.984	20
19317	RIM02g58	35618507	35619386	879	694	185	GCTCAGG	59.886	18
19394	RIM02g58	35820889	35821137	248	215	33	GAAGCATT	60.081	20
19410	RIM02g58	35876314	35878570	2256	2224	32	GCTCCTGG	59.962	20
19412	RIM02g58	35878692	35879304	612	586	26	AATGTAGG	59.978	20
19627	RIM03g01	454724	455599	875	903	28	GCACCTG	61.777	18
19635	RIM03g01	478768	479409	641	597	44	CCTACTGG	61.758	18
19637	RIM03g01	27031800	27032026	226	378	152	ATTTGTCT	59.973	20
19639	RIM03g01	27027856	27028015	159	187	28	ATATATGG	59.813	20
19666	RIM03g01	511255	512612	1357	1488	131	TCTGGAT	59.788	21
19674	RIM03g01	536756	538250	1494	1546	52	AGTAGCC	59.357	20
19732	RIM03g02	652218	653230	1012	1036	24	ATTCGAT	59.41	20
19771	RIM03g02	679826	679992	166	197	31	CCTGAGC	60.366	20
19853	RIM03g02	10382337	10384220	1883	1822	61	TGGAAGG	59.123	20
19898	RIM03g02	942451	943000	549	453	96	AAGAAGG	60.026	21
19920	RIM03g02	992543	993096	553	530	23	GGTGTTA	60.111	20
19923	RIM03g02	511218	512565	1347	1478	131	TCCACAGT	60.562	20
20033	RIM03g03	1395568	1397325	1757	1719	38	GGCTCTT	59.694	19
20078	RIM03g03	1477591	1478474	883	918	35	CCAAAGG	59.993	20
20099	RIM03g03	1631319	1633932	2613	2565	48	CTTCCGTC	60.331	20
20125	RIM03g03	1755301	1755472	171	210	39	CACCTGGT	60.149	20
20442	RIM03g05	22715273	22716266	993	958	35	CTCTTGTC	60.134	20
20443	RIM03g05	2993047	2993442	395	197	198	CCGCGAA	60.234	19
20449	RIM03g06	3020851	3021117	266	216	50	GCATCGT	59.658	20
20625	RIM03g07	3625674	3626507	833	922	89	CAAGATC	59.631	18
20651	RIM03g07	3676602	3676818	216	261	45	GTGGAAT	59.978	20
20704	RIM03g07	16843224	16843996	772	813	41	GAGAACG	59.511	20
20754	RIM03g07	3991137	3995988	4851	4876	25	GGACCAA	59.547	20
20783	RIM03g08	4094593	4095377	784	814	30	AGCACGC	59.904	20
20784	RIM03g08	4094593	4095377	784	814	30	AGCACGC	59.904	20
20785	RIM03g08	4094593	4095377	784	814	30	AGCACGC	59.904	20
20786	RIM03g08	4094593	4095377	784	814	30	AGCACGC	59.904	20
20827	RIM03g08	4266409	4269396	2987	2957	30	GACTTCG	59.882	20
20862	RIM03g08	4333721	4334340	619	583	36	CAGTGAA	59.581	21
20884	RIM03g08	4409860	4410435	575	631	56	GCTTGGA	59.629	20
20976	RIM03g08	4606342	4613243	6901	7001	100	CGTCGTCG	59.984	18
20977	RIM03g08	4613628	4613809	181	216	35	AGACGTG	60.829	18
20997	RIM03g09	4764128	4764851	723	749	26	TGATCAT	60.048	20
21025	RIM03g09	4877401	4878579	1178	1218	40	CGAGCAC	59.867	20
21067	RIM03g10	5033512	5036574	3062	3106	44	GCGTCTT	59.95	20
21108	RIM03g10	5270387	5270636	249	162	87	ACTACAAT	59.434	20
21165	RIM03g10	5458944	5459977	1033	1092	59	GAGGTCT	60.269	20
21266	RIM03g11	5777050	5777537	487	464	23	CCTCGCT	60.135	20
21267	RIM03g11	5777553	5777790	237	265	28	ATCTGCCA	60.269	20

21269	RIM03g113	5818626	5819454	828	742	86	GCATATGG	59.344	20
21289	RIM03g113	5863326	5863684	358	407	49	GTACTCAG	59.47	20
21292	RIM03g114	5865337	5866759	1422	1341	81	CGGAGTC	59.78	20
21372	RIM03g116	6041403	6042454	1051	993	58	CTCTCCCA	61.85	20
21374	RIM03g116	6042822	6046746	3924	3904	20	CAGAGAA	59.989	20
21490	RIM03g123	9484674	9485362	688	718	30	CAGGGCT	59.688	20
21572	RIM03g125	6662646	6664468	1822	1752	70	GCAGGAA	60.386	20
21604	RIM03g126	6698218	6699002	784	758	26	GCTTGTTG	58.287	20
21612	RIM03g126	6702831	6703594	763	635	128	GGAGCACT	59.682	20
21636	RIM03g127	6816427	6817507	1080	1100	20	TGGAAGTT	57.008	23
21655	RIM03g128	6940816	6941711	895	790	105	ATGCAGTG	59.347	20
21665	RIM03g130	7023239	7024168	929	780	149	TGGTACCT	60.755	20
21671	RIM03g131	7074191	7074418	227	178	49	TTCCTTCGA	60.603	20
21830	RIM03g141	7668379	7668803	424	454	30	AGAGTCCA	60.159	20
21965	RIM03g153	8403341	8404258	917	794	123	CCCTGTCA	59.864	20
22062	RIM03g159	8814317	8815280	963	1025	62	GCAATTTG	59.781	20
22207	RIM03g170	9482797	9485260	2463	2484	21	TCATGAG	59.992	20
22217	RIM03g170	9493306	9495396	2090	1961	129	AATGTCTT	59.045	21
22257	RIM03g172	9628404	9628978	574	671	97	GATGTCC	60.363	20
22301	RIM03g176	9842809	9844265	1456	1436	20	TTGTTTT	59.71	18
22405	RIM03g182	10203766	10204173	407	364	43	CGTCGAT	62.128	19
22468	RIM03g184	10352559	10352801	242	210	32	ATGCTACG	59.347	20
22501	RIM03g186	10456302	10456470	168	276	108	GTTCGAC	61.337	20
22565	RIM03g192	10845610	10845965	355	375	20	ATACAAAG	60.416	20
22593	RIM03g194	10938419	10942021	3602	3518	84	CTCTTCCT	60.912	18
22617	RIM03g196	11047637	11048234	597	573	24	GCCAAAAA	60.76	19
22631	RIM03g196	11074658	11075139	481	445	36	TTTTTATT	59.586	20
22743	RIM03g205	11653152	11653624	472	319	153	GGAGGAT	60.133	20
22802	RIM03g208	11804871	11805614	743	775	32	GCTGCTCT	60.012	20
22834	RIM03g211	12018711	12019788	1077	1157	80	TCACACAA	59.924	20
23030	RIM03g219	12529209	12530068	859	880	21	GCTTTAAA	60.075	20
23041	RIM03g219	12600339	12601502	1163	1062	101	CGAATGGT	59.853	20
23051	RIM03g220	12610814	12611372	558	522	36	CTCCACTT	60.444	20
23054	RIM03g220	12626235	12627335	1100	1124	24	CTGGAGCT	60.778	19
23066	RIM03g221	12698667	12699728	1061	1033	28	AGGTTTTT	59.184	19
23186	RIM03g228	13178316	13180052	1736	1712	24	CAACTAC	59.844	20
23235	RIM03g229	13245114	13245814	700	724	24	GATGATCA	59.488	20
23263	RIM03g230	13305612	13305983	371	349	22	GGAGCTC	60.111	20
23301	RIM03g237	13463291	13465764	2473	2536	63	TCTTCGTT	59.894	20
23328	RIM03g241	23061144	23062087	943	870	73	GCTAAACT	59.213	20
23423	RIM03g248	14146982	14148244	1262	1311	49	ACCTCGCA	60.359	18
23464	RIM03g250	14275782	14277609	1827	1911	84	GTGGAAT	60.119	20
23480	RIM03g250	14315855	14317863	2008	2040	32	GTCAAGGT	60.31	19
23497	RIM03g251	14337811	14338865	1054	1077	23	TGCCAAGT	59.467	20
23519	RIM03g251	14381644	14385555	3911	3944	33	GTCAACAT	59.934	20
23521	RIM03g252	14424590	14425949	1359	1401	42	GTGATAAT	60.624	20
23523	RIM03g252	14431903	14432300	397	358	39	TGTGCGCA	60.423	20

23561	RIM03g25	14659119	14661221	2102	2125	23	GAGAGCA	60.082	24	
23586	RIM03g25	14807014	14807568	554	443	111	GGCACTTA	58.582	20	
23639	RIM03g26	14949607	14950908	1301	1271	30	TGTTGAAA	58.146	21	
23763	RIM03g26	15399372	15399924	552	522	30	AACCACTG	59.989	20	
23775	RIM03g26	15409675	15410557	882	903	21	TTTTATGG	60.067	20	
23827	RIM03g27	15605290	15606813	1523	1655	132	AAGGCTC	59.844	20	
23845	RIM03g27	15639601	15640882	1281	1119	162	TATCGATC	60.17	20	
23852	RIM03g27	15649224	15650095	871	917	46	GGAGGTC	60.103	21	
24068	RIM03g29	16555636	16556876	1240	1068	172	CCTGACAT	59.676	20	
24083	RIM03g29	16579419	16583118	3699	3648	51	GCTTTCCC	59.879	18	
24223	RIM03g30	3750083	3750240	157	178	21	CCATGTGA	59.105	20	
24245	RIM03g30	17275160	17275915	755	728	27	TCAGTTCC	59.984	20	
24360	RIM03g31	17773987	17774509	522	497	25	ATCTCCGG	59.691	20	
24418	RIM03g31	500769	500969	200	178	22	CGAAGAT	59.665	20	
24489	RIM03g31	18214119	18216045	1926	1951	25	TGCTTGGT	60.278	20	
24558	RIM03g32	18535392	18536083	691	749	58	TGAAGTC	59.52	20	
24579	RIM03g32	18734723	18735205	482	534	52	TGTGCATG	60.135	21	
24592	RIM03g32	18805796	18806747	951	924	27	AGTTTGTG	61.019	20	
24631	RIM03g33	19046165	19047004	839	814	25	GACAAGG	60.386	20	
24655	RIM03g33	25631175	25632004	829	783	46	AGTTACC	60.932	20	
24681	RIM03g33	9251162	9251522	360	298	62	AAATTTGT	59.801	20	
24713	RIM03g34	19421132	19422192	1060	1088	28	CTATGCAT	60.104	20	
24751	RIM03g35	10481148	10481656	508	538	30	ATGAGAT	60.059	20	
24868	RIM03g36	20379658	20381007	1349	1327	22	CTCAAGAT	60.206	20	
24943	RIM03g37	20706706	20708008	1302	1271	31	CTGGATA	60.21	20	
24946	RIM03g37	20712314	20713611	1297	1353	56	ACAACCGT	60.16	20	
24971	RIM03g37	13532039	13532216	177	122	55	CAGCGGT	60.291	20	
24984	RIM03g37	20905671	20906553	882	946	64	GGCTATG	59.644	19	
24994	RIM03g37	7865599	7866229	630	663	33	ATGGCAA	59.34	20	
25001	RIM03g38	21109267	21109890	623	690	67	AGAGCTG	59.874	20	
25010	RIM03g38	21156286	21156444	158	192	34	TGCACCTT	59.247	20	
25078	RIM03g38	10094488	10095087	599	554	45	CGGAGGG	59.926	20	
25085	RIM03g38	21548855	21549950	1095	1127	32	GTTAGGC	60.964	20	
25129	RIM03g39	1527243	1528270	1027	854	173	CAACAACG	61.381	20	
25170	RIM03g39	22048542	22050935	2393	2201	192	ACGGCAT	60.218	20	
25183	RIM03g39	22154810	22155324	514	541	27	CTCGGGT	60.103	20	
25197	RIM03g40	22261110	22262142	1032	920	112	CGGTCTTT	58.674	22	
25199	RIM03g40	22263369	22263512	143	165	22	TCATCACC	59.918	21	
25212	RIM03g40	14260296	14260971	675	653	22	TTTGGTTT	60.242	19	
25222	RIM03g40	22333140	22333283	143	178	35	GAAGTCA	59.997	20	
25228	RIM03g40	22376107	22377280	1173	1090	83	AGCCCCTG	59.187	20	
25266	RIM03g40	22616126	22617043	917	946	29	ATTGCGCT	60.213	20	
25296	RIM03g41	22826250	22827831	1581	1610	29	GCCCTTCG	59.219	18	
25316	RIM03g41	3770755	3771266	511	475	36	GAAGTTGA	59.997	20	
25323	RIM03g41	5062689	5063447	758	955	197	AGTATTTG	59.82	20	
25375	RIM03g41	23207411	23208036	625	698	73	CAATCACA	60.473	20	
25466	RIM03g42	23571292	23573218	1926	1850	76	GAGTTGG	59.218	20	

25495	RIM03g42	23732972	23733695	723	695	28	GACGTCG	59.31	20
25506	RIM03g42	17749816	17750780	964	987	23	ATCTTACG	59.955	20
25516	RIM03g42	23828246	23829186	940	920	20	ATTGCGG	60	19
25520	RIM03g42	23835684	23836326	642	672	30	ATTGTGG	59.846	19
25549	RIM03g42	23909918	23910957	1039	1007	32	GGTGGAG	59.841	20
25558	RIM03g42	23929458	23931905	2447	2527	80	AGTGCAT	59.973	20
25576	RIM03g43	23992770	23994864	2094	2038	56	GACATGCT	60.146	20
25579	RIM03g43	24027260	24028035	775	810	35	CTCTGTTG	60.348	20
25687	RIM03g44	3751593	3754381	2788	2949	161	AGACACC	60.711	20
25688	RIM03g44	3750083	3750240	157	178	21	CCATGTGA	59.105	20
25712	RIM03g44	24910577	24911424	847	793	54	TGGAGAA	59.375	20
25748	RIM03g44	25195570	25199365	3795	3754	41	GCTACGTG	59.67	20
25880	RIM03g46	26077474	26078810	1336	1357	21	GGGAGCT	59.843	20
25970	RIM03g47	26726035	26727048	1013	846	167	TACCTTTC	60.345	20
25973	RIM03g47	26754898	26755838	940	908	32	CCATCACT	60.363	20
25998	RIM03g47	26854473	26854826	353	322	31	CAGAGCA	58.104	20
26017	RIM03g47	26960029	26961377	1348	1326	22	TGCTGGA	59.261	20
26018	RIM03g47	26961358	26962724	1366	1339	27	GGTGGAA	60.051	20
26075	RIM03g47	27040040	27040575	535	572	37	GGCTGGT	60.096	20
26084	RIM03g47	27085316	27086677	1361	1384	23	TGGGAGG	59.701	20
26099	RIM03g47	27100791	27101695	904	881	23	AATGTCTC	60.111	20
26140	RIM03g47	27245431	27246183	752	793	41	CTACCTCG	60.27	18
26168	RIM03g48	27327730	27330182	2452	2535	83	ATCCTCGG	61.495	18
26172	RIM03g48	27344932	27347438	2506	2537	31	CATCAACG	60.419	19
26253	RIM03g48	3750083	3750240	157	178	21	CCATGTGA	59.105	20
26320	RIM03g48	27840331	27842507	2176	2060	116	TCGGAGT	60.353	20
26331	RIM03g48	27871687	27875054	3367	3471	104	TTGTTCTT	60.195	20
26345	RIM03g49	27911960	27912725	765	731	34	ACTTCCCC	60.428	19
26377	RIM03g49	27991402	27993699	2297	2395	98	CCATTTCT	59.67	20
26434	RIM03g49	28125922	28126444	522	549	27	ATGCAGG	60.162	20
26456	RIM03g49	28177925	28178751	826	806	20	ATCTTGTT	59.74	20
26494	RIM03g49	28366290	28367959	1669	1642	27	GCATGAA	59.611	18
26710	RIM03g51	29193908	29199537	5629	5660	31	CGTCGAC	61.546	20
26714	RIM03g51	29200516	29200967	451	431	20	AGCCAGG	59.318	20
26739	RIM03g51	29260121	29262084	1963	1806	157	GGAGGTT	60.894	20
26773	RIM03g51	3750083	3750240	157	178	21	CCATGTGA	59.105	20
26788	RIM03g51	29379760	29380673	913	862	51	GTGTACG	60.431	20
26857	RIM03g51	29759517	29760085	568	610	42	CTGAAGA	59.545	20
26941	RIM03g52	29999856	30001706	1850	1810	40	TGGCTCTT	59.989	20
26947	RIM03g52	30068127	30068429	302	331	29	CCTCCACT	62.38	19
27017	RIM03g52	30265461	30266301	840	860	20	ATGGGAG	60.173	20
27077	RIM03g53	30400904	30401963	1059	1003	56	GACGGAG	61.376	20
27084	RIM03g53	30507165	30508906	1741	1704	37	GAAGGAC	60.045	20
27104	RIM03g53	30634800	30636819	2019	2041	22	CACCTACG	61.716	18
27111	RIM03g53	30654751	30655755	1004	875	129	CTCATCCA	60.929	19
27391	RIM03g55	31434469	31435755	1286	1188	98	CCGACTCT	58.879	20
27477	RIM03g55	23721564	23722555	991	1038	47	CGGAGTC	60.044	20

27479	RIM03g558	13964764	13965435	671	634	37	TGTTGTGT	59.525	21
27480	RIM03g558	31791227	31791668	441	420	21	CAAAATTG	59.317	20
27484	RIM03g560	31881566	31883002	1436	1387	49	AGATGCC	60.526	19
27500	RIM03g561	31958533	31962340	3807	3842	35	GAGTTCTT	60.386	20
27782	RIM03g576	32852903	32853855	952	1003	51	TGGTCCCA	60.563	20
27828	RIM03g579	32996248	32997043	795	771	24	CCCAGCAA	60.073	20
27856	RIM03g580	33046836	33048605	1769	1806	37	TCCAGAA	59.788	21
27867	RIM03g580	33055234	33056459	1225	1042	183	GTCTCGCT	60.977	20
27911	RIM03g583	33236424	33237058	634	725	91	ATAAACCA	59.996	20
27931	RIM03g584	33306851	33307307	456	488	32	AGAAGGA	59.671	20
28016	RIM03g587	33447781	33449452	1671	1691	20	GCAGCAAT	59.869	20
28083	RIM03g591	33653252	33653692	440	460	20	CGATGCCT	59.552	20
28094	RIM03g591	33678738	33679483	745	629	116	GGCTACTT	59.882	20
28097	RIM03g591	33680215	33680579	364	392	28	AAGGAGA	62.236	18
28157	RIM03g595	33887936	33889129	1193	1017	176	GACCGCTT	60.924	18
28158	RIM03g595	33889185	33890621	1436	1351	85	CATTTAAA	60.448	20
28202	RIM03g600	3752316	3752764	448	502	54	GAACGAA	60.142	20
28204	RIM03g600	3750083	3750240	157	178	21	CCATGTGA	59.105	20
28226	RIM03g602	2508714	2509046	332	305	27	CAGCAGA	59.873	20
28329	RIM03g609	34613428	34614544	1116	1165	49	GTTGTTTG	60.156	20
28346	RIM03g609	34625664	34625862	198	164	34	TGATTGTT	59.578	21
28430	RIM03g617	34961318	34963012	1694	1644	50	ACGTGATT	59.572	20
28482	RIM03g618	1230376	1231671	1295	1340	45	TGGCAACA	59.875	20
28483	RIM03g618	35066780	35067502	722	626	96	CGATGATA	59.96	20
28538	RIM03g621	35208405	35209279	874	898	24	CCTTTCTC	57.883	24
28579	RIM03g625	35403700	35404911	1211	1234	23	GACCATC	59.893	20
28615	RIM03g626	35461252	35461444	192	159	33	GAGCCGTT	59.243	20
28640	RIM03g627	35505635	35506401	766	806	40	TTCTCGTC	59.74	20
28658	RIM03g629	35582783	35584441	1658	1627	31	AGATCGA	59.834	20
28695	RIM03g630	35662997	35663217	220	198	22	GGCTAATA	60.259	20
28719	RIM03g633	35783660	35784953	1293	1336	43	ATTGATGA	58.088	20
28872	RIM03g643	36340999	36341460	461	485	24	GCTTGATT	59.389	19
28890	RIM03g644	36389969	36391687	1718	1756	38	GAATACG	59.962	20
28917	RIM04g011	19637388	19637548	160	192	32	GCATTCAG	59.96	20
28953	RIM04g013	271683	273162	1479	1443	36	GGAGGAT	59.07	23
29031	RIM04g019	609779	611509	1730	1667	63	ATCTCCAC	60.073	20
29037	RIM04g022	755246	755431	185	208	23	GCTTCCAA	59.629	20
29056	RIM04g023	845144	846975	1831	1790	41	TGTTCAGG	60.246	20
29072	RIM04g026	980738	981531	793	860	67	GTCCCGT	59.028	20
29111	RIM04g029	1131861	1132719	858	805	53	GTCTCCT	59.481	18
29128	RIM04g029	1196842	1197750	908	957	49	GGCGCTA	60.702	20
29131	RIM04g029	1206776	1211326	4550	4516	34	GCCAAAG	59.035	20
29232	RIM04g036	1569816	1569974	158	183	25	TAAGGCCA	59.953	20
29275	RIM04g037	1697704	1697935	231	268	37	CTGCCAG	60.347	20
29348	RIM04g042	3750083	3750240	157	178	21	CCATGTGA	59.105	20
29362	RIM04g043	2016238	2017075	837	863	26	TGAGTTCG	60.049	20
29369	RIM04g043	2019925	2020879	954	916	38	GAGGAAA	59.889	21

29411	RIM04g049	2370094	2370726	632	590	42	GGCAGGTA	59.476	20
29509	RIM04g062	12748955	12750582	1627	1559	68	GTGGTGGT	59.053	20
29535	RIM04g064	876894	878015	1121	1039	82	TGTATTAA	59.64	20
29551	RIM04g066	1457616	1457973	357	336	21	CAGCCGA	61.188	18
29591	RIM04g071	3750083	3750240	157	178	21	CCATGTGA	59.105	20
29599	RIM04g071	3807706	3808101	395	271	124	CTTGAAAA	59.986	20
29602	RIM04g072	3821048	3821291	243	209	34	CCAAGGG	60.081	20
29672	RIM04g080	4256553	4256959	406	261	145	CGGTGGAA	60.255	20
29696	RIM04g080	4280499	4281063	564	543	21	CCAGGCTG	58.32	20
29712	RIM04g082	4406099	4407627	1528	1562	34	TTCTTGTC	59.978	21
29724	RIM04g083	4433646	4436708	3062	3176	114	TCTTAAAT	59.807	20
29755	RIM04g087	4759600	4760339	739	707	32	GACGATGA	60.324	18
29821	RIM04g095	5116749	5118131	1382	1361	21	TTGTGTGG	60.112	20
29844	RIM04g097	11298614	11299087	473	570	97	ATATGCTG	59.682	20
29922	RIM04g103	5620784	5621496	712	592	120	TTGCAGAT	59.733	20
29944	RIM04g105	5726563	5726880	317	338	21	TCCCTTGCA	58.826	20
29955	RIM04g107	5824084	5825021	937	968	31	GGTTTCA	60.791	20
29972	RIM04g109	3750083	3750240	157	178	21	CCATGTGA	59.105	20
29984	RIM04g109	3750083	3750240	157	178	21	CCATGTGA	59.105	20
30001	RIM04g111	6064205	6064489	284	263	21	AGGGGCTT	59.813	20
30041	RIM04g115	6297502	6298001	499	441	58	CCTCCTCAT	60.646	20
30071	RIM04g116	6374735	6375491	756	667	89	GATTAGA	60.218	20
30137	RIM04g119	6549397	6549558	161	138	23	TGAGAACA	59.84	20
30200	RIM04g124	29182	30883	1701	1642	59	GATTATG	59.929	20
30218	RIM04g126	7481097	7483061	1964	1993	29	AGAGCCT	60.156	20
30272	RIM04g133	7426690	7427321	631	672	41	ACTCGTGG	60.656	20
30278	RIM04g133	7439449	7439722	273	293	20	CGTCAGGA	60.312	20
30296	RIM04g134	7504535	7505441	906	926	20	TTTGTTCA	58.044	20
30309	RIM04g135	7541845	7543033	1188	1214	26	CAAGGACA	60.149	20
30320	RIM04g136	3750083	3750240	157	178	21	CCATGTGA	59.105	20
30406	RIM04g144	1475853	1476038	185	219	34	GTCAGGT	60.489	20
30419	RIM04g145	19779669	19779881	212	181	31	GCTTGTTC	60.807	20
30467	RIM04g155	8451877	8454840	2963	2988	25	CCGCCTTA	60.635	21
30478	RIM04g156	8524094	8526684	2590	2768	178	AGAAGGC	61.091	19
30514	RIM04g160	7351013	7351231	218	158	60	TTTCACATA	60.096	20
30621	RIM04g169	3173956	3174222	266	287	21	GTTGTGCG	60.577	20
30642	RIM04g170	9345552	9346773	1221	1198	23	TAACATTG	60.014	20
30669	RIM04g173	2647510	2648496	986	1029	43	GGGTGCAA	59.933	20
30691	RIM04g174	17120063	17120650	587	669	82	CAACATCG	60.263	20
30702	RIM04g175	9595252	9595638	386	360	26	CGAATCAT	60.036	20
30715	RIM04g176	17120063	17120650	587	669	82	CAACATCG	60.263	20
30772	RIM04g181	2196564	2198428	1864	1699	165	CGACTGGT	60.277	20
30777	RIM04g181	2990762	2991368	606	585	21	CAAGGCTA	59.83	20
31002	RIM04g198	11076796	11077044	248	222	26	AATTCATG	59.305	20
31007	RIM04g199	11088056	11088311	255	283	28	ACGTGGAT	59.997	20
31010	RIM04g199	9836576	9837221	645	706	61	TGATAATA	58.188	23
31040	RIM04g201	11214083	11215127	1044	1003	41	CGCGACGA	61.052	20

31055	RIM04g20	11265268	11267349	2081	1976	105	CGGCATTT	60.732	20	
31058	RIM04g20	11268435	11271157	2722	2825	103	GAGCCCA	59.463	21	
31062	RIM04g20	11272987	11273505	518	473	45	TTGAAGTT	58.9	20	
31076	RIM04g20	9911719	9911935	216	258	42	GATTTGG	59.934	20	
31095	RIM04g20	11452908	11454232	1324	1236	88	GGAAAAG	60.053	20	
31114	RIM04g20	11642172	11648816	6644	6761	117	CTCTTGCA	60.975	20	
31152	RIM04g21	11866761	11868952	2191	2163	28	TGTCTTTC	59.691	20	
31159	RIM04g21	11872855	11874481	1626	1655	29	AGCACTGT	60.205	20	
31165	RIM04g21	11887603	11888657	1054	1030	24	ACGGAGG	59.679	20	
31292	RIM04g22	12638484	12639815	1331	1367	36	CTATGCTG	59.449	20	
31302	RIM04g22	12654757	12655398	641	489	152	ATCCGTGA	60.218	20	
31307	RIM04g22	12657218	12658950	1732	1569	163	ATTTCAGG	60.103	20	
31308	RIM04g22	12660619	12661180	561	590	29	GTTCTCGC	62.908	18	
31314	RIM04g22	12663499	12664237	738	708	30	TTGGTAAA	58.637	24	
31396	RIM04g23	5825023	5825427	404	359	45	GACAAGT	59.992	20	
31472	RIM04g23	3750083	3750240	157	178	21	CCATGTGA	59.105	20	
31498	RIM04g23	13517389	13519934	2545	2493	52	GGTGCGA	59.939	20	
31536	RIM04g23	13690421	13691114	693	670	23	TCAAGCTC	59.701	20	
31569	RIM04g24	3750083	3750240	157	178	21	CCATGTGA	59.105	20	
31576	RIM04g24	13893646	13894475	829	805	24	ATGCTGC	59.886	19	
31588	RIM04g24	4548686	4548880	194	173	21	AATTCTGC	60.073	20	
31618	RIM04g24	4989583	4989750	167	197	30	CACCGGTT	60.796	20	
31635	RIM04g24	14049914	14050763	849	914	65	GCTTTGAA	60.578	20	
31651	RIM04g24	14084464	14085111	647	614	33	TGGCGATT	59.688	20	
31729	RIM04g25	14599997	14601050	1053	987	66	ACTCACTG	60.408	20	
31740	RIM04g25	14666882	14667984	1102	970	132	ACCTTCGA	59.918	19	
31786	RIM04g25	23014951	23015142	191	221	30	GACCGAT	61.27	19	
31812	RIM04g26	3750083	3750240	157	178	21	CCATGTGA	59.105	20	
31833	RIM04g26	3750083	3750240	157	178	21	CCATGTGA	59.105	20	
31860	RIM04g26	15526160	15527376	1216	1375	159	TTAGAGG	60.353	20	
31905	RIM04g26	15717402	15720349	2947	2923	24	CGACAAG	59.631	18	
31911	RIM04g26	15736081	15738282	2201	2232	31	TAGCTTAC	57.512	20	
31999	RIM04g27	16282247	16283042	795	764	31	CAAGCCA	58.651	20	
32075	RIM04g28	16581910	16583018	1108	1143	35	CTGTTGCT	60.397	20	
32116	RIM04g28	16776475	16777303	828	788	40	CAGTTTGC	58.626	20	
32126	RIM04g28	25160808	25161542	734	689	45	ACCCCTTA	59.757	20	
32200	RIM04g29	17036923	17037200	277	248	29	GGGAGCT	60.961	19	
32293	RIM04g29	17666484	17667065	581	603	22	CTCACCGT	59.978	20	
32342	RIM04g30	3750083	3750240	157	178	21	CCATGTGA	59.105	20	
32408	RIM04g31	18352831	18354034	1203	1248	45	CTGGAAC	60.042	20	
32409	RIM04g31	18354015	18355319	1304	1401	97	GATGGTG	59.837	20	
32469	RIM04g31	18531072	18532515	1443	1473	30	TCGTGCTC	60.175	20	
32476	RIM04g31	18560615	18562101	1486	1440	46	GATTTGAA	60.133	20	
32551	RIM04g32	19065668	19066086	418	456	38	CGTCCTAC	59.673	20	
32583	RIM04g32	19202477	19202927	450	424	26	CTTTTGAA	59.67	20	
32755	RIM04g33	20080258	20080636	378	232	146	GGCTCGC	58.823	20	
32800	RIM04g33	20229177	20230076	899	927	28	TTGTGACT	59.344	23	

32813	RIM04g33	20252434	20252907	473	498	25	GCCAACG	62.764	18
32821	RIM04g33	20277187	20277965	778	798	20	TTGCTAAC	59.464	20
32879	RIM04g34	20552298	20553099	801	836	35	GTACCTA	60.235	20
32911	RIM04g34	20702549	20703068	519	543	24	GGAGATT	59.546	23
32934	RIM04g34	20754275	20755634	1359	1443	84	GAAGCAG	59.47	20
32969	RIM04g34	1455375	1456447	1072	1153	81	AACGTGA	60.157	20
33003	RIM04g35	16524833	16525453	620	714	94	AACCATTG	59.374	20
33077	RIM04g35	21343373	21344361	988	1010	22	CATCTTCA	59.543	22
33197	RIM04g36	22038860	22040724	1864	1902	38	ATCTTCCT	60.073	20
33217	RIM04g36	22080630	22080810	180	203	23	GCGGCTG	60.454	19
33237	RIM04g37	22151153	22151869	716	736	20	CCAAGAT	60.924	20
33260	RIM04g37	22192377	22193471	1094	1068	26	CTTGCTGG	61.671	18
33374	RIM04g38	22701646	22705208	3562	3490	72	TCTGGAG	60.481	20
33523	RIM04g40	23676017	23676253	236	162	74	TCAGTTCC	60.242	21
33726	RIM04g41	24282818	24283328	510	347	163	CACATCA	59.415	20
33809	RIM04g41	24432044	24432832	788	819	31	ATCGGTTG	60.074	20
33817	RIM04g41	24436555	24437151	596	633	37	AATGTGA	60.924	20
33829	RIM04g41	24448525	24449225	700	764	64	GGGCGAT	59.61	20
33837	RIM04g41	11179099	11179380	281	427	146	TGAAGAA	59.989	20
33844	RIM04g41	5175286	5176218	932	800	132	GTGGCAC	61.296	19
33877	RIM04g41	24652829	24653847	1018	991	27	GCATGAA	60.263	20
33916	RIM04g42	24827317	24828055	738	781	43	ATCTGCCG	60.226	20
33918	RIM04g42	24828540	24828751	211	249	38	CGTGGTC	59.726	21
33977	RIM04g42	24983245	24983744	499	526	27	CGTTGCG	59.999	19
34041	RIM04g43	25277225	25278244	1019	1050	31	GAAATGC	60.081	20
34092	RIM04g43	25473563	25476483	2920	3069	149	CAATTGG	60.173	20
34142	RIM04g43	17028661	17029577	916	894	22	GACCTCG	60.574	18
34335	RIM04g45	26453740	26454734	994	933	61	AGAAACC	60.119	20
34342	RIM04g45	26463308	26463683	375	556	181	CCAAGAG	59.859	21
34553	RIM04g46	27420660	27422021	1361	1388	27	TCTACAAA	58.741	20
34599	RIM04g46	27609410	27609741	331	365	34	TGCACCA	60.027	20
34759	RIM04g48	28643066	28644184	1118	1094	24	CCAACGTT	60.291	20
34767	RIM04g48	28659686	28660241	555	531	24	CTGGGGC	60.096	19
34859	RIM04g49	12455531	12456861	1330	1383	53	TTATTCCT	58.978	20
34871	RIM04g49	29126083	29126868	785	750	35	CTCACTGT	59.603	20
34999	RIM04g50	18703977	18704364	387	420	33	CAAAAGT	59.719	20
35016	RIM04g50	29827273	29828116	843	707	136	AACGACC	60.393	19
35047	RIM04g51	30025350	30026991	1641	1781	140	CTGGGAC	60.277	20
35049	RIM04g51	30056853	30057251	398	474	76	GAGCTAC	59.593	19
35052	RIM04g51	30057835	30059730	1895	1866	29	TTTTTGTC	60.053	20
35260	RIM04g52	30838003	30838668	665	578	87	TGTGGTC	60.246	20
35273	RIM04g52	30850082	30850789	707	757	50	CGACCTCT	61.262	18
35274	RIM04g52	30850870	30853112	2242	2313	71	ATGGAGA	60.575	20
35337	RIM04g52	30988714	30989228	514	537	23	GCTCGCG	61.572	20
35413	RIM04g52	31220089	31220585	496	522	26	CGTTGCTT	59.904	20
35433	RIM04g52	31312609	31314735	2126	2071	55	ATCAAGG	60.517	20
35436	RIM04g52	31339616	31340490	874	894	20	GCACAGA	59.723	21

35576	RIM04g534	31635705	31637232	1527	1430	97	GTCCAGCG	60.209	20
35585	RIM04g534	31642247	31642512	265	233	32	GCAAGTTG	58.926	20
35623	RIM04g536	31810690	31812826	2136	1991	145	CCTCCAAG	59.335	18
35653	RIM04g538	31875019	31875847	828	851	23	GCTCCGAT	59.81	20
35674	RIM04g538	31896164	31896353	189	285	96	GGAAGGTA	59.993	20
35679	RIM04g538	31896164	31896353	189	285	96	GGAAGGTA	59.993	20
35719	RIM04g541	32055084	32055412	328	307	21	GCTGAGAA	59.867	20
35823	RIM04g547	3270514	3270687	173	210	37	AAGAACA	60.119	20
36029	RIM04g558	33069187	33070167	980	936	44	GCGACTG	58.525	20
36093	RIM04g561	33248314	33248555	241	217	24	GTCAAAGA	59.43	20
36117	RIM04g562	33346512	33348065	1553	1530	23	GCCTCCAC	60.538	20
36156	RIM04g564	33480349	33481077	728	770	42	GATACCCT	59.384	20
36434	RIM04g584	34602981	34604043	1062	1090	28	CGTCGAC	61.188	19
36454	RIM04g586	34708468	34709162	694	714	20	GTTCCACC	60.048	20
36456	RIM04g586	34709630	34709777	147	203	56	AGCAAACT	60.059	20
36459	RIM04g586	34710199	34710387	188	228	40	CGAGGAAA	59.55	20
36536	RIM04g593	35126124	35126490	366	395	29	TGCGAGCA	59.028	20
36545	RIM04g594	35160067	35160212	145	125	20	CAAGGAC	60.081	20
36656	RIM05g013	215431	216248	817	857	40	TGGGTATT	60.439	20
36721	RIM05g016	365404	365884	480	453	27	ACTCGGGA	60.073	20
36739	RIM05g017	437608	442775	5167	5140	27	CTATGACG	59.83	20
36753	RIM05g018	486965	487925	960	939	21	GGTCGCCA	60.255	20
36759	RIM05g019	514146	514968	822	802	20	CAATTTCA	59.933	20
36761	RIM05g019	530228	530923	695	636	59	GAGGAAC	59.345	18
36804	RIM05g020	22215458	22216278	820	787	33	TGAACAAT	60.103	21
36835	RIM05g022	712852	714394	1542	1517	25	CTCAACAT	59.44	20
36853	RIM05g024	852036	854524	2488	2449	39	GAGCACC	59.827	20
36944	RIM05g030	1142340	1142592	252	213	39	GTGTCGTC	60.69	20
36967	RIM05g030	9498475	9499024	549	521	28	CAGCATG	59.297	20
36989	RIM05g031	1241925	1242805	880	847	33	AAGGTGA	59.886	22
37022	RIM05g034	1431198	1433092	1894	1941	47	TAAATGGA	60.014	20
37104	RIM05g042	1932171	1932940	769	745	24	GCCGCCTC	60.377	19
37118	RIM05g043	2010455	2013737	3282	3364	82	CCTCATCT	60.408	20
37129	RIM05g045	2081397	2082053	656	598	58	TCCTCAAA	59.853	20
37165	RIM05g046	2207050	2208721	1671	1712	41	CGCTATGA	60.08	20
37188	RIM05g050	16374062	16374220	158	135	23	TCTTGTCC	58.568	20
37301	RIM05g056	2796843	2797118	275	299	24	AGATCCCT	60.596	20
37328	RIM05g057	2855981	2856423	442	413	29	CCAATGTT	60.119	20
37385	RIM05g061	3051152	3051760	608	643	35	CTCTCTCT	59.117	19
37400	RIM05g061	3055177	3055617	440	391	49	AAGCCTCC	60.243	20
37405	RIM05g061	3060375	3061139	764	831	67	AATGGCA	59.791	20
37418	RIM05g062	3154072	3154618	546	569	23	TCGTTACT	61.147	20
37427	RIM05g062	3204591	3205410	819	875	56	CCAAAGGA	59.864	20
37560	RIM05g067	3490152	3491192	1040	1081	41	CTCCGTAC	60.156	20
37571	RIM05g067	3548793	3549821	1028	948	80	GTAACTTG	60.602	20
37628	RIM05g070	3696419	3696942	523	583	60	GATGAGC	60.269	20
37673	RIM05g073	42511130	42511421	291	336	45	CACTCTCT	60.275	20

37675	RIM05g07	42511130	42511421	291	336	45	CACTCTCT	60.275	20
37679	RIM05g07	4076104	4077146	1042	990	52	AGCGAGC	61.393	20
37707	RIM05g07	4250889	4253253	2364	2396	32	TTAATCTT	60.439	20
37727	RIM05g07	4302220	4305264	3044	3080	36	GCCAGGG	60.195	20
37760	RIM05g08	4478542	4480360	1818	1732	86	ATGGCTG	61.529	20
37821	RIM05g08	4868154	4868997	843	876	33	GCCGAGT	61.66	18
37892	RIM05g09	15705015	15705496	481	516	35	ATTCACG	60.08	20
37963	RIM05g09	18319925	18320106	181	347	166	GCACTAG	59.985	20
37965	RIM05g09	7995976	7996433	457	531	74	TGGGTGT	59.924	20
38010	RIM05g10	16584395	16585159	764	709	55	GAGAGCT	61.212	20
38119	RIM05g10	6135516	6136114	598	639	41	AGCAGAG	60.656	18
38134	RIM05g11	6316828	6318361	1533	1553	20	ATGGCTCT	61.043	20
38247	RIM05g12	7140669	7141849	1180	1135	45	TCAACAAT	57.511	20
38290	RIM05g13	7462741	7463595	854	889	35	TATCCGG	60.991	20
38326	RIM05g13	7650932	7651689	757	789	32	AGGAGTA	60.096	20
38330	RIM05g13	7653812	7654451	639	673	34	CTAGTCGA	60.103	20
38336	RIM05g13	7732897	7733779	882	783	99	CAAGGGT	59.45	20
38344	RIM05g14	3750083	3750240	157	178	21	CCATGTGA	59.105	20
38414	RIM05g14	3750083	3750240	157	178	21	CCATGTGA	59.105	20
38516	RIM05g14	8440807	8444635	3828	3924	96	TCTGCAC	59.682	20
38717	RIM05g16	22829165	22831189	2024	2121	97	AGTCGAC	60.001	19
38840	RIM05g17	3750083	3750240	157	178	21	CCATGTGA	59.105	20
38880	RIM05g17	9811820	9812238	418	379	39	GAAGCCC	59.324	20
38972	RIM05g17	10313703	10315212	1509	1560	51	ACGCAGA	59.982	20
39041	RIM05g18	1457616	1457973	357	336	21	CAGCCGA	61.188	18
39050	RIM05g18	3750083	3750240	157	178	21	CCATGTGA	59.105	20
39164	RIM05g19	21003752	21005222	1470	1501	31	GCTGCTA	60.326	18
39199	RIM05g19	11595896	11596269	373	270	103	GTCCGAC	59.788	19
39218	RIM05g19	27446821	27447045	224	364	140	GGCTACG	60.199	20
39279	RIM05g20	12141981	12142088	107	135	28	GAAGAAC	59.997	20
39302	RIM05g20	15594516	15595076	560	370	190	GAGGATG	60.189	20
39331	RIM05g21	12421203	12421550	347	389	42	CGCCGAA	60.096	20
39354	RIM05g21	15594769	15595134	365	175	190	CTTGAAGT	58.957	20
39539	RIM05g23	13566636	13567290	654	687	33	TCTGGTGA	59.705	20
39573	RIM05g23	13678080	13678671	591	565	26	GACCGCGT	59.934	19
39598	RIM05g23	13722408	13723587	1179	1023	156	CCAGCAG	60.175	20
39637	RIM05g24	19753553	19755059	1506	1533	27	GCCAGTT	60.081	20
39663	RIM05g24	13993429	13994208	779	826	47	GCTCAGC	59.874	20
39748	RIM05g24	14354624	14355304	680	700	20	ATTCGAG	59.985	20
39751	RIM05g24	14473375	14474649	1274	1325	51	CGCTTCTT	61.316	20
39773	RIM05g25	14418408	14418567	159	240	81	TAACCAAA	60.701	20
39787	RIM05g25	14455150	14456253	1103	1136	33	GGGTGAT	58.85	21
39843	RIM05g25	14693284	14695487	2203	2390	187	AGATCTCA	58.719	20
39868	RIM05g25	14822288	14822508	220	261	41	GCATCATG	60.066	20
39881	RIM05g25	14892319	14894847	2528	2504	24	GACATCCT	60.181	20
39904	RIM05g25	14989620	14991798	2178	2223	45	CCAGAGC	59.942	18
39924	RIM05g26	15079004	15080846	1842	1888	46	GATACTC	60.599	20

39932	RIM05g26	15085530	15086285	755	896	141	CGGTACCT	59.891	20
39976	RIM05g26	13015732	13016772	1040	958	82	TGCGTGCA	59.694	20
40000	RIM05g26	3406424	3406589	165	210	45	AGGATTT	60.853	20
40097	RIM05g27	1455345	1455875	530	590	60	AACGAGCT	59.875	20
40116	RIM05g27	16172095	16172640	545	719	174	GGAAGGA	60.293	20
40160	RIM05g28	16494999	16496063	1064	1094	30	GAGCTCGA	60.636	20
40183	RIM05g28	16516532	16519163	2631	2584	47	AAAGGCTT	59.63	20
40184	RIM05g28	16519267	16519501	234	259	25	CTCACAGA	60.408	20
40186	RIM05g28	16527061	16528077	1016	930	86	TAAAAGG	59.968	20
40405	RIM05g30	17472408	17472820	412	381	31	TGAAGATA	59.435	21
40429	RIM05g30	17506971	17508967	1996	2019	23	TCTAAAGG	59.985	20
40442	RIM05g30	17524088	17524899	811	851	40	AGCTGTTT	60.11	20
40481	RIM05g30	17810728	17812289	1561	1530	31	GCTGGCTT	59.997	20
40532	RIM05g31	17995167	17995448	281	352	71	CTGAACAG	59.758	20
40548	RIM05g31	24750423	24750575	152	126	26	GAGCGTA	60.022	20
40611	RIM05g31	18492980	18493878	898	1028	130	ATGAACTG	59.927	20
40683	RIM05g32	17120063	17120650	587	669	82	CAACATCG	60.263	20
40703	RIM05g32	18834026	18834550	524	552	28	GCTATTTA	59.95	20
40710	RIM05g32	18840930	18842721	1791	1766	25	ATGGCAC	59.925	20
40711	RIM05g32	18843010	18843740	730	709	21	TGCTATTG	58.62	24
40798	RIM05g32	11702623	11702960	337	376	39	CTGAGAG	59.785	20
40811	RIM05g32	19118700	19119504	804	829	25	GATGAAT	59.488	20
40814	RIM05g32	19141205	19142011	806	865	59	CCAAGCA	59.846	20
40863	RIM05g33	19353313	19354128	815	682	133	ATTTCCCT	60.208	20
40877	RIM05g33	19408842	19409146	304	280	24	ATCGGCA	60.257	20
40882	RIM05g33	19418480	19418848	368	455	87	GGGCCAT	60.492	20
40918	RIM05g33	19710077	19711084	1007	877	130	AACTTCGG	60.434	20
40926	RIM05g33	19716492	19717039	547	484	63	CGAACAC	59.691	20
40930	RIM05g33	19771763	19772244	481	457	24	AGGGAGA	60.878	18
40936	RIM05g33	2507587	2507898	311	336	25	TGACTTGG	59.967	20
40945	RIM05g33	19865174	19867396	2222	2144	78	TGGAAGTT	59.42	21
40987	RIM05g34	16042143	16042309	166	237	71	TGGGAGA	60.218	20
41021	RIM05g34	20317308	20317623	315	337	22	TTGCGAAA	59.697	20
41047	RIM05g34	20400835	20402978	2143	2169	26	TGGTCACT	59.893	20
41066	RIM05g34	20444758	20445468	710	902	192	GTGGGCTA	59.699	20
41075	RIM05g34	20526684	20527045	361	388	27	CTCCTCGT	59.648	20
41091	RIM05g34	20568571	20569383	812	845	33	CCAACAAG	60.152	20
41101	RIM05g34	20585324	20585795	471	497	26	CATGTTCA	59.823	20
41141	RIM05g35	13684899	13686453	1554	1749	195	AGATGAA	59.923	20
41145	RIM05g35	20870362	20871350	988	1024	36	GCCGGACA	60.538	20
41387	RIM05g38	22293684	22294901	1217	1326	109	GTGCTGTT	60.299	20
41393	RIM05g38	22321941	22323472	1531	1496	35	CTACTCCA	59.721	20
41453	RIM05g38	22534056	22534841	785	591	194	CTTCGTGG	60.247	19
41528	RIM05g39	22870625	22872211	1586	1630	44	GATGGAG	60.457	20
41538	RIM05g39	22926902	22928169	1267	1243	24	TCTTGCTT	59.992	20
41556	RIM05g39	22949063	22950111	1048	1011	37	CTCGTCTG	62.729	18
41562	RIM05g39	10724109	10725537	1428	1470	42	TCGTTTTG	60.052	20

41596	RIM05g39	3750083	3750240	157	178	21	CCATGTGA	59.105	20
41673	RIM05g40	23570363	23570691	328	355	27	CCTCAAGG	61.188	18
41674	RIM05g40	23570747	23570935	188	267	79	TCATCGAC	61.208	20
41695	RIM05g40	23594730	23594913	183	222	39	TAACTTCA	60.766	20
41698	RIM05g40	23595493	23596103	610	658	48	TTCCATCG	60.044	20
41709	RIM05g40	23666429	23674382	7953	7898	55	TTCCACAA	60.232	20
41822	RIM05g41	24136399	24136574	175	201	26	TGGAAAAT	59.199	21
41871	RIM05g41	24253140	24253682	542	565	23	GTGCTCGT	59.997	20
41886	RIM05g41	24308826	24310982	2156	2116	40	GGTTCTTG	59.957	20
41912	RIM05g41	24418489	24418757	268	246	22	CTCTCCTC	60.489	20
42000	RIM05g42	3750083	3750240	157	178	21	CCATGTGA	59.105	20
42103	RIM05g43	25174713	25174893	180	204	24	GCTGTCAG	59.795	21
42192	RIM05g43	25502706	25503130	424	564	140	CGGCGACA	59.846	19
42258	RIM05g44	25737882	25739062	1180	1158	22	CATTTCAG	58.048	20
42270	RIM05g44	12842983	12843641	658	679	21	GTTGAGG	59.31	20
42320	RIM05g44	26042226	26043050	824	853	29	AGATCGTG	58.845	20
42437	RIM05g45	17104504	17105355	851	814	37	CAGATCTG	61.749	18
42781	RIM05g47	27255646	27257070	1424	1389	35	TACCACCA	62.851	18
42793	RIM05g47	27291696	27294149	2453	2271	182	AAGAACGA	59.137	20
42839	RIM05g48	27494725	27495242	517	567	50	GCTTTTTG	58.961	20
42866	RIM05g48	27564073	27564647	574	614	40	TGCTCAAG	60.887	20
42898	RIM05g48	27604796	27605892	1096	1117	21	CCTTCACC	59.526	20
42904	RIM05g48	27616804	27619594	2790	2820	30	AGATAGCA	60.277	20
42974	RIM05g48	27881631	27882541	910	884	26	GCTCCTTT	60.549	19
43090	RIM05g49	28228756	28230162	1406	1460	54	GTGAGTG	59.943	20
43091	RIM05g49	28234123	28234444	321	343	22	AGCCTCGT	60.428	20
43098	RIM05g49	28273989	28274653	664	620	44	ACGGTGGA	59.997	20
43113	RIM05g49	28329638	28330716	1078	1054	24	TCCGCGTT	61.008	20
43133	RIM05g49	28338160	28338648	488	565	77	ACATACTG	59.975	18
43152	RIM05g49	16346147	16346855	708	747	39	ACCACCTC	59.153	20
43336	RIM05g50	3750083	3750240	157	178	21	CCATGTGA	59.105	20
43409	RIM05g51	29409972	29410161	189	169	20	CTCGGTTT	60.386	20
43413	RIM05g51	29420167	29421073	906	739	167	GGGCTACA	59.947	21
43523	RIM06g01	167178	171143	3965	3872	93	GCTTTGGG	60.038	20
43527	RIM06g01	179478	179971	493	516	23	GATTCAAC	59.697	20
43618	RIM06g01	358959	359500	541	505	36	CATCATCA	59.816	20
43708	RIM06g02	587355	588023	668	697	29	CTGGAACT	60.178	20
43742	RIM06g02	695626	696693	1067	1017	50	AAGTCTCA	59.505	20
43855	RIM06g03	700434	700655	221	161	60	GGCCTGAT	60.066	20
43864	RIM06g03	17035652	17038662	3010	2900	110	GCCAGTTC	60.418	20
44230	RIM06g05	2582264	2582479	215	170	45	GGATCCAA	60.662	20
44249	RIM06g05	2659266	2659889	623	694	71	TTGCGTTT	59.708	20
44356	RIM06g06	2994991	2996571	1580	1556	24	GCCCTCAT	61.152	18
44369	RIM06g06	3043854	3044506	652	676	24	AGGCGGAT	59.645	20
44496	RIM06g07	3503185	3505614	2429	2320	109	GTGAGGA	60.277	20
44497	RIM06g07	3505594	3506670	1076	1178	102	AAAAGTTG	59.538	22
44502	RIM06g07	3512297	3513012	715	738	23	GGCCAATC	60.124	21

44545	RIM06g07	33435791	33436044	253	174	79	TCCATTGA	59.369	20
44560	RIM06g07	3778685	3779695	1010	974	36	AACCGAA	60.291	20
44681	RIM06g08	4250233	4251358	1125	990	135	CGTTGTG	59.984	20
44689	RIM06g08	4255152	4255992	840	863	23	TTACGATC	59.499	20
44714	RIM06g08	4320935	4321832	897	764	133	AAGAGCG	60.453	20
44719	RIM06g08	4362001	4363057	1056	1087	31	TGGATCTG	60.028	18
44720	RIM06g08	4363028	4363531	503	461	42	GAGCAAC	59.844	20
44781	RIM06g09	4611871	4612617	746	712	34	ACGCGCA	60.74	20
44828	RIM06g09	4867993	4868893	900	923	23	GCATTTCG	60.207	19
44882	RIM06g10	5237079	5238806	1727	1769	42	AGGTGGA	59.474	20
44911	RIM06g10	11482642	11483550	908	799	109	GAGCTAG	59.947	20
44913	RIM06g10	3750083	3750240	157	178	21	CCATGTGA	59.105	20
44992	RIM06g10	5621819	5623596	1777	1797	20	GGGAGGT	59.817	20
45073	RIM06g11	6158219	6158385	166	198	32	GAATCAG	59.245	20
45092	RIM06g11	3750083	3750240	157	178	21	CCATGTGA	59.105	20
45105	RIM06g11	6372906	6374099	1193	1365	172	CGTCAACA	59.777	18
45219	RIM06g12	7084311	7086858	2547	2606	59	GAGATGG	59.952	20
45221	RIM06g12	7096596	7097460	864	820	44	TGGATTC	60.042	20
45239	RIM06g13	7247240	7248256	1016	890	126	GACCGCTA	60.542	20
45243	RIM06g13	7259758	7261706	1948	2004	56	TCCGCTC	59.703	20
45258	RIM06g13	7334064	7334442	378	214	164	AGTTCCTG	59.844	20
45277	RIM06g13	7459972	7460352	380	403	23	AATTTCAC	57.003	24
45279	RIM06g13	7487866	7488901	1035	1008	27	GCGGAGG	59.597	20
45311	RIM06g13	7585789	7589390	3601	3625	24	TTCTTTCC	60.038	20
45358	RIM06g13	9216016	9216538	522	478	44	TGCAAGA	60.195	20
45359	RIM06g13	7739531	7740085	554	577	23	CGAAGAG	58.903	20
45362	RIM06g13	7785647	7786041	394	450	56	TTCCCTAC	60.538	20
45423	RIM06g14	8142580	8143379	799	771	28	GTGATCAA	60.272	19
45498	RIM06g14	8312659	8313049	390	368	22	AGCAAGG	60.111	20
45509	RIM06g14	8414061	8415712	1651	1736	85	ACCCCCTC	60.015	20
45520	RIM06g14	8235651	8236617	966	1052	86	GCGTCTA	60.721	20
45535	RIM06g15	8723652	8724324	672	703	31	TCAGGAC	60.036	20
45542	RIM06g15	8739473	8741954	2481	2400	81	CTCGTCCA	60.146	19
45547	RIM06g15	8782594	8784049	1455	1427	28	CAAAGGTT	59.852	22
45561	RIM06g15	8873130	8873788	658	682	24	ACACGTG	60.576	18
45590	RIM06g15	3750083	3750240	157	178	21	CCATGTGA	59.105	20
45610	RIM06g15	9094661	9094957	296	271	25	ATATTTGG	59.962	20
45616	RIM06g16	9117895	9119877	1982	2002	20	GGGCTGG	59.41	20
45617	RIM06g16	9120064	9121580	1516	1585	69	ACCAGCA	59.467	20
45687	RIM06g16	3750083	3750240	157	178	21	CCATGTGA	59.105	20
45693	RIM06g16	3750083	3750240	157	178	21	CCATGTGA	59.105	20
45736	RIM06g16	3750083	3750240	157	178	21	CCATGTGA	59.105	20
45839	RIM06g18	9611846	9614321	2475	2371	104	TCGAAATT	59.79	23
45845	RIM06g18	4326639	4327687	1048	943	105	GCACTGG	60.52	20
45847	RIM06g18	3750083	3750240	157	178	21	CCATGTGA	59.105	20
45853	RIM06g18	10684956	10688184	3228	3248	20	GGAGCTT	60.012	20
45865	RIM06g18	33435791	33436044	253	174	79	TCCATTGA	59.369	20

45937	RIM06g19	11211137	11211604	467	487	20	CCTGAGGA	59.284	22
46105	RIM06g20	11760601	11760980	379	311	68	GGGCAATT	60.129	20
46142	RIM06g21	20962839	20962996	157	183	26	ACCTCGAG	60.096	20
46143	RIM06g21	1458355	1458523	168	188	20	ACGAAGAA	59.993	20
46151	RIM06g21	12217000	12219282	2282	2476	194	CCCGTCAC	59.813	20
46261	RIM06g21	33435791	33436044	253	174	79	TCCATTGA	59.369	20
46266	RIM06g21	12571640	12572676	1036	913	123	GCAAGGG	60.883	20
46278	RIM06g21	12572294	12572676	382	273	109	ACGTGTTC	60.009	20
46335	RIM06g22	12838623	12840107	1484	1564	80	ATACAAGC	60.183	20
46349	RIM06g22	12905742	12905923	181	224	43	CAAGGAA	60.309	20
46374	RIM06g22	12989242	12989509	267	223	44	CCAGATGT	59.55	20
46400	RIM06g22	13166229	13167802	1573	1553	20	GCAGAGG	60.854	20
46425	RIM06g22	13386731	13388833	2102	2032	70	CGACGGCT	59.781	20
46438	RIM06g23	13440078	13440249	171	195	24	GATGGAAA	59.62	19
46452	RIM06g23	13487443	13489440	1997	1934	63	AGGAGCA	59.405	20
46465	RIM06g23	13538329	13539374	1045	1078	33	CTGCGATG	62.816	19
46532	RIM06g23	13894996	13896316	1320	1344	24	CATCGTCA	60.105	19
46535	RIM06g23	13948852	13949886	1034	1006	28	CGTCACCG	60.104	19
46544	RIM06g23	13975623	13976378	755	707	48	GACCCTCG	59.965	19
46588	RIM06g24	14228489	14229744	1255	1220	35	AGTAGGG	61.238	18
46591	RIM06g24	14265142	14268884	3742	3702	40	GCAATCAG	60.066	20
46605	RIM06g24	11526812	11527165	353	327	26	CCTTTGCG	59.741	20
46634	RIM06g24	5950515	5950633	118	145	27	ACCGATG	60.317	20
46636	RIM06g24	4466877	4467437	560	634	74	GGGACCA	60.689	20
46725	RIM06g25	14929753	14930062	309	222	87	ATCGGGGT	59.813	20
46812	RIM06g26	15293548	15294112	564	523	41	GGGAGAG	60.16	18
46906	RIM06g27	15742651	15742990	339	318	21	TGTTGGTC	60.088	20
46916	RIM06g27	3750083	3750240	157	178	21	CCATGTGA	59.105	20
46925	RIM06g27	17144051	17145697	1646	1593	53	AAGATCAA	59.966	20
46965	RIM06g28	16127629	16127867	238	204	34	GGCTCTAG	60.386	20
46980	RIM06g28	16141132	16141352	220	178	42	TGCTCCCG	58.771	20
47075	RIM06g29	16676078	16678977	2899	2848	51	GCTTGCAT	60.686	18
47134	RIM06g29	16790391	16791812	1421	1387	34	GGCATCTG	59.992	21
47150	RIM06g29	8104048	8104379	331	359	28	TGACTTCT	59.648	20
47162	RIM06g29	14606113	14606511	398	432	34	ATGAAGC	59.723	20
47261	RIM06g30	33433793	33434121	328	294	34	CCGATTTG	60.044	20
47274	RIM06g30	17434198	17436268	2070	1954	116	TCAAACAG	57.487	22
47280	RIM06g30	8102411	8103329	918	1028	110	ATACCACA	60.103	20
47357	RIM06g30	3750083	3750240	157	178	21	CCATGTGA	59.105	20
47369	RIM06g30	17774528	17776547	2019	2046	27	CAAAATTT	59.013	20
47400	RIM06g31	876894	878015	1121	1039	82	TGTATTAA	59.64	20
47447	RIM06g31	17727071	17727676	605	548	57	AAGAGAGA	58.718	20
47466	RIM06g31	1327945	1328366	421	481	60	TTGTTCGT	60.074	20
47510	RIM06g32	1457616	1457973	357	336	21	CAGCCGA	61.188	18
47518	RIM06g32	42511130	42511421	291	336	45	CACTCTCT	60.275	20
47524	RIM06g32	15308462	15308921	459	438	21	AAGAGTTT	59.993	20
47546	RIM06g32	18996805	18997044	239	406	167	CAAAACTA	60.132	20

47608	RIM06g33	9563001	9563386	385	312	73	GGTTCAT	60.05	20
47632	RIM06g331	3750083	3750240	157	178	21	CCATGTGA	59.105	20
47654	RIM06g332	19383387	19383812	425	393	32	AGTTAACT	61.052	20
47726	RIM06g341	19853152	19855471	2319	2183	136	GAGAAGGA	60.215	19
47745	RIM06g343	19958691	19959417	726	758	32	TACGGAGA	59.916	20
47856	RIM06g352	20549697	20549851	154	98	56	CATTGGAA	59.518	20
47926	RIM06g359	20940480	20942010	1530	1564	34	CTCAAGG	60.863	18
47960	RIM06g361	21162701	21165716	3015	3074	59	CCAAGAA	59.869	20
47973	RIM06g362	21207447	21210965	3518	3468	50	GCTATGGA	59.976	21
47983	RIM06g364	11441452	11442872	1420	1519	99	AACTATGT	60.975	20
48028	RIM06g36	10458550	10458834	284	325	41	GGCATGAA	60.014	20
48033	RIM06g36	37257576	37257965	389	347	42	TGAAGGC	59.872	20
48200	RIM06g38	22497250	22497524	274	254	20	TGGCCAAT	60.214	20
48224	RIM06g383	22698452	22699022	570	629	59	GTACACCT	60.179	19
48276	RIM06g388	23054448	23055198	750	724	26	CTGTTGGT	59.135	20
48313	RIM06g391	2647510	2648157	647	707	60	AGAACCGA	59.978	20
48410	RIM06g398	23686438	23686824	386	352	34	GAAGATGA	60.426	20
48431	RIM06g399	391157	393192	2035	1996	39	CAAAACT	58.934	20
48536	RIM06g40	7630175	7630606	431	462	31	CGTTGCA	60.209	20
48565	RIM06g407	24311198	24311788	590	622	32	TGTGTTGT	58.09	21
48566	RIM06g407	24311828	24313924	2096	1916	180	CACCAAG	59.389	20
48603	RIM06g411	24573902	24575279	1377	1558	181	CCTTCGAT	61.115	20
48622	RIM06g412	24683398	24684966	1568	1594	26	GGTTATC	59.794	19
48671	RIM06g418	25117333	25119023	1690	1528	162	AGAACCA	60.299	20
48698	RIM06g419	25158442	25162456	4014	3891	123	GTCACCAA	61.146	20
48750	RIM06g423	14081542	14081772	230	253	23	TAATGGC	60.088	20
48795	RIM06g427	25683573	25683970	397	366	31	CTCAACCA	60.461	20
48820	RIM06g43	25834665	25835672	1007	1037	30	ACTCTCGG	60.615	20
48834	RIM06g431	25933360	25933765	405	369	36	GCGTCTCA	60.119	20
48840	RIM06g431	25941609	25941788	179	155	24	TTCCACAA	60.073	20
48843	RIM06g432	25988042	25988436	394	338	56	GTATCCTA	59.866	20
48857	RIM06g432	908884	909096	212	252	40	AAGCTTGT	59.539	24
48897	RIM06g43	26284347	26287196	2849	2828	21	AGAATTGA	58.253	21
48991	RIM06g44	26533959	26535345	1386	1256	130	CACAACTA	58.468	20
49036	RIM06g442	2442093	2442528	435	390	45	TCACCCAG	59.924	20
49043	RIM06g443	26739105	26740783	1678	1699	21	CCTTCCAG	59.393	20
49067	RIM06g444	26834016	26834539	523	583	60	AGCAACGT	60.001	19
49074	RIM06g44	26936632	26939425	2793	2717	76	ATAGCCTG	60.36	20
49150	RIM06g45	27231381	27231611	230	146	84	AGCACTGT	60.056	20
49183	RIM06g453	27435095	27436223	1128	993	135	AGTCCCA	60.395	20
49205	RIM06g454	27466866	27467114	248	228	20	CAGAGGAT	57.778	21
49241	RIM06g457	11719590	11720683	1093	1136	43	CCGACAAA	61.176	20
49351	RIM06g462	28009436	28010111	675	704	29	CTGCAGCA	59.133	21
49361	RIM06g463	28102195	28103220	1025	995	30	GGCCAGAA	60.142	20
49382	RIM06g463	28144257	28144800	543	597	54	GTAATTA	57.012	24
49395	RIM06g465	28242256	28243546	1290	1318	28	GACCGCG	60.346	19
49461	RIM06g471	2506873	2507034	161	108	53	CTTGGGCA	59.864	20

49462	RIM06g47	28616822	28617960	1138	1163	25	CAACATCA	60.112	20
49511	RIM06g47	28691997	28692529	532	380	152	CAAAGCT	59.512	20
49513	RIM06g47	28695564	28697016	1452	1486	34	AGATCCT	59.258	20
49561	RIM06g47	4841203	4841747	544	409	135	TATTGTTC	59.924	20
49721	RIM06g49	29696443	29699919	3476	3376	100	TAACCGAT	60.146	20
49882	RIM06g49	30125269	30125701	432	618	186	GTGGAGAT	59.933	20
49929	RIM06g50	30408033	30409763	1730	1751	21	GCCCAAG	59.818	19
50055	RIM06g51	30958553	30959267	714	748	34	ACAAGATT	59.962	20
50056	RIM06g51	30959248	30959641	393	416	23	GCCTCTAC	59.694	20
50057	RIM06g51	30959634	30960366	732	690	42	TTTGCCAA	59.849	20
50061	RIM06g51	30961167	30961381	214	191	23	GAGGAGTT	60.238	20
50066	RIM06g51	30966533	30966826	293	233	60	TGTTCGG	60.636	20
50083	RIM06g51	30969530	30969739	209	183	26	CATGCGT	61.75	19
50087	RIM06g51	30996899	30999409	2510	2489	21	CCCAACC	59.926	20
50096	RIM06g51	31016764	31017223	459	483	24	TATCGCAC	60.366	20
50127	RIM06g51	22632637	22633143	506	529	23	AGCTGCTT	59.745	20
50133	RIM06g51	31118170	31118405	235	257	22	GCATGTGT	59.42	20
50204	RIM07g01	35705	39113	3408	3443	35	GTCCTCT	59.783	19
50212	RIM07g01	78061	78492	431	288	143	CCCATTGA	60.096	20
50260	RIM07g01	259429	261001	1572	1727	155	AACTTCAC	61.019	20
50267	RIM07g01	23958490	23960119	1629	1579	50	CAGACAG	60.063	19
50302	RIM07g01	537099	538357	1258	1231	27	GTCGGAC	60.52	19
50319	RIM07g01	577809	578498	689	725	36	ACAAGCAT	59.727	20
50359	RIM07g02	6799533	6799588	55	158	103	GAGCAAA	59.82	20
50424	RIM07g03	1299133	1300238	1105	1081	24	ACAAGGC	60.142	20
50426	RIM07g03	1300492	1302275	1783	1639	144	AGGACCT	60.274	20
50434	RIM07g03	1273137	1273763	626	567	59	ATCTTCTT	59.284	20
50443	RIM07g03	1273137	1273763	626	567	59	ATCTTCTT	59.284	20
50469	RIM07g03	1566048	1570244	4196	4227	31	GTCGCAG	61.041	18
50669	RIM07g05	2543984	2544190	206	182	24	CTGGATC	60.426	20
50690	RIM07g05	2696297	2696568	271	435	164	GATGAGG	59.297	20
50814	RIM07g06	3253493	3253659	166	195	29	TCTTCACC	58.342	20
50817	RIM07g06	3258737	3260672	1935	1975	40	ACTCCAAG	60.393	19
50833	RIM07g06	3325540	3326325	785	765	20	TTCAAGAT	59.795	20
50997	RIM07g07	3871418	3872585	1167	1048	119	CTCACCT	59.962	20
51020	RIM07g07	3987631	3989319	1688	1554	134	TCTGTCAT	60.146	20
51075	RIM07g08	4199550	4199877	327	358	31	ACCACCT	60.69	20
51086	RIM07g08	4263308	4264268	960	980	20	GCTTGACT	60.386	20
51164	RIM07g08	4547872	4548927	1055	1078	23	TGAAGGG	59.958	21
51178	RIM07g08	4584254	4584464	210	242	32	GTCTTGC	60.205	18
51192	RIM07g08	4641666	4643020	1354	1318	36	AGGCTCC	60.402	19
51263	RIM07g09	4914709	4914926	217	197	20	CACTGTC	60.534	19
51361	RIM07g09	1463910	1464565	655	679	24	AGGTTTA	59.845	20
51491	RIM07g10	5768631	5769037	406	366	40	CCTCCTCG	60.634	20
51635	RIM07g11	4242662	4244006	1344	1313	31	TTGTTGGA	60.139	21
51687	RIM07g12	6810554	6810917	363	403	40	CCAAATG	59.285	20
51749	RIM07g12	7309668	7310505	837	866	29	ACGCTCTA	60.187	20

51766	RIM07g128	7368257	7368558	301	474	173	CAATTGAA	59	23
51840	RIM07g131	10095133	10095630	497	426	71	CTTTCGAC	60.291	20
51853	RIM07g133	7652279	7652771	492	528	36	CGTATCTT	60.288	20
51856	RIM07g133	4841203	4841747	544	409	135	TATTGTTC	59.924	20
51927	RIM07g137	7873531	7874605	1074	995	79	CGACATGA	60.272	20
51990	RIM07g143	14179526	14179755	229	122	107	ATGGCGA	59.96	20
52015	RIM07g146	8351535	8353509	1974	1933	41	AAGGAGG	61.363	18
52077	RIM07g151	8666343	8667421	1078	1139	61	TGGGCTT	59.953	20
52089	RIM07g152	8797581	8797724	143	199	56	CATATTTG	59.84	20
52139	RIM07g156	9098520	9099319	799	837	38	GGAAGCT	59.094	20
52157	RIM07g157	9139402	9139585	183	282	99	GGCAAGG	59.845	20
52172	RIM07g158	9206215	9207350	1135	1166	31	ACTCTCTT	59.492	20
52179	RIM07g158	9209701	9209995	294	163	131	TTCCTAAA	59.948	20
52185	RIM07g159	9253384	9254712	1328	1302	26	GGCACCG	60.464	20
52215	RIM07g161	9401525	9402196	671	777	106	TATGGATG	59.305	20
52228	RIM07g164	12260098	12261343	1245	1280	35	ACTGTCAC	61.501	18
52278	RIM07g168	3751593	3754381	2788	2949	161	AGACACC	60.711	20
52280	RIM07g168	3750083	3750240	157	178	21	CCATGTGA	59.105	20
52286	RIM07g168	9881149	9881396	247	312	65	GTGCCGTT	60.074	20
52305	RIM07g171	10065792	10066570	778	581	197	GCTGGTGA	59.836	20
52314	RIM07g172	13854763	13855480	717	811	94	TTCACCTT	59.415	20
52332	RIM07g174	14654286	14656081	1795	1744	51	ACCAAGCA	59.745	20
52338	RIM07g174	10298287	10298943	656	679	23	CGAGGAC	59.837	20
52340	RIM07g175	3750083	3750240	157	178	21	CCATGTGA	59.105	20
52422	RIM07g181	10733858	10734295	437	414	23	TGGTGGA	60.656	20
52442	RIM07g182	3750083	3750240	157	178	21	CCATGTGA	59.105	20
52463	RIM07g183	10894024	10894231	207	131	76	GTCCATGG	59.75	18
52491	RIM07g187	11073263	11073873	610	672	62	TCCTGAAG	59.697	20
52494	RIM07g187	11107140	11107443	303	340	37	ATGAAGG	60.226	20
52495	RIM07g187	11107852	11108350	498	520	22	TGATGTAG	60.423	20
52517	RIM07g188	11175459	11180380	4921	4859	62	ACGGTGT	60.14	20
52559	RIM07g192	11404693	11405244	551	583	32	CATTTTCC	59.77	21
52560	RIM07g192	13684899	13687577	2678	2821	143	AAGCCGA	60.132	20
52575	RIM07g194	11502360	11503398	1038	1120	82	GAGGAAC	60.386	20
52595	RIM07g201	11646432	11647277	845	881	36	GCACTTCT	59.428	23
52638	RIM07g206	5960182	5960648	466	488	22	AGACGAA	59.834	20
52738	RIM07g223	8102564	8103681	1117	1211	94	CATGTTGC	60.119	20
52770	RIM07g225	12711229	12712235	1006	983	23	AATCGTGC	60.255	20
52832	RIM07g231	13031518	13031716	198	171	27	GCTTGAGA	59.763	22
52853	RIM07g232	13098233	13102271	4038	4068	30	GGAGAGG	59.534	20
52861	RIM07g233	3750083	3750240	157	178	21	CCATGTGA	59.105	20
52867	RIM07g233	3747489	3748028	539	613	74	CGAAGAA	60.006	20
52871	RIM07g234	13218871	13222285	3414	3544	130	TTTCAAAA	60.181	20
52889	RIM07g235	13314171	13315224	1053	1088	35	CAGGACA	59.691	20
52941	RIM07g238	13496512	13499228	2716	2739	23	AATGTTGG	60.111	20
53052	RIM07g244	13921026	13921678	652	730	78	ATGAAGG	60.569	20
53192	RIM07g254	14601619	14603422	1803	1744	59	CAACAGG	60.647	20

53203	RIM07g25	14657773	14659241	1468	1411	57	CGAACTCA	60.269	20
53347	RIM07g26	15344046	15346248	2202	2255	53	TGCATCCG	59.799	20
53351	RIM07g26	15346727	15347765	1038	1004	34	GATTGCTT	59.805	20
53358	RIM07g26	15358609	15358813	204	179	25	GTGTACA	60.721	20
53361	RIM07g26	15358609	15358813	204	179	25	GTGTACA	60.721	20
53363	RIM07g26	8944300	8944502	202	97	105	TACACCGT	59.787	18
53379	RIM07g26	15488091	15488257	166	111	55	CTGCTCCG	60.125	20
53421	RIM07g27	16963230	16963538	308	333	25	CGTGTGAT	59.918	20
53469	RIM07g27	15883769	15884385	616	661	45	CCAGATC	62.875	18
53485	RIM07g27	15914754	15915129	375	354	21	AAACCAT	59.933	20
53498	RIM07g27	15990289	15992452	2163	2142	21	CGTCTCCA	59.142	18
53546	RIM07g27	16221149	16222732	1583	1556	27	AGGATTG	59.593	20
53583	RIM07g28	16375452	16376105	653	633	20	TTTGGTTG	59.024	20
53630	RIM07g28	16525452	16527032	1580	1496	84	AGGTGGA	59.962	20
53654	RIM07g28	16654583	16655784	1201	1141	60	GAATGCA	58.879	20
53765	RIM07g28	17000779	17001960	1181	1150	31	GGCGAAG	61.357	20
53788	RIM07g29	1455375	1456447	1072	1153	81	AACGTGA	60.157	20
53789	RIM07g29	7234283	7234438	155	176	21	CCATGTGA	59.105	20
53809	RIM07g29	17130789	17131238	449	364	85	TGAGGCT	60.13	19
53841	RIM07g29	17400489	17401480	991	1056	65	AGAAGGT	60.001	19
53900	RIM07g29	7234283	7234438	155	176	21	CCATGTGA	59.105	20
53925	RIM07g30	17771722	17772224	502	481	21	TGTGTTGT	60.16	20
54023	RIM07g30	18127923	18128351	428	475	47	GACCCAG	59.841	20
54033	RIM07g30	3750083	3750240	157	178	21	CCATGTGA	59.105	20
54052	RIM07g30	18250037	18251177	1140	1120	20	GTGATGTT	60.373	18
54162	RIM07g31	18642276	18642533	257	294	37	ATCTTCT	60.073	20
54178	RIM07g31	18672020	18673026	1006	912	94	ACAAGGC	59.353	20
54218	RIM07g31	18840692	18840949	257	323	66	AGCTCGCA	60.02	20
54268	RIM07g32	19223935	19225756	1821	1851	30	CGAGAGC	59.308	20
54311	RIM07g32	19495563	19495971	408	432	24	ATCCAGAT	60.881	20
54339	RIM07g32	3751593	3754381	2788	2949	161	AGACACC	60.711	20
54340	RIM07g32	1457763	1457956	193	172	21	CCATGTGA	59.105	20
54431	RIM07g33	19965961	19967120	1159	1138	21	GGCCTCCT	59.713	20
54461	RIM07g33	20045324	20045544	220	198	22	GATGGAT	60.008	20
54467	RIM07g33	20045324	20045544	220	198	22	GATGGAT	60.008	20
54472	RIM07g33	20045324	20045544	220	198	22	GATGGAT	60.008	20
54524	RIM07g34	20342085	20342726	641	489	152	TGATGTCA	59.535	21
54539	RIM07g34	3750083	3750240	157	178	21	CCATGTGA	59.105	20
54552	RIM07g34	20409974	20413376	3402	3356	46	GCCCAAG	60.517	20
54580	RIM07g34	20587178	20587629	451	471	20	CAGTGAT	60.154	20
54583	RIM07g34	20618003	20619426	1423	1383	40	TATGTTGT	60.517	20
54642	RIM07g34	20814235	20814527	292	159	133	TGAGGCT	59.05	20
54666	RIM07g35	20969871	20972995	3124	3016	108	TCTTCAAG	60.05	20
54668	RIM07g35	20973293	20973515	222	250	28	GACAACTT	60.402	19
54706	RIM07g35	21128361	21129678	1317	1259	58	CTTTCTTC	62.877	18
54722	RIM07g35	21147266	21147656	390	425	35	ACGGGAG	59.962	20
54740	RIM07g35	13020131	13021631	1500	1468	32	TTGTGGT	59.726	20

54773	RIM07g359	21504340	21504573	233	285	52	GGTCTTCT	59.803	20
54797	RIM07g361	21624753	21626058	1305	1326	21	ATGGACGA	60.215	19
54844	RIM07g366	21953739	21954628	889	938	49	AGATGGG	59.929	20
54899	RIM07g374	3750083	3750240	157	178	21	CCATGTGA	59.105	20
54953	RIM07g377	30914992	30915671	679	711	32	GGTGTCAT	62.041	20
54978	RIM07g379	22742698	22743711	1013	1040	27	AGCCGACA	59.978	20
54984	RIM07g379	22781998	22782468	470	446	24	CGAGGAAT	59.852	21
55064	RIM07g388	23298176	23299163	987	1007	20	GAGACGG	61.449	20
55065	RIM07g388	23301737	23303060	1323	1357	34	CTCCTCTC	61.196	18
55087	RIM07g389	23357851	23358141	290	318	28	ACAACCTC	59.67	19
55091	RIM07g389	23362814	23363366	552	572	20	CAATGGCA	59.969	20
55151	RIM07g395	23677500	23678211	711	678	33	TCAACTGC	60.183	20
55167	RIM07g396	23753319	23754339	1020	992	28	CTTCCTCGA	59.861	20
55224	RIM07g399	23984489	23985022	533	561	28	CTCCTCCCA	60.662	19
55226	RIM07g399	23985534	23986067	533	569	36	AGACAGC	59.834	20
55229	RIM07g399	23987860	23988490	630	661	31	GCTCATCA	59.359	22
55349	RIM07g409	24505434	24506341	907	760	147	TACTTCCA	59.284	20
55390	RIM07g413	24772607	24774337	1730	1802	72	CTGCTTCG	60.419	20
55400	RIM07g413	24799553	24800582	1029	966	63	GAGCTCGT	61.109	19
55540	RIM07g422	25302757	25303879	1122	1075	47	GAAGGCAT	59.955	20
55567	RIM07g423	25359489	25359853	364	340	24	TGGTGATC	60.21	20
55658	RIM07g426	25540507	25540798	291	318	27	CAGAGCCT	60.331	20
55708	RIM07g429	25740415	25741921	1506	1479	27	CTTGGCCT	59.869	20
55735	RIM07g432	25887885	25888036	151	171	20	GAGATCTC	61.41	20
55811	RIM07g436	26149318	26150198	880	956	76	GGGTATTG	59.269	20
55817	RIM07g437	26158222	26160155	1933	1913	20	ATGGCCAA	59.708	20
55827	RIM07g438	26211127	26211713	586	445	141	CGGCTCCG	62.236	18
55832	RIM07g438	26231387	26232082	695	674	21	TACGAGCA	59.278	19
55855	RIM07g439	26256489	26257769	1280	1301	21	GAGATCTC	59.409	18
55901	RIM07g442	26421536	26422363	827	899	72	CTTAACAT	59.926	20
55956	RIM07g444	26559122	26559837	715	610	105	CGTCGTCC	59.98	18
56012	RIM07g450	26847567	26848061	494	459	35	GAATCTGC	59.962	20
56022	RIM07g450	26879875	26880440	565	596	31	AAGGCAC	59.574	20
56090	RIM07g454	27087297	27087728	431	408	23	TTGATGTT	60.654	20
56094	RIM07g454	6978562	6978816	254	287	33	TTCATGCA	60.126	20
56100	RIM07g454	27131638	27133841	2203	2110	93	TCGGTTCA	60.688	20
56154	RIM07g457	27329824	27330392	568	524	44	GACGGGG	59.651	20
56177	RIM07g459	27421933	27422237	304	434	130	CCAAGCCA	60.397	20
56183	RIM07g459	27442391	27442811	420	394	26	GCAGTGCA	59.445	20
56222	RIM07g461	27531573	27531971	398	451	53	CGAGCTCA	60.769	20
56236	RIM07g461	27550741	27551440	699	733	34	GCACCTTT	59.316	20
56322	RIM07g463	27684551	27684754	203	228	25	TACAATGC	59.395	20
56325	RIM07g464	27694383	27694899	516	486	30	TGAATGTG	59.984	20
56326	RIM07g464	27695090	27695849	759	642	117	AGGATCA	59.415	20
56352	RIM07g464	27720190	27720988	798	734	64	TCAGGAGA	59.181	21
56457	RIM07g469	28041190	28042381	1191	1367	176	GGAGGGG	59.679	20
56458	RIM07g469	28042298	28042460	162	338	176	TTGTCAAA	60.616	20

56624	RIM07g47	28500218	28501080	862	805	57	GTCACCGT	60.097	18
56667	RIM07g47	28648831	28649412	581	495	86	GTCGAGA	60.134	20
56708	RIM07g48	28881453	28883853	2400	2421	21	CCGTCTTC	61.131	20
56822	RIM07g48	29209214	29209397	183	313	130	CAGGATGT	60.111	20
56968	RIM07g49	29523441	29523885	444	479	35	ATACTGC	60.265	20
57084	RIM08g01	101908	104674	2766	2716	50	CGCAACT	60.406	19
57108	RIM08g01	341978	343771	1793	1757	36	ACGACGTG	59.758	20
57119	RIM08g01	394393	394612	219	241	22	GACTTCCA	60.466	18
57158	RIM08g01	459183	459460	277	301	24	GAACACTT	59.973	20
57196	RIM08g02	685582	691625	6043	6107	64	CAACGGCT	60.128	19
57302	RIM08g03	26552277	26552807	530	553	23	CGTCTTAC	60.008	20
57336	RIM08g03	1560934	1564010	3076	3127	51	GGGACTCA	60.073	20
57398	RIM08g03	3750083	3750240	157	178	21	CCATGTGA	59.105	20
57404	RIM08g03	1794941	1795342	401	245	156	CGTGATTG	59.972	20
57408	RIM08g03	1794941	1795342	401	245	156	CGTGATTG	59.972	20
57465	RIM08g04	2065886	2066106	220	192	28	CCAAGCA	60.656	20
57468	RIM08g04	2078885	2079147	262	212	50	AGCTGCCT	59.836	20
57524	RIM08g04	2305681	2306154	473	524	51	CGGAGTG	59.984	20
57590	RIM08g05	3750083	3750240	157	178	21	CCATGTGA	59.105	20
57611	RIM08g05	2918251	2919709	1458	1364	94	GATGGACA	59.488	20
57617	RIM08g05	2926039	2926284	245	282	37	GAAGGAA	59.158	20
57713	RIM08g05	3146217	3148647	2430	2476	46	GGTTGTCG	60.009	20
57738	RIM08g06	3307162	3307726	564	584	20	GAGAGAT	60.24	20
57760	RIM08g06	1463910	1464565	655	679	24	AGGTTTA	59.845	20
57879	RIM08g07	3961739	3963112	1373	1335	38	GCTACAA	59.459	20
57896	RIM08g07	17367112	17367409	297	271	26	ACAACGAA	60.149	20
57901	RIM08g07	4052350	4052722	372	403	31	GAGGGTGT	59.835	20
57926	RIM08g07	4225508	4226482	974	1000	26	GTCATCCT	60.113	19
57933	RIM08g07	4240151	4240739	588	609	21	CTTGCAGG	59.288	20
57935	RIM08g07	4263197	4263895	698	656	42	ATCCCGCG	59.656	18
57936	RIM08g07	12536803	12537561	758	793	35	TTCCTTCGA	60.134	20
58000	RIM08g07	4492575	4492727	152	118	34	CCCTTTAG	60.029	20
58036	RIM08g08	4588337	4588678	341	365	24	GAAGCGA	60	20
58100	RIM08g08	7234145	7234438	293	314	21	ATTCCTCCT	60.073	20
58145	RIM08g08	5096294	5098101	1807	1695	112	TTTTGCTGA	59.027	21
58161	RIM08g08	5166758	5167130	372	397	25	CACCAAAT	60.552	20
58165	RIM08g08	5167818	5168556	738	816	78	CAAATTCC	59.955	20
58170	RIM08g08	3750083	3750240	157	178	21	CCATGTGA	59.105	20
58185	RIM08g09	5255540	5256998	1458	1513	55	AACAGCGA	60.678	18
58193	RIM08g09	26552277	26552807	530	553	23	CGTCTTAC	60.008	20
58343	RIM08g10	3750083	3750240	157	178	21	CCATGTGA	59.105	20
58541	RIM08g10	12715437	12716211	774	832	58	GACGAAG	60.466	18
58578	RIM08g11	10423701	10424339	638	662	24	GGCTGTGT	59.597	20
58596	RIM08g11	6655743	6656043	300	325	25	GGAAGTT	59.989	20
58600	RIM08g11	6731348	6731563	215	245	30	AAGGATTT	60.443	20
58691	RIM08g12	36071197	36071608	411	374	37	GGCAAGG	59.978	20
58702	RIM08g12	3750083	3750240	157	178	21	CCATGTGA	59.105	20

58734	RIM08g12	7497958	7498487	529	553	24	AAGCACT	60.277	20
58781	RIM08g12	3750083	3750240	157	178	21	CCATGTGA	59.105	20
58796	RIM08g12	7658823	7662161	3338	3382	44	GGTGGTT	59.997	20
58804	RIM08g12	7675677	7676094	417	449	32	GACTACG	59.866	20
58809	RIM08g13	7734641	7735145	504	477	27	ACTGGGC	61.533	20
58855	RIM08g13	8121124	8121895	771	742	29	ATGGGGG	60.278	20
58901	RIM08g13	8388595	8390040	1445	1556	111	TAAGGGG	60.345	20
58910	RIM08g14	9743238	9744736	1498	1544	46	TCTTCAGG	60.34	20
58947	RIM08g14	26552277	26552807	530	553	23	CGTCTTAC	60.008	20
58956	RIM08g14	8631598	8632284	686	622	64	CGAGCTT	62.263	20
59004	RIM08g14	10777494	10778316	822	848	26	CGATCACA	61.034	20
59018	RIM08g14	8874231	8875256	1025	999	26	CAAGGAC	60.363	18
59019	RIM08g14	8875408	8876890	1482	1439	43	ATCAGGG	61.661	20
59085	RIM08g15	9299213	9300269	1056	1029	27	ATTGACG	59.736	20
59093	RIM08g15	9385111	9385442	331	308	23	CAACGGC	60.255	20
59103	RIM08g15	9407586	9408621	1035	1199	164	CCAACGAT	59.982	22
59135	RIM08g15	11135086	11135425	339	378	39	AATGAAT	57.017	20
59171	RIM08g16	9852371	9853517	1146	1054	92	CATCGTCG	60.987	19
59187	RIM08g16	18139610	18139980	370	333	37	CATGAGG	60.073	20
59198	RIM08g16	10012238	10013286	1048	1075	27	GAGAATC	60.155	20
59209	RIM08g16	10077481	10078082	601	574	27	TCTTTCCT	59.813	20
59233	RIM08g16	10151685	10153039	1354	1329	25	AGTGGTG	61.492	20
59275	RIM08g16	7585625	7586394	769	699	70	TGTTGTG	59.729	20
59276	RIM08g16	10347020	10348182	1162	1196	34	TCCTCAC	59.036	20
59277	RIM08g16	10348242	10348971	729	813	84	TCTTCCTC	60.386	20
59291	RIM08g17	10435409	10436625	1216	1265	49	TTTGGGTA	59.926	20
59309	RIM08g17	13088667	13088887	220	254	34	AAGGCGA	59.813	20
59326	RIM08g17	10628297	10628911	614	668	54	AGGGCCA	60.645	18
59393	RIM08g17	10942248	10942534	286	325	39	CACCTCAT	59.831	20
59411	RIM08g17	10962580	10965519	2939	2856	83	ACTGCTTT	60.361	20
59438	RIM08g18	11102878	11103056	178	222	44	TTTTTGTT	59.973	19
59459	RIM08g18	4706192	4706322	130	251	121	CACGGAC	59.989	20
59461	RIM08g18	757466	758802	1336	1207	129	TGTCATAT	59.198	22
59465	RIM08g18	18942375	18943566	1191	1159	32	GCCTGGG	60.464	20
59505	RIM08g19	3770790	3771266	476	440	36	CGAGTTG	59.715	20
59556	RIM08g19	11819315	11820906	1591	1559	32	AAAGAAC	60.156	20
59642	RIM08g20	12119347	12120065	718	560	158	CGAGCTG	59.339	20
59722	RIM08g20	12418654	12419884	1230	1181	49	TTTTAGCA	59.976	20
59724	RIM08g20	12426602	12426949	347	427	80	ATGGTTG	61.383	20
59782	RIM08g21	2916785	2918151	1366	1271	95	ACGTCATT	62.556	19
59825	RIM08g21	17523874	17524091	217	300	83	CTATTGCA	59.864	20
60036	RIM08g23	13964776	13965435	659	639	20	TGTTGGT	59.35	21
60117	RIM08g23	14316681	14316819	138	61	77	TCATGGTT	59.374	20
60128	RIM08g23	14360294	14360532	238	195	43	GCAGTCT	60.873	20
60183	RIM08g24	15683302	15685247	1945	1884	61	CCCCAAGT	59.994	21
60226	RIM08g24	14753659	14755255	1596	1562	34	TTAGATCA	61.141	20
60306	RIM08g24	15117699	15119433	1734	1827	93	ATCGTTG	59.2	20

60339	RIM08g25	15305725	15307314	1589	1542	47	ATTTTGCC	59.087	20
60384	RIM08g25	15493197	15494521	1324	1299	25	CCCACTCG	59.36	20
60449	RIM08g25	15684805	15685732	927	975	48	GTCTCACT	59.377	20
60460	RIM08g25	15712136	15712956	820	797	23	AGATGGA	60.356	19
60492	RIM08g26	17461554	17463017	1463	1507	44	TAGAGCCT	60.012	20
60545	RIM08g26	16370222	16371029	807	837	30	GGAAACA	60.119	20
60565	RIM08g26	9044430	9044737	307	284	23	CCAAGTCT	60.012	20
60584	RIM08g27	16584742	16584904	162	129	33	GTTTGCCA	60.299	20
60626	RIM08g27	34210593	34210919	326	364	38	GCAAAAA	59.938	21
60634	RIM08g27	16756874	16759460	2586	2635	49	GAGCTGA	60.181	20
60638	RIM08g27	16762191	16762979	788	726	62	CGAGCGA	60.175	20
60697	RIM08g28	10120627	10120815	188	143	45	ATCACAGT	60.111	20
60714	RIM08g28	17169129	17169937	808	846	38	GATCGAG	60.16	20
60715	RIM08g28	17169994	17170130	136	162	26	TTGGGATT	59.301	20
60734	RIM08g28	17237763	17238349	586	512	74	ATACCTCC	60.328	20
60744	RIM08g28	17346868	17347389	521	500	21	TACACGC	60.538	20
60795	RIM08g28	17684669	17686585	1916	1946	30	CTCGGGTT	61.754	20
60838	RIM08g29	17846314	17846858	544	412	132	GTCATTGG	59.94	19
60847	RIM08g29	17852208	17852471	263	319	56	CCACAAA	59.82	20
60852	RIM08g29	3751593	3754381	2788	2949	161	AGACACC	60.711	20
60860	RIM08g29	17894306	17894716	410	458	48	CGTGATT	59.75	20
60908	RIM08g29	18155468	18156383	915	858	57	ATGCCTTG	59.535	20
60967	RIM08g29	7387799	7388489	690	649	41	TGTTGTGT	59.525	21
61023	RIM08g30	18510840	18511172	332	288	44	CAAGGAT	59.894	20
61024	RIM08g30	14821776	14821943	167	113	54	TTTCCCTC	59.872	20
61051	RIM08g30	8790266	8790857	591	562	29	TCTGAAGA	59.376	21
61070	RIM08g30	3188629	3189378	749	728	21	CGGTCTAA	59.456	20
61080	RIM08g30	18832173	18833435	1262	1286	24	ACACGAC	59.751	20
61132	RIM08g30	19019601	19021305	1704	1650	54	CGTGCTCA	59.984	20
61163	RIM08g30	19122329	19123272	943	917	26	ACGCAAG	60.386	20
61217	RIM08g31	19455364	19455548	184	329	145	AGGATGC	59.874	20
61254	RIM08g31	19727874	19728930	1056	1036	20	CTCCTCCT	61.243	20
61261	RIM08g31	19797216	19797733	517	541	24	TCTTACCA	59.96	20
61339	RIM08g32	20213545	20214226	681	561	120	GAATTTTC	60.137	21
61370	RIM08g32	20350489	20350892	403	379	24	CACTTCTC	59.77	20
61429	RIM08g33	20473960	20475307	1347	1454	107	TGCCAGAT	60.624	20
61456	RIM08g33	20556821	20557335	514	409	105	GAGAAAG	59.737	18
61518	RIM08g33	3750083	3750240	157	178	21	CCATGTGA	59.105	20
61544	RIM08g33	21079620	21080937	1317	1160	157	TGATTTTG	57.837	24
61588	RIM08g33	21238421	21238673	252	205	47	GAGGAGA	60.497	20
61616	RIM08g34	21352894	21353948	1054	1081	27	AGAAGTC	59.98	18
61695	RIM08g34	16004928	16005593	665	485	180	TTTTAGCG	59.872	20
61711	RIM08g34	21976320	21977978	1658	1679	21	ACTACGT	60.201	20
61712	RIM08g34	21984548	21986807	2259	2336	77	CGATATTT	59.953	20
61884	RIM08g36	3750083	3750240	157	178	21	CCATGTGA	59.105	20
61902	RIM08g36	23271053	23272958	1905	1927	22	GACTTCGA	60.606	19
61908	RIM08g36	23280460	23281927	1467	1504	37	AGGTGCT	59.782	20

61927	RIM08g36	23390787	23395851	5064	5122	58	CAGCTTGT	59.864	20
61935	RIM08g36	23399296	23399897	601	575	26	CTCGTTTG	59.597	20
61950	RIM08g37	23559634	23560015	381	406	25	GGTTAAG	60.321	20
62187	RIM08g38	24522653	24523977	1324	1406	82	CACCATTG	60.173	20
62268	RIM08g39	24858745	24860658	1913	1937	24	GTGACGG	59.982	20
62284	RIM08g39	24887195	24888057	862	883	21	CGCCCTAA	59.993	20
62407	RIM08g40	25496856	25498296	1440	1479	39	AGCTCAG	59.959	19
62440	RIM08g40	25608421	25610117	1696	1816	120	ACAGATA	60.395	20
62516	RIM08g41	25978359	25978679	320	288	32	CAAGCTTA	60.28	20
62531	RIM08g41	26022273	26023334	1061	1143	82	AGCTCCAG	60.556	19
62533	RIM08g41	26024305	26025943	1638	1705	67	ATTCAAAA	59.867	20
62569	RIM08g41	26174739	26175020	281	257	24	TAGCTAG	61.75	19
62623	RIM08g41	26397109	26397922	813	696	117	TCTTCCAG	60.349	20
62806	RIM08g42	27032501	27033921	1420	1361	59	CCTCTCCT	59.945	20
62848	RIM08g43	27235984	27237950	1966	1830	136	AAAATCAG	59.851	20
62904	RIM08g43	27494870	27496478	1608	1582	26	TCACCAAG	60.386	20
63003	RIM08g44	27802408	27804008	1600	1634	34	GGTTCGTT	59.978	20
63051	RIM08g44	27892141	27892686	545	695	150	CTGGTCT	60.252	20
63074	RIM08g44	27914112	27917465	3353	3305	48	AGATCTA	59.603	20
63075	RIM08g44	27917578	27917793	215	190	25	ACCTCGA	60.542	20
63147	RIM08g44	28067017	28067404	387	351	36	GTGAACA	61.708	20
63165	RIM08g44	28110652	28111005	353	310	43	TCCTTCCT	60.366	20
63167	RIM08g44	28117071	28118242	1171	1144	27	CGAGCTCT	59.43	20
63207	RIM08g45	28368020	28368223	203	227	24	CTTCTTCC	60.045	20
63334	RIM09g01	490806	492404	1598	1627	29	TTCTGGCT	60.195	20
63347	RIM09g01	599897	600347	450	480	30	CATCATTG	60.216	20
63395	RIM09g02	1000951	1001964	1013	981	32	ATGGAGA	60.961	20
63465	RIM09g02	1451072	1451649	577	764	187	TGCCTGAG	60.049	20
63489	RIM09g02	1382684	1382847	163	185	22	GAAGCCG	59.803	20
63500	RIM09g03	3750083	3750240	157	178	21	CCATGTGA	59.105	20
63581	RIM09g03	1764176	1764596	420	454	34	TGTGTGGT	59.55	20
63617	RIM09g03	20692873	20693145	272	230	42	AATCTGA	61.335	18
63657	RIM09g03	14807014	14807568	554	443	111	GGCACTTA	58.582	20
63659	RIM09g03	1987446	1988440	994	967	27	GTGCAAA	59.469	20
63748	RIM09g04	17120063	17120650	587	669	82	CAACATCG	60.263	20
63753	RIM09g04	17120063	17120650	587	669	82	CAACATCG	60.263	20
63774	RIM09g04	2455305	2455494	189	216	27	AGCGCCT	60.52	19
63782	RIM09g04	13341722	13342867	1145	1111	34	TTGCATGG	60.088	20
63827	RIM09g05	2729433	2729828	395	438	43	CTGCTTCA	60.397	20
63853	RIM09g06	8972683	8973342	659	636	23	TGAAGAA	60.003	20
63887	RIM09g06	3098091	3098640	549	495	54	AAGTGGT	59.867	20
63964	RIM09g07	3485545	3487373	1828	1806	22	CAAAAAG	60.348	20
63966	RIM09g07	3509747	3510909	1162	1012	150	GAAGACG	59.727	20
63967	RIM09g07	3511015	3511405	390	475	85	AACTCATG	59.312	20
64000	RIM09g07	3621292	3625181	3889	3866	23	ACCATGG	60.096	20
64050	RIM09g07	3857645	3858113	468	503	35	GAGGGGA	59.112	20
64068	RIM09g07	3949140	3951047	1907	1937	30	GACTTCA	60.823	19

64124	RIM09g08	4164808	4168009	3201	3167	34	TATGATG	60.269	20
64144	RIM09g08	4293705	4294435	730	686	44	GGGTCAC	59.682	20
64163	RIM09g08	4400689	4402832	2143	1988	155	AAGAGCG	60.285	20
64214	RIM09g08	4593296	4594016	720	827	107	CGGTCCG	59.292	20
64312	RIM09g09	5175480	5177143	1663	1765	102	GCCCTCC	60.952	21
64371	RIM09g09	11815822	11816865	1043	1022	21	TCGTTTCA	60.103	20
64434	RIM09g10	5877921	5878355	434	381	53	TGCAGTT	59.831	20
64456	RIM09g10	5918184	5919197	1013	1034	21	TTCGATCA	60.096	20
64463	RIM09g10	5921706	5925484	3778	3848	70	TTGGCTCG	60.074	20
64498	RIM09g11	19713056	19714219	1163	1111	52	GGAGGAA	60.945	19
64575	RIM09g11	6447317	6447548	231	259	28	CCAAGAT	59.996	22
64683	RIM09g12	7169259	7169426	167	255	88	GCAGATG	60.226	20
64685	RIM09g12	7184674	7185789	1115	1187	72	AGAGTAC	59.218	20
64700	RIM09g12	7197984	7199758	1774	1802	28	GTTCCTG	60.299	19
64701	RIM09g12	7199957	7200388	431	452	21	GCCCAGA	60.08	20
64746	RIM09g12	7330480	7331161	681	655	26	CAAAGAC	59.67	20
64749	RIM09g12	7333565	7333916	351	375	24	CGGCACA	59.926	19
64755	RIM09g12	7351013	7351231	218	158	60	TTTCACAT	60.096	20
64758	RIM09g12	27755863	27756265	402	432	30	GGCGAAT	57.99	20
64787	RIM09g13	13964764	13965435	671	634	37	TGTTGTGT	59.525	21
64803	RIM09g13	1455334	1455875	541	601	60	GAACGAA	59.076	20
64830	RIM09g13	3750083	3750240	157	178	21	CCATGTGA	59.105	20
65073	RIM09g15	9359733	9360405	672	716	44	TGGAAAG	58.074	21
65158	RIM09g15	9739407	9740180	773	809	36	TCAGGTG	58.821	20
65164	RIM09g16	9776741	9777422	681	787	106	CTACGAG	60.119	20
65215	RIM09g16	10241237	10242128	891	838	53	GAGAGAA	58.423	24
65218	RIM09g16	12523313	12524317	1004	875	129	GGTTTGG	60.353	20
65263	RIM09g17	3750083	3750240	157	178	21	CCATGTGA	59.105	20
65269	RIM09g17	10630979	10631602	623	644	21	ACTTCAG	60.363	20
65271	RIM09g17	42511130	42511421	291	336	45	CACTCTCT	60.275	20
65339	RIM09g17	10944652	10944917	265	369	104	TTCATCAT	59.604	20
65407	RIM09g18	11319441	11320230	789	749	40	GAGCACA	60.759	20
65424	RIM09g18	27410409	27411045	636	605	31	AGGACGC	60.205	18
65451	RIM09g19	11558774	11559100	326	380	54	AAGGCAA	59.434	20
65511	RIM09g19	11796265	11796562	297	267	30	GTGTGAA	59.425	20
65631	RIM09g20	8310519	8312373	1854	1881	27	TCGTCGG	59.997	21
65665	RIM09g20	12204062	12206409	2347	2310	37	ACGCTTG	59.845	20
65676	RIM09g20	12304907	12305946	1039	938	101	AGACGAC	59.867	20
65692	RIM09g20	12389343	12390230	887	925	38	AGTGTTTT	59.598	20
65710	RIM09g20	12475616	12476144	528	587	59	AGCCCAA	59.993	20
65714	RIM09g20	12536255	12538357	2102	2081	21	TAGCAGC	60.081	20
65727	RIM09g21	12722486	12723460	974	944	30	TACGTCGT	59.904	20
65782	RIM09g21	13010408	13011499	1091	942	149	GATTTTG	60.038	20
65845	RIM09g22	13319011	13320900	1889	1922	33	CGCTCGT	60.89	19
65860	RIM09g22	13351044	13351985	941	963	22	CCTTTGAT	59.974	22
65898	RIM09g22	4325919	4326448	529	496	33	ATGCGCA	60.016	20
65944	RIM09g23	13618956	13619292	336	316	20	AATCCTCT	60.074	20

65971	RIM09g23	12150554	12151586	1032	1152	120	AACGTCGT	59.867	21
65972	RIM09g23	13750477	13750639	162	318	156	GACAAAT	59.61	25
65986	RIM09g23	13803554	13804365	811	708	103	GACAGGC	60.736	18
66160	RIM09g24	14598290	14598733	443	423	20	AATTTGTC	60.61	20
66187	RIM09g24	21238421	21238673	252	205	47	GAGGAGA	60.497	20
66199	RIM09g24	14838065	14838475	410	442	32	CACACCTA	61.138	19
66206	RIM09g24	14886351	14890332	3981	4006	25	CCATCTTC	60.624	20
66225	RIM09g25	15094158	15094808	650	548	102	AATCCGAG	60.296	19
66226	RIM09g25	15094823	15095542	719	744	25	GGAAGAT	60.065	19
66255	RIM09g25	15282758	15282957	199	168	31	ACCGCAA	60.706	19
66264	RIM09g25	15332451	15333462	1011	1071	60	GATCATGA	60.484	20
66318	RIM09g26	3750083	3750240	157	178	21	CCATGTGA	59.105	20
66334	RIM09g26	15789896	15791821	1925	1904	21	CTCAGCCT	60.555	20
66409	RIM09g26	16187585	16189264	1679	1653	26	GACGACA	59.525	20
66421	RIM09g26	18319925	18320100	175	341	166	GCAAGAA	60.177	20
66458	RIM09g26	16411924	16413177	1253	1228	25	CCCGTTTC	60.058	19
66515	RIM09g27	16705577	16708232	2655	2630	25	GCAATGT	58.639	21
66543	RIM09g27	16833247	16833809	562	589	27	TTTGTAAA	60.11	20
66753	RIM09g29	17881617	17882383	766	803	37	TGGATCCT	59.955	22
66789	RIM09g29	18033645	18033935	290	261	29	TCCACACT	59.293	20
66795	RIM09g29	18037098	18037412	314	284	30	GTGGCTT	60.065	19
66887	RIM09g30	18387178	18388716	1538	1518	20	ACTTCTCC	59.694	19
66941	RIM09g30	34336609	34338121	1512	1436	76	GCCTTCCC	59.602	19
66978	RIM09g31	18976183	18976627	444	421	23	CGGTGAG	59.775	18
67005	RIM09g32	19181023	19182379	1356	1389	33	TTCAATGC	59.443	21
67035	RIM09g32	19248098	19248805	707	732	25	TGGAAATT	58.43	21
67041	RIM09g32	19269082	19269817	735	773	38	ACGACTA	60.142	20
67043	RIM09g32	19281117	19281456	339	362	23	TGCTTCGA	58.233	24
67094	RIM09g32	19500341	19501142	801	780	21	TTCAGGGT	59.54	22
67259	RIM09g33	3233489	3234171	682	653	29	ATTCTGCC	60.226	20
67327	RIM09g33	20024144	20025184	1040	1157	117	GACCTTAA	59.043	20
67382	RIM09g34	20231254	20231690	436	621	185	GGTCAAG	60.119	20
67390	RIM09g34	20317897	20318620	723	599	124	GTTTCAGG	59.797	20
67440	RIM09g35	20430120	20431385	1265	1447	182	GTAGAGC	59.867	20
67479	RIM09g35	2507587	2507898	311	336	25	TGACTTGG	59.967	20
67567	RIM09g36	21002649	21003925	1276	1331	55	AATCCGC	59.909	20
67631	RIM09g36	21106969	21107169	200	225	25	GGGAGTG	59.957	20
67647	RIM09g36	21162112	21162799	687	633	54	GCAGGTA	59.74	20
67649	RIM09g36	21171870	21173114	1244	1278	34	ACAAGGA	59.844	20
67708	RIM09g37	3750083	3750240	157	178	21	CCATGTGA	59.105	20
67838	RIM09g38	21902686	21902943	257	306	49	GACCTCTA	60.02	20
67870	RIM09g38	1645886	1646218	332	303	29	AGCTCTCA	58.921	19
67874	RIM09g38	21960598	21960856	258	369	111	GAAGGAC	59.64	19
67896	RIM09g38	22030286	22031679	1393	1468	75	GACAAGA	59.636	20
67916	RIM09g38	22149786	22149989	203	178	25	GCCTCTAC	59.685	20
67948	RIM09g38	22245640	22245942	302	450	148	CATTCCTC	59.612	20
67951	RIM09g38	22246861	22247036	175	315	140	GCTGATCT	59.258	20

67963	RIM09g387	22269781	22270480	699	672	27	TGGCTCTG	60.402	21
68037	RIM09g391	3751593	3754381	2788	2949	161	AGACACC	60.711	20
68039	RIM09g391	3750083	3750240	157	178	21	CCATGTGA	59.105	20
68088	RIM09g393	22614247	22614899	652	624	28	GATGATTG	61.003	20
68092	RIM09g393	22624926	22626087	1161	1302	141	ATACAGG	60.24	20
68138	RIM09g395	22692648	22693711	1063	1037	26	CCGCAAGT	59.716	20
68146	RIM09g395	22714117	22714489	372	350	22	AATACCCT	59.387	20
68342	RIM10g015	18948196	18948413	217	250	33	ACCTCGAG	60.096	20
68348	RIM10g015	344205	344602	397	370	27	GGGTGAA	59.357	20
68393	RIM10g023	827067	828219	1152	1000	152	ACTAATTT	57.077	24
68394	RIM10g023	828401	830010	1609	1548	61	CGATGTAG	60.823	20
68407	RIM10g024	903343	904784	1441	1489	48	CAGAAGCA	59.711	20
68464	RIM10g029	1238722	1239387	665	724	59	TCAGTGAA	60.12	20
68498	RIM10g035	1529881	1530685	804	859	55	AGATCCTT	59.492	20
68505	RIM10g037	1672367	1673959	1592	1625	33	GATGTGG	60.135	20
68556	RIM10g043	2037534	2037850	316	282	34	ACAGGTTG	60.002	20
68560	RIM10g044	2084428	2085563	1135	944	191	CAAGTGCT	60.822	20
68586	RIM10g047	2259650	2260239	589	640	51	AGCTTGGA	60.382	20
68593	RIM10g048	2358022	2360773	2751	2656	95	ATTCAGAG	61.663	19
68648	RIM10g050	2491843	2494534	2691	2608	83	GCAAGAT	60.925	20
68655	RIM10g051	3750083	3750240	157	178	21	CCATGTGA	59.105	20
68679	RIM10g053	2618798	2621367	2569	2594	25	AGACAAC	60.135	20
68684	RIM10g054	2666371	2666508	137	92	45	CGAAGACA	60.001	21
68698	RIM10g057	2878599	2878931	332	358	26	AGGTCGAA	59.813	20
68724	RIM10g060	3090446	3091130	684	705	21	TACTGCAA	60.195	20
68761	RIM10g064	3270514	3270687	173	210	37	AAGAACA	60.119	20
68768	RIM10g064	13094667	13095515	848	1023	175	TCTCCGC	60.135	20
68777	RIM10g066	3750083	3750240	157	178	21	CCATGTGA	59.105	20
68835	RIM10g072	3812728	3814792	2064	2096	32	CGTTATTG	60.48	20
68856	RIM10g073	3880190	3882077	1887	1689	198	CTTTGTGC	59.288	20
68866	RIM10g074	3980583	3981520	937	917	20	TGTAGATG	59.621	22
68867	RIM10g075	3984893	3985141	248	220	28	ACGTCGA	59.597	20
68873	RIM10g075	3750083	3750240	157	178	21	CCATGTGA	59.105	20
68917	RIM10g080	4344174	4345059	885	827	58	ACCCATCG	59.75	20
68946	RIM10g082	4462808	4463710	902	935	33	ACACGCT	60.328	18
68995	RIM10g084	4617390	4618735	1345	1383	38	ACACGCT	60.328	18
68998	RIM10g085	4643231	4644152	921	867	54	AATACTA	59.883	20
69048	RIM10g089	4829605	4830437	832	666	166	CTCGCCAG	62.237	18
69099	RIM10g093	5063090	5063466	376	354	22	GTCAGAC	59.261	20
69102	RIM10g093	13964764	13965435	671	634	37	TGTTGTGT	59.525	21
69133	RIM10g097	5259207	5259965	758	732	26	TTCAGGAA	59.716	20
69261	RIM10g107	5922503	5923983	1480	1386	94	AATCCGAT	60.461	20
69317	RIM10g112	1457616	1457973	357	336	21	CAGCCGA	61.188	18
69351	RIM10g117	6523094	6525744	2650	2561	89	TCCTGCCA	59.947	21
69416	RIM10g123	6886276	6891351	5075	5142	67	AAGTTGAT	59.09	20
69435	RIM10g125	6963077	6966015	2938	2880	58	GCATTCGG	59.083	20
69464	RIM10g127	7114943	7115359	416	552	136	CAGGAGAT	60.862	20

69496	RIM10g134	7278294	7279046	752	664	88	ATGCCCA	59.962	20
69545	RIM10g13	7443768	7444279	511	443	68	AGTGATGA	58.618	20
69624	RIM10g152	7997008	7997490	482	376	106	GGCCTTC	59.691	20
69769	RIM10g17	7766754	7767006	252	447	195	ATCTCAAG	59.39	20
69779	RIM10g17	8849292	8851332	2040	2011	29	GTCTTTGG	59.676	20
69801	RIM10g177	17539391	17540664	1273	1099	174	AAGGAGGT	59.212	20
69810	RIM10g177	8929950	8930277	327	304	23	GAATGCAA	57.639	20
69814	RIM10g178	42511130	42511421	291	336	45	CACTCTCT	60.275	20
69816	RIM10g178	8956831	8957140	309	339	30	CTCAGTGT	60.463	20
69840	RIM10g18	9113550	9119487	5937	5869	68	CATGTCGT	61.449	18
69881	RIM10g183	9261287	9263774	2487	2452	35	ACATCTG	60.657	20
69887	RIM10g184	9279990	9281110	1120	1145	25	ACCTACGT	59.208	20
69906	RIM10g185	13015732	13016769	1037	955	82	TGCGTGCA	59.694	20
69934	RIM10g189	9597009	9597800	791	686	105	CTGCAGG	60.455	20
69963	RIM10g193	1457763	1457956	193	172	21	CCATGTGA	59.105	20
69968	RIM10g193	4558462	4559041	579	615	36	ACCACAC	62.042	20
69988	RIM10g198	9839963	9840631	668	639	29	CTGTGGCA	59.905	20
70019	RIM10g20	10008995	10009464	469	536	67	CTGAAGCA	59.864	20
70021	RIM10g20	10019036	10020832	1796	1775	21	GGCAAGTT	59.844	20
70079	RIM10g20	22050325	22051182	857	1017	160	TCTCCGCC	60.135	20
70096	RIM10g209	10523054	10523936	882	925	43	CCCGAAGA	60.044	20
70107	RIM10g209	11184685	11185534	849	974	125	ACTCATTTT	60.27	20
70110	RIM10g209	10551090	10551592	502	530	28	TGAAGAA	59.813	20
70134	RIM10g21	10614632	10615911	1279	1299	20	CCCTAACG	60.171	20
70137	RIM10g21	10617378	10617523	145	213	68	TGGTCCAA	59.215	20
70161	RIM10g211	10718934	10719721	787	665	122	CCTACGC	59.587	20
70162	RIM10g212	10768022	10768161	139	94	45	TTCTATTG	60.066	20
70183	RIM10g213	10838827	10839910	1083	983	100	TGAAATC	58.104	23
70284	RIM10g22	11333863	11334747	884	938	54	CCTAGATG	59.759	23
70342	RIM10g227	11770293	11770607	314	392	78	GGTGCTT	60.621	22
70448	RIM10g243	12380242	12381049	807	954	147	GGCGAAGA	60.763	19
70449	RIM10g243	12381091	12381365	274	178	96	TGGGTGA	59.697	21
70467	RIM10g244	12434069	12435934	1865	1928	63	GAGAAAG	62.014	18
70509	RIM10g24	1918831	1919330	499	417	82	TATGGCTA	60.288	20
70541	RIM10g249	12751981	12752178	197	230	33	GTCAGACT	61.009	20
70633	RIM10g253	13052282	13053328	1046	984	62	CGCCTCGT	60.52	18
70759	RIM10g264	13707780	13709513	1733	1704	29	CTCTCTCT	59.4	20
70820	RIM10g268	3750083	3750240	157	178	21	CCATGTGA	59.105	20
70965	RIM10g284	10860831	10861421	590	551	39	GCCAAGAT	59.893	20
70973	RIM10g28	14850977	14851726	749	775	26	CTCTTCAC	61.819	18
71005	RIM10g29	3750083	3750240	157	178	21	CCATGTGA	59.105	20
71012	RIM10g29	13877906	13878951	1045	1016	29	TCAGGATG	58.254	23
71019	RIM10g293	15177646	15178859	1213	1246	33	AAACTTCA	59.837	18
71038	RIM10g294	15255920	15257082	1162	1202	40	GGGTATTA	60.773	20
71048	RIM10g295	15255920	15257082	1162	1202	40	GGGTATTA	60.773	20
71054	RIM10g295	15259903	15262852	2949	2781	168	TCGAGTTA	60.053	20
71082	RIM10g29	15343303	15343508	205	234	29	TTCTTGAG	59.955	20

71090	RIM10g29	15349474	15350141	667	645	22	ATGCTTGG	60.119	20
71237	RIM10g30	16023651	16024914	1263	1307	44	ATCCTCAG	60.073	20
71268	RIM10g31	16191753	16193675	1922	1899	23	AATGAGAT	59.239	20
71319	RIM10g31	16586689	16587217	528	713	185	AGCTTGTT	59.968	21
71384	RIM10g31	16726154	16726456	302	338	36	TGTCGAGT	58.8	20
71466	RIM10g32	17106506	17107102	596	636	40	AGACCATA	58.868	20
71516	RIM10g33	17244337	17244989	652	623	29	CTGGACTT	60.261	20
71520	RIM10g33	17344579	17347089	2510	2562	52	GTGGACCT	59.892	18
71545	RIM10g33	17495804	17498955	3151	3191	40	CCTCGAC	60.298	20
71563	RIM10g33	17580944	17582064	1120	1192	72	AGCAGCTT	60.978	18
71582	RIM10g33	17651394	17652627	1233	1210	23	CATGGACT	60.096	19
71652	RIM10g33	17718790	17719896	1106	1163	57	GACGAAT	60.504	20
71654	RIM10g33	17720108	17720737	629	818	189	AAGTCTTG	59.478	20
71696	RIM10g33	17845992	17846198	206	80	126	CCCAGTAA	60.025	20
71698	RIM10g33	17902527	17903439	912	882	30	CTGCAGCT	59.688	20
71719	RIM10g33	17966449	17967163	714	866	152	GGGGAGT	59.894	20
71747	RIM10g34	18098544	18100380	1836	1709	127	AACGCCT	60.156	20
71813	RIM10g34	18340262	18342327	2065	2022	43	CCACGACT	60.252	18
71844	RIM10g34	18404043	18411904	7861	7917	56	ACGACTC	60.001	19
71927	RIM10g35	18596059	18597102	1043	980	63	AAATCGG	60.15	18
72032	RIM10g35	18911441	18912753	1312	1364	52	CCGTACGA	60.206	20
72039	RIM10g35	18916690	18916975	285	227	58	CCCCTGGT	61.084	20
72092	RIM10g35	19015030	19015674	644	597	47	GGTTGTT	59.091	21
72292	RIM10g37	19928334	19928608	274	254	20	AGCGTGCT	59.942	18
72357	RIM10g37	20105442	20107189	1747	1670	77	GTCGACAA	60.009	20
72409	RIM10g38	20291581	20292811	1230	1420	190	GTTCTCTT	60.142	20
72433	RIM10g38	20482486	20482697	211	169	42	CTTCTGGG	61.168	18
72465	RIM10g38	20674156	20674353	197	261	64	CATCGAGA	60.277	20
72667	RIM10g40	21461737	21464468	2731	2693	38	CAAGAAG	59.691	20
72673	RIM10g40	21473925	21474222	297	277	20	AAATATC	59.006	20
72693	RIM10g40	21530320	21532512	2192	2107	85	TACCTTGG	59.784	20
72700	RIM10g40	21537702	21538049	347	378	31	TGAAAGCA	58.869	20
72705	RIM10g40	21582814	21583226	412	384	28	GCAACTTG	59.534	21
72915	RIM10g42	22527854	22529229	1375	1409	34	ATGAAGCA	60	19
72916	RIM10g42	22529200	22529694	494	363	131	CTTTGCAA	60.397	20
72917	RIM10g42	22536249	22536872	623	583	40	CCTTCTGA	59.508	20
73013	RIM10g42	23036303	23036456	153	175	22	GCGAGGA	59.34	20
73118	RIM11g01	177095	178911	1816	1849	33	TAGGAGG	60.284	20
73119	RIM11g01	194531	195755	1224	1407	183	AACCACTG	59.914	20
73126	RIM11g01	234858	235092	234	212	22	CCAAAGTT	59.728	20
73221	RIM11g01	485595	486003	408	455	47	CAAGGTCA	59.984	20
73318	RIM11g02	19160736	19161270	534	569	35	CCGATATG	59.784	20
73322	RIM11g02	1018953	1019465	512	546	34	ATTCCATA	60.173	20
73325	RIM11g02	1022013	1022854	841	815	26	GCATGCA	60.016	20
73328	RIM11g02	1029647	1032299	2652	2564	88	CTGCGAA	60.65	19
73381	RIM11g03	1224241	1224702	461	492	31	GGAAGAAT	59.033	21
73469	RIM11g03	1502609	1503311	702	655	47	GACGATCT	59.532	20

73493	RIM11g039	1606122	1606529	407	379	28	GAATCCTT	59.727	20
73579	RIM11g046	1983333	1983546	213	182	31	TTCACCGA	60.156	21
73592	RIM11g046	1991723	1992722	999	960	39	AAAAGCTC	59.955	20
73596	RIM11g047	2009912	2010684	772	746	26	TGACAGTG	58.871	21
73640	RIM11g051	2268169	2268957	788	815	27	TCCGGTAG	60.647	20
73664	RIM11g054	2431416	2431920	504	534	30	CGAGCCTC	60.34	18
73695	RIM11g055	2518549	2523745	5196	5161	35	TACAAGCA	60.073	20
73730	RIM11g059	3750083	3750240	157	178	21	CCATGTGA	59.105	20
73793	RIM11g065	3752692	3754412	1720	1643	77	CGATTGAC	59.653	20
73795	RIM11g065	3750083	3750240	157	178	21	CCATGTGA	59.105	20
73859	RIM11g068	3353966	3354499	533	565	32	CCCTCGAG	60.317	20
73958	RIM11g071	14978192	14979289	1097	1056	41	TCTTCCTTC	60.569	20
73966	RIM11g078	4019219	4019756	537	557	20	CAGCGCGA	60.23	20
73969	RIM11g078	4020206	4020839	633	583	50	GCGATCAT	60.221	20
73991	RIM11g078	3750083	3750240	157	178	21	CCATGTGA	59.105	20
74058	RIM11g081	4244613	4245132	519	384	135	CACCTGGC	61.58	19
74094	RIM11g083	4371530	4372844	1314	1277	37	CTCGCATG	59.827	20
74106	RIM11g083	4382151	4382888	737	580	157	CGACCATC	59.95	20
74122	RIM11g085	4519113	4522620	3507	3680	173	CGGGGATT	59.916	20
74130	RIM11g085	4544137	4546706	2569	2615	46	TGGCAAGT	59.847	20
74135	RIM11g085	4547991	4549952	1961	1776	185	GTCAAAAC	59.853	20
74173	RIM11g088	4685643	4686389	746	726	20	CGGAATCC	60.908	19
74341	RIM11g108	3750083	3750240	157	178	21	CCATGTGA	59.105	20
74342	RIM11g108	3749650	3750000	350	371	21	ATTACCCTC	59.817	20
74348	RIM11g109	42511130	42511421	291	336	45	CACTCTCTC	60.275	20
74367	RIM11g110	6097020	6098491	1471	1552	81	ATTTTGCTC	60.022	20
74388	RIM11g112	6214592	6215426	834	855	21	TCCTACTTC	59.948	20
74413	RIM11g113	6317021	6318413	1392	1428	36	CATTCCTCA	60.822	20
74417	RIM11g114	6336025	6337107	1082	1044	38	CAACTACG	59.721	20
74426	RIM11g114	6372905	6373221	316	340	24	GCATGGAC	59.925	20
74445	RIM11g116	6477500	6478188	688	735	47	GTCCGGTG	59.965	19
74466	RIM11g118	6597001	6597513	512	478	34	GTGGAGAC	60.05	20
74467	RIM11g118	6597728	6598019	291	326	35	TTTGCCTAC	59.861	21
74494	RIM11g122	944848	946302	1454	1350	104	ATTACATA	59.95	20
74497	RIM11g122	6818657	6818963	306	258	48	GACAATTT	59.916	20
74541	RIM11g126	2990681	2990892	211	271	60	CGGCTAGC	60.403	19
74546	RIM11g127	7234283	7234438	155	176	21	CCATGTGA	59.105	20
74581	RIM11g136	7513641	7521788	8147	8030	117	GCGATCCG	59.668	20
74606	RIM11g138	7612209	7613569	1360	1291	69	CACCGACA	59.98	18
74666	RIM11g142	7941514	7942050	536	512	24	ATCGCACC	61.332	19
74678	RIM11g143	3750083	3750240	157	178	21	CCATGTGA	59.105	20
74708	RIM11g146	13763481	13764088	607	568	39	GTCGTCCG	61.834	18
74748	RIM11g149	8030312	8032581	2269	2245	24	GCTACACT	59.904	20
74752	RIM11g150	8451767	8452550	783	812	29	ACATGACG	60.018	20
74814	RIM11g153	3750083	3750240	157	178	21	CCATGTGA	59.105	20
74866	RIM11g156	10423694	10423908	214	235	21	GTTGTGGC	61.03	20
74931	RIM11g164	9097329	9098457	1128	1223	95	ACTTCCATC	58.586	18

74965	RIM11g17	9469471	9470814	1343	1366	23	GTGCACCT	59.726	20
74984	RIM11g17	9538420	9539462	1042	892	150	GTTGTCGT	59.665	18
75002	RIM11g17	13964764	13965435	671	634	37	TGTTGTGT	59.525	21
75026	RIM11g17	9743152	9745220	2068	2113	45	ATCGTGG	62.087	18
75035	RIM11g17	9753641	9754119	478	569	91	ACCAGTAT	59.596	20
75051	RIM11g17	9795971	9796885	914	965	51	CCCATATA	58.912	20
75061	RIM11g17	9799727	9800439	712	672	40	GGAGAAT	59.31	21
75110	RIM11g17	10093316	10095170	1854	1826	28	TCTTCTTC	59.778	20
75128	RIM11g18	10190811	10191227	416	448	32	AGTGCAG	60.134	20
75160	RIM11g18	10434206	10435174	968	928	40	GGAGGGG	62.94	18
75164	RIM11g18	3750083	3750240	157	178	21	CCATGTGA	59.105	20
75208	RIM11g18	10687127	10690879	3752	3798	46	GCTCGAT	59.843	20
75209	RIM11g18	10690976	10692220	1244	1187	57	CAAAGCC	60.066	20
75226	RIM11g18	10822263	10823504	1241	1116	125	TTCCATCA	60.24	20
75227	RIM11g18	10823485	10825017	1532	1595	63	CAGCCAT	60.152	20
75231	RIM11g19	10834952	10835143	191	166	25	GGTGTAT	59.67	20
75234	RIM11g19	10841501	10841868	367	502	135	ATCGTGG	60.243	20
75255	RIM11g19	10891843	10892080	237	258	21	ACGACCA	59.792	20
75277	RIM11g19	10930281	10931298	1017	1049	32	AGCTTCCC	61.348	18
75298	RIM11g19	10953162	10953304	142	168	26	GTGAATG	59.819	20
75346	RIM11g19	11177032	11177901	869	900	31	GCCAGTT	60.081	20
75384	RIM11g19	11324216	11324529	313	396	83	AAGTCAA	59.215	20
75432	RIM11g20	11578571	11580802	2231	2416	185	ATTCCAC	59.874	20
75441	RIM11g20	11667536	11668824	1288	1311	23	CTGAGGT	60.039	20
75468	RIM11g20	11841621	11842230	609	552	57	TGATTTCA	59.127	20
75528	RIM11g21	12075598	12076157	559	587	28	GAAGGCT	60.143	20
75609	RIM11g22	33435791	33436044	253	174	79	TCCATTGA	59.369	20
75625	RIM11g22	15593892	15594858	966	919	47	TCCTGGA	58.984	20
75666	RIM11g22	12522212	12522763	551	528	23	TGTTGTGT	59.525	21
75700	RIM11g22	41423157	41423722	565	519	46	TACCCAG	58.843	20
75703	RIM11g22	12705120	12705449	329	500	171	CTCTCCTT	60.134	20
75717	RIM11g22	12742073	12742601	528	554	26	TGTGCATA	59.557	21
75728	RIM11g23	12790698	12791340	642	682	40	TAGTGGA	61.084	20
75732	RIM11g23	12792365	12792814	449	474	25	TGGAAAG	60.249	22
75743	RIM11g23	17120063	17120650	587	669	82	CAACATCG	60.263	20
75747	RIM11g23	12811299	12812129	830	872	42	GGCAGAT	59.178	20
75787	RIM11g23	15986118	15986512	394	311	83	CTCCTGCA	59.933	20
75839	RIM11g24	13332079	13333106	1027	1056	29	GGCACCG	58.228	20
75930	RIM11g25	13838291	13838625	334	356	22	TTCAGTCT	59.956	19
75943	RIM11g25	13906902	13910308	3406	3315	91	TTGCACCA	59.864	20
75992	RIM11g25	14157425	14158450	1025	1059	34	GTGGCATT	59.415	20
76004	RIM11g25	13964764	13965435	671	634	37	TGTTGTGT	59.525	21
76014	RIM11g25	14241898	14250056	8158	8188	30	GACCGCT	62.088	18
76041	RIM11g25	14362205	14364462	2257	2201	56	TTGTAAAG	59.325	21
76078	RIM11g26	3766562	3768432	1870	1840	30	CACGTAG	59.864	20
76079	RIM11g26	1822123	1823143	1020	960	60	GGTAGCTA	60.716	21
76126	RIM11g26	14558439	14560105	1666	1472	194	GTAGCGAT	60.218	20

76175	RIM11g26	14826475	14828086	1611	1570	41	AGGCGGA	60.285	20
76190	RIM11g26	14996220	14998292	2072	1947	125	CCACCCTC	60.056	19
76193	RIM11g26	15054295	15054990	695	657	38	ATGCCAC	59.574	20
76250	RIM11g27	15243336	15249405	6069	5900	169	GTGACGA	60.215	19
76253	RIM11g27	15249933	15257452	7519	7567	48	AACACAG	59.844	20
76268	RIM11g27	15330192	15330939	747	646	101	GATGTTG	58.299	20
76306	RIM11g27	15504516	15504868	352	379	27	TGGTGCTA	60.164	21
76331	RIM11g27	22568614	22568961	347	324	23	CAAAAAT	60.644	20
76345	RIM11g28	15654402	15654709	307	354	47	GCGAGAT	60.243	20
76412	RIM11g28	15893457	15894514	1057	992	65	CGTGGGA	60.015	20
76483	RIM11g28	16313638	16314250	612	526	86	TGATGAA	58.979	20
76516	RIM11g29	16467511	16467985	474	524	50	GCTTCGAT	58.661	21
76518	RIM11g29	16468159	16469073	914	969	55	ATTTCTGC	59.882	20
76519	RIM11g29	16469051	16470036	985	965	20	GGTCACCT	60.125	21
76614	RIM11g29	16853216	16855260	2044	2157	113	TCAAAGA	59.262	20
76628	RIM11g29	16886630	16889096	2466	2332	134	GGCCGTC	59.978	20
76699	RIM11g30	17205063	17206020	957	1016	59	GCTGCTTG	60.154	20
76724	RIM11g30	3750083	3750240	157	178	21	CCATGTGA	59.105	20
76732	RIM11g30	17323959	17324559	600	668	68	ACATAAC	59.859	20
76766	RIM11g31	17599084	17599801	717	687	30	GGGTTTCA	59.973	20
76771	RIM11g31	17666210	17667048	838	990	152	ACCCATCA	60.255	20
76772	RIM11g31	17678090	17679326	1236	1377	141	CTGGTGG	60.767	19
76777	RIM11g31	3750083	3750240	157	178	21	CCATGTGA	59.105	20
76803	RIM11g31	17822469	17822709	240	162	78	ACCGATGT	59.769	20
76804	RIM11g31	17822972	17823893	921	973	52	AACCAGC	60.263	20
76805	RIM11g31	17828486	17828745	259	283	24	TCGACATT	59.837	20
76850	RIM11g31	17920033	17920180	147	168	21	CCATTTGT	60.517	20
76861	RIM11g31	17922631	17922808	177	157	20	TCAGGATT	58.381	21
76954	RIM11g31	18381333	18381775	442	258	184	TCAGCGTA	60.393	21
76967	RIM11g32	3750083	3750240	157	178	21	CCATGTGA	59.105	20
77035	RIM11g32	18702838	18704236	1398	1426	28	TGTTGACA	60.032	20
77063	RIM11g32	18920701	18921923	1222	1159	63	CGCCATTT	59.938	20
77123	RIM11g33	19114346	19118316	3970	3929	41	CCTCGCTC	59.495	19
77146	RIM11g33	19209273	19211085	1812	1789	23	TCCTACTC	59.797	20
77150	RIM11g33	27347744	27349742	1998	2034	36	CCTATGG	57.781	20
77151	RIM11g33	11564752	11565002	250	225	25	TGTTGGGT	60.309	20
77160	RIM11g33	19276642	19277659	1017	975	42	GGGGTGA	59.83	20
77270	RIM11g34	19859015	19859690	675	728	53	TGGAGAT	60.346	21
77288	RIM11g34	19899071	19899827	756	733	23	TTGTCAAA	59.715	22
77322	RIM11g34	19968463	19970704	2241	2301	60	GGATTTG	60.265	20
77331	RIM11g35	20057924	20058523	599	619	20	CAGAAGC	60.134	20
77391	RIM11g35	6447203	6447512	309	330	21	CGCAATG	60.243	20
77416	RIM11g35	20478051	20478839	788	822	34	GATCATAT	59.763	20
77442	RIM11g35	3770755	3771266	511	475	36	GAAGTTG	59.997	20
77476	RIM11g35	3750083	3750240	157	178	21	CCATGTGA	59.105	20
77504	RIM11g36	20869607	20871205	1598	1553	45	GACATGC	60.634	20
77535	RIM11g36	20983400	20984303	903	959	56	TCATATTC	60.177	20

77545	RIM11g364	21011197	21011597	400	367	33	ACATGATG	59.707	20
77600	RIM11g369	18703977	18704364	387	420	33	CAAAAGT	59.719	20
77605	RIM11g369	21319224	21319651	427	471	44	AATTCGTG	60.856	20
77611	RIM11g369	21330682	21331765	1083	1163	80	CGTCAAA	59.705	20
77621	RIM11g369	21102453	21102645	192	230	38	CTGGACT	59.982	20
77681	RIM11g375	21699384	21699666	282	304	22	CGTTCATC	59.84	20
77690	RIM11g375	21704606	21705324	718	645	73	GAAGGGT	59.703	20
77782	RIM11g382	22205312	22205979	667	518	149	GATTGGG	61.313	19
77867	RIM11g389	22715273	22716266	993	958	35	CTCTTGTC	60.134	20
77869	RIM11g389	22746497	22747393	896	994	98	CAGCTTCT	61.091	19
77874	RIM11g389	22748657	22749520	863	1046	183	GCCTATTG	59.044	20
77891	RIM11g391	22829165	22831189	2024	2121	97	AGTCGAC	60.001	19
78010	RIM11g401	23499763	23502060	2297	2244	53	GGGAGGT	60.195	20
78020	RIM11g405	23722101	23723020	919	856	63	GGCCCGA	60.32	20
78031	RIM11g406	23837584	23840728	3144	3202	58	GTGTTGAT	60.372	20
78033	RIM11g406	23841264	23841542	278	222	56	TGGTGCTA	59.89	21
78053	RIM11g409	3750083	3750240	157	178	21	CCATGTGA	59.105	20
78055	RIM11g409	1458355	1458523	168	188	20	ACGAAGA	59.993	20
78077	RIM11g411	24172282	24172933	651	845	194	GCTTGCCA	60.058	20
78080	RIM11g411	24176808	24177125	317	276	41	GGATAAC	59.933	20
78102	RIM11g411	22215458	22216278	820	787	33	TGAACAAT	60.103	21
78137	RIM11g413	24376336	24377329	993	963	30	AAAGCATT	59.945	20
78179	RIM11g416	22568614	22568971	357	334	23	ATCAAAGT	59.938	20
78273	RIM11g424	25079771	25080760	989	964	25	GATCTGCA	59.858	21
78296	RIM11g425	25171144	25171333	189	94	95	TCTTGGG	59.547	22
78318	RIM11g426	26543193	26545309	2116	2091	25	GGGACGG	60.11	20
78339	RIM11g428	25365137	25366779	1642	1535	107	CAAATTTT	59.353	20
78347	RIM11g429	19230217	19230719	502	543	41	CCATGGTT	59.024	20
78379	RIM11g433	25677664	25677908	244	266	22	GAGTTTTG	59.717	20
78395	RIM11g434	25742774	25742961	187	215	28	CTATTTTC	59.429	20
78443	RIM11g436	6548088	6549495	1407	1386	21	GGTTCGG	60.421	20
78470	RIM11g437	25971475	25971943	468	358	110	CACTGCAA	59.984	20
78497	RIM11g440	26146237	26147237	1000	1152	152	ATGATTG	59.933	20
78587	RIM11g444	3751593	3754381	2788	2949	161	AGACACC	60.711	20
78605	RIM11g445	26472355	26472992	637	798	161	ATCATCAT	60.507	20
78606	RIM11g445	26472973	26473754	781	944	163	CGAGTTTG	59.99	20
78628	RIM11g446	26544093	26544479	386	356	30	GCATGCT	60.104	20
78639	RIM11g446	26553133	26553256	123	143	20	ACCATAC	59.993	20
78650	RIM11g447	26559316	26559597	281	313	32	ACTGGGA	59.598	20
78660	RIM11g447	42511130	42511421	291	336	45	CACTCTCT	60.275	20
78714	RIM11g452	26939289	26940624	1335	1276	59	CCTCCTAC	60.317	18
78723	RIM11g454	27015991	27017502	1511	1442	69	GGTTGATG	59.973	20
78731	RIM11g455	27090091	27090509	418	392	26	ACGGCAT	61.126	19
78743	RIM11g456	1457616	1457973	357	336	21	CAGCCGA	61.188	18
78773	RIM11g460	27370014	27370525	511	582	71	CTTCTCCA	61.06	20
78830	RIM11g469	27717624	27717757	133	154	21	ACAACAT	59.973	20
78890	RIM11g473	27814386	27815288	902	928	26	GGTATCGA	59.911	21

78912	RIM11g474	12842983	12843641	658	679	21	GTTGAGG	59.31	20
78950	RIM11g477	28281269	28283265	1996	2016	20	GAGATGCT	60.945	20
78956	RIM11g478	28297715	28298341	626	552	74	ATCGGATG	60.125	20
79051	RIM12g012	147402	149946	2544	2487	57	GCTTTACC	60.061	20
79053	RIM12g012	151191	152240	1049	874	175	GTTAACAG	60.517	20
79069	RIM12g013	194531	195755	1224	1407	183	AACCACTG	59.914	20
79073	RIM12g013	243137	245746	2609	2414	195	CCAGGACT	59.697	20
79076	RIM12g013	234858	235092	234	212	22	CCAAAGTT	59.728	20
79176	RIM12g019	485595	486003	408	455	47	CAAGGTCA	59.984	20
79197	RIM12g021	594790	595679	889	869	20	CTTCTCCCT	59.399	19
79198	RIM12g021	595687	595922	235	266	31	GGGCATT	59.866	20
79206	RIM12g021	598501	599165	664	855	191	AGACCTGG	60.074	20
79276	RIM12g029	1177421	1177708	287	235	52	TACTCCTT	61.362	20
79345	RIM12g035	1398517	1399000	483	517	34	TGGCATTT	60.192	20
79368	RIM12g035	1426828	1427071	243	219	24	GTCAGAC	61.932	20
79488	RIM12g042	1818660	1819298	638	664	26	TCTGGCAG	60.004	21
79496	RIM12g044	1980738	1983123	2385	2228	157	AGGGTGCT	60.402	19
79497	RIM12g044	1983333	1983546	213	182	31	TTCACCGA	60.156	21
79510	RIM12g044	1896395	1897416	1021	1110	89	CGTACAGT	60.567	20
79514	RIM12g045	2009992	2010778	786	760	26	CCAGTTGT	59.976	21
79518	RIM12g046	1956151	1956484	333	283	50	CAGCAGA	59.873	20
79758	RIM12g067	3288036	3288832	796	834	38	CGTCATGT	60.056	19
79759	RIM12g067	3288813	3288904	91	125	34	CCAGTGAG	60.523	20
79761	RIM12g068	3320381	3320821	440	480	40	AAGCCAC	61.136	20
79805	RIM12g069	3375343	3376654	1311	1335	24	CAACCGAG	59.986	20
79859	RIM12g072	3583032	3584658	1626	1674	48	CTGCGTGT	59.072	18
79866	RIM12g073	3591437	3592879	1442	1464	22	TCTAAAAA	60.048	21
79868	RIM12g073	3593077	3593397	320	356	36	TGCAGCTT	60.22	20
79887	RIM12g073	3622045	3622587	542	522	20	GTTGCATG	59.805	20
79961	RIM12g077	36846446	36846560	114	148	34	TTTGGCTG	59.546	20
79985	RIM12g078	3969670	3969937	267	237	30	CGACCAT	59.95	20
80082	RIM12g086	4375249	4376081	832	954	122	GGATTCA	60.218	20
80162	RIM12g092	4862565	4869107	6542	6568	26	AGCAGCA	60.46	18
80176	RIM12g093	4903675	4904702	1027	1059	32	GGCCATCA	60.014	20
80186	RIM12g094	4930761	4931108	347	283	64	CAGTTCTG	59.831	20
80190	RIM12g094	4938592	4938818	226	247	21	GGATGGA	59.756	20
80223	RIM12g097	20652177	20653264	1087	1034	53	AGCAAGCT	59.037	20
80268	RIM12g102	5437535	5437902	367	317	50	GGTGGTA	59.527	20
80321	RIM12g106	5698973	5700905	1932	1971	39	CTCCTCCT	62.044	19
80391	RIM12g108	5821858	5822377	519	479	40	ACTACTGG	59.381	20
80396	RIM12g108	5828955	5831143	2188	2275	87	AGAAGAAT	60.36	20
80409	RIM12g108	5836890	5837522	632	496	136	TAGTTGGG	59.158	20
80410	RIM12g108	5837423	5838530	1107	978	129	CCCAAAAG	59.807	20
80449	RIM12g112	3766562	3768432	1870	1840	30	CACGTAG	59.864	20
80454	RIM12g112	3770755	3771266	511	475	36	GAAGTTGA	59.997	20
80533	RIM12g121	6676844	6677079	235	313	78	AGGATTG	60.491	19
80536	RIM12g121	2509727	2510083	356	292	64	CTCCGGAA	60.34	18

80542	RIM12g122	4903675	4904702	1027	1059	32	GGCCATCA	60.014	20
80546	RIM12g123	6775546	6776060	514	465	49	TTGTAAAG	60.214	20
80573	RIM12g125	2196561	2197471	910	818	92	CACTGGCT	60.293	19
80584	RIM12g125	6931729	6934450	2721	2752	31	GATGACCT	59.685	20
80585	RIM12g125	6934558	6935064	506	385	121	CCCTGAAC	58.313	20
80609	RIM12g127	7052966	7053600	634	662	28	TCAAGGGA	59.933	19
80612	RIM12g128	7063831	7065079	1248	1224	24	AAATATTC	59.791	20
80648	RIM12g130	7214834	7215010	176	376	200	TGACTCCG	59.839	19
80655	RIM12g130	7217911	7218098	187	166	21	GTGGGAAC	58.104	20
80694	RIM12g131	36981759	36981988	229	115	114	CATCGAGA	59.161	20
80702	RIM12g133	7418786	7423991	5205	5121	84	ACGAGAAC	59.144	19
80703	RIM12g133	7428301	7428967	666	622	44	ATCGTTCG	59.787	18
80741	RIM12g135	7619104	7621006	1902	1865	37	TGAGAGGC	58.838	20
80759	RIM12g138	1526207	1527338	1131	954	177	GTTGTTGG	60.179	20
80762	RIM12g139	7910055	7910211	156	177	21	CCATGTGA	59.105	20
80781	RIM12g140	7985253	7985959	706	750	44	GAGGCGGT	59.556	20
80788	RIM12g141	7995018	7995180	162	307	145	GTCCTCAG	59.723	18
80845	RIM12g146	8365240	8365817	577	541	36	TCTAGGTG	60.255	20
80866	RIM12g147	14568357	14568808	451	627	176	AATACATC	57.695	26
80873	RIM12g148	3750083	3750240	157	178	21	CCATGTGA	59.105	20
80908	RIM12g151	8610746	8611691	945	992	47	GACTCACC	59.751	20
80998	RIM12g160	9178678	9178895	217	195	22	AACAATCT	59.556	20
81041	RIM12g163	9358301	9360942	2641	2621	20	CACTCACT	58.333	20
81058	RIM12g164	9439023	9439184	161	207	46	GGGTTGAA	60.363	20
81074	RIM12g165	4903675	4904702	1027	1059	32	GGCCATCA	60.014	20
81122	RIM12g167	6478422	6478766	344	364	20	GGACAGGT	60.51	20
81188	RIM12g172	9893692	9894449	757	802	45	ACTACTGC	60.407	20
81193	RIM12g173	9931442	9931737	295	315	20	GCACCACT	60.621	20
81264	RIM12g181	10498547	10499131	584	558	26	TTCCTATTC	57.629	24
81287	RIM12g184	19620134	19620808	674	647	27	GTTGGGAC	59.783	19
81386	RIM12g193	11249447	11249998	551	585	34	AGATGTCG	59.927	20
81415	RIM12g194	11324743	11324957	214	265	51	ACATGCCC	60.214	20
81457	RIM12g197	26552277	26552807	530	553	23	CGTCTTAC	60.008	20
81520	RIM12g203	7385021	7385893	872	1059	187	GAGGAGCT	60.065	19
81521	RIM12g203	7385874	7386541	667	724	57	TCGGAAGT	59.734	20
81546	RIM12g215	12073071	12074628	1557	1533	24	TGTTAGAC	60.049	20
81548	RIM12g215	12077908	12080387	2479	2604	125	CTGCAAAG	58.675	20
81550	RIM12g215	12083583	12084562	979	812	167	TTTGCAAT	60.088	20
81612	RIM12g220	12423648	12425275	1627	1674	47	AGGAAGG	59.82	18
81613	RIM12g220	12425197	12425523	326	371	45	TTAGGCTT	58.128	23
81630	RIM12g221	12496807	12497509	702	805	103	AAAGAGGC	60.2	20
81708	RIM12g229	1457743	1457904	161	140	21	ATGACATC	60.279	20
81719	RIM12g230	13021641	13022886	1245	1213	32	CTCTATTTT	57.08	22
81727	RIM12g230	13026498	13026981	483	441	42	GGTGGGAC	60.088	20
81782	RIM12g234	18319924	18320092	168	334	166	GATGGCCA	59.722	20
81824	RIM12g237	13489778	13492879	3101	3046	55	CTACGGCG	61.216	18
81840	RIM12g238	3750083	3750240	157	178	21	CCATGTGA	59.105	20

81856	RIM12g23	13634508	13635351	843	819	24	TGGACCAT	59.763	24
81862	RIM12g24	13662101	13662999	898	968	70	CTCGGGA	60.612	20
81903	RIM12g24	3750083	3750240	157	178	21	CCATGTGA	59.105	20
81904	RIM12g24	1458355	1458523	168	188	20	ACGAAGA	59.993	20
81905	RIM12g24	13852830	13853466	636	711	75	GACTGAC	60.204	19
81923	RIM12g24	6978562	6978823	261	294	33	TTCATGCA	60.126	20
81942	RIM12g24	13974932	13976899	1967	1926	41	AGCGGTA	60.012	20
81975	RIM12g24	3750083	3750240	157	178	21	CCATGTGA	59.105	20
81993	RIM12g24	14197621	14198254	633	442	191	ACAACACA	60.291	20
82019	RIM12g25	10553473	10554209	736	688	48	CTGCCAAA	60.027	20
82070	RIM12g25	14629613	14629951	338	372	34	GTGGGTT	60.142	20
82165	RIM12g26	15508759	15509150	391	426	35	GGCAGAA	59.152	20
82265	RIM12g27	14081542	14081772	230	253	23	TAATGGC	60.088	20
82346	RIM12g28	13752315	13752629	314	293	21	CGTCAGG	59.45	19
82360	RIM12g28	3750083	3750240	157	178	21	CCATGTGA	59.105	20
82407	RIM12g29	13964764	13965435	671	634	37	TGTTGTGT	59.525	21
82419	RIM12g29	17606631	17607185	554	577	23	TCATGAAG	60.504	20
82490	RIM12g29	17858287	17859084	797	819	22	CAGAAAA	59.44	20
82531	RIM12g30	18089238	18090697	1459	1481	22	AGGAAGC	60.074	20
82555	RIM12g30	3750083	3750240	157	178	21	CCATGTGA	59.105	20
82563	RIM12g30	18274895	18275749	854	948	94	TCATCGAG	59.722	20
82598	RIM12g30	18318645	18320139	1494	1562	68	TGGAGCTT	59.933	20
82603	RIM12g30	3751593	3754381	2788	2949	161	AGACACC	60.711	20
82604	RIM12g30	3750083	3750240	157	178	21	CCATGTGA	59.105	20
82649	RIM12g31	3750083	3750240	157	178	21	CCATGTGA	59.105	20
82702	RIM12g31	18897416	18898003	587	623	36	AAATTGA	59.752	20
82708	RIM12g31	18902660	18902917	257	394	137	TTCACAGG	60.088	20
82780	RIM12g32	19426316	19427184	868	826	42	AGCTGGT	59.862	20
82801	RIM12g32	11857031	11858215	1184	1378	194	CAGGAGC	59.577	20
82804	RIM12g32	19487535	19489395	1860	1882	22	CAAGCGG	59.823	20
82868	RIM12g33	19919858	19923135	3277	3297	20	GTCTGCCT	61.981	18
82883	RIM12g33	19951343	19951564	221	244	23	TCGAAGTT	59.415	20
82976	RIM12g34	3751593	3754381	2788	2949	161	AGACACC	60.711	20
83044	RIM12g34	20819346	20820644	1298	1327	29	ACTGGTTT	60.488	20
83051	RIM12g34	3750083	3750240	157	178	21	CCATGTGA	59.105	20
83062	RIM12g34	14243565	14243813	248	169	79	TCCATTGA	59.369	20
83199	RIM12g35	21530975	21534600	3625	3570	55	AGAATGG	60.212	20
83256	RIM12g35	908884	909035	151	191	40	AAGCTTGT	59.539	24
83274	RIM12g35	7234145	7234438	293	314	21	ATTCCTCC	60.073	20
83277	RIM12g35	37257576	37257965	389	347	42	TGAAGGC	59.872	20
83336	RIM12g36	3750083	3750240	157	178	21	CCATGTGA	59.105	20
83395	RIM12g36	22558312	22559414	1102	1036	66	GTCGAGG	60.008	18
83412	RIM12g36	22602648	22603440	792	826	34	TTGTGTTT	59.751	20
83445	RIM12g37	13684861	13685049	188	310	122	CTTCACTA	59.869	20
83465	RIM12g37	3750083	3750240	157	178	21	CCATGTGA	59.105	20
83473	RIM12g37	22886660	22887887	1227	1281	54	ACCGAAA	60.11	20
83517	RIM12g37	23031181	23031620	439	462	23	TTTGCAGG	60.257	20

83538	RIM12g375	23049256	23050307	1051	1133	82	CCACAGG	61.001	20
83541	RIM12g376	23058828	23059722	894	797	97	CGGAGTC	59.966	20
83624	RIM12g381	23418797	23419822	1025	953	72	AGATCGA	59.95	20
83646	RIM12g383	23512157	23512382	225	252	27	AGGCGAT	59.97	21
83649	RIM12g383	23513080	23513664	584	560	24	GGGTTCTG	59.381	20
83751	RIM12g389	23889063	23889360	297	339	42	CGTACACG	59.895	20
83780	RIM12g390	23973892	23974115	223	186	37	ATTGCCGA	60.312	20
83882	RIM12g396	24442161	24443011	850	755	95	CAGCGTCA	60.003	18
83899	RIM12g396	24459040	24461735	2695	2674	21	GAAGCAG	60.225	19
84012	RIM12g404	24986641	24987598	957	935	22	TCGCACCT	59.805	21
84028	RIM12g405	25025081	25026851	1770	1791	21	TAGACCTG	59.973	20
84138	RIM12g409	25324951	25325354	403	441	38	ACGACGA	61.34	20
84282	RIM12g416	25760183	25760835	652	674	22	TATACATG	59.712	20
84331	RIM12g422	26148193	26149904	1711	1571	140	ATTGGGGA	59.471	20
84468	RIM12g430	26690895	26691313	418	545	127	ACCCCTCA	61.268	20
84474	RIM12g430	26719492	26719910	418	394	24	AATGCATT	60.081	20
84475	RIM12g430	26720069	26720775	706	774	68	TGTCCGGT	60.238	20
84492	RIM12g433	26842433	26843210	777	713	64	GGCTACTA	59.904	20
84528	RIM12g435	27013809	27015340	1531	1433	98	TCGAGAG	59.623	20
84612	RIM12g443	27431564	27432549	985	818	167	CTGGCTCT	61.507	18

REVERSE P	Tm(°C)	Primer_siz	PRODUCT	start_posit	end_position_in _gene(2)
CGTCTTTCA	59.77	20	201	687	887
ACCACTCC	60.314	20	176	415	590
AATTCGTG	59.882	20	1082	4719	5800
GCCAGAA	58.802	20	1330	502	1831
TGGAAAAT	59.844	22	580	1232	1811
GACAGGAT	60.081	20	2047	5545	7591
TCACGTAC	60.309	20	1420	742	2161
AACAACAT	59.781	20	218	511	728
CTGCCTCTA	60.005	20	745	2291	3035
TGGATTAT	60.089	23	1230	852	2081
AACTGGA	60.074	20	207	1035	1241
AACATTGA	58.661	23	144	4964	5107
CCATGTCA	59.712	23	1077	313	1389
CGGCCTG	59.873	19	194	816	1009
TGCTCAAC	60.596	20	856	4969	5824
GAAAAGG	59.906	21	577	794	1370
TAGCAAGT	59.875	20	482	3115	3596
CCTGTAAA	59.304	20	408	1213	1620
CAAATCTG	59.984	20	155	7587	7741
CACCAGCA	59.823	20	588	1338	1925
CACATGAA	60.473	20	497	478	974
AAGACGTT	59.74	20	605	287	891
GAAAATC	59.91	20	242	1698	1939
CTGGGTGA	59.807	20	468	3616	4083
GTGCTCCA	59.758	20	732	428	1159
CCTGGCTT	61.176	20	744	407	1150
TTGGAATT	59.894	20	178	1190	1367
AGCTACCA	59.639	20	1871	3016	4886
CCACTCCT	60.517	20	696	9315	10010
GACGCCCA	59.291	18	1070	870	1939
CCCCCAAC	60.332	20	584	1688	2271
CGCATGTG	59.676	20	1017	5867	6883
GACTTCCG	59.713	20	675	1970	2644
CCGTAGG	59.48	21	1972	382	2353
CCGGATGT	60.827	20	412	692	1103
GGTAAGTA	59.872	21	175	1367	1541
CTTTGTGTA	59.904	20	769	3101	3869
TCGACGA	59.551	20	657	2697	3353
CATCCAGG	59.691	20	2055	57	2111
TGCACCAA	59.964	20	948	40	987
CTTCAGCT	59.828	19	596	636	1231
AGTTGACG	59.969	20	3386	3938	7323
AATGCGGT	59.195	20	5363	2037	7399
GTCGCGT	61.672	20	3189	1225	4413
CAGCAACA	60.31	20	840	4570	5409
TACAGGGT	61.208	20	236	7704	7939

GTTCTTGG	60.349	20	2064	798	2861
TTTCCTGT	57.255	21	1115	31	1145
GGAGTGG	58.672	20	207	3934	4140
ACCTCTGA	59.653	20	604	3050	3653
TCACTCTT	59.522	20	1072	401	1472
CTCTGAAA	59.95	20	1629	584	2212
ATCACTGT	59.583	20	2266	993	3258
CCAGTGAT	60.003	25	479	3623	4101
TCCTCTTT	58.978	20	910	6215	7124
ACTCGTCG	59.794	18	1016	763	1778
TCCCTGAA	60.111	20	620	3431	4050
ACCCTTTA	59.734	20	873	126	998
GAACAGC	59.56	20	668	979	1646
GGACTGG	59.799	20	495	1196	1690
TCGAGAA	60.238	20	228	2421	2648
CGACTGC	62.254	19	1130	2963	4092
GCCTCTAA	59.284	20	231	2098	2328
AGGGACT	59.986	20	951	398	1348
CTTGACCT	61.009	20	484	25	508
CAAGGGA	60.019	19	989	2430	3418
TTCATCCG	59.348	20	1034	1702	2735
ACAGTTG	59.905	20	707	1481	2187
GGGAACA	59.82	20	957	1350	2306
TTGTGACA	60.225	21	550	4690	5239
CAACATCT	58.945	20	1198	1424	2621
TGATGTG	59.6	23	1708	1385	3092
CAACGTGA	60.008	20	696	1933	2628
CTCCTGAG	61.688	20	1080	268	1347
ATCAGCA	60.269	20	4623	2917	7539
TTCTTCGT	59.597	24	704	2961	3664
AGGCCTGT	59.155	21	2705	95	2799
ACTTACCC	61.15	20	7355	565	7919
GTCGGAC	60.563	18	161	2540	2700
CCCACTG	59.685	20	1427	798	2224
ACGATCA	59.786	20	1940	3927	5866
GTACAAG	60.517	20	2371	640	3010
TTCATCCA	59.945	19	181	6126	6306
GTCCGAC	59.955	20	187	4	190
TACTCGTT	59.694	20	980	443	1422
CATGTTGT	59.063	20	1448	713	2160
CTTCCCTC	59.948	20	2250	3107	5356
ACTCCTCT	60.48	20	555	152	706
CGATAGCA	60.22	21	1564	3934	5497
CACCTCTG	60.399	20	1850	339	2188
AAACGAAT	60.074	20	932	3149	4080
AAAGACA	59.328	20	1566	3016	4581
GAATGGTT	59.973	20	825	2866	3690

CCAAGGT	59.966	20	112	261	372
CAGCAGC	60.445	20	2804	855	3658
GCTTTTAG	58.863	23	191	6543	6733
CTCGACG	60.012	20	3999	1562	5560
ATCCAGGT	59.957	20	600	155	754
ATGTCCGG	60.672	19	198	477	674
CTGCTCCA	60.552	18	1020	264	1283
AACTTGAG	60.453	20	994	2605	3598
ATTGCTAC	59.993	20	3031	1164	4194
AACTTGTA	60.14	20	153	642	794
AGTACCTG	59.062	20	158	2474	2631
GACCCCAA	60.096	20	1036	1275	2310
CTCCCATT	59.137	20	501	381	881
TTTGCTCA	57.867	20	1279	8464	9742
GCGAATG	60.243	20	185	286	470
TGGTCAA	59.899	21	7221	3205	10425
CTGTGGGT	59.139	20	614	1091	1704
GAGCACTT	57.797	20	301	5059	5359
ACACTCAG	60.467	20	1292	1411	2702
TGAACAGA	59.992	20	722	547	1268
CAGGTTC	59.716	20	1640	5844	7483
AGACCCTT	58.646	20	388	1566	1953
CACTGTCA	59.997	20	10368	4631	14998
AACCTACG	60.621	20	1724	4798	6521
AACGCAAT	59.186	20	769	3028	3796
AGCCACTT	60.277	20	458	1301	1758
CCCTGTTG	60.297	21	2035	492	2526
CTCCCCAG	61.749	18	1587	593	2179
CAGTTGAA	60.883	20	1631	1555	3185
CAACCAC	60.081	20	983	2004	2986
CCAGAAGA	58.785	20	641	2836	3476
ACCTGCAT	60.469	20	1026	6546	7571
CTGGTTG	60.873	20	265	9303	9567
AAGTTCCA	59.366	20	748	9740	10487
AGGTCTT	59.697	20	368	10670	11037
GGTGCGT	58.28	18	1359	1373	2731
ATGAAGG	61.819	20	500	1080	1579
AGTACCTG	59.062	20	158	2670	2827
GAGCGTT	59.052	20	1762	146	1907
TTCTTGGG	59.762	20	244	2861	3104
TCCTTTGC	59.813	20	4196	1475	5670
TGCCTTGA	59.208	21	1097	2671	3767
GTCACGG	59.973	20	6397	201	6597
ACCACTTG	59.851	20	855	123	977
AGCTCGTG	59.717	19	193	476	668
ATCCTCTC	59.978	20	522	1583	2104
GATTCAG	60.045	20	1260	792	2051

GGGTGGT	59.997	21	1070	4810	5879
TTCATGTA	59.572	20	713	3380	4092
AAGTCCTA	60.505	19	1829	20	1848
GCAGATTT	59.822	20	1406	2095	3500
CCAAGAG	60.975	19	679	1674	2352
CGGAGGA	60.618	19	258	58	315
CATTCAAA	59.985	21	323	2036	2358
AGTCAAG	59.685	20	1032	790	1821
ACAGCACT	60.195	19	2006	449	2454
GTCGCATA	59.348	20	1347	541	1887
AGTACCTG	59.062	20	158	1380	1537
AGTACCTG	59.062	20	158	2705	2862
CGTCCAAG	59.716	20	2128	649	2776
AATAGAA	59.708	20	1322	1209	2530
TTGTGTGT	59.565	20	1338	5773	7110
GCTTTGGA	60.44	20	2579	391	2969
TTGACTGC	60.011	20	1013	1026	2038
CAGCATCA	59.673	20	657	948	1604
TGCCACTG	60.008	20	884	366	1249
AGTTGATT	59.373	20	918	1030	1947
AACACCCA	59.06	20	452	1760	2211
AGGATGC	59.09	20	235	1915	2149
AGGATGC	59.09	20	235	1666	1900
TTTCTCAT	60.656	20	622	588	1209
GGCCTAA	59.875	20	1874	63	1936
GCCGGTA	60.365	20	942	1652	2593
CTTTCCAG	60.241	20	653	650	1302
TGTAGCAG	59.522	22	168	1550	1717
TGTTCTCT	59.884	22	588	186	773
AATACGG	59.056	20	949	331	1279
AGAGGAA	59.939	20	1994	1346	3339
CACCACGT	60.252	18	219	5145	5363
TATCACCA	59.924	20	2446	81	2526
CCTTCCTC	60.311	20	1207	449	1655
GCCCCACA	58.647	20	292	2210	2501
GACCAGCT	60.628	20	800	2305	3104
GCTTCACG	60.466	19	297	650	946
TGGGAAA	60.626	20	621	446	1066
TGGTTATT	60.606	20	690	6246	6935
ATCTTGCC	60.569	20	365	1555	1919
TGCATAGG	59.825	22	942	876	1817
GCGATGAT	59.679	20	758	1772	2529
TCAGCTCT	60.142	22	1250	3810	5059
TTCAGCTC	59.793	21	857	1820	2676
AAGCGCCT	60.682	20	637	934	1570
GGCATCA	59.847	20	668	2872	3539
TTTCTCAC	58.949	23	1650	469	2118

TATTTGAA	59.901	20	1339	8675	10013
TTTCGAAT	58.742	22	380	10406	10785
GAGGCCG	59.668	20	728	153	880
AACTCCGT	59.969	20	388	375	762
AACTAAG	60.14	20	745	4574	5318
TGCCGGG	60.192	18	805	214	1018
CTCTTTTG	60.452	20	807	2396	3202
TTGAGTG	59.002	20	706	272	977
CGGGTCG	62.561	20	3045	758	3802
AGCAACG	59.911	20	692	85	776
CAGCCTG	60.624	20	1824	885	2708
AGCAGAT	59.222	20	1460	0	1459
AGCTGCCA	59.603	20	806	307	1112
CCGGTCG	60.692	20	244	161	404
CGTATGTT	58.759	21	4924	107	5030
GCTCCTCA	62.203	19	293	313	605
ATCGTCTC	62.397	18	3338	2005	5342
CGCTTGAT	58.95	20	1796	4676	6471
CTCTCCCG	61.18	20	2075	1006	3080
TTACCCCG	60.103	20	1892	1214	3105
CACACTAT	60.382	21	525	536	1060
ATGAGGA	62.261	20	209	8	216
ATGAAAC	59.96	20	639	3525	4163
GCCTGTA	60.182	20	1016	665	1680
GACAGGA	60.12	20	603	3308	3910
TCTGTTGC	60.05	20	1043	3049	4091
AGGAAGA	60.766	20	1205	4372	5576
TCTTGTCC	59.262	25	890	46	935
TCACTCGG	60.263	20	288	433	720
AATGAACT	58.969	21	665	427	1091
GATCAGC	60.517	20	247	3530	3776
AAGTGGC	60.24	20	527	4969	5495
TCATCTTG	59.002	20	1682	2954	4635
TCGCATAT	59.375	20	519	131	649
CATCTTCA	59.91	20	1536	1803	3338
GTTGTGG	60.105	19	195	5567	5761
GCACAATG	59.879	20	1014	4284	5297
TCTCCTTC	59.926	20	924	1410	2333
TGCTTTTC	59.405	20	2005	838	2842
CTGCATCA	59.531	19	638	2462	3099
CACCAGGT	59.044	19	2474	204	2677
CCTGTGCA	60.559	20	1541	1034	2574
CGCTCTTC	60.096	20	1829	516	2344
GGAACAT	59.996	20	485	3128	3612
GTCTGCAG	60.743	20	435	416	850
GACCGGT	59.81	20	509	2478	2986
CAATTGTC	59.706	20	1582	227	1808

ACATCACC	60.005	20	434	3149	3582
GGGTTGGT	59.454	20	597	1196	1792
GATGTCTC	59.776	21	656	2275	2930
TGATGATC	59.478	20	1088	222	1309
CATTAGGA	59.917	20	303	5527	5829
GAGATGCC	60.052	21	384	1885	2268
AGTACCTG	59.062	20	179	915	1093
GATCCTGA	60.615	20	234	1164	1397
TTCACCAT	59.946	20	936	18618	19553
TGAGAGCA	60.413	20	1211	437	1647
GGGAGCTT	60.538	20	841	4667	5507
CAATCCTTC	60.363	20	282	4849	5130
TTGTGGTA	59.911	20	1198	385	1582
CGGAAGCA	59.971	20	171	5004	5174
GAACGAAC	60.032	20	2319	469	2787
ATACATGC	59.801	20	17159	1914	19072
ACCCTTGG	59.679	20	682	14354	15035
GCAGTCGA	58.864	20	1199	1550	2748
TCAAAAAG	59.716	20	606	1713	2318
GTCTGTTT	60.395	20	1082	2229	3310
AGGCACAT	60.37	20	292	1161	1452
GATTCGTG	58.256	20	474	727	1200
TGGTTGCC	60.357	20	174	766	939
CTTTTGCCA	59.747	20	766	3369	4134
TTCCACCA	60.422	20	810	40	849
TTCCCTGG	60.214	20	296	2169	2464
TGATGAGC	60.632	20	1477	7061	8537
TCTTCCATC	60.84	20	2438	432	2869
CCGGCTTT	61.129	20	607	4700	5306
TGATTGCA	59.676	20	325	6038	6362
TCTCCAGG	59.948	20	1821	1401	3221
GCATCAAT	59.762	20	166	1742	1907
TGGCAGAC	60.207	20	428	34	461
ACAGGAGC	59.801	20	391	1293	1683
CGATCCTC	60.228	19	1396	571	1966
ATCAAAGC	59.971	20	515	669	1183
AATCCGAT	59.611	20	205	1678	1882
AGTACCTG	59.062	20	158	624	781
CTTGCAAC	59.572	20	968	10568	11535
TCAAATTG	60.378	22	2538	6	2543
GGTATGGC	59.813	20	209	0	208
CCTGGCTT	60.132	20	722	2562	3283
CGTACCTT	59.193	18	156	169	324
CCCTTTTCA	59.502	22	649	2114	2762
TTAGAACT	59.807	20	306	2320	2625
ACCTCGTC	60.467	20	304	165	468
TGGGTTTT	59.139	20	750	1146	1895

CTGACATT	60.056	19	362	914	1275
ACATGAA	59.786	20	881	2565	3445
ATACCTGG	60.328	20	206	1935	2140
GTGAGCC	60.231	20	542	2114	2655
CCGCTTGA	59.773	20	2080	4813	6892
TTCTGGCC	60.202	20	729	1198	1926
CCGAGCTT	59.978	20	939	2359	3297
ATTGCCAG	59.853	20	147	632	778
CATGGAGT	60.517	22	779	106	884
AAAGGTG	59.376	22	725	1810	2534
CAGACCAT	59.522	20	585	5153	5737
ACCATTCC	59.991	20	484	2021	2504
TGTGGATG	59.94	21	345	114	458
CTGATTGC	59.56	21	1120	3633	4752
GTCGTGG	60.02	20	168	1897	2064
AGATACCT	59.014	20	9489	709	10197
GTTGTCGT	61.501	18	179	320	498
TGTCCAAG	59.831	20	705	4157	4861
CCTTTTCA	59.202	20	1162	249	1410
AGTACCTG	59.062	20	158	1380	1537
GCCGTCAA	59.905	20	1700	610	2309
GCTCGAG	61.873	18	2216	1310	3525
CAACTCCC	59.682	20	971	272	1242
GCCTGCCA	60.492	20	989	213	1201
GCGGCTCT	60.104	20	670	2219	2888
CTAGCCGC	60.384	20	1022	30	1051
CTATGTCA	57.273	27	3440	563	4002
AGTACCTG	59.062	20	158	1380	1537
ATCGACCT	59.685	20	482	240	721
AATCTCTT	59.955	20	483	4149	4631
GCTGATTT	59.596	20	849	1033	1881
GGCAGAC	60.134	20	350	88	437
TGAAAGG	59.931	20	214	1876	2089
AGCCCAAA	59.993	20	254	1229	1482
CGATCCAC	60.111	20	624	1208	1831
TCGAACTG	60.028	22	1044	6441	7484
CACACGTT	60.833	20	365	3742	4106
GTTTCACC	59.661	20	573	576	1148
GAGACTTG	59.813	20	662	751	1412
ATGTATTG	60.211	19	3134	479	3612
CACCAGTA	60.011	20	433	4410	4842
GCCTCTGT	59.224	20	1041	55	1095
CATTCCTT	59.836	20	220	1843	2062
ACTTTCGG	60.32	20	1205	1493	2697
TAATGCCT	60.118	20	103	2068	2170
GCTCTTGG	60.195	20	862	525	1386
CGTTGATG	59.086	20	833	263	1095

TCGTGATC	58.617	23	345	1729	2073
GGGCTGT	59.703	20	132	1490	1621
TATCATTG	60.029	20	739	10126	10864
CCTCTAAG	59.647	20	1103	13143	14245
GCTCAAGT	60.056	20	212	2698	2909
AATCTCCG	60.073	20	1234	566	1799
ATGGGAG	60.034	20	654	731	1384
TCCAGGAA	59.648	20	1009	1014	2022
TCGATGAG	59.843	22	1014	2989	4002
ATTCTGGG	60.801	20	7652	5692	13343
AAATCATC	58.937	20	618	527	1144
TGGAGCTA	59.74	20	1364	3469	4832
GGATGTG	59.615	25	295	1040	1334
TGCACGGT	60.401	20	1272	3294	4565
GATCTGGT	59.957	20	403	164	566
GATTCCTC	61.002	20	1572	1205	2776
CAGAGACA	59.831	20	3001	1015	4015
CAAACGG	60.317	20	399	1514	1912
AGTGAGCA	59.887	20	5960	591	6550
TCCCGTAC	59.839	20	1674	519	2192
CTCCCCAG	60.375	20	696	3983	4678
GGATAGCT	60.619	20	1168	1868	3035
CCTCCGCG	59.655	19	1073	3012	4084
AGTACCTG	59.062	20	179	5416	5594
GGTATTCT	58.958	22	336	6645	6980
CAGCTGAT	60.758	20	1168	1862	3029
CCAAGAGA	60.136	20	467	4	470
TGAACAA	60.154	22	1321	190	1510
AGCTCCCT	59.994	20	720	1100	1819
CAACAAAA	61.032	20	194	3245	3438
ATCCAAAG	59.874	20	153	20	172
ATTGAACT	60.173	20	229	985	1213
AATACTCC	59.845	20	400	3424	3823
ATTTCAGA	60.461	20	1418	822	2239
TTGTCCTG	60.301	20	892	2487	3378
TGTTCTCA	59.844	22	294	6410	6703
CTCTGCTT	60.23	19	354	2354	2707
TGCACCAT	60.263	20	1443	372	1814
CCATACAA	60.28	20	261	1497	1757
CAGTACTG	60.012	20	2147	2938	5084
GTACATG	59.997	20	1910	1177	3086
TGTATGTT	59.708	24	2058	1934	3991
CGTAGTCA	59.165	20	2249	3279	5527
GCCAAGCT	60.081	20	848	596	1443
AAAACCA	59.546	20	5965	4474	10438
AGCTTGAA	59.778	21	163	1350	1512
CGACCTTC	59.992	19	627	2256	2882

CGACCTTC	59.992	19	629	784	1412
CGACCTTC	59.992	19	629	784	1412
CGACCTTC	59.992	19	629	784	1412
CGACCTTC	59.992	19	629	784	1412
CGACCTTC	59.992	19	631	784	1414
CCATTCCT	59.83	20	884	811	1694
CCTAGCAT	59.795	21	612	1521	2132
CTGCAGGA	60.218	20	2476	148	2623
TCGGTCAT	60.239	21	2037	296	2332
CTGAATTT	60.111	20	507	367	873
GGAATTG	59.645	20	149	917	1065
TACGTAAG	59.856	20	459	3825	4283
GATTGCAT	59.805	20	767	40	806
GGAAGGCT	58.672	20	1746	93	1838
CATGGAA	60.812	18	5278	472	5749
AGGTACCT	59.499	18	401	5960	6360
GCATGGCT	59.917	20	753	1432	2184
TATGAACC	59.523	20	1618	467	2084
GCGAGCT	59.981	20	1042	77	1118
GCCTTCAC	59.283	21	506	4317	4822
AGGTGGCA	59.989	20	168	77	244
TTCTTCGTA	59.597	24	704	178	881
CCTCTTCT	59.844	20	2413	290	2702
CCCTTGAA	60.245	19	192	126	317
AGATCATG	59.09	20	327	2445	2771
CTTCATGT	60.112	20	3722	2777	6498
TTTTGCTC	60.117	21	265	2677	2941
GCCGAGTT	59.95	20	507	642	1148
GTGCAACA	59.888	20	900	3684	4583
GAGAAGCA	59.962	20	1966	157	2122
GATGAAC	60.326	20	868	541	1408
GCAGCAA	60.844	20	238	1256	1493
TCTGGATT	60.192	20	750	87	836
GTGAGGA	60.311	19	236	348	583
CACGGCGA	60.193	20	394	698	1091
GTGACTCC	59.841	20	794	1325	2118
TTTAAAGG	59.424	23	1351	1274	2624
GACCTCAA	60.05	20	1574	499	2072
AAGGGAC	59.795	20	553	2214	2766
GGGTGAT	60.064	19	5165	2698	7862
TTCAGTTG	59.691	20	1118	1298	2415
AATCACCA	59.933	20	429	911	1339
ATTCCTCA	60.408	20	2350	4290	6639
GACGGCTT	59.129	20	1107	196	1302
GGCTGTGA	60.874	20	584	1445	2028
GTCAAAGC	59.973	20	211	3011	3221
GCACTTGC	60.14	20	1269	1215	2483

CCACTTCA	60.298	20	1008	2439	3446
GTGGTGA	60.348	20	389	4639	5027
CCTGCTGC	60.419	20	1370	643	2012
CTCACCCT	59.859	21	199	677	875
TTAAGATT	60.067	20	173	742	914
GGCACAT	60.776	20	503	894	1396
ACGTCCAT	60.79	20	287	430	716
TACTCGTC	60.065	20	1512	1318	2829
GCCTGCAT	59.415	20	390	1834	2223
TGCTTGG	60.318	20	217	11368	11584
ACACACC	60.159	20	476	455	930
AGTACCTG	59.062	20	163	2960	3122
CAGATGG	59.946	21	1488	874	2361
AGCTCAGA	60.406	20	615	1562	2176
TGTTCTGC	59.67	20	2289	430	2718
TCAGTTC	59.751	22	510	593	1102
GCCGATGT	59.425	20	6274	162	6435
TGGAATC	60.797	20	785	277	1061
TCGAATCA	57.957	24	787	1274	2060
GTGAGCT	61.021	20	656	3977	4632
ATGGGAAT	60.155	20	1728	4576	6303
TGTGAAG	59.867	21	945	1588	2532
TTGCTCGA	59.596	20	210	1174	1383
AACCTTTA	59.476	20	162	458	619
TGCAACTC	59.992	20	1068	1694	2761
TAGCTTCC	58.824	20	628	1145	1772
ATCGAGTA	60.081	19	1054	1081	2134
GCAATAGT	59.091	20	695	6676	7370
TCCTCCAA	59.2	20	451	7702	8152
CTCTCACG	59.82	20	889	2694	3582
GATTTTCA	60.17	20	1075	1287	2361
TGCAAGG	58.675	20	208	1895	2102
GGCCCAAT	60.664	20	480	223	702
CCTCAGG	59.728	20	905	818	1722
CAAGCTTC	59.96	20	182	2912	3093
TTCCTTGG	60.187	20	246	3137	3382
GACGGTA	59.851	20	532	3829	4360
GCAACAGT	60.032	20	755	1914	2668
AGGTCAAT	59.962	20	2912	3144	6055
ACTCGTTT	59.78	20	513	1505	2017
AAATCCCT	60.074	20	656	1309	1964
GTGATCTC	61.893	20	756	690	1445
GCACGTTT	59.882	20	1001	1616	2616
CGGTTTTG	59.706	20	505	1024	1528
ACCTTTAT	59.569	20	908	1241	2148
CAGTCTGG	59.92	20	1269	356	1624
TAATGTAC	60.776	20	382	193	574

GAACCTTG	59.463	21	751	1513	2263
ATACAGC	59.978	20	138	3174	3311
TTCACAG	59.113	20	553	1916	2468
TCATGAG	60.195	20	2848	584	3431
TGAGAGG	58.827	20	880	239	1118
TTTGCAGG	59.562	20	249	3762	4010
AAATTGCT	60.424	20	2257	1336	3592
GCATCGA	60.221	20	613	3714	4326
CGGAGAT	60.088	20	876	3327	4202
CCATCCG	60.626	20	642	603	1244
CGTAAAC	59.415	20	373	135	507
CATTTGTG	59.971	20	201	713	913
GCCGCGG	61.243	21	1358	1662	3019
GTACACA	60.24	20	1495	149	1643
TATCGGTG	59.369	20	1013	21	1033
ACTCAAC	59.797	20	167	6141	6307
GTAGTAC	59.898	20	206	1946	2151
CCTTTGCT	60.366	20	550	759	1308
CATCGCCT	61.434	18	554	2456	3009
TCACATTC	59.502	20	1484	886	2369
TACCTGG	60.419	20	1758	2141	3898
TCATCCTC	60.656	20	884	2258	3141
TAGATGC	59.999	20	2614	359	2972
AGTCGGG	60.489	20	172	4145	4316
GGGATGTT	59.797	20	975	1775	2749
TCTCGTAG	60.154	20	396	1255	1650
GCTCGAA	59.875	20	267	609	875
GTTCGGA	60.05	20	834	286	1119
GATCAGA	59.359	20	217	3459	3675
GTCTTCCT	58.467	20	764	1501	2264
TCACGGTG	59.931	20	4852	2036	6887
GTACTTGG	59.851	20	785	403	1187
GTACTTGG	59.851	20	678	403	1080
GTACTTGG	59.851	20	692	403	1094
GTACTTGG	59.851	20	670	409	1078
GCTATCCT	59.985	20	2988	429	3416
CTGACATT	59.591	20	620	7333	7952
GCTCGCCA	60.44	20	576	1783	2358
CCCCCATC	60.05	20	6902	395	7296
ACCAGTT	60.975	20	182	7681	7862
TTGGCTTC	59.989	20	724	1370	2093
CTCGACT	60.861	20	1179	1888	3066
CCATCCCA	60.155	20	3063	342	3404
CTTCCCGT	60.432	19	163	141	303
AAGTTCA	60.883	20	1034	1848	2881
ATTCCATC	59.629	20	488	274	761
CGAACTCG	60.015	20	238	777	1014

TAGACCGA	59.555	20	829	1749	2577
TCGGGGAT	60.16	20	359	269	627
TGTTGTTC	59.943	20	1423	1261	2683
GGTTCCTC	60.861	20	1052	1158	2209
TCCCTGTG	59.879	20	3925	2577	6501
TTTCTACA	60.244	20	719	3119	3837
CATGCAAA	59.801	20	1823	6042	7864
CTCCAATT	60.217	19	785	945	1729
CGCATTAA	58.413	21	764	5558	6321
CACCTTGC	60.397	20	1081	1278	2358
CTGCGACT	60.31	20	896	1313	2208
TCGAGCAG	60.249	20	930	1397	2326
GGTGCTCT	59.043	20	228	509	736
AGTGCTGG	59.31	20	425	1519	1943
GGATATAC	59.917	20	918	5586	6503
GTTCGGTG	59.429	20	964	357	1320
TGGTCGAA	60.256	21	2464	3755	6218
GAGGTAAC	60.651	19	2091	1480	3570
CCTTGATG	59.024	20	575	665	1239
AGGTGGG	62.725	18	1457	546	2002
GCACTCTT	60.69	20	408	31	438
CCGCTTCA	59.984	20	243	8699	8941
AGTAGGCC	60.008	18	169	402	570
TATCTCGT	59.547	20	356	3664	4019
GTACGCGT	59.399	18	3603	583	4185
TGCCCTCT	60.029	20	598	431	1028
TTGCCATG	58.675	20	482	4046	4527
CTTCCATC	60.362	20	473	435	907
CAGTTCCT	57.211	21	744	964	1707
GAGCCGA	59.43	20	1078	825	1902
GATGCCAA	59.533	20	860	1426	2285
ATGTTCCT	59.934	20	1164	2154	3317
TTGACATT	60.894	20	559	285	843
GTGCAGCC	59.178	20	1101	227	1327
GCGAAAT	59.9	20	1062	4703	5764
CACCAGCC	58.558	18	1737	428	2164
TTTGGAAG	59.795	20	701	9713	10413
CCCCACAT	60.11	22	372	12939	13310
TGGACTTC	60.533	20	2474	4180	6653
CGGATCCT	60.152	18	942	9	950
GCGGAAT	60.296	20	1263	615	1877
CCTCCAAT	59.974	20	1828	618	2445
CCTGACAT	59.648	20	2009	1079	3087
TAGATCAC	60.144	20	1055	2001	3055
TTCTTCAT	60.57	20	3912	1657	5568
CTTTGACT	59.63	21	1360	1272	2631
CAAATAGA	58.566	21	398	1585	1982

ACAGATTG	60.112	20	2103	4192	6294
CCAGAATT	59.184	21	555	1711	2265
TCAAGAAA	58.623	20	1302	4315	5616
CCAAGTTC	59.836	20	553	310	862
TCTCGGCC	59.277	20	883	596	1478
TCATGCAC	60.79	20	1524	2813	4336
CCCTTTGC	59.342	20	1282	3113	4394
GATGTGCT	60.444	20	872	1676	2547
TGCACGTT	59.902	20	1241	5637	6877
GCATCAAT	60.19	20	3700	623	4322
AGTACCTG	59.062	20	158	2499	2656
TCGTTGGT	59.525	20	756	668	1423
CGGCTCTT	59.496	20	523	866	1388
GCGTTTCT	59.875	20	179	4840	5018
GCAATCCC	59.916	20	1927	3965	5891
CTTAGAGT	59.996	20	692	1252	1943
TCCACGAT	59.478	20	483	929	1411
TTTGAGGA	60.042	20	952	52	1003
GAGGGGA	60.473	20	840	3916	4755
GTAGACC	60.662	19	755	1179	1933
CTTCGCCC	59.916	20	361	3241	3601
TCCCTTTC	60.163	19	1061	1189	2249
CAAGTAAA	60.361	23	477	610	1086
TTCGTCGT	59.873	20	1350	1531	2880
TCAACGTA	59.694	20	1303	1170	2472
GTTGATCT	59.992	20	1298	2568	3865
CGCACTTT	60.443	19	123	2830	2952
CACCCTGA	60.852	20	883	305	1187
AAATATGA	59.843	20	631	165	795
CTGTACAC	60.005	21	624	1993	2616
GGTTTCTT	59.691	20	159	99	257
GCAATTGC	60.089	21	600	730	1329
ACCGGGA	60.586	20	1096	84	1179
GGACGAC	59.827	20	1309	153	1461
GAACGCA	60.089	22	2394	1565	3958
CTAACTCG	60.008	20	515	2704	3218
TTTTATTG	59.901	20	1033	92	1124
CCAAAGCA	60.436	20	144	2351	2494
TGGAACAT	60.256	21	607	320	926
TGAATCCT	60.201	20	144	2389	2532
GCTTCCCA	60.058	19	1174	4694	5867
AACTTCTT	59.697	20	918	1751	2668
TCCAAAGG	59.322	21	1582	335	1916
GGCTTGA	59.997	20	434	1404	1837
GGATGAG	59.839	23	979	1765	2743
CTCCAAAT	60.719	19	626	889	1514
ACCAGCTA	60.044	20	1927	5574	7500

CGCATGCT	60.011	20	724	218	941
TGTAACCA	57.783	26	985	2529	3513
ATGCACCG	60.785	19	941	2439	3379
ACTTCACC	60.12	20	643	1447	2089
TCTGAACC	58.867	21	1040	4096	5135
GTTAGAA	61.407	20	2448	5707	8154
AGGATGA	60.543	19	2095	5456	7550
GACATGTG	60.081	20	776	824	1599
ATATCTGT	60.059	20	2690	5671	8360
AGTACCTG	59.062	20	158	9713	9870
GACAGAG	59.811	19	848	716	1563
GCATGCTA	59.839	20	3796	432	4227
GCGTATGT	59.862	20	1337	679	2015
GATTTCTC	59.803	20	1014	213	1226
TAGTGCAC	60.273	20	941	623	1563
TTTTGTTG	57.824	25	354	1867	2220
TCCTCAAA	60.051	20	1349	4271	5619
GGCATCTG	60.226	20	1367	5600	6966
TTGCAGCA	59.879	20	536	2875	3410
CCAGCAAT	59.868	22	1362	3436	4797
GTCGCAAC	59.837	20	905	7286	8190
GCCTCCAC	60.255	20	753	440	1192
GATGTCCC	59.602	19	2453	474	2926
GAGCCCCT	60.649	20	2507	250	2756
AGTACCTG	59.062	20	158	1380	1537
AGGCTGTG	60.057	20	2177	305	2481
CCGGATAG	60.134	20	3368	690	4057
ATGCTTCC	59.965	19	766	219	984
TGCGATCC	59.462	21	2298	533	2830
TGGCCTTC	59.844	20	523	4191	4713
GTCCTCTT	59.989	20	827	4644	5470
GCTCTGAC	60.422	18	1670	1390	3059
TCCCCTAG	59.767	20	5630	646	6275
TTCTCCTG	59.803	20	452	7254	7705
ACTTGACT	59.598	20	1964	6551	8514
AGTACCTG	59.062	20	158	1377	1534
CTTCTCCT	61.16	20	914	520	1433
CCTTAGCG	59.694	20	569	345	913
AGGTGCTT	60.007	20	1851	3861	5711
TAGCCTCC	59.743	18	303	164	466
ACCCTTGC	60.382	20	841	9946	10786
TGTCAGGC	59.986	20	1060	1185	2244
AGTCCTTT	59.478	20	1742	420	2161
CCTTCTCG	59.879	18	2020	431	2450
TGAACAAA	59.715	22	1005	30	1034
GAGGACC	59.688	20	1287	836	2122
TTTTTGAA	59.736	22	981	27	1007

TCCACACG	59.697	20	656	2424	3079
TGCACAAA	59.248	20	442	4290	4731
CCAATTGG	59.387	20	1437	326	1762
ATCCCGTG	60.331	20	3808	1074	4881
ATCATGCC	59.893	20	953	973	1925
TATGCTGA	60.51	20	796	3876	4671
CACCCTGT	60.751	21	1770	4633	6402
TCAAGTTG	59.875	20	1226	1007	2232
TTTGGTGC	59.773	20	635	3288	3922
GCAGCTCC	59.574	20	457	3570	4026
CGTATGGC	60.585	20	1672	1506	3177
TGCGATGT	59.697	20	441	815	1255
TCGGGCTT	60.082	21	746	63	808
CCTTTGGC	60.431	20	365	1540	1904
GCGTCTTC	58.158	20	1194	257	1450
TGATTGCA	59.847	20	1437	1506	2942
GCTCCAAT	60.173	20	393	137	529
AGTACCTG	59.062	20	158	2781	2938
CATTAGGA	60.18	19	333	657	989
AGCACCTT	59.7	20	1117	2301	3417
TCCAAAAA	59.438	21	199	2049	2247
GCCAAACA	60.04	22	1695	2956	4650
GGTCGCTA	59.513	20	1297	322	1618
GAAATGAA	59.61	18	723	1767	2489
GCTCTCAG	58.961	20	875	2673	3547
GGCGTTCC	60.242	19	1212	408	1619
CTCATCGA	60.527	19	193	753	945
AGCCTTAA	58.663	21	767	1447	2213
CCAATGGC	59.648	20	1659	164	1822
GACCTCTT	60.443	20	221	473	693
TTCTTTCAT	59.091	22	1294	744	2037
CTCCTTCC	60.206	20	462	327	788
TTGCTGGA	60.118	21	1719	2326	4044
ACTTTTGC	60.11	20	193	2827	3019
TAAGCGTG	59.872	20	1480	2	1481
CCTTCTCCT	59.803	20	1731	657	2387
TCTTGAAT	59.415	21	186	572	757
CTTCGTGC	61.819	18	1832	1421	3252
CACGTACA	60.049	20	794	643	1436
CATGTCCT	59.855	20	859	432	1290
TAGCTTGT	60.98	20	909	90	998
TCCATATC	59.993	20	4551	1729	6279
TGTGCCAT	60.22	20	159	387	545
TCTTCATG	59.992	20	232	152	383
AGTACCTG	59.062	20	158	2553	2710
CTCCTGTG	60.419	19	838	1422	2259
GCTTCAAG	58.92	20	955	5109	6063

GAAGAGA	59.676	20	633	21	653
CAACGATT	59.966	20	1598	3797	5394
TCTGTTGC	60.05	20	1045	1934	2978
GAGTATC	59.653	20	357	1233	1589
AGTACCTG	59.062	20	158	2795	2952
GGTGCAA	60.195	20	396	7679	8074
AACCCCTA	59.848	20	244	1559	1802
TTCTGGC	60.195	20	407	988	1394
CGGTAGTA	58.592	21	565	10008	10572
CCCTCGTA	59.315	20	1529	2138	3666
CCATAAAA	60.227	20	3063	1186	4248
ATGCTCCG	60.667	20	740	5	744
AAGAGAA	60.725	20	1383	280	1662
ATAATTCC	59.929	20	573	695	1267
ATCAATGT	59.955	20	713	16603	17315
GTTGGTCT	60.227	20	318	3125	3442
GCTGCCG	60.154	20	938	2	939
AGTACCTG	59.062	20	158	1380	1537
AGTACCTG	59.062	20	158	7320	7477
TCTGATCT	57.916	26	285	2206	2490
CACTCTTG	59.201	21	500	69	568
AGTCGAA	59.076	21	757	535	1291
GTGGACT	60.833	20	162	915	1076
ACTTGTGG	60.149	20	1643	2127	3769
CGTCTTCA	59.685	20	1994	2790	4783
GACCTCCT	59.604	19	632	4645	5276
AGTACCTG	59.062	20	274	1264	1537
GGTTTCC	60.526	20	907	5268	6174
CCCAATTT	60.111	20	1189	1298	2486
AGTACCTG	59.062	20	158	9856	10013
GCAAACC	60.504	20	220	45	264
GGTGGAA	57.734	21	214	4030	4243
TGATGGG	58.253	20	2964	2776	5739
GGAAATG	60.081	20	2591	309	2899
TCATGATT	59.127	20	218	1524	1741
CCGGCTGT	60.117	22	288	22	309
TCTAGCAT	60.018	22	1222	2623	3844
AAGGAGT	60.045	20	1048	3514	4561
GCGGCTCT	60.104	20	669	2212	2880
GAGAGGG	60.05	20	387	381	767
GCGGCTCT	60.104	20	670	2226	2895
CCATTCCT	59.83	20	893	133	1025
CATGCCA	59.95	20	613	761	1373
TGCACTCT	59.047	20	249	215	463
CTGGAAGT	60.255	20	256	1262	1517
CATATCAA	60.323	20	646	3379	4024
CCTTCTCC	60.031	20	1045	198	1242

TCCTGTCA	60.246	20	2082	2071	4152
TCTGCTTG	59.577	20	2723	5238	7960
CCCATCAC	60.801	20	519	9790	10308
ATGAGAT	59.685	20	259	1236	1494
GCTTTGAT	59.597	20	1325	115	1439
CATTTGCA	59.988	20	6645	1072	7716
TGTCTTGC	60.262	21	2192	6925	9116
CAATATAT	59.161	20	1627	13019	14645
ACCAACA	60.002	20	1055	2210	3264
CCAGGAAT	59.933	20	1332	1954	3285
AAAGCTTG	59.861	20	642	2087	2728
ACATAGCA	59.936	20	1733	4548	6280
TTCAGCA	60.671	19	562	109	670
CAGTGACT	60.022	20	739	2989	3727
CCGACAT	59.882	20	339	63	401
AGTACCTG	59.062	20	158	1380	1537
GCAGCCC	59.74	20	2546	735	3280
TGTTGTTG	60.449	20	694	1762	2455
AGTACCTG	59.062	20	158	2993	3150
TCAGATT	60.226	22	830	23	852
ATGCGCAT	60.663	20	215	129	343
CACCTTGT	59.716	20	198	2971	3168
CGCTTAAG	60.669	20	850	2799	3648
AGTTGCCT	60.418	20	648	8363	9010
TGGTGGT	59.824	20	1054	500	1553
GATTATG	59.923	20	1103	842	1944
TCACACAA	57.356	21	192	679	870
AGTACCTG	59.062	20	158	1344	1501
AGTACCTG	59.062	20	158	915	1072
TTCATATC	59.023	23	1217	33	1249
CGATGCTT	59.833	20	2948	554	3501
GGTGCTA	60.428	20	2202	729	2930
AACATTGT	59.911	20	796	4709	5504
AAGATGG	60.056	19	1109	310	1418
CTGCTTG	60.347	20	829	3228	4056
GCTGTGT	59.758	22	340	1396	1735
AGCTGCTT	59.895	18	249	22	270
GCATCTCT	59.658	20	582	438	1019
AGTACCTG	59.062	20	158	1380	1537
TCTCGTTG	59.837	20	1204	4375	5578
TCTTCCAC	60.36	21	1305	5559	6863
TGGATCGT	59.361	20	1444	319	1762
GATGGTTT	59.429	20	1487	27	1513
CATCCTCA	60.008	20	419	976	1394
TGAAGAT	59.831	20	451	750	1200
TTGGAAA	59.691	20	379	2123	2501
GCAATTTG	59.148	22	900	3040	3939

GGTCCAG	60.104	19	474	2219	2692
ACTTCTTG	59.875	20	779	2276	3054
CTGGAAC	60.668	20	802	17	818
AATATCTT	59.186	20	520	1170	1689
TTTGGCTT	60.068	20	1360	330	1689
CAGTACTG	60.012	20	903	90	992
CACCTCTC	59.148	20	635	17	651
CTTTTCAC	58.808	21	989	1853	2841
TCAAATGA	59.992	20	1865	256	2120
ATGAACA	59.596	20	181	1135	1315
GCCCTGTT	60.111	20	717	1259	1975
TGGCTCA	60.187	20	1095	460	1554
TGCTTACT	60.111	20	3563	114	3676
AGCTGATG	59.56	21	237	1940	2176
TAGTCGG	59.867	20	511	6811	7321
GACAAGA	59.997	20	789	1628	2416
AAGCGTG	60.156	20	597	6139	6735
AATGCTGA	59.758	20	701	2433	3133
CCCATTCG	59.975	20	428	200	627
TTCCACCA	60.422	20	811	40	850
CCATCTTT	60.044	20	1019	3567	4585
TAAGCGT	60.352	20	739	475	1213
CCAGTTGT	59.308	24	212	1698	1909
CCAAACA	60.051	20	500	2694	3193
CAATAGT	59.697	20	1020	2118	3137
TGTACCGA	59.44	20	2921	475	3395
TGTCACA	60.143	21	885	65	949
TTCTTCAC	60.69	20	995	1047	2041
AATTCACA	59.971	20	376	4412	4787
GTTGGTGT	61.891	18	1362	633	1994
CGCCAAA	60.015	20	332	2749	3080
AGCTGCT	59.985	20	1119	797	1915
TGTGCTCA	60.694	23	556	4334	4889
GCCATGC	59.42	22	1376	981	2356
GATATTCC	59.656	21	786	2974	3759
AGACCCTT	58.646	20	388	1558	1945
TGGAAAC	59.845	21	844	287	1130
ACTCTGGG	59.989	20	1642	1347	2988
CCCTTGAG	59.95	20	399	391	789
ATTTCTGC	59.574	20	1896	1373	3268
CAGCGAC	59.94	20	666	3756	4421
TGTTCCTC	60.074	20	708	152	859
CGTATATT	58.652	22	2243	940	3182
CCACGCTT	59.694	21	515	4811	5325
ATTGCCTC	59.445	20	497	1826	2322
GCCAGCA	59.975	18	2127	456	2582
CATCCTTA	59.462	21	875	103	977

AGAACGC	60.44	20	1528	1352	2879
CTCACCTG	58.13	20	266	3267	3532
AGCTCCAG	59.56	20	2137	385	2521
GAACGTT	60.833	20	829	606	1434
GATCAGCT	59.957	20	190	2721	2910
GATCAGCT	59.957	20	186	2296	2481
ACCACCAT	59.579	20	329	1817	2145
GCCGATTT	59.962	20	174	2056	2229
CGACCAC	60.005	20	981	382	1362
CAATGCA	59.464	20	242	4348	4589
GACGACG	60.941	19	1554	1552	3105
TTAACCTC	60.596	20	729	443	1171
AACTTATG	59.962	20	1063	724	1786
GCTTCCTT	60.088	20	695	644	1338
CTTTTGGA	60.817	20	148	1806	1953
CTGCTGGT	59.823	20	189	2375	2563
CGAAGGT	58.707	21	367	980	1346
GGGATCTT	59.927	20	146	873	1018
CAAGGCTT	59.711	20	818	1864	2681
CCTTCTCA	59.844	20	481	2904	3384
AACCTGTA	60.081	21	5168	598	5765
ACACCGTG	61.146	20	961	912	1872
GCCAGTCA	60.159	20	823	36	858
AGGGCAG	60.096	20	696	716	1411
TGTTTTCC	60.671	20	173	4841	5013
ATTAGCAC	60.606	20	1543	1303	2845
GAAGAAC	59.998	22	2489	301	2789
CCACCACG	60.232	20	253	329	581
TTGTGACA	60.225	21	514	5814	6327
TTCTGTGG	59.771	19	881	1642	2522
ACCAAAG	60.11	20	1895	4285	6179
CCATGTAC	60.529	20	770	299	1068
CTTCTCCG	62.255	18	3283	358	3640
CAGTGAG	60.008	20	657	820	1476
AGGGGAT	59.923	20	1672	69	1740
AAAGGGC	60.074	20	159	3249	3407
TGTTGTAA	60.838	20	276	432	707
GGGAATC	59.674	20	443	3160	3602
CATAATGC	58.906	21	609	400	1008
GGTCATCC	59.545	21	441	4425	4865
GAGCAAG	60.215	19	765	2538	3302
ATACTCTC	59.653	20	547	991	1537
GAGCGGT	60.021	22	820	1573	2392
CCCAAGAA	61.41	20	1041	1009	2049
TCCCATCA	60.173	20	1029	2461	3489
GTACTCGC	59.318	20	524	6488	7011
AGGCACAT	60.37	20	294	698	991

AGGCACAT	60.37	20	294	698	991
GCGCTTGT	59.935	21	1043	120	1162
ATGTTGGT	59.271	20	2365	916	3280
AAGGGAT	59.811	20	3045	810	3854
CTGGACG	60.255	20	1819	21	1839
GTCATCTT	60.622	20	844	136	979
TGTCGTTA	59.758	20	517	2141	2657
CAAGCTTC	59.96	20	182	2744	2925
GACGGTAA	59.851	20	458	3905	4362
GTTCGGA	61.121	19	716	5	720
CCATGTTT	59.861	21	599	1840	2438
TGCTTAGG	59.238	21	1534	0	1533
AACCCCAA	59.335	22	1181	2021	3201
CAGACGAT	59.95	20	855	380	1234
GTTCTCCG	61.032	20	758	1584	2341
GGGTAAG	60.074	20	640	4464	5103
AAAAATAT	59.212	20	883	248	1130
AGTACCTG	59.062	20	158	1380	1537
AGTACCTG	59.062	20	158	1380	1537
CGGTTGTG	59.353	20	3829	445	4273
GCTGCTTG	61.006	20	1945	289	2233
AGTACCTG	59.062	20	158	11329	11486
ATAGAGT	59.653	20	419	4749	5167
ACCTTCCT	60.096	19	1510	433	1942
GAGTATC	59.653	20	337	2368	2704
AGTACCTG	59.062	20	179	916	1094
TACCCGCT	60.074	20	1479	26	1504
CAACCACG	59.751	20	374	2194	2567
TCATTTAC	61.345	20	228	890	1117
CGAAGGA	60.898	19	108	1446	1553
ATCGGGG	60.195	20	371	150	520
ATCCGTTG	61.767	20	348	3119	3466
CTCTCCCG	60.328	20	175	233	407
ATCATTCT	58.981	20	655	2313	2967
CATTCCCT	59.943	20	592	1469	2060
CAGCTTCA	58.463	21	1180	7606	8785
CTCGTCCC	59.803	20	1531	55	1585
AAAATGCT	59.158	20	780	555	1334
AGTACAG	59.604	20	681	4174	4854
AATGCAA	59.41	20	1268	8	1275
TTGCTTAA	59.964	20	160	2342	2501
CGAGCGT	60.796	20	1104	2274	3377
AAGCGAA	60.599	20	2204	985	3188
CACATCTG	60.778	20	221	309	529
CCTCGCA	59.757	20	2529	2766	5294
ACGCTGAT	58.961	20	2179	348	2526
ACTAGCC	60.132	20	1843	174	2016

TCGAGAA	59.507	23	756	6700	7455
GCCTCTGT	59.224	20	1041	2071	3111
AAGCATTC	60.49	20	211	1103	1313
GTCGCACC	60.526	20	659	351	1009
GGGCAAG	60.096	20	546	132	677
CGGCTTGC	60.05	20	1065	299	1363
TAGAGCAC	60.157	20	2632	7509	10140
AGCCCTTT	59.17	20	235	10244	10478
CGCCCCA	59.993	20	1017	43	1059
GCCTTCTT	59.803	20	413	2622	3034
TTTGAGGA	59.396	21	1997	1246	3242
GCCAGTG	59.997	20	812	3186	3997
GATGGGA	60.303	20	1562	1194	2755
CCAAACGA	60.081	20	282	3109	3390
TGTAAGTG	59.716	20	127	2585	2711
ATATTGGT	59.653	20	899	3126	4024
GCGGCTCT	60.104	20	670	2218	2887
CATTTGTT	59.542	20	525	4561	5085
TCCCCCTC	60.177	22	1792	27	1818
TGTCATGA	59.743	23	731	2107	2837
CCAGTATA	58.791	25	338	3628	3965
TTCAAGTT	58.315	21	805	2850	3654
AAGCCCAC	60.326	18	807	33	839
AGGAAAT	59.973	20	816	440	1255
AACAAATC	59.883	21	305	1132	1436
ATCGGGA	60.787	20	369	182	550
CCGTCCTA	59.528	20	1008	3813	4820
CATTGGCT	58.931	21	548	2534	3081
TTGGATCC	60.329	20	482	279	760
ATGTCCGG	60.578	20	311	1805	2115
GTATACGG	59.022	20	2223	4531	6753
CTACAACA	59.392	20	167	120	286
ATGCCATT	60.511	20	316	369	684
AACCACCA	59.859	20	2144	1636	3779
CGTCCCAC	59.499	18	711	17	727
CACGCCAT	59.656	18	362	3002	3363
GGGAAGA	60.693	20	813	1088	1900
ACTTGACC	60.159	20	472	3175	3646
CGTCTTGC	58.917	20	1710	3367	5076
ATCAGCAC	60.231	20	989	1807	2795
TGCTTATC	60.011	20	1218	2246	3463
TTGCCTAC	59.123	20	1532	362	1893
GACAAAG	59.549	20	786	196	981
GCGCTTCA	59.596	20	1587	536	2122
GCCAGCG	60.221	20	1268	1231	2498
AAGATGC	60.729	19	1049	2408	3456
AAATCCTC	59.483	20	1425	3859	5283

AGTACCTG	59.062	20	158	1380	1537
CAGCACC	62.799	18	329	658	986
GATGCAAT	61.369	20	189	1042	1230
GATCAGGA	59.658	20	184	3912	4095
CAAATTTC	60.044	20	611	4675	5285
GGGTCCGT	60.121	18	7954	506	8459
GGCTATG	59.714	21	176	1766	1941
CAACTTCC	59.844	20	543	2868	3410
CAGCATG	60.333	20	2157	193	2349
CCAAAGCA	59.844	20	269	317	585
AGTACCTG	59.062	20	158	1380	1537
GTTGCCAA	59.889	20	181	1452	1632
ATCGCCC	60.483	20	425	777	1201
TTGTGCAG	59.288	20	1181	4164	5344
AAATCCTC	59.483	20	655	93	747
AAGTGAT	59.323	24	825	3587	4411
CATCAAG	60.263	20	815	77	891
CCATAATA	58.597	24	1425	877	2301
TTGCAATA	59.502	21	3471	818	4288
ATCAACCA	59.813	20	518	4779	5296
GCCAATA	59.7	20	575	4062	4636
GAACAGGT	60.307	20	1097	1113	2209
ATCTCCTTT	60.226	20	2791	5512	8302
AACAAGT	60.453	20	911	261	1171
TACAGGC	59.829	20	1407	1572	2978
AGCTCTTC	60.996	20	322	93	414
TTCCATGC	59.474	20	665	1889	2553
ATATAGTT	60.081	20	1079	94	1172
GTCCCACG	60.397	20	489	97	585
AACTTGAA	59.621	20	748	2269	3016
AGTACCTG	59.062	20	179	2281	2459
CCTCAAG	59.982	20	190	2606	2795
CACCAGAT	59.566	20	907	1879	2785
AATGAAG	59.037	20	3966	814	4779
TTAGCTGG	60.11	20	494	263	756
CGGCCAG	60.241	20	542	290	831
TTGACAG	59.007	20	669	811	1479
GATGCTG	60.205	18	1068	591	1658
GCGATAG	60.31	20	162	4008	4169
GGCTTAT	60.733	20	2927	200	3126
GACATCG	60.475	20	216	481	696
CTTCGCAA	60.003	20	624	8196	8819
CAGTGAAT	58.352	20	1581	223	1803
CGCTCATT	60.924	20	653	2663	3315
TTTGGAC	59.886	22	2430	127	2556
CAGAACCT	60.042	20	1077	2536	3612
TTTTCCACT	60.465	20	716	3621	4336

GCAGCCG	59.962	20	250	1921	2170
AAAATGG	59.938	20	1011	31	1041
CTCCAGAA	60.042	20	1126	504	1629
TGCCAAT	59.921	21	841	5423	6263
TAACAATT	59.875	20	898	327	1224
TAGCAGC	59.971	20	1057	303	1359
TCTTGCTT	60.117	21	504	1330	1833
CATCAAAT	59.894	20	747	621	1367
GGCCTCTG	60.096	20	901	1149	2049
TGTCGAAT	59.526	20	1728	181	1908
CTTCCCTC	60.044	19	1021	356	1376
AGTACCTG	59.062	20	179	2700	2878
CCAACTTC	59.982	20	1778	892	2669
TCATCCCA	59.927	20	167	3278	3444
AGTACCTG	59.062	20	179	1379	1557
TCGCTTCC	59.901	20	1194	1552	2745
AGTTGCAG	61.413	20	2548	220	2767
ACCTGGTT	59.844	20	865	1	865
CATGGCAT	59.969	19	1017	510	1526
AGTTTGG	60.776	20	1949	350	2298
TTGAAAGT	60.18	20	379	1785	2163
AAGCATCT	59.95	20	381	1504	1884
TATGCGCT	59.718	20	1036	799	1834
CTCTGTCT	60.096	20	3602	2008	5609
TGACAGA	60.136	20	505	4409	4913
GACCAGC	59.894	20	555	4989	5543
ATGAACA	59.962	20	395	1096	1490
TGGTCGG	60.336	20	800	928	1727
TCCATGGT	59.2	20	391	11878	12268
TCCCTACA	60	22	1652	63	1714
TAATAGG	60.11	20	341	94	434
CAGGATTT	60.111	20	673	4093	4765
GGTGTCCG	60.097	18	2482	1041	3522
ATTTCATT	60.061	20	1456	2403	3858
TACCTACT	59.989	20	659	1645	2303
AGTACCTG	59.062	20	158	1380	1537
TTTGCCCT	60.195	20	297	4644	4940
CTGCATCT	60.16	20	1983	1950	3932
CTCAATCA	60.111	20	1517	4119	5635
AGTACCTG	59.062	20	158	1380	1537
AGTACCTG	59.062	20	158	1380	1537
AGTACCTG	59.062	20	158	1883	2040
AGGGTCC	60.471	20	2044	4110	6153
TAGTGCA	60.273	20	958	470	1427
AGTACCTG	59.062	20	158	7251	7408
TTCTACCT	60.529	20	3229	359	3587
GCAGCCG	59.962	20	254	1978	2231

GCTTCAAT	60.532	21	468	2311	2778
CTTTGTCG	60.557	18	380	340	719
GGAGCAT	59.945	20	184	1629	1812
CTCCTTGA	60.022	20	189	1973	2161
GCTTGATG	59.016	21	2557	45	2601
GCAGCCG	59.962	20	254	1980	2233
ACGAACA	60.776	20	1037	44	1080
ACGAACA	60.776	20	409	726	1134
GTTGGGG	60.232	20	1485	241	1725
TTGGTGTT	59.726	20	182	2766	2947
TTACACCT	58.773	20	268	2057	2324
TTCAATGA	59.67	20	1574	4327	5900
ACCCTGAT	60.342	19	2103	12227	14329
ATCACATC	60.395	20	172	225	396
CTTGCAAG	60.796	20	1998	215	2212
TTGCTGTC	60.032	20	1046	458	1503
AGCTGCC	59.786	20	1321	3524	4844
AGCGACG	60.081	20	1035	3058	4092
GGGTTCT	59.532	20	756	960	1715
TCAATGTT	59.287	21	1256	347	1602
CGGCGGT	60.481	20	3743	81	3823
CGGACATT	59.927	20	354	7200	7553
ATCTTTGG	59.811	20	150	1888	2037
GAAAATT	59.829	20	614	2609	3222
CTCCACGG	61.184	20	223	689	911
GTAACGC	61.066	20	565	401	965
AACCCATG	59.874	20	340	5264	5603
AGTACCTG	59.062	20	179	1991	2169
AGCACGA	60.058	20	1612	573	2184
CACTGTTC	59.467	20	239	2531	2769
GGTGATAT	59.894	20	221	2838	3058
GAACACA	60.009	20	2900	598	3497
GATGCTGT	60.165	20	1422	169	1590
TGAGTCTG	59.415	20	360	477	836
GGCGAATT	59.433	20	407	0	406
AGCCGATT	59.925	20	329	6218	6546
AACCTCAT	59.557	20	2071	1076	3146
CGAATCTT	59.126	20	940	3120	4059
AGTACCTG	59.062	20	179	2942	3120
AGACGGC	60.796	20	2020	3934	5953
TCTGTTGC	60.05	20	1045	3686	4730
CGTCCTGA	59.77	21	587	885	1471
TTCATATC	60.001	24	421	54	474
GAGTATC	59.653	20	337	1233	1569
AGGCACAT	60.37	20	292	1165	1456
TCACAAC	60.088	20	439	1997	2435
CCATTCGT	59.933	20	240	2026	2265

GACCTTGT	59.657	24	317	2687	3003
AGTACCTG	59.062	20	158	2568	2725
ACGATGTA	60.7	20	426	3791	4216
ATGAGCT	60.226	20	2320	32	2351
GCATTCAA	61.535	20	727	2772	3498
CTTGATCA	58.23	20	155	3989	4143
ATCAGGA	60.7	20	1531	357	1887
TGCTCTGT	59.989	20	3016	480	3495
GTGATTAT	58.595	18	3519	252	3770
CCAACTTT	59.432	24	215	693	907
TACCCCTT	59.82	20	183	834	1016
GTCTTTCT	59.813	20	387	6039	6425
GGCCATGA	59.78	20	275	1654	1928
TCAATCAG	61.129	20	571	408	978
GTCCATCC	60.128	19	751	1023	1773
AAGGAGTT	60.045	20	707	2451	3157
CCTGGTTG	59.82	20	387	2256	2642
ACGACGA	60.766	19	2002	507	2508
GGTGCCT	60.585	19	430	1113	1542
AACAAGAA	60.012	20	591	887	1477
GTTTAATA	60.061	20	2097	1517	3613
TTCATCTG	60.539	20	1378	606	1983
TCCATTCC	60.266	20	1569	122	1690
CCAACAG	59.813	20	1535	337	1871
TCCCAGCT	60.24	20	4015	1144	5158
AGCCCAAA	59.993	20	254	3915	4168
CCCATCTG	59.933	20	398	47	444
GATCAGA	60.226	20	1008	3021	4028
ATCTGGCG	60	20	406	1928	2333
CCAGCCCA	58.949	20	180	966	1145
ACCGTCCT	59.655	18	395	160	554
GCAGGAA	60.263	20	253	3700	3952
TCCTCCTT	59.926	21	2850	5540	8389
TCATGAGA	59.856	20	1387	5658	7044
TTGCAATA	59.758	22	436	3731	4166
TTGGAGT	60.229	20	1679	3499	5177
TCCCCCAC	62.361	18	524	1153	1676
CATATAGT	59.449	20	2794	482	3275
ACTTCAGA	59.579	20	231	5759	5989
CTCAGGTT	60.563	20	1129	2774	3902
CTGTCCAT	60.218	20	249	1498	1746
ACCGAAA	59.927	18	1109	177	1285
CACCCCAG	60.634	20	676	3149	3824
AAGATGT	59.243	20	1026	2392	3417
TGACTCGA	59.989	20	544	1383	1926
GTCCCTCC	61.85	20	1291	77	1367
GAGCAACA	59.88	20	108	2009	2116

CTGGAGG	58.889	20	1139	373	1511
GCTGGAA	59.141	20	533	4201	4733
CTTGGCG	59.993	20	1453	1711	3163
AGATCCTG	60.421	20	545	1849	2393
CCTCCGGA	60.962	20	3477	881	4357
GTGCCATT	60.272	20	433	3448	3880
AGCAATG	60.118	20	1731	385	2115
CGAGGAT	59.694	20	715	1980	2694
TTGGCAA	59.356	22	394	2675	3068
AGGGATT	60.061	20	733	3061	3793
GCAGGAA	62.088	20	215	4594	4808
TGGAGTT	59.609	20	294	212	505
ACTTACGT	60.285	20	184	3557	3740
TCAAGAG	59.496	22	2511	18	2528
TCACGTTT	60.14	22	460	4031	4490
TTTTCCAT	59.656	21	523	983	1505
ATCCACCA	59.67	20	236	421	656
ATGACCAT	59.925	20	3409	592	4000
TGTCCCGT	59.904	20	432	5899	6330
GAGGAGT	60.156	20	1573	717	2289
ACTCATCA	59.685	20	562	52	613
CACCTTCG	60.074	20	1259	118	1376
GGAGCAG	60.284	21	690	3874	4563
ATCAGCA	59.722	20	159	9849	10007
ACCACGGT	59.997	20	1106	535	1640
GAAGTTG	59.682	18	1784	1894	3677
GCCTTGTC	60.776	20	567	3243	3809
GCCTTGTC	60.776	20	567	3243	3809
CAGAAGA	57.856	22	4197	984	5180
AATCTTGA	59.843	20	207	5690	5896
CCTTCTGT	60.298	20	272	2286	2557
ACGGTCTT	58.943	20	167	3392	3558
CTAGGAA	59.688	20	1936	1499	3434
TTGCATAG	59.996	22	786	2800	3585
CCTCAGGA	58.803	20	1168	283	1450
ATTAAGC	61.452	19	1689	17	1705
GCATCCC	59.757	20	328	1301	1628
GCAGCCTT	59.275	20	961	1135	2095
CCTTAGCA	59.059	22	1056	3959	5014
GGGATCA	60.226	20	211	45	255
CGATGTCT	60.02	21	1355	156	1510
TAATGATG	60.67	20	218	1100	1317
TCGAGGA	59.91	20	654	94	747
AAGTTGC	59.837	18	407	81	487
TGGAACTA	59.933	20	1315	2895	4209
GTGGCAC	61.292	20	364	2762	3125
TGACCATG	59.097	22	838	451	1288

GAAGACGT	60.801	20	302	5711	6012
GTTGCTGA	59.993	20	496	135	630
TGGCTCTC	59.989	20	493	4908	5400
AGATCCTG	60.421	20	545	1849	2393
CCAGGCAC	59.898	20	418	697	1114
TGAGAAGC	59.621	20	123	1285	1407
CCGCTGAA	60.481	20	1975	446	2420
CCCTTCTTC	59.844	20	1079	1952	3030
GCCAAGTT	59.166	20	144	1260	1403
TGCTTTAC	59.332	21	800	417	1216
CCAAATCA	59.499	20	184	2128	2311
AGCATGTG	59.905	20	1136	712	1847
CCTTGACC	59.52	20	295	4198	4492
ATACAAAT	61.149	20	1329	1986	3314
GACACTGC	60.032	20	672	3133	3804
TTGAATGC	58.16	20	1252	139	1390
ATATCTGT	60.059	20	2860	6732	9591
AGTACCTG	59.062	20	158	10944	11101
CAACAGAT	57.679	24	248	969	1216
TCCAACGA	59.941	20	779	2579	3357
GCGCAAGC	59.505	18	764	4543	5306
CTCGGCAG	59.978	20	270	79	348
GGGTCCTT	58.664	20	657	311	967
AGTACCTG	59.062	20	158	2919	3076
TTGCGATT	60.775	20	438	10253	10690
AGTACCTG	59.062	20	158	2679	2836
CCTCGAAC	60.224	20	208	1567	1774
CTCTGCTTC	59.378	22	611	9467	10077
CAGTGTTC	58.765	22	304	150	453
AGAAGCGA	60.362	20	499	862	1360
GAAGGATT	60.008	20	4922	5565	10486
TAACACAA	59.395	20	552	482	1033
CGTCTTGC	58.917	20	2626	1936	4561
CTCCGAAA	60.51	20	1039	6702	7740
GACTCGTG	60.226	20	846	5	850
GATAGTTC	60.606	20	489	949	1437
CTAGCATG	60.096	20	1227	3229	4455
CCTACCTA	60.423	20	1007	1854	2860
AACCTTCTC	58.792	20	199	6071	6269
TTCTTCTTC	60.066	20	4039	616	4654
AGTACCTG	59.062	20	158	9761	9918
ACCCTTTG	60.225	20	594	11972	12565
CCGCTGGT	61.235	20	3415	184	3598
CGGCTGAA	59.923	20	1054	1611	2664
GTTGGATG	59.697	20	2717	9230	11946
CTTCAACC	59.989	20	653	19	671
ATGAGCTC	60.226	20	1804	136	1939

ACTCATAG	58.816	20	1469	219	1687
CCTGCATC	60.136	20	2203	6126	8328
CCCATCAG	59.708	21	1039	8807	9845
ACCATGAA	60.544	18	205	642	846
ACCATGAA	60.544	18	184	539	722
ACCATGAA	60.544	18	193	629	821
TCCGGAA	59.638	21	167	1116	1282
CAGGGGT	60.103	20	334	3384	3717
TGACAACT	58.917	20	617	405	1021
TATCTCTC	60.537	20	376	2875	3250
CTTCGAG	59.95	20	2164	400	2563
CTGTCACC	59.962	20	1584	2035	3618
AACAAAC	60.156	20	654	1386	2039
GTCATTGG	60.12	20	1581	46	1626
TTTTTCTC	60.43	20	1202	5199	6400
CAAATGCA	59.819	20	1182	32	1213
CAGTACTG	60.012	20	1225	265	1489
TACCTGAA	59.959	20	177	2805	2981
TTTACCGG	59.887	20	450	722	1171
TTCCGGTT	60.452	20	992	1659	2650
TACCTGAA	59.959	20	156	1380	1535
CCATCCTG	58.254	20	503	721	1223
ACCCGTCA	60.119	20	429	145	573
AGTACCTG	59.062	20	158	2303	2460
AGAACTG	59.478	20	1141	108	1248
GAGATGG	61.795	18	258	249	506
TCACACCA	57.16	21	1007	141	1147
CACGTTGA	59.664	20	258	1438	1695
ACGAGAT	60.622	20	1822	1000	2821
ATCCCGTA	61.019	20	409	4954	5362
ATATCTGT	60.059	20	2431	1784	4214
CGGCCTG	59.873	19	173	5567	5739
AAATTCCA	59.126	20	1160	1285	2444
GTCAAAG	59.989	20	221	471	691
GTCAAAG	59.989	20	199	456	654
GTCAAAG	59.989	20	199	2163	2361
GAACTCG	60.218	20	642	2072	2713
AGTACCTG	59.062	20	158	2594	2751
CATCAGTG	59.449	20	3403	416	3818
ATCACCG	59.009	20	452	122	573
ACGGTGAT	59.874	20	1424	3282	4705
GCACTGGA	60.013	20	293	2346	2638
GATCGCCA	61.264	18	3125	883	4007
GCTATCTC	59.797	20	223	4305	4527
GCTGTGC	60.065	24	1318	742	2059
GCTCCCAG	60.012	20	391	1780	2170
GTAACCG	60.176	20	1501	2548	4048

TATACCAC	59.257	20	234	1518	1751
TGATTCAT	59.781	20	1306	127	1432
TCTAATTT	60.066	20	890	1891	2780
AGTACCTG	59.062	20	158	3183	3340
TGGTACG	60.301	20	681	2251	2931
CTGTCTTT	59.161	20	1014	5584	6597
CACTGGT	59.966	20	471	2883	3353
CACCAAG	60.375	20	988	857	1844
CTGCACCA	58.311	18	1324	111	1434
AAGAACT	60.298	20	291	1161	1451
CCTCCAAT	59.623	20	553	2673	3225
GTCTTGTC	60.214	18	712	630	1341
AAGAATT	59.268	23	1021	1205	2225
CCTTGGAT	60.21	20	534	209	742
CTCTTTCC	58.861	20	534	1254	1787
GATGTGA	59.975	20	631	3580	4210
GGAAGGA	59.036	18	908	1262	2169
TCCTTTCC	58.568	20	1731	325	2055
GTGGCAA	60.003	19	1030	15	1044
GGACCAT	60.727	21	1123	5308	6430
TTGATCCC	60.713	20	365	2642	3006
CCATCTTT	59.09	20	292	1054	1345
CCCGTTGG	60.005	20	1507	395	1901
CCATGGC	61.566	19	152	1372	1523
GTGCTAA	60.807	20	881	1291	2171
CTCACATT	59.831	20	1934	866	2799
ATTGTGA	59.939	20	587	376	962
CCACTGGA	60.044	20	696	1710	2405
TTGGCGA	60.729	19	1281	1005	2285
TTTGATCC	58.541	20	828	5572	6399
CTGGCTCA	58.882	20	506	14	519
TTGCTCCA	59.864	20	495	3840	4334
GAATGCA	60.081	20	566	628	1193
GGTGGTG	59.844	20	432	3451	3882
AACCCCAA	60.246	20	254	680	933
TAAAAGC	59.975	20	2204	221	2424
CACCGATG	60.144	20	569	502	1070
TTCTGCCC	58.298	20	435	5832	6266
CACCTTTT	59.993	20	421	1115	1535
CTGGTCCT	60.073	20	399	4014	4412
CCAGTTAT	59.55	20	700	903	1602
TCTGTTCG	59.525	20	204	1185	1388
AGCAGCA	59.621	20	517	754	1270
TTGCTGA	60.885	20	760	1461	2220
GGAGAAG	60.19	20	799	7862	8660
ACTACAGA	58.65	20	1192	4156	5347
GAGAAGT	60.192	20	163	5264	5426

ATAACACG	60.015	20	863	295	1157
CGTGATTA	59.002	20	582	128	709
ACGTGCA	60.021	19	2401	291	2691
TCGACAG	59.712	20	184	650	833
ACCGAAAT	59.154	20	445	1991	2435
ACGAGACT	60.466	20	2767	781	3547
CCATGCTT	59.691	20	1794	763	2556
GGAGCTT	60.34	20	220	165	384
TCCACAG	59.551	20	278	1650	1927
CTGAAGA	59.344	20	6044	294	6337
CCATTCCC	59.955	20	527	4176	4702
GTTCCTGG	60.105	19	3077	178	3254
AGTACCTG	59.062	20	179	1380	1558
ATACTAG	59.364	20	402	147	548
ATACTAG	59.364	20	246	437	682
CCCCGATG	60.647	20	221	654	874
CATCAAGA	59.648	20	263	2648	2910
AGCAACT	60.058	20	474	869	1342
AGTACCTG	59.062	20	158	2643	2800
CCCGTAGA	61.504	19	1459	612	2070
GATGCAA	59.992	20	246	2843	3088
CTGATGAA	59.596	20	2431	726	3156
GTGGCCGT	59.82	20	565	639	1203
TCGAGGAT	59.91	20	657	1165	1821
TTGGAAGT	59.133	21	1374	2273	3646
AGGAGGG	60.258	20	298	598	895
TATCACCG	61.003	20	373	194	566
CCGTCGTT	60.154	20	975	317	1291
TTCAGCCT	59.583	21	589	4138	4726
GGCCTTGT	60.211	19	699	311	1009
CAAGTAA	60.361	23	711	59	769
GGAGCATT	59.091	21	153	5845	5997
GGTGTCG	59.927	19	342	2856	3197
TACCTGAA	59.959	20	294	2756	3049
GTCACCAT	59.941	19	1808	473	2280
GTGCAAG	60.407	20	373	545	917
TACATTGT	60.111	20	739	1605	2343
AGTACCTG	59.062	20	158	2742	2899
GAGGGCT	60.261	20	1459	100	1558
CCATTCCC	59.955	20	530	558	1087
AGTACCTG	59.062	20	158	63	220
AAATACCG	60.131	20	827	172	998
AGGAATC	59.166	20	641	157	797
ATGAGGA	59.929	20	301	766	1066
TCCCTCAG	60.191	20	216	4079	4294
AATACTCC	59.845	20	412	3378	3789
AGTACCTG	59.062	20	158	7016	7173

CTCCCTTG	60.081	20	530	10300	10829
AGTACCTG	59.062	20	158	1380	1537
TCTGCATA	59.694	20	3339	7235	10573
TACTTCTC	61.348	20	418	855	1272
CTCCCTCT	60.149	20	505	144	648
CAATTTGT	59.17	20	772	2450	3221
AAGATAAT	60.103	20	1446	205	1650
CGTAATAC	60.004	21	1896	307	2202
CCATTCCC	59.955	20	527	153	679
TACGGTAA	58.093	20	687	1635	2321
CGGTTAG	59.084	20	957	3259	4215
CCTGCCTC	58.67	20	1026	1048	2073
TGCATCAA	60.665	20	1483	2225	3707
GCGCCAAT	59.851	20	1057	1208	2264
GTAAGCCT	59.757	20	332	2767	3098
GTACCAGG	60.249	20	1036	2894	3929
TGAGTTCT	59.069	24	378	7933	8310
TCCATTCC	60.266	20	1147	16	1162
GCAACATT	58.872	20	372	2703	3074
TGAATAGC	59.528	20	1049	959	2007
ACCATATC	59.805	20	602	1053	1654
AACCATAC	59.732	21	1355	610	1964
ACACTCCC	59.187	20	763	701	1463
AACGCGGT	61.016	19	1163	1521	2683
CACATTCC	59.716	20	730	2743	3472
CCGTGAAG	59.989	20	1217	3899	5115
CTTGCAAA	59.225	20	255	355	609
AACCAGAT	59.925	20	615	226	840
AGGGACTT	60.307	20	287	4799	5085
TGAACCTC	60.232	20	2940	3533	6472
CTGAGGCA	59.322	20	179	1150	1328
GTTTCTTC	59.676	20	131	408	538
TAAGTTGT	59.964	20	1337	2239	3575
GCTCCTAA	59.942	26	689	5341	6029
GGCTTGAG	59.997	20	426	5630	6055
ACAACACA	59.82	20	1592	98	1689
TTCTCCGT	59.682	20	719	4759	5477
TTTCACCA	60.033	21	1231	7818	9048
CCTTATCC	57.348	20	348	678	1025
CCGGCTGC	60.419	20	1378	49	1426
TGGGTCAA	59.935	20	301	4799	5099
TCCACACG	59.697	20	645	1763	2407
AAGCAAAC	60.257	20	139	7357	7495
TAGAGTAT	60.374	20	239	372	610
GTGTCACA	60.009	20	1942	2054	3995
CATTGAGA	59.209	21	1597	3764	5360
CCTCCTTT	59.886	22	1735	4993	6727

TGAAGGC	59.938	20	1590	5722	7311
TCTTCATG	60.182	20	1325	1673	2997
GATCTTCT	59.434	20	928	107	1034
AGCTGTAG	60.74	20	821	4069	4889
AGCGATAC	59.971	20	1552	1160	2711
GCTGCTGG	59.957	20	808	866	1673
TCCATTCA	60.067	23	285	2826	3110
CTCCTCGA	60.978	20	163	300	462
TCCACACG	59.697	20	349	2099	2447
CCTCGCGT	60.944	20	2587	1714	4300
GCAGACAT	59.83	20	789	7031	7819
TTCCCTGG	60.214	20	190	2362	2551
CAAACTCC	59.734	20	809	137	945
CAACAACT	60.023	23	137	1002	1138
AAGCAGGA	60.015	20	587	316	902
CCAAGTGG	60.865	19	522	127	648
TGGACTCC	58.366	25	1917	207	2123
AGCATGAC	60.945	20	545	4838	5382
GCCCCCTG	61.203	20	264	3017	3280
ATATCTGT	60.059	20	3210	6071	9280
CGAACTTT	59.711	20	411	93	503
TCGGAGAT	59.773	20	916	1474	2389
AACCAGAA	59.786	20	641	403	1043
TCTAATTG	59.777	19	333	1888	2220
ATGTATCG	60.469	20	114	2364	2477
GTTTAACA	57.98	20	594	927	1520
TCATCCAA	60.331	20	729	5118	5846
GAAACAAA	58.653	24	1263	29	1291
GCCATATT	58.453	20	1705	499	2203
TGCAGAGC	60.539	20	944	610	1553
GGCTTGAC	60.118	20	185	1640	1824
TGCCTTTT	60.237	21	1033	179	1211
CATGTCGA	59.028	20	518	3480	3997
CTTCCGAA	59.948	20	682	7398	8079
GGAATGAA	59.939	20	404	2097	2500
CACTTCCA	59.873	20	1348	3080	4427
CTTTTATC	60.031	20	515	513	1027
AGTACCTG	59.062	20	158	1380	1537
TCAAGTGG	59.726	21	1318	4194	5511
GATGTCGT	60.12	20	253	539	791
TGGTCAGG	59.112	22	1055	224	1278
TAACACAA	59.964	20	490	910	1399
CCGTGTTC	60.302	19	1659	965	2623
CTCGGAAT	59.086	20	2260	88	2347
AGTACCTG	59.062	20	158	1380	1537
TGAAAACC	59.654	21	1906	446	2351
ATGGTGCT	59.859	20	1468	80	1547

CTGCAACC	60.136	20	5065	2823	7887
AGGTGGTG	59.962	20	602	11332	11933
GGCTTGCT	59.979	20	382	508	889
TGATCCAT	59.327	20	1325	806	2130
GAAATGCT	58.966	23	1914	322	2235
CTTCCCATC	60.111	20	863	2148	3010
CGGCATGT	60.596	20	1441	1706	3146
AGGAGACT	60.073	20	1697	789	2485
CAAAAATT	59.809	20	321	1602	1922
TTGAAGTT	59.67	20	1062	273	1334
TCCCCGTT	59.04	20	1639	2305	3943
TTGCTGTC	59.905	20	282	3439	3720
CGGAACCA	59.219	20	814	1499	2312
TGCACTGT	58.732	20	1421	286	1706
CAGTTGCA	59.64	20	1967	1414	3380
GCAGTACA	59.101	20	1609	394	2002
GTCTTGAT	60.887	19	1601	2088	3688
TCTTGCAT	60.334	20	546	1618	2163
CTTCTCCTT	59.555	19	3354	513	3866
TTGGCACA	59.992	20	216	3979	4194
CCATGAAG	60.192	20	388	431	818
TCAGGCTT	60.493	20	354	557	910
CCCTGTCG	61.302	20	1172	1053	2224
GATCTTGT	61.484	19	204	166	369
GCAAGACC	59.455	20	1599	876	2474
ACGACCCT	60.306	20	451	939	1389
GCCTCGCA	59.786	20	1014	0	1013
TGTCGTTA	59.758	20	577	2370	2946
CCGTAGAC	59.641	19	164	2535	2698
AGTACCTG	59.062	20	179	5000	5178
CCAGTCGG	60.232	20	421	585	1005
GAGCTGCC	62.254	18	273	1443	1715
CCAGAATT	59.184	21	443	19546	19988
CGTCATAC	60.217	22	995	2814	3808
GCGGCTCT	60.104	20	670	2387	3056
GCGGCTCT	60.104	20	670	6164	6833
GCCTGACG	59.644	20	190	1072	1261
TCAATAGG	59.694	20	1111	2535	3645
GGCTGAAT	59.923	20	396	3846	4241
CTCCGTGG	59.966	20	726	1409	2134
TTGGGCAA	60.012	20	550	2401	2950
CTCGGAAC	60.089	20	1829	369	2197
AACATCGG	57.916	21	1163	894	2056
CTTCATCTT	60.452	20	391	2162	2552
TTGCCGAC	59.952	21	3890	2229	6118
CCATGGTG	60.634	20	469	3429	3897
TCCAAACT	60.103	20	1908	296	2203

GCTATGCG	60.022	20	3202	411	3612
ACCACGAT	59.166	20	731	759	1489
ACCTTCCG	60.786	20	2144	477	2620
AAGGTTG	60.111	20	721	2126	2846
TTTCTCCTT	60.184	20	1664	315	1978
AACCTTCG	59.308	20	1046	5745	6790
ACTGAAAT	59.878	19	435	3949	4383
TGGGAAG	60.042	20	1014	1107	2120
GTAGATG	58.573	20	3779	4629	8407
CCGTAAAT	57.396	23	817	120	936
CAAGCGA	59.942	20	232	2266	2497
CGCATGA	59.132	19	168	3686	3853
ACCGACA	59.245	20	1116	456	1571
CATGCAAG	59.911	20	1775	351	2125
AGAAACCT	59.328	20	432	2324	2755
ACGCTTTT	61.019	20	682	1940	2621
CTTCTTCT	60.126	20	352	394	745
TCATGATT	59.127	20	218	1378	1595
GCCATAAT	59.513	20	426	2839	3264
TCCACACG	59.697	20	657	10012	10668
GTCGCAC	60.526	20	663	148	810
AGTACCTG	59.062	20	158	1380	1537
AAAACAA	59.976	20	673	2779	3451
TTCTGATT	60.426	20	774	331	1104
CGTGTTGT	59.64	20	682	215	896
GGAAAAC	59.916	20	892	265	1156
AACAGAA	60.253	19	1017	1879	2895
AGTACCTG	59.062	20	158	1380	1537
TCTCCTCG	62.453	18	624	778	1401
AGGCACAT	60.37	20	292	698	989
TCCTATGA	59.138	21	266	2167	2432
TGAACTCG	57.287	20	790	147	936
GAGGTCC	59.492	20	653	751	1403
ACCCATCG	60.622	20	327	222	548
AGCACGG	59.746	20	298	1220	1517
GCTAGCTA	60.914	20	1597	2901	4497
TGCCTTAA	60.258	21	2348	2663	5010
GCTAGCTA	60.914	20	1040	382	1421
TTGCAGAA	60.637	20	888	1168	2055
TACCTCGC	60.27	20	529	1147	1675
GGAGAGC	60.576	18	2103	635	2737
GGCCATCT	59.508	20	975	1973	2947
CATCCAGT	59.962	20	1092	1218	2309
CTCCCTCG	60.038	18	1890	189	2078
TCCGTCCT	57.888	20	942	33	974
TCATAATG	60.467	21	497	2444	2940
TCGTGATT	59.287	21	337	966	1302

CACAAATG	59.507	25	1168	3226	4393
TAATCTTG	60.036	20	163	4371	4533
GCCTTTGT	58.629	22	812	52	863
CTCCTTGC	59.679	20	444	265	708
GATGTCGT	60.12	20	179	301	479
CCCTTCTC	58.866	20	411	6014	6424
GAACACCA	61.318	20	3982	301	4282
GTACCAAC	59.41	20	651	763	1413
CAGAATAC	59.971	20	720	1428	2147
ACCCTGTC	60.856	19	200	2491	2690
AGCTGAAC	60.015	20	1012	507	1518
AGTACCTG	59.062	20	158	1380	1537
TATCCTTC	59.622	20	1926	129	2054
ATCAGCCT	61.118	18	1680	2306	3985
CAAGCTTC	59.96	20	176	2770	2945
GGAACTGA	59.762	22	1254	1774	3027
TGACGCTC	58.089	23	2656	1973	4628
AGAACTCA	59.988	18	563	5326	5888
AGCGCACT	60.602	20	767	799	1565
GATCAGGA	60.278	20	291	525	815
GCTATCAC	60.348	20	315	3978	4292
GCTGTATT	61.401	20	1539	707	2245
GATCGAC	59.901	20	1514	282	1795
TCCTCGAG	59.973	20	445	553	997
TGTAGAG	59.312	20	1357	1397	2753
TGTTGGTG	60.152	20	708	3593	4300
ATGATCTG	60.769	20	736	788	1523
CTGAGCTG	60.096	20	340	1672	2011
TGGTGCTA	60.678	20	802	1792	2593
AGAAACTC	60.247	20	721	127	847
AAATCCAT	60.074	20	1041	678	1718
CAGCAGCA	59.988	20	437	3065	3501
TCAGGTCT	59.003	21	724	1468	2191
TCTCCCAT	60.135	20	1266	153	1418
ATGTCCGG	60.578	20	313	1805	2117
GAGGCCTC	59.499	18	1277	38	1314
CAAGGGC	60.964	20	201	2822	3022
AGTCGTCC	59.969	20	688	350	1037
TTCTTTCC	60.375	20	1245	698	1942
AGTACCTG	59.062	20	158	1380	1537
AGGCCCGA	59.962	20	258	453	710
TCCCTCTG	61.35	18	305	116	420
AGCGTCGA	60.35	19	259	137	395
ATGAAGCA	60.255	20	1394	1568	2961
GGTAACTT	60.111	20	204	528	731
GGGAATG	59.661	20	303	2228	2530
TGTACCCA	59.82	20	176	3449	3624

TCACTGGA	59.803	20	700	1160	1859
ATATCTGT	60.059	20	2940	3237	6176
AGTACCTG	59.062	20	158	7524	7681
AGTTCTGC	59.067	21	653	4332	4984
CCCTGTGA	59.401	20	1162	262	1423
CACTTCTT	60.571	20	1064	462	1525
CGCTCTTG	59.945	20	373	1318	1690
AGTCAGTG	60.757	20	242	1418	1659
CAATCCTG	60.363	20	398	875	1272
AGAAACG	59.904	20	1153	987	2139
CCCGGCGA	62.168	20	1610	2321	3930
GCACCTCA	60.035	20	1442	19	1460
CTAACCTC	60.299	20	666	5678	6343
ATGGGACA	59.82	20	805	345	1149
GGGGATC	60.169	20	1593	1103	2695
TTGGCTAG	60.344	20	317	3423	3739
CTCCTAGC	60.012	20	1136	325	1460
CCTTGTCC	58.287	20	590	3183	3772
TCGTACTT	59.441	20	2752	255	3006
GCTCAGG	59.604	20	2692	278	2969
AGTACCTG	59.062	20	158	6110	6267
GGCCATGA	60.812	20	2570	323	2892
TCCAGCCA	60.112	20	138	329	466
TATATCCC	59.64	20	333	3656	3988
AGGGATAT	60.006	19	685	873	1557
GCCGATTT	59.962	20	174	2052	2225
CTAGCCG	60.384	20	1027	30	1056
AGTACCTG	59.062	20	158	1380	1537
GTCCCTCT	59.986	20	2065	2544	4608
TTTGCATG	59.271	21	1888	2926	4813
ATTGTCTC	60.226	20	938	2478	3415
GTACGTG	60.397	20	249	306	554
AGTACCTG	59.062	20	158	2473	2630
CACGGGA	59.3	20	886	892	1777
GGGGAAG	59.955	20	903	871	1773
GCCATTG	59.962	20	1346	914	2259
CAAACAAA	60.351	19	922	1461	2382
TCGAGCTT	60.235	21	833	1513	2345
GGCTTCAG	58.659	21	377	274	650
TCCACACG	59.697	20	671	2321	2991
ATCTCGTA	59.904	20	759	515	1273
AAGGACA	60.015	20	1481	39	1519
GAGTATC	59.653	20	337	1233	1569
GAGGGAG	59.651	20	2651	10403	13053
AGTTCCAT	61.192	20	5076	2167	7242
GATGCAGT	59.261	20	2939	616	3554
TAGGCAA	59.836	20	417	258	674

CAGATTGT	60.112	20	753	7430	8182
CACCATGT	60.008	20	444	443	886
TCAAGGG	59.953	20	483	317	799
TTCTCAGC	59.836	20	253	2602	2854
TATGTGCG	59.93	20	2041	170	2210
CATGATAA	60.227	22	1256	2781	4036
ATACGCTA	60.832	19	328	386	713
AGGCACAT	60.37	20	293	722	1014
ATTTCTCC	59.629	20	310	172	481
GTTGACA	59.819	20	5938	104	6041
CATGGGCT	60.073	20	2488	1821	4308
CCAGCATT	59.239	20	1121	2118	3238
TCTGTTGC	60.05	20	1039	1138	2176
GCACTTGG	59.847	20	792	1021	1812
CGGCCTG	59.873	19	173	1380	1552
AGCATGTG	59.905	20	410	12	421
CAGTGCA	60.449	20	669	3839	4507
TACAGAA	60.246	20	470	783	1252
GCAGAAG	59.902	19	1797	765	2561
GCTGACG	59.297	20	1018	30	1047
GTTTCTCG	59.333	20	883	1208	2090
TCCATTCC	60.266	20	929	1104	2032
AAGACTTG	60.118	20	503	200	702
TTGCTGCA	59.948	20	1280	619	1898
TCACAGA	59.637	20	146	3365	3510
GAACGAC	59.569	20	788	1119	1906
TACCGCGT	57.081	21	140	104	243
AAACCATA	59.939	24	1084	509	1592
CTCCGGCT	61.965	18	885	337	1221
CAACAGA	59.389	20	315	341	655
CTGCCACT	60.218	20	808	1055	1862
TCAACCTT	58.823	21	275	1904	2178
GCTTCACC	59.997	20	1866	249	2114
CTCAACAA	59.626	21	501	182	682
AAGCAGA	60.277	20	198	1442	1639
CGTCTTTC	62.278	18	1047	288	1334
GGCCACA	60.142	20	1734	213	1946
AGTACCTG	59.062	20	158	1380	1537
GTCTCCTC	58.388	18	554	876	1429
TGCCCCAG	59.836	20	750	288	1037
AGTACCTG	59.062	20	179	1380	1558
TCATTTGG	59.767	20	1015	2980	3994
ATCTGGTA	60.285	20	1214	123	1336
GGCCTTGA	60.214	20	1163	2689	3851
GGCCTTGA	60.214	20	1163	478	1640
GGAAACC	59.897	20	2950	525	3474
GTTGATGA	59.776	20	206	338	543

TCAATTCC	59.525	20	668	6509	7176
GAAGTCGT	59.152	20	1264	2106	3369
TCCATCTC	59.886	20	1923	2025	3947
AAAAAGG	59.94	19	529	6176	6704
AGCTGATC	59.222	22	303	9764	10066
ATTGGAGT	60.074	20	597	2017	2613
CGTCACCC	59.984	20	653	3303	3955
GCCATTCT	59.81	20	2511	204	2714
ATCGACTC	60.222	19	3152	2864	6015
TCGACAGA	59.88	20	1121	70	1190
TCACATTG	59.525	20	1234	154	1387
GGGAGTCA	58.912	22	1107	11515	12621
TGGTAAGA	59.124	21	630	12833	13462
GCGTCCAT	60.34	20	207	3402	3608
CTGCCGCT	59.911	20	913	159	1071
CAGCACCT	59.152	20	715	1131	1845
GTACAGCT	59.501	20	1837	882	2718
ACCAGGTA	60.517	20	2066	199	2264
TTCCTTTCA	59.659	23	7862	463	8324
AACCCAAA	60.399	20	1044	326	1369
GGACTTGA	61.16	20	1313	1558	2870
AGCCGTCT	59.882	20	286	1428	1713
CGCTGAG	60.678	20	645	2179	2823
CATAATTG	60.235	19	275	2066	2340
CGTCGCCA	58.905	18	1748	1313	3060
GGCTGCA	59.542	19	1231	2154	3384
CTCCGCCT	60.024	18	168	378	545
CTTCGAAC	59.873	20	198	1256	1453
CCATGTTC	58.623	20	2732	2763	5494
GCACCGA	60.47	20	298	50	347
CCTTGCTG	60.119	19	2193	248	2440
AACTGCCT	60.074	20	348	7630	7977
GAGGAAG	58.796	21	413	2304	2716
GGCGAGG	59.241	18	1376	4302	5677
TCCAGTGA	59.986	20	495	5648	6142
TCCACACC	59.283	20	624	142	765
ACACCACC	60.151	20	154	328	481
GACCACCT	60.421	20	1817	3842	5658
CCTCCAAA	59.143	20	1225	1353	2577
CCAAATTA	59.564	20	235	1684	1918
CCCTCTTC	60.175	20	409	1797	2205
CCCCCTCT	60.042	20	535	2628	3162
ATTTTTCCA	60.029	20	513	9	521
GGCAGAT	60.126	21	842	3069	3910
AGGTGAT	59.697	20	2653	237	2889
GTTGCATC	60.492	20	462	2440	2901
GCTGGTCT	59.851	20	703	1871	2573

TTTTTCGT	60.227	20	408	3425	3832
TCCAGTGT	60.001	20	214	995	1208
CAACACCG	60.065	20	1000	438	1437
AAGATCAA	59.753	24	773	683	1455
CCTTCTTC	60.067	20	789	1305	2093
AGCATGTC	60.032	19	505	2586	3090
CAAGATCC	60.073	20	5197	462	5658
AGTACCTG	59.062	20	158	1380	1537
CGATCGTT	60.397	20	1683	6759	8441
AGTACCTG	59.062	20	158	10995	11152
ATCTCCAC	59.685	20	534	797	1330
TTAACCAA	60.399	20	859	1363	2221
TTTTTGGT	57.025	21	538	1619	2156
AAACGAGT	59.992	21	634	2606	3239
AGTACCTG	59.062	20	158	8755	8912
CTTGTTCT	60.11	20	520	1412	1931
CCAATTCT	59.903	20	1315	347	1661
GATCACCG	60.054	18	738	5464	6201
CAGAACTC	59.889	21	3508	872	4379
GGTTCACC	60.353	20	2570	25896	28465
GAGGTCGG	59.312	20	1962	29750	31711
GGCATTGA	60.304	20	747	549	1295
AGTACCTG	59.062	20	158	7243	7400
CGTCAACT	59.494	20	345	7483	7827
AGGCACAT	60.37	20	293	698	990
TCTGGTGC	59.897	20	1472	88	1559
GGGAATAC	60.096	20	835	342	1176
GGCGGTAC	59.572	18	1393	5	1397
TTCTCCCT	58.875	22	1083	4380	5462
AAAGCCAA	59.843	20	317	6	322
GGATATCG	60.861	18	689	1028	1716
CATTTGGA	60.096	19	513	4874	5386
GAAGCGCA	60.971	20	292	5601	5892
CAATTGAA	61.266	20	1334	366	1699
TTTGGGTG	59.297	20	307	2434	2740
GTGGTGGA	60.088	18	212	4629	4840
TACCTGAA	59.959	20	156	1344	1499
TTCCAGTC	60.051	20	8148	6011	14158
AGGTTGGC	59.736	19	1361	2001	3361
CCAATCGC	61.607	18	537	7	543
AGTACCTG	59.062	20	179	1380	1558
CTGGCCTT	60.366	20	598	449	1046
CACCACTG	60.627	20	2291	205	2495
ATGGCTTC	60.111	20	784	22	805
AGTACCTG	59.062	20	158	2534	2691
ATCCTGAA	59.67	20	235	10	244
CAGAGTTT	59.201	21	1129	26	1154

AAATATGC	59.929	20	1344	3373	4716
CAGTACTG	60.012	20	1043	4967	6009
TCCACACG	59.697	20	635	1819	2453
TGCCTTCC	59.953	20	2069	196	2264
CCTGGAAA	60.067	20	479	4105	4583
CCTTAAAA	60.792	20	915	6486	7400
TGTTCATA	59.972	24	713	10242	10954
GGATGGCC	60.99	19	1855	2633	4487
TAAGGGAA	59.308	20	417	63	479
TCCTCGGT	60.111	20	969	96	1064
AGTACCTG	59.062	20	158	1380	1537
CCTTCACT	59.521	20	3753	642	4394
TGGTCCAT	60.402	20	1245	4491	5735
CACTTTGG	60.152	20	1242	2315	3556
CCTGCAGC	60.374	20	1533	3537	5069
TCCTCCGC	60.218	20	192	595	786
TAGGGACT	60.452	20	368	1651	2018
AGAGGGTA	59.848	20	238	954	1191
AGGTTGTA	60.126	19	1018	582	1599
TGATGGTT	59.727	20	143	2099	2241
CGAACCCT	60.149	20	870	49	918
TCTGTCCC	59.827	20	314	108	421
TGCATTGT	59.67	20	2232	864	3095
TAGTCTGA	59.897	20	1289	100	1388
GCAATATC	58.342	23	610	4030	4639
ATGTCAGG	59.82	20	560	4368	4927
GCAGCCGA	59.962	20	254	1973	2226
TTTGCAGG	60.214	20	956	178	1133
CACACGAC	59.676	20	507	3660	4166
CCTCCCTCT	60.6	18	480	6832	7311
ACTGCCAT	59.535	19	330	624	953
CCAATGAG	61.001	20	529	86	614
GCAGTTGA	59.366	20	643	8	650
CGTAGAGT	59.034	20	450	1675	2124
GCGGCTCT	60.104	20	670	7279	7948
CGATCGAG	59.859	20	831	15	845
GCTCACTG	58.95	21	312	2703	3014
AAATGCAC	59.939	20	1028	15	1042
TGCAGGAC	59.415	20	335	18	352
ACACGACC	59.853	20	3407	64	3470
TGCCTCTCT	60.277	20	1026	2792	3817
TCCACACG	59.697	20	657	1617	2273
ACATCTCC	61.192	20	8159	369	8527
TTCCTCATT	59.631	21	2258	2349	4606
AGCTACCA	59.639	20	1798	280	2077
TCCCTCTGG	60.624	20	811	2071	2881
TAGCTACC	60.11	20	1667	6641	8307

GATGTGG	60.135	20	1612	739	2350
AGTAAGG	59.994	20	2073	449	2521
TGCTCAAT	59.68	24	696	87	782
CCCGTACT	59.721	20	6070	230	6299
CAGCAAG	60.073	20	7520	6827	14346
TGATATCC	59.883	20	748	755	1502
TTTGGGTG	59.297	20	353	3223	3575
TCCACACG	59.697	20	309	755	1063
TATCAATA	58.599	20	308	854	1161
GTGCGGA	59.694	20	1058	9139	10196
AGCTGAA	59.401	22	613	3883	4495
AGGTCGTT	59.34	20	475	6848	7322
TGTCATCG	59.332	21	915	7496	8410
CTCGAAT	57.865	20	986	8388	9373
TAGTCGTT	59.745	20	2045	446	2490
CTTCTTCA	60.291	20	2467	693	3159
TGCCAACT	59.591	20	958	728	1685
AGTACCTG	59.062	20	158	2631	2788
GTACGGC	59.502	19	601	4965	5565
GATTGAG	59.878	19	718	1581	2298
ATTTCACC	59.945	20	839	23	861
GCATCAG	59.207	20	1237	79	1315
AGTACCTG	59.062	20	179	1378	1556
AGTGCTT	59.817	20	241	253	493
GCACGAA	58.909	20	922	756	1677
CGTTCGTT	60.073	20	260	218	477
ACGCTTCA	60.132	20	148	4154	4301
GAATGCT	59.973	20	178	6752	6929
GGGCACT	59.942	19	443	425	867
AGTACCTG	59.062	20	158	2521	2678
AGAAGCC	59.357	20	1399	3135	4533
TCACGTTT	60.134	20	1223	2008	3230
AGCCAAT	59.7	20	3971	352	4322
TGCTGTT	59.873	20	1813	574	2386
AGGAGTG	60.695	19	219	1335	1553
CCGAGTA	59.823	20	249	1695	1943
TAGGTGG	59.591	20	1018	515	1532
GCAAAGC	59.726	20	676	3760	4435
TCCATTGT	59.956	21	757	5230	5986
GTGTCTTG	59.912	20	2242	1224	3465
TGGTCGA	59.187	20	600	2233	2832
TGAACCAT	60.453	23	330	2674	3003
GGAAGAT	60.169	20	789	1733	2521
GGCTTGA	59.997	20	404	2759	3162
AGTACCTG	59.062	20	158	2596	2753
CTGTATCG	60.668	20	1599	396	1994
TGAGGTA	60.081	21	904	6471	7374

GACAACCA	59.555	20	401	1626	2026
AGACCCTT	58.646	20	388	543	930
CCTTCTTT	59.067	23	428	1689	2116
TAGCCCC	60.514	20	1084	19	1102
CCACAAA	60.298	20	193	1656	1848
AGAAACA	59.076	21	283	6004	6286
TCCTGGGA	59.123	20	719	11226	11944
TGAACAA	59.293	20	668	231	898
GGGATGT	59.797	20	916	1714	2629
GCAACAT	59.82	20	897	159	1055
TGGACTTT	60.565	21	864	2319	3182
GCTGCTTG	61.006	20	2025	183	2207
TGGTTCTT	60.666	23	2298	1096	3393
CATGTTCA	60.343	20	920	3621	4540
TGACAAA	60.297	21	3145	1196	4340
CCCCCTGT	59.473	20	279	4876	5154
AGTACCTG	59.062	20	158	2749	2906
CTCCTTGA	60.022	20	189	3320	3508
CGATGTTG	60.152	20	652	927	1578
GGTGCTC	60.361	20	318	442	759
TGTTTTCC	60.671	20	173	2833	3005
CCACCAA	59.873	20	994	4155	5148
TCCACACG	59.697	20	374	1396	1769
TCGTCGAT	59.813	20	990	3192	4181
GGTGATG	60.924	20	190	4139	4328
CTTCTTCT	59.993	20	2127	11535	13661
TTGAAAG	61.046	20	1643	1992	3634
AGGTCTC	60.527	20	544	5014	5557
CTTCAAAT	60.201	18	245	322	566
GAGCATC	59.837	20	188	1324	1511
CCGAGTA	59.823	20	273	2374	2646
CAAGCAC	60.065	21	469	62	530
CAAGCAG	60.065	21	1001	514	1514
ATATCTGT	60.059	20	3143	5741	8883
CTTCGCCT	59.99	20	638	3949	4586
GATGTTTG	60.272	20	782	4567	5348
AGCTGCT	60.916	20	387	348	734
GCAGCTG	59.992	20	124	316	439
TAGCGCT	60.14	20	282	1084	1365
AGGCACAT	60.37	20	292	698	989
TACCATTT	60.096	20	1336	4	1339
CTTCTCCT	59.864	20	1512	701	2212
GTGGGTGT	60.395	20	419	43	461
GAGTATC	59.653	20	337	1233	1569
TGGGATCT	60.003	20	512	115	626
GAACAGA	59.663	18	134	4831	4964
ACCAGCT	59.907	20	914	238	1151

AAATCCTC	59.483	20	657	93	749
GCTAAACC	60.214	20	1997	242	2238
CAAACGGA	60.745	20	627	171	797
TGGGATAC	60.537	20	2545	217	2761
TCTTGGTC	60.266	20	1050	4006	5055
CCTCCAAA	59.143	20	1423	1352	2774
CTTTACGC	59.96	20	2610	1169	3778
CCAAATTA	59.564	20	213	1536	1748
CCCTCTTCT	60.175	20	398	1727	2124
GAGGCAAA	59.234	21	870	433	1302
CCCCATCC	60.011	20	268	1310	1577
CACCAAGC	59.734	20	851	4066	4916
TACTCCCC	59.55	20	236	2499	2734
TGTCAACT	58.767	24	484	2125	2608
AAAATCAG	57.669	23	244	52	295
TCATCAAG	59.955	20	639	2048	2686
CCTTGGAT	60.495	20	2208	2317	4524
TCCAGTGT	60.001	20	183	4734	4916
CTTTCTTC	59.252	20	1022	1362	2383
GAGAGCCC	59.989	20	787	745	1531
CCATTAGG	61.326	20	334	270	603
TCCTTCCTC	60.523	20	797	15	811
TTGATCTT	60.461	20	92	792	883
TCGTGGTA	59.74	20	441	246	686
TTTTGGGA	59.767	20	1312	871	2182
AAGAGGCA	57.387	18	1627	605	2231
ACCGACCC	60.132	20	1443	1296	2738
TTTTCCTC	59.361	20	321	2936	3256
TAAAAGCA	60.368	20	543	3695	4237
TGGTTTAC	59.964	20	149	3837	3985
ACGATCAG	60.16	18	268	3951	4218
CACCACAA	59.52	20	833	41	873
TTGAGACT	59.831	20	6543	320	6862
AACTTGAT	61.014	20	1028	219	1246
ATATCATT	59.468	20	348	74	421
ACCACTCG	59.105	20	227	1066	1292
ACGACCTC	61.262	18	1092	1213	2304
CAGGGTTC	60.073	20	368	2586	2953
TCGAGGCA	59.717	20	1933	201	2133
CCTGCAGT	60.555	20	520	277	796
TCTTCCTCA	59.929	23	2189	25	2213
TGAACAAT	60.002	21	633	7960	8592
GCTTGGCA	59.985	20	975	8626	9600
AGCTACCA	59.639	20	2205	4154	6358
GGCTTGAC	59.997	20	509	8622	9130
GGAGAACA	60.048	20	236	297	532
AAGGTTTT	58.129	23	357	686	1042

AACTTGAT	61.014	20	1043	992	2034
GCCCGACA	59.734	19	515	55	569
GATCCATT	60.036	20	818	946	1763
TATCACCT	60.073	20	2722	257	2978
TTGGCCAC	60.051	20	507	3086	3592
GTCTTCTC	59.166	20	635	2871	3505
ATTGCTAC	60.278	20	1249	497	1745
AGCTTCAG	59.176	19	177	7	183
TCAGACTT	59.903	20	188	3084	3271
GAACTGCA	59.88	20	231	3994	4224
CACGACAG	59.988	19	5206	1725	6930
TTGAAATT	60.049	20	667	364	1030
TGCATGTA	59.895	20	1903	40	1942
CAGGCGGA	60.246	18	333	176	508
GTACCTGA	59.449	20	157	9578	9734
CAGATGTG	59.831	20	707	1686	2392
GTGATCAC	59.189	20	163	229	391
TGTTAGAC	60.088	20	578	629	1206
GTCGCACC	60.526	20	282	432	713
AGTACCTG	59.062	20	158	702	859
GCCCAGAA	60.051	20	946	37	982
ATGCGTCC	60.12	20	218	9585	9802
TTGAAAGT	58.551	23	2642	10037	12678
GCATGGTG	61.188	19	162	2815	2976
AACTTGAT	61.014	20	1071	177	1247
ATGATCCC	59.843	20	365	612	976
GAAGATG	59.694	20	758	8167	8924
CCAATCAC	59.648	20	296	1508	1803
CTGAGTCG	60.668	20	585	6831	7415
TTTGTCGC	60.643	18	676	404	1079
TGGTTCTA	58.96	21	552	9540	10091
AGGTCATT	60.074	20	215	585	799
CCATTCCC	59.955	20	527	5675	6201
ACCCTTTA	59.734	20	1062	374	1435
GAACAGC	59.56	20	725	1416	2140
TGAAGAAT	60.051	20	1558	623	2180
AGCAGAC	60.255	20	2480	5460	7939
CCTCTGAG	60.262	21	980	11135	12114
TTGGCAGA	59.869	21	1628	926	2553
TGGCATG	60.201	20	327	2475	2801
GCTTCTCA	59.457	20	703	2432	3134
GCCACCTT	59.682	20	141	1360	1500
ATCCCCTT	59.594	20	1246	2375	3620
TGGAGCAA	60.03	23	484	7232	7715
GCAAGCTT	59.96	20	169	741	909
GCAGAAGA	59.957	20	3102	405	3506
AGTACCTG	59.062	20	179	2336	2514

TTCCTTCAT	60.195	20	844	5435	6278
GGCTCAA	59.844	20	899	3135	4033
AGTACCTG	59.062	20	179	7010	7188
CTCCTTGA	60.022	20	189	7603	7791
GGTCGTTG	60.823	19	637	178	814
GGATCAAA	60.032	20	264	360	623
AGGGGCG	60.476	20	1968	11	1978
AGTACCTG	59.062	20	179	4511	4689
CCATCCAC	60.353	20	634	329	962
TCTAAGGA	59.982	20	650	770	1419
AACAGCC	60.497	18	339	28	366
GCTATGA	60.142	20	392	1797	2188
AGCCCAAA	59.993	20	254	3782	4035
GGAATCG	59.955	20	294	1255	1548
AGTACCTG	59.062	20	158	1380	1537
TCCACACG	59.697	20	673	1819	2491
CCAAGCT	60.134	20	555	300	854
CTCTCCAC	61.16	20	798	172	969
GCCATTCG	59.951	20	1460	1894	3353
AGTACCTG	59.062	20	158	1380	1537
CGTGCTCT	59.473	20	855	2234	3088
AGGCTTCT	59.529	21	1495	12544	14038
ATATCTGT	60.059	20	3372	5864	9235
AGTACCTG	59.062	20	158	10588	10745
AGTACCTG	59.062	20	158	1380	1537
TAATCCAA	59.901	20	588	3177	3764
ATCTGTTG	59.927	20	258	8421	8678
AACATCCC	60.14	20	869	2677	3545
TTAGCTGT	60.529	20	1375	2287	3661
GTCTTGCC	60.622	20	1861	2754	4614
CCCTTTAGT	60.626	21	3278	300	3577
GTGTAGGA	60.261	20	222	3001	3222
ATATCTGT	60.059	20	2797	4673	7469
AACAAAA	60.059	20	1299	9	1307
AGTACCTG	59.062	20	158	624	781
CGATTTCT	60.904	20	248	1441	1688
ACGGTGT	60.005	20	3626	7004	10629
TGACATCA	60.256	21	192	3699	3890
TACCTGAA	59.959	20	294	1912	2205
GTCTTTCT	59.813	20	390	3500	3889
AGTACCTG	59.062	20	158	2450	2607
CTTGTATA	60.292	20	1103	197	1299
TGAGCATT	60.136	20	793	375	1167
GCTTCCCA	60.483	22	337	3019	3355
AGTACCTG	59.062	20	158	1380	1537
CAGGTATT	60.357	20	1228	94	1321
GGCGTAGT	59.63	22	440	3540	3979

AATTCAAA	57.821	20	1052	2815	3866
CCACTTGC	59.598	20	895	732	1626
AGGACCA	59.867	20	792	127	918
GCAGCTT	60.504	20	226	334	559
ATCCAAA	60.058	19	585	1257	1841
CTCACGT	60.112	20	298	3703	4000
AATTTCG	60.832	19	224	84	307
TCGGCTTT	59.813	20	851	611	1461
TCTCCTCG	60.247	19	2696	57	2752
TTTTCGCC	60.236	20	958	5152	6109
AACTCAA	60	20	1771	1541	3311
GCTTCTG	59.222	20	404	64	467
TAGTGCTT	59.452	20	653	3080	3732
CAATTAGT	60.508	20	1712	1640	3351
ATGTTTTG	59.797	20	419	2694	3112
GCTATCTG	59.983	20	419	106	524
AGGGGTA	59.813	20	707	683	1389
AACCCGG	59.856	20	778	3284	4061
CAGCAGC	60.104	20	1532	1216	2747
CAAATTCT	58.836	22	986	429	1414