

SeqID	refPos	refStran	refBase	cov	C_count	methRa	mut_cou	mutRat	CalledB	CB_cou	state	c95_CI	c95_CI	p_value	p_value	score	seqContext	candidateName	
chr1	892380	-	C	36	10	0.278	0	0	T	26	M	0.158	0.44	5E-14	2E-06	5E-14	21.112	ggagatggagCggaggaagga	m5C_65
chr1	2835877	-	C	56	21	0.375	0	0	T	35	M	0.26	0.506	0	5E-08	0	109.24	ggagacgggCagggaagacag	m5C_666
chr1	3409584	-	C	33	11	0.333	0	0	T	22	M	0.198	0.504	2E-16	3E-06	2E-16	34.007	gggggggCtCggacgggg	m5C_671
chr1	3409586	-	C	35	21	0.6	0	0	C	21	M	0.436	0.744	0	5E-05	0	183	tcggggggaCtctggacgg	m5C_659
chr1	6673481	-	C	31	12	0.387	0	0	T	19	M	0.237	0.562	0	5E-06	0	56.959	tcggggggcCggggggggga	m5C_519
chr1	8925499	-	C	31	20	0.645	0	0	C	20	M	0.469	0.789	0	4E-05	0	187.79	gctggctacaCtgaataagg	m5C_1303
chr1	11968263	+	C	49	18	0.367	0	0	T	31	M	0.247	0.507	0	8E-07	0	88.794	ctaaagatttCtggggagga	m5C_108
chr1	11968264	+	C	55	16	0.291	0	0	T	39	M	0.188	0.421	0	7E-09	0	60.067	taagatttCtggggagagaa	m5C_112
chr1	11968276	+	C	130	60	0.462	0	0	T	70	M	0.378	0.547	0	3E-14	0	453.81	tggaagagaaCgaaggaggt	m5C_100
chr1	11968287	+	C	82	44	0.537	0	0	C	44	M	0.429	0.64	0	5E-10	0	377.91	gaggggggCtgaaccaat	m5C_124
chr1	11968293	+	C	65	42	0.646	0	0	C	42	M	0.525	0.751	0	2E-07	0	440.79	gagctgaaaCcaattttttg	m5C_115
chr1	11968307	+	C	61	36	0.59	0	0	C	36	M	0.465	0.705	0	6E-08	0	334.8	tttttgaggCctggcgttc	m5C_105
chr1	11968312	+	C	68	37	0.544	0	0	C	37	M	0.427	0.657	0	8E-08	0	315.66	tgaggccttgCgtttctagc	m5C_109
chr1	11968317	+	C	67	37	0.552	0	0	C	37	M	0.434	0.665	0	8E-08	0	320.84	cctggctttCtagcagggc	m5C_113
chr1	11968322	+	C	55	32	0.582	0	0	C	32	M	0.45	0.703	0	7E-07	0	288.21	cgtttctagCagggtctatt	m5C_107
chr1	11968327	+	C	61	35	0.574	0	0	C	35	M	0.449	0.69	0	5E-08	0	314.27	cttagcaggCttattttaag	m5C_106
chr1	12306131	+	C	38	10	0.263	0	0	T	28	M	0.15	0.42	9E-14	2E-06	1E-13	19.504	tccaggctgaCtggggggag	m5C_331
chr1	15755130	+	C	32	11	0.344	0	0	T	21	M	0.204	0.517	2E-16	3E-06	2E-16	35.144	aggaaggaCaaaggcagagc	m5C_93
chr1	15755135	+	C	49	12	0.245	0	0	T	37	M	0.146	0.381	2E-15	7E-08	2E-15	25.801	gagatcaaggCagagcaggag	m5C_92
chr1	15755140	+	C	55	11	0.2	0	0	T	44	M	0.116	0.324	3E-13	4E-10	3E-13	15.923	caaggcagagCaggaagaaag	m5C_95
chr1	16134098	-	C	35	16	0.457	0	0	T	19	M	0.305	0.618	0	2E-05	0	97.49	tcggagatCtggagagagag	m5C_784
chr1	16134107	-	C	31	17	0.548	0	0	C	17	M	0.378	0.708	0	2E-05	0	128.42	cttaccgaatCcggaagatct	m5C_782
chr1	16861780	-	C	338	82	0.243	0	0	T	256	M	0.2	0.291	0	0	0	327.94	gattccgggCagggaatttg	m5C_827
chr1	16861784	-	C	337	114	0.338	0	0	T	223	M	0.29	0.39	0	0	0	660.83	gttcgattccCggtcagggaa	m5C_817
chr1	16861785	-	C	326	115	0.353	0	0	T	211	M	0.303	0.406	0	0	0	696.62	gggtcgattCcggtcagggga	m5C_799
chr1	16861786	-	C	335	119	0.355	0	0	T	216	M	0.306	0.408	0	0	0	728	gggtcgattCccgggcaggg	m5C_800
chr1	16861799	-	C	338	138	0.408	0	0	T	200	M	0.357	0.461	0	0	0	985.87	accgcgcggCccgggttga	m5C_785
chr1	16861802	-	C	308	97	0.316	1	0.003	T	210	M	0.267	0.37	0	0	0	517.02	ttcacgcgcCggccggggt	m5C_816
chr1	16861804	-	C	303	121	0.399	0	0	T	182	M	0.346	0.455	0	0	0	836.8	ctttaccgcCgcggcccg	m5C_807
chr1	16861805	-	C	286	92	0.322	0	0	T	194	M	0.27	0.378	0	0	0	497.19	gctttaccgcCgcggcccg	m5C_805
chr1	16861807	-	C	258	86	0.333	0	0	T	172	M	0.279	0.393	0	0	0	479.24	gcgctttacCgcgcggccc	m5C_812
chr1	16861808	-	C	251	72	0.287	0	0	T	179	M	0.234	0.346	0	0	0	337.6	ggcgctttcaCcgccgcggc	m5C_810
chr1	16861810	-	C	235	68	0.289	0	0	T	167	M	0.235	0.35	0	0	0	319.79	tcggcgctttCaccgcgcgg	m5C_789
chr1	16861814	-	C	199	65	0.327	0	0	T	134	M	0.265	0.395	0	0	0	344.88	ggatccggcCttttaccgcc	m5C_811
chr1	16861816	-	C	186	73	0.392	0	0	T	113	M	0.325	0.464	0	0	0	474.72	taggaatcgCgctttaccgc	m5C_795
chr1	16861819	-	C	173	56	0.324	0	0	T	117	M	0.258	0.397	0	0	0	289.48	ggctaggaatCggcgctttca	m5C_802
chr1	16861834	-	C	104	24	0.231	0	0	T	80	M	0.16	0.32	0	2E-16	0	76.926	ccctggggtCtagggctag	m5C_806
chr1	16861842	-	C	32	7	0.219	0	0	T	25	M	0.11	0.388	8E-10	3E-07	9E-10	6.9997	ctgggtgccCtgggggtca	m5C_796
chr1	17004798	-	C	39	8	0.205	0	0	T	31	M	0.108	0.355	2E-10	7E-07	2E-10	8.4438	gcctcccatgCgggaagaccg	m5C_820
chr1	17004802	-	C	40	22	0.55	0	0	C	22	M	0.398	0.693	0	6E-05	0	175.25	tctgccttcCatgcccagga	m5C_783
chr1	17004806	-	C	81	30	0.37	0	0	T	51	M	0.273	0.479	0	1E-11	0	163.99	gaattctcgcTctccatcg	m5C_804
chr1	17004807	-	C	95	43	0.453	0	0	T	52	M	0.356	0.553	0	1E-11	0	306.44	agaattctgcCtcccatg	m5C_825
chr1	17004809	-	C	103	60	0.583	0	0	C	60	M	0.486	0.673	0	2E-11	0	583.2	gtagaattcCgctccccatg	m5C_818
chr1	17004811	-	C	124	78	0.629	0	0	C	78	M	0.541	0.709	0	1E-12	0	844.47	tggaatattCtgcctcccca	m5C_792
chr1	17004835	-	C	77	36	0.468	0	0	T	41	M	0.36	0.578	0	2E-09	0	259.42	tccagagaggCgtgggggt	m5C_788
chr1	17052083	+	C	31	19	0.613	0	0	C	19	M	0.438	0.763	0	3E-05	0	166.53	taggggttatCatgttgctt	m5C_709
chr1	17199089	+	C	156	37	0.237	0	0	T	119	M	0.177	0.31	0	0	0	131.17	ccctggggtCtagggctag	m5C_729
chr1	17199104	+	C	214	79	0.373	2	0.009	T	133	M	0.31	0.439	0	0	0	490.37	ggctaggattCggcgctttca	m5C_778
chr1	17199107	+	C	229	86	0.376	0	0	T	143	M	0.315	0.44	0	0	0	542.42	taggaattcgCgctttaccgc	m5C_680
chr1	17199109	+	C	240	81	0.34	2	0.008	T	157	M	0.283	0.403	0	0	0	458.62	ggatccggcCttttaccgcc	m5C_724
chr1	17199113	+	C	265	101	0.381	0	0	T	164	M	0.325	0.441	0	0	0	656	tcggcgctttCaccgcgcggg	m5C_757
chr1	17199115	+	C	277	95	0.343	0	0	T	182	M	0.29	0.401	0	0	0	550.14	ggcgctttcaCgcgcgcggc	m5C_698
chr1	17199116	+	C	284	132	0.465	0	0	T	152	M	0.408	0.523	0	0	0	1076.2	gcgctttacCgcgcggccc	m5C_712
chr1	17199118	+	C	284	74	0.261	0	0	T	210	M	0.213	0.315	0	0	0	315.16	gctttaccgcCgcggcccg	m5C_705
chr1	17199119	+	C	292	107	0.369	2	0.007	T	183	M	0.315	0.426	0	0	0	675.13	ctttaccgcCgcgcgcggg	m5C_727
chr1	17199121	+	C	293	119	0.409	2	0.007	T	172	M	0.354	0.466	0	0	0	842.5	ttcacgcgcCggccggggt	m5C_764
chr1	17199124	+	C	295	136	0.472	7	0.024	T	152	M	0.415	0.53	0	0	0	1129.6	accgcgcggCccgggttga	m5C_696
chr1	17199132	+	C	290	82	0.283	0	0	T	208	M	0.234	0.337	0	0	0	383.81	ggccggggtCgattccggc	m5C_776
chr1	17199137	+	C	302	87	0.29	2	0.007	T	213	M	0.242	0.344	0	0	0	420.32	gggttcgattCcgggcagg	m5C_762
chr1	17199138	+	C	299	121	0.407	2	0.007	T	176	M	0.353	0.464	0	0	0	854.39	gggtcgattCcggcaggga	m5C_694
chr1	17199139	+	C	287	102	0.358	2	0.007	T	183	M	0.304	0.415	0	0	0	621.11	gttcgattccCgggcaggaa	m5C_758
chr1	17199143	+	C	288	101	0.353	2	0.007	T	185	M	0.3	0.41	0	0	0	606.07	gattccggcCagggaatttg	m5C_689
chr1	17439797	-	C	55	17	0.309	0	0	T	38	M	0.203	0.44	0	1E-08	0	68.959	ccctggggtCtaggggttag	m5C_798
chr1	21012796	+	C	47	17	0.362	0	0	T	30	M	0.24	0.505	0	6E-07	0	81.484	agggagagaaCagggaagaga	m5C_74
chr1	21103142	-	C	42	16	0.381	0	0	T	26	M	0.25	0.532	0	4E-07	0	79.998	aaagggggaCctgaagatga	m5C_86
chr1	25554662	-	C	33	15	0.455	0	0	T	18	M	0.298	0.62	0	1E-05	0	89.528	gcagaagatgCagaaagatgg	m5C_175
chr1	28358600	-	C	47	30	0.638	0	0	C	30	M	0.495	0.76	0	1E-05	0	297.21	ggctgtagtCgctatgctga	m5C_2374
chr1	28358608	-	C	42	29	0.69	0	0	C	29	M	0.54	0.809	0	1E-05	0	313.05	gagtcctggCtgaaggcgc	m5C_2375
chr1	28358613	-	C	38	29	0.763	0	0	C	29	M	0.608	0.87	0	0.0002	0	352.6	cccaggatgCtgggcttag	m5C_2343
chr1	28833879	+	C	34	12	0.353	0	0	T	22	M	0.215	0.521	0	5E-06	0	51.571	actgattgCcaacgggata	m5C_2288
chr1	28833882	+	C	47	33	0.702	0	0	C	33	M	0.56	0.813	0	2E-05	0	369.75	gatttgcaacCgggatacac	m5C_2292
chr1	28833892	+	C	77	36	0.468	0	0	T	41	M	0.36	0.578	0	2E-09	0	259.42	cggtgatacaCccggagggtc	m5C_2306
chr1	28833893	+	C	73	40	0.548	0	0	C	40	M	0.434	0.657	0	6E-09	0	347.39	grrggatacacCgggaaggca	m5C_2291
chr1	28833																		

chr1	28906280	-	C	87	18	0.207	0	0	T	69	M	0.135	0.304	0	4E-14	0	48.626	tagttcagaCagggttcaga	m5C_2369
chr1	28906284	-	C	100	40	0.4	0	0	T	60	M	0.309	0.498	0	6E-12	0	247.52	gggctagttCagacaggttt	m5C_2317
chr1	28906291	-	C	104	30	0.288	0	0	T	74	M	0.21	0.382	0	5E-15	0	126.09	ggcatgtgggCtagtttcaga	m5C_2325
chr1	28906299	-	C	76	23	0.303	0	0	T	53	M	0.211	0.413	0	4E-11	0	97.019	tggatattggCatgtgggcta	m5C_2355
chr1	28906996	-	C	43	14	0.326	0	0	T	29	M	0.205	0.475	0	2E-07	0	57.381	tgggctgggCatagccatgg	m5C_2372
chr1	28907007	-	C	69	27	0.391	0	0	T	42	M	0.285	0.509	0	7E-09	0	153.8	tttccaagggCtgaggctgt	m5C_2342
chr1	28907014	-	C	72	28	0.389	0	0	T	44	M	0.285	0.504	0	3E-10	0	159.41	cagcatgtttCcaaggctgt	m5C_2328
chr1	28975167	+	C	41	9	0.22	0	0	T	32	M	0.12	0.367	8E-12	1E-08	9E-12	11.962	gctctgctgCggatcgaca	m5C_2289
chr1	28975173	+	C	41	11	0.268	0	0	T	30	M	0.157	0.419	6E-15	4E-08	7E-15	24.554	cgggggaatCgacatcaaga	m5C_2302
chr1	28975234	+	C	38	18	0.474	0	0	T	20	M	0.325	0.627	0	3E-05	0	116.92	gatctgttggCccggccctt	m5C_2273
chr1	28975235	+	C	34	16	0.471	0	0	T	18	M	0.315	0.633	0	2E-05	0	100.64	atcgttggcCggggccctt	m5C_2282
chr1	28975236	+	C	35	8	0.229	0	0	T	27	M	0.121	0.39	6E-11	7E-07	6E-11	9.8969	tcgttggcccCgggcccctt	m5C_2303
chr1	28975239	+	C	37	15	0.405	0	0	T	22	M	0.263	0.565	0	1E-05	0	79.039	tgtgtcccgCgccccttctt	m5C_2290
chr1	29793170	+	C	61	25	0.41	0	0	T	36	M	0.295	0.535	0	4E-09	0	147.68	gttcaggacaCtgttgacaac	m5C_2311
chr1	35650115	-	C	32	12	0.375	0	0	T	20	M	0.229	0.547	0	5E-06	0	55.041	ggaactcgagCaggatattgt	m5C_552
chr1	35653642	-	C	49	19	0.388	0	0	T	30	M	0.264	0.528	0	1E-06	0	100.43	gattctgcaaCgtggatgtga	m5C_570
chr1	35653675	-	C	114	29	0.254	0	0	T	85	M	0.183	0.341	0	0	0	106.34	ggagggaacgaCtgaagaagaga	m5C_569
chr1	35653690	-	C	75	23	0.307	0	0	T	52	M	0.214	0.418	0	4E-11	0	98.379	tatttctaggCaagaaggagga	m5C_576
chr1	38435347	-	C	95	19	0.2	0	0	T	76	M	0.132	0.291	0	9E-16	0	50.139	agggaagaagCggaagaaga	m5C_629
chr1	38435364	-	C	80	20	0.25	0	0	T	60	M	0.168	0.355	0	2E-13	0	67.224	cgcaagcaagCcaaggacagga	m5C_616
chr1	38435368	-	C	78	20	0.256	0	0	T	58	M	0.173	0.363	0	1E-11	0	69.021	acagcgcaagCaagcaggagc	m5C_628
chr1	38435372	-	C	63	16	0.254	0	0	T	47	M	0.163	0.373	0	1E-10	0	52.097	atgtcacgpcCaagcaagcca	m5C_614
chr1	38435374	-	C	56	19	0.339	0	0	T	37	M	0.229	0.47	0	2E-08	0	87.095	aaatgtacagCgcaagcaagc	m5C_619
chr1	40538448	-	C	33	10	0.303	0	0	T	23	M	0.174	0.473	2E-14	2E-06	2E-14	23.982	ggataagagCaagaagtgtg	m5C_435
chr1	41270699	+	C	74	26	0.351	0	0	T	48	M	0.252	0.465	0	1E-10	0	131.24	gaggggcaaCtggcccagggt	m5C_411
chr1	41270705	+	C	71	23	0.324	0	0	T	48	M	0.227	0.439	0	4E-11	0	104.22	tgaactggccCagggtcagaaa	m5C_423
chr1	43162445	+	C	34	10	0.294	0	0	T	24	M	0.168	0.462	2E-14	2E-06	3E-14	22.956	gcaaaattacCagatatgtga	m5C_444
chr1	43162471	+	C	101	27	0.267	0	0	T	74	M	0.191	0.361	0	1E-15	0	102.98	gggaagaagaCtggggatcgg	m5C_443
chr1	45241548	+	C	289	65	0.225	0	0	T	224	M	0.181	0.276	0	0	0	234.73	tgtatgatgaCaactcggtaa	m5C_1445
chr1	45241551	+	C	295	76	0.259	1	0.003	T	218	M	0.212	0.311	0	0	0	321.93	atgatgacaaCtggtaatgc	m5C_1449
chr1	45241553	+	C	304	81	0.266	0	0	T	223	M	0.22	0.319	0	0	0	356.22	gatgacaactCggtaatgctg	m5C_1456
chr1	45241561	+	C	288	67	0.234	2	0.007	T	219	M	0.189	0.287	0	0	0	253.13	ctcgttaatCtgcatactcc	m5C_1447
chr1	45241564	+	C	292	81	0.277	0	0	T	211	M	0.229	0.331	0	0	0	371.28	gggaatgctCatactcccga	m5C_1442
chr1	45241570	+	C	300	81	0.27	0	0	T	219	M	0.223	0.323	0	0	0	361.1	gctgcatactCccgagggcg	m5C_1429
chr1	45241578	+	C	296	78	0.265	2	0.007	T	216	M	0.218	0.319	0	0	0	340.24	ctcccgaatgCgctgggggga	m5C_1468
chr1	45241592	+	C	328	86	0.262	0	0	T	242	M	0.218	0.312	0	0	0	374.18	gggggaagcCaaccttggag	m5C_1446
chr1	45241595	+	C	339	74	0.218	0	0	T	265	M	0.178	0.265	0	0	0	262.86	gggaagccaaCttggagagagc	m5C_1427
chr1	45241596	+	C	346	123	0.355	0	0	T	223	M	0.307	0.407	0	0	0	754.96	ggaagcgaacCttggagaagct	m5C_1423
chr1	45241605	+	C	276	63	0.228	0	0	T	213	M	0.183	0.281	0	0	0	230.17	cccttggaagCtgaagtgagc	m5C_1452
chr1	45241610	+	C	169	55	0.327	1	0.006	T	113	M	0.261	0.402	0	0	0	287.07	gagagctgaagCgagcgaccgg	m5C_1463
chr1	45242184	+	C	91	44	0.484	0	0	T	47	M	0.384	0.585	0	2E-11	0	337.57	gaaaaagaatCcttagggctg	m5C_1424
chr1	45242185	+	C	81	39	0.481	0	0	T	42	M	0.376	0.589	0	2E-10	0	293.28	aaaaagaatCcttagggctg	m5C_1425
chr1	45242191	+	C	54	43	0.796	0	0	C	43	M	0.671	0.882	0	4E-06	0	577.04	aatccttaggCggtgggtggg	m5C_1464
chr1	45242202	+	C	58	42	0.724	0	0	C	42	M	0.598	0.822	0	4E-06	0	502.28	gtgggtgggCgctttggcc	m5C_1469
chr1	45242203	+	C	55	36	0.655	0	0	C	36	M	0.523	0.766	0	2E-06	0	376.23	tgggttgggCgtcttggtca	m5C_1436
chr1	45242206	+	C	55	38	0.691	0	0	C	38	M	0.56	0.797	0	2E-06	0	425.38	tggggcgtCttggacacct	m5C_1444
chr1	45242212	+	C	52	39	0.75	0	0	C	39	M	0.618	0.848	0	2E-06	0	481.99	ccgttgggCacctgtgtgc	m5C_1434
chr1	45242214	+	C	54	35	0.648	0	0	C	35	M	0.515	0.762	0	1E-06	0	360.39	gttcttggtCctgtgtgcca	m5C_1430
chr1	45242215	+	C	51	33	0.647	0	0	C	33	M	0.51	0.764	0	9E-07	0	336.51	tcttgtcacCtggggccac	m5C_1461
chr1	45242222	+	C	53	37	0.698	0	0	C	37	M	0.565	0.805	0	2E-06	0	417.83	cacctgtgtgCacctgtgcaa	m5C_1462
chr1	45242223	+	C	56	35	0.625	0	0	C	35	M	0.494	0.74	0	1E-06	0	345.84	acctgtgtgCactgtgcaat	m5C_1476
chr1	45242225	+	C	53	31	0.585	0	0	C	31	M	0.451	0.707	0	6E-07	0	279.58	ctgtgtgccaCttgccaatgc	m5C_1450
chr1	45242229	+	C	55	32	0.582	0	0	C	32	M	0.45	0.703	0	7E-07	0	288.21	gtgcactgtCcaatgcaagg	m5C_1470
chr1	45242230	+	C	53	32	0.604	0	0	C	32	M	0.469	0.724	0	7E-07	0	300.42	tggccaatgCcaatgcaaga	m5C_1451
chr1	45242235	+	C	54	33	0.611	0	0	C	33	M	0.478	0.73	0	9E-07	0	315.4	cttgccaatgCaaggactgt	m5C_1433
chr1	45242241	+	C	52	35	0.673	0	0	C	35	M	0.538	0.785	0	1E-06	0	376.29	aatgcaaggCctgtcatagt	m5C_1474
chr1	45242246	+	C	50	34	0.68	0	0	C	34	M	0.542	0.792	0	2E-05	0	368.49	aaggactgtCatagtacac	m5C_1477
chr1	45242254	+	C	48	27	0.562	0	0	C	27	M	0.423	0.693	0	7E-06	0	228.28	gcatagtaCactgactgt	m5C_1480
chr1	45242256	+	C	48	29	0.604	0	0	C	29	M	0.463	0.73	0	1E-05	0	268.6	catagtacaCtgaactgtgc	m5C_1458
chr1	45242260	+	C	52	35	0.673	0	0	C	35	M	0.538	0.785	0	1E-06	0	376.29	gttacaagCtgtgtgcttc	m5C_1432
chr1	45243516	+	C	52	17	0.327	0	0	T	35	M	0.215	0.462	0	1E-08	0	73.174	ctccagcttCtctggatgaa	m5C_1438
chr1	45243518	+	C	52	21	0.404	0	0	T	31	M	0.282	0.539	0	5E-08	0	118.27	ccagcttctCggtatgaaaa	m5C_1440
chr1	45243529	+	C	103	43	0.417	0	0	T	60	M	0.327	0.514	0	4E-13	0	281.12	gtgatgaaaCtctgtccagt	m5C_1453
chr1	45243531	+	C	106	33	0.311	0	0	T	73	M	0.231	0.405	0	2E-14	0	152.51	gatgaaaaatCtggccagttc	m5C_1439
chr1	45243535	+	C	108	34	0.315	0	0	T	74	M	0.235	0.407	0	2E-14	0	159.71	aaaactgtgCaggttctgt	m5C_1479
chr1	45243536	+	C	114	59	0.518	0	0	C	59	M	0.427	0.607	0	7E-13	0	503.56	aaactgtgCaggttctgtca	m5C_1428
chr1	45243541	+	C	105	32	0.305	0	0	T	73	M	0.225	0.398	0	1E-14	0	143.94	ctgtccaggtCtgtacttgaa	m5C_1467
chr1	45243544	+	C	107	80	0.755	1	0.009	C	80	M	0.665	0.827	0	6E-10	0	1063.8	tccagttctCtactgaagg	m5C_1441
chr1	45243547	+	C	107	33	0.308	0	0	T	74	M	0.229	0.401	0	2E-14	0	151.02	agttctgtcaCtgaaggagga	m5C_1426
chr1	45243568	+	C	71	21	0.296	0	0	T	50	M	0.202	0.41	0	2E-11	0	84.978	gagatgagagCctttaggct	m5C_1471
chr1	45243569	+	C	70	25	0.357	0	0	T	45	M	0.255	0.474	0	4E-09	0	127.52	agatgagagCttttaggctg	m5C_1460
chr1	45243577	+	C	57	41	0.719	0	0	C	41	M	0.592	0.819	0	3E-06	0	485.19	gccttttaggCtgaagaaggc	m5C_1459
chr1	45244077	+	C	52	15	0.288	0	0	T	37	M	0.183	0.423	0	5E-09	0	54.989	gtgatgaaaaCttttccagt	m5C_1472
chr1	45244083	+	C	49	13	0.265	0	0											

chr1	91853088	-	C	111	77	0.694	0	0	C	77	M	0.603	0.772	0	2E-11	0	928.09	aacgggaacgCagggtgctta	m5C_4018
chr1	91853090	-	C	92	72	0.783	0	0	C	72	M	0.688	0.855	0	3E-09	0	990.62	caaacggtaaCgcagggtgcc	m5C_4032
chr1	93302861	+	C	55	16	0.291	0	0	T	39	M	0.188	0.421	0	7E-09	0	60.067	atgatgatCccactaactg	m5C_1364
chr1	93302863	+	C	58	12	0.207	0	0	T	46	M	0.123	0.328	2E-14	9E-10	2E-14	20.116	gatgataccCactaactgag	m5C_1368
chr1	93302865	+	C	56	14	0.25	0	0	T	42	M	0.155	0.377	0	3E-09	0	43.447	tgatattcccaCtaactgagca	m5C_1369
chr1	93302869	+	C	57	15	0.263	0	0	T	42	M	0.166	0.39	0	5E-09	0	49.937	atccacataaCtgagcagca	m5C_1371
chr1	93302874	+	C	58	13	0.224	0	0	T	45	M	0.136	0.347	7E-16	2E-09	7E-16	26.819	actaactgagCagtcagtagt	m5C_1352
chr1	93302878	+	C	58	12	0.207	0	0	T	46	M	0.123	0.328	2E-14	9E-10	2E-14	20.116	actgagcagtCagtagtggg	m5C_1359
chr1	93302899	+	C	58	25	0.431	0	0	T	33	M	0.312	0.559	0	2E-07	0	155.91	cttttggtgCatatgatgag	m5C_1355
chr1	93302908	+	C	64	49	0.766	0	0	C	49	M	0.649	0.853	0	6E-07	0	635.69	gcatatgatgCgataattgtt	m5C_1367
chr1	93302920	+	C	76	16	0.211	0	0	T	60	M	0.134	0.315	0	1E-12	0	42.864	ataattgttCaagacgggac	m5C_1360
chr1	93302925	+	C	80	23	0.287	0	0	T	57	M	0.2	0.395	0	7E-13	0	91.939	tggttcaagaCgggactgatg	m5C_1361
chr1	93302930	+	C	75	53	0.707	0	0	C	53	M	0.596	0.798	0	6E-08	0	631.33	caagacgggaCtgatggcagc	m5C_1353
chr1	93306289	+	C	31	11	0.355	0	0	T	20	M	0.211	0.531	1E-16	3E-06	1E-16	37.059	caaaactgatCactagtcttg	m5C_1363
chr1	93306310	+	C	32	12	0.375	0	0	T	20	M	0.229	0.547	0	5E-06	0	55.041	cggatgtggCagaagaagaag	m5C_1372
chr1	93981875	+	C	38	17	0.447	0	0	T	21	M	0.301	0.603	0	2E-05	0	102.5	gagcatttgaCtgcatcaaa	m5C_1373
chr1	93981894	-	C	51	37	0.725	0	0	C	37	M	0.591	0.829	0	2E-06	0	436.99	gggtatagctCagggtgtaga	m5C_1382
chr1	93981896	-	C	54	23	0.426	0	0	T	31	M	0.303	0.558	0	9E-08	0	139.53	ggggatagctCtagggggga	m5C_1383
chr1	94058374	-	C	46	15	0.326	0	0	T	31	M	0.209	0.47	0	3E-07	0	62.597	ctttgggacctCactgccaga	m5C_1205
chr1	108113330	-	C	34	17	0.5	0	0	CT	17	M	0.341	0.659	0	2E-05	0	115.83	tccggaggggCggagatggac	m5C_1745
chr1	108113484	-	C	31	20	0.645	0	0	C	20	M	0.469	0.789	0	4E-05	0	187.79	cttcaaaaggCgaaggggaga	m5C_1715
chr1	108113565	-	C	136	34	0.25	0	0	T	102	M	0.185	0.329	0	0	0	125.64	gtcttgaaGCcagggtctggg	m5C_1743
chr1	108113566	-	C	151	84	0.556	0	0	C	84	M	0.477	0.633	0	3E-16	0	800.73	agcttgaaGCccaggctggg	m5C_1733
chr1	108113573	-	C	163	76	0.466	0	0	T	87	M	0.391	0.543	0	0	0	594.83	tgccggaggtCttgaagccca	m5C_1711
chr1	108113581	-	C	172	62	0.36	0	0	T	110	M	0.292	0.435	0	0	0	362.68	agggccgtgtCggtaggtctt	m5C_1748
chr1	108113584	-	C	159	68	0.428	0	0	T	91	M	0.353	0.505	0	0	0	480.58	aggaaggccgcCtgcggggagt	m5C_1718
chr1	108113586	-	C	144	43	0.299	0	0	T	101	M	0.23	0.378	0	0	0	197.7	ggaggagggcCgctgcggga	m5C_1737
chr1	108113587	-	C	122	56	0.459	0	0	T	66	M	0.373	0.547	0	1E-14	0	417.98	agtagaggggCgcgtgcggg	m5C_1742
chr1	109642907	+	C	48	21	0.438	0	0	T	27	M	0.307	0.577	0	2E-06	0	128.94	tgtaggtggaCgctggaggtg	m5C_1695
chr1	111991798	-	C	31	14	0.452	0	0	T	17	M	0.292	0.622	0	9E-06	0	81.652	gagttggaaCggtggagatgc	m5C_1286
chr1	120543995	-	C	126	93	0.738	0	0	C	93	M	0.655	0.807	0	1E-11	0	1218.5	cgtaggaacCtgatgtgcaa	m5C_1585
chr1	120543996	-	C	124	61	0.492	0	0	T	63	M	0.406	0.579	0	4E-14	0	494.73	ccgtagcaggtCctgatgtgca	m5C_1601
chr1	120544000	-	C	225	168	0.747	0	0	C	168	M	0.686	0.799	0	0	0	2305	aggctccgagCagttcctgatg	m5C_1592
chr1	120544006	-	C	235	91	0.387	0	0	T	144	M	0.327	0.451	0	0	0	595.58	tggtggaggtCcgtagcagtc	m5C_1588
chr1	120544019	-	C	181	138	0.762	0	0	C	138	M	0.695	0.819	0	3E-16	0	1919.2	ccagagaanaCtctgtggagag	m5C_1580
chr1	145277346	+	C	59	47	0.797	0	0	C	47	M	0.677	0.88	0	8E-06	0	636.68	cagggcaagcCagaaggaaac	m5C_1846
chr1	145277347	+	C	72	54	0.75	0	0	C	54	M	0.639	0.836	0	7E-08	0	690.19	agggcaaaGCcagaaggaaact	m5C_1854
chr1	145277356	+	C	98	63	0.643	0	0	C	63	M	0.544	0.731	0	8E-10	0	685.76	ccagagaanaCtctgtggagag	m5C_1850
chr1	145277358	+	C	101	66	0.653	0	0	C	66	M	0.557	0.739	0	6E-11	0	734.68	agagaanaactCtggggaggt	m5C_1840
chr1	145277370	+	C	96	62	0.646	0	0	C	62	M	0.546	0.734	0	7E-10	0	677.34	ggggagggcCgtagcagttcc	m5C_1856
chr1	145277375	+	C	99	63	0.636	0	0	C	63	M	0.538	0.724	0	8E-10	0	678.08	aggtccgagCagttcctgatg	m5C_1849
chr1	145277379	+	C	94	25	0.266	0	0	T	69	M	0.187	0.363	0	3E-14	0	93.557	ccgtagcaggtCctgatgtgca	m5C_1838
chr1	145277418	+	C	109	87	0.798	0	0	C	87	M	0.713	0.863	0	1E-09	0	1241.1	gggttaggggCgaagaactaa	m5C_1852
chr1	145277434	+	C	108	84	0.778	0	0	C	84	M	0.691	0.846	0	9E-10	0	1160.2	actaattgaaCcatctagtag	m5C_1842
chr1	145277435	+	C	51	40	0.784	0	0	C	40	M	0.654	0.875	0	3E-06	0	522.99	ctaattgaaCcatctagtagc	m5C_1843
chr1	145395523	-	C	51	15	0.294	0	0	T	36	M	0.187	0.43	0	5E-09	0	56.126	ccacgtgggCgctgtgtttt	m5C_1919
chr1	145395530	-	C	60	18	0.3	0	0	T	42	M	0.199	0.425	0	3E-10	0	71.633	tcgagccccaCgtggggcgt	m5C_1901
chr1	145395533	-	C	62	17	0.274	0	0	T	45	M	0.179	0.396	0	2E-10	0	60.795	gggtcagaccCacgtggggc	m5C_1860
chr1	145395535	-	C	61	18	0.295	0	0	T	43	M	0.196	0.419	0	3E-10	0	70.398	tggttcgagCcccacgtggg	m5C_1869
chr1	145395539	-	C	63	29	0.46	0	0	T	34	M	0.343	0.582	0	1E-08	0	198.99	gttcgggggtCgagcccccag	m5C_1912
chr1	145395547	-	C	58	35	0.603	0	0	C	35	M	0.475	0.719	0	1E-06	0	332.45	atctcagggtCggtgggtcga	m5C_1878
chr1	145395555	-	C	36	28	0.778	0	0	C	28	M	0.619	0.883	0	0.0002	0	346.72	gactcttaattCtaggggtcgt	m5C_1900
chr1	145457073	-	C	31	13	0.419	0	0	T	18	M	0.264	0.592	0	7E-06	0	68.68	gaagaaattCagaaggagag	m5C_1875
chr1	146556212	-	C	74	47	0.635	0	0	C	47	M	0.521	0.736	0	2E-08	0	490.04	gtgggaaggtCgactgcataa	m5C_1545
chr1	149194111	-	C	39	13	0.333	0	0	T	26	M	0.206	0.49	0	7E-06	0	53.645	ttcgctttCccctgaattt	m5C_2058
chr1	149194115	-	C	47	18	0.4	2	0.043	T	27	M	0.27	0.545	0	8E-07	0	97.289	tggttcgcgcCtttccccgt	m5C_2049
chr1	149194117	-	C	44	9	0.205	0	0	T	35	M	0.112	0.345	2E-11	1E-08	2E-11	10.781	actgctgtcgCgtttccctt	m5C_2041
chr1	149194126	-	C	51	21	0.412	0	0	T	30	M	0.288	0.548	0	5E-08	0	120.77	tagtgggggaCtgcgttcgag	m5C_2042
chr1	150193024	-	C	42	11	0.262	0	0	T	31	M	0.153	0.411	8E-15	4E-08	9E-15	23.69	aaacgagatgCtgaagacat	m5C_1963
chr1	150193031	-	C	46	12	0.261	0	0	T	34	M	0.156	0.403	7E-16	7E-08	7E-16	28.412	gaagagaanaCgagatgtga	m5C_1962
chr1	150199001	-	C	37	18	0.486	0	0	T	19	M	0.334	0.641	0	3E-05	0	120.41	gaagcaggtCagaagtggga	m5C_1951
chr1	150199007	-	C	37	20	0.541	0	0	C	20	M	0.384	0.69	0	4E-05	0	153.54	gaagatgaagCaggttcagag	m5C_1972
chr1	150199079	-	C	89	49	0.551	0	0	C	49	M	0.447	0.65	0	1E-09	0	438.32	gctgtccacCggaaggatat	m5C_1958
chr1	150199082	-	C	94	38	0.404	0	0	T	56	M	0.311	0.505	0	4E-12	0	236.13	gaagctggcCaccgggaagga	m5C_1954
chr1	150199083	-	C	89	18	0.202	0	0	T	71	M	0.132	0.297	0	4E-14	0	47.497	tgaagctggcCaccgggaagg	m5C_1961
chr1	150199123	-	C	74	34	0.63	20	0.27	C	34	M	0.496	0.746	0	1E-06	0	337.47	ttaaaatggCgatgaagatg	m5C_1950
chr1	153591391	-	C	54	11	0.204	0	0	T	43	M	0.118	0.329	2E-13	4E-10	3E-13	16.362	gaagaagaacCtgaagatcag	m5C_1769
chr1	153591392	-	C	57	36	0.632	0	0	C	36	M	0.502	0.745	0	2E-06	0	361.28	agaagaagaCtgaagaatca	m5C_1768
chr1	153591417	-	C	37	19	0.514	0	0	C	19	M	0.359	0.666	0	3E-05	0	136.4	ggggagctggCcaaggaaatc	m5C_1764
chr1	153591421	-	C	33	23	0.697	0	0	C	23	M	0.527	0.826	0	8E-05	0	242.24	gattggggagCtggccaagga	m5C_1771
chr1	153634963	-	C	40	22	0.55	0	0	C	22	M	0.398	0.693	0	6E-05	0	175.25	tatgaagaacCaccagagaag	m5C_1763
chr1	153634984	-	C	41	18	0.439	0	0	T	23	M	0.299	0.59	0	8E-07	0	107.6	gtaacacctCagaanaaggct	m5C_1766
chr1	155889719	-	C	89	39	0.438	0	0	T	50	M	0.34	0.542	0	2E-10	0			

chr1	161450386	+	C	83	50	0.602	0	0	C	50	M	0.495	0.701	0	2E-09	0	494.85	gaattcttgcCtgccacgcag	m5C_2444
chr1	161450389	+	C	56	27	0.482	0	0	T	29	M	0.357	0.61	0	2E-07	0	192.61	ttcttgctgcCcacgcaggag	m5C_2475
chr1	161450390	+	C	52	25	0.481	0	0	T	27	M	0.351	0.613	0	2E-07	0	175.52	tcttgctgcCacgcaggag	m5C_2479
chr1	161450394	+	C	47	25	0.532	0	0	C	25	M	0.392	0.667	0	4E-06	0	196.16	gcctgcacgcCaggaggccca	m5C_2456
chr1	161493636	-	C	94	66	0.702	0	0	C	66	M	0.603	0.785	0	1E-09	0	796.26	ggccaatgcaCittcatitt	m5C_2560
chr1	161493638	-	C	109	32	0.294	0	0	T	77	M	0.216	0.385	0	1E-14	0	138.42	ccgcgaatgcCacttcatitt	m5C_2520
chr1	161493643	-	C	117	29	0.248	0	0	T	88	M	0.178	0.333	0	0	0	103.52	gattccccgcCaatgcacttt	m5C_2543
chr1	161493644	-	C	120	41	0.342	0	0	T	79	M	0.263	0.43	0	1E-16	0	215.58	cgattccccgcCcaatgcactt	m5C_2545
chr1	161493647	-	C	117	49	0.419	0	0	T	68	M	0.333	0.509	0	7E-14	0	326.71	gttcgattccCggccaatgca	m5C_2542
chr1	161493648	-	C	124	58	0.468	0	0	T	66	M	0.382	0.555	0	2E-14	0	443.37	ggctgcacgcCggccaatgc	m5C_2552
chr1	161493649	-	C	120	27	0.225	0	0	T	93	M	0.159	0.308	0	0	0	86.125	gggtcgattCccggccaatg	m5C_2491
chr1	161493654	-	C	118	38	0.322	0	0	T	80	M	0.244	0.411	0	2E-15	0	185.81	ggccggggtCgattccccgc	m5C_2510
chr1	161493669	-	C	105	44	0.419	0	0	T	61	M	0.329	0.515	0	6E-13	0	289.67	gcctgcacgcCggaggcccg	m5C_2503
chr1	161493673	-	C	102	27	0.265	0	0	T	75	M	0.189	0.358	0	1E-15	0	101.93	tctgcctgcCacgcggagg	m5C_2549
chr1	161493674	-	C	106	28	0.264	0	0	T	78	M	0.19	0.355	0	2E-15	0	106.14	ttcttgctgcCcacgcaggag	m5C_2556
chr1	161493677	-	C	106	35	0.33	0	0	T	71	M	0.248	0.424	0	3E-14	0	173.58	gaattctgcCtgccacgcgg	m5C_2511
chr1	161493678	-	C	108	29	0.269	0	0	T	79	M	0.194	0.359	0	3E-15	0	112.49	agaattctgcCtgccacgcg	m5C_2494
chr1	161493680	-	C	104	30	0.288	0	0	T	74	M	0.21	0.382	0	5E-15	0	126.09	ggaattctCgctgcacgc	m5C_2537
chr1	161493682	-	C	101	42	0.416	0	0	T	59	M	0.325	0.513	0	3E-13	0	272.61	tggagattCcgctctgcca	m5C_2555
chr1	161493695	-	C	83	21	0.253	0	0	T	62	M	0.172	0.356	0	3E-13	0	72.177	attgggggtCaggggagaa	m5C_2535
chr1	161493706	-	C	38	9	0.237	0	0	T	29	M	0.13	0.392	4E-12	1E-06	4E-12	13.374	ctgacagagCattggggtt	m5C_2551
chr1	161500904	+	C	39	19	0.487	0	0	T	20	M	0.339	0.638	0	3E-05	0	128.69	accgggaacCgtgggggga	m5C_2488
chr1	161500925	+	C	89	39	0.443	1	0.011	T	49	M	0.344	0.547	0	2E-10	0	268.27	tagggggagCatagtgcct	m5C_2447
chr1	161500930	+	C	98	60	0.612	0	0	C	60	M	0.513	0.703	0	5E-10	0	615.94	gggacatagCtgcttccaa	m5C_2468
chr1	161500933	+	C	96	42	0.438	0	0	T	54	M	0.343	0.537	0	1E-11	0	287.76	agcatactgcCttccaaaga	m5C_2445
chr1	161500934	+	C	94	42	0.447	0	0	T	52	M	0.35	0.547	0	1E-11	0	294.3	gcatagtgcCttccaagcag	m5C_2449
chr1	161500937	+	C	94	45	0.479	0	0	T	49	M	0.381	0.579	0	2E-11	0	342.51	tagctgcctCcaagcagttg	m5C_2461
chr1	161500938	+	C	94	52	0.553	0	0	C	52	M	0.453	0.65	0	1E-10	0	470.67	agctgcctCcaagcagttga	m5C_2472
chr1	161500942	+	C	93	43	0.462	0	0	T	50	M	0.365	0.563	0	1E-11	0	313.51	gcctccaagCagttgaccgc	m5C_2474
chr1	161582507	+	C	54	30	0.556	0	0	C	30	M	0.424	0.68	0	5E-07	0	254.25	aaaccggggaCgctggggg	m5C_2434
chr1	161582530	+	C	80	17	0.212	0	0	T	63	M	0.137	0.314	0	2E-14	0	46.622	tagggggagCacagctgcct	m5C_2454
chr1	161582539	+	C	43	23	0.535	0	0	C	23	M	0.389	0.675	0	3E-06	0	179.01	gcacagtcCtttcaagcag	m5C_2466
chr1	161582554	+	C	43	12	0.279	0	0	T	31	M	0.167	0.427	2E-16	7E-08	2E-16	31.457	aagcagtaaaCgcgggtcga	m5C_2471
chr1	161582568	+	C	43	11	0.256	0	0	T	32	M	0.149	0.402	1E-14	4E-08	1E-14	22.889	ggctgcattCcggttaacga	m5C_2483
chr1	166975289	+	C	382	294	0.77	0	0	C	294	M	0.725	0.809	0	0	0	4262.1	tgagagactgcCtgggaatac	m5C_2710
chr1	166975299	+	C	481	365	0.759	0	0	C	365	M	0.719	0.795	0	0	0	5246.1	cctgggaataCtgggtgctg	m5C_2718
chr1	166975306	+	C	473	375	0.793	0	0	C	375	M	0.754	0.827	0	0	0	5655	atactgggtCtgtagcttt	m5C_2720
chr1	171461724	+	C	41	9	0.22	0	0	T	32	M	0.12	0.367	8E-12	1E-08	9E-12	11.962	taacaggtgcCtgaggagg	m5C_1991
chr1	171461725	+	C	43	16	0.372	0	0	T	27	M	0.244	0.521	0	4E-07	0	78.004	aacaggtgcCtgaggagg	m5C_1992
chr1	171501770	+	C	31	21	0.677	0	0	C	21	M	0.501	0.814	0	5E-05	0	210.59	agaaaaagaaCgggaagctga	m5C_2011
chr1	171501776	+	C	46	22	0.478	0	0	T	24	M	0.341	0.619	0	2E-06	0	150.15	agaaagggaagCgtgaaaga	m5C_1993
chr1	171501800	+	C	48	38	0.792	0	0	C	38	M	0.657	0.883	0	4E-05	0	499.63	tgaaaaagaaCaagaacagga	m5C_1994
chr1	171501806	+	C	60	12	0.2	0	0	T	48	M	0.118	0.318	3E-14	8E-12	4E-14	19.13	agaacaagaaCaggagcagga	m5C_2004
chr1	173833976	-	C	43	17	0.395	0	0	T	26	M	0.264	0.544	0	6E-07	0	89.641	tcgtctctatCtgatglatct	m5C_3662
chr1	173833980	-	C	39	16	0.41	0	0	T	23	M	0.271	0.566	0	2E-05	0	86.653	ttcttcgtCtctatgtatg	m5C_3612
chr1	173833983	-	C	42	17	0.405	0	0	T	25	M	0.27	0.555	0	6E-07	0	91.945	aagctttgcCtctatctga	m5C_3631
chr1	173833985	-	C	42	18	0.429	0	0	T	24	M	0.291	0.578	0	8E-07	0	104.82	ttaagttctCgctctatct	m5C_3633
chr1	173833989	-	C	41	17	0.415	0	0	T	24	M	0.278	0.566	0	6E-07	0	94.372	aatattaagtCtttcgtcct	m5C_3630
chr1	173834000	-	C	42	14	0.333	0	0	T	28	M	0.21	0.484	0	2E-07	0	58.834	cgcctgatgagCaataataagt	m5C_3600
chr1	173834008	-	C	40	17	0.425	0	0	T	23	M	0.285	0.578	0	6E-07	0	96.931	cagactaacCtgatgagcaa	m5C_3581
chr1	173834010	-	C	44	18	0.409	0	0	T	26	M	0.277	0.556	0	8E-07	0	99.676	agcagactaaCgctgatgagc	m5C_3669
chr1	173834014	-	C	52	17	0.327	0	0	T	35	M	0.215	0.462	0	1E-08	0	73.174	gttcagcagaCtaacgctgat	m5C_3599
chr1	173834018	-	C	53	16	0.302	0	0	T	37	M	0.195	0.435	0	7E-09	0	62.458	catagttcagCagactaacgc	m5C_3651
chr1	173834021	-	C	55	16	0.291	0	0	T	39	M	0.188	0.421	0	7E-09	0	60.067	taacattgtCagcagactaa	m5C_3613
chr1	173834028	-	C	54	14	0.259	0	0	T	40	M	0.161	0.389	0	3E-09	0	45.132	atgatataaCatagttcagc	m5C_3611
chr1	173834496	-	C	67	25	0.373	0	0	T	42	M	0.267	0.493	0	4E-09	0	133.59	taatcttaaaCtgaacaagaa	m5C_3570
chr1	173834502	-	C	80	49	0.613	0	0	C	49	M	0.503	0.712	0	3E-08	0	492.88	ggagattaatCttaactgaa	m5C_3593
chr1	173834526	-	C	138	47	0.341	0	0	T	91	M	0.267	0.423	0	0	0	250.78	gggaatctctCtgaagaagaa	m5C_3666
chr1	173834528	-	C	140	47	0.336	0	0	T	93	M	0.263	0.417	0	0	0	247.03	atgggaatctCtctgaagaag	m5C_3579
chr1	173834769	-	C	101	21	0.208	0	0	T	80	M	0.14	0.297	0	0	0	58.887	acaaaggtaaCactgaagaac	m5C_3585
chr1	173834786	-	C	109	32	0.294	0	0	T	77	M	0.216	0.385	0	1E-14	0	138.42	ctgaatgagCatgtagacaa	m5C_3668
chr1	173834796	-	C	114	24	0.211	0	0	T	90	M	0.146	0.294	0	0	0	69.961	aatgctgagCtgaatgagc	m5C_3620
chr1	173834797	-	C	112	37	0.33	0	0	T	75	M	0.25	0.422	0	1E-15	0	185.11	aaatgctgagCtgaatgag	m5C_3617
chr1	173834808	-	C	109	25	0.229	0	0	T	84	M	0.16	0.317	0	4E-16	0	80.227	tgatgtgatCaaatgctgag	m5C_3626
chr1	173835107	-	C	144	65	0.451	0	0	T	79	M	0.372	0.533	0	1E-16	0	484.15	ctctaactgaCtaaggcatt	m5C_3618
chr1	173835111	-	C	196	72	0.367	0	0	T	124	M	0.303	0.437	0	0	0	436.33	ttagctctaaCtgactaaagg	m5C_3615
chr1	173835115	-	C	219	77	0.352	0	0	T	142	M	0.291	0.417	0	0	0	448.78	ttaattagctCtaactgacta	m5C_3595
chr1	173835117	-	C	239	99	0.414	0	0	T	140	M	0.354	0.478	0	0	0	700.15	tcttaattagCtctaactgac	m5C_3635
chr1	173835126	-	C	255	86	0.337	0	0	T	169	M	0.282	0.397	0	0	0	485.08	acatgaaggCtctaattagct	m5C_3604
chr1	173835135	-	C	288	115	0.399	0	0	T	173	M	0.344	0.457	0	0	0	792.18	gctgactgaaCatgaaggct	m5C_3589
chr1	173835140	-	C	324	121	0.373	0	0	T	203	M	0.323	0.427	0	0	0	780.59	caaagtctgaCtgaactgaa	m5C_3652
chr1	173835144	-	C	351	72	0.205	0	0	T	279	M	0.166	0.25	0	0	0	239.31	taagcaaatgCtgactgaaca	m5C_3567
chr1	173835150	-	C	354	83	0.236	2	0.006	T	269	M	0.194	0.283	0	0	0	322.79	tgatgataagCaaatgctgac	m5C_3572
chr1	1738																		

chr1	173836830	-	C	189	77	0.407	0	0	T	112	M	0.34	0.479	0	0	0	523.41	atgatgaatgCcaaccgctct	m5C_3607
chr1	173836852	-	C	168	41	0.244	0	0	T	127	M	0.185	0.314	0	0	0	151.94	ttggagggaCatctgagag	m5C_3638
chr1	173836868	-	C	151	35	0.232	0	0	T	116	M	0.172	0.305	0	0	0	120.15	tctgtagaGCctgtgtgtg	m5C_3649
chr1	173836879	-	C	70	16	0.229	0	0	T	54	M	0.146	0.34	0	1E-12	0	46.681	cggtccctgcCtctgatgaag	m5C_3627
chr1	173836880	-	C	67	19	0.284	0	0	T	48	M	0.19	0.401	0	5E-10	0	72.087	tcgtgacctgcCtctgatga	m5C_3598
chr1	185276170	-	C	64	30	0.469	0	0	T	34	M	0.352	0.589	0	2E-08	0	211.05	agaatggagaCagcttggaag	m5C_2699
chr1	185276185	-	C	68	34	0.5	0	0	CT	34	M	0.384	0.616	0	4E-08	0	261.38	agcgtgacTCtggagaatg	m5C_2688
chr1	185276193	-	C	56	18	0.321	0	0	T	38	M	0.214	0.452	0	2E-08	0	77.043	ctgggtgcagCgtgacatctg	m5C_2687
chr1	185276196	-	C	57	18	0.316	0	0	T	39	M	0.21	0.445	0	2E-08	0	75.615	caactgggtgCagcgtgacat	m5C_2700
chr1	202129921	-	C	65	26	0.4	0	0	T	39	M	0.29	0.521	0	6E-09	0	150.65	tcgggaaggcCtggccctca	m5C_2609
chr1	202129922	-	C	65	23	0.354	0	0	T	42	M	0.249	0.475	0	2E-09	0	114.43	gtcgggaaggCctggccctc	m5C_2615
chr1	204475656	+	C	77	23	0.299	0	0	T	54	M	0.208	0.408	0	4E-11	0	95.697	ttcggagcgcCccgatagtc	m5C_3023
chr1	204475658	+	C	74	42	0.568	0	0	C	42	M	0.454	0.674	0	9E-09	0	381.47	cggagagccCggaatgctca	m5C_3022
chr1	205687439	-	C	37	20	0.541	0	0	C	20	M	0.384	0.69	0	4E-05	0	153.54	gatgaagggTCtgaagatgaa	m5C_3035
chr1	205689662	-	C	192	102	0.531	0	0	C	102	M	0.461	0.601	0	0	0	939.92	tgaagaaagaCaagaaagga	m5C_3040
chr1	205689675	-	C	216	67	0.31	0	0	T	149	M	0.252	0.375	0	0	0	338.03	aagatgggcCagtgaagaa	m5C_3037
chr1	205689690	-	C	95	31	0.326	0	0	T	64	M	0.24	0.426	0	4E-13	0	149.04	gagagatgcTCatggaagatg	m5C_3041
chr1	205689692	-	C	82	21	0.256	0	0	T	61	M	0.174	0.36	0	3E-13	0	73.094	gagagagatgCtcatggaaga	m5C_3038
chr1	205698702	-	C	90	20	0.222	0	0	T	70	M	0.149	0.318	0	2E-15	0	59.485	tctgatgagTCgtgaaagt	m5C_3070
chr1	205698724	-	C	44	16	0.364	0	0	T	28	M	0.238	0.511	0	4E-07	0	76.107	tgattactaCagtttcagga	m5C_3030
chr1	212454147	+	C	50	32	0.64	0	0	C	32	M	0.501	0.759	0	7E-07	0	320.9	ggattgggtCtcttctctgc	m5C_4522
chr1	212454149	+	C	33	22	0.667	0	0	C	22	M	0.496	0.802	0	6E-05	0	218.27	atttggtgctCtctctcgag	m5C_4521
chr1	223943237	+	C	36	19	0.528	0	0	C	19	M	0.37	0.68	0	3E-05	0	140.62	aggatgaggaCgaaggaggatg	m5C_2778
chr1	225706984	-	C	31	15	0.484	0	0	T	16	M	0.32	0.652	0	1E-05	0	95.91	gagactggaaCggggaaggca	m5C_2761
chr1	225706999	-	C	48	32	0.667	0	0	C	32	M	0.525	0.783	0	2E-05	0	336.26	acgagagaggCTggaagagact	m5C_2771
chr1	225707230	-	C	36	22	0.611	0	0	C	22	M	0.449	0.752	0	6E-05	0	197.4	ggagctggagCgggaaggct	m5C_2765
chr1	225707236	-	C	32	11	0.344	0	0	T	21	M	0.204	0.517	2E-16	3E-06	2E-16	35.144	gcaaaaggagCTggaagcggga	m5C_2757
chr1	226349320	-	C	80	32	0.4	0	0	T	48	M	0.3	0.51	0	8E-10	0	191.75	ggaaagaaacCtgaagagaga	m5C_2812
chr1	226349338	-	C	84	62	0.738	0	0	C	62	M	0.635	0.82	0	1E-08	0	787.58	agaactctgCaaaggaggga	m5C_2818
chr1	226349341	-	C	76	56	0.737	0	0	C	56	M	0.628	0.823	0	9E-08	0	703.57	aagaagacgtCtgcaaaagga	m5C_2817
chr1	226349344	-	C	55	43	0.782	0	0	C	43	M	0.656	0.871	0	4E-06	0	564.42	agaagagaaCgtctgcaaaa	m5C_2825
chr1	226349365	-	C	33	11	0.333	0	0	T	22	M	0.198	0.504	2E-16	3E-06	2E-16	34.007	gcgaaggcgcCgtgaagagga	m5C_2828
chr1	229673634	+	C	42	32	0.762	0	0	C	32	M	0.615	0.865	0	2E-05	0	393.42	gaattctacCtgcattca	m5C_2864
chr1	236431200	+	C	35	17	0.486	0	0	T	18	M	0.33	0.644	0	2E-05	0	112.18	taggagctgTctcatcact	m5C_3155
chr1	236431223	+	C	94	20	0.213	0	0	T	74	M	0.142	0.366	0	2E-15	0	56.867	tcgcatcgacCtggattgca	m5C_3150
chr1	236431237	+	C	184	56	0.304	0	0	T	128	M	0.242	0.374	0	0	0	271.52	tattgcagaCttcaggaacg	m5C_3158
chr1	236431254	+	C	130	31	0.238	0	0	T	99	M	0.173	0.319	0	0	0	107.5	aacggtgacCctctggggg	m5C_3146
chr1	239847440	+	C	51	32	0.627	0	0	C	32	M	0.49	0.747	0	7E-07	0	313.76	atgggtggtCagtggaagaa	m5C_2931
chr1	240964260	+	C	32	10	0.312	0	0	T	22	M	0.18	0.486	1E-14	2E-06	1E-14	25.084	taggggtctCtggggggca	m5C_2967
chr1	241793554	-	C	42	21	0.5	0	0	CT	21	M	0.355	0.645	0	2E-06	0	149.21	aaaaagagaCattgggaagat	m5C_2982
chr1	242247840	-	C	39	10	0.256	0	0	T	29	M	0.146	0.411	1E-13	2E-06	1E-13	18.775	tcaggagggCgaaggtctg	m5C_2964
chr1	242247841	-	C	35	15	0.429	0	0	T	20	M	0.28	0.591	0	1E-05	0	83.953	gtcagagcggCcgatgggtct	m5C_2962
chr1	245021336	-	C	71	40	0.563	0	0	C	40	M	0.448	0.673	0	6E-09	0	358.17	accaaaaggggCtgaagagaa	m5C_3006
chr1	245021345	-	C	46	20	0.435	0	0	T	26	M	0.302	0.578	0	1E-06	0	120.84	agttagaggaCcaaggggcc	m5C_3001
chr1	245027364	-	C	149	32	0.215	0	0	T	117	M	0.156	0.287	0	0	0	100.12	cggccggcggCgaagaagagg	m5C_3005
chr1	245027367	-	C	151	70	0.464	0	0	T	81	M	0.386	0.543	0	0	0	540.3	ccggggccggCggcgtggaag	m5C_3002
chr1	245027370	-	C	148	86	0.581	0	0	C	86	M	0.501	0.658	0	1E-14	0	860.9	agggcggcggCggcgtgatg	m5C_2997
chr1	245027374	-	C	110	37	0.336	0	0	T	73	M	0.255	0.429	0	1E-15	0	188.64	caggagggcgCggccggggcg	m5C_3008
chr1	245027376	-	C	105	75	0.714	0	0	C	75	M	0.622	0.792	0	3E-10	0	932.27	agcaggagggCggggccggcg	m5C_3009
chr1	245027377	-	C	96	26	0.271	0	0	T	70	M	0.192	0.367	0	5E-14	0	99.859	gagcaggaggCcgggccggc	m5C_3000
chr1	249168121	+	C	54	20	0.37	0	0	T	34	M	0.254	0.504	0	3E-08	0	101.69	gctttctgtCtccgatgga	m5C_3483
chr1	249168123	+	C	62	24	0.387	0	0	T	38	M	0.276	0.512	0	3E-09	0	132.41	tttctggtCtCggatggagg	m5C_3491
chr1	249168448	+	C	68	18	0.265	0	0	T	50	M	0.174	0.38	0	3E-10	0	62.819	atcatgcttCctctgggtgc	m5C_3462
chr1	249168449	+	C	70	31	0.443	0	0	T	39	M	0.332	0.559	0	6E-10	0	206.15	tcattgcttCtggaggtct	m5C_3485
chr1	249168450	+	C	68	34	0.5	0	0	CT	34	M	0.384	0.616	0	4E-08	0	261.38	catgcttccTCtgggtgcta	m5C_3493
chr1	249168458	+	C	167	108	0.647	0	0	C	108	M	0.572	0.715	0	1E-15	0	1234.8	ccctgggggCtaggggttag	m5C_3481
chr1	249168473	+	C	178	97	0.545	0	0	C	97	M	0.472	0.616	0	0	0	914.92	ggtagattCggcgctctca	m5C_3464
chr1	249168476	+	C	178	93	0.522	0	0	C	93	M	0.449	0.595	0	0	0	835.87	taggattcggCgtctaccgc	m5C_3466
chr1	249168478	+	C	177	87	0.492	0	0	T	90	M	0.419	0.565	0	0	0	728.78	ggattcggcgCtctaccgcc	m5C_3489
chr1	249168480	+	C	174	88	0.506	0	0	C	88	M	0.432	0.579	0	0	0	760.57	attcgcgctCagcacgcgc	m5C_3470
chr1	249168482	+	C	176	104	0.591	0	0	C	104	M	0.517	0.661	0	0	0	1075.5	tcggcgctctCaccgcggcg	m5C_3488
chr1	249168484	+	C	168	88	0.527	1	0.006	C	88	M	0.451	0.601	0	0	0	794.59	ggcgcttcaCgcgcggcgc	m5C_3465
chr1	249168485	+	C	163	76	0.466	0	0	T	87	M	0.391	0.543	0	0	0	594.83	gcgcttcacCgcgcggccc	m5C_3492
chr1	249168487	+	C	137	44	0.321	0	0	T	93	M	0.249	0.403	0	0	0	218.92	gcttcaccgcCgcgggccgg	m5C_3468
chr1	249168488	+	C	125	52	0.416	0	0	T	73	M	0.333	0.504	0	4E-15	0	346.69	ctctaccgcCgcggccggg	m5C_3474
chr1	249168490	+	C	107	54	0.505	0	0	C	54	M	0.411	0.598	0	6E-12	0	444.35	ctcacgcgcCggccgggt	m5C_3476
chr1	249168493	+	C	100	44	0.44	0	0	T	56	M	0.347	0.538	0	6E-13	0	305.11	accgcgcgcCccgggttga	m5C_3473
chr1	249168506	+	C	52	12	0.231	0	0	T	40	M	0.137	0.361	4E-15	9E-10	5E-15	23.637	gggttcgattCccggtcagga	m5C_3460
chr1	249168507	+	C	51	19	0.373	0	0	T	32	M	0.253	0.51	0	2E-08	0	96.217	gggttcgattCctgagagaa	m5C_3486
chr1	249168508	+	C	50	11	0.22	0	0	T	39	M	0.128	0.352	9E-14	4E-10	9E-14	18.334	gttcgattccCggcagagaa	m5C_3463
chr10	1759668	-	C	43	11	0.256	0	0	T	32	M	0.149	0.402	1E-14	4E-08	1E-14	22.889	aagaaagaaCagaaagaa	m5C_20544
chr10	5794938	-	C	61	34	0.557	0	0	C	34	M	0.433	0.675	0	4E-08	0	294.46	ctctggcggtCtaggggttag	m5C_20674
chr10	17272665	+	C	38	8	0.211	0	0	T	30	M	0.111	0.363	1E-10	7E-07	1E-10	8.7725	ggaggaagatgCttcagagaga	

chr10	101590102 +	C	36	26	0.722	0	0	C	26	M	0.56	0.842	0	0.0001	0	291.24	tgactatgggCtgatccag	m5C_21534
chr10	101590109 +	C	35	11	0.314	0	0	T	24	M	0.186	0.48	7E-16	3E-06	7E-16	30.969	gggctgatatCcaggtggaa	m5C_21535
chr10	103124607 -	C	76	25	0.329	0	0	T	51	M	0.234	0.441	0	9E-11	0	116.9	gaacggggaCtctgcctgg	m5C_21616
chr10	103124620 -	C	113	26	0.23	0	0	T	87	M	0.162	0.316	0	0	0	84.308	gcagtaacctCaggaaacgg	m5C_21639
chr10	103124624 -	C	115	40	0.348	0	0	T	75	M	0.267	0.439	0	4E-15	0	213.58	tattcgagaCctccaggaa	m5C_21628
chr10	103124655 -	C	67	28	0.418	0	0	T	39	M	0.307	0.537	0	1E-08	0	172.16	cttgcctcgCcaactccatgc	m5C_21643
chr10	103124659 -	C	76	21	0.276	0	0	T	55	M	0.188	0.386	0	2E-11	0	79.128	ggagcttgctCctgccaatcc	m5C_21631
chr10	103124684 -	C	131	65	0.496	0	0	T	66	M	0.412	0.581	0	4E-15	0	535.47	attttggagCagggagatgg	m5C_21634
chr10	103577786 -	C	41	13	0.317	0	0	T	28	M	0.196	0.47	0	1E-07	0	50.868	cggccgggggCaggaagatgg	m5C_21647
chr10	103577792 -	C	43	17	0.395	0	0	T	26	M	0.264	0.544	0	6E-07	0	89.641	tgccagcggcCggggcagga	m5C_21630
chr10	103577796 -	C	45	13	0.289	0	0	T	32	M	0.177	0.434	0	1E-07	0	46.098	gagggggcagCggccggggc	m5C_21617
chr10	103923338 +	C	31	10	0.323	0	0	T	21	M	0.186	0.499	7E-15	2E-06	8E-15	26.273	agtagcgggaCctagccagac	m5C_21608
chr10	105154061 -	C	97	58	0.598	0	0	C	58	M	0.498	0.69	0	3E-10	0	578.18	tgccgtcggCgggaagata	m5C_21499
chr10	105154065 -	C	117	47	0.402	0	0	T	70	M	0.317	0.492	0	4E-14	0	298.33	ggcgtggcgtCggcgtggga	m5C_21502
chr10	105154068 -	C	117	43	0.368	0	0	T	74	M	0.286	0.458	0	1E-14	0	245.67	ctcggcgggCgtcggcggg	m5C_21487
chr10	105154073 -	C	111	33	0.297	0	0	T	78	M	0.22	0.388	0	2E-16	0	145.34	atcgactcggCgtggcgtcgg	m5C_21483
chr10	105154078 -	C	44	11	0.25	0	0	T	33	M	0.146	0.394	2E-14	4E-08	2E-14	22.132	tgccaatgaCtccggcgggc	m5C_21484
chr10	120797810 -	C	77	39	0.506	0	0	C	39	M	0.397	0.615	0	5E-09	0	309.81	gacaaggaccCtggagagaa	m5C_21872
chr10	120797811 -	C	73	20	0.274	0	0	T	53	M	0.185	0.386	0	1E-11	0	73.965	tgacaaggacCtggagagaa	m5C_21890
chr10	120797832 -	C	60	20	0.333	0	0	T	40	M	0.227	0.459	0	7E-10	0	90.916	taatcaagatCggggaggaa	m5C_21891
chr10	120797838 -	C	99	26	0.263	0	0	T	73	M	0.186	0.357	0	5E-14	0	96.71	cagagataatCaagatcggga	m5C_21909
chr10	120797848 -	C	82	46	0.561	0	0	C	46	M	0.453	0.663	0	8E-10	0	416.97	aagaaagggaCagagataatc	m5C_21878
chr10	120797866 -	C	68	40	0.588	0	0	C	40	M	0.47	0.697	0	1E-07	0	375.69	gtgaatgggaCagagaaaaag	m5C_21911
chr10	120797926 -	C	45	26	0.578	0	0	C	26	M	0.433	0.71	0	6E-06	0	225.16	aagaaaaagcCagagaggga	m5C_21905
chr10	120797927 -	C	52	25	0.481	0	0	T	27	M	0.351	0.613	0	2E-07	0	175.52	aaagaaaaagCcaagaggga	m5C_21907
chr10	120801508 -	C	36	21	0.583	0	0	C	21	M	0.422	0.729	0	5E-05	0	177.24	ttagtcaagCaggtaaaatt	m5C_21881
chr10	120802244 -	C	35	14	0.4	0	0	T	21	M	0.256	0.564	0	9E-06	0	71.541	ggcagggctCatagagaga	m5C_21903
chr10	120809363 -	C	219	78	0.356	0	0	T	141	M	0.296	0.422	0	0	0	461.33	agaaagagaaCggcgtagaga	m5C_21902
chr10	120809369 -	C	239	83	0.347	0	0	T	156	M	0.29	0.41	0	0	0	481.01	aattgaagaaCagaaacggcg	m5C_21908
chr10	120809393 -	C	116	50	0.431	0	0	T	66	M	0.345	0.522	0	9E-14	0	344.55	gaaaaaacgcCaaaggaggt	m5C_21877
chr10	120809394 -	C	103	33	0.32	0	0	T	70	M	0.238	0.416	0	2E-14	0	157.17	ggaaaaaacgcCaaaggaggt	m5C_21889
chr10	120809396 -	C	90	24	0.267	0	0	T	66	M	0.186	0.366	0	2E-14	0	89.394	aaggaaaaaaCgcraaggga	m5C_21882
chr10	120817632 -	C	31	7	0.226	0	0	T	24	M	0.114	0.398	6E-10	3E-07	7E-10	7.3321	ccagaaaggcCggaaggctga	m5C_21894
chr10	120817659 -	C	37	16	0.432	0	0	T	21	M	0.287	0.591	0	2E-05	0	91.749	agaattggaaCagagggaagc	m5C_21874
chr10	131239934 +	C	53	27	0.509	0	0	C	27	M	0.379	0.639	0	2E-07	0	204.57	aacagggtgcCggggggaga	m5C_21715
chr10	135062936 -	C	44	17	0.386	0	0	T	27	M	0.257	0.534	0	6E-07	0	87.451	tgcaagggtgcCtggcagggtg	m5C_22444
chr11	532453 -	C	31	19	0.613	0	0	C	19	M	0.438	0.763	0	3E-05	0	166.53	gaaggagaggaCggaagcaagg	m5C_21841
chr11	568115 -	C	41	13	0.317	0	0	T	28	M	0.196	0.47	0	1E-07	0	50.868	gtgacggcggCtgatctgtgc	m5C_21830
chr11	568121 -	C	44	17	0.386	0	0	T	27	M	0.257	0.534	0	6E-07	0	87.451	gtgcgtgtgaCagcggctgat	m5C_21829
chr11	812631 +	C	58	12	0.207	0	0	T	46	M	0.123	0.328	2E-14	9E-10	2E-14	20.116	gccctgtgtcCaggaaagggt	m5C_21794
chr11	812793 +	C	73	38	0.521	0	0	C	38	M	0.408	0.631	0	4E-09	0	309.94	aaggaggaggtCtgaagatca	m5C_21790
chr11	833461 +	C	34	12	0.353	0	0	T	22	M	0.215	0.521	0	5E-06	0	51.571	gcggggtcggCggcggcggtg	m5C_21811
chr11	833464 +	C	35	17	0.486	0	0	T	18	M	0.33	0.644	0	2E-05	0	112.18	gggtcggcggCggcggggacc	m5C_21786
chr11	833467 +	C	33	21	0.636	0	0	C	21	M	0.466	0.778	0	5E-05	0	195.79	tcggcggcggCgggtacctca	m5C_21816
chr11	833473 +	C	33	19	0.576	0	0	C	19	M	0.408	0.728	0	3E-05	0	155.07	gcggcgggtgaCctcatgtcag	m5C_21806
chr11	2016650 -	C	42	15	0.357	0	0	T	27	M	0.23	0.508	0	3E-07	0	68.967	tacgaaggcgCgtgggtgtga	m5C_22286
chr11	2017542 -	C	42	17	0.405	0	0	T	25	M	0.27	0.555	0	6E-07	0	91.945	acggcgagggaCagagaggcgg	m5C_22371
chr11	2017551 -	C	117	29	0.248	0	0	T	88	M	0.178	0.333	0	0	0	103.52	tcgggtgtgaCggcgaggaca	m5C_22379
chr11	2017894 -	C	40	14	0.35	0	0	T	26	M	0.221	0.505	0	2E-07	0	61.976	aatgagctctCaggagggagg	m5C_22285
chr11	2017896 -	C	43	28	0.651	0	0	C	28	M	0.502	0.776	0	8E-06	0	280.96	tgaatgagctCtcagagaggga	m5C_22370
chr11	2017925 -	C	31	16	0.516	0	0	C	16	M	0.348	0.68	0	2E-05	0	111.49	ccagataaggCgaaggcggtg	m5C_22327
chr11	2017930 -	C	45	33	0.733	0	0	C	33	M	0.59	0.84	0	2E-05	0	389.14	cgaaccagaaCtagggcgggc	m5C_22337
chr11	2017934 -	C	41	17	0.415	0	0	T	24	M	0.278	0.566	0	6E-07	0	94.372	ggggcgagaaCagataggcgt	m5C_22284
chr11	2017940 -	C	37	11	0.297	0	0	T	26	M	0.175	0.458	1E-15	3E-06	2E-15	28.551	gggcatggggCgaaccagaa	m5C_22366
chr11	2018037 -	C	80	23	0.287	0	0	T	57	M	0.2	0.395	0	7E-13	0	91.939	cggagagggcCcacaggggac	m5C_22376
chr11	2018038 -	C	86	19	0.221	0	0	T	67	M	0.146	0.319	0	8E-14	0	55.574	gcggagaggggCccacagggga	m5C_22383
chr11	2018187 -	C	43	18	0.419	0	0	T	25	M	0.284	0.567	0	8E-07	0	102.18	aggcaggtgcCgggaaggtgc	m5C_22358
chr11	2018194 -	C	52	17	0.327	0	0	T	35	M	0.215	0.462	0	1E-08	0	73.174	gggaagacaggCaggtctcggg	m5C_22320
chr11	2018206 -	C	57	29	0.509	0	0	C	29	M	0.383	0.634	0	4E-07	0	221.91	ggctggagagCgggaagacag	m5C_22356
chr11	2018222 -	C	55	11	0.2	0	0	T	44	M	0.116	0.324	3E-13	4E-10	3E-13	15.923	atgctggagcCtctggaggctg	m5C_22319
chr11	2018223 -	C	43	17	0.395	0	0	T	26	M	0.264	0.544	0	6E-07	0	89.641	tatgcggaggCctcgagggtct	m5C_22294
chr11	2018229 -	C	36	20	0.556	0	0	C	20	M	0.396	0.705	0	4E-05	0	158.32	caggcctatgcCggagccttcg	m5C_22288
chr11	2018324 -	C	33	20	0.606	0	0	C	20	M	0.437	0.753	0	4E-05	0	174.73	gcaggagacaCaggacagagg	m5C_22316
chr11	2018333 -	C	69	16	0.232	0	0	T	53	M	0.148	0.344	0	1E-10	0	47.385	agggaatggCaggggacaca	m5C_22334
chr11	2018338 -	C	80	46	0.575	0	0	C	46	M	0.466	0.677	0	8E-10	0	428.44	cagacagggaCatggcagggg	m5C_22295
chr11	2018344 -	C	70	43	0.614	0	0	C	43	M	0.497	0.72	0	2E-07	0	427.55	ctgggtcagaCaggacatgg	m5C_22269
chr11	2018348 -	C	60	15	0.25	0	0	T	45	M	0.158	0.372	0	6E-11	0	47.329	aggcctgggtCagacagggac	m5C_22308
chr11	2018354 -	C	49	17	0.347	0	0	T	32	M	0.229	0.487	0	6E-07	0	77.942	taccccaaggCtgggtcagac	m5C_22268
chr11	2018355 -	C	37	29	0.784	0	0	C	29	M	0.628	0.886	0	0.0002	0	364.27	gtacccaaggCctgggtcaga	m5C_22378
chr11	2018464 -	C	62	14	0.23	1	0.016	T	47	M	0.142	0.349	0	3E-11	0	39.741	gccgagactgcCgcaaggctgg	m5C_22373
chr11	2018467 -	C	67	15	0.224	0	0	T	52	M	0.141	0.337	0	6E-11	0	42.191	ggagccggaaCtgcgcgaaggc	m5C_22342
chr11	2018472 -	C	61	35	0.574	0	0	C	35	M	0.449	0.69	0	5E-08	0	314.27	cggggggagcCggaactgcgc	m5C_22368
chr11	2018473 -	C	49	35	0.714	0	0	C	35	M	0.576	0.822	0	3E-05	0	403.14	tcggggggagCcggaactgcg	m5C_22298
chr11	2018482 -	C	35	19	0.543	0	0	C	19	M	0.382	0.695	0	3E-05	0	145.12	gacatcttctCggggggagcc	m5C_22270
chr11	201																	

chr11	2018845 -	C	49	20	0.408	0	0 T	29 M	0.282	0.548	0	1E-06	0	112.86	ggcgccaggCcatgctgcaga	m5C_22279
chr11	2018850 -	C	61	21	0.344	0	0 T	40 M	0.237	0.47	0	1E-09	0	99.739	gagtagggcCcaggcatcgt	m5C_22346
chr11	2018851 -	C	58	19	0.328	0	0 T	39 M	0.221	0.456	0	2E-08	0	83.916	ggagtagggcCccaggcatcg	m5C_22380
chr11	2018853 -	C	68	17	0.25	0	0 T	51 M	0.162	0.364	0	2E-10	0	55.199	gtggagtagggCgcccaggcat	m5C_22350
chr11	2018875 -	C	93	54	0.581	0	0 C	54 M	0.479	0.676	0	2E-10	0	517.44	gggctggaggCagggagggag	m5C_22305
chr11	2018881 -	C	91	54	0.593	0	0 C	54 M	0.491	0.689	0	2E-10	0	529.95	ctggggggCtggagccagt	m5C_22387
chr11	2018882 -	C	91	35	0.385	0	0 T	56 M	0.291	0.487	0	1E-12	0	203.88	gtgtggggCctgagggcag	m5C_22377
chr11	2018891 -	C	62	45	0.726	0	0 C	45 M	0.604	0.821	0	3E-07	0	543.67	cggagcaggCtggggggcc	m5C_22347
chr11	2018919 -	C	94	69	0.734	0	0 C	69 M	0.637	0.813	0	2E-09	0	878.81	ggaggtatgaCggggggagg	m5C_22382
chr11	2018931 -	C	65	15	0.231	0	0 T	50 M	0.145	0.346	0	6E-11	0	43.541	tggagctggCaggaggtatg	m5C_22367
chr11	2019000 -	C	47	20	0.426	0	0 T	27 M	0.295	0.567	0	1E-06	0	118.05	gaggggcaacCaggggaagat	m5C_22310
chr11	2019004 -	C	41	24	0.585	0	0 C	24 M	0.434	0.722	0	4E-06	0	208.16	aaccgagggCcaaccaggga	m5C_22275
chr11	3178797 +	C	37	28	0.757	0	0 C	28 M	0.599	0.866	0	0.0002	0	335.34	gggggggctCacaggcagc	m5C_22261
chr11	3810678 -	C	117	36	0.308	0	0 T	81 M	0.231	0.396	0	1E-15	0	166.53	ggataaagaCagagatgtga	m5C_22384
chr11	4142910 +	C	36	8	0.222	0	0 T	28 M	0.117	0.381	7E-11	7E-07	8E-11	9.4968	aagaagaacaCaggaagaaga	m5C_21759
chr11	4159503 +	C	69	21	0.304	0	0 T	48 M	0.208	0.421	0	1E-09	0	87.568	taaggagaagCtaaaagataa	m5C_21761
chr11	4159525 +	C	173	37	0.214	0	0 T	136 M	0.159	0.281	0	0	0	117.91	gaaaaggatCaaaaaggaa	m5C_21771
chr11	4159596 +	C	329	87	0.264	0	0 T	242 M	0.22	0.315	0	0	0	382.27	agatgaatgtCtgaatggg	m5C_21763
chr11	4159609 +	C	357	91	0.255	0	0 T	266 M	0.212	0.303	0	0	0	386.69	atgtgggatCtgaagaaag	m5C_21764
chr11	4159610 +	C	336	93	0.277	0	0 T	243 M	0.232	0.327	0	0	0	430.91	tgtgggatCtgaagaaaga	m5C_21770
chr11	7256443 +	C	57	31	0.544	0	0 C	31 M	0.416	0.666	0	6E-07	0	257.86	tggggggcagCttattggcc	m5C_22017
chr11	7256452 +	C	56	24	0.429	0	0 T	32 M	0.308	0.559	0	1E-07	0	147.69	gtttattgcCcatcaattt	m5C_22015
chr11	8705781 +	C	69	18	0.261	0	0 T	51 M	0.172	0.375	0	3E-10	0	61.868	gtcatcgaggCtagagtcag	m5C_22114
chr11	8705788 +	C	62	13	0.21	0	0 T	49 M	0.127	0.326	2E-15	2E-11	2E-15	24.322	aggctagagtCacgtctggg	m5C_22102
chr11	8705790 +	C	65	18	0.277	0	0 T	47 M	0.183	0.396	0	3E-10	0	65.856	gctagagatCgcttgggat	m5C_22108
chr11	8705792 +	C	61	18	0.295	0	0 T	43 M	0.196	0.419	0	3E-10	0	70.398	tagagtcagCttagggatcg	m5C_22111
chr11	8705804 +	C	52	18	0.346	0	0 T	34 M	0.232	0.482	0	2E-08	0	83.343	tgggatcggCtattgctga	m5C_22110
chr11	8705811 +	C	42	13	0.31	0	0 T	29 M	0.191	0.46	0	1E-07	0	49.584	cggctatgcCtgaatgtgct	m5C_22112
chr11	10530739 -	C	72	49	0.681	0	0 C	49 M	0.566	0.777	0	3E-08	0	554.75	ctgaccgctCtgaaccaaac	m5C_21998
chr11	10530743 -	C	76	57	0.75	0	0 C	57 M	0.642	0.834	0	1E-07	0	732.14	tcaactgacCgctctgagcc	m5C_22004
chr11	10530744 -	C	72	49	0.681	0	0 C	49 M	0.566	0.777	0	3E-08	0	554.75	ctcaactcaCgctctgagc	m5C_21996
chr11	10530749 -	C	77	54	0.701	0	0 C	54 M	0.592	0.792	0	7E-08	0	638.82	tcaactcaaCtgaaccgtc	m5C_21989
chr11	10530754 -	C	73	42	0.575	0	0 C	42 M	0.461	0.682	0	9E-09	0	387.23	gagattcaaCtcaactgac	m5C_21992
chr11	10530757 -	C	73	41	0.562	0	0 C	41 M	0.448	0.67	0	7E-09	0	367.01	taggagattCcaactcaatt	m5C_22003
chr11	18425324 +	C	37	18	0.486	0	0 T	19 M	0.334	0.641	0	3E-05	0	120.41	agataaggaaCagtggaagaa	m5C_22510
chr11	21022435 -	C	66	51	0.773	0	0 C	51 M	0.658	0.857	0	8E-07	0	671.47	atacggggCttagggctgt	m5C_22039
chr11	35684961 +	C	45	14	0.311	0	0 T	31 M	0.195	0.457	0	2E-07	0	54.68	gagagtaggtCggaggaagag	m5C_22500
chr11	35684997 +	C	43	22	0.733	13	0.302 C	22 M	0.556	0.858	0	6E-05	0	244.43	gagagcgagaCagaggaagag	m5C_22491
chr11	35685022 +	C	96	52	0.542	0	0 C	52 M	0.442	0.638	0	1E-10	0	460.01	aggatggagCgatggagga	m5C_22492
chr11	35828474 +	C	48	19	0.396	0	0 T	29 M	0.27	0.537	0	1E-06	0	102.68	agatggatgaCtggaaaaagg	m5C_22502
chr11	45848213 -	C	31	22	0.71	0	0 C	22 M	0.534	0.839	0	6E-05	0	234.99	gtgtgtggCtagtgcattc	m5C_22673
chr11	45848228 -	C	51	11	0.216	0	0 T	40 M	0.125	0.346	1E-13	4E-10	1E-13	17.806	tttctcaattCtgggggtgt	m5C_22684
chr11	45848235 -	C	73	40	0.548	0	0 C	40 M	0.434	0.657	0	6E-09	0	347.39	atagctctttCtcaattctgt	m5C_22682
chr11	45848239 -	C	123	68	0.553	0	0 C	68 M	0.465	0.638	0	2E-13	0	632	attgatagtCtttctcaatt	m5C_22688
chr11	45848241 -	C	115	63	0.548	0	0 C	63 M	0.457	0.636	0	2E-12	0	575.55	aggatgatagCtttcttcaa	m5C_22668
chr11	45848252 -	C	140	84	0.6	0	0 C	84 M	0.517	0.677	0	8E-15	0	868.94	acaggatgaCagattgatag	m5C_22669
chr11	45848261 -	C	131	75	0.573	0	0 C	75 M	0.487	0.654	0	3E-14	0	730.39	tggacaggaCagattgagaca	m5C_22695
chr11	45848265 -	C	110	55	0.5	0	0 CT	55 M	0.408	0.592	0	3E-13	0	448.97	aggctggacaCggagaggatt	m5C_22686
chr11	45848267 -	C	106	52	0.491	0	0 T	54 M	0.397	0.584	0	4E-12	0	413.3	ccagcttgaCacggacagga	m5C_22674
chr11	45848272 -	C	85	38	0.447	0	0 T	47 M	0.346	0.553	0	1E-10	0	262.91	ctcaccagcCtggacacgga	m5C_22689
chr11	45848273 -	C	82	36	0.439	0	0 T	46 M	0.337	0.547	0	7E-11	0	242.45	cttcaccagCctggacacgg	m5C_22692
chr11	45848276 -	C	56	25	0.446	0	0 T	31 M	0.324	0.576	0	2E-07	0	161.93	aaactcaccCagcctggaca	m5C_22687
chr11	45848277 -	C	48	24	0.5	0	0 CT	24 M	0.364	0.636	0	4E-06	0	174.67	gaaccttacCagccttgac	m5C_22675
chr11	45848278 -	C	50	24	0.48	0	0 T	26 M	0.348	0.615	0	1E-07	0	167.03	ggaaactcaCccagcttga	m5C_22671
chr11	45848280 -	C	48	21	0.438	0	0 T	27 M	0.307	0.577	0	2E-06	0	128.94	cgggaacctCaccagccttg	m5C_22691
chr11	45848282 -	C	41	20	0.488	0	0 T	21 M	0.343	0.635	0	1E-06	0	137.02	cacgggaaaCtcaaccagcc	m5C_22696
chr11	45848283 -	C	42	21	0.5	0	0 CT	21 M	0.355	0.645	0	2E-06	0	149.21	acacgggaaaCtccaccagc	m5C_22690
chr11	46265717 +	C	33	23	0.697	0	0 C	23 M	0.527	0.826	0	8E-05	0	242.24	atgggctggCcgagtgacg	m5C_22539
chr11	46265718 +	C	33	16	0.485	0	0 T	17 M	0.325	0.648	0	2E-05	0	104.01	tgggctggCgagtgacgtg	m5C_22535
chr11	46265739 +	C	32	12	0.375	0	0 T	20 M	0.229	0.547	0	5E-06	0	55.041	gtgttgcaaCtaactgatca	m5C_22550
chr11	46784009 -	C	51	26	0.51	0	0 C	26 M	0.377	0.641	0	2E-07	0	195.94	gccattgatCagggtataca	m5C_22582
chr11	46784031 -	C	63	38	0.603	0	0 C	38 M	0.48	0.715	0	1E-07	0	364.65	tgatgattgtCacactgtgg	m5C_22555
chr11	57094201 -	C	34	13	0.382	0	0 T	21 M	0.239	0.555	0	7E-06	0	62.14	agaacaagagCaaaaagaaga	m5C_22785
chr11	57094207 -	C	39	16	0.41	0	0 T	23 M	0.271	0.566	0	2E-05	0	86.653	cgggagagaaCaaagacaaa	m5C_22790
chr11	57095222 -	C	32	12	0.375	0	0 T	20 M	0.229	0.547	0	5E-06	0	55.041	agaagcaggCgagatttga	m5C_22784
chr11	57097820 -	C	77	44	0.571	0	0 C	44 M	0.46	0.676	0	1E-08	0	404.89	aggaggaaggCaaatccggg	m5C_22788
chr11	58346746 +	C	31	22	0.71	0	0 C	22 M	0.534	0.839	0	6E-05	0	234.99	gggggacggaCaagccccgat	m5C_22598
chr11	58346751 +	C	32	19	0.594	0	0 C	19 M	0.423	0.745	0	3E-05	0	160.59	acggacaagcCccgatgcgg	m5C_22600
chr11	58346753 +	C	31	9	0.29	0	0 T	22 M	0.161	0.466	4E-13	1E-06	4E-13	18.015	ggacaaggccCgatgcgggg	m5C_22599
chr11	58379201 +	C	47	21	0.447	0	0 T	26 M	0.314	0.588	0	2E-06	0	131.93	ggatgaggaacCtccaagaa	m5C_22619
chr11	58379204 +	C	43	12	0.279	0	0 T	31 M	0.167	0.427	2E-16	7E-08	2E-16	31.457	tgaggaaacctCaaaggaagg	m5C_22613
chr11	58379205 +	C	36	8	0.222	0	0 T	28 M	0.117	0.381	7E-11	7E-07	8E-11	9.4968	gaggaaacctCaaaggaagg	m5C_22607
chr11	61732280 -	C	34	17	0.5	0	0 CT	17 M	0.341	0.659	0	2E-05	0	115.83	ccaacttgcCaaagtggaag	m5C_23321
chr11	61732298 -	C	36	16	0.444	0	0 T	20 M	0.295	0.604	0	2E-05	0	94.531	aattggggaCcacgtgacca	m5C_23311
chr11	61732554 -	C	53	19	0.358	0	0 T	34 M	0.243	0.493	0	2E-08	0	92.347	ggagagcgggCtgaatgcaat	m5C_23319
chr11	61732558 -	C	54	19	0.352	0	0 T	35 M	0.238	0.485	0	2E-08	0	90.527	actggagagCgggctgaat	m5C_23317
chr11	61915997 +	C	54	30	0.556	0	0 C	30 M	0.424	0.68	0	5E-07	0	254.25	ggagcagctgCagaggggaat	m5C_23297
chr11	62400707 -	C	33	16	0.485	0	0 T	17 M	0.325	0.648	0	2E-05	0	104.01	gaagatgagCagagagctg	m5C_26337
chr11	62400721 -	C	31	19												

chr11	62609138	-	C	312	160	0.513	0	0	C	160	M	0.458	0.568	0	0	0	1464.1	ccgtccactCacgcatcga	m5C_26353
chr11	62609139	-	C	314	177	0.564	0	0	C	177	M	0.508	0.617	0	0	0	1799.7	tcgtccactCcacgcatcga	m5C_26252
chr11	62609141	-	C	305	203	0.666	0	0	C	203	M	0.611	0.716	0	0	0	2480.1	gctccgccaCttccacgcatc	m5C_26283
chr11	62609143	-	C	283	168	0.594	0	0	C	168	M	0.536	0.649	0	0	0	1799.4	ttgtccgctCactccacgca	m5C_26249
chr11	62609144	-	C	280	174	0.621	0	0	C	174	M	0.563	0.676	0	0	0	1960.4	cttgcctcgtCcactccacgc	m5C_26243
chr11	62609147	-	C	251	188	0.749	0	0	C	188	M	0.692	0.799	0	0	0	2601.5	gagctgtctCgtccatcca	m5C_26218
chr11	62609148	-	C	237	148	0.624	0	0	C	148	M	0.561	0.684	0	0	0	1661.4	ggagctgtctCgtccactcc	m5C_26360
chr11	62609150	-	C	232	158	0.681	0	0	C	158	M	0.619	0.738	0	0	0	1954.5	taggagcttgCttcgccact	m5C_26226
chr11	62609154	-	C	199	128	0.643	0	0	C	128	M	0.575	0.706	0	0	0	1470.8	ggaataggagCttgtccgic	m5C_26241
chr11	62609198	-	C	221	162	0.733	0	0	C	162	M	0.671	0.787	0	0	0	2174.3	tatccgaggaCaatatattaa	m5C_26335
chr11	62609204	-	C	203	114	0.562	0	0	C	114	M	0.493	0.628	0	0	0	1123.6	gctctctatCggaggacaata	m5C_26233
chr11	62609205	-	C	203	116	0.571	0	0	C	116	M	0.503	0.638	0	0	0	1166.1	cgctctatCcgaggacaat	m5C_26348
chr11	62609209	-	C	206	153	0.743	0	0	C	153	M	0.679	0.798	0	0	0	2077.6	gatacgctctCtatccgagga	m5C_26228
chr11	62609211	-	C	189	141	0.746	0	0	C	141	M	0.679	0.803	0	4E-16	0	1916.2	ctgatacgtCtctatccgag	m5C_26347
chr11	62609212	-	C	188	121	0.644	0	0	C	121	M	0.573	0.709	0	0	0	1386.4	tcgtatagctCtctatccga	m5C_26230
chr11	62609215	-	C	172	119	0.692	0	0	C	119	M	0.619	0.756	0	3E-16	0	1473.9	atatctgataCgtctctatc	m5C_26229
chr11	62620390	-	C	99	23	0.232	0	0	T	76	M	0.16	0.325	0	1E-14	0	73.641	aaggacttgCtaggggatga	m5C_26300
chr11	62620394	-	C	100	33	0.333	1	0.01	T	66	M	0.248	0.431	0	8E-13	0	163.84	ccagaaggaaCtgtctgagg	m5C_26380
chr11	62620403	-	C	93	43	0.462	0	0	T	50	M	0.365	0.563	0	1E-11	0	313.51	agatttgtcCagaaggaaact	m5C_26242
chr11	62620404	-	C	87	23	0.264	0	0	T	64	M	0.183	0.366	0	7E-13	0	84.226	aagatttgtCcaagaaggaa	m5C_26368
chr11	62620429	-	C	137	62	0.453	0	0	T	75	M	0.372	0.536	0	2E-15	0	460.83	ctggagctggCtggggagaa	m5C_26377
chr11	62620433	-	C	138	83	0.601	0	0	C	83	M	0.518	0.679	0	1E-13	0	860.01	ccactgggaCtggctggagg	m5C_26245
chr11	62620439	-	C	137	51	0.372	0	0	T	86	M	0.296	0.456	0	1E-16	0	301.75	gggagcccaCtgggactggc	m5C_26291
chr11	62620442	-	C	119	33	0.277	0	0	T	86	M	0.205	0.364	0	2E-16	0	135.17	aaagggaacCcactgggact	m5C_26269
chr11	62620443	-	C	113	45	0.398	0	0	T	68	M	0.313	0.49	0	2E-14	0	281.47	taaaagggaCccactgggac	m5C_26305
chr11	62620801	-	C	89	27	0.303	0	0	T	62	M	0.218	0.405	0	4E-12	0	117.53	atttctggagCtggagactg	m5C_26332
chr11	62620806	-	C	184	56	0.304	0	0	T	128	M	0.242	0.374	0	0	0	271.52	aagattttCtggagcttga	m5C_26248
chr11	62620820	-	C	238	65	0.273	0	0	T	173	M	0.22	0.333	0	0	0	286.57	caatgttgaCtgaaaggat	m5C_26270
chr11	62620830	-	C	224	85	0.379	0	0	T	139	M	0.318	0.445	0	0	0	541.37	ccagctgatCaatgttgagac	m5C_26232
chr11	62620835	-	C	228	74	0.325	0	0	T	154	M	0.267	0.388	0	0	0	395.35	ccgccccagCtgatcaatg	m5C_26340
chr11	62620839	-	C	231	74	0.32	0	0	T	157	M	0.264	0.383	0	0	0	390.03	aataccgccCagictgata	m5C_26341
chr11	62620840	-	C	231	63	0.273	0	0	T	168	M	0.219	0.334	0	0	0	276.4	gaataccgccCagictgatc	m5C_26343
chr11	62620841	-	C	228	71	0.311	0	0	T	157	M	0.255	0.374	0	0	0	361.87	tgaataccgcCccagctgat	m5C_26237
chr11	62620842	-	C	224	63	0.281	0	0	T	161	M	0.226	0.343	0	0	0	285.32	ttgaataccgCccagcttga	m5C_26317
chr11	62620844	-	C	233	74	0.318	0	0	T	159	M	0.261	0.38	0	0	0	386.56	agttgaataCgccccagct	m5C_26214
chr11	62620845	-	C	239	71	0.298	1	0.004	T	167	M	0.244	0.359	0	0	0	346.15	gagttgaataCgccccagc	m5C_26312
chr11	62620862	-	C	100	26	0.26	0	0	T	74	M	0.184	0.354	0	7E-16	0	95.704	tgtctctacCagtgatgag	m5C_26314
chr11	62620863	-	C	94	26	0.277	0	0	T	68	M	0.196	0.374	0	5E-14	0	102.08	ttgtctgtaCcaagatgag	m5C_26220
chr11	62621143	-	C	292	114	0.39	0	0	T	178	M	0.336	0.447	0	0	0	766.59	acctgaaatCtgattttctg	m5C_26365
chr11	62621150	-	C	345	120	0.348	0	0	T	225	M	0.299	0.4	0	0	0	718.78	tgttgagactCtgaatactga	m5C_26293
chr11	62621152	-	C	357	130	0.364	0	0	T	227	M	0.316	0.415	0	0	0	821.4	gcttgtgagaCttcgaatct	m5C_26325
chr11	62621161	-	C	377	128	0.34	0	0	T	249	M	0.294	0.389	0	0	0	751.5	tgtgacttgCtgnrgagact	m5C_26282
chr11	62621165	-	C	368	145	0.394	0	0	T	223	M	0.345	0.445	0	0	0	1001.8	cggttgatgaCttgtcttga	m5C_26304
chr11	62621172	-	C	361	152	0.421	0	0	T	209	M	0.371	0.473	0	0	0	1128.5	ttctgtcggCtggatcttg	m5C_26219
chr11	62621175	-	C	354	187	0.528	0	0	C	187	M	0.476	0.58	0	0	0	1781.1	gaatctggtCcggttgatga	m5C_26262
chr11	62621179	-	C	347	142	0.409	0	0	T	205	M	0.359	0.462	0	0	0	1018.9	catggaatctCgttcggctga	m5C_26344
chr11	62621181	-	C	353	165	0.467	0	0	T	188	M	0.416	0.52	0	0	0	1372.8	tacatggaatCtctgtcgct	m5C_26234
chr11	62621189	-	C	358	157	0.439	0	0	T	201	M	0.388	0.49	0	0	0	1218.5	tgtatgactaCattggaattc	m5C_26209
chr11	62621193	-	C	355	133	0.375	0	0	T	222	M	0.326	0.426	0	0	0	866.87	tttgatgaCttacatggaa	m5C_26208
chr11	62621387	-	C	47	19	0.404	0	0	T	28	M	0.276	0.547	0	1E-06	0	105.03	aatacatgaaCaccctgagaa	m5C_26299
chr11	62621393	-	C	52	22	0.423	0	0	T	30	M	0.299	0.558	0	7E-08	0	131.42	agtgaaataaCattgaacact	m5C_26336
chr11	62621404	-	C	51	19	0.373	0	0	T	32	M	0.253	0.51	0	2E-08	0	96.217	ctatgacgaCagtgaaaata	m5C_26213
chr11	62621407	-	C	50	28	0.56	0	0	C	28	M	0.423	0.688	0	8E-06	0	236.91	tcactatgacCgacagtgaaa	m5C_26329
chr11	62621414	-	C	52	12	0.231	0	0	T	40	M	0.137	0.361	4E-15	9E-10	5E-15	23.637	taactgactaCtatgacgac	m5C_26216
chr11	62621416	-	C	54	23	0.426	0	0	T	31	M	0.303	0.558	0	9E-08	0	139.53	caaactagctCactatgaccg	m5C_26255
chr11	62621418	-	C	56	32	0.571	0	0	C	32	M	0.441	0.692	0	7E-07	0	282.48	atcaactagCttactatgac	m5C_26363
chr11	62621422	-	C	54	11	0.204	0	0	T	43	M	0.118	0.329	2E-13	4E-10	3E-13	16.362	atgaataaaaCtagctcaact	m5C_26238
chr11	62621426	-	C	55	15	0.273	0	0	T	40	M	0.173	0.402	0	5E-09	0	51.842	tatgatgaatCaaactagctc	m5C_26374
chr11	62622495	-	C	55	42	0.764	0	0	C	42	M	0.637	0.856	0	4E-06	0	534.67	tgtactttaCtactgagaag	m5C_26278
chr11	62622499	-	C	55	41	0.745	0	0	C	41	M	0.617	0.842	0	3E-06	0	505.92	ggatgcatctCttactatga	m5C_26273
chr11	62622512	-	C	57	41	0.732	1	0.018	C	41	M	0.604	0.83	0	3E-06	0	495.32	gctgaactttCaaagtgatgc	m5C_26265
chr11	62622516	-	C	52	36	0.692	0	0	C	36	M	0.557	0.801	0	2E-06	0	401.26	tatggctgaaCttcaaggga	m5C_26376
chr11	62622532	-	C	41	26	0.634	0	0	C	26	M	0.481	0.764	0	6E-06	0	250.23	cacaaaatgaCaagcatatgg	m5C_26330
chr11	62622540	-	C	35	19	0.543	0	0	C	19	M	0.382	0.695	0	3E-05	0	145.12	atgatgaaCaataatgacaa	m5C_26254
chr11	62622542	-	C	33	18	0.545	0	0	C	18	M	0.38	0.702	0	3E-05	0	136.75	ccatgatgaaCacaaaatgac	m5C_26281
chr11	62622772	-	C	231	119	0.515	0	0	C	119	M	0.451	0.579	0	0	0	1073.3	acagaaaatCtggatgagac	m5C_26231
chr11	62622781	-	C	264	100	0.379	0	0	T	164	M	0.322	0.439	0	0	0	644.81	ggggagaaaaCagaaaattct	m5C_26277
chr11	62622802	-	C	230	108	0.47	0	0	T	122	M	0.406	0.534	0	0	0	877.17	ctctctcttCtgatggata	m5C_26211
chr11	62622806	-	C	228	99	0.434	0	0	T	129	M	0.371	0.499	0	0	0	735.55	tgaactttCtttctgagg	m5C_26306
chr11	62622808	-	C	226	99	0.438	0	0	T	127	M	0.375	0.503	0	0	0	742.37	actgaactctCttcttctgt	m5C_26224
chr11	62622810	-	C	230	102	0.443	0	0	T	128	M	0.381	0.508	0	0	0	776.68	gaactgaactCtcttcttct	m5C_26327
chr11	62622812	-	C	231	137	0.593	0	0	C	137	M	0.529	0.654	0	0	0	1448.6	acgaactgaaCtctcttttc	m5C_26302
chr11	62622817	-	C	246	98	0.398	0	0	T	148	M	0.339	0.461	0	0	0	664.85	atttt	

chr11	65266734	+	C	33	14	0.424	0	0	T	19	M	0.272	0.592	0	9E-06	0	76.259	agaaagtagCatgaggaagg	m5C_26014
chr11	65267103	+	C	609	157	0.261	7	0.011	T	445	M	0.227	0.297	0	0	0	713.78	taggatgaaaCaatttgaga	m5C_26030
chr11	65267137	+	C	875	394	0.45	0	0	T	481	M	0.418	0.483	0	0	0	3290.8	aagtggaaaaCtgggaagacag	m5C_25987
chr11	65267145	+	C	849	232	0.274	1	0.001	T	616	M	0.245	0.305	0	0	0	1135.2	aactgggaagCagaagtagcgg	m5C_26038
chr11	65267153	+	C	589	214	0.364	1	0.002	T	374	M	0.326	0.404	0	0	0	1395.5	gacagaagracgggaaggcga	m5C_25949
chr11	65267161	+	C	659	157	0.245	19	0.029	T	483	M	0.214	0.28	0	0	0	670.58	tacgggaagcCgaagaaaga	m5C_25977
chr11	65267301	+	C	51	17	0.333	0	0	T	34	M	0.22	0.47	0	1E-08	0	74.697	gcacaaatgaCaaacttagaa	m5C_25933
chr11	65267667	+	C	58	17	0.293	0	0	T	41	M	0.192	0.42	0	1E-08	0	65.205	ttaaaaaaaCtaaggcagaa	m5C_26048
chr11	65267961	+	C	250	69	0.276	0	0	T	181	M	0.224	0.334	0	0	0	309.53	gactgaggaagCaagcgagcaa	m5C_26008
chr11	65267965	+	C	280	68	0.243	0	0	T	212	M	0.196	0.296	0	0	0	267.01	gaggagcaagCgagcaagcrag	m5C_26039
chr11	65267976	+	C	319	92	0.288	0	0	T	227	M	0.241	0.34	0	0	0	444.25	gagcaagcagCagttcgngt	m5C_25935
chr11	65267981	+	C	348	85	0.244	0	0	T	263	M	0.202	0.292	0	0	0	343.51	agcagcagttCgtgggaaga	m5C_25940
chr11	65268012	+	C	293	62	0.212	0	0	T	231	M	0.169	0.262	0	0	0	209.21	gtccaggagcCagtcgattt	m5C_26009
chr11	65268017	+	C	338	89	0.263	0	0	T	249	M	0.219	0.313	0	0	0	390.19	ggagccagtcCgatttgtna	m5C_26043
chr11	65268034	+	C	288	63	0.219	0	0	T	225	M	0.175	0.27	0	0	0	220.35	gtgaggaagCtaggaagaag	m5C_26005
chr11	65268054	+	C	46	17	0.37	0	0	T	29	M	0.245	0.514	0	6E-07	0	83.38	ggagggagcCtaacgatttg	m5C_26004
chr11	65268058	+	C	49	32	0.653	0	0	C	32	M	0.513	0.771	0	2E-05	0	328.39	ggagcgctaaCgatttggtg	m5C_25999
chr11	65268074	+	C	66	22	0.333	0	0	T	44	M	0.232	0.453	0	1E-09	0	101.89	gggtgggaagCtaggaaaaa	m5C_25914
chr11	65268090	+	C	56	15	0.268	0	0	T	41	M	0.17	0.396	0	5E-09	0	50.871	aaaaagattcCagaagagagc	m5C_26012
chr11	65268439	+	C	41	21	0.512	0	0	C	21	M	0.365	0.657	0	2E-06	0	153.23	tgagggcagaCtgccaagtc	m5C_25929
chr11	65268449	+	C	39	27	0.692	0	0	C	27	M	0.536	0.814	0	0.0001	0	289.32	ctgcgaagcCtgggaagata	m5C_26035
chr11	65268671	+	C	49	18	0.367	0	0	T	31	M	0.247	0.507	0	8E-07	0	88.794	ggatgtgtaaCtaggggggg	m5C_25944
chr11	65270538	+	C	49	30	0.612	0	0	C	30	M	0.472	0.736	0	1E-05	0	283.47	gagtggtgCaaagtgattg	m5C_26036
chr11	65270560	+	C	53	42	0.792	0	0	C	42	M	0.665	0.88	0	4E-06	0	558.95	ggaggtgtgtCtgggtccaa	m5C_25938
chr11	65270568	+	C	33	26	0.788	0	0	C	26	M	0.622	0.893	0	0.0001	0	323.69	tgtgtgtgtCaatgtttgt	m5C_26050
chr11	65270996	+	C	32	11	0.344	0	0	T	21	M	0.204	0.517	2E-16	3E-06	2E-16	35.144	gcattgtgtgtCgttagaatc	m5C_26006
chr11	65271247	+	C	93	25	0.269	0	0	T	68	M	0.189	0.367	0	3E-14	0	94.606	aggtattgagCgggaagacga	m5C_25962
chr11	65271255	+	C	106	30	0.283	0	0	T	76	M	0.206	0.375	0	5E-15	0	123.61	agcggaagaaCgaatgtaact	m5C_26001
chr11	65273299	+	C	74	24	0.324	0	0	T	50	M	0.229	0.437	0	6E-11	0	109.75	gggaataataCatgttcaaga	m5C_26040
chr11	65273330	+	C	240	58	0.242	0	0	T	182	M	0.192	0.3	0	0	0	222.55	tgggtgggaCatgtaactgt	m5C_25931
chr11	65273337	+	C	243	114	0.469	0	0	T	129	M	0.407	0.532	0	0	0	928.77	gaacatgaaCttgagactgt	m5C_25994
chr11	65273345	+	C	51	31	0.608	0	0	C	31	M	0.471	0.73	0	6E-07	0	291.93	aactgtgaaCtgggaagat	m5C_26049
chr11	65661664	+	C	51	26	0.51	0	0	C	26	M	0.377	0.641	0	2E-07	0	195.94	catgtggccCagtggtgaga	m5C_26010
chr11	66234545	+	C	34	10	0.294	0	0	T	24	M	0.168	0.462	2E-14	2E-06	3E-14	22.956	caggcgggcCcgaggggcgc	m5C_22747
chr11	66234546	+	C	36	12	0.333	0	0	T	24	M	0.202	0.497	0	5E-06	0	48.515	agcggggcCggcgggcg	m5C_22748
chr11	66234549	+	C	33	16	0.485	0	0	T	17	M	0.325	0.648	0	2E-05	0	104.01	cgggccccCggcggggg	m5C_22758
chr11	70918775	-	C	35	18	0.514	0	0	C	18	M	0.356	0.67	0	3E-05	0	128.05	ctgagagagCgggtcacac	m5C_22811
chr11	75380203	+	C	43	33	0.767	0	0	C	33	M	0.623	0.868	0	2E-05	0	410.88	cactgtgtCgtcagcttgc	m5C_23400
chr11	75380206	+	C	39	28	0.718	0	0	C	28	M	0.562	0.835	0	0.0002	0	314.86	ctgtgtgtCagcttgcgt	m5C_23406
chr11	85195023	+	C	31	20	0.645	0	0	C	20	M	0.469	0.789	0	4E-05	0	187.79	ccgggtcttCaggaagtcgg	m5C_24945
chr11	85195024	+	C	33	21	0.636	0	0	C	21	M	0.466	0.778	0	5E-05	0	195.79	ccgggtcttCaggaagtcgg	m5C_24960
chr11	85195038	+	C	124	86	0.694	0	0	C	86	M	0.608	0.768	0	4E-12	0	1045.1	agtcgggtgtCttgggaatgc	m5C_24923
chr11	85195048	+	C	180	93	0.517	0	0	C	93	M	0.444	0.589	0	0	0	825.99	cttgggaatgCagccaaagc	m5C_24929
chr11	85195051	+	C	182	71	0.392	1	0.005	T	110	M	0.324	0.465	0	0	0	460.19	gggaatgcagCccaaagggg	m5C_24928
chr11	85195052	+	C	177	84	0.475	0	0	T	93	M	0.402	0.548	0	0	0	675.92	gggaatgcagCcaaaaggggt	m5C_24973
chr11	85195053	+	C	189	89	0.471	0	0	T	100	M	0.401	0.542	0	0	0	713.83	gaatgcagctCaaagcggng	m5C_24969
chr11	85195058	+	C	181	104	0.605	9	0.05	C	104	M	0.53	0.675	0	0	0	1102.5	cagcccaagCgggtggaaa	m5C_24936
chr11	85195069	+	C	106	59	0.557	0	0	C	59	M	0.462	0.648	0	2E-11	0	544.8	gggtggaaaCttcatttaag	m5C_24975
chr11	85195072	+	C	71	31	0.437	0	0	T	40	M	0.327	0.552	0	6E-10	0	203.02	tggtaaaactCatttaaggct	m5C_24927
chr11	85195081	+	C	109	36	0.33	0	0	T	73	M	0.249	0.423	0	5E-14	0	179.34	ccatttaaggCtaataaccgg	m5C_24925
chr11	85195088	+	C	138	51	0.37	0	0	T	87	M	0.294	0.453	0	1E-16	0	299.45	aggttaataCcggcacgaga	m5C_24966
chr11	85195089	+	C	152	42	0.276	0	0	T	110	M	0.211	0.352	0	0	0	177.58	ggctaataacCggcacgagac	m5C_24954
chr11	85195092	+	C	160	53	0.333	1	0.006	T	106	M	0.265	0.41	0	0	0	280.64	taataacggCacgagaccga	m5C_24958
chr11	85195094	+	C	180	76	0.422	0	0	T	104	M	0.352	0.495	0	0	0	535.7	aataccggCaCagaccgata	m5C_24967
chr11	85195099	+	C	249	124	0.498	0	0	T	125	M	0.436	0.56	0	0	0	1082.3	cggcacgagaCcgatagcaa	m5C_24934
chr11	85195100	+	C	252	123	0.488	0	0	T	129	M	0.427	0.55	0	0	0	1050.5	ggcacgagaCcgatagcaac	m5C_24956
chr11	85195107	+	C	399	155	0.391	3	0.008	T	241	M	0.345	0.44	0	0	0	1068.3	gaccgatagtCaacaagtaac	m5C_24971
chr11	85195110	+	C	480	188	0.392	0	0	T	292	M	0.349	0.436	0	0	0	1312.3	cgatagcaaCaagaccgga	m5C_24942
chr11	85195116	+	C	629	276	0.439	0	0	T	353	M	0.4	0.478	0	0	0	2210.7	tcaacaagracCgtaagggga	m5C_24983
chr11	85195117	+	C	705	314	0.446	1	0.001	T	390	M	0.41	0.483	0	0	0	2572.9	caacaagtagCtaaggggaaa	m5C_24955
chr11	85195139	+	C	1611	763	0.474	0	0	T	848	M	0.449	0.498	0	0	0	6856.8	ttagaaagaaCtttgaagaga	m5C_24941
chr11	85195155	+	C	537	241	0.449	0	0	T	296	M	0.407	0.491	0	0	0	1962.9	agagagagaCaaagggggt	m5C_24968
chr11	85195163	+	C	641	386	0.602	0	0	C	386	M	0.564	0.639	0	0	0	4352.5	tacaagggcCgtgaaacctg	m5C_24980
chr11	85195170	+	C	479	159	0.332	0	0	T	320	M	0.291	0.375	0	0	0	926.19	ggcggtgaaaCcgtaagagg	m5C_24952
chr11	85195171	+	C	459	126	0.275	0	0	T	333	M	0.236	0.317	0	0	0	593.92	ggcggaaacCgttaagaggr	m5C_24961
chr11	85195195	+	C	57	29	0.509	0	0	C	29	M	0.383	0.634	0	4E-07	0	221.91	tgggtcaggtCcgcgagtc	m5C_24939
chr11	85195196	+	C	73	23	0.315	0	0	T	50	M	0.22	0.429	0	4E-11	0	101.22	gggtcaggtCcgcgagtc	m5C_24962
chr11	85195198	+	C	102	41	0.41	2	0.02	T	59	M	0.319	0.508	0	2E-13	0	261.31	gtcaggccgcCgagtcgcc	m5C_24951
chr11	85195200	+	C	109	32	0.294	0	0	T	77	M	0.216	0.385	0	1E-14	0	138.42	caggtccgcgcCagtcgcccg	m5C_24949
chr11	85195204	+	C	143	44	0.308	0	0	T	99	M	0.238	0.388	0	0	0	209.35	tccgcgcagtcCgcggggagg	m5C_24976
chr11	85195207	+	C	153	32	0.209	0	0	T	121	M	0.152	0.28	0	0	0	97.425	gcgcagtcgcCccggggatt	m5C_24926
chr11	85195209	+	C	165	48	0.291	0	0	T	117	M	0.227	0.364	0	0	0	217.91	gcagtcgcgcCggaaggattca	m5C_24959
chr11	85195221	+	C	96	27	0.281	0	0	T	69	M	0.201	0.378	0	7E-14	0	1		

chr11	93466415	-	C	37	26	0.703	0	0	C	26	M	0.542	0.825	0	0.0001	0	281.93	cgggcatgaaCtaaaacttaa	m5C_24436
chr11	93466421	-	C	39	28	0.718	0	0	C	28	M	0.562	0.835	0	0.0002	0	314.86	tgataacgggCatgaactaaa	m5C_24415
chr11	93466436	-	C	46	35	0.761	0	0	C	35	M	0.621	0.861	0	3E-05	0	434.45	tgtcaactcgCtgatgataa	m5C_24400
chr11	93466439	-	C	46	35	0.761	0	0	C	35	M	0.621	0.861	0	3E-05	0	434.45	aactgttcaaCtgcgtaatga	m5C_24420
chr11	93466447	-	C	47	36	0.766	0	0	C	36	M	0.628	0.864	0	3E-05	0	451.98	atgaatttaaCtgtcaactg	m5C_24409
chr11	93466720	-	C	62	43	0.694	0	0	C	43	M	0.57	0.794	0	2E-07	0	490.48	gccttgcacatCgttggaaacg	m5C_24413
chr11	93466723	-	C	63	44	0.698	0	0	C	44	M	0.576	0.798	0	3E-07	0	507.23	gtagcttcgaCgatgtggaa	m5C_24422
chr11	93466729	-	C	59	40	0.678	0	0	C	40	M	0.551	0.783	0	3E-06	0	440.84	tttcttggagCtgcacatcg	m5C_24419
chr11	93466735	-	C	37	19	0.514	0	0	C	19	M	0.359	0.666	0	3E-05	0	136.4	ggggcttttCtggagcttcg	m5C_24402
chr11	93466736	-	C	37	20	0.541	0	0	C	20	M	0.384	0.69	0	4E-05	0	153.54	tggggcttttCtggagcttcg	m5C_24433
chr11	93466741	-	C	45	20	0.444	0	0	T	25	M	0.309	0.588	0	1E-06	0	123.75	cccgatggggCttttcttga	m5C_24385
chr11	93466749	-	C	38	18	0.474	0	0	T	20	M	0.325	0.627	0	3E-05	0	116.92	aggctatcccCgatgggagctt	m5C_24428
chr11	93466751	-	C	37	18	0.486	0	0	T	19	M	0.334	0.641	0	3E-05	0	120.41	tggagttcatCccgatggggc	m5C_24429
chr11	102100518	+	C	58	39	0.672	0	0	C	39	M	0.544	0.779	0	2E-06	0	424.51	caaatgggaCcttggaaacac	m5C_24618
chr11	102100526	+	C	82	29	0.354	0	0	T	53	M	0.259	0.462	0	8E-12	0	150.14	gaccttggaaCactggaagaa	m5C_24623
chr11	102100548	+	C	86	26	0.302	0	0	T	60	M	0.215	0.406	0	3E-12	0	112.03	atggaaatgaaCatagaaggag	m5C_24619
chr11	108593985	+	C	40	19	0.475	0	0	T	21	M	0.329	0.625	0	1E-06	0	125.15	aagaagaagaCgatgaagaag	m5C_24569
chr11	118622539	-	C	75	27	0.36	0	0	T	48	M	0.261	0.473	0	2E-10	0	140.75	ggaaaggggaCaaggaagaa	m5C_24717
chr11	119181097	-	C	44	20	0.455	0	0	T	24	M	0.317	0.599	0	1E-06	0	126.82	gggctcttcgCagggcagcag	m5C_24707
chr11	119181101	-	C	43	19	0.442	0	0	T	24	M	0.304	0.589	0	1E-06	0	115.65	agatgggcttCtgcaggga	m5C_24702
chr11	120356317	+	C	56	26	0.464	0	0	T	30	M	0.34	0.593	0	2E-07	0	176.9	ggaaagggaCggggaaggga	m5C_24587
chr11	122022988	-	C	33	18	0.545	0	0	C	18	M	0.38	0.702	0	3E-05	0	136.75	tagatccgaCtttgtgatt	m5C_24801
chr11	122930045	-	C	34	17	0.5	0	0	CT	17	M	0.341	0.659	0	2E-05	0	115.83	gattgttcgagCgaggatag	m5C_24792
chr11	122930050	-	C	38	18	0.474	0	0	T	20	M	0.325	0.627	0	3E-05	0	116.92	ccttggaatCtggagcagag	m5C_24813
chr11	122930059	-	C	41	20	0.488	0	0	T	21	M	0.343	0.635	0	1E-06	0	137.02	caacaccttCtttgatgct	m5C_24790
chr11	122930063	-	C	42	20	0.476	0	0	T	22	M	0.334	0.623	0	1E-06	0	133.44	atggcaaacCtttcttgat	m5C_24807
chr11	122930066	-	C	39	20	0.513	0	0	C	20	M	0.362	0.661	0	4E-05	0	144.8	atgatggcaaCaccttcttg	m5C_24818
chr11	122930069	-	C	39	18	0.474	1	0.026	T	20	M	0.325	0.627	0	3E-05	0	116.92	ctaattgggCaacaccttcc	m5C_24802
chr11	122930106	-	C	48	34	0.708	0	0	C	34	M	0.568	0.818	0	2E-05	0	386.38	gattgttaaCatttgatgt	m5C_24808
chr11	122930127	-	C	33	9	0.273	0	0	T	24	M	0.151	0.442	8E-13	1E-06	8E-13	16.442	aggagctcgCtggatgag	m5C_24798
chr12	970269	+	C	43	11	0.256	0	0	T	32	M	0.149	0.402	1E-14	4E-08	1E-14	22.889	gaacagagaCagcgccaggt	m5C_25139
chr12	970284	+	C	78	43	0.551	0	0	C	43	M	0.441	0.657	0	1E-08	0	379.34	gcagttggaCgggaagagca	m5C_25130
chr12	970293	+	C	84	35	0.417	0	0	T	49	M	0.317	0.523	0	6E-11	0	222	acgggaagggaCaagaaaaaaa	m5C_25122
chr12	3563416	+	C	40	11	0.275	0	0	T	29	M	0.161	0.428	4E-15	3E-06	5E-15	25.45	ctttgactcCtgcagggga	m5C_24871
chr12	3563421	+	C	39	16	0.41	0	0	T	23	M	0.271	0.566	0	2E-05	0	86.653	gactccctgaCgggagcctg	m5C_24877
chr12	3563428	+	C	32	20	0.625	0	0	C	20	M	0.453	0.771	0	4E-05	0	181.02	tgacggggagCcttgcagggt	m5C_24866
chr12	6878771	+	C	41	10	0.244	0	0	T	31	M	0.138	0.393	2E-13	2E-08	3E-13	17.447	ctttgaggaCctgaagga	m5C_25211
chr12	6879098	+	C	39	14	0.359	0	0	T	25	M	0.227	0.516	0	9E-06	0	63.677	aggaaggagaCggggctgagg	m5C_25207
chr12	6879124	+	C	106	29	0.274	0	0	T	77	M	0.198	0.365	0	3E-15	0	114.7	gaagaagaaaCtgccgaggat	m5C_25210
chr12	6879127	+	C	114	53	0.465	0	0	T	61	M	0.376	0.556	0	2E-13	0	398.55	gaagaactgcCgagggatgga	m5C_25191
chr12	6879128	+	C	129	35	0.271	0	0	T	94	M	0.202	0.354	0	0	0	141.42	aagaactgcCgaaggatgag	m5C_25200
chr12	6976778	+	C	47	30	0.638	0	0	C	30	M	0.495	0.76	0	1E-05	0	297.21	gggaagatgaaCgggaggagc	m5C_25199
chr12	6976782	+	C	48	31	0.646	0	0	C	31	M	0.504	0.766	0	1E-05	0	312.72	gatgaacgggCggaagcagag	m5C_25193
chr12	6976788	+	C	35	26	0.743	0	0	C	26	M	0.579	0.858	0	0.0001	0	301.24	cgggcggaagCagagcttggg	m5C_25190
chr12	17143740	+	C	37	16	0.432	0	0	T	21	M	0.287	0.591	0	2E-05	0	91.749	gagaaggaggCtgcttagatg	m5C_25069
chr12	17143743	+	C	35	17	0.486	0	0	T	18	M	0.33	0.644	0	2E-05	0	112.18	aaggaggctgCttagatggga	m5C_25067
chr12	19877513	+	C	79	27	0.342	0	0	T	52	M	0.247	0.452	0	2E-10	0	133.22	agggggggaCtgggttgcg	m5C_25149
chr12	19877524	+	C	82	22	0.268	0	0	T	60	M	0.184	0.373	0	4E-13	0	81.118	tgggttgcgCtttcccttgg	m5C_25148
chr12	20704372	+	C	57	37	0.649	0	0	C	37	M	0.519	0.76	0	2E-06	0	384.37	acaggatgaCagattgatag	m5C_26967
chr12	20704391	+	C	278	97	0.349	0	0	T	181	M	0.295	0.407	0	0	0	572.87	agctcttttCgatctctggg	m5C_26953
chr12	20704396	+	C	442	280	0.633	0	0	C	280	M	0.588	0.677	0	0	0	3290.5	tttctgattCtgggggggt	m5C_26963
chr12	20704397	+	C	468	162	0.367	27	0.058	T	279	M	0.324	0.413	0	0	0	1048.7	ttctgattcCtgggggggg	m5C_26945
chr12	20704435	+	C	1043	520	0.499	0	0	T	523	M	0.468	0.529	0	0	0	4870.1	gttggggagCgattgtctg	m5C_26966
chr12	20704499	+	C	155	78	0.503	0	0	C	78	M	0.425	0.581	0	1E-16	0	663.61	acgcgaccccCgagcgggtct	m5C_26950
chr12	21791334	-	C	48	19	0.396	0	0	T	29	M	0.27	0.537	0	1E-06	0	102.68	tgggaactgaCaatgatagtg	m5C_27016
chr12	21791338	-	C	49	28	0.571	0	0	C	28	M	0.433	0.7	0	8E-06	0	242.31	gaaatgggaCtgaacatgat	m5C_27023
chr12	21796993	-	C	59	15	0.254	0	0	T	44	M	0.161	0.378	0	5E-09	0	48.168	ctgcaggagaCcgctcagcaag	m5C_26987
chr12	21797000	-	C	45	24	0.533	0	0	C	24	M	0.391	0.671	0	4E-06	0	187.57	gtggaaactgCaggagctcg	m5C_27007
chr12	21797003	-	C	40	14	0.35	0	0	T	26	M	0.221	0.505	0	2E-07	0	61.976	gtagtgtaaCtgcaggagtc	m5C_27010
chr12	22079792	+	C	42	17	0.405	0	0	T	25	M	0.27	0.555	0	6E-07	0	91.945	ccagtgattcCagacagatg	m5C_25403
chr12	22079797	+	C	41	16	0.39	0	0	T	25	M	0.257	0.543	0	4E-07	0	82.099	gattccagacCagatgtgcat	m5C_25401
chr12	27908142	+	C	74	29	0.392	0	0	T	45	M	0.289	0.506	0	4E-10	0	167.42	aaaagaagaCtgaagcagac	m5C_25533
chr12	27908148	+	C	66	14	0.212	0	0	T	52	M	0.131	0.325	2E-16	3E-11	2E-16	28.66	aagatggaCgagacatgaa	m5C_25521
chr12	31479284	+	C	33	20	0.606	0	0	C	20	M	0.437	0.753	0	4E-05	0	174.73	agcttcgaggCgagggaacg	m5C_25270
chr12	34356839	+	C	32	22	0.688	0	0	C	22	M	0.514	0.82	0	6E-05	0	226.31	tctgggaatgCggggagctgt	m5C_25325
chr12	34356840	+	C	31	23	0.742	0	0	C	23	M	0.568	0.863	0	8E-05	0	261.07	ctgggaatgcCgggggtctga	m5C_25324
chr12	34356846	+	C	32	19	0.594	0	0	C	19	M	0.423	0.745	0	3E-05	0	160.59	atgcgggggtCtgtaggctt	m5C_25315
chr12	42707688	-	C	50	39	0.78	0	0	C	39	M	0.648	0.872	0	2E-06	0	505.11	gtctctgaacCagagaagaa	m5C_25364
chr12	42707689	-	C	52	21	0.404	0	0	C	31	M	0.282	0.539	0	5E-08	0	118.27	agctcttgaaCcagaagaga	m5C_25365
chr12	42707694	-	C	45	11	0.244	0	0	T	34	M	0.142	0.387	2E-14	4E-08	2E-14	21.411	aagaagaactCtgaaccagaa	m5C_25355
chr12	42707697	-	C	39	18	0.462	0	0	T	21	M	0.316	0.614	0	3E-05	0	113.64	aaaaagaagCtcttgacca	m5C_25363
chr12	45581244	-	C	69	18	0.261	0	0	T	51	M	0.172	0.375	0	3E-10	0	61.868	caagttgggtCgagggtgtgtg	m5C_25343
chr12	45581245	-	C	63	28	0.4													

chr12	57037519	-	C	48	32	0.667	0	0	C	32	M	0.525	0.783	0	2E-05	0	336.26	ctgatgagaCgttctgactt	m5C_25682
chr12	57108175	-	C	37	8	0.216	0	0	T	29	M	0.114	0.372	1E-10	7E-07	1E-10	9.1227	taaagcaaaCagagtcggag	m5C_25687
chr12	58112019	+	C	79	52	0.658	0	0	C	52	M	0.548	0.753	0	5E-08	0	570.43	tgtaccagaaCggcagagaga	m5C_25489
chr12	58112022	+	C	75	44	0.587	0	0	C	44	M	0.474	0.691	0	1E-08	0	416.82	tcagaacggCagagagagat	m5C_25490
chr12	58190322	+	C	32	18	0.6	2	0.062	C	18	M	0.423	0.754	0	3E-05	0	152.35	agactttggCggtttgaatg	m5C_25491
chr12	58388801	-	C	32	20	0.625	0	0	C	20	M	0.453	0.771	0	4E-05	0	181.02	gcacttgctCattccccatt	m5C_25496
chr12	58388806	-	C	32	18	0.562	0	0	C	18	M	0.393	0.718	0	3E-05	0	141.57	gagttgcattCtgctcatccc	m5C_25503
chr12	58388810	-	C	34	9	0.265	0	0	T	25	M	0.146	0.431	1E-12	1E-06	1E-12	15.739	ctggagttgCcatctgtcta	m5C_25499
chr12	58388820	-	C	37	10	0.27	0	0	T	27	M	0.154	0.43	7E-14	2E-06	7E-14	20.282	tgcggatgcCtgggagtgc	m5C_25507
chr12	58388821	-	C	37	15	0.405	0	0	T	22	M	0.263	0.565	0	1E-05	0	79.039	ttgcgggatgCctgggagtgtg	m5C_25506
chr12	62997488	+	C	59	30	0.508	0	0	C	30	M	0.384	0.632	0	5E-07	0	230.61	gtagtttggCtgttgctgg	m5C_26090
chr12	76443543	-	C	59	17	0.288	0	0	T	42	M	0.188	0.414	0	1E-08	0	64.044	gggaaagaagCggatgagga	m5C_25779
chr12	90024332	-	C	31	20	0.69	2	0.065	C	20	M	0.508	0.827	0	0.001	0	203.08	tacttggagCtggaggtgaa	m5C_25786
chr12	93750936	-	C	43	32	0.744	0	0	C	32	M	0.598	0.851	0	2E-05	0	382.47	ccctgatggCtaggggctag	m5C_26122
chr12	96429859	+	C	163	40	0.245	0	0	T	123	M	0.186	0.317	0	0	0	148.56	gggtgattcCccgacgggga	m5C_26474
chr12	98850879	+	C	32	19	0.594	0	0	C	19	M	0.423	0.745	0	3E-05	0	160.59	agggagagcgcCggtgcacag	m5C_26421
chr12	98897306	+	C	57	22	0.386	0	0	T	35	M	0.271	0.516	0	7E-08	0	119.08	tggtagtatCcccgcctgtc	m5C_26420
chr12	98897307	+	C	54	19	0.352	0	0	T	35	M	0.238	0.485	0	2E-08	0	90.527	ggtagatcCccgcctgtca	m5C_26424
chr12	98897308	+	C	57	19	0.333	0	0	T	38	M	0.225	0.463	0	2E-08	0	85.476	gttagtaccCgcgtctcac	m5C_26410
chr12	98897309	+	C	58	24	0.414	0	0	T	34	M	0.296	0.542	0	1E-07	0	142.21	tagtatcccCgcgtgcacg	m5C_26427
chr12	98897311	+	C	59	25	0.424	0	0	T	34	M	0.306	0.551	0	2E-07	0	153.06	agatcccgcCctgtcacggt	m5C_26425
chr12	98897312	+	C	51	12	0.235	0	0	T	39	M	0.14	0.368	3E-15	9E-10	4E-15	24.331	gtatcccgcCtgtcacggg	m5C_26429
chr12	98897327	+	C	86	25	0.291	0	0	T	61	M	0.205	0.394	0	2E-12	0	102.66	acgcgggagaCcggggttcaa	m5C_26422
chr12	98897328	+	C	83	64	0.771	0	0	C	64	M	0.67	0.848	0	2E-08	0	857.49	cgcggagagcCggggttcaat	m5C_26426
chr12	98897335	+	C	85	17	0.2	0	0	T	68	M	0.129	0.297	0	2E-14	0	43.788	gaccggggtCaattccccga	m5C_26414
chr12	98897340	+	C	84	32	0.381	0	0	T	52	M	0.284	0.488	0	2E-11	0	182.06	gggttcaattCcccgcgggg	m5C_26417
chr12	98897341	+	C	84	20	0.238	0	0	T	64	M	0.16	0.339	0	2E-13	0	63.898	gggtcaattCccgacgggga	m5C_26416
chr12	104325338	+	C	31	22	0.71	0	0	C	22	M	0.534	0.839	0	6E-05	0	234.99	gtggatgggaCagtagaagag	m5C_26813
chr12	104325352	+	C	70	23	0.329	0	0	T	47	M	0.23	0.445	0	4E-11	0	105.79	agaaagagatCtgggtaaaag	m5C_26803
chr12	104325374	+	C	191	77	0.403	0	0	T	114	M	0.336	0.474	0	0	0	517.67	agaaaggaatCaaggacggat	m5C_26801
chr12	104341102	+	C	34	14	0.412	0	0	T	20	M	0.264	0.578	0	9E-06	0	73.824	gaagaagagcCtgaagaagaa	m5C_26814
chr12	104341114	+	C	45	21	0.467	0	0	T	24	M	0.329	0.609	0	2E-06	0	138.33	gaagaagaacCtgaagagaca	m5C_26805
chr12	104341123	+	C	45	22	0.489	0	0	T	23	M	0.35	0.63	0	2E-06	0	153.81	cctgaagagaCagcagaagac	m5C_26812
chr12	104720177	+	C	97	33	0.34	0	0	T	64	M	0.254	0.439	0	8E-13	0	167.39	ggcttagaaaCctgaggggg	m5C_26806
chr12	106573499	-	C	32	24	0.75	0	0	C	24	M	0.579	0.867	0	9E-05	0	277.89	gactccaatCaggcgcaatg	m5C_26449
chr12	106573504	-	C	34	27	0.794	0	0	C	27	M	0.632	0.897	0	0.0001	0	341.29	tgttgactcCagatcaggcg	m5C_26447
chr12	110867827	-	C	31	23	0.742	0	0	C	23	M	0.568	0.863	0	8E-05	0	261.07	ggggcagaccCaataaacttg	m5C_26648
chr12	112460375	+	C	47	33	0.702	0	0	C	33	M	0.56	0.813	0	2E-05	0	369.75	agatgaggtCgggaagaagg	m5C_26569
chr12	117908958	+	C	33	8	0.242	0	0	T	25	M	0.128	0.41	3E-11	7E-07	3E-11	10.787	tctgtctcCctcatcccc	m5C_26519
chr12	120729574	-	C	73	17	0.233	0	0	T	56	M	0.151	0.342	0	2E-12	0	51.268	ttgacagtctCtaccgagact	m5C_26728
chr12	120729576	-	C	71	17	0.239	0	0	T	54	M	0.155	0.35	0	2E-12	0	52.771	ttttgacagtCtctacggaga	m5C_26716
chr12	120729590	-	C	72	21	0.292	0	0	T	51	M	0.199	0.405	0	2E-11	0	83.739	tcggcattggCaatttttgac	m5C_26726
chr12	120729615	-	C	72	19	0.264	0	0	T	53	M	0.176	0.376	0	7E-12	0	66.856	cccgcctagaCgacttgaat	m5C_26699
chr12	120729621	-	C	42	21	0.5	0	0	CT	21	M	0.355	0.645	0	2E-06	0	149.21	caatacccccCcatgagact	m5C_26705
chr12	123466284	+	C	122	66	0.541	0	0	C	66	M	0.453	0.627	0	1E-13	0	597.51	agtaacaaggCaagagaaggga	m5C_26920
chr12	123466318	+	C	74	25	0.338	0	0	T	49	M	0.24	0.451	0	9E-11	0	120.23	gaggaagaagCtgaagaagaa	m5C_26922
chr12	125406302	-	C	38	16	0.421	0	0	T	22	M	0.279	0.578	0	2E-05	0	89.127	ccggcatctCatttgagttt	m5C_27155
chr12	125406303	-	C	40	29	0.725	0	0	C	29	M	0.572	0.839	0	1E-05	0	331.56	cccgcatctCatttgagtt	m5C_27152
chr12	125406305	-	C	39	24	0.615	0	0	C	24	M	0.459	0.751	0	9E-05	0	220.31	tcctccggcatCctcattgag	m5C_27156
chr12	125406308	-	C	37	24	0.649	0	0	C	24	M	0.488	0.782	0	9E-05	0	234.04	cgatcccccCattcttcattg	m5C_27148
chr12	125406311	-	C	41	19	0.463	0	0	T	22	M	0.321	0.613	0	1E-06	0	121.81	gttcgatcccCggcatctcca	m5C_27171
chr12	125406312	-	C	41	18	0.439	0	0	T	23	M	0.299	0.59	0	8E-07	0	107.6	gggtgatcccCggcatctccc	m5C_27166
chr12	125406313	-	C	39	19	0.487	0	0	T	20	M	0.339	0.638	0	3E-05	0	128.69	gggttcgatCccggcatctc	m5C_27149
chr12	125406318	-	C	41	26	0.634	0	0	C	26	M	0.481	0.764	0	6E-06	0	250.23	gccccgggtCgatccccggc	m5C_27164
chr12	125406324	-	C	36	23	0.639	0	0	C	23	M	0.476	0.775	0	8E-05	0	218.84	tatgagggcccCgggttcgatc	m5C_27129
chr12	125406326	-	C	38	18	0.474	0	0	T	20	M	0.325	0.627	0	3E-05	0	116.92	tgtatgaggCccgggttcga	m5C_27123
chr12	127650600	-	C	31	19	0.613	0	0	C	19	M	0.438	0.763	0	3E-05	0	166.53	ggcgccgcCctctgcccggt	m5C_28021
chr12	127650601	-	C	32	20	0.625	0	0	C	20	M	0.453	0.771	0	4E-05	0	181.02	agggcgccgcCctctgccccg	m5C_28056
chr12	127650604	-	C	47	26	0.553	0	0	C	26	M	0.412	0.686	0	6E-06	0	214.48	gaaaaggcgCgcgcctctcgc	m5C_28059
chr12	127650605	-	C	50	31	0.62	0	0	C	31	M	0.482	0.741	0	6E-07	0	298.53	ggaaggcggCgcgcctctcgc	m5C_28062
chr12	127650608	-	C	50	7	0.259	23	0.46	G	23	M	0.132	0.447	2E-10	3E-05	2E-10	8.9677	gcccgaaggCggcgcccttc	m5C_28028
chr12	127650616	-	C	113	46	0.407	0	0	T	67	M	0.321	0.499	0	3E-14	0	295.32	ggggcgccgcCggaaggcgg	m5C_28011
chr12	127650617	-	C	109	40	0.367	0	0	T	69	M	0.282	0.461	0	2E-13	0	225.96	cggggcgccgcCggaaggcgg	m5C_28040
chr12	127650620	-	C	120	43	0.358	0	0	T	77	M	0.278	0.447	0	2E-16	0	239.22	aaacggggcgCggcggaag	m5C_28073
chr12	127650627	-	C	89	42	0.472	0	0	T	47	M	0.372	0.575	0	3E-10	0	312.08	tcctgggaaaCggggcgccgc	m5C_28006
chr13	42030115	-	C	60	18	0.383	13	0.217	T	29	M	0.258	0.526	0	8E-07	0	92.846	tgtctaggtCtagagtttcg	m5C_26912
chr13	42030121	-	C	58	38	0.655	0	0	C	38	M	0.527	0.764	0	2E-06	0	400.27	ccctgggggCtaggtcttag	m5C_26916
chr13	45912861	-	C	35	19	0.543	0	0	C	19	M	0.382	0.695	0	3E-05	0	145.12	ctctattggaCtaacgttagg	m5C_27799
chr13	46549602	-	C	55	27	0.491	0	0	T	28	M	0.364	0.619	0	2E-07	0	196.43	ggagagagagCggaacggga	m5C_27479
chr13	46948618	-	C	695	269	0.388	1	0.001	T	425	M	0.352	0.424	0	0	0	1894.2	attttggagCagggaacatgg	m5C_27477
chr13	46948643	-	C	712	205	0.288	0	0	T	507	M	0.256	0.322	0	0	0	1049.1	tatccggagaCaatatataa	m5C_27476
chr13	46948657	-	C	176	61	0.347	0	0	T	115	M	0.28	0.419	0	0	0	341.89	tctgatattCctctatccga	m5C_27480
chr13	58458610	-																	

chr14	20811292	-	C	71	24	0.338	0	0	T	47	M	0.239	0.454	0	6E-11	0	114.65	agttcaatggCtgaggtgagg	m5C_28319
chr14	20811313	-	C	53	14	0.264	0	0	T	39	M	0.164	0.396	0	3E-09	0	46.024	agactcacggCagcgaaagg	m5C_28312
chr14	20811324	-	C	61	17	0.279	0	0	T	44	M	0.182	0.402	0	2E-10	0	61.841	gagcttggaacCagactcacgg	m5C_28276
chr14	20811331	-	C	41	19	0.463	0	0	T	22	M	0.321	0.613	0	1E-06	0	121.81	ttgcccggagCttggaaacaga	m5C_28321
chr14	20811337	-	C	38	10	0.263	0	0	T	28	M	0.15	0.42	9E-14	2E-06	1E-13	19.504	gcctccttgCggagcttgg	m5C_28318
chr14	20811352	-	C	56	13	0.232	0	0	T	43	M	0.141	0.358	4E-16	2E-09	5E-16	28.14	aggggcccggCggaatgctcc	m5C_28271
chr14	20811356	-	C	57	17	0.298	0	0	T	40	M	0.195	0.427	0	1E-08	0	66.41	ggggagggggCcgcggaatgc	m5C_28293
chr14	20811377	-	C	32	23	0.719	0	0	C	23	M	0.546	0.844	0	8E-05	0	251.28	atgcctgggaCcccgcccttc	m5C_28289
chr14	20811393	-	C	222	170	0.766	0	0	C	170	M	0.706	0.817	0	0	0	2399.8	tcagactgggCaggagatgcc	m5C_28258
chr14	20811398	-	C	208	66	0.317	0	0	T	142	M	0.258	0.383	0	0	0	340.37	cgaggtcagaCtgggcaggag	m5C_28270
chr14	20811408	-	C	116	37	0.319	0	0	T	79	M	0.241	0.408	0	1E-15	0	178.43	gggctccgcCgaggtcagac	m5C_28279
chr14	20811410	-	C	80	33	0.412	0	0	T	47	M	0.311	0.522	0	3E-11	0	205.3	cggggctccgCgcgaggtcag	m5C_28299
chr14	20811413	-	C	76	37	0.487	0	0	T	39	M	0.378	0.597	0	3E-09	0	279.6	gaacgggggctCcgcgcgagg	m5C_28291
chr14	20811415	-	C	57	41	0.719	0	0	C	41	M	0.592	0.819	0	3E-06	0	485.19	gagaacggggCtccgcgcgag	m5C_28303
chr14	20811428	-	C	31	21	0.677	0	0	C	21	M	0.501	0.814	0	5E-05	0	210.59	aggtgagttCacagagaacgg	m5C_28268
chr14	20811429	-	C	32	10	0.312	0	0	T	22	M	0.18	0.486	1E-14	2E-06	1E-14	25.084	gaggtgagttCcagagaacg	m5C_28311
chr14	20811471	-	C	43	9	0.209	0	0	T	34	M	0.114	0.352	1E-11	1E-08	2E-11	11.152	gggccaaggCggcctaaca	m5C_28278
chr14	20811477	-	C	48	18	0.375	0	0	T	30	M	0.252	0.516	0	8E-07	0	90.774	agactagggCagagggcgacc	m5C_28287
chr14	20811484	-	C	57	27	0.474	0	0	T	30	M	0.35	0.601	0	2E-07	0	188.93	aggtctggaCtagggccaga	m5C_28313
chr14	20811527	-	C	66	16	0.242	0	0	T	50	M	0.155	0.358	0	1E-10	0	49.629	gagctgagggCgctctgtcac	m5C_28310
chr14	20811534	-	C	170	94	0.553	0	0	C	94	M	0.478	0.626	0	1E-16	0	898.36	gggcccagagCtgagggctgc	m5C_28262
chr14	20811538	-	C	208	60	0.288	0	0	T	148	M	0.231	0.353	0	0	0	277.4	aggggggccaCagctgagtg	m5C_28322
chr14	20811540	-	C	217	75	0.346	0	0	T	142	M	0.286	0.411	0	0	0	428.29	tcagtgggggCacgagctgag	m5C_28317
chr14	20811541	-	C	238	126	0.529	0	0	C	126	M	0.466	0.592	0	0	0	1174.4	atcagggggCcacgagctga	m5C_28267
chr14	20811549	-	C	363	190	0.523	0	0	C	190	M	0.472	0.574	0	0	0	1793.8	ggaaagtcatCaggggggcca	m5C_28256
chr14	20811552	-	C	377	95	0.252	0	0	T	282	M	0.211	0.298	0	0	0	400.55	gaggggaagtCatcagtgggg	m5C_28301
chr14	20811554	-	C	408	214	0.525	0	0	C	214	M	0.476	0.573	0	0	0	2037.5	cgggggaagCtcatcagggg	m5C_28273
chr14	20811564	-	C	386	147	0.381	0	0	T	239	M	0.334	0.43	0	0	0	981.33	ttccataggCggaggggaagc	m5C_28255
chr14	21679971	-	C	31	16	0.516	0	0	C	16	M	0.348	0.68	0	2E-05	0	111.49	agcaacaagCaggaaatgg	m5C_28297
chr14	24606632	+	C	38	12	0.316	0	0	T	26	M	0.191	0.475	0	5E-06	0	45.803	gcccgaagaaCagcagggggc	m5C_27666
chr14	31602811	-	C	45	11	0.244	0	0	T	34	M	0.142	0.387	2E-14	4E-08	2E-14	21.411	gagaattaaaCagatgggaa	m5C_27860
chr14	31602826	-	C	48	19	0.396	0	0	T	29	M	0.27	0.537	0	1E-06	0	102.68	aggggggagaCatgtgagaat	m5C_27858
chr14	39649914	+	C	39	12	0.308	0	0	T	27	M	0.186	0.464	0	5E-06	0	44.558	atagaggaagCaggagaagaa	m5C_28091
chr14	39649991	+	C	40	11	0.275	0	0	T	29	M	0.161	0.428	4E-15	3E-06	5E-15	25.45	agaacaaaaCaggaaatgga	m5C_28100
chr14	50320335	-	C	55	40	0.727	0	0	C	40	M	0.598	0.827	0	3E-06	0	478.14	gacctgtctCttttgatttc	m5C_28453
chr14	50320337	-	C	54	38	0.704	0	0	C	38	M	0.572	0.809	0	2E-06	0	434.51	gagacctgtCctttttgatt	m5C_28529
chr14	50320342	-	C	62	47	0.77	1	0.016	C	47	M	0.651	0.858	0	4E-07	0	611.81	atagtgagacCctgtctcttt	m5C_28477
chr14	50320343	-	C	60	43	0.717	0	0	C	43	M	0.592	0.815	0	2E-07	0	509.4	catagtgaCctgtctcttt	m5C_28554
chr14	50320353	-	C	65	47	0.723	0	0	C	47	M	0.604	0.817	0	4E-07	0	567.94	gcctggggcaCatagtggagac	m5C_28538
chr14	50320356	-	C	65	47	0.723	0	0	C	47	M	0.604	0.817	0	4E-07	0	567.94	ccagctgggCaacatagga	m5C_28486
chr14	50320361	-	C	67	51	0.761	0	0	C	51	M	0.647	0.847	0	8E-07	0	659.67	gcactccagCctgggcaacat	m5C_28488
chr14	50320362	-	C	69	51	0.739	0	0	C	51	M	0.625	0.828	0	8E-07	0	637.39	tgactctcagCctgggcaaca	m5C_28437
chr14	50320365	-	C	67	49	0.731	0	0	C	49	M	0.615	0.823	0	6E-07	0	602.52	cactgtcactCagctgggca	m5C_28535
chr14	50320366	-	C	66	48	0.75	2	0.03	C	48	M	0.632	0.84	0	5E-07	0	606.56	ccactgtactCagctgggca	m5C_28540
chr14	50320368	-	C	62	44	0.71	0	0	C	44	M	0.587	0.808	0	3E-07	0	516.67	agccactgcaCtccagcttgg	m5C_28551
chr14	50320370	-	C	64	45	0.703	0	0	C	45	M	0.582	0.801	0	3E-07	0	524.07	atagccactgtCactccagctt	m5C_28548
chr14	50320373	-	C	73	54	0.74	0	0	C	54	M	0.629	0.827	0	7E-08	0	679.22	tgaatagccaCtgcactccag	m5C_28568
chr14	50320375	-	C	70	52	0.743	0	0	C	52	M	0.63	0.831	0	5E-08	0	654.93	tgtgaatagCactgtcactcc	m5C_28470
chr14	50320376	-	C	71	52	0.732	0	0	C	52	M	0.619	0.821	0	5E-08	0	644.24	ctgtgaatagCactgtcactc	m5C_28559
chr14	50320389	-	C	72	54	0.75	0	0	C	54	M	0.639	0.836	0	7E-08	0	690.19	aggggattgCgctgtggaat	m5C_28474
chr14	50329296	-	C	36	16	0.457	1	0.028	T	19	M	0.305	0.618	0	2E-05	0	97.49	gcactccagCtgggcaaat	m5C_28484
chr14	50329297	-	C	38	20	0.526	0	0	C	20	M	0.373	0.675	0	4E-05	0	149.03	tgactctcagCctgggcaaca	m5C_28520
chr14	50329300	-	C	38	18	0.474	0	0	T	20	M	0.325	0.627	0	3E-05	0	116.92	cactgtcactCagcttgagca	m5C_28514
chr14	50329301	-	C	43	21	0.488	0	0	T	22	M	0.346	0.632	0	2E-06	0	145.39	ccactgtactCagcttgagc	m5C_28509
chr14	50329305	-	C	37	19	0.514	0	0	C	19	M	0.359	0.666	0	3E-05	0	136.4	atagccactgtCactccagctt	m5C_28490
chr14	50329308	-	C	38	17	0.447	0	0	T	21	M	0.301	0.603	0	2E-05	0	102.5	tgaatagccaCtgcactccag	m5C_28476
chr14	50329310	-	C	42	25	0.595	0	0	C	25	M	0.445	0.73	0	4E-06	0	222.47	tgtgaatagCactgtcactcc	m5C_28531
chr14	50329311	-	C	42	20	0.476	0	0	T	22	M	0.334	0.623	0	1E-06	0	133.44	ctgtgaatagCactgtcactc	m5C_28550
chr14	50329321	-	C	42	25	0.595	0	0	C	25	M	0.445	0.73	0	4E-06	0	222.47	gggattcgcCtgtgaatagc	m5C_28481
chr14	50329322	-	C	45	28	0.622	0	0	C	28	M	0.476	0.749	0	8E-06	0	266.73	tgggattcgcCtgtgaatag	m5C_28442
chr14	50329324	-	C	34	26	0.765	0	0	C	26	M	0.6	0.876	0	0.0001	0	312.02	aggggattcgCgctgtggaat	m5C_28541
chr14	50329326	-	C	32	22	0.688	0	0	C	22	M	0.514	0.82	0	6E-05	0	226.31	gtaggggatCgctgtgga	m5C_28503
chr14	50329407	-	C	34	14	0.412	0	0	T	20	M	0.264	0.578	0	9E-06	0	73.824	cggggaccacCaggttgctt	m5C_28508
chr14	50329410	-	C	32	13	0.419	1	0.031	T	18	M	0.264	0.592	0	7E-06	0	68.68	gagcgggggaCcaccaagggtg	m5C_28468
chr14	50329423	-	C	31	21	0.677	0	0	C	21	M	0.501	0.814	0	5E-05	0	210.59	gggagcttccCgggaggggg	m5C_28560
chr14	50329427	-	C	34	13	0.382	0	0	T	21	M	0.239	0.555	0	7E-06	0	62.14	atatgtgacCtcccgggagc	m5C_28466
chr14	50329428	-	C	33	12	0.364	0	0	T	21	M	0.222	0.534	0	5E-06	0	53.249	aatatggggaCtctccgggag	m5C_28565
chr14	50329439	-	C	51	18	0.353	0	0	T	33	M	0.236	0.49	0	2E-08	0	85.084	agttgggatCaatatggga	m5C_28566
chr14	50329442	-	C	51	18	0.353	0	0	T	33	M	0.236	0.49	0	2E-08	0	85.084	ctaagttcggCatcaatatgg	m5C_28534
chr14	50329445	-	C	65	30	0.462	0	0	T	35	M	0.346	0.581	0	2E-08	0	207.54	gcactaaagtCggcatcaata	m5C_28447
chr14	50329452	-	C	62	28	0.452	0	0	T	34	M	0.334	0.575	0	1E-08	0	187.15	ggggccgcaCtaagttcggc	m5C_28530
chr14	50329454	-	C	63	34	0.54	0	0	C	34	M	0.418	0.657	0	4E-08	0	284.17	cgggtgtccgCactaaattcg	m5C_28479
chr14	50329456	-	C	54	27	0.5													

chr14	73576100	+	C	107	28	0.262	0	0	T	79	M	0.188	0.352	0	2E-15	0	105.11	gaatgggaagCagatgaacga	m5C_28891
chr14	73576108	+	C	106	57	0.538	0	0	C	57	M	0.443	0.63	0	1E-11	0	505.21	agcagatgaCgagataggaa	m5C_28876
chr14	96851069	+	C	326	153	0.469	0	0	T	173	M	0.416	0.524	0	0	0	1272.4	attttggagCaggagagatag	m5C_28955
chr14	102549471	-	C	61	36	0.59	0	0	C	36	M	0.465	0.705	0	6E-08	0	334.8	ctggaaacttCagagagatga	m5C_29625
chr14	102549472	-	C	54	16	0.296	0	0	T	38	M	0.191	0.428	0	7E-09	0	61.239	cctggaaacttCagagagatga	m5C_29636
chr14	102549475	-	C	49	21	0.429	0	0	T	28	M	0.3	0.567	0	2E-06	0	126.1	agccctggaaCttccagagga	m5C_29631
chr14	102549482	-	C	35	7	0.2	0	0	T	28	M	0.1	0.359	2E-09	3E-07	2E-09	6.1388	ccaaagaaggCctggaaactt	m5C_29629
chr14	102551211	-	C	36	11	0.306	0	0	T	25	M	0.18	0.469	1E-15	3E-06	1E-15	29.708	gatgtgggtCtgaatgagaa	m5C_29634
chr14	102551279	-	C	223	53	0.238	0	0	T	170	M	0.187	0.298	0	0	0	197.73	aaaaagaagaCaaagaagaag	m5C_29619
chr14	102551306	-	C	140	32	0.229	0	0	T	108	M	0.167	0.305	0	0	0	106.76	aagaagtaagCagatgagag	m5C_29622
chr14	102551323	-	C	34	18	0.529	0	0	C	18	M	0.367	0.685	0	3E-05	0	132.25	ggagaaggaaCgagataaaga	m5C_29632
chr14	102551697	-	C	241	65	0.27	0	0	T	176	M	0.218	0.329	0	0	0	282.9	cttggaggaaCgaagaataaa	m5C_29613
chr14	102551714	-	C	85	24	0.282	0	0	T	61	M	0.198	0.386	0	1E-12	0	94.89	gaagaacaaaCtgagtacttg	m5C_29614
chr14	102551718	-	C	49	18	0.367	0	0	T	31	M	0.247	0.507	0	8E-07	0	88.794	gaaagaagacCaaactgagga	m5C_29615
chr14	102551719	-	C	50	14	0.28	0	0	T	36	M	0.175	0.417	0	2E-07	0	48.927	tgaagaagaCcaactgagt	m5C_29627
chr14	105179578	+	C	31	10	0.323	0	0	T	21	M	0.186	0.499	7E-15	2E-06	8E-15	26.273	gcggcgaaggCagagaggagg	m5C_29083
chr15	41988398	+	C	31	12	0.387	0	0	T	19	M	0.237	0.562	0	5E-06	0	56.959	ggggaaggccCagaaggggac	m5C_29254
chr15	45010017	+	C	36	10	0.278	0	0	T	26	M	0.158	0.44	5E-14	2E-06	5E-14	21.112	tctagagggCtggcaactta	m5C_29328
chr15	45010021	+	C	33	19	0.576	0	0	C	19	M	0.408	0.728	0	3E-05	0	155.07	ggagaggaaCcaacttagagg	m5C_29315
chr15	45010024	+	C	31	17	0.548	0	0	C	17	M	0.378	0.708	0	2E-05	0	128.42	gggctggcaaCttaagagggg	m5C_29310
chr15	53140881	-	C	52	13	0.25	0	0	T	39	M	0.152	0.382	1E-16	2E-09	1E-16	31.595	ggggggggCggatattctgc	m5C_29647
chr15	55652580	-	C	38	9	0.237	0	0	T	29	M	0.13	0.392	4E-12	1E-06	4E-12	13.374	aaacaaggaaCagatggaaaa	m5C_29407
chr15	64008585	-	C	48	31	0.646	0	0	C	31	M	0.504	0.766	0	1E-05	0	312.72	aatggaaagaCaggctgagag	m5C_29782
chr15	65588459	+	C	186	110	0.591	0	0	C	110	M	0.52	0.66	0	0	0	1143.1	agaggaacaaCctgagcttt	m5C_29761
chr15	65588487	+	C	173	103	0.595	0	0	C	103	M	0.521	0.666	0	0	0	1073.1	tttttgaggCttgtttttgg	m5C_29776
chr15	65588492	+	C	165	70	0.424	0	0	T	95	M	0.351	0.501	0	0	0	491.96	tgaggccttgCttggcaagg	m5C_29751
chr15	66794400	-	C	36	15	0.417	0	0	T	21	M	0.271	0.578	0	1E-05	0	81.421	cttaattggCcggttttttg	m5C_29573
chr15	66794410	-	C	33	13	0.394	0	0	T	20	M	0.247	0.563	0	7E-06	0	64.175	tgagattccaCttaattgttc	m5C_29575
chr15	66795588	-	C	117	91	0.778	0	0	C	91	M	0.694	0.844	0	2E-10	0	1263.6	ctcggatgttCtgaatgttt	m5C_29563
chr15	66795598	-	C	118	86	0.729	0	0	C	86	M	0.642	0.801	0	8E-11	0	1104.8	acatgattttCtgggatgttc	m5C_29576
chr15	69072774	-	C	212	55	0.261	1	0.005	T	156	M	0.206	0.324	0	0	0	226.69	aggtagatgaCgaggaagatg	m5C_29711
chr15	69072792	-	C	196	74	0.378	0	0	T	122	M	0.313	0.447	0	0	0	462.72	aaggtataaCgatgagaagg	m5C_29701
chr15	69076763	-	C	33	9	0.273	0	0	T	24	M	0.151	0.442	8E-13	1E-06	8E-13	16.442	cggaggggCtggatgata	m5C_29712
chr15	70961196	-	C	37	18	0.486	0	0	T	19	M	0.334	0.641	0	3E-05	0	120.41	gaagaagaagCacagatagg	m5C_30387
chr15	70961219	-	C	44	19	0.432	0	0	T	25	M	0.297	0.578	0	1E-06	0	112.79	tgaaatggagCgagaagaaga	m5C_30388
chr15	72491725	-	C	87	24	0.276	0	0	T	63	M	0.193	0.378	0	1E-12	0	92.612	ccccctggagCagatggcaag	m5C_30754
chr15	72491726	-	C	165	90	0.545	0	0	C	90	M	0.469	0.62	0	0	0	844.75	gccctggagCagatggcaa	m5C_30774
chr15	72491732	-	C	169	44	0.26	0	0	T	125	M	0.2	0.331	0	0	0	176.04	ctggaggcccCtggagccaga	m5C_30789
chr15	72491733	-	C	167	37	0.222	0	0	T	130	M	0.165	0.29	0	0	0	122.27	actggaggccCctggagccag	m5C_30769
chr15	72491747	-	C	166	35	0.211	0	0	T	131	M	0.156	0.279	0	0	0	108.98	aggaagaatgCtgaactggag	m5C_30776
chr15	73212641	-	C	45	28	0.622	0	0	C	28	M	0.476	0.749	0	8E-06	0	266.73	tcagtgcttCaaattgtaat	m5C_30771
chr15	73212665	-	C	236	176	0.746	0	0	C	176	M	0.687	0.797	0	0	0	2416.8	ccctcgggtCtaagggttag	m5C_30786
chr15	73212673	-	C	102	70	0.686	0	0	C	70	M	0.591	0.768	0	1E-10	0	827.2	cctcgtctcCtcgggicta	m5C_30794
chr15	73212674	-	C	82	54	0.659	0	0	C	54	M	0.551	0.752	0	4E-09	0	594.95	ccctcgtctCctcgggict	m5C_30783
chr15	73212675	-	C	74	26	0.351	0	0	T	48	M	0.252	0.465	0	1E-10	0	131.24	tcctcgtctCctcgggict	m5C_30762
chr15	74682179	-	C	75	36	0.48	0	0	T	39	M	0.371	0.591	0	2E-09	0	266.9	gccctggagaCggggggggcc	m5C_29675
chr15	74682186	-	C	33	8	0.242	0	0	T	25	M	0.128	0.41	3E-11	7E-07	3E-11	10.787	ccatggggccCtgggagcgg	m5C_29680
chr15	83424779	+	C	51	32	0.627	0	0	C	32	M	0.49	0.747	0	7E-07	0	313.76	tagacaaggCttgtttgcaa	m5C_31768
chr15	90226451	-	C	35	21	0.6	0	0	C	21	M	0.436	0.744	0	5E-05	0	183	agggccaagaaCggagaaggga	m5C_30122
chr15	90226458	-	C	35	21	0.6	0	0	C	21	M	0.436	0.744	0	5E-05	0	183	agagatgaggCcaagaacgga	m5C_30113
chr15	91187006	+	C	74	30	0.405	0	0	T	44	M	0.301	0.519	0	5E-10	0	180.54	aggaagagaaCctgaagagag	m5C_30099
chr15	91187008	+	C	70	41	0.586	0	0	C	41	M	0.469	0.694	0	2E-07	0	384.42	gaggaagaaccCtgaaggagag	m5C_30094
chr15	96289141	+	C	43	18	0.419	0	0	T	25	M	0.284	0.567	0	8E-07	0	102.18	attttggagCagagagatgg	m5C_29859
chr15	99610024	+	C	34	7	0.206	0	0	T	27	M	0.103	0.368	1E-09	3E-07	2E-09	6.4054	tggagaagagCggcctggagg	m5C_29985
chr16	686735	-	C	35	24	0.686	0	0	C	24	M	0.52	0.814	0	9E-05	0	249.7	gggggggccaCttagttttt	m5C_30211
chr16	686737	-	C	37	15	0.405	0	0	T	22	M	0.263	0.565	0	1E-05	0	79.039	ccgggggggCacttagtttt	m5C_30205
chr16	686739	-	C	44	17	0.386	0	0	T	27	M	0.257	0.534	0	6E-07	0	87.451	tcgggggggCgcaacttagt	m5C_30210
chr16	686742	-	C	40	15	0.375	0	0	T	25	M	0.242	0.53	0	3E-07	0	72.668	gattccggggCggggcaacta	m5C_30176
chr16	686746	-	C	45	16	0.356	0	0	T	29	M	0.232	0.502	0	4E-07	0	74.3	gttcgattccCgggggggcca	m5C_30206
chr16	686747	-	C	43	32	0.744	0	0	C	32	M	0.598	0.851	0	2E-05	0	382.47	gggtcattccCggggggggc	m5C_30201
chr16	686748	-	C	42	21	0.5	0	0	CT	21	M	0.355	0.645	0	2E-06	0	149.21	gggttcgattCccgggggggg	m5C_30188
chr16	686753	-	C	44	25	0.568	0	0	C	25	M	0.422	0.703	0	4E-06	0	211.12	gaccgggggtCgattccgggg	m5C_30204
chr16	686761	-	C	47	25	0.532	0	0	C	25	M	0.392	0.667	0	4E-06	0	196.16	atttctgcaCccgggttcga	m5C_30199
chr16	686764	-	C	45	26	0.578	0	0	C	26	M	0.433	0.71	0	6E-06	0	225.16	ccattcttgCgaccggggt	m5C_30184
chr16	686768	-	C	42	19	0.452	0	0	T	23	M	0.312	0.601	0	1E-06	0	118.65	gattccattCttgggacccg	m5C_30187
chr16	686772	-	C	38	17	0.447	0	0	T	21	M	0.301	0.603	0	2E-05	0	102.5	gcaagattccCattttggga	m5C_30195
chr16	686773	-	C	34	7	0.206	0	0	T	27	M	0.103	0.368	1E-09	3E-07	2E-09	6.4054	tgcaagattCcaattcttgc	m5C_30182
chr16	686774	-	C	34	13	0.382	0	0	T	21	M	0.239	0.55	0	7E-06	0	62.14	atgcaagattCcaattcttgc	m5C_30186
chr16	686781	-	C	33	7	0.212	0	0	T	26	M	0.107	0.378	1E-09	3E-07	1E-09	6.6917	tggatcatgCaaagattccca	m5C_30197
chr16	686785	-	C	38	9	0.237	0	0	T	29	M	0.13	0.392	4E-12	1E-06	4E-12	13.374	gtaggggtatCatgcaagatt	m5C_30191
chr16	686800	-	C	33	7	0.212	0	0	T	26	M	0.107	0.378	1E-09	3E-07	1E-09	6.6917	gacagcgccgCtggggtagg	m5C_30173
chr16	11990523	-	C	39	14	0.359	0	0	T	25	M	0.227	0.516	0	9E-06	0	63.677	ggaaagggcCcatgaatgat	m5C_30230
chr16	11990524	-	C	41	17	0.415	0	0	T	24	M								

chr16	33963347	+	C	58	35	0.603	0	0	C	35	M	0.475	0.719	0	1E-06	0	332.45	gcctggatcCgcagctagga	m5C_31353
chr16	33963349	+	C	64	40	0.625	0	0	C	40	M	0.503	0.733	0	1E-07	0	402	ctggataccgCagctaggaat	m5C_31313
chr16	33963352	+	C	77	53	0.688	0	0	C	53	M	0.578	0.781	0	6E-08	0	612.68	gataccgcagCtaggaataat	m5C_31314
chr16	33963373	+	C	113	88	0.779	0	0	C	88	M	0.694	0.845	0	1E-10	0	1221	ggaataggaCgcggcttat	m5C_31300
chr16	33963423	+	C	48	38	0.792	0	0	C	38	M	0.657	0.883	0	4E-05	0	499.63	ttaagaggaCagctgggggc	m5C_31325
chr16	33963426	+	C	46	13	0.283	0	0	T	33	M	0.173	0.425	0	1E-07	0	45.043	agagggacagCtggggcatt	m5C_31238
chr16	33963535	+	C	187	65	0.348	0	0	T	122	M	0.283	0.418	0	0	0	367.94	gaatgaagCtggaggttcga	m5C_31273
chr16	33963543	+	C	178	135	0.758	0	0	C	135	M	0.691	0.815	0	4E-15	0	1864.4	grcggaggtCgaagacgac	m5C_31333
chr16	33963549	+	C	167	130	0.783	1	0.006	C	130	M	0.714	0.839	0	3E-14	0	1857.5	gggtcgaagaCgatcatgac	m5C_31387
chr16	33963666	+	C	67	45	0.672	0	0	C	45	M	0.553	0.772	0	3E-07	0	497.32	tttttaggtCcgggggaggt	m5C_31311
chr16	33963667	+	C	76	50	0.658	0	0	C	50	M	0.546	0.755	0	4E-08	0	545.96	tttttaggtCcgggggaggt	m5C_31229
chr16	33963684	+	C	77	58	0.753	0	0	C	58	M	0.646	0.836	0	1E-07	0	749.9	agtagggtCaaagctgaat	m5C_31259
chr16	33963689	+	C	53	34	0.642	0	0	C	34	M	0.507	0.757	0	1E-06	0	344.7	gggtgcaagCtgaacttaa	m5C_31430
chr16	33963734	+	C	62	43	0.694	0	0	C	43	M	0.57	0.794	0	2E-07	0	490.48	aggaaggagCctgcggctta	m5C_31446
chr16	33963735	+	C	59	41	0.695	0	0	C	41	M	0.569	0.797	0	3E-06	0	466.2	ggagggagCtgcgggttaa	m5C_31377
chr16	33963738	+	C	58	40	0.69	0	0	C	40	M	0.562	0.794	0	3E-06	0	449.57	gggagctgcCggcttaatt	m5C_31356
chr16	33963741	+	C	56	43	0.768	0	0	C	43	M	0.642	0.859	0	4E-06	0	552.39	gagctcggCttaatttgac	m5C_31293
chr16	33964508	+	C	97	26	0.268	0	0	T	71	M	0.19	0.364	0	5E-14	0	98.787	gccctgagCcggaagaactc	m5C_31337
chr16	33964509	+	C	108	44	0.407	0	0	T	64	M	0.319	0.502	0	6E-13	0	281.13	ccctgagagCcggaagactcg	m5C_31324
chr16	33964516	+	C	137	32	0.234	0	0	T	105	M	0.171	0.311	0	0	0	109.18	agccggagaaCtggggaggga	m5C_31253
chr16	33964518	+	C	137	78	0.569	0	0	C	78	M	0.486	0.649	0	6E-14	0	757.61	ccggagaactCgggaaggaga	m5C_31343
chr16	33964962	+	C	35	27	0.771	0	0	C	27	M	0.61	0.879	0	0.0001	0	329.3	cgcgttcggCgcggaggttt	m5C_31431
chr16	33965201	+	C	40	23	0.575	0	0	C	23	M	0.422	0.715	0	3E-06	0	194.1	gtgcaccgtCtggggggggc	m5C_31455
chr16	33965210	+	C	119	27	0.227	0	0	T	92	M	0.161	0.31	0	0	0	86.873	gctggggggCgggaatcccc	m5C_31264
chr16	33965217	+	C	157	61	0.389	0	0	T	96	M	0.316	0.467	0	0	0	385.3	ggcggggaatCcccgggcgc	m5C_31367
chr16	33965219	+	C	153	51	0.333	0	0	T	102	M	0.264	0.411	0	0	0	268.8	gcgggaatccCcgggcgcccg	m5C_31280
chr16	33965220	+	C	149	42	0.282	0	0	T	107	M	0.216	0.359	0	0	0	181.29	cgggaatcccCgggcggcgt	m5C_31369
chr16	33965224	+	C	141	76	0.539	0	0	C	76	M	0.457	0.619	0	2E-15	0	694.31	aatccggggCgcccggggg	m5C_31278
chr16	33965226	+	C	140	35	0.25	0	0	T	105	M	0.186	0.328	0	0	0	129.92	tcctccgggCccggggggg	m5C_31432
chr16	33965227	+	C	131	58	0.443	0	0	T	73	M	0.361	0.528	0	7E-16	0	418.21	ccccgggcCcgggggggc	m5C_31331
chr16	47539114	+	C	34	15	0.441	0	0	T	19	M	0.289	0.605	0	1E-05	0	86.65	gggaagaagCcgcgcttgct	m5C_30556
chr16	47539115	+	C	34	16	0.471	0	0	T	18	M	0.315	0.633	0	2E-05	0	100.64	gggaagaagCcgcgctgtcg	m5C_30546
chr16	47539116	+	C	36	26	0.722	0	0	C	26	M	0.56	0.842	0	0.0001	0	291.24	gtaagaagccCgggtctggtg	m5C_30555
chr16	47539119	+	C	34	15	0.441	0	0	T	19	M	0.289	0.605	0	1E-05	0	86.65	agaaagcccgCtgcgttgct	m5C_30561
chr16	47539123	+	C	32	15	0.469	0	0	T	17	M	0.309	0.636	0	1E-05	0	92.607	gccccgttcCtggcggtgg	m5C_30554
chr16	47539156	+	C	37	18	0.486	0	0	T	19	M	0.334	0.641	0	3E-05	0	120.41	aatggaagCctagggggcc	m5C_30557
chr16	47539157	+	C	36	19	0.528	0	0	C	19	M	0.37	0.68	0	3E-05	0	140.62	atggaagtcCtagggggcgc	m5C_30544
chr16	49854070	+	C	39	23	0.59	0	0	C	23	M	0.434	0.729	0	8E-05	0	199.72	gaaggaagCagtagtgtag	m5C_30890
chr16	50132200	+	C	35	11	0.314	0	0	T	24	M	0.186	0.48	7E-16	3E-06	7E-16	30.969	agggggaatCaggactatt	m5C_30637
chr16	50132205	+	C	35	22	0.629	0	0	C	22	M	0.463	0.768	0	6E-05	0	203.88	gtatcaggaCttattaatc	m5C_30638
chr16	57697472	-	C	33	9	0.273	0	0	T	24	M	0.151	0.442	8E-13	1E-06	8E-13	16.442	ggaggaaggtCtgcggagct	m5C_30718
chr16	57697479	-	C	37	19	0.514	0	0	C	19	M	0.359	0.666	0	3E-05	0	136.4	tgcggctggaCgaaggtctgc	m5C_30713
chr16	58633481	+	C	32	20	0.625	0	0	C	20	M	0.453	0.771	0	4E-05	0	181.02	gaggttggtCagagcgagg	m5C_31075
chr16	58633502	+	C	31	10	0.323	0	0	T	21	M	0.186	0.499	7E-15	2E-06	8E-15	26.273	gtgttacaaCtaattgatca	m5C_31066
chr16	58804587	+	C	34	7	0.206	0	0	T	27	M	0.103	0.368	1E-09	3E-07	2E-09	6.4054	tggagactgcCaggctgtcta	m5C_31072
chr16	58804595	+	C	46	16	0.348	0	0	T	30	M	0.227	0.492	0	4E-07	0	72.579	gccaggctgcCtaaggagggg	m5C_31069
chr16	58804610	+	C	41	26	0.634	0	0	C	26	M	0.481	0.764	0	6E-06	0	250.23	gaggggggaaCtggccaggt	m5C_31065
chr16	58804614	+	C	34	8	0.235	0	0	T	26	M	0.124	0.4	4E-11	7E-07	4E-11	10.326	gggaagctgcCcaaggcaggt	m5C_31078
chr16	67663332	+	C	31	19	0.613	0	0	C	19	M	0.438	0.763	0	3E-05	0	166.53	gataattggtCtggccagat	m5C_30851
chr16	67663337	+	C	34	11	0.324	0	0	T	23	M	0.191	0.492	4E-16	3E-06	5E-16	32.399	ttgtctggtCcaagatggct	m5C_30848
chr16	67663338	+	C	34	19	0.559	0	0	C	19	M	0.395	0.711	0	3E-05	0	149.92	tgtgtggcCagatggcgta	m5C_30846
chr16	67663345	+	C	37	12	0.333	1	0.027	T	24	M	0.202	0.497	0	5E-06	0	48.515	gccccagtgCtgaagggggg	m5C_30857
chr16	69814947	+	C	37	21	0.568	0	0	C	21	M	0.409	0.713	0	5E-05	0	171.84	acaggttggtCctgggtagt	m5C_31167
chr16	69814948	+	C	36	16	0.444	0	0	T	20	M	0.295	0.604	0	2E-05	0	94.531	caggttggtCtgggtgagtg	m5C_31159
chr16	69814965	+	C	34	17	0.5	0	0	CT	17	M	0.341	0.659	0	2E-05	0	115.83	agggggaatCagaactatt	m5C_31172
chr16	69814970	+	C	31	17	0.548	0	0	C	17	M	0.378	0.708	0	2E-05	0	128.42	gtatcaggaCttattaatc	m5C_31169
chr16	70296395	-	C	41	23	0.561	0	0	C	23	M	0.41	0.701	0	3E-06	0	188.79	gggtatggtCtgcgaggga	m5C_31011
chr16	70812154	-	C	32	18	0.562	0	0	C	18	M	0.393	0.718	0	3E-05	0	141.57	gaattctgcCtgcacgagg	m5C_31027
chr16	70812157	-	C	31	11	0.367	1	0.032	T	19	M	0.219	0.545	0	3E-06	0	48.122	ggaattctCgctgcacgc	m5C_31012
chr16	70822609	+	C	73	57	0.781	0	0	C	57	M	0.673	0.86	0	1E-07	0	767.48	attgggtgtCagtgtagaag	m5C_30990
chr16	70822626	+	C	72	50	0.694	0	0	C	50	M	0.58	0.789	0	4E-08	0	580.46	agaattctgcCtgcgatcgc	m5C_30996
chr16	70822627	+	C	66	43	0.652	0	0	C	43	M	0.531	0.755	0	2E-07	0	456.76	gaattctgcCtgcgatcgcg	m5C_30983
chr16	70822630	+	C	37	19	0.514	0	0	C	19	M	0.359	0.666	0	3E-05	0	136.4	ttctgcgtCcatgcgggcg	m5C_30976
chr16	70822631	+	C	34	18	0.529	0	0	C	18	M	0.367	0.685	0	3E-05	0	132.25	tctgcctgcCattgcgggcg	m5C_30993
chr16	70823422	+	C	97	67	0.691	0	0	C	67	M	0.593	0.774	0	1E-09	0	794.56	attgggggtCagtgtagaag	m5C_30967
chr16	70823435	+	C	88	59	0.67	0	0	C	59	M	0.567	0.76	0	8E-09	0	668.97	tgggaattCtgcctgccca	m5C_30992
chr16	70823437	+	C	84	56	0.667	0	0	C	56	M	0.561	0.758	0	5E-09	0	627.79	gtgaattctCgctgcacgc	m5C_30985
chr16	70823439	+	C	59	28	0.475	0	0	T	31	M	0.353	0.6	0	3E-07	0	197.49	agaattctgcCtgcacgcgc	m5C_30988
chr16	70823440	+	C	48	23	0.479	0	0	T	25	M	0.345	0.617	0	3E-06	0	158.57	gaattctgcCtgcacgcgcg	m5C_30975
chr16	70823443	+	C	32	10	0.312	0	0	T	22	M	0.18	0.486	1E-14	2E-06	1E-14	25.084	ttctgcctgcCacgcggag	m5C_30980
chr16	74339527	+	C	55	23	0.418	0	0	T	32	M	0.297	0.55	0	9E-08	0	136.79	gaaagaaggCaggaagaaga	m5C_30955
chr16	74339544	+	C	73	34	0.466	0	0	T	39	M	0.356	0.579	0	1E-09	0	242.02	aagaagagagCaaaaaggata	m5C_30958
chr16	74339565	+	C	99	46	0.465	0	0	T	5									

chr16	89627871	+	C	147	106	0.721	0	0	C	106	M	0.644	0.787	0	3E-13	0	1364.6	cgctgacggCcttgatgaaa	m5C_31644
chr16	89627872	+	C	147	81	0.551	0	0	C	81	M	0.47	0.629	0	4E-15	0	761.94	gctgacggcCttgatgaaag	m5C_31666
chr16	89627883	+	C	143	74	0.517	0	0	C	74	M	0.436	0.598	0	1E-15	0	645.58	ttgatgaaacCacatttgaac	m5C_31655
chr16	89627885	+	C	141	80	0.567	0	0	C	80	M	0.485	0.646	0	4E-15	0	775.81	gatgaaagcCatttgaaccc	m5C_31651
chr16	89627893	+	C	143	87	0.608	0	0	C	87	M	0.527	0.685	0	1E-14	0	916.21	cacatttgaacCcttttccat	m5C_31671
chr16	89627894	+	C	133	92	0.692	0	0	C	92	M	0.609	0.764	0	6E-13	0	1120.2	acatttgaacCcttttccatc	m5C_31652
chr16	89627895	+	C	139	87	0.626	0	0	C	87	M	0.543	0.702	0	3E-13	0	944.97	catttgaaccCtttccatct	m5C_31657
chr16	89627900	+	C	139	96	0.691	0	0	C	96	M	0.61	0.761	0	1E-12	0	1170.3	gaacccttttCcatctgattg	m5C_31658
chr16	89627901	+	C	133	80	0.602	0	0	C	80	M	0.517	0.681	0	8E-14	0	826.52	aacccttttCcatctgattgc	m5C_31646
chr16	89627904	+	C	114	75	0.658	0	0	C	75	M	0.567	0.739	0	1E-11	0	850.4	ccttttccatCtgattgctga	m5C_31663
chr17	1368040	-	C	38	15	0.395	0	0	T	23	M	0.256	0.553	0	1E-05	0	76.794	cgcttagacCatagagggtg	m5C_31999
chr17	1368041	-	C	40	17	0.425	0	0	T	23	M	0.285	0.578	0	6E-07	0	96.931	ccgcttagaCatagagggtt	m5C_31993
chr17	1368047	-	C	46	20	0.435	0	0	T	26	M	0.302	0.578	0	1E-06	0	120.84	ggaaaggccgCttagaccata	m5C_31991
chr17	1437431	-	C	31	14	0.452	0	0	T	17	M	0.292	0.622	0	9E-06	0	81.652	ggacgacattCgaaggatgga	m5C_31987
chr17	1437435	-	C	33	14	0.424	0	0	T	19	M	0.272	0.592	0	9E-06	0	76.259	ccatggagcgaCattcgaagga	m5C_32005
chr17	2236259	-	C	65	30	0.462	0	0	T	35	M	0.346	0.581	0	2E-08	0	207.54	gaggaggaatCtcaggaaagg	m5C_31839
chr17	2319545	-	C	41	21	0.512	0	0	C	21	M	0.365	0.657	0	2E-06	0	153.23	ctgctgaagcCgcggcatttc	m5C_31838
chr17	2593832	-	C	32	12	0.375	0	0	T	20	M	0.229	0.547	0	5E-06	0	55.041	agcccgactgCgggagaaagg	m5C_31862
chr17	2593835	-	C	31	10	0.323	0	0	T	21	M	0.186	0.499	7E-15	2E-06	8E-15	26.273	ggagcccgCgtcgaggagaa	m5C_31846
chr17	4448417	-	C	49	29	0.592	0	0	C	29	M	0.452	0.718	0	1E-05	0	262.43	aaaggagagcCagggggagg	m5C_31962
chr17	4448447	-	C	52	21	0.404	0	0	T	31	M	0.282	0.539	0	5E-08	0	118.27	aaaggagagCaacgaagct	m5C_31957
chr17	6356314	-	C	40	10	0.25	0	0	T	30	M	0.142	0.402	2E-13	2E-08	2E-13	18.091	gaaggagagCtagggagagag	m5C_32174
chr17	7218281	-	C	41	22	0.537	0	0	C	22	M	0.387	0.679	0	2E-06	0	170.48	gcgcaagcggCaggggagcc	m5C_32159
chr17	7478041	+	C	43	14	0.326	0	0	T	29	M	0.205	0.475	0	2E-07	0	57.381	tgccttgacCtgggagagat	m5C_32145
chr17	7480130	+	C	34	8	0.235	0	0	T	26	M	0.124	0.4	4E-11	7E-07	4E-11	10.326	ggaaaggagCtctggaatgg	m5C_32140
chr17	7480145	+	C	86	28	0.326	0	0	T	58	M	0.236	0.43	0	6E-12	0	132.08	tgatggagcCcatgctggcga	m5C_32094
chr17	7480149	+	C	86	20	0.233	0	0	T	66	M	0.156	0.332	0	2E-13	0	62.356	ggagcccatgCggtgcatctg	m5C_32133
chr17	7480157	+	C	90	46	0.511	0	0	C	46	M	0.41	0.612	0	3E-11	0	376.75	tgcgtgcatCtggagctcttg	m5C_32082
chr17	7480162	+	C	68	43	0.632	0	0	C	43	M	0.514	0.737	0	2E-07	0	441.66	gtcatctgacCctctggcttc	m5C_32085
chr17	7480174	+	C	37	14	0.378	0	0	T	23	M	0.241	0.539	0	9E-06	0	67.379	tctgcttccCtgcagtgca	m5C_32074
chr17	7480177	+	C	42	17	0.405	0	0	T	25	M	0.27	0.555	0	6E-07	0	91.945	ggcttccctgCcaaggcagcc	m5C_32090
chr17	7480254	+	C	50	15	0.3	0	0	T	35	M	0.191	0.438	0	5E-09	0	57.31	aaggatcagCtttgactctt	m5C_32080
chr17	7480261	+	C	53	21	0.396	0	0	T	32	M	0.276	0.531	0	5E-08	0	115.87	agcttttgaCtctgagagca	m5C_32108
chr17	7809273	+	C	36	18	0.5	0	0	CT	18	M	0.345	0.655	0	3E-05	0	124.11	gggttggtgCgggaacttgag	m5C_32097
chr17	7809279	+	C	39	21	0.538	0	0	C	21	M	0.386	0.684	0	5E-05	0	161.99	gggtgCgggaCtggggggcaa	m5C_32113
chr17	7809287	+	C	37	11	0.297	0	0	T	26	M	0.175	0.458	1E-15	3E-06	2E-15	28.551	acctgaggggCaagactgaga	m5C_32105
chr17	8029076	+	C	35	13	0.371	0	0	T	22	M	0.232	0.537	0	7E-06	0	60.231	attgggggtCagggtaagaa	m5C_31712
chr17	8029089	+	C	34	18	0.529	0	0	C	18	M	0.367	0.685	0	3E-05	0	132.25	tggtagaatCtgcgctgcca	m5C_31705
chr17	8029091	+	C	33	11	0.333	0	0	T	22	M	0.198	0.504	2E-16	3E-06	2E-16	34.007	tgagattctCgctgcacag	m5C_31700
chr17	8029093	+	C	33	12	0.364	0	0	T	21	M	0.222	0.534	0	5E-06	0	53.249	agaattctgCctgcacgcg	m5C_31718
chr17	8090194	+	C	109	50	0.459	0	0	T	59	M	0.368	0.552	0	3E-12	0	368.17	gacgaggtggCgagtggtta	m5C_31702
chr17	8090195	+	C	113	36	0.319	0	0	T	77	M	0.24	0.409	0	1E-15	0	172.7	acgagggggCgaggggttaa	m5C_31698
chr17	8090208	+	C	49	14	0.286	0	0	T	35	M	0.178	0.424	0	2E-07	0	49.978	gggttaaggCgatggactgc	m5C_31706
chr17	16343352	+	C	69	42	0.609	0	0	C	42	M	0.491	0.715	0	2E-07	0	412.22	tgttgtagctgCtctgagaaa	m5C_33009
chr17	16343354	+	C	78	49	0.628	0	0	C	49	M	0.517	0.727	0	3E-08	0	506.96	cttgactgctCttaggaattc	m5C_33044
chr17	16343364	+	C	215	159	0.74	0	0	C	159	M	0.677	0.794	0	0	0	2153	ctgtagaatCactaatagga	m5C_33020
chr17	16343366	+	C	222	127	0.572	0	0	C	127	M	0.506	0.635	0	0	0	1286	gatgaataatCtaataaggaag	m5C_33050
chr17	16343379	+	C	235	139	0.591	0	0	C	139	M	0.528	0.652	0	0	0	1466.9	ataggaaaggCgcgcagaagc	m5C_33047
chr17	16343380	+	C	231	122	0.528	0	0	C	122	M	0.464	0.592	0	0	0	1131.7	taggaagggtCgacgaagcg	m5C_33058
chr17	16343383	+	C	237	116	0.489	0	0	T	121	M	0.426	0.553	0	0	0	989.45	gaagggccgtCagaagcgata	m5C_33025
chr17	16343389	+	C	238	123	0.517	0	0	C	123	M	0.454	0.58	0	0	0	1115.8	ccgtcagaagCgataactgac	m5C_33027
chr17	16343395	+	C	235	132	0.562	0	0	C	132	M	0.498	0.624	0	0	0	1314.1	gaagcgataaCtgcagaagac	m5C_33036
chr17	16343399	+	C	237	148	0.627	1	0.004	C	148	M	0.564	0.686	0	0	0	1669	cgataactgaCgaagactact	m5C_33038
chr17	16343405	+	C	235	163	0.694	0	0	C	163	M	0.632	0.749	0	0	0	2060.2	ctgcagaagaCtactctctgc	m5C_33048
chr17	16343408	+	C	227	138	0.613	2	0.009	C	138	M	0.548	0.675	0	0	0	1513.3	acgaagactaCctctgtctga	m5C_33018
chr17	16343410	+	C	229	132	0.576	0	0	C	132	M	0.512	0.639	0	0	0	1350.8	gaagactactCtctgtgatt	m5C_33063
chr17	16343411	+	C	215	153	0.712	0	0	C	153	M	0.648	0.768	0	0	0	1982.2	aagactactCtctgtgattg	m5C_33013
chr17	16343415	+	C	182	129	0.709	0	0	C	129	M	0.639	0.77	0	1E-16	0	1648.7	ctactctgtCtgatgcagt	m5C_33064
chr17	16344539	+	C	47	16	0.34	0	0	T	31	M	0.222	0.483	0	4E-07	0	70.935	aaaaagatatCaaatgtagaa	m5C_33023
chr17	16344552	+	C	172	40	0.233	0	0	T	132	M	0.176	0.301	0	0	0	140.55	atgatgaatCaccaccaataa	m5C_33046
chr17	16344554	+	C	177	72	0.409	1	0.006	T	104	M	0.339	0.483	0	0	0	488.37	gatgaataatCccaaaatagc	m5C_33022
chr17	16344555	+	C	173	63	0.364	0	0	T	110	M	0.296	0.438	0	0	0	373.12	atgaataatCccaaaatagct	m5C_33061
chr17	16344556	+	C	168	46	0.274	0	0	T	122	M	0.212	0.346	0	0	0	195.04	tgaataatCccaaaatagctg	m5C_33017
chr17	16344564	+	C	169	73	0.432	0	0	T	96	M	0.36	0.507	0	0	0	525.02	cccaaatagCtgggaattacc	m5C_33035
chr17	16344573	+	C	171	72	0.421	0	0	T	99	M	0.35	0.496	0	0	0	503.4	gctggaattaCgggcagattg	m5C_33033
chr17	16344574	+	C	170	62	0.365	0	0	T	108	M	0.296	0.439	0	0	0	367.14	ctggaaattacCggcagattgt	m5C_33043
chr17	16344577	+	C	179	55	0.307	0	0	T	124	M	0.244	0.378	0	0	0	268.75	gaattaccggCagatttgga	m5C_33055
chr17	16344596	+	C	226	70	0.31	0	0	T	156	M	0.253	0.373	0	0	0	354.27	tagggggaaCctatggtttt	m5C_33057
chr17	16344597	+	C	220	61	0.277	0	0	T	159	M	0.222	0.34	0	0	0	271.24	aggggggaacCtatggttttc	m5C_33052
chr17	16344607	+	C	163	72	0.442	0	0	T	91	M	0.368	0.518	0	0	0	529.48	ctatggttttCtgaagatatc	m5C_33054
chr17	18150121	-	C	42	23	0.548	0	0	C	23	M	0.399	0.688	0	3E-06	0	183.76	ctggggagtaCgagggggagg	m5C_34167
chr17	18150131	-	C	40	27	0.675	0	0	C	27	M	0.52	0.799	0	0.0001	0	280.89	tactgggtgCtgggagagac	m5C_34170
chr17	18965433	+	C	58	21	0.362	0	0	T	37	M	0.251	0.491	0</					

chr17	19093508	-	C	41	12	0.293	0	0	T	29	M	0.176	0.445	1E-16	7E-08	1E-16	33.713	agagaagttCtctgaacgtg	m5C_34165
chr17	19764205	+	C	38	30	0.789	0	0	C	30	M	0.637	0.889	0	0.0002	0	381.92	gaattctcgcCtcccacgag	m5C_34123
chr17	20135081	+	C	35	9	0.257	0	0	T	26	M	0.142	0.421	1E-12	1E-06	2E-12	15.086	gtatgtgagCaaagctgag	m5C_32242
chr17	20135085	+	C	34	17	0.5	0	0	CT	17	M	0.341	0.659	0	2E-05	0	115.83	tgtatcaagCtggaggaaca	m5C_32247
chr17	20135101	+	C	36	13	0.361	0	0	T	23	M	0.225	0.524	0	7E-06	0	58.436	gaacagaagCagacctggag	m5C_32251
chr17	20135118	+	C	31	10	0.323	0	0	T	21	M	0.186	0.499	7E-15	2E-06	8E-15	26.273	ggagaggcagCtgaagactct	m5C_32249
chr17	20135125	+	C	31	21	0.677	0	0	C	21	M	0.501	0.814	0	5E-05	0	210.59	cagctgaagCtctgaccaag	m5C_32253
chr17	27047600	+	C	69	25	0.362	0	0	T	44	M	0.259	0.48	0	4E-09	0	129.48	aatctctgaCacttggatg	m5C_32632
chr17	27047602	+	C	70	21	0.3	0	0	T	49	M	0.205	0.415	0	2E-11	0	86.253	tctctgacaCtggatgtrc	m5C_32613
chr17	27047623	+	C	68	24	0.353	0	0	T	44	M	0.25	0.472	0	3E-09	0	120.01	tcaaaaggaaCactgatgca	m5C_32622
chr17	27047624	+	C	67	17	0.254	0	0	T	50	M	0.165	0.369	0	2E-10	0	56.058	tcaaaaggaaCactgatgcac	m5C_32614
chr17	27050450	+	C	152	42	0.276	0	0	T	110	M	0.211	0.352	0	0	0	177.58	grrctctgggCtaatgagga	m5C_32599
chr17	27050466	+	C	376	111	0.295	0	0	T	265	M	0.251	0.343	0	0	0	558.03	atggaaaaatCattattgaa	m5C_32601
chr17	27050502	+	C	373	126	0.338	0	0	T	247	M	0.292	0.387	0	0	0	735.02	aaaggaaCtgaagggccg	m5C_32615
chr17	28444120	+	C	140	28	0.2	0	0	T	112	M	0.142	0.274	0	0	0	79.606	ggctgaggggCagagagcgag	m5C_32406
chr17	31149420	+	C	131	93	0.71	0	0	C	93	M	0.627	0.781	0	7E-13	0	1166.4	gcgctggagCgttatccctc	m5C_32469
chr17	31149422	-	C	124	68	0.548	0	0	C	68	M	0.461	0.633	0	2E-13	0	626.49	cggcgctggaCgcgttatccc	m5C_32501
chr17	31149427	-	C	143	72	0.503	0	0	C	72	M	0.423	0.584	0	7E-16	0	608.45	acggacggcgCtggagcggt	m5C_32493
chr17	31149429	+	C	152	84	0.553	0	0	C	84	M	0.473	0.629	0	3E-16	0	795.07	ggacggagcgCgtggacgcg	m5C_32461
chr17	31149432	-	C	194	113	0.582	0	0	C	113	M	0.512	0.65	0	0	0	1157.4	aacggacggaCggcgctggac	m5C_32481
chr17	31149436	-	C	147	38	0.437	60	0.408	A	60	M	0.337	0.541	0	1E-10	0	256.44	gacgaacggaCggaaggcgt	m5C_32482
chr17	31149440	-	C	672	324	0.482	0	0	T	348	M	0.445	0.52	0	0	0	2880.8	ggagaacgaaCggaaggacgg	m5C_32503
chr17	31149444	-	C	843	308	0.365	0	0	T	535	M	0.334	0.398	0	0	0	2054.6	gggaggaagaCgaaggagcgg	m5C_32451
chr17	31149459	-	C	969	569	0.587	0	0	C	569	M	0.556	0.618	0	0	0	6326.4	cgggagagggCgggaaggag	m5C_32452
chr17	31149460	-	C	940	491	0.523	1	0.001	C	491	M	0.491	0.555	0	0	0	4820.8	gcggagagggCgggaaggag	m5C_32443
chr17	31149469	-	C	581	283	0.487	0	0	T	298	M	0.447	0.528	0	0	0	2528.1	ccgtgtcggCgggagagagcc	m5C_32457
chr17	31149472	-	C	470	348	0.74	0	0	C	348	M	0.699	0.778	0	0	0	4864.7	tgccctgggCggggagagag	m5C_32487
chr17	31149478	-	C	154	52	0.338	0	0	T	102	M	0.268	0.415	0	0	0	278.44	caccactgcCgtggcgcgcg	m5C_32490
chr17	31149479	-	C	133	47	0.353	0	0	T	86	M	0.277	0.438	0	0	0	260.66	ccaccactgcCcggtgcgac	m5C_32491
chr17	31149480	-	C	110	36	0.327	0	0	T	74	M	0.247	0.419	0	1E-15	0	177.63	cccaccactgCccgggtcgg	m5C_32464
chr17	31149524	-	C	372	82	0.22	0	0	T	290	M	0.181	0.265	0	0	0	297.3	accgaagaagCggcgcgcca	m5C_32480
chr17	31149532	-	C	728	371	0.51	0	0	C	371	M	0.473	0.546	0	0	0	3512.2	aggcgggaaCgaagaagcgg	m5C_32468
chr17	31149533	-	C	740	374	0.505	0	0	C	374	M	0.469	0.541	0	0	0	3511.5	gaggcgggaaCgaagaagcgg	m5C_32453
chr17	31149539	-	C	694	391	0.563	0	0	C	391	M	0.526	0.6	0	0	0	4115.3	ggggagagggCgggaaccgaa	m5C_32492
chr17	31149605	-	C	36	18	0.5	0	0	CT	18	M	0.345	0.655	0	3E-05	0	124.11	gcggcgccctCcgcggttccc	m5C_32483
chr17	31149607	-	C	54	18	0.333	0	0	T	36	M	0.222	0.466	0	2E-08	0	80.068	gcgcggcgCctccgggttc	m5C_32436
chr17	31149608	-	C	54	36	0.667	0	0	C	36	M	0.534	0.778	0	2E-06	0	384.2	ggcgggcgCctccgcggt	m5C_32460
chr17	31149610	-	C	52	17	0.327	0	0	T	35	M	0.215	0.462	0	1E-08	0	73.174	tcggcgggCgcctccggcg	m5C_32497
chr17	31149611	-	C	57	18	0.316	0	0	T	39	M	0.21	0.445	0	2E-08	0	75.615	ctcgcgggCcgctctcgcg	m5C_32448
chr17	31149614	-	C	81	43	0.531	0	0	C	43	M	0.423	0.636	0	4E-10	0	364.01	cggtcggcgCggcgccctcc	m5C_32456
chr17	31149616	-	C	93	61	0.656	0	0	C	61	M	0.555	0.745	0	6E-10	0	676.99	cccggctcgCgcggcgccct	m5C_32435
chr17	31149619	-	C	95	43	0.453	0	0	T	52	M	0.356	0.553	0	1E-11	0	306.44	ggcgccggcCggcgggcg	m5C_32442
chr17	31149621	-	C	80	18	0.225	0	0	T	62	M	0.147	0.328	0	4E-14	0	53.039	acgggcccgcCtggcgggc	m5C_32472
chr17	31149624	-	C	76	50	0.658	0	0	C	50	M	0.546	0.755	0	4E-08	0	545.96	gccacgggcCggctggcg	m5C_32455
chr17	31149625	-	C	72	35	0.486	0	0	T	37	M	0.374	0.599	0	2E-09	0	262.03	ggcacgggcCcgctcgggcg	m5C_32474
chr17	31149626	-	C	69	28	0.406	0	0	T	41	M	0.298	0.524	0	1E-08	0	166.82	gggcacgggCccggctcggc	m5C_32473
chr17	31149630	-	C	55	11	0.2	0	0	T	44	M	0.116	0.324	3E-13	4E-10	3E-13	15.923	cggcgggccaCgggcccggct	m5C_32476
chr17	31149632	-	C	41	16	0.39	0	0	T	25	M	0.257	0.543	0	4E-07	0	82.099	gcgcggggCacgggcccgg	m5C_32462
chr17	31149633	-	C	43	27	0.628	0	0	C	27	M	0.479	0.756	0	7E-06	0	258.44	ggcggggggCcacgggccc	m5C_32458
chr17	31149663	-	C	44	24	0.545	0	0	C	24	M	0.401	0.683	0	4E-06	0	192.32	ggggcccgcCggcacccccc	m5C_32498
chr17	31149665	-	C	49	16	0.327	0	0	T	33	M	0.212	0.466	0	4E-07	0	67.863	ccggggcccCggcgccaccc	m5C_32445
chr17	31149667	-	C	48	27	0.562	0	0	C	27	M	0.423	0.693	0	7E-06	0	228.28	caccggggcCgcggggcac	m5C_32502
chr17	31149674	-	C	45	16	0.356	0	0	T	29	M	0.232	0.502	0	4E-07	0	74.3	gcgcgcccaCggggcccgcg	m5C_32465
chr17	31149677	-	C	41	32	0.78	0	0	C	32	M	0.633	0.88	0	2E-05	0	405.09	gtggcgcccCacggggggccc	m5C_32441
chr17	31149679	-	C	36	14	0.389	0	0	T	22	M	0.248	0.551	0	9E-06	0	69.397	gggtggccgcCccaccggggc	m5C_32499
chr17	33478193	-	C	659	462	0.701	0	0	C	462	M	0.665	0.735	0	0	0	6144.8	agatttcctCagtaagagg	m5C_35677
chr17	33478195	-	C	676	484	0.716	0	0	C	484	M	0.681	0.749	0	0	0	6590.5	ccagatttcCtaagtaagg	m5C_35657
chr17	33478196	-	C	657	459	0.699	0	0	C	459	M	0.662	0.732	0	0	0	6081.5	accaggattCctcgaatg	m5C_35634
chr17	33478197	-	C	657	464	0.706	0	0	C	464	M	0.67	0.74	0	0	0	6220.3	aaccaggattCcttcagtaat	m5C_35690
chr17	33478205	-	C	636	501	0.788	0	0	C	501	M	0.754	0.818	0	0	0	7557.9	aagaactaaCaggattccc	m5C_35679
chr17	33478223	-	C	679	459	0.676	0	0	C	459	M	0.64	0.71	0	0	0	5874.2	tattgtcagCggaggaaag	m5C_35648
chr17	33478226	-	C	674	416	0.617	0	0	C	416	M	0.58	0.653	0	0	0	4825.2	gcattattgtCagcgaggaa	m5C_35678
chr17	33478235	-	C	929	463	0.499	1	0.001	T	463	M	0.467	0.531	0	0	0	4322.8	tgattttaagCattattgca	m5C_35682
chr17	33478246	-	C	936	384	0.41	0	0	T	552	M	0.379	0.442	0	0	0	2912.1	tggcgacccgCtgaatttaag	m5C_35662
chr17	33478248	-	C	944	395	0.418	0	0	T	549	M	0.387	0.45	0	0	0	3060.1	cggcgaccCagtgaattta	m5C_35665
chr17	33478249	-	C	940	418	0.445	0	0	T	522	M	0.413	0.477	0	0	0	3454.4	acgtggaccCcgctgaattt	m5C_35681
chr17	33478250	-	C	937	439	0.469	1	0.001	T	497	M	0.437	0.501	0	0	0	3839	gacgtggcgaCccgtgaatt	m5C_35649
chr17	33478253	-	C	934	439	0.473	5	0.005	T	490	M	0.441	0.505	0	0	0	3868.7	tcagacgggCgacccgctga	m5C_35661
chr17	33478258	-	C	938	450	0.483	6	0.006	T	482	M	0.451	0.515	0	0	0	4058	tcagatcagaCggggcgacc	m5C_35700
chr17	33478262	-	C	863	386	0.447	0	0	T	477	M	0.414	0.481	0	0	0	3199.2	gactcagatCagacgtggcg	m5C_35698
chr17	33478267	-	C	834	366	0.439	0	0	T	468	M	0.406	0.473	0	0	0	2968.4	cccgcgacctCagatcagag	m5C_35645
chr17	33478269	-	C	804	321	0.4	1	0.001	T	482	M	0.366	0.434	0	0	0	2352.4	ggcccggaCctcagatcaga	m5C_35680
chr17	33478270	-	C	764	348	0.455	0	0	T	416	M	0.42	0.491	0					

chr17	33478341	+	C	51	25	0.49	0	0	T	26	M	0.359	0.623	0	2E-07	0	179.29	ccgtacgccacattccccg	m5C_35593
chr17	34151156	+	C	34	16	0.485	1	0.029	T	17	M	0.325	0.648	0	2E-05	0	104.01	agggagagggcggggggata	m5C_32217
chr17	34151170	+	C	37	26	0.703	0	0	C	26	M	0.542	0.825	0	0.0001	0	281.93	ggggatatgaCaaggatgaa	m5C_32216
chr17	37009131	-	C	39	18	0.462	0	0	T	21	M	0.316	0.614	0	3E-05	0	113.64	ttgttcaatCgggggtgga	m5C_32304
chr17	37009135	-	C	37	11	0.297	0	0	T	26	M	0.175	0.458	1E-15	3E-06	2E-15	28.551	ttgtttcttCaatcgggtg	m5C_32334
chr17	37009196	-	C	37	9	0.243	0	0	T	28	M	0.134	0.401	3E-12	1E-06	3E-12	13.907	attgagccgtCaagaagggg	m5C_32323
chr17	37009200	-	C	39	13	0.333	0	0	T	26	M	0.206	0.49	0	7E-06	0	53.645	acctattgagCgtcaagaaa	m5C_32329
chr17	37009208	-	C	43	14	0.326	0	0	T	29	M	0.205	0.475	0	2E-07	0	57.381	ggctaatacCtattgagcgc	m5C_32307
chr17	37017996	-	C	35	13	0.371	0	0	T	22	M	0.232	0.537	0	7E-06	0	60.231	gggatagctCaggggagag	m5C_32324
chr17	37017998	-	C	35	12	0.343	0	0	T	23	M	0.208	0.508	0	5E-06	0	49.996	gggggatagCtccaggagag	m5C_32333
chr17	37023908	+	C	33	8	0.242	0	0	T	25	M	0.128	0.41	3E-11	7E-07	3E-11	10.787	gggggatagCtccaggagag	m5C_32285
chr17	37023910	+	C	36	15	0.417	0	0	T	21	M	0.271	0.578	0	1E-05	0	81.421	gggatagctCaggggagag	m5C_32275
chr17	37023921	+	C	35	24	0.686	0	0	C	24	M	0.52	0.814	0	9E-05	0	249.7	aggggatagCattgaatgc	m5C_32290
chr17	37360816	+	C	57	18	0.316	0	0	T	39	M	0.21	0.445	0	2E-08	0	75.615	accaaggagCagcaagcgc	m5C_32295
chr17	37360836	+	C	44	13	0.295	0	0	T	31	M	0.182	0.442	0	1E-07	0	47.204	ccgtgaagagCgctccaggc	m5C_32270
chr17	37360842	+	C	39	12	0.308	0	0	T	27	M	0.186	0.464	0	5E-06	0	44.558	agagcgcctCaggccaagaa	m5C_32266
chr17	38282517	+	C	31	10	0.323	0	0	T	21	M	0.186	0.499	7E-15	2E-06	8E-15	26.273	caagctgtttCagggtatga	m5C_32347
chr17	38399482	+	C	42	19	0.452	0	0	T	23	M	0.312	0.601	0	1E-06	0	118.65	tgaggctggcTtgatggagt	m5C_32359
chr17	38399500	+	C	38	13	0.342	0	0	T	25	M	0.212	0.501	0	7E-06	0	55.152	aggggatagCagagcttatt	m5C_32366
chr17	38399505	+	C	35	17	0.486	0	0	T	18	M	0.33	0.644	0	2E-05	0	112.18	gttatcagagCttataaacat	m5C_32343
chr17	39624284	+	C	34	11	0.324	0	0	T	23	M	0.191	0.492	4E-16	3E-06	5E-16	32.309	cgctcccatCtggagacaac	m5C_32365
chr17	39624291	+	C	40	11	0.275	0	0	T	29	M	0.161	0.428	4E-15	3E-06	5E-15	25.45	catctgaggaCaacattataa	m5C_32360
chr17	40489528	-	C	31	8	0.258	0	0	T	23	M	0.137	0.432	2E-11	7E-07	2E-11	11.818	gaggagctggcTtgatggag	m5C_32590
chr17	40489532	-	C	41	11	0.268	0	0	T	30	M	0.157	0.419	6E-15	4E-08	7E-15	24.554	ggagggagagCtgagtgactg	m5C_32576
chr17	40489539	-	C	53	42	0.792	0	0	C	42	M	0.665	0.88	0	4E-06	0	558.95	ctctcacgagCagggagctgg	m5C_32565
chr17	40489545	-	C	41	24	0.585	0	0	C	24	M	0.434	0.722	0	4E-06	0	208.16	agaaaacctCacggagcagg	m5C_32568
chr17	40489547	-	C	40	24	0.6	0	0	C	24	M	0.446	0.737	0	4E-06	0	214.06	gcagaaaactCtccagcaga	m5C_32556
chr17	40574893	-	C	37	22	0.595	0	0	C	22	M	0.435	0.737	0	6E-05	0	191.34	tcaagcacagCtggagagcgc	m5C_32577
chr17	41400535	+	C	57	39	0.684	0	0	C	39	M	0.555	0.79	0	2E-06	0	433.06	cgcgtggtgCggaagcaga	m5C_32525
chr17	41400541	+	C	79	36	0.48	4	0.051	T	39	M	0.371	0.591	0	2E-09	0	266.9	tggcgggagCgagagatga	m5C_32510
chr17	41400563	+	C	116	24	0.207	0	0	T	92	M	0.143	0.289	0	0	0	68.717	gagataagaCagaagcaaa	m5C_32539
chr17	41400570	+	C	98	29	0.296	0	0	T	69	M	0.215	0.393	0	2E-13	0	124.49	agacagaaagCaagagatag	m5C_32546
chr17	41464613	-	C	128	44	0.344	0	0	T	84	M	0.267	0.43	0	4E-16	0	235.05	tgacagacctCaggatggg	m5C_32571
chr17	41464616	-	C	138	48	0.348	0	0	T	90	M	0.273	0.43	0	0	0	262.52	tattcgatgaCctccaggaa	m5C_32583
chr17	41464630	-	C	89	25	0.281	0	0	T	64	M	0.198	0.382	0	2E-12	0	99.047	acgcgtcgaCtggattgca	m5C_32559
chr17	41464634	-	C	68	19	0.279	0	0	T	49	M	0.187	0.396	0	5E-10	0	70.976	ctccacgcgtCgacctggat	m5C_32558
chr17	42088964	-	C	71	29	0.408	0	0	T	42	M	0.302	0.525	0	4E-10	0	174.98	gaggggagagCagaggaaagg	m5C_33000
chr17	46133870	+	C	33	15	0.455	0	0	T	18	M	0.298	0.62	0	1E-05	0	89.528	gagatggagCgagcaggaca	m5C_32693
chr17	46133874	+	C	33	14	0.424	0	0	T	19	M	0.272	0.592	0	9E-06	0	76.259	tggaagcagCaggacacctg	m5C_32697
chr17	46133879	+	C	34	19	0.559	0	0	C	19	M	0.395	0.711	0	3E-05	0	149.92	gcagcaggaCacctgggcag	m5C_32698
chr17	46133891	+	C	32	13	0.406	0	0	T	19	M	0.255	0.577	0	7E-06	0	66.35	cctggcagagCgagggcgcgg	m5C_32691
chr17	46657275	-	C	74	55	0.743	0	0	C	55	M	0.633	0.829	0	8E-08	0	696.8	cctgatgacCgaatttggt	m5C_32719
chr17	46657285	-	C	36	22	0.611	0	0	C	22	M	0.449	0.752	0	6E-05	0	197.4	ctgatatacCctgagatcc	m5C_32717
chr17	46657286	-	C	36	23	0.639	0	0	C	23	M	0.476	0.775	0	8E-05	0	218.84	tctgatataCcttgatgatc	m5C_32703
chr17	46685176	-	C	59	17	0.288	0	0	T	42	M	0.188	0.414	0	1E-08	0	64.044	gaggaaagagCatgaaagagg	m5C_32709
chr17	46685188	-	C	83	22	0.265	0	0	T	61	M	0.182	0.369	0	4E-13	0	80.099	ggagaaagggCagagggaagag	m5C_32714
chr17	48462587	-	C	59	28	0.475	0	0	T	31	M	0.353	0.6	0	3E-07	0	197.49	actgcggagCgggagaaagg	m5C_32926
chr17	48462596	-	C	73	35	0.479	0	0	T	38	M	0.369	0.592	0	2E-09	0	258.14	ggagcgggaaCtgcggaaagcg	m5C_32946
chr17	48462602	-	C	63	20	0.317	0	0	T	43	M	0.216	0.44	0	7E-10	0	86.346	agctcaggaCgggaactgctg	m5C_32941
chr17	48462608	-	C	42	25	0.595	0	0	C	25	M	0.445	0.73	0	4E-06	0	222.47	taaggaaagCaggagcggga	m5C_32950
chr17	48823123	+	C	31	20	0.645	0	0	C	20	M	0.469	0.789	0	4E-05	0	187.79	tcgtgatgagCgctaaaaaa	m5C_32903
chr17	48823126	+	C	31	11	0.355	0	0	T	20	M	0.211	0.531	1E-16	3E-06	1E-16	37.059	tgatgagcgtCtaaaaaagga	m5C_32912
chr17	48823168	+	C	54	27	0.5	0	0	CT	27	M	0.371	0.629	0	2E-07	0	200.42	agaaaaagaaCggagagagga	m5C_32892
chr17	55868719	-	C	118	91	0.771	0	0	C	91	M	0.688	0.838	0	2E-10	0	1251.4	tcagtgggtCtgaagatgg	m5C_32754
chr17	55868720	-	C	120	95	0.792	0	0	C	95	M	0.711	0.855	0	2E-11	0	1350	gtcagttggcCtggagagatg	m5C_32761
chr17	55868746	-	C	97	75	0.773	0	0	C	75	M	0.68	0.845	0	5E-09	0	1020.6	ttattggaaCagcagttgaa	m5C_32755
chr17	57918642	+	C	119	94	0.79	0	0	C	94	M	0.708	0.853	0	2E-10	0	1331.5	ggagcttatCagactgatgt	m5C_33323
chr17	57918656	+	C	63	49	0.778	0	0	C	49	M	0.661	0.863	0	6E-07	0	647.66	ctgatgtgaCtggtaactc	m5C_33324
chr17	58160993	-	C	34	15	0.441	0	0	T	19	M	0.289	0.605	0	1E-05	0	86.65	tgagtgaggaCtaccagggat	m5C_32781
chr17	62223457	+	C	309	95	0.308	1	0.003	T	213	M	0.259	0.362	0	0	0	493.02	tgatgacattCaattaaagc	m5C_33164
chr17	62223458	+	C	299	65	0.218	1	0.003	T	233	M	0.175	0.268	0	0	0	227.48	gatgacattCaattaaagca	m5C_33150
chr17	62223481	+	C	334	72	0.216	1	0.003	T	261	M	0.175	0.264	0	0	0	252.53	tgttagactCtgcagcgggt	m5C_33171
chr17	62223485	+	C	379	102	0.271	2	0.005	T	275	M	0.228	0.318	0	0	0	465.51	agactgctgaCgcggggatg	m5C_33170
chr17	62223500	+	C	393	100	0.254	0	0	T	293	M	0.214	0.3	0	0	0	427.82	gtgatgcgaCtggagcttga	m5C_33161
chr17	62223512	+	C	206	46	0.223	0	0	T	160	M	0.172	0.285	0	0	0	158.05	ggagctgagCctgcccgagc	m5C_33158
chr17	62223513	+	C	174	55	0.316	0	0	T	119	M	0.252	0.389	0	0	0	276.78	gagctgagcCtgcggagcg	m5C_33148
chr17	62223817	+	C	45	12	0.267	0	0	T	33	M	0.16	0.41	6E-16	7E-08	6E-16	29.226	gccttttaaCcgcgagcgac	m5C_33162
chr17	62223818	+	C	45	12	0.267	0	0	T	33	M	0.16	0.41	6E-16	7E-08	6E-16	29.226	ccttttaacCgcgagcgaca	m5C_33154
chr17	73030524	-	C	34	25	0.735	0	0	C	25	M	0.569	0.854	0	0.0001	0	284.41	cctgggggtCgagaggggct	m5C_33280
chr17	73030558	-	C	46	34	0.739	0	0	C	34	M	0.597	0.844	0	2E-05	0	406.24	ctctctaagCagggaattgg	m5C_33274
chr17	73030559	-	C	34	17	0.5	0	0	CT	17	M	0.341	0.659	0	2E-05	0	115.83	gcctcctaagCagggaattg	m5C_33278
chr17	73035328	-	C	56	20	0.357	0	0	T	36	M	0.245	0.488	0	3E-08	0	97.826	ttcctaaaggCaggattgag	m5C_33294
chr17	73035329	-	C	51															

chr18	19209026	+	C	68	15	0.221	0	0	T	53	M	0.138	0.333	0	6E-11	0	41.547	ctctcagtgCaggaagagggc	m5C_33737
chr18	44790111	+	C	32	10	0.312	0	0	T	22	M	0.18	0.486	1E-14	2E-06	1E-14	25.084	atcgcatagcCagccggatc	m5C_33815
chr18	47017661	-	C	32	20	0.625	0	0	C	20	M	0.453	0.771	0	4E-05	0	181.02	ttaataattCtgagcagcca	m5C_34022
chr18	47017679	-	C	39	27	0.692	0	0	C	27	M	0.536	0.814	0	0.0001	0	289.32	ttggattacCtgaaaatta	m5C_34016
chr18	47017691	-	C	38	27	0.711	0	0	C	27	M	0.552	0.83	0	0.0001	0	298.31	cttagaacacCttggatta	m5C_34010
chr18	47017692	-	C	38	28	0.737	0	0	C	28	M	0.58	0.85	0	0.0002	0	324.75	tcttaggacaCcttgattg	m5C_33989
chr18	47017701	-	C	39	27	0.692	0	0	C	27	M	0.536	0.814	0	0.0001	0	289.32	tgatgacctCttagacacc	m5C_34006
chr18	47811112	-	C	59	33	0.559	0	0	C	33	M	0.433	0.678	0	9E-07	0	285.71	gaggaagagCtgaagaagaag	m5C_33994
chr18	47811128	-	C	31	12	0.387	0	0	T	19	M	0.237	0.562	0	5E-06	0	56.959	gcattggaagCtgcgggagaa	m5C_33978
chr18	48810123	-	C	41	19	0.463	0	0	T	22	M	0.321	0.613	0	1E-06	0	121.81	tagggggggaCtggggggg	m5C_34439
chr18	57022805	-	C	32	9	0.281	0	0	T	23	M	0.156	0.454	5E-13	1E-06	6E-13	17.198	caaaagggcCttgggaact	m5C_34469
chr18	58072215	+	C	74	39	0.527	0	0	C	39	M	0.415	0.637	0	5E-09	0	323.52	gagtgatggtCagacagggga	m5C_33899
chr18	58072219	+	C	67	34	0.507	0	0	C	34	M	0.391	0.623	0	4E-08	0	265.63	gatgttcagaCagggaanaag	m5C_33909
chr18	70999774	+	C	34	26	0.765	0	0	C	26	M	0.6	0.876	0	0.0001	0	312.02	ccagcagagcCagatctgagc	m5C_34462
chr18	70999779	+	C	32	15	0.469	0	0	T	17	M	0.309	0.636	0	1E-05	0	92.607	agagccagatCtgaagtgga	m5C_34457
chr19	926319	+	C	67	31	0.463	0	0	T	36	M	0.349	0.581	0	2E-08	0	216.12	ggggggggcCcgagctggga	m5C_34366
chr19	3539410	-	C	32	21	0.656	0	0	C	21	M	0.483	0.796	0	5E-05	0	202.91	cggagggggaCaggaagaagct	m5C_34280
chr19	3539425	-	C	42	20	0.476	0	0	T	22	M	0.334	0.623	0	1E-06	0	133.44	tgaggggccaCtggccggagg	m5C_34261
chr19	3539428	-	C	36	13	0.361	0	0	T	23	M	0.225	0.524	0	7E-06	0	58.436	cagtgagcggCactggccgg	m5C_34286
chr19	3539660	-	C	32	17	0.531	0	0	C	17	M	0.364	0.691	0	2E-05	0	123.93	aagacagaagCagagaccggg	m5C_34292
chr19	3976158	-	C	58	24	0.414	0	0	T	34	M	0.296	0.542	0	1E-07	0	142.21	gaaaggaacaCgcgggagat	m5C_34283
chr19	3976160	-	C	50	16	0.32	0	0	T	34	M	0.208	0.458	0	7E-09	0	66.426	gggaagaggaCacgcgggag	m5C_34281
chr19	3977953	-	C	31	13	0.419	0	0	T	18	M	0.264	0.592	0	7E-06	0	68.68	tgggacgrrggCtgaagccgc	m5C_34276
chr19	3977958	-	C	45	17	0.378	0	0	T	28	M	0.251	0.524	0	6E-07	0	85.367	acgagggggaCgrrgctgag	m5C_34298
chr19	4423372	+	C	48	13	0.271	0	0	T	35	M	0.166	0.41	0	1E-07	0	43.071	agaaagagaaCcggttaagga	m5C_34608
chr19	4446369	-	C	43	22	0.512	0	0	C	22	M	0.368	0.654	0	2E-06	0	161.71	cggaccaaggCcatgrrggag	m5C_34663
chr19	4510607	-	C	301	147	0.488	0	0	T	154	M	0.432	0.545	0	0	0	1271.3	gagrrggggaCgttccacca	m5C_34664
chr19	4724112	+	C	103	55	0.534	0	0	C	55	M	0.438	0.627	0	8E-12	0	481.98	agcatagctCcttccaagca	m5C_34633
chr19	4724113	+	C	101	36	0.356	0	0	T	65	M	0.27	0.454	0	5E-14	0	194.3	gcatagctgcCttccaagcag	m5C_34621
chr19	4724117	+	C	99	36	0.364	0	0	T	63	M	0.276	0.462	0	2E-12	0	198.44	agctgccttCaagcagttga	m5C_34620
chr19	5600214	-	C	33	7	0.212	0	0	T	26	M	0.107	0.378	1E-09	3E-07	1E-09	6.6917	agcctgaagCattaagaagg	m5C_34643
chr19	5600221	-	C	36	19	0.528	0	0	C	19	M	0.37	0.68	0	3E-05	0	140.62	gaaaaaagcCtgaagacatt	m5C_34670
chr19	6589226	-	C	39	11	0.282	0	0	T	28	M	0.165	0.438	3E-15	3E-06	3E-15	26.4	aggaagataaCagagaaggaag	m5C_34348
chr19	6589254	-	C	34	10	0.294	0	0	T	24	M	0.168	0.462	2E-14	2E-06	3E-14	22.956	gaaagaaagcCagagaagaga	m5C_34342
chr19	6589255	-	C	33	21	0.636	0	0	C	21	M	0.466	0.778	0	5E-05	0	195.79	agaaagaaagCcaagagaagg	m5C_34347
chr19	8793673	-	C	38	29	0.763	0	0	C	29	M	0.608	0.87	0	0.0002	0	352.6	gaattctgcCtgcacaatg	m5C_34317
chr19	8793691	-	C	110	87	0.791	0	0	C	87	M	0.706	0.856	0	9E-11	0	1228	atcaggggtCagrrgagaa	m5C_34312
chr19	10670331	-	C	34	10	0.294	0	0	T	24	M	0.168	0.462	2E-14	2E-06	3E-14	22.956	aggaagagcCagaaaggaag	m5C_34758
chr19	11170485	+	C	40	20	0.5	0	0	CT	20	M	0.352	0.648	0	1E-06	0	140.8	ggcagaatatCgaagaaggag	m5C_34750
chr19	11170500	+	C	39	19	0.487	0	0	T	20	M	0.339	0.638	0	3E-05	0	128.69	aggaagaggaCaggaagggc	m5C_34729
chr19	11306387	-	C	36	19	0.528	0	0	C	19	M	0.37	0.68	0	3E-05	0	140.62	gagacagagaCgrrgagagac	m5C_34794
chr19	11306393	-	C	50	13	0.26	0	0	T	37	M	0.159	0.396	0	2E-09	0	41.266	cgcagagagaCagagacgggg	m5C_34784
chr19	11306415	-	C	34	7	0.206	0	0	T	27	M	0.103	0.368	1E-09	3E-07	2E-09	6.4054	aggaacagagaCgrrgagagag	m5C_34779
chr19	11553280	+	C	58	17	0.293	0	0	T	41	M	0.192	0.42	0	1E-08	0	65.205	aaaggggaagCtgaagaagcca	m5C_34741
chr19	11553289	+	C	57	36	0.632	0	0	C	36	M	0.502	0.745	0	2E-06	0	361.28	gctgaagagCagagaagagag	m5C_34751
chr19	12814428	-	C	130	73	0.562	0	0	C	73	M	0.476	0.644	0	2E-14	0	694.51	gggaatgattCgactgctg	m5C_34569
chr19	12814442	-	C	127	28	0.22	0	0	T	99	M	0.157	0.3	0	0	0	88.016	actggaaccaCattggagatg	m5C_34548
chr19	12814444	-	C	129	52	0.403	0	0	T	77	M	0.322	0.489	0	4E-15	0	335.34	tgactgtgacCacattggat	m5C_34547
chr19	12814445	-	C	128	44	0.344	0	0	T	84	M	0.267	0.43	0	4E-16	0	235.05	atgactgtgacCacattggga	m5C_34550
chr19	12814460	-	C	124	25	0.202	0	0	T	99	M	0.14	0.281	0	0	0	70.228	gagcaataccCggggatgact	m5C_34544
chr19	12817265	-	C	68	52	0.765	0	0	C	52	M	0.651	0.85	0	9E-07	0	677.5	ctggctgatCtgaatggccc	m5C_34541
chr19	12817266	-	C	69	24	0.348	0	0	T	45	M	0.246	0.466	0	3E-09	0	118.17	actggctgatCtgaatggcc	m5C_34602
chr19	12817271	-	C	84	33	0.393	0	0	T	51	M	0.295	0.5	0	3E-11	0	194.9	ttcgaactggCtgaactgag	m5C_34585
chr19	12817275	-	C	88	34	0.386	0	0	T	54	M	0.291	0.491	0	4E-11	0	198.17	cgtaactggaCtggctgatcc	m5C_34545
chr19	12817279	-	C	82	29	0.354	0	0	T	53	M	0.259	0.462	0	8E-12	0	150.14	atcgctgattCgactggctg	m5C_34530
chr19	12817285	-	C	87	45	0.517	0	0	C	45	M	0.414	0.619	0	6E-10	0	372.37	tgattatcgCgattcgac	m5C_34599
chr19	12817287	-	C	83	31	0.373	0	0	T	52	M	0.277	0.481	0	2E-11	0	171.86	actgattatCtgcgattcgt	m5C_34537
chr19	12817296	-	C	88	33	0.375	0	0	T	55	M	0.281	0.479	0	3E-11	0	185.51	tgatgggaaCtgattatcg	m5C_34584
chr19	12817310	-	C	92	33	0.359	0	0	T	59	M	0.268	0.461	0	8E-13	0	176.99	acactgtggaCtggatgggg	m5C_34561
chr19	12817316	-	C	81	36	0.444	0	0	T	45	M	0.341	0.553	0	7E-11	0	245.66	gtgacgaacCtgggactgtt	m5C_34577
chr19	12817317	-	C	84	58	0.69	0	0	C	58	M	0.585	0.779	0	7E-09	0	678.73	agtgatgacaCtctgactgt	m5C_34598
chr19	12817319	-	C	72	29	0.403	0	0	T	43	M	0.297	0.518	0	4E-10	0	172.38	gaagtgatgaCacctggaact	m5C_34564
chr19	13041089	-	C	112	58	0.518	0	0	C	58	M	0.426	0.608	0	6E-13	0	494.47	ggctgaagaagCtgggggagaa	m5C_34600
chr19	13054554	+	C	35	19	0.543	0	0	C	19	M	0.382	0.695	0	3E-05	0	145.12	gaaggacaaaCaggaccagga	m5C_34516
chr19	13054559	+	C	47	19	0.404	0	0	T	28	M	0.276	0.547	0	1E-06	0	105.03	acaacaggaCgagagcagga	m5C_34526
chr19	13054572	+	C	40	23	0.575	0	0	C	23	M	0.422	0.715	0	3E-06	0	194.1	ggagcagaggCttaaaggagga	m5C_34518
chr19	13054643	+	C	78	32	0.41	0	0	T	46	M	0.308	0.521	0	8E-10	0	197	atgatgaggaCaagaatgagg	m5C_34523
chr19	13054673	+	C	171	86	0.503	0	0	C	86	M	0.429	0.577	0	0	0	737.44	atggagaggaCaaggaggaag	m5C_34529
chr19	13065108	-	C	44	13	0.295	0	0	T	31	M	0.182	0.442	0	1E-07	0	47.204	ggaggaaaaaCagaacggaa	m5C_34571
chr19	13065123	-	C	47	11	0.234	0	0	T	36	M	0.136	0.372	4E-14	4E-08	4E-14	20.086	gcgcaagcgcCtcaaggagga	m5C_34582
chr19	13065124	-	C	41	12	0.293	0	0	T	29	M	0.176	0.445	1E-16	7E-08	1E-16	33.713	agcgaagcgcCtcaaggaggg	m5C_34572
chr19	13947419	-	C	35	17	0.486	0	0	T	18	M	0.33	0.644	0	2E-05	0	112.18	atcacattgcCagggatctcc	m5C_34559
chr19	14524009	-	C	33	16	0.485	0	0											

chr19	24184811 -	C	32	14	0.438	0	0 T	18 M	0.282	0.607	0	9E-06	0	78.862	tatgcttgggCagggcgaagc	m5C_35206
chr19	24184918 -	C	46	26	0.565	0	0 C	26 M	0.422	0.698	0	6E-06	0	219.69	ccttgaggctCtccagttgc	m5C_35179
chr19	24184920 -	C	44	11	0.25	0	0 T	33 M	0.146	0.394	2E-14	4E-08	2E-14	22.132	atcttgaggCtctccagtt	m5C_35146
chr19	24184921 -	C	47	17	0.362	0	0 T	30 M	0.24	0.505	0	6E-07	0	81.484	gatctgaggCtctccagtt	m5C_35121
chr19	24184956 -	C	123	46	0.374	0	0 T	77 M	0.294	0.462	0	7E-16	0	270.03	aagggaaggCtgatgcgtg	m5C_35111
chr19	24184971 -	C	203	68	0.335	0	0 T	135 M	0.274	0.402	0	0	0	372.16	cacttgaggCcaatgaagg	m5C_35209
chr19	24184973 -	C	165	54	0.327	0	0 T	111 M	0.26	0.402	0	0	0	281.14	gccactgggCgcaatgaagg	m5C_35215
chr19	24184981 -	C	55	37	0.673	0	0 C	37 M	0.541	0.782	0	2E-06	0	400.36	gcacgaaggCacttggggc	m5C_35108
chr19	24184988 -	C	67	20	0.299	0	0 T	47 M	0.202	0.417	0	7E-10	0	80.925	ggggctgcacGaaggccact	m5C_35182
chr19	24184990 -	C	64	17	0.266	0	0 T	47 M	0.173	0.385	0	2E-10	0	58.807	caggggctgcCacgaagcca	m5C_35229
chr19	24184994 -	C	47	13	0.277	0	0 T	34 M	0.169	0.418	0	1E-07	0	44.035	gagtcagggCctgcacgaaa	m5C_35186
chr19	24185132 -	C	63	37	0.587	0	0 C	37 M	0.464	0.7	0	8E-08	0	343.47	gctgcgggCtgggggaact	m5C_35227
chr19	24185141 -	C	48	26	0.542	0	0 C	26 M	0.403	0.674	0	6E-06	0	209.51	gctgggttgCtgcgggct	m5C_35200
chr19	24185476 -	C	48	11	0.229	0	0 T	37 M	0.133	0.365	5E-14	4E-08	5E-14	19.471	aaaggcccgCagggaagg	m5C_35143
chr19	24185479 -	C	51	22	0.431	0	0 T	29 M	0.305	0.567	0	7E-08	0	134.2	tggaaaggCggcaggggaag	m5C_35123
chr19	24185480 -	C	57	22	0.386	0	0 T	35 M	0.271	0.516	0	7E-08	0	119.08	ctggaaaggCcgacaggaaa	m5C_35145
chr19	24185481 -	C	57	18	0.316	0	0 T	39 M	0.21	0.445	0	2E-08	0	75.615	gctggaaaggCccggcaggga	m5C_35196
chr19	24185490 -	C	216	71	0.329	0	0 T	145 M	0.27	0.394	0	0	0	382.73	tctggagcggCtggaaaggcc	m5C_35136
chr19	24185493 -	C	259	91	0.351	0	0 T	168 M	0.296	0.411	0	0	0	538.3	ggctctgggaCggctggaag	m5C_35119
chr19	24185499 -	C	301	136	0.452	0	0 T	165 M	0.397	0.508	0	0	0	1078.7	gtgactggcCtgggacggct	m5C_35132
chr19	24185501 -	C	292	95	0.325	0	0 T	197 M	0.274	0.381	0	0	0	520.93	ccgtgactggCtctgggaagg	m5C_35222
chr19	24185505 -	C	249	57	0.229	0	0 T	192 M	0.181	0.285	0	0	0	206.44	tgcgctgggaCtgcctctggg	m5C_35171
chr19	24185510 -	C	150	41	0.273	0	0 T	109 M	0.208	0.35	0	0	0	170.84	gggtgctgcCgtgactggct	m5C_35192
chr19	24185511 -	C	130	31	0.238	0	0 T	99 M	0.173	0.319	0	0	0	107.5	tgggtgctgcCgtgactggc	m5C_35224
chr19	24185513 -	C	97	34	0.351	0	0 T	63 M	0.263	0.45	0	1E-12	0	178.78	tgggtgctgcCgtgacttg	m5C_35212
chr19	24185524 -	C	51	12	0.235	0	0 T	39 M	0.14	0.368	3E-15	9E-10	4E-15	24.331	tgcattccaCtgggggctg	m5C_35115
chr19	24185526 -	C	38	11	0.289	0	0 T	27 M	0.17	0.448	2E-15	3E-06	2E-15	27.449	gatgcattcCacttgggtgc	m5C_35240
chr19	24185527 -	C	40	17	0.425	0	0 T	23 M	0.285	0.578	0	6E-07	0	96.931	agatgctattCcaactgggtg	m5C_35245
chr19	24185790 -	C	163	47	0.288	0	0 T	116 M	0.224	0.362	0	0	0	210.85	gggcgtgaaaCcgtaagact	m5C_35174
chr19	24185797 -	C	173	71	0.41	0	0 T	102 M	0.34	0.485	0	0	0	482.55	ttcaagaaggCggaaaccgt	m5C_35141
chr19	24185812 -	C	37	12	0.444	10	0.27 T	15 M	0.276	0.627	0	0.0002	0	66.205	actttgaagaCgcagtccaag	m5C_35202
chr19	24185821 -	C	530	228	0.43	0	0 T	302 M	0.389	0.473	0	0	0	1772.4	ttagaaagaaCtttgaagacg	m5C_35221
chr19	24185844 -	C	131	29	0.221	0	0 T	102 M	0.159	0.3	0	0	0	92.097	tcaacaagtaCttagaaggaa	m5C_35237
chr19	24185973 -	C	62	25	0.403	0	0 T	37 M	0.29	0.527	0	4E-09	0	145.12	cgggtggaggCcttagcagc	m5C_35199
chr19	24185990 -	C	82	41	0.5	0	0 CT	41 M	0.394	0.606	0	3E-10	0	323.27	cccagccagcCtgggaacgg	m5C_35139
chr19	24185991 -	C	54	19	0.352	0	0 T	35 M	0.238	0.485	0	2E-08	0	90.527	gccacgcagCctgggacgg	m5C_35189
chr19	24187261 -	C	46	17	0.37	0	0 T	29 M	0.245	0.514	0	6E-07	0	83.38	aagaatgcagCagctgtgag	m5C_35168
chr19	24187264 -	C	38	12	0.316	0	0 T	26 M	0.191	0.475	0	5E-06	0	45.803	atgaagaatgCagcacactgt	m5C_35103
chr19	36066545 +	C	92	52	0.565	0	0 C	52 M	0.463	0.662	0	1E-10	0	481.85	ttgatatagaCagcaggacgg	m5C_35330
chr19	36066548 +	C	106	61	0.575	0	0 C	61 M	0.48	0.665	0	3E-11	0	586.04	atatagacagCaggacggagg	m5C_35319
chr19	36066553 +	C	95	72	0.758	0	0 C	72 M	0.663	0.833	0	3E-09	0	954.48	gacacaggaCggggccatg	m5C_35311
chr19	36540055 +	C	267	80	0.3	0	0 T	187 M	0.248	0.357	0	0	0	396.54	tggagctggCcgagtgtttg	m5C_35327
chr19	36540056 +	C	266	57	0.215	1	0.004 T	208 M	0.17	0.268	0	0	0	193.66	ggagctggcCgaggtgtgtg	m5C_35316
chr19	38795565 +	C	37	28	0.757	0	0 C	28 M	0.599	0.866	0	0.0002	0	335.34	aggaagaaggCaaagaaggaa	m5C_35411
chr19	39340555 -	C	36	12	0.333	0	0 T	24 M	0.202	0.497	0	5E-06	0	48.515	gcggctgggCagagggcagca	m5C_35421
chr19	39340561 -	C	34	14	0.412	0	0 T	20 M	0.264	0.578	0	9E-06	0	73.824	gcgtggcggCtgggacagag	m5C_35425
chr19	39340564 -	C	37	10	0.27	0	0 T	27 M	0.154	0.43	7E-14	2E-06	7E-14	20.282	ggcggcggcCggctggagca	m5C_35438
chr19	39340570 -	C	38	23	0.605	0	0 C	23 M	0.447	0.744	0	8E-05	0	205.7	ggagaagcgcCgtcgccgct	m5C_35440
chr19	39340573 -	C	31	12	0.387	0	0 T	19 M	0.237	0.562	0	5E-06	0	56.959	ggcggagaagCggcgtcgccg	m5C_35439
chr19	39877126 -	C	37	15	0.429	2	0.054 T	20 M	0.28	0.591	0	1E-05	0	83.953	aaagtggggCtcaaggaaat	m5C_35434
chr19	43910975 -	C	58	46	0.793	0	0 C	46 M	0.672	0.877	0	7E-06	0	618.52	gtttaaaactCaaaagggtcag	m5C_34912
chr19	45381734 +	C	45	10	0.222	0	0 T	35 M	0.125	0.363	7E-13	2E-08	8E-13	15.216	ttccattgaaCcagatggcaa	m5C_34933
chr19	45381735 +	C	47	14	0.298	0	0 T	33 M	0.187	0.44	0	2E-07	0	52.223	cccatggaaCagatggcaag	m5C_34934
chr19	45381742 +	C	53	20	0.377	0	0 T	33 M	0.259	0.512	0	3E-08	0	103.74	aaccagatggCaaagatgagg	m5C_34928
chr19	45981916 -	C	33	15	0.455	0	0 T	18 M	0.298	0.62	0	1E-05	0	89.528	gcttgggggCaggcttcaa	m5C_34957
chr19	45981924 -	C	37	16	0.432	0	0 T	21 M	0.287	0.591	0	2E-05	0	91.749	cctcaggtgCtggggcagc	m5C_34963
chr19	45981933 -	C	39	19	0.487	0	0 T	20 M	0.339	0.638	0	3E-05	0	128.69	ccggtgatcCtcaagtgtct	m5C_34938
chr19	45981934 -	C	38	8	0.211	0	0 T	30 M	0.111	0.363	1E-10	7E-07	1E-10	8.7725	cccggatgatCctcaggggc	m5C_34962
chr19	46142272 -	C	51	12	0.235	0	0 T	39 M	0.14	0.368	3E-15	9E-10	4E-15	24.331	acacggcctgCagagaaggcag	m5C_35502
chr19	46142275 -	C	54	33	0.611	0	0 C	33 M	0.478	0.73	0	9E-07	0	315.4	agcacacggCtgcagagaagg	m5C_35499
chr19	46142279 -	C	52	27	0.519	0	0 C	27 M	0.387	0.649	0	2E-07	0	208.9	gcaaaagacaCggcctgcaga	m5C_35480
chr19	46142281 -	C	51	22	0.431	0	0 T	29 M	0.305	0.567	0	7E-08	0	134.2	gagcaaaagcaCaggcctgcga	m5C_35472
chr19	47858242 -	C	37	19	0.514	0	0 C	19 M	0.359	0.666	0	3E-05	0	136.4	gggtaccagCctggcccttg	m5C_35497
chr19	48427137 +	C	59	12	0.203	0	0 T	47 M	0.12	0.323	3E-14	9E-10	3E-14	19.611	ccacatgggCggaaaaaagg	m5C_35931
chr19	48448273 +	C	41	11	0.275	1	0.024 T	29 M	0.161	0.428	4E-15	3E-06	5E-15	25.45	gcttggrccaCatgggctgga	m5C_35899
chr19	49120041 -	C	37	12	0.324	0	0 T	25 M	0.196	0.485	0	5E-06	0	47.119	aaacaagcgcCggtgtgttg	m5C_35964
chr19	49120044 -	C	37	25	0.676	0	0 C	25 M	0.515	0.804	0	0.0001	0	257.32	gaaaaaaggaCggcgtgggt	m5C_35968
chr19	49120049 -	C	35	13	0.371	0	0 T	22 M	0.232	0.537	0	7E-06	0	60.231	ggcgggaaaaCaagacggcgc	m5C_35963
chr19	49120057 -	C	39	27	0.692	0	0 C	27 M	0.536	0.814	0	0.0001	0	289.32	gcttctggcCgggaaaaacaa	m5C_35971
chr19	49120058 -	C	38	24	0.649	1	0.026 C	24 M	0.488	0.782	0	9E-05	0	234.04	agttctctggCgggaaaaaca	m5C_35973
chr19	49993889 +	C	32	22	0.688	0	0 C	22 M	0.514	0.82	0	6E-05	0	226.31	gttagagaaCttctccact	m5C_35918
chr19	49993892 +	C	31	24	0.774	0	0 C	24 M	0.602	0.886	0	9E-05	0	288.9	atgagaactCtccactcac	m5C_35881
chr19	49993894 +	C	32	22	0.688	0	0 C	22 M	0.514	0.82	0	6E-05	0	226.31	gagaacttCtccactacat	m5C_35888
chr19	49993896 +	C	34	25	0.735	0	0 C	25 M	0.569	0.854	0	0.0001	0	284.41	gaacttctccCactcacatc	m5C_35894
chr19	49993898 +	C	31	20	0.645	0	0 C	20 M	0.469	0.789	0	4E-05	0	187.79	acttctgacaCtcaattcga	m5C_35945
chr19	49994177 +	C	77	18	0.234	0	0 T	59 M	0.153	0.34	0	4E-12	0	55.186	ccatgatgtCcgcaactacc	m5C_35887
chr19	49994221 +	C	91	49	0.538	0	0 C	49 M	0.437	0.637	0	6E-11	0	427.83	gcgactggtCtggagcgcca	m5C_35932
chr19	49994227 +	C	78	18	0.231	0	0 T	60 M	0.151	0.336	0	4E-12	0	54.451		

chr19	51302737 -	C	46	24	0.545	2	0.043	C	24	M	0.401	0.683	0	4E-06	0	192.32	ggacacgggGccccgggac	m5C_35261
chr19	51302757 -	C	41	23	0.561	0	0	C	23	M	0.41	0.701	0	3E-06	0	188.79	tgggtccgaCtgccactgag	m5C_35280
chr19	51302760 -	C	39	19	0.487	0	0	T	20	M	0.339	0.638	0	3E-05	0	128.69	cactgggtcCgactgccact	m5C_35268
chr19	51302761 -	C	41	18	0.439	0	0	T	23	M	0.299	0.59	0	8E-07	0	107.6	gcactgggtCcgactgccac	m5C_35253
chr19	51302763 -	C	42	20	0.476	0	0	T	22	M	0.334	0.623	0	1E-06	0	133.44	cagcactgggCtccgactgcc	m5C_35290
chr19	51302770 -	C	40	16	0.4	0	0	T	24	M	0.263	0.554	0	2E-05	0	84.314	tgatgtccagCactgggtctcc	m5C_35294
chr19	51305603 -	C	93	31	0.333	0	0	T	62	M	0.246	0.434	0	4E-13	0	152.41	cttttgacCctggggctctg	m5C_35277
chr19	51305604 -	C	96	51	0.531	0	0	C	51	M	0.432	0.628	0	9E-11	0	440.8	accttgacaCctggggctct	m5C_35291
chr19	51305606 -	C	93	23	0.247	0	0	T	70	M	0.171	0.344	0	1E-14	0	78.578	ggactttgaCacctgggggt	m5C_35270
chr19	51305612 -	C	103	52	0.505	0	0	C	52	M	0.41	0.599	0	4E-12	0	426.27	accccgaggCtttgacacct	m5C_35271
chr19	51305613 -	C	103	31	0.301	0	0	T	72	M	0.221	0.395	0	7E-15	0	136.93	caccccgaggCtttgacacct	m5C_35295
chr19	51305619 -	C	84	25	0.298	0	0	T	59	M	0.21	0.402	0	2E-12	0	105.22	acagggaccCaggacctttt	m5C_35252
chr19	51305623 -	C	68	20	0.294	0	0	T	48	M	0.199	0.411	0	7E-10	0	79.675	ggacacagtGcacccgaggac	m5C_35288
chr19	51305639 -	C	48	22	0.458	0	0	T	26	M	0.326	0.597	0	2E-06	0	143.33	ctctgatcacCcttgaggaca	m5C_35279
chr19	53284658 +	C	46	25	0.543	0	0	C	25	M	0.402	0.678	0	4E-06	0	200.9	ggaggaggagCgtgggtctga	m5C_35014
chr19	55390060 -	C	292	199	0.682	0	0	C	199	M	0.626	0.732	0	0	0	2491.5	tcggatctCtaaggagtgt	m5C_35864
chr19	55390063 -	C	290	191	0.659	0	0	C	191	M	0.602	0.711	0	0	0	2300.7	aagtcggatCtctaaggag	m5C_35875
chr2	1607499 -	C	54	23	0.426	0	0	T	31	M	0.303	0.558	0	9E-08	0	139.53	tgggtatcggCggggggatcc	m5C_3079
chr2	26357845 +	C	36	9	0.25	0	0	T	27	M	0.138	0.411	2E-12	1E-06	2E-12	14.476	atgtatgatCagcagtggag	m5C_3786
chr2	26357848 +	C	47	20	0.426	0	0	T	27	M	0.295	0.567	0	1E-06	0	118.05	tagatatcagCagtggaggag	m5C_3767
chr2	26357865 +	C	41	18	0.439	0	0	T	23	M	0.299	0.59	0	8E-07	0	107.6	ggaggcggaCaggctgggaag	m5C_3781
chr2	27274092 +	C	66	44	0.667	0	0	C	44	M	0.547	0.768	0	3E-07	0	480.97	ggggattagCtcaatggga	m5C_3782
chr2	27274094 +	C	66	43	0.652	0	0	C	43	M	0.531	0.755	0	2E-07	0	456.76	gggtattgtCaaatggtaga	m5C_3787
chr2	27603889 -	C	33	23	0.697	0	0	C	23	M	0.527	0.826	0	8E-05	0	242.24	gcggctgccCctcgcccttc	m5C_3806
chr2	27603891 -	C	36	9	0.25	0	0	T	27	M	0.138	0.411	2E-12	1E-06	2E-12	14.476	tcgggtctgcCctcgccccc	m5C_3798
chr2	27603895 -	C	36	26	0.722	0	0	C	26	M	0.56	0.842	0	0.0001	0	291.24	gggtcgcggCtgcctctgc	m5C_3795
chr2	27603898 -	C	36	9	0.25	0	0	T	27	M	0.138	0.411	2E-12	1E-06	2E-12	14.476	gcgggtctgcCgggtcccttc	m5C_3807
chr2	27606873 -	C	92	28	0.304	0	0	T	64	M	0.22	0.405	0	1E-13	0	123.05	ctgaagaagCgatagaagaag	m5C_3810
chr2	27606892 -	C	59	36	0.61	0	0	C	36	M	0.483	0.724	0	2E-06	0	347.52	gaggatgacaCcgaggagact	m5C_3800
chr2	27606894 -	C	66	40	0.606	0	0	C	40	M	0.485	0.715	0	1E-07	0	388.39	atgaggatgaCaccgaggagg	m5C_3812
chr2	27606954 -	C	46	21	0.457	0	0	T	25	M	0.322	0.598	0	2E-06	0	135.05	ggcaggaatgCagcaggaag	m5C_3802
chr2	27607546 -	C	107	26	0.243	0	0	T	81	M	0.172	0.332	0	7E-16	0	89.21	aagaaggagaCaggaggtaa	m5C_3813
chr2	29136544 +	C	53	29	0.547	0	0	C	29	M	0.415	0.673	0	4E-07	0	240.43	tggatgagCcttaatatgt	m5C_4123
chr2	29136561 +	C	49	27	0.551	0	0	C	27	M	0.413	0.681	0	7E-06	0	223.1	attgggtttCgactactga	m5C_4122
chr2	29136566 +	C	49	27	0.551	0	0	C	27	M	0.413	0.681	0	7E-06	0	223.1	gggttcactCactgagatga	m5C_4130
chr2	29136568 +	C	49	27	0.551	0	0	C	27	M	0.413	0.681	0	7E-06	0	223.1	tttcgactaCtgaagataa	m5C_4128
chr2	36647854 +	C	37	25	0.676	0	0	C	25	M	0.515	0.804	0	0.0001	0	257.32	gcagagaaggCatagggaacat	m5C_4167
chr2	36647862 +	C	34	23	0.676	0	0	C	23	M	0.508	0.809	0	8E-05	0	233.88	ggcatagggCatggggtaag	m5C_4170
chr2	45508265 +	C	39	30	0.769	0	0	C	30	M	0.617	0.874	0	0.0002	0	369.98	gacgcggcgCtgaatggag	m5C_3525
chr2	47507895 -	C	52	41	0.788	0	0	C	41	M	0.66	0.878	0	3E-06	0	540.93	tcgctgacaCaattacaacg	m5C_3845
chr2	54871721 +	C	67	22	0.328	0	0	T	45	M	0.228	0.447	0	1E-09	0	100.28	gaaaaagcaaCaggcaaggg	m5C_3891
chr2	54886309 +	C	45	20	0.444	0	0	T	25	M	0.309	0.588	0	1E-06	0	123.75	actggaaaggCgcagacagca	m5C_3899
chr2	54886315 +	C	48	18	0.375	0	0	T	30	M	0.252	0.516	0	8E-07	0	90.774	agggcgagaCagcaagaagg	m5C_3870
chr2	54886318 +	C	47	17	0.362	0	0	T	30	M	0.24	0.505	0	6E-07	0	81.484	gcgcagacagCaagaaggaga	m5C_3875
chr2	55277338 -	C	71	33	0.465	0	0	T	38	M	0.354	0.58	0	1E-09	0	233.36	agcccgaggCgaaggaggag	m5C_3908
chr2	55277345 -	C	39	14	0.359	0	0	T	25	M	0.227	0.516	0	9E-06	0	63.677	ggaggggagCcgaggacgag	m5C_3910
chr2	71654044 +	C	32	8	0.25	0	0	T	24	M	0.133	0.421	2E-11	7E-07	2E-11	11.283	cgctggtaaCtgggaatga	m5C_4438
chr2	72949096 +	C	31	17	0.548	0	0	C	17	M	0.378	0.708	0	2E-05	0	128.42	atgcatcacCtggcatatga	m5C_4553
chr2	72949105 +	C	52	12	0.231	0	0	T	40	M	0.137	0.361	4E-15	9E-10	5E-15	23.637	cctggcatgCagtaacctca	m5C_4550
chr2	72949110 +	C	56	13	0.232	0	0	T	43	M	0.141	0.358	4E-16	2E-09	5E-16	28.14	cattgcagtaCctccaggaa	m5C_4548
chr2	72949113 +	C	57	25	0.439	0	0	T	32	M	0.318	0.567	0	2E-07	0	158.86	tgcagtaactCcaaggatgtg	m5C_4557
chr2	72949114 +	C	59	12	0.203	0	0	T	47	M	0.12	0.323	3E-14	9E-10	3E-14	19.611	gcagtaacctCaggaaatggg	m5C_4547
chr2	86259406 -	C	45	11	0.244	0	0	T	34	M	0.142	0.387	2E-14	4E-08	2E-14	21.411	caaggagaagCaggagaaggga	m5C_4494
chr2	86363024 +	C	49	29	0.592	0	0	C	29	M	0.452	0.718	0	1E-05	0	262.43	ggggcgaggCctcagctgag	m5C_4476
chr2	115695115 -	C	56	29	0.518	0	0	C	29	M	0.39	0.643	0	4E-07	0	226.26	ggcggtgaacCttaagggtaa	m5C_5659
chr2	115695116 -	C	81	37	0.457	0	0	T	44	M	0.353	0.565	0	1E-10	0	261.02	ggcggtgaacCttaagggtga	m5C_5656
chr2	115695123 -	C	406	322	0.793	0	0	C	322	M	0.751	0.83	0	0	0	4836.7	tccaagggcggtgaaccttc	m5C_5658
chr2	115695131 -	C	440	158	0.359	0	0	T	282	M	0.316	0.405	0	0	0	997.49	agagagagtCaagggggtg	m5C_5660
chr2	115695147 -	C	113	42	0.372	0	0	T	71	M	0.288	0.464	0	8E-15	0	242.07	ttggaagaaCtttgagaaga	m5C_5657
chr2	131058804 +	C	43	29	0.674	0	0	C	29	M	0.525	0.795	0	1E-05	0	304.59	ttgtgtgtgCgtcgacact	m5C_5199
chr2	133010728 -	C	36	9	0.25	0	0	T	27	M	0.138	0.411	2E-12	1E-06	2E-12	14.476	gtctgagcgCacttgcacat	m5C_6788
chr2	133010731 -	C	46	10	0.217	0	0	T	36	M	0.123	0.356	1E-12	2E-08	1E-12	14.731	cctgtctgagCgtacttgc	m5C_6833
chr2	133010736 -	C	50	24	0.438	0	0	T	26	M	0.348	0.615	0	1E-07	0	167.03	ctatgcctgtCtgaagctcac	m5C_6592
chr2	133010740 -	C	48	25	0.521	0	0	C	25	M	0.383	0.655	0	4E-06	0	191.64	agggctatgcCtgtctgagcg	m5C_6868
chr2	133010857 -	C	135	84	0.622	0	0	C	84	M	0.538	0.7	0	2E-13	0	904.05	ggggatcactCagctctctgg	m5C_6839
chr2	133010859 -	C	172	125	0.727	0	0	C	125	M	0.656	0.788	0	9E-16	0	1639.3	tgggtatataCtcagctcttg	m5C_6656
chr2	133010861 -	C	184	119	0.647	0	0	C	119	M	0.575	0.712	0	0	0	1369.3	aggggggatCactagctcc	m5C_6671
chr2	133010876 -	C	230	102	0.443	0	0	T	128	M	0.381	0.508	0	0	0	776.68	ccttgatgaCtttagtgtt	m5C_6805
chr2	133012252 -	C	78	59	0.756	0	0	C	59	M	0.651	0.838	0	1E-07	0	767.71	tgcacggcgCtatactgact	m5C_6678
chr2	133012254 -	C	76	55	0.724	0	0	C	55	M	0.614	0.812	0	8E-08	0	675.67	gttcacggcgCgtatactga	m5C_6664
chr2	133012256 -	C	84	60	0.714	0	0	C	60	M	0.61	0.8	0	9E-09	0	731.97	gggttcacgCgcgtactact	m5C_6590
chr2	133012258 -	C	83	60	0.723	0	0	C	60	M	0.618	0.808	0	9E-09	0	742.06	cagggttgcCgcgcgtaca	m5C_6731
chr2	133012260 -	C	77	51	0.662	0	0	C	51	M	0.551	0.758	0	4E-08	0	562.27	tccagggtcgCacggcgcta	m5C_6706
chr2	133012268 -	C	66	39	0.591	0	0	C	39	M	0.47	0.701	0	1E-07	0	366.98	cttaaatgcCagggtctgac	m5C_6587
chr2	133012269 -	C	59	32	0.542	0	0	C	32	M	0.417	0.663	0	7E-07	0	266.61	cctta	

chr2	133012744	-	C	155	57	0.368	0	0	T	98	M	0.296	0.446	0	0	0	337.31	gaacgaagcCggaggttcga	m5C_6817
chr2	133012851	-	C	51	39	0.765	0	0	C	39	M	0.632	0.86	0	2E-06	0	493.25	agagggacggCcggggcatt	m5C_6842
chr2	133013105	-	C	99	65	0.657	0	0	C	65	M	0.559	0.743	0	1E-09	0	726.38	aaagtgtgtCagttaaaaag	m5C_6596
chr2	133013422	-	C	31	10	0.323	0	0	T	21	M	0.186	0.499	7E-15	2E-06	8E-15	26.273	atgacctattCgaatgtctgc	m5C_6538
chr2	133014841	-	C	50	10	0.2	0	0	T	40	M	0.112	0.33	3E-12	2E-10	3E-12	13.024	accggtttcCgggcacggg	m5C_6540
chr2	133014856	-	C	44	14	0.318	0	0	T	30	M	0.2	0.466	0	2E-07	0	55.98	cgaccgggtcCgacgaccgg	m5C_6795
chr2	133014857	-	C	39	24	0.615	0	0	C	24	M	0.459	0.751	0	9E-05	0	220.31	gcgacgggtcCgacgaccgt	m5C_6780
chr2	133015207	-	C	38	12	0.316	0	0	T	26	M	0.191	0.475	0	5E-06	0	45.803	agaggtgtcCttgggttac	m5C_6782
chr2	133015208	-	C	38	27	0.711	0	0	C	27	M	0.552	0.83	0	0.0001	0	298.31	gagaggtgtcCttggggga	m5C_6694
chr2	133015220	-	C	74	34	0.459	0	0	T	40	M	0.351	0.572	0	1E-09	0	238.5	ctctagcgatCtgagaggtgt	m5C_6572
chr2	133032466	-	C	31	9	0.29	0	0	T	22	M	0.161	0.466	4E-13	1E-06	4E-13	18.015	attagccaggCctgggtcgt	m5C_6663
chr2	133037880	-	C	56	40	0.714	0	0	C	40	M	0.585	0.816	0	3E-06	0	468.2	tgaacttgaCacaagctgg	m5C_6589
chr2	133037885	-	C	71	55	0.775	0	0	C	55	M	0.665	0.856	0	8E-08	0	731.33	gggtgtgactCtggaacaaag	m5C_6864
chr2	133037887	-	C	78	38	0.487	0	0	T	40	M	0.379	0.596	0	4E-09	0	288.41	gggtgttgaCtctggacaca	m5C_6703
chr2	133038365	-	C	47	10	0.213	0	0	T	37	M	0.12	0.349	1E-12	2E-08	1E-12	14.271	aattgtgtcCcccgagagag	m5C_6566
chr2	133038367	-	C	50	17	0.34	0	0	T	33	M	0.224	0.478	0	6E-07	0	76.285	ggaatgggtCgccccgagag	m5C_6773
chr2	133038441	-	C	42	14	0.333	0	0	T	28	M	0.21	0.484	0	2E-07	0	58.834	gtgactgaccCtgggaagca	m5C_6536
chr2	133038442	-	C	40	14	0.35	0	0	T	26	M	0.221	0.505	0	2E-07	0	61.976	tgtgactgacCctgggaagc	m5C_6594
chr2	133038447	-	C	48	12	0.25	0	0	T	36	M	0.149	0.388	1E-15	7E-08	1E-15	26.634	ggaaatgacCtgacccttga	m5C_6680
chr2	133038458	-	C	39	9	0.231	0	0	T	30	M	0.126	0.383	5E-12	1E-06	5E-12	12.874	gcgtccaggCggaaatgtga	m5C_6652
chr2	133038509	-	C	44	35	0.795	0	0	C	35	M	0.655	0.888	0	3E-05	0	458.49	gagttgggtCagatccccga	m5C_6815
chr2	133038877	-	C	37	15	0.405	0	0	T	22	M	0.263	0.565	0	1E-05	0	79.039	atgggagcgcCaggggcaat	m5C_6617
chr2	133038880	-	C	69	26	0.377	0	0	T	43	M	0.272	0.495	0	6E-09	0	141.35	tggatgggagCggcaggggca	m5C_6810
chr2	133038989	-	C	609	420	0.69	0	0	C	420	M	0.652	0.725	0	0	0	5475.3	tgggaatccCtaaggaggtgt	m5C_6801
chr2	133038991	-	C	676	452	0.669	0	0	C	452	M	0.632	0.703	0	0	0	5715.9	agttggaatCgctaaggaggt	m5C_6534
chr2	133038992	-	C	735	524	0.713	0	0	C	524	M	0.679	0.744	0	0	0	7117.8	aaagtggatCcgctaaaggag	m5C_6542
chr2	133039007	-	C	828	554	0.669	0	0	C	554	M	0.636	0.7	0	0	0	7050.4	ggatgggtcCattggaatgt	m5C_6646
chr2	133039008	-	C	837	512	0.613	2	0.002	C	512	M	0.58	0.646	0	0	0	5936.1	aggaatgggtCcatgggaagt	m5C_6768
chr2	133039019	-	C	597	334	0.559	0	0	C	334	M	0.519	0.599	0	0	0	3469.5	atatagacagCaggatgtgt	m5C_6559
chr2	133039022	-	C	472	253	0.536	0	0	C	253	M	0.491	0.581	0	0	0	2484	ttagtatagaCagcaggatgg	m5C_6618
chr2	133039177	-	C	31	19	0.613	0	0	C	19	M	0.438	0.763	0	3E-05	0	166.53	ggtaagaagCttgctgtgt	m5C_6699
chr2	133039178	-	C	32	9	0.281	0	0	T	23	M	0.156	0.454	5E-13	1E-06	6E-13	17.198	gggaagaagCctgtgtgtgt	m5C_6519
chr2	136691493	-	C	51	32	0.627	0	0	C	32	M	0.49	0.747	0	7E-07	0	313.76	cggtctgaggCagaaggagaa	m5C_4817
chr2	136691499	-	C	51	18	0.353	0	0	T	33	M	0.236	0.49	0	2E-08	0	85.084	cgctgtcggCtgagccagaa	m5C_4816
chr2	136691500	-	C	49	19	0.388	0	0	T	30	M	0.264	0.528	0	1E-06	0	100.43	tgtgtgtcggCtgaaggcaga	m5C_4814
chr2	136691503	-	C	52	20	0.385	0	0	C	32	M	0.265	0.52	0	3E-08	0	105.88	tgtgtgtgtCggcctgaggc	m5C_4819
chr2	136691508	-	C	49	17	0.347	0	0	T	32	M	0.229	0.487	0	6E-07	0	77.942	ctggatgatCtgttcggct	m5C_4818
chr2	149583272	-	C	52	14	0.269	0	0	T	38	M	0.168	0.403	0	3E-09	0	46.953	tgcagtacctCagaagatgt	m5C_4836
chr2	149583275	-	C	53	13	0.245	0	0	T	40	M	0.149	0.376	2E-16	2E-09	2E-16	30.388	tattgcagaCctccaggaa	m5C_4834
chr2	169020359	-	C	34	20	0.588	0	0	C	20	M	0.422	0.736	0	4E-05	0	168.89	aatacatgtCaaccgaggag	m5C_4980
chr2	211518768	+	C	40	15	0.375	0	0	T	25	M	0.242	0.53	0	3E-07	0	72.668	gggtgctgaCaaaatttgt	m5C_5514
chr2	211518786	+	C	144	35	0.243	0	0	T	109	M	0.18	0.319	0	0	0	126.19	gttgaagggtCccgagaagga	m5C_5523
chr2	211518788	+	C	160	34	0.212	0	0	T	126	M	0.156	0.282	0	0	0	106.24	tgaagggtccCgagaagtga	m5C_5521
chr2	211518805	+	C	239	101	0.423	0	0	T	138	M	0.362	0.486	0	0	0	730.59	tagaaatggaCgctgtggca	m5C_5511
chr2	211518807	+	C	232	83	0.358	0	0	T	149	M	0.299	0.421	0	0	0	496.1	gaaatggagCtgtgtggcaca	m5C_5520
chr2	211518814	+	C	167	48	0.287	0	0	T	119	M	0.224	0.36	0	0	0	215.21	acgctgtgtCaaagatggaa	m5C_5512
chr2	213403502	+	C	31	12	0.387	0	0	T	19	M	0.237	0.562	0	5E-06	0	56.959	tccgtgtgtCgcttggcgt	m5C_5377
chr2	230045489	-	C	194	135	0.696	0	0	C	135	M	0.628	0.756	0	0	0	1695.2	cggagatgggCgaggtggagt	m5C_6023
chr2	230045499	-	C	314	213	0.678	0	0	C	213	M	0.625	0.728	0	0	0	2661.6	tccgaggtggCggagatgggc	m5C_6021
chr2	230045507	-	C	300	200	0.667	0	0	C	200	M	0.612	0.718	0	0	0	2446	tccccgaatCcgaggtgggg	m5C_6016
chr2	230045508	-	C	276	180	0.652	0	0	C	180	M	0.594	0.706	0	0	0	2139.3	atccccgaatCcgaggtgggc	m5C_6029
chr2	230045513	-	C	179	109	0.609	0	0	C	109	M	0.536	0.677	0	0	0	1168.2	ttcagatcccCgaatccggag	m5C_6049
chr2	230045514	-	C	166	113	0.681	0	0	C	113	M	0.606	0.747	0	3E-15	0	1370.5	gttcagatccCggaatccgga	m5C_6017
chr2	230045515	-	C	155	95	0.613	0	0	C	95	M	0.534	0.686	0	3E-15	0	1015.3	gggtcagatCCcggaatccgg	m5C_6014
chr2	230045516	-	C	152	113	0.743	0	0	C	113	M	0.669	0.806	0	4E-14	0	1511	gggttcagatCcccgaatccg	m5C_6012
chr2	230045521	-	C	133	91	0.684	0	0	C	91	M	0.601	0.757	0	5E-13	0	1093.8	gagtcgggtCagatccccga	m5C_6051
chr2	230045527	-	C	120	85	0.708	0	0	C	85	M	0.622	0.782	0	7E-11	0	1056.6	gaaggagagCgggttcagat	m5C_6047
chr2	230045577	-	C	87	68	0.782	0	0	C	68	M	0.684	0.855	0	3E-08	0	930.11	agcgccgtcCgaaggagacag	m5C_6045
chr2	230045578	-	C	91	57	0.626	0	0	C	57	M	0.524	0.719	0	3E-10	0	597.08	gagcgccgtCggaaggagaca	m5C_6036
chr2	230045582	-	C	105	73	0.695	0	0	C	73	M	0.602	0.775	0	2E-10	0	878.33	gggcgaagcgcGttccgaagg	m5C_6050
chr2	230045583	-	C	97	62	0.639	0	0	C	62	M	0.54	0.728	0	7E-10	0	669.59	tgggcgaagcCcggtccgaag	m5C_6028
chr2	230045585	-	C	103	58	0.563	0	0	C	58	M	0.467	0.655	0	1E-11	0	541.44	gatggcgagCagcgttccga	m5C_6035
chr2	230045589	-	C	109	68	0.624	0	0	C	68	M	0.53	0.709	0	9E-11	0	721.01	gagagatgggCgaagccgtt	m5C_6027
chr2	230045601	-	C	90	64	0.711	0	0	C	64	M	0.61	0.795	0	9E-10	0	781.26	tcagtcgggtCtgaagatgg	m5C_6015
chr2	230045602	-	C	83	46	0.554	0	0	C	46	M	0.447	0.656	0	8E-10	0	411.47	gtcagtcggCtgaagatgat	m5C_6041
chr2	230045606	-	C	67	43	0.642	0	0	C	43	M	0.522	0.746	0	2E-07	0	449.08	acgggtcagCggtcctgaga	m5C_6031
chr2	230045673	-	C	46	21	0.457	0	0	T	25	M	0.322	0.598	0	2E-06	0	135.05	gagagaggggCccgtgcttg	m5C_6033
chr2	231183792	+	C	41	23	0.561	0	0	C	23	M	0.41	0.701	0	3E-06	0	188.79	acactgggtCtgcaggtcaa	m5C_5941
chr2	231736691	-	C	34	16	0.471	0	0	T	18	M	0.315	0.633	0	2E-05	0	100.64	ctaagtgaactCaggacaggcc	m5C_6026
chr2	232322446	-	C	65	46	0.708	0	0	C	46	M	0.588	0.804	0	4E-07	0	540.99	aagcaggagaaCagagatcgt	m5C_7360
chr2	232322467	-	C	66	36	0.545	0	0	C	36	M	0.426	0.66	0	6E-08	0	306.83	gcagagaaaaCtttgaagaa	m5C_7368
chr2	232322488	-	C	61	15	0.246	0	0	T	46	M	0.155	0.367	0	6E-11	0	46.52	gaatttaagaCagaagtgtat	m5C_7387
chr2	232325082	-	C	61	15	0.246	0	0	T	46	M	0.155	0.367	0	6E-11	0	46.52	t	

chr20	2634884	+	C	41	9	0.22	0	0	T	32	M	0.12	0.367	8E-12	1E-08	9E-12	11.962	cgaatcaaatCtgcgaatccc	m5C_35995
chr20	2634902	+	C	32	13	0.406	0	0	T	19	M	0.255	0.577	0	7E-06	0	66.35	ccccctgaggCaatcactgat	m5C_35991
chr20	2634906	+	C	33	13	0.394	0	0	T	20	M	0.247	0.563	0	7E-06	0	64.175	tgagtgcaatCactgatgctc	m5C_35998
chr20	2634908	+	C	32	12	0.375	0	0	T	20	M	0.229	0.547	0	5E-06	0	55.041	agtgcaatcaCtgcgtctcc	m5C_36009
chr20	2634915	+	C	34	12	0.353	0	0	T	22	M	0.215	0.521	0	5E-06	0	51.571	tcactgatgCtccatgctc	m5C_35992
chr20	2634917	+	C	32	14	0.438	0	0	T	18	M	0.282	0.607	0	9E-06	0	78.862	actgatgctCcaatgctctg	m5C_35987
chr20	2634918	+	C	32	13	0.406	0	0	T	19	M	0.255	0.577	0	7E-06	0	66.35	ctgatgctcCattgctctga	m5C_36001
chr20	2634923	+	C	35	16	0.457	0	0	T	19	M	0.305	0.618	0	2E-05	0	97.49	gctccatgCtctgagcaat	m5C_35984
chr20	2634925	+	C	31	11	0.355	0	0	T	20	M	0.211	0.531	1E-16	3E-06	1E-16	37.059	ctccatgctCtgcgaatgc	m5C_35996
chr20	2637602	+	C	205	57	0.278	0	0	T	148	M	0.221	0.343	0	0	0	252.2	gatgaactgCtgcagctgac	m5C_36015
chr20	2637607	+	C	196	72	0.367	0	0	T	124	M	0.303	0.437	0	0	0	436.33	actgctgagCtgcacctgtg	m5C_35988
chr20	2637608	+	C	193	47	0.245	1	0.005	T	145	M	0.189	0.31	0	0	0	178.01	ctgctgagCtgcacctgga	m5C_36002
chr20	2637613	+	C	196	47	0.24	0	0	T	149	M	0.185	0.304	0	0	0	174.27	tgagctgacCttgtagaatg	m5C_35997
chr20	2637628	+	C	150	39	0.283	12	0.08	T	99	M	0.214	0.363	0	0	0	167.05	agaatggaggCaaaaaaactg	m5C_36011
chr20	2637636	+	C	158	57	0.361	0	0	T	101	M	0.29	0.438	0	0	0	330.61	ggcaaaaaaCttgtaaatg	m5C_35993
chr20	2637649	+	C	107	24	0.224	0	0	T	83	M	0.156	0.312	0	2E-16	0	74.695	attaatgagCtgcattcaat	m5C_35990
chr20	2637650	+	C	107	32	0.299	0	0	T	75	M	0.221	0.392	0	1E-14	0	141.13	tttaatgagCtgcaccaata	m5C_36003
chr20	2637656	+	C	52	21	0.404	0	0	T	31	M	0.282	0.539	0	5E-08	0	118.27	gagctgatCaaataaagcca	m5C_36005
chr20	3765604	-	C	43	25	0.581	0	0	C	25	M	0.433	0.716	0	4E-06	0	216.64	ggggggaggaCtctgattcac	m5C_36022
chr20	9089476	+	C	37	21	0.568	0	0	C	21	M	0.409	0.713	0	5E-05	0	171.84	gggggaaaagCtagggagaaa	m5C_35765
chr20	9089493	+	C	36	16	0.444	0	0	T	20	M	0.295	0.604	0	2E-05	0	94.531	gaagcaaaagCcaattgcagg	m5C_35768
chr20	17469759	+	C	59	23	0.39	0	0	T	36	M	0.276	0.517	0	9E-08	0	126.86	agcacaaagCaggtgttagg	m5C_36445
chr20	17469761	+	C	78	43	0.551	0	0	C	43	M	0.441	0.657	0	1E-08	0	379.34	cacaaggaCaggttaggac	m5C_36448
chr20	17469771	+	C	100	62	0.62	0	0	C	62	M	0.522	0.709	0	3E-11	0	647.4	cggttaggaCctgaaaagtg	m5C_36449
chr20	17469772	+	C	101	78	0.772	0	0	C	78	M	0.681	0.843	0	4E-10	0	1063	gtgttaggaCtgaagaatgg	m5C_36443
chr20	17601423	-	C	46	30	0.652	0	0	C	30	M	0.508	0.773	0	1E-05	0	304.62	tgcaagaagCgtggaggagg	m5C_36475
chr20	17601434	-	C	49	14	0.286	0	0	T	35	M	0.178	0.424	0	2E-07	0	49.978	gctcagagaCtgcagaagaag	m5C_36462
chr20	17601435	-	C	50	18	0.36	0	0	T	32	M	0.241	0.499	0	2E-08	0	86.899	tgctcagagaCctgcagaaga	m5C_36455
chr20	17640938	-	C	45	17	0.378	0	0	T	28	M	0.251	0.524	0	6E-07	0	85.367	aaagcaagaCcaagaaaaag	m5C_36470
chr20	17943355	-	C	66	17	0.258	0	0	T	49	M	0.167	0.374	0	2E-10	0	56.946	aaaactgatCactgtctga	m5C_36460
chr20	18246414	-	C	33	11	0.333	0	0	T	22	M	0.198	0.504	2E-16	3E-06	2E-16	34.007	atttttgagCaggagaatgg	m5C_35813
chr20	20536858	-	C	32	14	0.438	0	0	T	18	M	0.282	0.607	0	9E-06	0	78.862	ggacttggggCtgaeggagcg	m5C_36131
chr20	23345941	+	C	56	20	0.357	0	0	T	36	M	0.245	0.488	0	3E-08	0	97.826	agggagggagCgaagaagggg	m5C_36158
chr20	26188847	-	C	55	14	0.255	0	0	T	41	M	0.158	0.383	0	3E-09	0	44.274	atcccggggCgtgttttct	m5C_36328
chr20	26188848	-	C	53	12	0.226	0	0	T	41	M	0.135	0.355	6E-15	9E-10	6E-15	22.989	gatccggggCcggtttttcc	m5C_36339
chr20	26188851	-	C	58	30	0.517	0	0	C	30	M	0.392	0.641	0	5E-07	0	234.97	tgggatcccgCggccgtgtt	m5C_36334
chr20	26188864	-	C	40	19	0.475	0	0	T	21	M	0.329	0.625	0	1E-06	0	125.15	gtgctgggCggggagatcc	m5C_36350
chr20	26188870	-	C	31	22	0.71	0	0	C	22	M	0.534	0.839	0	6E-05	0	234.99	gcccctgggtCtgggggggt	m5C_36317
chr20	26188882	-	C	38	19	0.5	0	0	CT	19	M	0.348	0.652	0	3E-05	0	132.43	cgccgggggaCcgccctcgg	m5C_36364
chr20	26188887	-	C	40	17	0.425	0	0	T	23	M	0.285	0.578	0	6E-07	0	96.931	cggggcgccgCgggaaccgcc	m5C_36325
chr20	26188892	-	C	40	24	0.6	0	0	C	24	M	0.446	0.737	0	4E-06	0	214.06	ccaggcggggCgcccgggac	m5C_36358
chr20	26188897	-	C	38	16	0.421	0	0	T	22	M	0.279	0.578	0	2E-05	0	89.127	gcgtccaggCggggcgccg	m5C_36304
chr20	26189012	-	C	184	59	0.321	0	0	T	125	M	0.257	0.391	0	0	0	303.82	gaatcacagCgatggggcc	m5C_36321
chr20	26189018	-	C	228	58	0.254	0	0	T	170	M	0.202	0.315	0	0	0	234.61	ggagagaatCacgagcgatg	m5C_36319
chr20	26189025	-	C	278	77	0.277	0	0	T	201	M	0.228	0.332	0	0	0	350.63	ggaggaatgacCgaagaatcac	m5C_36301
chr20	26189036	-	C	201	70	0.348	0	0	T	131	M	0.286	0.416	0	0	0	400.12	gggaaccgggCggaggataga	m5C_36312
chr20	26189041	-	C	187	42	0.225	0	0	T	145	M	0.171	0.29	0	0	0	143.37	ggagcgggacCgggctggagg	m5C_36330
chr20	26189042	-	C	184	55	0.299	0	0	T	129	M	0.237	0.369	0	0	0	261.17	cgagcggggaCgggtcgagag	m5C_36320
chr20	26189047	-	C	235	66	0.281	0	0	T	169	M	0.227	0.341	0	0	0	300	ttccccggagCgggaaccggg	m5C_36363
chr20	26189052	-	C	170	35	0.206	0	0	T	135	M	0.152	0.273	0	0	0	106.35	gcccgtctccCggagcgggac	m5C_36353
chr20	26189053	-	C	149	40	0.268	0	0	T	109	M	0.204	0.345	0	0	0	163.02	cgccggtctcCggagcgggga	m5C_36356
chr20	26189056	-	C	117	51	0.436	0	0	T	66	M	0.349	0.526	0	1E-13	0	356.49	gcgcgccggCtcccggagcg	m5C_36335
chr20	26189061	-	C	116	39	0.336	0	0	T	77	M	0.257	0.426	0	3E-15	0	200.24	tgggggcgcgCgggtctcccg	m5C_36302
chr20	26189063	-	C	115	31	0.27	0	0	T	84	M	0.197	0.357	0	1E-16	0	122.07	ggggggcgcgCggcggtctcc	m5C_36342
chr20	26189065	-	C	105	39	0.371	0	0	T	66	M	0.285	0.467	0	1E-13	0	222.36	acgggggggCgcgccggtct	m5C_36352
chr20	26189074	-	C	51	32	0.627	0	0	C	32	M	0.49	0.747	0	7E-07	0	313.76	aagcgcccaCggggggggcg	m5C_36343
chr20	26189327	-	C	82	27	0.329	0	0	T	55	M	0.237	0.437	0	4E-12	0	128.09	ccgagcgcgCctgtcgcta	m5C_36349
chr20	26189330	-	C	90	19	0.211	0	0	T	71	M	0.14	0.306	0	9E-16	0	53.019	tgccgagcgCgggtctgtgc	m5C_36354
chr20	26189337	-	C	121	52	0.43	0	0	T	69	M	0.345	0.519	0	4E-15	0	358.85	cggggggggCcgagcgggcg	m5C_36345
chr20	26189351	-	C	58	24	0.414	0	0	T	34	M	0.296	0.542	0	1E-07	0	142.21	ttccggggCcaacgggggg	m5C_36361
chr20	26189961	-	C	55	19	0.345	0	0	T	36	M	0.234	0.477	0	2E-08	0	88.778	cgcgccctcCcaacggggga	m5C_36331
chr20	26189964	-	C	53	17	0.321	0	0	T	36	M	0.211	0.455	0	1E-08	0	71.713	agacgcgccCtcccacggcg	m5C_36322
chr20	26189965	-	C	54	19	0.352	0	0	T	35	M	0.238	0.485	0	2E-08	0	90.527	gagacgcgcCctcccacggg	m5C_36351
chr20	26189966	-	C	53	13	0.25	1	0.019	T	39	M	0.152	0.382	1E-16	2E-09	1E-16	31.595	cgagacgcgcCcttcccacgc	m5C_36329
chr20	26189967	-	C	51	11	0.216	0	0	T	40	M	0.125	0.346	1E-13	4E-10	1E-13	17.806	acgagacgcgCccctcccacg	m5C_36324
chr20	26189969	-	C	55	13	0.236	0	0	T	42	M	0.144	0.363	2E-16	2E-09	2E-16	29.235	agacgagacgCgcccctcca	m5C_36347
chr20	26189971	-	C	80	34	0.425	0	0	T	46	M	0.323	0.534	0	4E-11	0	219.34	tgagacgagaCgcgcccttc	m5C_36340
chr20	26189976	-	C	78	45	0.577	0	0	C	45	M	0.466	0.68	0	2E-08	0	419.59	ttgagagagaCgaagcggcc	m5C_36336
chr20	26189989	-	C	249	119	0.478	0	0	T	130	M	0.417	0.54	0	0	0	991.69	gggttcgagGCgggtgagga	m5C_36348
chr20	26189994	-	C	236	83	0.352	0	0	T	153	M	0.294	0.415	0	0	0	487.36	gtggggggCgaaggcggtg	m5C_36305
chr20	26190009	-	C	286	66	0.232	1	0.003	T	219	M	0.186	0.284	0	0	0	246.01	tgaggagactCgtgggggg	m5C_36323
chr20	26190020	-	C	168	92	0.548	0	0	C	92	M	0.472	0.621	0	0	0	868.72	cgcgtggggtCtgaaggagct	m5C_36303
chr20	26190021	-	C	167	70	0.419	0	0	T	97	M	0.34							

chr20	37053954	-	C	137	60	0.438	0	0	T	77	M	0.358	0.522	0	1E-15	0	429.23	tgatcgggggCtgctttggc	m5C_36898
chr20	37053960	-	C	137	34	0.248	0	0	T	103	M	0.183	0.327	0	0	0	124.69	cgaagatgCggggctgcc	m5C_36865
chr20	37053977	-	C	65	18	0.277	0	0	T	47	M	0.183	0.396	0	3E-10	0	65.856	tattttgccCtgattccgaa	m5C_36916
chr20	37053978	-	C	60	14	0.233	0	0	T	46	M	0.144	0.354	0	3E-11	0	40.43	ctattttgCctgattcca	m5C_36873
chr20	37053979	-	C	61	26	0.426	0	0	T	35	M	0.31	0.551	0	6E-09	0	161.28	cctattttgCctgtattcg	m5C_36887
chr20	37056044	-	C	33	11	0.333	0	0	T	22	M	0.198	0.504	2E-16	3E-06	2E-16	34.007	gtgcctaggCattgatagg	m5C_36868
chr20	37056056	-	C	33	9	0.273	0	0	T	24	M	0.151	0.442	8E-13	1E-06	8E-13	16.442	cataggctgCtgtgctagg	m5C_36891
chr20	37056057	-	C	32	10	0.312	0	0	T	22	M	0.18	0.486	1E-14	2E-06	1E-14	25.084	tcataggctgCtgtgcttag	m5C_36905
chr20	37056060	-	C	32	7	0.219	0	0	T	25	M	0.11	0.388	8E-10	3E-07	9E-10	6.9997	tgatcataggCtgctctggc	m5C_36846
chr20	37056066	-	C	32	11	0.344	0	0	T	21	M	0.204	0.517	2E-16	3E-06	2E-16	35.144	cgaagatgCataggctgcc	m5C_36906
chr20	37056077	-	C	32	23	0.719	0	0	C	23	M	0.546	0.844	0	8E-05	0	251.28	gtcctcgatCgaaaggat	m5C_36863
chr20	37056080	-	C	31	7	0.226	0	0	T	24	M	0.114	0.398	6E-10	3E-07	7E-10	7.3321	tctgctctgCatccgaaatg	m5C_36866
chr20	37062600	-	C	157	48	0.306	0	0	T	109	M	0.239	0.382	0	0	0	229.46	gtgctctggCattgatagg	m5C_36899
chr20	37062605	-	C	167	98	0.587	0	0	C	98	M	0.511	0.659	0	2E-16	0	1001.6	tgcttggtccCtggcatga	m5C_36875
chr20	37062607	-	C	154	34	0.221	0	0	T	120	M	0.163	0.293	0	0	0	110.51	gtctgctggCctgtgcat	m5C_36882
chr20	37062612	-	C	154	48	0.312	0	0	T	106	M	0.244	0.389	0	0	0	234.11	ctggggctgCtgtgctctgg	m5C_36913
chr20	37062613	-	C	155	38	0.245	0	0	T	117	M	0.184	0.319	0	0	0	139.95	tcggggctgCtgtgctctg	m5C_36860
chr20	37062616	-	C	154	45	0.292	0	0	T	109	M	0.226	0.368	0	0	0	203.52	tgatcggggCtgctctggc	m5C_36911
chr20	37062622	-	C	151	50	0.331	0	0	T	101	M	0.261	0.41	0	0	0	261.07	cgaagatgCtggggctgcc	m5C_36869
chr20	37062632	-	C	142	45	0.317	0	0	T	97	M	0.246	0.397	0	0	0	221.45	cacctgattCgaaaggatc	m5C_36892
chr20	37062640	-	C	48	10	0.208	0	0	T	38	M	0.117	0.343	2E-12	2E-08	2E-12	13.834	ctttttgcaCctgattcca	m5C_36902
chr20	39653012	+	C	124	30	0.242	0	0	T	94	M	0.175	0.324	0	0	0	105.03	gattgcagtaCctccaggaat	m5C_36278
chr20	39653016	+	C	152	32	0.212	1	0.007	T	119	M	0.154	0.284	0	0	0	98.753	gcagtcctcCagggaatggg	m5C_36271
chr20	39653029	+	C	105	34	0.324	0	0	T	71	M	0.242	0.418	0	2E-14	0	164.49	gaatgggcaCctctctacc	m5C_36272
chr20	39653030	+	C	96	36	0.375	0	0	T	60	M	0.285	0.475	0	2E-12	0	205	aattgggacCctcttacca	m5C_36274
chr20	43530409	+	C	58	21	0.362	0	0	T	37	M	0.251	0.491	0	5E-08	0	105.23	gaagaagcagCagatgggcaa	m5C_36583
chr20	55063820	+	C	51	30	0.588	0	0	C	30	M	0.452	0.712	0	5E-07	0	270.99	tacctatcaaCagactggagg	m5C_36384
chr20	55084444	+	C	31	9	0.29	0	0	T	22	M	0.161	0.466	4E-13	1E-06	4E-13	18.015	gtgctgagaaCaaggatggag	m5C_36376
chr20	57570385	-	C	34	17	0.5	0	0	CT	17	M	0.341	0.659	0	2E-05	0	115.83	caactggggCaaataatgg	m5C_36618
chr20	57570395	-	C	31	15	0.484	0	0	T	16	M	0.32	0.652	0	1E-05	0	95.91	ttgatttggCaactggggc	m5C_36616
chr20	60963536	+	C	34	13	0.382	0	0	T	21	M	0.239	0.55	0	7E-06	0	62.14	gagaaatcaCagatgggaa	m5C_37060
chr21	9825711	+	C	32	13	0.406	0	0	T	19	M	0.255	0.577	0	7E-06	0	66.35	ccgcgtcccCggcgcggcc	m5C_38149
chr21	9825714	+	C	38	10	0.263	0	0	T	28	M	0.15	0.42	9E-14	2E-06	1E-13	19.504	cgcccccgCgcgcgcttg	m5C_38080
chr21	9825718	+	C	43	27	0.628	0	0	C	27	M	0.479	0.756	0	7E-06	0	258.44	ccccggcgCgctttgggaa	m5C_38150
chr21	9825720	+	C	44	15	0.341	0	0	T	29	M	0.219	0.489	0	3E-07	0	65.627	ccggcgcgcgCttggggacc	m5C_38244
chr21	9825721	+	C	46	29	0.63	0	0	C	29	M	0.486	0.755	0	1E-05	0	281.88	cgggcgcgCttggggaccg	m5C_38012
chr21	9825729	+	C	45	13	0.289	0	0	T	32	M	0.177	0.434	0	1E-07	0	46.098	gccttggggaCgggtgggg	m5C_38091
chr21	9825730	+	C	36	10	0.278	0	0	T	26	M	0.158	0.44	5E-14	2E-06	5E-14	21.112	ccttgggggaCgggtgggg	m5C_37928
chr21	9825778	+	C	42	22	0.524	0	0	C	22	M	0.377	0.666	0	2E-06	0	165.98	ccgaggggtCcgggggcgg	m5C_37933
chr21	9825779	+	C	44	10	0.233	1	0.023	T	33	M	0.132	0.377	4E-13	2E-08	5E-13	16.268	cgaagggttcCgggggtcggc	m5C_38025
chr21	9825786	+	C	36	22	0.611	0	0	C	22	M	0.449	0.752	0	6E-05	0	197.4	ttccgggggtCggcctggcg	m5C_38070
chr21	9825789	+	C	33	9	0.273	0	0	T	24	M	0.151	0.442	8E-13	1E-06	8E-13	16.442	cgggggctggCctggggcg	m5C_38132
chr21	9825790	+	C	37	9	0.243	0	0	T	28	M	0.134	0.401	3E-12	1E-06	3E-12	13.907	ggggggcgCtggggcggt	m5C_37987
chr21	9825793	+	C	50	16	0.32	0	0	T	34	M	0.208	0.458	0	7E-09	0	66.426	ggcgcgctgCggcgcggtg	m5C_38046
chr21	9825796	+	C	61	23	0.377	0	0	T	38	M	0.266	0.503	0	2E-09	0	122.43	cggtctggcgCggtggcggg	m5C_37907
chr21	9825798	+	C	79	23	0.291	0	0	T	56	M	0.203	0.399	0	4E-11	0	93.159	gccttggcgCgtgggggaa	m5C_37970
chr21	9825802	+	C	90	44	0.489	0	0	T	46	M	0.388	0.59	0	2E-11	0	341.62	ggcgcggtgCggggggagag	m5C_38193
chr21	9825814	+	C	109	30	0.275	0	0	T	79	M	0.2	0.366	0	5E-15	0	120.07	gggggaaggaaCggttcgggg	m5C_38210
chr21	9825819	+	C	70	24	0.343	0	0	T	46	M	0.242	0.46	0	6E-11	0	116.38	gggaagggtCggggggaccg	m5C_38121
chr21	9825820	+	C	63	13	0.206	0	0	T	50	M	0.125	0.322	2E-15	2E-11	3E-15	23.698	gagacgggtCgggggaccg	m5C_38045
chr21	9825827	+	C	45	20	0.444	0	0	T	25	M	0.309	0.588	0	1E-06	0	123.75	ttccgggggaCggcgcgac	m5C_38014
chr21	9825828	+	C	55	16	0.291	0	0	T	39	M	0.188	0.421	0	7E-09	0	60.067	tcgggggacCggcgcgact	m5C_38037
chr21	9825831	+	C	52	30	0.577	0	0	C	30	M	0.442	0.701	0	5E-07	0	265.16	gggggaccgCcgcgactcg	m5C_37997
chr21	9825832	+	C	44	13	0.295	0	0	T	31	M	0.182	0.442	0	1E-07	0	47.204	gggggaccgCcgcgactcg	m5C_38172
chr21	9825840	+	C	34	9	0.265	0	0	T	25	M	0.146	0.431	1E-12	1E-06	1E-12	15.739	ggcgcgactgCggcgcggtg	m5C_38158
chr21	9825861	+	C	40	10	0.25	0	0	T	30	M	0.142	0.402	2E-13	2E-08	2E-13	18.091	gggggggagCcgcggggacc	m5C_38219
chr21	9825862	+	C	53	34	0.642	0	0	C	34	M	0.507	0.757	0	1E-06	0	344.7	tggggggagCcgcgggatcg	m5C_38235
chr21	9825864	+	C	66	15	0.227	0	0	T	51	M	0.143	0.342	0	6E-11	0	42.855	gggggagcggCggggatgcc	m5C_38155
chr21	9825871	+	C	82	26	0.317	0	0	T	56	M	0.226	0.424	0	3E-12	0	117.77	ccgggggagCagcgaggacc	m5C_38180
chr21	9825874	+	C	93	40	0.43	0	0	T	53	M	0.334	0.532	0	6E-12	0	267.39	cggggatcgCgagggccgtg	m5C_37991
chr21	9825880	+	C	66	14	0.212	0	0	T	52	M	0.131	0.325	2E-16	3E-11	2E-16	28.66	tcgcccgggCcgggcgccg	m5C_38242
chr21	9825881	+	C	58	30	0.517	0	0	C	30	M	0.392	0.641	0	5E-07	0	234.97	cgccgaggacCggcgcgcc	m5C_38187
chr21	9825900	+	C	68	18	0.265	0	0	T	50	M	0.174	0.38	0	3E-10	0	62.819	gccccgggCcgcggggtg	m5C_37996
chr21	9825901	+	C	73	30	0.411	0	0	T	43	M	0.305	0.526	0	5E-10	0	183.19	ccccgggtgCgcggggtgc	m5C_38015
chr21	9825903	+	C	104	33	0.317	0	0	T	71	M	0.236	0.412	0	2E-14	0	155.58	ccggggcgCcgcgggcgcg	m5C_38125
chr21	9825910	+	C	130	44	0.338	0	0	T	86	M	0.263	0.423	0	0	0	231.26	ccgcggggCcgcgggggc	m5C_38151
chr21	9825911	+	C	129	37	0.287	0	0	T	92	M	0.216	0.37	0	0	0	159.71	cgcggggtgCcgcgggcg	m5C_38251
chr21	9825914	+	C	140	40	0.286	0	0	T	100	M	0.217	0.365	0	0	0	173.91	ggggggcgCggcggggtg	m5C_38237
chr21	9825917	+	C	152	33	0.217	0	0	T	119	M	0.159	0.289	0	0	0	104.92	gtgctggcgCggcggggag	m5C_38166
chr21	9825929	+	C	150	51	0.34	0	0	T	99	M	0.269	0.419	0	0	0	274.41	ggcgggggcCccgcggtg	m5C_38021
chr21	9825930	+	C	159	85	0.538	1	0.006	C	85	M	0.46	0.614	0	4E-16	0	782.44	cggggggacCcgcggggtg	m5C_38040
chr21	9825935	+	C	147	47	0.32	0	0	T	100	M	0.25	0.399	0	0	0	234.77	aggccccgCgtgtgccg	m5C_37930
chr21	9825943	+	C	67	20	0.299	0	0</											

chr21	9826239	+	C	106	27	0.255	0	0	T	79	M	0.181	0.345	0	1E-15	0	97.936	tggtccctccCggacaggcgt	m5C_38055
chr21	9826247	+	C	122	32	0.262	0	0	T	90	M	0.192	0.347	0	0	0	123.11	ccggacaggCgtcgcgga	m5C_38117
chr21	9826255	+	C	206	48	0.233	0	0	T	158	M	0.18	0.295	0	0	0	173.27	ggcgttcgCgacgtggcg	m5C_38247
chr21	9826258	+	C	258	97	0.376	0	0	T	161	M	0.319	0.436	0	0	0	619.04	gttcgcggaCgtggggcgtg	m5C_38078
chr21	9826265	+	C	234	97	0.415	0	0	T	137	M	0.353	0.479	0	0	0	685.37	cgcgtgggCggggcgac	m5C_37974
chr21	9826272	+	C	134	28	0.209	0	0	T	106	M	0.149	0.285	0	0	0	83.278	tggtgggCgacctccgcc	m5C_38152
chr21	9826276	+	C	65	29	0.446	0	0	T	36	M	0.332	0.567	0	1E-08	0	192.38	ggggcgacCttccgcttgc	m5C_37962
chr21	9826414	+	C	55	19	0.345	0	0	T	36	M	0.234	0.477	0	2E-08	0	88.778	ccttggcgtCgtggggcgtg	m5C_38111
chr21	9826421	+	C	57	18	0.316	0	0	T	39	M	0.21	0.445	0	2E-08	0	75.615	cgctggggCgtggcgacc	m5C_38029
chr21	9826427	+	C	49	18	0.367	0	0	T	31	M	0.247	0.507	0	8E-07	0	88.794	ggggcggtCcaaccttgcg	m5C_38230
chr21	9826428	+	C	51	12	0.235	0	0	T	39	M	0.14	0.368	3E-15	9E-10	4E-15	24.331	tggtgtgcCacctctgcgc	m5C_38022
chr21	9826449	+	C	36	12	0.333	0	0	T	24	M	0.202	0.497	0	5E-06	0	48.515	ccgcgccgcCggggggctc	m5C_38089
chr21	9826452	+	C	40	14	0.35	0	0	T	26	M	0.221	0.505	0	2E-07	0	61.976	cgcccgccgCgggtctgga	m5C_38213
chr21	9826459	+	C	38	21	0.553	0	0	C	21	M	0.397	0.699	0	5E-05	0	166.77	cgggggctCggagccgggc	m5C_38056
chr21	9826508	+	C	62	20	0.323	0	0	T	42	M	0.22	0.446	0	7E-10	0	87.817	gaccgggCggggtctgcg	m5C_37981
chr21	9826514	+	C	76	27	0.355	0	0	T	49	M	0.257	0.467	0	2E-10	0	138.79	tgcgggcgCtgcggccgca	m5C_38058
chr21	9826520	+	C	76	20	0.263	0	0	T	56	M	0.177	0.372	0	1E-11	0	70.917	ggcgctgcgCcgacggcgc	m5C_38190
chr21	9826521	+	C	55	18	0.327	0	0	T	37	M	0.218	0.459	0	2E-08	0	78.526	gcgtgcggCgcacggcgcg	m5C_38248
chr21	9826523	+	C	56	20	0.353	0	0	T	36	M	0.245	0.488	0	3E-08	0	97.826	gtcggccgCacggcgac	m5C_38205
chr21	9826572	+	C	35	18	0.514	0	0	C	18	M	0.356	0.67	0	3E-05	0	128.05	ctctgctcgCcgccggagc	m5C_38186
chr21	9826577	+	C	44	22	0.5	0	0	CT	22	M	0.358	0.642	0	2E-06	0	157.66	gtctgcgcCggagctcgag	m5C_38168
chr21	9826581	+	C	52	13	0.25	0	0	T	39	M	0.152	0.382	1E-16	2E-09	1E-16	31.595	gcgcgccgaCgtcgggcgcg	m5C_37992
chr21	9826584	+	C	57	30	0.526	0	0	C	30	M	0.399	0.65	0	5E-07	0	239.51	gcccggagCggggcgccc	m5C_38170
chr21	9826589	+	C	60	32	0.533	0	0	C	32	M	0.409	0.654	0	3E-08	0	261.72	gacgtgggCgcccccgcg	m5C_38109
chr21	9826593	+	C	69	28	0.406	0	0	T	41	M	0.298	0.524	0	1E-08	0	166.82	tcggggcgCcgcgggagcg	m5C_38241
chr21	9826594	+	C	62	32	0.516	0	0	C	32	M	0.394	0.636	0	3E-08	0	252.46	cggggcgccCcgggggcgg	m5C_38197
chr21	9826595	+	C	63	39	0.619	0	0	C	39	M	0.496	0.729	0	1E-07	0	386.56	ggggcgcccCggggggggg	m5C_38209
chr21	9826597	+	C	62	24	0.387	0	0	T	38	M	0.276	0.512	0	3E-09	0	132.41	ggcgccccCggggcgagc	m5C_37912
chr21	9826643	+	C	45	12	0.267	0	0	T	33	M	0.16	0.41	6E-16	7E-08	6E-16	29.226	cccggggCcgccgcgcgc	m5C_37935
chr21	9826644	+	C	48	23	0.479	0	0	T	25	M	0.345	0.617	0	3E-06	0	158.57	ccggggcgCggccgcgcgc	m5C_38156
chr21	9826647	+	C	43	13	0.302	0	0	T	30	M	0.186	0.451	0	1E-07	0	48.365	cggggcgccCcgcgcgcg	m5C_38189
chr21	9826648	+	C	44	10	0.227	0	0	T	34	M	0.128	0.37	6E-13	2E-08	6E-13	15.727	ggggcgggCgcgcgcgcgc	m5C_38127
chr21	9826650	+	C	55	18	0.327	0	0	T	37	M	0.218	0.459	0	2E-08	0	78.526	gcgcggcgCgcgcgcgcgc	m5C_38020
chr21	9826654	+	C	66	20	0.303	0	0	T	46	M	0.206	0.422	0	7E-10	0	82.215	cggcgcgcgCgcgcgcgcgt	m5C_38065
chr21	9826658	+	C	61	22	0.361	0	0	T	39	M	0.252	0.486	0	1E-09	0	110.77	cgcgcgcgcCgcgcgcgcgc	m5C_38079
chr21	9826671	+	C	40	8	0.2	0	0	T	32	M	0.105	0.348	2E-10	5E-09	2E-10	8.135	gcgtggcgCgggtccctcc	m5C_37995
chr21	9826675	+	C	37	8	0.216	0	0	T	29	M	0.114	0.372	1E-10	7E-07	1E-10	9.1227	ggcgccggCctctccgcgc	m5C_38110
chr21	9826722	+	C	79	50	0.633	0	0	C	50	M	0.523	0.731	0	4E-08	0	522.77	tcctcgggCggggcgagc	m5C_38103
chr21	9826726	+	C	120	36	0.3	0	0	T	84	M	0.225	0.387	0	0	0	162.18	cggggcgCgcgcgaaga	m5C_38006
chr21	9826728	+	C	126	33	0.262	0	0	T	93	M	0.193	0.345	0	0	0	127.38	cggggggCgacgaagaag	m5C_38211
chr21	9826731	+	C	129	37	0.287	0	0	T	92	M	0.216	0.37	0	0	0	159.71	gcggcgcgCgaagaagcgt	m5C_38131
chr21	9826744	+	C	65	19	0.292	0	0	T	46	M	0.196	0.412	0	5E-10	0	74.416	agaagcgCgggtctggg	m5C_38105
chr21	9826749	+	C	62	32	0.516	0	0	C	32	M	0.394	0.636	0	3E-08	0	252.46	cgtcgggCtggggcgag	m5C_37975
chr21	9826757	+	C	40	23	0.575	0	0	C	23	M	0.422	0.715	0	3E-06	0	194.1	gtctggcgCggggcccgcc	m5C_38137
chr21	9826931	+	C	31	9	0.29	0	0	T	22	M	0.161	0.466	4E-13	1E-06	4E-13	18.015	gcttggggCgcccggcccg	m5C_37911
chr21	9826933	+	C	32	21	0.656	0	0	C	21	M	0.483	0.796	0	5E-05	0	202.91	ttcgggcgCcgggccgctc	m5C_37965
chr21	9826934	+	C	32	9	0.281	0	0	T	23	M	0.156	0.454	5E-13	1E-06	6E-13	17.198	tgcgggcgCggggccgtcc	m5C_37955
chr21	9827007	+	C	204	48	0.235	0	0	T	156	M	0.182	0.298	0	0	0	175.02	tacctacctCctgttgatc	m5C_37927
chr21	9827008	+	C	213	64	0.3	0	0	T	149	M	0.243	0.365	0	0	0	310.89	acctacctCttgtgatcc	m5C_38179
chr21	9827017	+	C	510	201	0.394	0	0	T	309	M	0.353	0.437	0	0	0	1417.7	cctgttgatCctgcagtag	m5C_38206
chr21	9827018	+	C	502	191	0.38	0	0	T	311	M	0.339	0.424	0	0	0	1295.2	ctgttgatCctgcagtagc	m5C_38042
chr21	9827021	+	C	523	178	0.34	0	0	T	345	M	0.301	0.382	0	0	0	1071.7	gttgatctcgCagtagcata	m5C_38113
chr21	9827022	+	C	518	185	0.357	0	0	T	333	M	0.317	0.399	0	0	0	1173.2	ttgatctcgCagtagcatat	m5C_37963
chr21	9827028	+	C	508	235	0.463	0	0	T	273	M	0.42	0.506	0	0	0	1972.5	ctgcagtagCatagtctgt	m5C_38092
chr21	9827034	+	C	419	153	0.366	1	0.002	T	265	M	0.321	0.413	0	0	0	983.06	gtagcatatgCttgtctcaa	m5C_37932
chr21	9827039	+	C	381	197	0.517	0	0	C	197	M	0.467	0.567	0	0	0	1839.8	atatctgttCtcaaatgta	m5C_37917
chr21	9827041	+	C	339	136	0.401	0	0	T	203	M	0.35	0.454	0	0	0	953.07	atgttgttCaaagattaag	m5C_38229
chr21	9827052	+	C	172	109	0.634	0	0	C	109	M	0.56	0.702	0	0	0	1219.8	aaagattaagCcatgatgct	m5C_37982
chr21	9827053	+	C	166	108	0.655	1	0.006	C	108	M	0.579	0.723	0	1E-15	0	1251.1	aaagattaagCcatgatgct	m5C_38081
chr21	9827057	+	C	164	117	0.713	0	0	C	117	M	0.64	0.777	0	5E-15	0	1497.5	ttaaagcatgCatgtctaagt	m5C_38200
chr21	9827062	+	C	183	138	0.754	0	0	C	138	M	0.687	0.811	0	3E-16	0	1895.9	ccatgatgtCtaagtagcca	m5C_37937
chr21	9827069	+	C	196	145	0.74	0	0	C	145	M	0.674	0.796	0	0	0	1955.1	tgctaaagaCgcacggccgg	m5C_37952
chr21	9827073	+	C	211	151	0.716	0	0	C	151	M	0.651	0.772	0	0	0	1967	taagtagccaCggcggtaca	m5C_37920
chr21	9827076	+	C	199	129	0.648	0	0	C	129	M	0.58	0.711	0	0	0	1495.5	gtacgcacggCcggtacagc	m5C_38142
chr21	9827077	+	C	186	140	0.753	0	0	C	140	M	0.686	0.809	0	4E-16	0	1920.8	tacgcacggCggtagcagga	m5C_38253
chr21	9827082	+	C	198	119	0.601	0	0	C	119	M	0.532	0.667	0	0	0	1265	acggcggaCagtagaaactg	m5C_38083
chr21	9827090	+	C	261	198	0.759	0	0	C	198	M	0.703	0.807	0	0	0	2784.7	tacagtgaatCgtgaatgac	m5C_38162
chr21	9827093	+	C	250	164	0.656	0	0	C	164	M	0.595	0.712	0	0	0	1952.1	agtagaaactgCgaatgctca	m5C_37948
chr21	9827102	+	C	202	137	0.678	0	0	C	137	M	0.611	0.739	0	0	0	1674.1	gcgaatggctCattaaatcag	m5C_37976
chr21	9827199	+	C	325	242	0.747	1	0.003	C	242	M	0.697	0.791	0	0	0	3372.8	gcgtgacccCcttcggggg	m5C_37925
chr21	9827200	+	C	314	228	0.726	0	0	C	228	M	0.674	0.772	0	0	0	3074.7	cgtgaccccCttcgggggg	m5C_37979
chr21	9827203	+	C	311	155	0.498	0	0	T	156	M	0.443	0.554	0	0	0	1373.9	tgacctcttCgccccggga	m5C_37929
chr21	9827205	+	C	318	140	0.47	20	0.063	T	158	M	0.414	0.526	0	0	0	1158.9	accccttctCgggggggatg	m5C_37958
chr21	9827																		

chr21	9827288 +	C	339	211	0.622	0	0	C	211	M	0.57	0.672	0	0	0	2404.2	gcgcggcgCtttggtgact	m5C_38066
chr21	9827297 +	C	460	315	0.685	0	0	C	315	M	0.641	0.726	0	0	0	4037.9	gcttgggaCtctagataac	m5C_37977
chr21	9827299 +	C	474	326	0.688	0	0	C	326	M	0.645	0.728	0	0	0	4203.3	tttggtgactCtagataacct	m5C_37983
chr21	9827307 +	C	483	322	0.667	0	0	C	322	M	0.623	0.707	0	0	0	4015.1	ctctagataaCctcgggctga	m5C_38087
chr21	9827308 +	C	498	347	0.697	0	0	C	347	M	0.655	0.736	0	0	0	4546	tctagataaCtctgggctgat	m5C_38099
chr21	9827310 +	C	529	352	0.665	0	0	C	352	M	0.624	0.704	0	0	0	4393.9	tagataacctCgggtgatcg	m5C_38224
chr21	9827314 +	C	523	351	0.671	0	0	C	351	M	0.63	0.71	0	0	0	4420.8	taacctgggCtgatcgacag	m5C_38031
chr21	9827319 +	C	563	339	0.602	0	0	C	339	M	0.561	0.642	0	0	0	3804.5	tcgggctgatCgcacgcccc	m5C_37968
chr21	9827321 +	C	602	324	0.538	0	0	C	324	M	0.498	0.578	0	0	0	3228.8	gggtgatcgCacgcccccg	m5C_38250
chr21	9827323 +	C	612	395	0.645	0	0	C	395	M	0.607	0.682	0	0	0	4793.1	gctgatcgcaCgcccccg	m5C_38153
chr21	9827325 +	C	552	248	0.451	2	0.004	T	302	M	0.41	0.493	0	0	0	2032.6	tgatcgacgCccccgggc	m5C_38082
chr21	9827326 +	C	570	266	0.467	0	0	T	304	M	0.426	0.508	0	0	0	2266.7	gatcgacgCccccgggc	m5C_38238
chr21	9827327 +	C	640	228	0.357	2	0.003	T	410	M	0.321	0.395	0	0	0	1464.4	atcgacgcccCccccgggc	m5C_38232
chr21	9827328 +	C	637	185	0.29	0	0	T	452	M	0.257	0.327	0	0	0	949.09	tcgcacgcccCccgggggc	m5C_38167
chr21	9827329 +	C	640	201	0.314	0	0	T	439	M	0.279	0.351	0	0	0	1122.8	cgcacgccccCggggcgagc	m5C_37960
chr21	9827330 +	C	644	177	0.276	2	0.003	T	465	M	0.243	0.312	0	0	0	858.61	gcacgccccCggggcgaga	m5C_37923
chr21	9827335 +	C	651	187	0.288	2	0.003	T	462	M	0.255	0.324	0	0	0	952.27	cccccgggCggcgacgacc	m5C_38008
chr21	9827338 +	C	660	205	0.312	2	0.003	T	453	M	0.277	0.348	0	0	0	1137.1	cccgggcgCgacgacctat	m5C_37918
chr21	9827341 +	C	645	167	0.259	0	0	T	478	M	0.227	0.294	0	0	0	756.87	gggcggcgCaaccattcg	m5C_38023
chr21	9827344 +	C	609	152	0.25	0	0	T	457	M	0.217	0.285	0	0	0	659.25	gcggcgacgaCccattcgac	m5C_38207
chr21	9827345 +	C	598	190	0.318	1	0.002	T	407	M	0.282	0.357	0	0	0	1072.2	cggcgacgaCcatcgacag	m5C_38140
chr21	9827350 +	C	543	122	0.225	0	0	T	421	M	0.192	0.262	0	0	0	467.45	acgacctatCgaacgtctg	m5C_38048
chr21	9827357 +	C	380	94	0.247	0	0	T	286	M	0.207	0.293	0	0	0	388.51	attcgacgtCtgccctatca	m5C_38147
chr21	9827360 +	C	236	48	0.203	0	0	T	188	M	0.157	0.259	0	0	0	150.7	cgaacgtctgCcttatcaact	m5C_38128
chr21	9827361 +	C	184	43	0.234	0	0	T	141	M	0.178	0.3	0	0	0	153.41	gaacgtctgCctatacaatt	m5C_38183
chr21	9827362 +	C	141	40	0.284	0	0	T	101	M	0.216	0.363	0	0	0	172.63	aacgtctgcCtatcaactt	m5C_38161
chr21	9827366 +	C	119	78	0.655	0	0	C	78	M	0.566	0.735	0	2E-11	0	883.62	tctgacctatCaactttgat	m5C_38243
chr21	9827373 +	C	135	42	0.311	0	0	T	93	M	0.239	0.394	0	0	0	200.89	tatcaacttCgatggagtc	m5C_38234
chr21	9827383 +	C	61	30	0.492	0	0	T	31	M	0.371	0.614	0	2E-08	0	222.36	cgatggagtcCggcgacctt	m5C_38122
chr21	9827385 +	C	71	41	0.577	0	0	C	41	M	0.462	0.685	0	7E-09	0	378.43	atggagtcgCcggtctacc	m5C_38192
chr21	9827386 +	C	71	30	0.423	0	0	T	41	M	0.315	0.538	0	5E-10	0	188.72	tggtagtcgCggcgctacca	m5C_38226
chr21	9827390 +	C	72	39	0.542	0	0	C	39	M	0.427	0.652	0	5E-09	0	333.37	agtcggcgCctacattgat	m5C_38090
chr21	9827391 +	C	72	38	0.528	0	0	C	38	M	0.414	0.639	0	4E-09	0	314.64	gtcgcggtgCtaccatggg	m5C_38017
chr21	9827394 +	C	86	38	0.442	0	0	T	48	M	0.342	0.547	0	1E-10	0	259.64	gcggcgctcaCcatggagacc	m5C_38175
chr21	9827395 +	C	100	47	0.47	0	0	T	53	M	0.375	0.567	0	1E-12	0	352.6	ccgtgcctacCatggagacca	m5C_38114
chr21	9827403 +	C	149	63	0.423	0	0	T	86	M	0.346	0.503	0	0	0	436.48	accatggggaCcacgggtgac	m5C_38249
chr21	9827404 +	C	157	63	0.406	2	0.013	T	92	M	0.332	0.485	0	0	0	418.69	ccatggggaCacggggagcg	m5C_38104
chr21	9827406 +	C	188	91	0.484	0	0	T	97	M	0.414	0.555	0	0	0	752.83	atgggagccaCggggagggg	m5C_38223
chr21	9827413 +	C	294	168	0.571	0	0	C	168	M	0.514	0.627	0	0	0	1728	ccacggggaCgggggaatcag	m5C_37984
chr21	9827421 +	C	346	91	0.263	0	0	T	255	M	0.219	0.312	0	0	0	399.31	gacggggaatCagggttcgat	m5C_38160
chr21	9827428 +	C	423	220	0.52	0	0	C	220	M	0.473	0.567	0	0	0	2079.1	aatcagggtCgattccggag	m5C_37908
chr21	9827433 +	C	357	223	0.625	0	0	C	223	M	0.573	0.673	0	0	0	2557.1	gggttcgattCgggagggga	m5C_37946
chr21	9827434 +	C	374	266	0.711	0	0	C	266	M	0.663	0.755	0	0	0	3528.9	gggtcgattcCgggaggggag	m5C_38003
chr21	9827476 +	C	152	121	0.796	0	0	C	121	M	0.725	0.852	0	1E-13	0	1754.7	ccaaggaaaggCagcagggcg	m5C_38041
chr21	18827143 -	C	48	14	0.292	0	0	T	34	M	0.182	0.432	0	2E-07	0	51.076	tctgcctgcCacgcgggagg	m5C_36709
chr21	18827147 -	C	100	37	0.37	0	0	T	63	M	0.282	0.468	0	7E-14	0	208.55	gaattctcgcCtgcacagcg	m5C_36715
chr21	18827148 -	C	126	61	0.484	0	0	T	65	M	0.399	0.571	0	4E-14	0	486.33	agaattctgcCctgcacgcg	m5C_36714
chr21	18827150 -	C	139	68	0.489	0	0	T	71	M	0.408	0.571	0	7E-15	0	554.23	gagagaatttcGcctgcacg	m5C_36720
chr21	18827152 -	C	166	101	0.608	0	0	C	101	M	0.533	0.679	0	3E-16	0	1075.7	tggagaattCtgccttcca	m5C_36704
chr21	18827165 -	C	259	128	0.494	0	0	T	131	M	0.434	0.555	0	0	0	1110.7	atgggtgggtCagtgagaga	m5C_36707
chr21	18827176 -	C	108	43	0.398	0	0	T	65	M	0.311	0.492	0	4E-13	0	267.34	tctatcggtCcatgggtggt	m5C_36719
chr21	26197468 -	C	34	19	0.559	0	0	C	19	M	0.395	0.711	0	3E-05	0	149.92	gggactgagaCatgggaattg	m5C_37284
chr21	26197474 -	C	38	22	0.579	0	0	C	22	M	0.422	0.721	0	6E-05	0	185.65	gaaccggggaCtgagacatgg	m5C_37298
chr21	26946306 +	C	37	24	0.649	0	0	T	24	M	0.488	0.782	0	9E-05	0	234.04	taatgctaCtgatagggg	m5C_37261
chr21	27354674 -	C	31	16	0.516	0	0	C	16	M	0.348	0.68	0	2E-05	0	111.49	ggccaagcacCgagagagaat	m5C_37281
chr21	27354681 -	C	31	13	0.419	0	0	T	18	M	0.264	0.592	0	7E-06	0	68.68	gggttgaggCaaagaccgag	m5C_37276
chr21	27354682 -	C	32	18	0.562	0	0	C	18	M	0.393	0.718	0	3E-05	0	141.57	aggcttgaggCcaagaccga	m5C_37287
chr21	27394280 -	C	283	77	0.272	0	0	T	206	M	0.224	0.327	0	0	0	344.26	atgacgggaCgatggggatg	m5C_37294
chr21	27394286 -	C	242	79	0.326	0	0	T	163	M	0.27	0.388	0	0	0	427.36	ccgatgatgaCgagagacgat	m5C_37306
chr21	27394295 -	C	149	51	0.342	0	0	T	98	M	0.271	0.422	0	0	0	276.34	aagaagaagcCgatgatgac	m5C_37271
chr21	27394296 -	C	117	33	0.282	0	0	T	84	M	0.208	0.37	0	2E-16	0	137.58	gaagaagaagCcgatgatgac	m5C_37283
chr21	40717093 -	C	86	37	0.43	0	0	T	49	M	0.331	0.536	0	1E-10	0	244.79	ctgcgaaaaCggggaaaacga	m5C_37173
chr21	40717100 -	C	74	39	0.527	0	0	C	39	M	0.415	0.637	0	5E-09	0	323.52	gacttactgcCggaaacggg	m5C_37178
chr21	40717108 -	C	36	22	0.611	0	0	C	22	M	0.449	0.752	0	6E-05	0	197.4	ctaaagaagaCttactcggg	m5C_37170
chr22	20228628 +	C	45	9	0.2	0	0	T	36	M	0.109	0.338	2E-11	1E-08	2E-11	10.429	gggggctgcccCgggcagctg	m5C_37209
chr22	24001056 -	C	50	32	0.64	0	0	C	32	M	0.501	0.759	0	7E-07	0	320.9	aatgaatgaaCaagatgaggt	m5C_37339
chr22	29664292 +	C	52	27	0.519	0	0	C	27	M	0.387	0.649	0	2E-07	0	208.9	gagagggggaCggacgttga	m5C_37589
chr22	32795677 -	C	35	15	0.429	0	0	T	20	M	0.28	0.591	0	1E-05	0	83.953	gggctgagaCaaggagcaact	m5C_37419
chr22	32795690 -	C	38	20	0.526	0	0	C	20	M	0.373	0.675	0	4E-05	0	149.03	gaagggtatgCtgggctgaa	m5C_37421
chr22	36236450 -	C	45	30	0.667	0	0	C	30	M	0.521	0.786	0	1E-05	0	312.42	gagagactgcCagagaggaag	m5C_37639
chr22	36236451 -	C	56	20	0.357	0	0	T	36	M	0.245	0.488	0	3E-08	0	97.826	ggagagactgCagagagga	m5C_37648
chr22	36236454 -	C	56	32	0.571	0	0	C	32	M	0.441	0.692	0	7E-07	0	282.48	gggggagagaCtgccagagag	m5C_37671
chr22	36681186 -	C	31	12	0.387	0	0	T	19	M	0.237	0.562	0	5E-06	0	56.959	gctggaggggCagctggacaa	m5C_37650
chr22	36681270 -	C	37	19	0.514	0	0	C	19	M	0.359	0.666	0	3E-05	0	136.4	taaggcaagCtgacggagat	m5C_37636
chr22	36681282 -	C	39	19	0.487	0	0	T	20	M	0.339	0.638	0	3E-05	0	128.69	gaacaaggagCttaaggcca	m5C

chr22	39709899 -	C	178	37	0.209	1	0.006 T	140 M	0.156	0.275	0	0	0	115.17	aggatgaggCctggaaatgtg	m5C_37833
chr22	39709910 -	C	78	22	0.282	0	0 T	56 M	0.194	0.39	0	3E-11	0	85.471	ctcagctggtCaggtgatgag	m5C_37842
chr22	39711269 -	C	72	32	0.444	0	0 T	40 M	0.335	0.559	0	8E-10	0	214.65	ggatcagcgcCcgaaatcgac	m5C_37819
chr22	39711275 -	C	71	21	0.296	0	0 T	50 M	0.202	0.41	0	2E-11	0	84.978	gcgctgggtgCagcgcccgaa	m5C_37809
chr22	39711284 -	C	107	28	0.262	0	0 T	79 M	0.188	0.352	0	2E-15	0	105.11	tcagagggagCgctgggtaca	m5C_37825
chr22	39711293 -	C	153	43	0.281	0	0 T	110 M	0.216	0.357	0	0	0	185.63	tgatgagggtCagagggagcg	m5C_37807
chr22	39711295 -	C	158	48	0.304	0	0 T	110 M	0.237	0.379	0	0	0	227.95	gtgatgaggCtcagagggag	m5C_37801
chr22	39711306 -	C	67	31	0.463	0	0 T	36 M	0.349	0.581	0	2E-08	0	216.12	cccagctggtCggtgatgag	m5C_37802
chr22	39715062 -	C	173	77	0.445	0	0 T	96 M	0.373	0.52	0	0	0	574.45	ttgcacgtCtgattgggt	m5C_37810
chr22	39715066 -	C	203	69	0.34	0	0 T	134 M	0.278	0.407	0	0	0	383.99	ctgattgcaCgttctgatt	m5C_37822
chr22	39715068 -	C	230	65	0.283	0	0 T	165 M	0.228	0.344	0	0	0	296.86	tgctgattgCacgtctgat	m5C_37836
chr22	39715076 -	C	253	59	0.233	0	0 T	194 M	0.185	0.289	0	0	0	218.68	aaactgtggCtgatgtcac	m5C_37837
chr22	39715083 -	C	244	58	0.238	0	0 T	186 M	0.189	0.295	0	0	0	218.8	cggacagaaaCtgtgtgtga	m5C_37817
chr22	39715097 -	C	233	133	0.571	0	0 C	133 M	0.507	0.633	0	0	0	1347.6	aactattgaCggggcgacag	m5C_37814
chr22	39715105 -	C	235	47	0.2	0	0 T	188 M	0.154	0.256	0	0	0	144.63	agatgatgaaCttattgacgg	m5C_37811
chr22	39715116 -	C	93	39	0.419	0	0 T	54 M	0.324	0.521	0	5E-12	0	252.89	gcagaaaccaCagatgatgaa	m5C_37805
chr22	39918100 +	C	46	14	0.304	0	0 T	32 M	0.191	0.448	0	2E-07	0	53.423	tagagctgggCagtgaaatgg	m5C_37799
chr22	39918117 +	C	76	20	0.263	0	0 T	56 M	0.177	0.372	0	1E-11	0	70.917	gtggatatcaCtgaaggagat	m5C_37788
chr22	41226885 -	C	39	11	0.282	0	0 T	28 M	0.165	0.438	3E-15	3E-06	3E-15	26.4	aagaatgaaCgaagttaaga	m5C_37751
chr22	41461643 -	C	56	31	0.554	0	0 C	31 M	0.424	0.676	0	6E-07	0	262.96	cttggtgtgtCcgatggtagt	m5C_37759
chr22	43011333 +	C	49	19	0.388	0	0 T	30 M	0.264	0.528	0	1E-06	0	100.43	aaatttgagCggggtaaagt	m5C_37694
chr22	43011348 +	C	33	13	0.394	0	0 T	20 M	0.247	0.563	0	7E-06	0	64.175	aaagctgcgcCtcaagggtac	m5C_37683
chr22	43011363 +	C	44	27	0.614	0	0 C	27 M	0.466	0.743	0	7E-06	0	251.77	ggggaccgcCtactttgcgg	m5C_37688
chr22	43011379 +	C	127	41	0.325	1	0.008 T	85 M	0.25	0.411	0	1E-16	0	204.84	tgcgggatgcCtgggaatgac	m5C_37701
chr22	43011393 +	C	138	40	0.29	0	0 T	98 M	0.221	0.37	0	0	0	176.53	gagttgcgatCtggccgaacct	m5C_37702
chr22	43011396 +	C	131	57	0.435	0	0 T	74 M	0.353	0.521	0	4E-16	0	402.72	ttcgatgtgCccgaccttat	m5C_37689
chr22	43011397 +	C	116	91	0.784	0	0 C	91 M	0.701	0.85	0	2E-10	0	1276.2	tgcgatctgcCcgaccttat	m5C_37684
chr22	43579085 -	C	33	19	0.576	0	0 C	19 M	0.408	0.728	0	3E-05	0	155.07	gacgagcgagCccggagggag	m5C_37727
chr22	43579088 -	C	35	22	0.629	0	0 C	22 M	0.463	0.768	0	6E-05	0	203.88	gaggacgagCagcccggagag	m5C_37733
chr22	43579093 -	C	52	39	0.75	0	0 C	39 M	0.618	0.848	0	2E-06	0	481.99	agggagggagCggggcagccc	m5C_37714
chr3	12881931 -	C	42	27	0.643	0	0 C	27 M	0.492	0.77	0	7E-06	0	265.5	gggatcgatCtgggaatgac	m5C_5809
chr3	12881936 -	C	36	14	0.389	0	0 T	22 M	0.248	0.551	0	9E-06	0	69.397	ctctgggatCgcatctggag	m5C_5810
chr3	12881943 -	C	37	11	0.297	0	0 T	26 M	0.175	0.458	1E-15	3E-06	2E-15	28.551	ccctgacctCtgggatcgca	m5C_5808
chr3	15094934 -	C	31	12	0.387	0	0 T	19 M	0.237	0.562	0	5E-06	0	56.959	agaccaagaaCaataaggagaa	m5C_5927
chr3	18543289 +	C	37	12	0.324	0	0 T	25 M	0.196	0.485	0	5E-06	0	47.119	gttttggtgCtgcgtttgt	m5C_5829
chr3	21591529 -	C	48	37	0.787	1	0.021 C	37 M	0.651	0.88	0	3E-05	0	481.71	ccctcggtgCtaggggttag	m5C_6122
chr3	22423842 +	C	41	20	0.488	0	0 T	21 M	0.343	0.635	0	1E-06	0	137.02	gtgtcaaggCtgaaaaaagc	m5C_6132
chr3	33144658 +	C	32	9	0.281	0	0 T	23 M	0.156	0.454	5E-13	1E-06	6E-13	17.198	aaacggggagCaccaaggtgc	m5C_8318
chr3	33144660 +	C	49	11	0.224	0	0 T	38 M	0.13	0.359	7E-14	4E-08	7E-14	18.889	caggggaccaCaggttgctct	m5C_8319
chr3	33144669 +	C	144	44	0.306	0	0 T	100 M	0.236	0.385	0	0	0	207.84	accaggttgcCtaaggagggg	m5C_8315
chr3	33144688 +	C	168	45	0.268	0	0 T	123 M	0.207	0.339	0	0	0	185.97	gggaattggCcaaggttga	m5C_8314
chr3	33144689 +	C	192	40	0.208	0	0 T	152 M	0.157	0.271	0	0	0	125.51	gtgaattggCcaaggttgaa	m5C_8337
chr3	33185660 +	C	38	20	0.526	0	0 C	20 M	0.373	0.675	0	4E-05	0	149.03	tgaaaagagCaaatagattt	m5C_8336
chr3	33185672 +	C	68	45	0.662	0	0 C	45 M	0.543	0.763	0	3E-07	0	489.03	ataggatttgCtgaagatttg	m5C_8302
chr3	39452562 +	C	46	14	0.304	0	0 T	32 M	0.191	0.448	0	2E-07	0	53.423	atgttagagCtggagttga	m5C_6197
chr3	39452575 +	C	34	10	0.294	0	0 T	24 M	0.168	0.462	2E-14	2E-06	3E-14	22.956	ggagtgaggtCtactgactgg	m5C_6201
chr3	48614446 -	C	31	10	0.323	0	0 T	21 M	0.186	0.499	7E-15	2E-06	8E-15	26.273	aaactggggaCccctggagaag	m5C_7965
chr3	48642186 -	C	39	19	0.487	0	0 T	20 M	0.339	0.638	0	3E-05	0	128.69	tggcaggtCctggagaagga	m5C_7958
chr3	48642187 -	C	42	24	0.571	0	0 C	24 M	0.422	0.709	0	4E-06	0	202.59	ctggcaggtCctggagaagg	m5C_7959
chr3	48642197 -	C	33	23	0.697	0	0 C	23 M	0.527	0.826	0	8E-05	0	242.24	aaagatggcCtggcaggtgc	m5C_7950
chr3	48642201 -	C	33	8	0.242	0	0 T	25 M	0.128	0.41	3E-11	7E-07	3E-11	10.787	aacaaagaaCggcctggcag	m5C_7978
chr3	49135878 -	C	38	16	0.421	0	0 T	22 M	0.279	0.578	0	2E-05	0	89.127	tggaggtgacCtgcagacggg	m5C_7977
chr3	50152909 +	C	58	39	0.672	0	0 C	39 M	0.544	0.779	0	2E-06	0	424.51	tgaaggagagCtggggagagag	m5C_6932
chr3	50152921 +	C	41	13	0.317	0	0 T	28 M	0.196	0.47	0	1E-07	0	50.868	gggtgagagCttgaagtga	m5C_6929
chr3	50314507 +	C	34	24	0.706	0	0 C	24 M	0.538	0.832	0	9E-05	0	258.39	acaggtgggCtgcctggaggt	m5C_6933
chr3	52724816 +	C	38	26	0.684	0	0 C	26 M	0.525	0.809	0	0.0001	0	273.23	tgaaaaattaCaaagtcaac	m5C_7436
chr3	52724828 +	C	32	25	0.781	0	0 C	25 M	0.612	0.89	0	0.0001	0	306.22	agatccaatCtgaattcagc	m5C_7411
chr3	52726761 +	C	46	12	0.261	0	0 T	34 M	0.156	0.403	7E-16	7E-08	7E-16	28.412	aaatgtgaagCaaatgatgat	m5C_7415
chr3	52726775 +	C	120	54	0.45	0	0 T	66 M	0.364	0.539	0	2E-13	0	393.03	tgatgataaaCtgacttgac	m5C_7435
chr3	52726781 +	C	123	42	0.341	0	0 T	81 M	0.264	0.429	0	2E-16	0	221.42	taaacctgatCtgactgactg	m5C_7433
chr3	52726785 +	C	123	42	0.341	0	0 T	81 M	0.264	0.429	0	2E-16	0	221.42	ctggatctgaCtgaactgtct	m5C_7425
chr3	52726789 +	C	133	93	0.699	0	0 C	93 M	0.617	0.771	0	7E-13	0	1146.9	atctgaactgaCtgaactgagt	m5C_7442
chr3	52726794 +	C	143	105	0.734	0	0 C	105 M	0.656	0.8	0	2E-13	0	1378.5	actgaactgCtgaacttgtt	m5C_7410
chr3	52726800 +	C	140	48	0.343	0	0 T	92 M	0.269	0.425	0	0	0	258.59	tgtctgtagCtgttcaatcc	m5C_7439
chr3	52726805 +	C	141	58	0.411	0	0 T	83 M	0.334	0.494	0	0	0	386.89	tgaacttgtCaaatcaaccc	m5C_7444
chr3	52726809 +	C	137	55	0.401	0	0 T	82 M	0.323	0.485	0	2E-16	0	355.46	tctgtcaatCcaaccttgag	m5C_7417
chr3	52726810 +	C	136	53	0.39	0	0 T	83 M	0.312	0.474	0	2E-16	0	330.56	ctgttcaatCcaaccttgagc	m5C_7419
chr3	52726813 +	C	127	76	0.598	0	0 C	76 M	0.511	0.68	0	8E-13	0	777.46	ttaatccaaCccctgacttc	m5C_7430
chr3	52726814 +	C	127	79	0.622	0	0 C	79 M	0.535	0.702	0	1E-12	0	845.78	tcaatccaaCctgaacttca	m5C_7424
chr3	52726815 +	C	114	57	0.5	0	0 CT	57 M	0.41	0.59	0	5E-13	0	467.08	caatccaaCctgaacttcat	m5C_7426
chr3	52726820 +	C	71	35	0.493	0	0 T	36 M	0.38	0.607	0	2E-09	0	266.03	caaccttgagCttatgttct	m5C_7412
chr3	73160251 +	C	168	66	0.393	0	0 T	102 M	0.322	0.468	0	0	0	425.29	gttttggagCagggaagatgg	m5C_7216
chr3	99328405 -	C	49	27	0.551	0	0 C	27 M	0.413	0.681	0	7E-06	0	223.1	ccctgtgggCtaggggctaa	m5C_7185
chr3	101931074 +	C	46	11	0.239	0	0 T	35 M	0.139	0.379	3E-14	4E-08	3E-14	20.73	tgtggggggCttcaacccca	m5C_7240
chr3	108107939 +	C	67	32	0.478	0	0 T	35 M	0.363	0.595	0	3E-08	0	232	caaaagtgagCctcagaccag	m5C_7267
chr3	108107940 +	C	70	32	0.457	0	0 T	38 M	0.346	0.573	0	8E-10	0	221.26	aaaactgagCtcaagaccaga	m5C_7261
chr3	108107942 +	C	71	37	0.521	0	0 C	37 M	0.407	0.633	0	3E-09	0	301.07	aacgtgaactCagaccagagc	m5C_7263
chr3	108107947 +	C	61	32	0.525	0	0 C	32 M	0.402	0.645	0	3E-08	0	257	gacctcagagCagacgtgac	m5C_7262
chr3	108107951 +	C	62	38	0.613	0	0 C	3								

chr3	131948003	-	C	37	20	0.541	0	0	C	20	M	0.384	0.69	0	4E-05	0	153.54	gggtgagctCagtggtgag	m5C_7719
chr3	134076387	-	C	31	19	0.613	0	0	C	19	M	0.438	0.763	0	3E-05	0	166.53	agggagggaCccaggggag	m5C_7779
chr3	140216289	+	C	37	18	0.486	0	0	T	19	M	0.334	0.641	0	3E-05	0	120.41	tgcttctgaCcggaacct	m5C_7807
chr3	140216290	+	C	36	12	0.333	0	0	T	24	M	0.202	0.497	0	5E-06	0	48.515	gtctttgacGgaaccactg	m5C_7809
chr3	144268166	+	C	43	11	0.256	0	0	T	32	M	0.149	0.402	1E-14	4E-08	1E-14	22.889	gagcaggagCtgccagcat	m5C_7730
chr3	144268174	+	C	39	27	0.692	0	0	C	27	M	0.536	0.814	0	0.0001	0	289.32	tgcttgagCattgattcag	m5C_7732
chr3	149086944	-	C	43	19	0.442	0	0	T	24	M	0.304	0.589	0	1E-06	0	115.65	gatgactggCaaagaagaag	m5C_7892
chr3	149086949	-	C	43	14	0.326	0	0	T	29	M	0.205	0.475	0	2E-07	0	57.381	gtactgatgaCtgggcaaga	m5C_7897
chr3	149095313	-	C	33	18	0.545	0	0	C	18	M	0.38	0.702	0	3E-05	0	136.75	gaagrggcaCgatgcatcg	m5C_7908
chr3	149212583	+	C	41	16	0.39	0	0	T	25	M	0.257	0.543	0	4E-07	0	82.099	gagaaggagCtgtaagaag	m5C_7874
chr3	149212586	+	C	33	13	0.394	0	0	T	20	M	0.247	0.563	0	7E-06	0	64.175	aaggagctgCtaagaaggga	m5C_7879
chr3	155378883	+	C	32	21	0.656	0	0	C	21	M	0.483	0.796	0	5E-05	0	202.91	atgataccttCctggggc	m5C_8678
chr3	155378908	+	C	94	74	0.787	0	0	C	74	M	0.694	0.858	0	4E-09	0	1027.2	ggtaggattCggcactctca	m5C_8682
chr3	169384360	-	C	42	12	0.286	0	0	T	30	M	0.172	0.436	2E-16	7E-08	2E-16	32.247	ccggttgctgCtgggggttg	m5C_8743
chr3	169384363	-	C	41	16	0.39	0	0	T	25	M	0.257	0.543	0	4E-07	0	82.099	cgaccggttCtgctgggtg	m5C_8742
chr3	169384369	-	C	41	11	0.268	0	0	T	30	M	0.157	0.419	6E-15	4E-08	7E-15	24.554	cgagcggacCgggttgct	m5C_8746
chr3	169710762	+	C	37	8	0.222	1	0.027	T	28	M	0.117	0.381	7E-11	7E-07	8E-11	9.4968	aaaaagggaCtggaacagca	m5C_8728
chr3	169710768	+	C	42	9	0.214	0	0	T	33	M	0.117	0.359	1E-11	1E-08	1E-11	11.545	ggaactggaaCagcaaacaga	m5C_8734
chr3	169710771	+	C	40	10	0.303	7	0.175	T	23	M	0.174	0.473	2E-14	2E-06	2E-14	23.982	actggaacgCaaacagttgg	m5C_8727
chr3	169710775	+	C	39	15	0.385	0	0	T	24	M	0.249	0.541	0	1E-05	0	74.673	gaacgcaaaCagatgggat	m5C_8733
chr3	184039729	+	C	38	10	0.263	0	0	T	28	M	0.15	0.42	9E-14	2E-06	1E-13	19.504	ttcccgactCaggaggga	m5C_8406
chr3	184039793	+	C	257	96	0.374	0	0	T	161	M	0.317	0.434	0	0	0	608	gcaggaagaCtgaggtgag	m5C_8407
chr3	184042109	+	C	51	18	0.353	0	0	T	33	M	0.236	0.49	0	2E-08	0	85.084	tgagaagaagCaaaaagagat	m5C_8408
chr3	184042675	+	C	41	26	0.634	0	0	C	26	M	0.481	0.764	0	6E-06	0	250.23	ggcagaggaaCgaggacgct	m5C_8405
chr3	184042684	+	C	45	11	0.244	0	0	T	34	M	0.142	0.387	2E-14	4E-08	2E-14	21.411	acgagagcgcCtgaaggaga	m5C_8420
chr3	186502599	+	C	142	98	0.69	0	0	C	98	M	0.61	0.76	0	8E-14	0	1195.4	gaaatgaggCaaatcatctt	m5C_8505
chr3	186502603	+	C	165	111	0.673	0	0	C	111	M	0.598	0.74	0	2E-15	0	1327.4	tgatgcaatCattcttggg	m5C_8513
chr3	186502610	+	C	167	122	0.731	0	0	C	122	M	0.659	0.792	0	1E-14	0	1607	aatcatcttCggagctgacc	m5C_8528
chr3	186502615	+	C	163	124	0.761	0	0	C	124	M	0.69	0.82	0	1E-14	0	1710.5	ttcttgggaCtgacctgaa	m5C_8497
chr3	186502619	+	C	164	121	0.738	0	0	C	121	M	0.666	0.799	0	8E-15	0	1610.7	tcgggactgaCctgaatgaa	m5C_8512
chr3	186502620	+	C	161	118	0.733	0	0	C	118	M	0.66	0.795	0	5E-15	0	1557	cgggagctgaCtgaatgaag	m5C_8507
chr3	186502649	+	C	61	25	0.41	0	0	T	36	M	0.295	0.535	0	4E-09	0	147.68	cattgctgatCacttgattat	m5C_8493
chr3	186505099	+	C	77	49	0.636	0	0	C	49	M	0.525	0.735	0	3E-08	0	514.32	aagcaggatCagactacaat	m5C_8520
chr3	186505106	+	C	75	22	0.293	0	0	T	53	M	0.202	0.404	0	3E-11	0	89.056	attcagactaCaatatagctg	m5C_8485
chr3	186505114	+	C	70	30	0.429	0	0	T	40	M	0.319	0.545	0	5E-10	0	191.61	tacaatataCtgtaaggtgc	m5C_8482
chr3	186505124	+	C	68	24	0.353	0	0	T	44	M	0.25	0.472	0	3E-09	0	120.01	ctgtaaggtCtgtgtgtgc	m5C_8481
chr3	186505133	+	C	43	25	0.581	0	0	C	25	M	0.433	0.716	0	4E-06	0	216.64	gctgtgtgtCgtccccctg	m5C_8488
chr3	193458365	-	C	43	19	0.442	0	0	T	24	M	0.304	0.589	0	1E-06	0	115.65	gaggggggaaCtggctgaagt	m5C_8231
chr3	195903765	-	C	87	41	0.471	0	0	T	46	M	0.37	0.575	0	3E-10	0	303.25	aggattcaacCtgggtgggg	m5C_8657
chr3	195903766	-	C	86	19	0.221	0	0	T	67	M	0.146	0.319	0	8E-14	0	55.574	gaggattcaaCctgggtggg	m5C_8665
chr3	195903769	-	C	79	23	0.291	0	0	T	56	M	0.203	0.399	0	4E-11	0	93.159	ccggaggatCaaactgtggg	m5C_8656
chr4	2397458	-	C	31	22	0.71	0	0	C	22	M	0.534	0.839	0	6E-05	0	234.99	gtgtgggctCggccacctct	m5C_8457
chr4	12975460	-	C	44	12	0.273	0	0	T	32	M	0.163	0.418	4E-16	7E-08	5E-16	30.115	ggatccatgcCtgcttgagtg	m5C_8549
chr4	13578543	-	C	41	13	0.317	0	0	T	28	M	0.196	0.47	0	1E-07	0	50.868	gagcaggagCtgatgggga	m5C_8551
chr4	24578222	-	C	34	18	0.529	0	0	C	18	M	0.367	0.685	0	3E-05	0	132.25	agatatgagCgagagaggga	m5C_8647
chr4	69202874	-	C	45	15	0.333	0	0	T	30	M	0.214	0.479	0	3E-07	0	64.076	agatatgaaCaggatgagag	m5C_8998
chr4	70296621	-	C	52	27	0.519	0	0	C	27	M	0.387	0.649	0	2E-07	0	208.9	cgagagggaCggcagcagcc	m5C_9079
chr4	70296635	-	C	53	14	0.264	0	0	T	39	M	0.164	0.396	0	3E-09	0	46.024	ctgtgcccCagtcgagagt	m5C_9096
chr4	70296639	-	C	48	19	0.396	0	0	T	29	M	0.27	0.537	0	1E-06	0	102.68	caggctgngCggcgagcga	m5C_9099
chr4	70296669	-	C	146	109	0.747	0	0	C	109	M	0.67	0.81	0	4E-13	0	1461.3	atggatgggcCtggaggttg	m5C_9093
chr4	70296671	-	C	136	57	0.419	0	0	T	79	M	0.34	0.503	0	4E-16	0	387.06	aaatgagtgCgctggaggt	m5C_9080
chr4	70296685	-	C	116	85	0.733	0	0	C	85	M	0.646	0.805	0	7E-11	0	1097.7	tcaactgcccTgaaaaatgga	m5C_9094
chr4	70296686	-	C	110	87	0.791	0	0	C	87	M	0.706	0.856	0	9E-11	0	1228	atcaactgacCctgaaaatgg	m5C_9097
chr4	70296687	-	C	106	84	0.792	0	0	C	84	M	0.706	0.859	0	9E-10	0	1185.6	aatcaactgacCctgaaaatg	m5C_9082
chr4	70296735	-	C	38	25	0.658	0	0	C	25	M	0.499	0.788	0	0.0001	0	249.46	ccatgggaagtCagatccgct	m5C_9105
chr4	76654445	-	C	58	22	0.379	0	0	T	36	M	0.266	0.508	0	7E-08	0	116.88	ccctgggggCtatgggttag	m5C_10144
chr4	88813736	+	C	46	13	0.283	0	0	T	33	M	0.173	0.425	0	1E-07	0	45.043	gaagaagaagCaaagatcaa	m5C_9120
chr4	107249377	+	C	51	21	0.412	0	0	T	30	M	0.288	0.548	0	5E-08	0	120.77	gaaaaagaagCgaagaagaaa	m5C_9475
chr4	107924469	-	C	76	55	0.724	0	0	C	55	M	0.614	0.812	0	8E-08	0	675.67	tctgatggCagatcggtca	m5C_9483
chr4	107924477	-	C	238	155	0.651	0	0	C	155	M	0.589	0.709	0	0	0	1825.1	tgtatggctCtgatggcag	m5C_9486
chr4	110476768	+	C	31	19	0.613	0	0	C	19	M	0.438	0.763	0	3E-05	0	166.53	tgaaggctgCaaatatatgg	m5C_9384
chr4	122605923	-	C	37	15	0.405	0	0	T	22	M	0.263	0.565	0	1E-05	0	79.039	attcagggaCagatggaggg	m5C_9590
chr4	122605925	-	C	33	9	0.273	0	0	T	24	M	0.151	0.442	8E-13	1E-06	8E-13	16.442	aaatgcagagCacagatgag	m5C_9591
chr4	122607457	-	C	50	14	0.28	0	0	T	36	M	0.175	0.417	0	2E-07	0	48.927	cttcggaaggCtatgaaaggc	m5C_9582
chr4	127569076	+	C	41	20	0.488	0	0	T	21	M	0.343	0.635	0	1E-06	0	137.02	ccctagctgCtgggggct	m5C_9465
chr4	129191383	-	C	31	16	0.516	0	0	C	16	M	0.348	0.68	0	2E-05	0	111.49	atggatggcCtgaatggtg	m5C_9308
chr4	163917817	-	C	64	16	0.25	0	0	T	48	M	0.16	0.368	0	1E-10	0	51.247	ttgtgggggCggggggatag	m5C_9616
chr4	166256910	+	C	50	37	0.74	0	0	C	37	M	0.604	0.841	0	2E-06	0	447.3	tgggcagagCtagtgttta	m5C_9796
chr4	174253301	-	C	59	33	0.559	0	0	C	33	M	0.433	0.678	0	9E-07	0	285.71	aagaacgaagCagaagatgag	m5C_9786
chr4	174253302	-	C	31	12	0.387	0	0	T	19	M	0.237	0.562	0	5E-06	0	56.959	gaagaacgaCcaagaatgga	m5C_9785
chr5	6600233	-	C	101	62	0.614	0	0	C	62	M	0.516	0.703	0	3E-11	0	640.34	gatgtggggCtggaggatt	m5C_10321
chr5	6600248	-	C	38	13	0.342	0	0	T	25	M	0.212	0.501	0	7E-06	0	55.152	gtctcattatCtaaggatgat	m5C_10302
chr5	11082863	+	C	31	13	0.419	0	0	T	18	M	0.264	0.592	0	7E-06	0			

chr5	33445465	+	C	85	37	0.435	0	0	T	48	M	0.335	0.541	0	1E-10	0	247.87	aggaaaggaggCaaaaagaaga	m5C_10439
chr5	33445477	+	C	113	62	0.549	0	0	C	62	M	0.457	0.637	0	1E-12	0	566.46	aaaaagaagaCaaagaaggat	m5C_10458
chr5	34937728	+	C	32	21	0.656	0	0	C	21	M	0.483	0.796	0	5E-05	0	202.91	gaagctaagaCaggccaagg	m5C_10238
chr5	68562552	+	C	38	16	0.421	0	0	T	22	M	0.279	0.578	0	2E-05	0	89.127	aaaaaaggaaCcgatggatat	m5C_10482
chr5	71146744	+	C	36	18	0.5	0	0	CT	18	M	0.345	0.655	0	3E-05	0	124.11	aaatttttcCagggcgga	m5C_10959
chr5	71146749	+	C	146	66	0.452	0	0	T	80	M	0.374	0.533	0	2E-16	0	493.13	ttcttcaggCggaaaggga	m5C_10953
chr5	71146755	+	C	243	89	0.369	2	0.008	T	152	M	0.311	0.432	0	0	0	553.33	agggcggaacCggaccgatc	m5C_10932
chr5	71146760	+	C	309	109	0.353	0	0	T	200	M	0.302	0.408	0	0	0	657.44	ggaaacgggaCcgatcccga	m5C_10936
chr5	71146761	+	C	327	140	0.428	0	0	T	187	M	0.376	0.482	0	0	0	1051.8	gaacgggaCgatcccggag	m5C_10987
chr5	71146765	+	C	355	206	0.582	1	0.003	C	206	M	0.53	0.632	0	0	0	2183.3	cgggaccgatCccggagaagc	m5C_11000
chr5	71146766	+	C	358	174	0.486	0	0	T	184	M	0.435	0.538	0	0	0	1512.7	ggaccgatCccggagaagcc	m5C_10981
chr5	71146767	+	C	370	175	0.473	0	0	T	195	M	0.423	0.524	0	0	0	1479.2	tgaccgatCcggaagaccg	m5C_10964
chr5	71146775	+	C	394	216	0.548	0	0	C	216	M	0.499	0.597	0	0	0	2155	ccggagaagCcgccggagc	m5C_10931
chr5	71146776	+	C	405	186	0.459	0	0	T	219	M	0.411	0.508	0	0	0	1530.2	ccggagaagCcgccggagcc	m5C_10933
chr5	71146779	+	C	385	189	0.491	0	0	T	196	M	0.441	0.541	0	0	0	1668.1	gagaagccggCggagaagccg	m5C_10939
chr5	71146785	+	C	212	129	0.608	0	0	C	129	M	0.541	0.672	0	0	0	1396.9	ccggcggaagCccggggaga	m5C_10937
chr5	71146786	+	C	214	152	0.71	0	0	C	152	M	0.646	0.767	0	0	0	1964.5	cgccgggaagCccggggagag	m5C_10985
chr5	71146787	+	C	208	118	0.567	0	0	C	118	M	0.499	0.633	0	0	0	1178.5	ggcgggagccCcgggagagt	m5C_10940
chr5	71146788	+	C	213	133	0.627	1	0.005	C	133	M	0.561	0.69	0	0	0	1491.1	gcgggaagccCggggagagt	m5C_10960
chr5	71146799	+	C	133	103	0.774	0	0	C	103	M	0.696	0.837	0	3E-12	0	1434.3	ggggagagtCttttttt	m5C_10980
chr5	71146801	+	C	133	98	0.737	0	0	C	98	M	0.656	0.804	0	1E-12	0	1286	ggaggtttCttttttt	m5C_10996
chr5	71146806	+	C	54	25	0.463	0	0	T	29	M	0.337	0.594	0	2E-07	0	168.45	gtttttttCtttttgaag	m5C_10963
chr5	71146855	+	C	60	17	0.283	0	0	T	43	M	0.185	0.408	0	2E-10	0	62.923	gagagaagggCccggccttg	m5C_10989
chr5	71146856	+	C	57	40	0.702	0	0	C	40	M	0.573	0.805	0	3E-06	0	458.68	agagaagggcCcgggccttg	m5C_10951
chr5	71146857	+	C	57	15	0.263	0	0	T	42	M	0.166	0.39	0	5E-09	0	49.937	gagaagggcCcgcccttga	m5C_10982
chr5	71146861	+	C	81	50	0.617	0	0	C	50	M	0.508	0.716	0	2E-09	0	508.41	ggggcccttgCcttggaagc	m5C_10968
chr5	71146862	+	C	84	26	0.31	0	0	T	58	M	0.221	0.415	0	3E-12	0	114.83	gggcccgtCttgaaagcg	m5C_10969
chr5	71146871	+	C	112	49	0.438	0	0	T	63	M	0.349	0.53	0	7E-14	0	342.23	ccttggaagCgtgcgggtc	m5C_10975
chr5	71146874	+	C	118	40	0.339	0	0	T	78	M	0.26	0.428	0	4E-15	0	207.88	tgaaagcgCggtgtcttg	m5C_10966
chr5	71146876	+	C	122	52	0.426	0	0	T	70	M	0.342	0.515	0	4E-15	0	355.73	gaaagcgCggttctggg	m5C_10958
chr5	71146881	+	C	108	40	0.37	0	0	T	68	M	0.285	0.464	0	2E-13	0	228.17	cgctcggtCtgggggcatc	m5C_11002
chr5	71146885	+	C	113	61	0.54	0	0	C	61	M	0.448	0.629	0	1E-12	0	546.72	gcggttctggCggcatccgt	m5C_10934
chr5	71146888	+	C	93	54	0.581	0	0	C	54	M	0.479	0.676	0	2E-10	0	517.44	gttctggcgCcatccggag	m5C_10992
chr5	71146891	+	C	94	52	0.553	0	0	C	52	M	0.453	0.65	0	1E-10	0	470.67	ctggggcatCcgggagctc	m5C_10986
chr5	71146892	+	C	88	54	0.614	0	0	C	54	M	0.509	0.709	0	4E-09	0	549.92	tgccggcatCgggtgactct	m5C_10984
chr5	71146901	+	C	97	57	0.588	0	0	C	57	M	0.488	0.68	0	3E-10	0	556.49	ccggtgagtCtgcgtggccc	m5C_10943
chr5	71146903	+	C	88	44	0.5	0	0	CT	44	M	0.398	0.602	0	5E-10	0	350.01	gggagctcCgtgcgcttt	m5C_10990
chr5	71146905	+	C	64	47	0.734	0	0	C	47	M	0.615	0.827	0	4E-07	0	578.26	tgagctctcCtggcccttga	m5C_10961
chr5	71146909	+	C	47	29	0.617	0	0	C	29	M	0.474	0.742	0	1E-05	0	275.07	ctctcgctgCcttgaaaat	m5C_10949
chr5	71146910	+	C	52	27	0.519	0	0	C	27	M	0.387	0.649	0	2E-07	0	208.9	tctcgctggCcttgaaatc	m5C_10973
chr5	71146911	+	C	48	15	0.312	0	0	T	33	M	0.199	0.453	0	3E-07	0	59.837	ctcgctggcCttgaaatcc	m5C_10942
chr5	71146920	+	C	33	10	0.303	0	0	T	23	M	0.174	0.473	2E-14	2E-06	2E-14	23.982	ccttgaaatCcgggggaga	m5C_10978
chr5	71146921	+	C	33	22	0.667	0	0	C	22	M	0.496	0.802	0	6E-05	0	218.27	cttgaaatCggggggagg	m5C_10945
chr5	90606809	-	C	35	10	0.286	0	0	T	25	M	0.163	0.451	3E-14	2E-06	4E-14	21.999	gaaaaggggCggagggaa	m5C_10880
chr5	114937994	+	C	31	8	0.258	0	0	T	23	M	0.137	0.432	2E-11	7E-07	2E-11	11.818	gcgcggagCggggggccgc	m5C_11122
chr5	115110094	-	C	85	21	0.247	0	0	T	64	M	0.168	0.348	0	3E-13	0	70.411	attttggagCtagagagtg	m5C_11134
chr5	122518448	+	C	49	36	0.735	0	0	C	36	M	0.597	0.838	0	3E-05	0	430.11	ggctaaattCgtgtatatg	m5C_11273
chr5	122990634	+	C	33	18	0.545	0	0	C	18	M	0.38	0.702	0	3E-05	0	136.75	tgatttaagCatattgaca	m5C_11245
chr5	122990643	+	C	47	31	0.66	0	0	C	31	M	0.517	0.778	0	1E-05	0	320.36	gcattattgCagtgaggaa	m5C_11266
chr5	122990787	+	C	63	42	0.667	0	0	C	42	M	0.544	0.771	0	2E-07	0	456.68	tcatgggggCccaagctct	m5C_11261
chr5	122990789	+	C	69	48	0.696	0	0	C	48	M	0.579	0.792	0	5E-07	0	556	atggggggcCaaagctctct	m5C_11259
chr5	122990831	+	C	167	91	0.545	0	0	C	91	M	0.469	0.619	0	0	0	853.98	cggggggggCtggagggg	m5C_11263
chr5	132427041	+	C	36	11	0.306	0	0	T	25	M	0.18	0.469	1E-15	3E-06	1E-15	29.708	ccaatggaaCagatcgaat	m5C_11322
chr5	134099691	+	C	31	9	0.29	0	0	T	22	M	0.161	0.466	4E-13	1E-06	4E-13	18.015	agatgacagaCggtctaga	m5C_11553
chr5	137896733	-	C	53	35	0.66	0	0	C	35	M	0.526	0.773	0	1E-06	0	368.16	tgactgagcaCaaacctgtg	m5C_11482
chr5	137896740	-	C	110	84	0.764	0	0	C	84	M	0.676	0.833	0	6E-11	0	1136	aaactaatgCtgaacacaa	m5C_11481
chr5	137896747	-	C	115	85	0.739	0	0	C	85	M	0.652	0.811	0	7E-11	0	1108.5	gttggaaaaCtaatgactga	m5C_11475
chr5	138378337	-	C	42	17	0.405	0	0	T	25	M	0.27	0.555	0	6E-07	0	91.945	aaggaggggCagagatggag	m5C_11503
chr5	138378355	-	C	34	14	0.412	0	0	T	20	M	0.264	0.578	0	9E-06	0	73.824	agggactggCaaaattcaag	m5C_11500
chr5	138614648	+	C	34	9	0.265	0	0	T	25	M	0.146	0.431	1E-12	1E-06	1E-12	15.739	ggaggtgatCtagtctgggt	m5C_11494
chr5	138658591	+	C	58	19	0.328	0	0	T	39	M	0.221	0.456	0	2E-08	0	83.916	gaaaaaggaaCcatcagataa	m5C_11486
chr5	138658604	+	C	56	35	0.625	0	0	C	35	M	0.494	0.74	0	1E-06	0	345.84	tcagataaagCtgggaaaaa	m5C_11489
chr5	140038686	+	C	36	18	0.5	0	0	CT	18	M	0.345	0.655	0	3E-05	0	124.11	gagagcggaCggaagagag	m5C_11377
chr5	140038687	+	C	38	11	0.289	0	0	T	27	M	0.17	0.448	2E-15	3E-06	2E-15	27.449	agagcggaacCgagaagaga	m5C_11336
chr5	148808561	+	C	53	41	0.774	0	0	C	41	M	0.645	0.865	0	3E-06	0	528.68	cactgtagtCaggagaagga	m5C_11816
chr5	150005000	+	C	38	9	0.237	0	0	T	29	M	0.13	0.392	4E-12	1E-06	4E-12	13.374	tggggttggCtggccgggt	m5C_11663
chr5	153135020	+	C	43	30	0.698	0	0	C	30	M	0.549	0.814	0	1E-05	0	329.37	cacaggaagtCtgggttgag	m5C_11431
chr5	153135025	+	C	44	35	0.795	0	0	C	35	M	0.655	0.888	0	3E-05	0	458.49	gagttctggCtgaagtgg	m5C_11429
chr5	156814276	-	C	40	18	0.45	0	0	T	22	M	0.307	0.602	0	3E-05	0	110.54	tctgtggcCtagtggttag	m5C_11677
chr5	157403856	-	C	72	39	0.542	0	0	C	39	M	0.427	0.652	0	5E-09	0	333.37	attttggagCagggaagatag	m5C_11673
chr5	161501959	+	C	36	9	0.25	0	0	T	27	M	0.138	0.411	2E-12	1E-06	2E-12	14.476	tacctgattCcgaggcaga	m5C_11590
chr5	167987919	-	C	32	13	0.406	0	0	T	19	M	0.255	0.577	0	7E-06	0	66.35	cagcatttgaCagggctatga	m5C_11722
chr5	167987926	-	C	32	13	0.406	0	0	T	19	M	0.255	0.577	0	7E-06	0	6		

chr5	179150661	+	C	34	10	0.294	0	0	T	24	M	0.168	0.462	2E-14	2E-06	3E-14	22.956	tgttttcagCaggcggtgtg	m5C_12263
chr5	179150662	+	C	31	22	0.71	0	0	C	22	M	0.534	0.839	0	6E-05	0	234.99	gtttttcagCaggcggtgtg	m5C_12245
chr5	179150666	+	C	50	15	0.3	0	0	T	35	M	0.191	0.438	0	5E-09	0	57.31	ttcagccagcCgttggggggc	m5C_12235
chr5	179150676	+	C	60	25	0.417	0	0	T	35	M	0.301	0.543	0	2E-07	0	150.32	cggttgggggCagatgatcga	m5C_12246
chr5	179151695	+	C	96	24	0.25	0	0	T	72	M	0.174	0.345	0	2E-14	0	83.586	aaaactgatgCacctcaaccg	m5C_12226
chr5	179151704	+	C	243	72	0.296	0	0	T	171	M	0.242	0.357	0	0	0	349.08	gcacctcaacCggatgtgaag	m5C_12266
chr5	179151747	+	C	224	90	0.402	0	0	T	134	M	0.34	0.467	0	0	0	611.57	aggaaaaggaCaaagggaatg	m5C_12242
chr5	179151781	+	C	38	29	0.763	0	0	C	29	M	0.608	0.87	0	0.0002	0	352.6	agaaagaaaaCttgggaaga	m5C_12230
chr5	179153689	+	C	45	9	0.2	0	0	T	36	M	0.109	0.338	2E-11	1E-08	2E-11	10.429	agaaagaaaaCagaaaaggga	m5C_12240
chr5	179252180	+	C	34	18	0.529	0	0	C	18	M	0.367	0.685	0	3E-05	0	132.25	gtgtgaatttCctgaagaacg	m5C_12248
chr5	179252181	+	C	39	29	0.744	0	0	C	29	M	0.589	0.854	0	0.0002	0	341.72	tggtgaatttCtgaagaacgt	m5C_12260
chr5	180668824	-	C	42	33	0.786	0	0	C	33	M	0.641	0.883	0	2E-05	0	422.8	tcctgcaattCtgaagggtatt	m5C_12180
chr5	180668829	-	C	43	29	0.674	0	0	C	29	M	0.525	0.795	0	1E-05	0	304.59	acatgtcctgCaattctgaag	m5C_12170
chr5	180668833	-	C	44	30	0.682	0	0	C	30	M	0.534	0.8	0	1E-05	0	320.66	gaggacatgtCctgcaattct	m5C_12157
chr5	180668838	-	C	40	21	0.525	0	0	C	21	M	0.375	0.671	0	5E-05	0	157.49	ggagagaggaCatgtcttcca	m5C_12179
chr5	180670314	-	C	154	54	0.351	0	0	T	100	M	0.28	0.429	0	0	0	302.13	tgttttctgagCtggcgcctgg	m5C_12185
chr5	180670325	-	C	287	106	0.369	0	0	T	181	M	0.316	0.427	0	0	0	669.01	aatccagaggCtgttcttgag	m5C_12172
chr5	180670331	-	C	306	73	0.239	0	0	T	233	M	0.194	0.289	0	0	0	283.58	tgtgaattCagaaggcttgt	m5C_12155
chr5	180670339	-	C	311	106	0.341	0	0	T	205	M	0.29	0.395	0	0	0	615.62	atgtccgggCtgaattccag	m5C_12173
chr5	180670344	-	C	324	69	0.213	0	0	T	255	M	0.172	0.261	0	0	0	237.2	atctgaggtgCgggtctgaaa	m5C_12156
chr5	180670352	-	C	345	139	0.403	0	0	T	206	M	0.352	0.455	0	0	0	979.91	aacatgcatCtgaagtgtcgg	m5C_12183
chr5	180670355	-	C	339	96	0.283	0	0	T	243	M	0.238	0.333	0	0	0	456.69	cccaaatgtCaatctgaggt	m5C_12175
chr5	180670365	-	C	358	140	0.391	0	0	T	218	M	0.342	0.443	0	0	0	957.39	cggtgatgacCccaatgtcc	m5C_12176
chr5	180670366	-	C	364	82	0.225	0	0	T	282	M	0.185	0.271	0	0	0	303.98	gcgggaggaCcccaaatgtc	m5C_12181
chr5	180670375	-	C	154	34	0.221	0	0	T	120	M	0.163	0.293	0	0	0	110.51	ccggcggggCgggtgtgacc	m5C_12177
chr6	13615848	+	C	36	28	0.778	0	0	C	28	M	0.619	0.883	0	0.0002	0	346.72	tgcggaggaCgtgtgcaggt	m5C_12186
chr6	18249916	-	C	44	11	0.25	0	0	T	33	M	0.146	0.394	2E-14	4E-08	2E-14	22.132	aaggagaagtCttcatgtgat	m5C_12105
chr6	18264099	-	C	100	51	0.51	0	0	C	51	M	0.413	0.606	0	9E-11	0	421.75	acgagagacgCgaggagaggg	m5C_12100
chr6	18264102	-	C	90	49	0.544	0	0	C	49	M	0.442	0.643	0	6E-11	0	433.01	aggaagaggaCgaagagaggg	m5C_12103
chr6	18264108	-	C	89	29	0.326	0	0	T	60	M	0.237	0.429	0	8E-12	0	137.71	aggaagaggaCgaggacgagc	m5C_12114
chr6	18264123	-	C	42	10	0.238	0	0	T	32	M	0.135	0.385	3E-13	2E-08	3E-13	16.841	gagagaggaCgaggagaggaag	m5C_12099
chr6	26124066	-	C	68	20	0.294	0	0	T	48	M	0.199	0.411	0	7E-10	0	79.675	gaccaagagcCagaagaaaga	m5C_12997
chr6	26124068	-	C	74	29	0.392	0	0	T	45	M	0.289	0.506	0	4E-10	0	167.42	gtgaccaagCgcaagaagaaa	m5C_12960
chr6	26124073	-	C	68	15	0.221	0	0	T	53	M	0.138	0.333	0	6E-11	0	41.547	agggagagcCaaagcgcaga	m5C_12958
chr6	26158475	+	C	35	17	0.486	0	0	T	18	M	0.33	0.644	0	2E-05	0	112.18	agaaagaggaCgggaagaagc	m5C_12950
chr6	26158485	+	C	34	18	0.529	0	0	C	18	M	0.367	0.685	0	3E-05	0	132.25	cgggagaagcCgaagcgcag	m5C_12918
chr6	26250416	-	C	35	15	0.429	0	0	T	20	M	0.28	0.591	0	1E-05	0	83.953	ataagttgaCtgaagggtg	m5C_12982
chr6	26538319	+	C	52	39	0.75	0	0	C	39	M	0.618	0.848	0	2E-06	0	481.99	tcgtctcaacCgcgaaggttc	m5C_12908
chr6	27447478	+	C	72	27	0.375	0	0	T	45	M	0.272	0.49	0	2E-10	0	146.98	tggtgagatCcccgctgtgc	m5C_12932
chr6	27447479	+	C	76	45	0.592	0	0	C	45	M	0.48	0.696	0	2E-08	0	431.81	gggtgagatCCcgctgtgtca	m5C_12890
chr6	27447480	+	C	75	26	0.347	0	0	T	49	M	0.249	0.459	0	1E-10	0	129.39	gtgagatccCcgctgtgtcac	m5C_12898
chr6	27447481	+	C	72	15	0.208	0	0	T	57	M	0.131	0.316	0	6E-13	0	39.156	tgagatccccCgctgtgcacg	m5C_12914
chr6	27447484	+	C	95	24	0.253	0	0	T	71	M	0.176	0.348	0	2E-14	0	84.501	gtatccccCgtgtcacgagg	m5C_12953
chr6	27447488	+	C	116	47	0.405	0	0	T	69	M	0.32	0.496	0	4E-14	0	301.05	ccccgctgtCacgaggagga	m5C_12853
chr6	27447507	+	C	135	29	0.215	0	0	T	106	M	0.154	0.291	0	0	0	89.283	gaccggggtCgatcccccca	m5C_12917
chr6	27447513	+	C	136	31	0.228	0	0	T	105	M	0.165	0.305	0	0	0	102.6	gggtcattcCccgacgggga	m5C_12940
chr6	27447514	+	C	137	33	0.241	0	0	T	104	M	0.177	0.319	0	0	0	116.8	gttcgattccCgagggagga	m5C_12952
chr6	27471549	+	C	31	17	0.548	0	0	C	17	M	0.378	0.708	0	2E-05	0	128.42	gggtgagatCCcgctgtgtca	m5C_12887
chr6	27471550	+	C	33	14	0.424	0	0	T	19	M	0.272	0.592	0	9E-06	0	76.259	gtgagatcccCgctgtgtcac	m5C_12913
chr6	27471551	+	C	32	9	0.281	0	0	T	23	M	0.156	0.454	5E-13	1E-06	6E-13	17.198	tgagatccccCgctgtgtcac	m5C_12854
chr6	27471553	+	C	46	11	0.239	0	0	T	35	M	0.139	0.379	3E-14	4E-08	3E-14	20.73	aglatccccCgtgtcacg	m5C_12934
chr6	27471554	+	C	54	12	0.222	0	0	T	42	M	0.132	0.349	8E-15	9E-10	8E-15	22.361	gtatccccCgtgtcacgagg	m5C_12942
chr6	27471558	+	C	72	26	0.361	0	0	T	46	M	0.26	0.476	0	1E-10	0	135.1	ccccgctgtCacgaggagga	m5C_12945
chr6	27471583	+	C	80	17	0.212	0	0	T	63	M	0.137	0.314	0	2E-14	0	46.622	gggtcattcCccgacgggga	m5C_12920
chr6	27471584	+	C	72	17	0.236	0	0	T	55	M	0.153	0.346	0	2E-12	0	52.008	gttcgattccCgagggggag	m5C_12871
chr6	27551272	-	C	33	8	0.242	0	0	T	25	M	0.128	0.41	3E-11	7E-07	3E-11	10.787	ccccgctgtCacgaggagga	m5C_12981
chr6	27834874	+	C	35	12	0.343	0	0	T	23	M	0.208	0.508	0	5E-06	0	49.996	gccagaagggCtgcaggagcg	m5C_12984
chr6	28180817	+	C	32	22	0.688	0	0	C	22	M	0.514	0.82	0	6E-05	0	226.31	ctttgttgaCgggtggcgg	m5C_13607
chr6	28574987	+	C	34	25	0.735	0	0	C	25	M	0.569	0.854	0	0.0001	0	284.41	gtccccgggtCaatccccggc	m5C_13623
chr6	28574992	+	C	32	23	0.719	0	0	C	23	M	0.546	0.844	0	8E-05	0	251.28	gggttgaattCCcggcacctc	m5C_13601
chr6	28574993	+	C	34	26	0.765	0	0	C	26	M	0.6	0.876	0	0.0001	0	312.02	gggtcaatccCgggcacctcc	m5C_13650
chr6	28574994	+	C	34	25	0.735	0	0	C	25	M	0.569	0.854	0	0.0001	0	284.41	gttcaatcccCggacctcca	m5C_13608
chr6	28574997	+	C	35	27	0.771	0	0	C	27	M	0.61	0.879	0	0.0001	0	329.3	caatccccggCactctcacca	m5C_13665
chr6	28574999	+	C	35	22	0.629	0	0	C	22	M	0.463	0.768	0	6E-05	0	203.88	atccccgggaCctccaccagt	m5C_13641
chr6	28575000	+	C	31	23	0.742	0	0	C	23	M	0.568	0.863	0	8E-05	0	261.07	tcccccggacCtccaccagt	m5C_13636
chr6	28575003	+	C	34	24	0.706	0	0	C	24	M	0.538	0.832	0	9E-05	0	258.39	cgggcacctCaccagtttg	m5C_13619
chr6	28575006	+	C	33	24	0.727	0	0	C	24	M	0.558	0.849	0	9E-05	0	267.75	gcacctcacCagttttggga	m5C_13629
chr6	28726189	-	C	39	29	0.744	0	0	C	29	M	0.589	0.854	0	0.0002	0	341.72	aggtgtagagCacatgtttg	m5C_13675
chr6	28726200	-	C	40	13	0.325	0	0	T	27	M	0.201	0.48	0	1E-07	0	52.219	gggttgaagtCtgggttagag	m5C_13679
chr6	28831510	-	C	54	38	0.704	0	0	C	38	M	0.572	0.809	0	2E-06	0	434.51	aggtgtagagCgctgttttag	m5C_13685
chr6	28831521	-	C	59	37	0.627	0	0	C	37	M	0.5	0.739	0	2E-06	0	369.65	gggttgaagtCagttgttagag	m5C_13723
chr6	28831523	-	C	57	34	0.596	0	0	C	34	M	0.467	0.714	0	1E-06	0	317.54	gggttgttagCtcagtgttag	m5C_13695
chr6	28918816	+	C	31	8	0.258	0	0	T	23	M	0.137	0.432	2E-11	7E-07				

chr6	30552124	+	C	68	22	0.324	0	0	T	46	M	0.224	0.442	0	1E-09	0	98.725	ggagatggcgCaggggacacg	m5C_12596
chr6	30552131	+	C	32	12	0.375	0	0	T	20	M	0.229	0.547	0	5E-06	0	55.041	gcgcaggggaCacgggcaaa	m5C_12577
chr6	30671412	-	C	41	10	0.244	0	0	T	31	M	0.138	0.393	2E-13	2E-08	3E-13	17.447	tgcagagaagCCagggaaagg	m5C_12636
chr6	30671420	-	C	46	21	0.457	0	0	T	25	M	0.322	0.598	0	2E-06	0	135.05	gaagatactGCagagaagcca	m5C_12618
chr6	30671423	-	C	46	22	0.478	0	0	T	24	M	0.341	0.619	0	2E-06	0	150.15	gaagaagataCtgcagagaag	m5C_12634
chr6	31803052	+	C	123	46	0.374	0	0	T	77	M	0.294	0.462	0	7E-16	0	270.03	tgatgatgacCCagggaaact	m5C_12557
chr6	31803061	+	C	117	27	0.231	0	0	T	90	M	0.164	0.315	0	0	0	88.409	ccccaggtaaCtcttgaggtg	m5C_12588
chr6	31803076	+	C	117	32	0.274	0	0	T	85	M	0.201	0.361	0	2E-16	0	128.58	gagtggtcgcCtgcgtcatc	m5C_12585
chr6	31803082	+	C	120	29	0.242	0	0	T	91	M	0.174	0.326	0	0	0	100.84	grcgtgatgCcatcacccga	m5C_12561
chr6	31803086	+	C	117	31	0.265	0	0	T	86	M	0.193	0.351	0	1E-16	0	119.9	ctgatgcctCaccgcagcgc	m5C_12559
chr6	31803088	+	C	116	26	0.224	0	0	T	90	M	0.158	0.308	0	0	0	82.054	gatgcctacaCcgagcgctc	m5C_12553
chr6	31803096	+	C	114	30	0.265	1	0.009	T	83	M	0.193	0.354	0	0	0	115.65	caccgcagcgCtctgaccgc	m5C_12580
chr6	31803103	+	C	84	37	0.44	0	0	T	47	M	0.339	0.547	0	1E-10	0	251.03	gcgcctctgacCgccccctgg	m5C_12586
chr6	31804867	+	C	114	67	0.588	0	0	C	67	M	0.496	0.674	0	4E-12	0	664.56	atgatgattCacagactaga	m5C_12582
chr6	31804869	+	C	117	61	0.521	0	0	C	61	M	0.432	0.61	0	1E-12	0	526.57	gatgattcaCagactagaagt	m5C_12595
chr6	31804873	+	C	106	80	0.755	0	0	C	80	M	0.665	0.827	0	6E-10	0	1063.8	attcacagaCtagagctctc	m5C_12563
chr6	31804880	+	C	84	59	0.702	0	0	C	59	M	0.598	0.79	0	8E-09	0	705.06	agactagagCtccgatgctg	m5C_12575
chr6	31804882	+	C	83	55	0.663	0	0	C	55	M	0.556	0.755	0	4E-09	0	611.33	actagagctCcgatcgctg	m5C_12602
chr6	31804883	+	C	84	32	0.381	0	0	T	52	M	0.284	0.488	0	2E-11	0	182.06	ctagagctcCgatcgctgc	m5C_12572
chr6	31804888	+	C	62	40	0.656	1	0.016	C	40	M	0.53	0.763	0	1E-07	0	424.4	gtctccgatgCtggcatgat	m5C_12570
chr6	31804893	+	C	53	34	0.642	0	0	C	34	M	0.507	0.757	0	1E-06	0	344.7	cgatcgctggCgatggtcaa	m5C_12560
chr6	31804901	+	C	50	32	0.64	0	0	C	32	M	0.501	0.759	0	7E-07	0	320.9	grcatgatgCaaaactaagt	m5C_12593
chr6	31804906	+	C	54	32	0.604	1	0.019	C	32	M	0.469	0.724	0	7E-07	0	300.42	gatgcaaaaCtaagtctga	m5C_12556
chr6	31804913	+	C	50	29	0.58	0	0	C	29	M	0.442	0.706	0	4E-07	0	256.55	aaactaagtCtgaactattt	m5C_12597
chr6	31804917	+	C	47	28	0.596	0	0	C	28	M	0.453	0.724	0	8E-06	0	253.91	taagtctgaCtctattaggg	m5C_12565
chr6	31922470	-	C	37	18	0.486	0	0	T	19	M	0.334	0.641	0	3E-05	0	120.41	agaccgagatCgggagcggga	m5C_12632
chr6	33287796	-	C	33	12	0.364	0	0	T	21	M	0.222	0.534	0	5E-06	0	53.249	gaggaagaagCagcacagagt	m5C_12324
chr6	39463178	-	C	38	28	0.737	0	0	C	28	M	0.58	0.85	0	0.0002	0	324.75	caggatgctCtgaaggaggt	m5C_12351
chr6	41902812	-	C	34	19	0.559	0	0	C	19	M	0.395	0.711	0	3E-05	0	149.92	ctggagggtgCtgagcccttg	m5C_12450
chr6	43738275	+	C	33	12	0.364	0	0	T	21	M	0.222	0.534	0	5E-06	0	53.249	aaagaggtagCaagagctcca	m5C_12393
chr6	43738281	+	C	31	12	0.387	0	0	T	19	M	0.237	0.562	0	5E-06	0	56.959	gtagcaagagCtccagagaga	m5C_12390
chr6	43738718	+	C	58	26	0.448	0	0	T	32	M	0.327	0.575	0	2E-07	0	170.3	gagccgcagcCggaggagggg	m5C_12394
chr6	44218040	+	C	213	55	0.27	9	0.042	T	149	M	0.213	0.334	0	0	0	234.72	gggaagaagaaCggaagaagga	m5C_13037
chr6	44218068	+	C	505	201	0.406	10	0.02	T	294	M	0.364	0.45	0	0	0	1462	gatgatgaggCagaagaagag	m5C_13045
chr6	44219903	+	C	349	75	0.215	0	0	T	274	M	0.175	0.261	0	0	0	262.55	tctggagctgCtgaaggatga	m5C_13042
chr6	44219904	+	C	373	93	0.249	0	0	T	280	M	0.208	0.296	0	0	0	387.12	ctggagctgcCtgaaggatgag	m5C_13036
chr6	52132683	-	C	188	60	0.319	0	0	T	128	M	0.257	0.389	0	0	0	308.05	gccaaagagaaCcaaggagcaga	m5C_12726
chr6	52132692	-	C	121	54	0.446	0	0	T	67	M	0.361	0.535	0	8E-15	0	389.57	aggagaagaaGCaaaggagacc	m5C_12724
chr6	52132720	-	C	68	15	0.221	0	0	T	53	M	0.138	0.333	0	6E-11	0	41.547	gaggatgaatCagaagacagaa	m5C_12722
chr6	56557786	-	C	35	26	0.743	0	0	C	26	M	0.579	0.858	0	0.0001	0	301.24	tggggcaaaaCaatgaaaaatg	m5C_12682
chr6	64423352	+	C	32	9	0.281	0	0	T	23	M	0.156	0.454	5E-13	1E-06	6E-13	17.198	aaagacaagaaCagagacagaa	m5C_12755
chr6	64423358	+	C	34	14	0.412	0	0	T	20	M	0.264	0.578	0	9E-06	0	73.824	aggacagagaCagaaaaagca	m5C_12753
chr6	64423367	+	C	38	16	0.421	0	0	T	22	M	0.279	0.578	0	2E-05	0	89.127	acagaaaaagCaggagggaag	m5C_12748
chr6	70183134	-	C	56	20	0.357	0	0	T	36	M	0.245	0.488	0	3E-08	0	97.826	ccggagaagcCagctggagcc	m5C_12796
chr6	70183135	-	C	54	32	0.593	0	0	C	32	M	0.46	0.713	0	7E-07	0	294.19	cccggagaagCcaagtggagc	m5C_12800
chr6	70183143	-	C	64	27	0.422	0	0	T	37	M	0.309	0.544	0	7E-09	0	166.7	tgaatgctccCggagaagcca	m5C_12786
chr6	70183144	-	C	61	17	0.279	0	0	T	44	M	0.182	0.402	0	2E-10	0	61.841	gtgactgacCcggaagaagcc	m5C_12793
chr6	70183145	-	C	57	34	0.596	0	0	C	34	M	0.467	0.714	0	1E-06	0	317.54	cgtaggaagCccggagaagc	m5C_12801
chr6	70183150	-	C	64	24	0.375	0	0	T	40	M	0.267	0.497	0	3E-09	0	128	ggaaacgggaCtgaatcccgg	m5C_12803
chr6	73549645	+	C	49	31	0.633	0	0	C	31	M	0.493	0.753	0	1E-05	0	305.45	atgggtgggtCgggtggaaga	m5C_12810
chr6	76599944	+	C	43	12	0.279	0	0	T	31	M	0.167	0.427	2E-16	7E-08	2E-16	31.457	gtgaagagaaCgaaaaagctc	m5C_13118
chr6	76599954	+	C	39	13	0.333	0	0	T	26	M	0.206	0.49	0	7E-06	0	53.645	cgaaaaacgtCgaagaagagga	m5C_13115
chr6	86387061	-	C	263	209	0.795	0	0	C	209	M	0.742	0.839	0	0	0	3100.7	tatcccgaacCtgaactcttg	m5C_13282
chr6	86387062	-	C	259	207	0.799	0	0	C	207	M	0.746	0.843	0	0	0	3089.4	tatcccgaacCtgaactcttg	m5C_13276
chr6	86387068	-	C	274	214	0.781	0	0	C	214	M	0.728	0.826	0	0	0	3117.4	atgaatctatCccgaacctga	m5C_13280
chr6	86387073	-	C	268	209	0.78	0	0	C	209	M	0.726	0.825	0	0	0	3036.7	ctggatgatCtatacccga	m5C_13289
chr6	86387313	-	C	42	13	0.31	0	0	T	29	M	0.191	0.46	0	1E-07	0	49.584	gattcggcttCtgaattaag	m5C_13286
chr6	86387316	-	C	55	38	0.691	0	0	C	38	M	0.56	0.797	0	2E-06	0	425.38	acggattcggCttctgatgatt	m5C_13294
chr6	86387319	-	C	53	30	0.566	0	0	C	30	M	0.433	0.69	0	5E-07	0	259.59	agtaggaattCggctcttgag	m5C_13291
chr6	86387325	-	C	52	15	0.288	0	0	T	37	M	0.183	0.423	0	5E-09	0	54.989	aaaaataagaCggattcggt	m5C_13292
chr6	86387343	-	C	48	21	0.438	0	0	T	27	M	0.307	0.577	0	2E-06	0	128.94	aaactgataaCtgaagaanaa	m5C_13281
chr6	86387350	-	C	41	20	0.488	0	0	T	21	M	0.343	0.635	0	1E-06	0	137.02	tatcccgaagCtgaataacctg	m5C_13283
chr6	86387361	-	C	41	11	0.268	0	0	T	30	M	0.157	0.419	6E-15	4E-08	7E-15	24.554	atgatgaacCtatcccgaag	m5C_13272
chr6	86387362	-	C	37	9	0.243	0	0	T	28	M	0.134	0.401	3E-12	1E-06	3E-12	13.907	aatgatgaacCtatcccga	m5C_13287
chr6	109103258	+	C	31	9	0.29	0	0	T	22	M	0.161	0.466	4E-13	1E-06	4E-13	18.015	gggtggtggCaaggagggga	m5C_13394
chr6	111280000	+	C	43	11	0.256	0	0	T	32	M	0.149	0.402	1E-14	4E-08	1E-14	22.889	cgagcggaagCcaagagacgg	m5C_13251
chr6	111280008	+	C	36	11	0.306	0	0	T	25	M	0.18	0.469	1E-15	3E-06	1E-15	29.708	gtccagaggaCggagaagacg	m5C_13244
chr6	123066572	+	C	33	8	0.242	0	0	T	25	M	0.128	0.41	3E-11	7E-07	3E-11	10.787	agcaggtgcCtaaggagggg	m5C_13386
chr6	123066587	+	C	85	43	0.506	0	0	C	43	M	0.402	0.61	0	4E-10	0	345.43	gagggaggaCcgggccaggt	m5C_13384
chr6	123066588	+	C	84	27	0.321	0	0	T	57	M	0.231	0.427	0	4E-12	0	124.88	agggaggaacCggcccaggtc	m5C_13383
chr6	123066592	+	C	81	19	0.235	0	0	T	62	M	0.156	0.338	0	8E-14	0	59.137	ggggaccggcCagggcgga	m5C_13382
chr6	123066593	+	C	79	20	0.253	0	0	T	59	M	0.17	0.359	0	1E-11	0	68.111	tggaccggcCaggtcgga	m5C_13385
chr6	133137955	+	C	74	55	0.743	0	0	C	55	M	0.633	0.829	0	8E-08	0			

chr6	139308568	-	C	35	14	0.4	0	0 T	21 M	0.256	0.564	0	9E-06	0	71.541	cgccggggggCtggttctctg	m5C_13552
chr6	139308579	-	C	34	11	0.324	0	0 T	23 M	0.191	0.492	4E-16	3E-06	5E-16	32.309	tccttgggggCcgggggggg	m5C_13549
chr6	139308580	-	C	34	13	0.382	0	0 T	21 M	0.239	0.55	0	7E-06	0	62.14	ttcttgggggCcgggggggg	m5C_13561
chr6	144537695	+	C	47	25	0.532	0	0 C	25 M	0.392	0.667	0	4E-06	0	196.16	ccaggatggcCgaggggttaa	m5C_13753
chr6	150639786	+	C	39	8	0.205	0	0 T	31 M	0.108	0.355	2E-10	7E-07	2E-10	8.4438	gctctggggcCtaggggcagg	m5C_13780
chr6	151426777	-	C	36	13	0.361	0	0 T	23 M	0.225	0.524	0	7E-06	0	58.436	cccttggggcCtaggggctag	m5C_13787
chr6	159191860	-	C	97	32	0.33	0	0 T	65 M	0.244	0.428	0	5E-13	0	156.4	agatgtatgcccCggaaggagg	m5C_14092
chr6	159191890	-	C	105	33	0.314	0	0 T	72 M	0.233	0.408	0	2E-14	0	154.03	ggagagaacaCgggggagag	m5C_14108
chr6	159191891	-	C	100	33	0.333	1	0.01 T	66 M	0.248	0.431	0	8E-13	0	163.84	aggagagaaaCcgggggagag	m5C_14094
chr6	159191912	-	C	62	22	0.355	0	0 T	40 M	0.247	0.479	0	1E-09	0	108.87	cagctggaaaCagagaagaaa	m5C_14104
chr6	160525725	+	C	35	20	0.571	0	0 C	20 M	0.409	0.72	0	4E-05	0	163.43	gaagaagagaCagatgagaat	m5C_13902
chr6	160525740	+	C	32	18	0.562	0	0 C	18 M	0.393	0.718	0	3E-05	0	141.57	gagaatgaaaCagagggctg	m5C_13900
chr6	166365102	-	C	48	36	0.75	0	0 C	36 M	0.612	0.851	0	3E-05	0	440.75	aaggctggagCcgatgggaag	m5C_13982
chr6	166365108	-	C	46	16	0.348	0	0 T	30 M	0.227	0.492	0	4E-07	0	72.579	gaaagggaaggCtggagccaga	m5C_13972
chr6	166400055	-	C	41	18	0.439	0	0 T	23 M	0.299	0.59	0	8E-07	0	107.6	gagagagagaCtggagagggg	m5C_13975
chr7	1314568	+	C	35	18	0.514	0	0 C	18 M	0.356	0.67	0	3E-05	0	128.05	ctgtccggggCtgcattgtgtg	m5C_14880
chr7	1314571	+	C	38	20	0.526	0	0 C	20 M	0.373	0.675	0	4E-05	0	149.03	tccggggctgCatgtgtgtgt	m5C_14890
chr7	26233292	-	C	31	16	0.516	0	0 C	16 M	0.348	0.68	0	2E-05	0	111.49	gagtagcccCggttatggag	m5C_14333
chr7	26233293	-	C	31	14	0.452	0	0 T	17 M	0.292	0.622	0	9E-06	0	81.652	ggaggaagccCcggttatgga	m5C_14326
chr7	26233295	-	C	34	15	0.441	0	0 T	19 M	0.289	0.605	0	1E-05	0	86.65	tggagggtagCcccggttatg	m5C_14338
chr7	26236054	-	C	34	17	0.5	0	0 CT	17 M	0.341	0.659	0	2E-05	0	115.83	aaatttcggaCcaggaccagg	m5C_14331
chr7	26236058	-	C	36	18	0.5	0	0 CT	18 M	0.345	0.655	0	3E-05	0	124.11	gtggaaatttcCaggaccaggac	m5C_14329
chr7	44608551	-	C	31	10	0.323	0	0 T	21 M	0.186	0.499	7E-15	2E-06	8E-15	26.273	attcggggaggCaagattgaag	m5C_15993
chr7	45024985	-	C	35	18	0.514	0	0 C	18 M	0.356	0.67	0	3E-05	0	128.05	atagaatttCagacaattgac	m5C_15989
chr7	45025074	-	C	34	14	0.412	0	0 T	20 M	0.264	0.578	0	9E-06	0	73.824	ctgcccgggacCctatgcattc	m5C_15970
chr7	45025084	-	C	34	18	0.529	0	0 C	18 M	0.367	0.685	0	3E-05	0	132.25	gtgttgggtCtgcggtagcc	m5C_15973
chr7	45025095	-	C	36	13	0.361	0	0 T	23 M	0.225	0.524	0	7E-06	0	58.436	aagcttcagCgtgctgggtg	m5C_15990
chr7	45025101	-	C	36	19	0.528	0	0 C	19 M	0.37	0.68	0	3E-05	0	140.62	ggtagcaagCtccagcgggc	m5C_15977
chr7	45952686	-	C	56	26	0.464	0	0 T	30 M	0.34	0.593	0	2E-07	0	176.9	gtaggaggggCagagagaacag	m5C_15991
chr7	53843937	+	C	248	76	0.306	0	0 T	172 M	0.252	0.366	0	0	0	383.63	atttttggagCaggagagatgg	m5C_14425
chr7	55275228	+	C	33	10	0.303	0	0 T	23 M	0.174	0.473	2E-14	2E-06	2E-14	23.982	gagcacagaCagaggaggttg	m5C_14609
chr7	55275242	+	C	37	10	0.27	0	0 T	27 M	0.154	0.43	7E-14	2E-06	7E-14	20.282	gaggttgggtCctgctctgag	m5C_14617
chr7	55275243	+	C	36	17	0.472	0	0 T	19 M	0.32	0.63	0	2E-05	0	108.75	aggttgggtCtgcctgagga	m5C_14619
chr7	55275247	+	C	33	16	0.485	0	0 T	17 M	0.325	0.648	0	2E-05	0	104.01	tgggtcctgcCtggagagacc	m5C_14618
chr7	75959222	-	C	36	16	0.444	0	0 T	20 M	0.295	0.604	0	2E-05	0	94.531	gaagtggccaCcggaagagaaa	m5C_14720
chr7	80963038	+	C	53	37	0.698	0	0 C	37 M	0.565	0.805	0	2E-06	0	417.83	attaaattgCtgcagttaaa	m5C_15058
chr7	80963067	+	C	66	13	0.203	2	0.03 T	51 M	0.123	0.317	3E-15	2E-11	3E-15	23.172	agttggatcCggagcagagc	m5C_15064
chr7	80963073	+	C	42	18	0.429	0	0 T	24 M	0.291	0.578	0	8E-07	0	104.82	atctcgggagCaggcgtgagg	m5C_15067
chr7	80963129	-	C	40	30	0.75	0	0 C	30 M	0.598	0.858	0	1E-05	0	358.83	gagggggcgcCgagagttaac	m5C_15107
chr7	80963130	-	C	38	23	0.605	0	0 C	23 M	0.447	0.744	0	8E-05	0	205.7	cgagggggcgcCgagaggttaa	m5C_15110
chr7	80963132	-	C	37	22	0.595	0	0 C	22 M	0.435	0.737	0	6E-05	0	191.34	atcgagggggCggcagaggtt	m5C_15108
chr7	80963140	-	C	41	16	0.39	0	0 T	25 M	0.257	0.543	0	4E-07	0	82.099	gctagagcatCgagggggcgc	m5C_15100
chr7	97481517	-	C	32	15	0.469	0	0 T	17 M	0.309	0.636	0	1E-05	0	92.607	tggatggggaCtgggggtaga	m5C_15368
chr7	99691444	-	C	67	19	0.284	0	0 T	48 M	0.19	0.401	0	5E-10	0	72.087	gctgttcgtgCaggtagtgtg	m5C_15304
chr7	99691448	-	C	70	45	0.643	0	0 C	45 M	0.526	0.745	0	3E-07	0	473.29	aagtgctgtgtCgtgcaggtag	m5C_15306
chr7	99691453	-	C	72	15	0.208	0	0 T	57 M	0.131	0.316	0	6E-13	0	39.156	ctccaaagtgCtgtctgagca	m5C_15323
chr7	99691460	-	C	33	8	0.242	0	0 T	25 M	0.128	0.41	3E-11	7E-07	3E-11	10.787	ctggggggcCaaaagtgtgt	m5C_15322
chr7	99691675	-	C	56	40	0.714	0	0 C	40 M	0.585	0.816	0	3E-06	0	468.2	aaagtgctgaCagtcagata	m5C_15319
chr7	99691679	-	C	53	17	0.321	0	0 T	36 M	0.211	0.455	0	1E-08	0	71.713	ggctaaagtgCtgcaggtgca	m5C_15318
chr7	100482634	+	C	32	14	0.438	0	0 T	18 M	0.282	0.607	0	9E-06	0	78.862	agagaggggcCaggtctgga	m5C_15194
chr7	100482638	+	C	31	19	0.613	0	0 C	19 M	0.438	0.763	0	3E-05	0	166.53	agcggcagggCtggagagagag	m5C_15201
chr7	102782156	-	C	48	28	0.583	0	0 C	28 M	0.443	0.712	0	8E-06	0	247.97	ggcatatgggCatagggaagc	m5C_15147
chr7	102782176	-	C	50	21	0.42	0	0 T	29 M	0.294	0.558	0	5E-08	0	123.37	cttggcctgcCggagagggcag	m5C_15148
chr7	102782177	-	C	48	22	0.458	0	0 T	26 M	0.326	0.597	0	2E-06	0	143.33	cttggcctgcCgggaaggcca	m5C_15146
chr7	102782181	-	C	38	14	0.368	0	0 T	24 M	0.234	0.527	0	9E-06	0	65.475	aaacaccttggCctgcgggaag	m5C_15144
chr7	129410288	-	C	40	30	0.75	0	0 C	30 M	0.598	0.858	0	1E-05	0	358.83	agaactcacCtggggagga	m5C_15594
chr7	129410290	-	C	58	42	0.724	0	0 C	42 M	0.598	0.822	0	4E-06	0	502.28	gtagaactcaCactgtgtagg	m5C_15577
chr7	129410292	-	C	60	45	0.75	0	0 C	45 M	0.628	0.842	0	3E-07	0	564.91	tggtagaactCacactgtgga	m5C_15582
chr7	134851421	-	C	37	11	0.297	0	0 T	26 M	0.175	0.458	1E-15	3E-06	2E-15	28.551	agcagagaccCtggagagagag	m5C_15838
chr7	134851423	-	C	39	18	0.462	0	0 T	21 M	0.316	0.614	0	3E-05	0	113.64	gtagcagagCcttgaggagg	m5C_15839
chr7	139094341	+	C	41	19	0.463	0	0 T	22 M	0.321	0.613	0	1E-06	0	121.81	agaaaagaaaCagggaacggc	m5C_15726
chr7	139094348	+	C	71	23	0.324	0	0 T	48 M	0.227	0.439	0	4E-11	0	104.22	aaaccaggaaCggctgaaacg	m5C_15729
chr7	139094351	+	C	69	28	0.406	0	0 T	41 M	0.298	0.524	0	1E-08	0	166.82	ccaggaacggCtgaagacgaag	m5C_15732
chr7	139094357	+	C	74	26	0.351	0	0 T	48 M	0.252	0.465	0	1E-10	0	131.24	acggctgaaaCgaaagagaaga	m5C_15720
chr7	141304706	-	C	36	8	0.222	0	0 T	28 M	0.117	0.381	7E-11	7E-07	8E-11	9.4968	tatgtatcccCagatggtagt	m5C_15484
chr7	141304708	-	C	37	10	0.27	0	0 T	27 M	0.154	0.43	7E-14	2E-06	7E-14	20.282	aatatgtgatCccagattgga	m5C_15476
chr7	148638588	+	C	104	32	0.308	0	0 T	72 M	0.227	0.402	0	1E-14	0	145.38	acagttgggcCgaggtgtgtg	m5C_16248
chr7	148638627	+	C	109	32	0.294	0	0 T	77 M	0.216	0.385	0	1E-14	0	138.42	ttaacattgtCtcccccaacc	m5C_16252
chr7	148638630	+	C	111	44	0.396	0	0 T	67 M	0.31	0.489	0	2E-14	0	273.09	acattgtctCccccacaacc	m5C_16249
chr7	148638649	+	C	189	59	0.312	0	0 T	130 M	0.25	0.381	0	0	0	295.47	ccgcgcttgaCtagcttctg	m5C_16247
chr7	148638657	+	C	162	55	0.34	0	0 T	107 M	0.271	0.415	0	0	0	298.16	gactagcttCtgttttgac	m5C_16251
chr7	148684289	-	C	55	38	0.691	0	0 C	38 M	0.56	0.797	0	2E-06	0	425.38	cagtcagttaCagatcgaact	m5C_16269
chr7	148684295	-	C	69	43	0.623	0	0 C	43 M	0.505	0.728	0	2E-07	0	434.49	tgttcacagtCagttacagat	m5C_16260
chr7	148684299	-	C	76	47	0.618	0	0 C	47 M	0.506	0.719	0	2E-08	0	475.65	tgattgttcaCagtcagttac	m5C_16253
chr7	148684301	-	C	76	48	0.632	0	0 C	48 M	0.519	0.731	0	3E-08	0	498.48	attgattgttCacagtcagrt	m5C_16263
chr7	148684313	-	C	64	32	0.5	0	0 CT	32 M	0.381	0.619	0	3E-08	0	243.85	tgagtattctCa	

chr8	22576077	+	C	33	11	0.333	0	0	T	22	M	0.198	0.504	2E-16	3E-06	2E-16	34.007	ctgagtggtgCccggagtggc	m5C_16114
chr8	23147913	+	C	44	34	0.773	0	0	C	34	M	0.63	0.872	0	2E-05	0	428.45	aggaagaggaCgaagaggaagg	m5C_16111
chr8	30432335	-	C	32	19	0.594	0	0	C	19	M	0.423	0.745	0	3E-05	0	160.59	tgtatgtgaaCagtgaggagag	m5C_16301
chr8	33371030	+	C	51	15	0.294	0	0	T	36	M	0.187	0.43	0	5E-09	0	56.126	attgggtgttCatacgttgt	m5C_16191
chr8	33371034	+	C	53	19	0.358	0	0	T	34	M	0.243	0.493	0	2E-08	0	92.347	gggttcataCgcttgggtga	m5C_16185
chr8	33371036	+	C	50	13	0.26	0	0	T	37	M	0.159	0.396	0	2E-09	0	41.266	tgtcatacgtCttgggtgaga	m5C_16195
chr8	33371051	+	C	39	13	0.333	0	0	T	26	M	0.206	0.49	0	7E-06	0	53.645	gtgagatgtgCacccttgaa	m5C_16192
chr8	33371052	+	C	40	16	0.4	0	0	T	24	M	0.263	0.554	0	2E-05	0	84.314	tgagatgtgcCacccttgaa	m5C_16201
chr8	33371054	+	C	37	15	0.405	0	0	T	22	M	0.263	0.565	0	1E-05	0	79.039	agatgtgccCacccttgaa	m5C_16187
chr8	33371055	+	C	40	15	0.375	0	0	T	25	M	0.242	0.53	0	3E-07	0	72.668	gatgtgcacCcttgaa	m5C_16197
chr8	33371056	+	C	37	19	0.514	0	0	C	19	M	0.359	0.666	0	3E-05	0	136.4	atgtgccaccCttgaaccttg	m5C_16198
chr8	33371062	+	C	39	16	0.41	0	0	T	23	M	0.271	0.566	0	2E-05	0	86.653	cacccttgaaCcttgataga	m5C_16200
chr8	33371063	+	C	42	15	0.357	0	0	T	27	M	0.23	0.508	0	3E-07	0	68.967	acccttgaaCcttgataga	m5C_16189
chr8	33371070	+	C	60	20	0.339	1	0.017	T	39	M	0.231	0.466	0	3E-08	0	92.55	aaccttgtaCgacgtgggga	m5C_16178
chr8	33371073	+	C	68	23	0.338	0	0	T	45	M	0.237	0.457	0	2E-09	0	109.08	cttgatagaCggggacat	m5C_16193
chr8	33371079	+	C	73	31	0.425	0	0	T	42	M	0.318	0.539	0	6E-10	0	197.06	acgacgggCacattaccgc	m5C_16184
chr8	33371081	+	C	78	26	0.333	0	0	T	52	M	0.239	0.444	0	1E-10	0	124.14	gacgtggggaCattaccgtc	m5C_16186
chr8	33371086	+	C	81	29	0.358	0	0	T	52	M	0.262	0.467	0	8E-12	0	152.1	gggacattacCcggtga	m5C_16203
chr8	33371087	+	C	81	40	0.494	0	0	T	41	M	0.388	0.6	0	2E-10	0	310.18	ggacattacCgctga	m5C_16179
chr8	33371088	+	C	83	22	0.265	0	0	T	61	M	0.182	0.369	0	4E-13	0	80.099	gcattaccCgctga	m5C_16188
chr8	33371091	+	C	75	38	0.507	0	0	C	38	M	0.396	0.617	0	4E-09	0	300.95	cattaccgcCtgacctga	m5C_16181
chr8	33371095	+	C	75	34	0.453	0	0	T	41	M	0.346	0.566	0	1E-09	0	235.07	accgtctgaCtgga	m5C_16194
chr8	33371096	+	C	59	23	0.39	0	0	T	36	M	0.276	0.517	0	9E-08	0	126.86	cccgctgaCtgga	m5C_16182
chr8	40449638	+	C	99	33	0.333	0	0	T	66	M	0.248	0.431	0	8E-13	0	163.84	gggtgggaaCatgagtgt	m5C_16335
chr8	41917311	+	C	40	17	0.425	0	0	T	23	M	0.285	0.578	0	6E-07	0	96.931	gatggaggaCagattacta	m5C_16326
chr8	46951851	-	C	39	19	0.487	0	0	T	20	M	0.339	0.638	0	3E-05	0	128.69	ctcgatagCgggtctctgc	m5C_16423
chr8	46951852	-	C	43	22	0.512	0	0	C	22	M	0.368	0.654	0	2E-06	0	161.71	cctcgatagCgggtctctgc	m5C_16432
chr8	46951859	-	C	44	23	0.523	0	0	C	23	M	0.379	0.662	0	3E-06	0	174.5	tgggtgctCggatagccgg	m5C_16428
chr8	46951861	-	C	44	22	0.5	0	0	CT	22	M	0.358	0.642	0	2E-06	0	157.66	cttggtggCctcgatagcc	m5C_16433
chr8	46951862	-	C	44	23	0.523	0	0	C	23	M	0.379	0.662	0	3E-06	0	174.5	ccttggtggCctcgatagcc	m5C_16422
chr8	56755213	-	C	69	20	0.29	0	0	T	49	M	0.196	0.406	0	7E-10	0	78.464	atcgccgacCtgggtatagg	m5C_16505
chr8	56755214	-	C	62	40	0.645	0	0	C	40	M	0.521	0.753	0	1E-07	0	416.65	catcgccgaCctgggtatag	m5C_16510
chr8	56986427	-	C	38	29	0.763	0	0	C	29	M	0.608	0.87	0	0.0002	0	352.6	tgttgatgaCgggtatatt	m5C_16502
chr8	67834714	-	C	40	21	0.525	0	0	C	21	M	0.375	0.671	0	5E-05	0	157.49	aattttaagaCtgatgcca	m5C_16742
chr8	67834736	-	C	58	41	0.707	0	0	C	41	M	0.58	0.808	0	3E-06	0	475.49	ctgagtggtCttgagaaaa	m5C_16746
chr8	67834746	-	C	54	23	0.426	0	0	T	31	M	0.303	0.558	0	9E-08	0	139.53	gtttaccagCtgaggtgtc	m5C_16747
chr8	67834749	-	C	54	32	0.593	0	0	C	32	M	0.46	0.713	0	7E-07	0	294.19	gccgtttaccCagctgaggt	m5C_16744
chr8	67834750	-	C	53	26	0.491	0	0	T	27	M	0.361	0.621	0	2E-07	0	187.84	tgccgtttacCagctgaggt	m5C_16734
chr8	67834751	-	C	57	24	0.421	0	0	T	33	M	0.302	0.555	0	1E-07	0	144.9	ttgccgtttaCccagctgagg	m5C_16743
chr8	67834757	-	C	57	36	0.632	0	0	C	36	M	0.502	0.745	0	2E-06	0	361.28	tacttttgcCgtttaccag	m5C_16737
chr8	67834758	-	C	55	24	0.436	0	0	T	31	M	0.314	0.567	0	1E-07	0	150.59	ttaacttttgcCgtttacca	m5C_16735
chr8	67834765	-	C	51	32	0.627	0	0	C	32	M	0.49	0.747	0	7E-07	0	313.76	acttaaatatCttttgccgt	m5C_16733
chr8	67834774	-	C	55	25	0.455	0	0	T	30	M	0.33	0.585	0	2E-07	0	165.13	acaatgatgaCttaaattact	m5C_16745
chr8	68070802	+	C	50	29	0.58	0	0	C	29	M	0.442	0.706	0	4E-07	0	256.55	tgaagaggaCaggaaaaaga	m5C_16528
chr8	69218664	-	C	43	25	0.581	0	0	C	25	M	0.433	0.716	0	4E-06	0	216.64	ggaggtggagCatgagcacag	m5C_16530
chr8	70602423	-	C	318	183	0.575	0	0	C	183	M	0.521	0.629	0	0	0	1905.3	acctatcCagcgaaacca	m5C_17994
chr8	70602432	-	C	444	189	0.426	0	0	T	255	M	0.381	0.472	0	0	0	1438.3	actgccctaCctatctcca	m5C_17949
chr8	98725892	+	C	33	10	0.303	0	0	T	23	M	0.174	0.473	2E-14	2E-06	2E-14	23.982	aacctaaaggCttcatgatag	m5C_16926
chr8	100218905	-	C	45	29	0.644	0	0	C	29	M	0.498	0.768	0	1E-05	0	289.05	gggtttagacCagatgttaa	m5C_16860
chr8	110594886	-	C	31	12	0.387	0	0	T	19	M	0.237	0.562	0	5E-06	0	56.959	atgatgatgaCgatgatgat	m5C_17575
chr8	117862909	-	C	46	10	0.217	0	0	T	36	M	0.123	0.356	1E-12	2E-08	1E-12	14.731	gaactctgcCagaaaaaag	m5C_16989
chr8	125785419	-	C	76	56	0.737	0	0	C	56	M	0.628	0.823	0	9E-08	0	703.57	aaggagcatCctaggggtct	m5C_17222
chr8	125785420	-	C	68	46	0.676	0	0	C	46	M	0.558	0.776	0	4E-07	0	513.77	caaggagcatCcttaggggtc	m5C_17206
chr8	142233886	-	C	41	21	0.512	0	0	C	21	M	0.365	0.657	0	2E-06	0	153.23	ggcacgtctCctctgggtgc	m5C_17264
chr8	142233892	-	C	40	30	0.75	0	0	C	30	M	0.598	0.858	0	1E-05	0	358.83	tctgggggaCgggtctctgc	m5C_17258
chr8	142233894	-	C	41	10	0.244	0	0	T	31	M	0.138	0.393	2E-13	2E-08	3E-13	17.447	cctctgggggaCaggtctctc	m5C_17250
chr8	144997043	-	C	49	18	0.367	0	0	T	31	M	0.247	0.507	0	8E-07	0	88.794	ggacaagggaCagatggcgca	m5C_17426
chr8	144997050	-	C	57	29	0.509	0	0	C	29	M	0.383	0.634	0	4E-07	0	221.91	tgacagaggaCaaggagcaga	m5C_17421
chr8	144997058	-	C	50	16	0.32	0	0	T	34	M	0.208	0.458	0	7E-09	0	66.426	gcggggctgCaggagagacaa	m5C_17419
chr9	4793080	-	C	71	38	0.535	0	0	C	38	M	0.42	0.646	0	4E-09	0	319.5	tgccgctgcCagaaagacg	m5C_17305
chr9	17578939	-	C	47	20	0.426	0	0	T	27	M	0.295	0.567	0	1E-06	0	118.05	ggggatgggCtcagcggcac	m5C_18508
chr9	19063673	-	C	31	18	0.581	0	0	C	18	M	0.408	0.736	0	3E-05	0	146.76	tcgaacggaCagatagggg	m5C_17487
chr9	21512158	-	C	82	28	0.341	0	0	T	54	M	0.248	0.449	0	6E-12	0	138.88	gctgcatagCtggtaactg	m5C_17855
chr9	21512163	-	C	95	51	0.537	0	0	C	51	M	0.437	0.634	0	9E-11	0	445.84	aagatgctggCatactgttg	m5C_17848
chr9	35657751	-	C	93	44	0.473	0	0	T	49	M	0.375	0.574	0	2E-11	0	329.77	ctcagcgggCtggttttgt	m5C_18100
chr9	35657754	-	C	103	49	0.476	0	0	T	54	M	0.382	0.571	0	2E-12	0	374.26	atttcagcgcgggttttt	m5C_18137
chr9	35657761	-	C	110	24	0.218	0	0	T	86	M	0.151	0.304	0	0	0	72.59	ggggctcattCtcagcgggc	m5C_18101
chr9	35657765	-	C	108	51	0.472	0	0	T	57	M	0.381	0.566	0	3E-12	0	388.26	acacggggctCattctcag	m5C_18106
chr9	35657767	-	C	99	31	0.313	0	0	T	68	M	0.23	0.41	0	4E-13	0	142.73	ccacacgggctCtattctcag	m5C_18135
chr9	35657774	-	C	71	25	0.352	0	0	T	46	M	0.251	0.468	0	9E-11	0	125.61	gcaccaaccaCacggggctca	m5C_18121
chr9	35657780	-	C	64	28	0.438	0	0	T	36	M	0.323	0.559	0	1E-08	0	180.85	gtccgcgcacCaaccacacgg	m5C_18128
chr9	35657785	-	C	64	28	0.438	0	0	T	36	M	0.323	0.559	0	1E-08	0	180.85	tgctgtccgcCgcaccaacca	m5C_18125
chr9	35657787	-	C	62	32	0.516	0	0	C	32	M	0.394	0.636	0	3E-08	0	252.46	agtgctgtgcCgcgcaccaac	m5C_18142
chr9	35657838	-	C																

chr9	79186679	+	C	54	20	0.37	0	0	T	34	M	0.254	0.504	0	3E-08	0	101.69	cctcgggtggcCctcggatagc	m5C_18231
chr9	79186680	+	C	52	36	0.692	0	0	C	36	M	0.557	0.801	0	2E-06	0	401.26	ctcgggtggcCtcggatagcc	m5C_18249
chr9	79186682	+	C	59	27	0.458	0	0	T	32	M	0.337	0.583	0	2E-07	0	181.99	cggtggcctCggatagccgg	m5C_18244
chr9	79186683	-	C	31	14	0.452	0	0	T	17	M	0.292	0.622	0	9E-06	0	81.652	accggctatcCgagggccaacc	m5C_18262
chr9	79186688	-	C	48	11	0.229	0	0	T	37	M	0.133	0.365	5E-14	4E-08	5E-14	19.471	gggggaccggCtatccgaggc	m5C_18265
chr9	79186691	-	C	64	31	0.484	0	0	T	33	M	0.366	0.604	0	2E-08	0	227.13	ggcgggggaCcggtatccga	m5C_18305
chr9	79186692	-	C	68	22	0.324	0	0	T	46	M	0.224	0.442	0	1E-09	0	98.725	agggcgggggaCcggtatccg	m5C_18280
chr9	79186699	-	C	84	52	0.619	0	0	C	52	M	0.512	0.716	0	2E-09	0	532.64	cggggacaggCgggggaccgg	m5C_18324
chr9	79186703	-	C	81	33	0.407	0	0	T	48	M	0.307	0.516	0	3E-11	0	202.59	ccggcgggggaCagggggggga	m5C_18294
chr9	79186709	-	C	56	22	0.393	0	0	T	34	M	0.276	0.524	0	7E-08	0	121.35	ggcccgccggCggggacaggc	m5C_18298
chr9	79186712	-	C	44	18	0.409	0	0	T	26	M	0.277	0.556	0	8E-07	0	99.676	ggcggcccgCggcggggaca	m5C_18278
chr9	89037857	-	C	190	56	0.295	0	0	T	134	M	0.234	0.363	0	0	0	262.63	aattgggcacCaaaaaaaaaa	m5C_17826
chr9	89037858	-	C	156	80	0.513	0	0	C	80	M	0.435	0.59	0	2E-16	0	696.04	gaatggggcaCcaaaaaaaaa	m5C_17825
chr9	89037860	-	C	182	40	0.22	0	0	T	142	M	0.166	0.285	0	0	0	132.6	aggaatgggCaccaaaaaaaa	m5C_17824
chr9	89037890	-	C	111	29	0.261	0	0	T	82	M	0.189	0.35	0	0	0	109.33	catgcattgaCctggattgc	m5C_17827
chr9	97109699	-	C	55	20	0.364	0	0	T	35	M	0.249	0.496	0	3E-08	0	99.721	aggaaggctgaCaatgaaggag	m5C_18381
chr9	97109703	-	C	59	29	0.492	0	0	T	30	M	0.368	0.616	0	4E-07	0	213.69	gagcaggaggCtgacaatgag	m5C_18375
chr9	100773572	+	C	100	33	0.33	0	0	T	67	M	0.246	0.427	0	2E-14	0	162.12	atgaggaagaCgaggaatgatg	m5C_19793
chr9	100773578	+	C	82	30	0.366	0	0	T	52	M	0.27	0.474	0	1E-11	0	161.87	aagacgagaCgatgaggatg	m5C_19791
chr9	100773650	+	C	111	26	0.234	0	0	T	85	M	0.165	0.321	0	0	0	85.881	gggatgagggaCgacgatgaag	m5C_19789
chr9	100773653	+	C	107	35	0.327	0	0	T	72	M	0.246	0.421	0	3E-14	0	171.88	atgaggaagaCgatgaatgca	m5C_19788
chr9	100774718	+	C	56	35	0.625	0	0	C	35	M	0.494	0.74	0	1E-06	0	345.84	agaattgggaCttgatgaaga	m5C_19792
chr9	104314872	+	C	37	17	0.459	0	0	T	20	M	0.31	0.616	0	2E-05	0	105.53	ggagagggggaCgagaagaaga	m5C_18178
chr9	104328738	-	C	33	12	0.364	0	0	T	21	M	0.222	0.534	0	5E-06	0	53.249	tgcagggttcCgagcgatg	m5C_18188
chr9	111754688	-	C	276	103	0.373	0	0	T	173	M	0.318	0.432	0	0	0	655.56	ctgagcggtgCtaaaaaaaaa	m5C_19384
chr9	111754693	-	C	318	70	0.22	0	0	T	248	M	0.178	0.269	0	0	0	249.31	catgctgagCgttgctaaa	m5C_19377
chr9	111754698	-	C	330	108	0.327	0	0	T	222	M	0.279	0.38	0	0	0	602.4	ctatgcattgCtggcggtgc	m5C_19378
chr9	111754703	-	C	347	95	0.274	0	0	T	252	M	0.23	0.323	0	0	0	436.1	cggggctatgCtatgctgagc	m5C_19344
chr9	111754708	-	C	374	91	0.243	0	0	T	283	M	0.203	0.289	0	0	0	368.7	cctccggggCtatgcatgct	m5C_19357
chr9	111754713	-	C	387	83	0.214	0	0	T	304	M	0.176	0.258	0	0	0	292.97	gggtctctccCggggctatgc	m5C_19356
chr9	111754714	-	C	391	102	0.261	0	0	T	289	M	0.22	0.307	0	0	0	448.43	tgggtctctcCggggctatg	m5C_19360
chr9	111754715	-	C	385	131	0.34	0	0	T	254	M	0.295	0.389	0	0	0	772.16	ctgggtctctCccggggctat	m5C_19346
chr9	111754717	-	C	375	146	0.389	0	0	T	229	M	0.341	0.44	0	0	0	996.72	cccttggttcCtccggggct	m5C_19381
chr9	111754718	-	C	383	101	0.264	0	0	T	282	M	0.222	0.31	0	0	0	448.6	cccttggttcCtccggggct	m5C_19375
chr9	111754725	-	C	335	112	0.334	0	0	T	223	M	0.286	0.386	0	0	0	640.51	acttggtggcCtgggtctct	m5C_19341
chr9	111754726	-	C	325	92	0.283	0	0	T	233	M	0.237	0.334	0	0	0	435.81	cacttggtgcCctgggtctct	m5C_19359
chr9	111754727	-	C	316	74	0.234	0	0	T	242	M	0.191	0.284	0	0	0	282.46	gcacttgggCctgggtctct	m5C_19347
chr9	111754734	-	C	173	45	0.26	0	0	T	128	M	0.2	0.33	0	0	0	180.41	gttgatggaCtgggtccct	m5C_19342
chr9	111754736	-	C	159	33	0.208	0	0	T	126	M	0.152	0.277	0	0	0	100.17	acgtggaatgCacttgggtcc	m5C_19383
chr9	111754801	-	C	945	272	0.288	0	0	T	673	M	0.26	0.318	0	0	0	1413.7	aagaatgcagCtagctgggg	m5C_19365
chr9	111754804	-	C	1126	301	0.267	0	0	T	825	M	0.242	0.294	0	0	0	1458.6	atgaagaatgCagtagctgtg	m5C_19352
chr9	111754816	-	C	1552	479	0.309	0	0	T	1073	M	0.286	0.332	0	0	0	2741.3	gcttggtgtgCgatgaagaat	m5C_19355
chr9	111754825	-	C	1414	365	0.258	0	0	T	1049	M	0.236	0.282	0	0	0	1722.8	gattgcttggCttgggtgtgc	m5C_19343
chr9	111754830	-	C	1305	531	0.407	0	0	T	774	M	0.381	0.434	0	0	0	4041.5	tgggttgatgCtgggttgg	m5C_19358
chr9	111754845	-	C	992	262	0.264	0	0	T	730	M	0.238	0.292	0	0	0	1245.2	ttttatgactCtaggtgggg	m5C_19348
chr9	111754847	-	C	646	200	0.31	0	0	T	446	M	0.275	0.346	0	0	0	1100.6	cttttatgaCtcttagggg	m5C_19382
chr9	116171145	-	C	31	18	0.581	0	0	C	18	M	0.408	0.736	0	3E-05	0	146.76	atgatgaagaCgaagaaggc	m5C_18445
chr9	116171157	-	C	34	12	0.353	0	0	T	22	M	0.215	0.521	0	5E-06	0	51.571	gggatgagggaCaatgatgaag	m5C_18436
chr9	127620265	-	C	41	21	0.512	0	0	C	21	M	0.365	0.657	0	2E-06	0	153.23	cgaaggagaacCtgaagaccaa	m5C_18658
chr9	127620266	-	C	40	11	0.275	0	0	T	29	M	0.161	0.428	4E-15	3E-06	5E-15	25.45	acgaaggagaCctgaagacca	m5C_18649
chr9	127620275	-	C	39	18	0.462	0	0	T	21	M	0.316	0.614	0	3E-05	0	113.64	tcaacaagcaCgagaaggacc	m5C_18647
chr9	127623819	-	C	68	29	0.426	0	0	T	39	M	0.316	0.545	0	1E-08	0	183.26	gatcaaggctCgagatcttcg	m5C_18670
chr9	127623821	-	C	59	17	0.288	0	0	T	42	M	0.188	0.414	0	1E-08	0	64.044	aagatcaaggCctcgaatctt	m5C_18665
chr9	131456179	+	C	38	13	0.342	0	0	T	25	M	0.212	0.501	0	7E-06	0	55.152	tttaagggtCcgatgatgat	m5C_18561
chr9	135894974	+	C	41	24	0.585	0	0	C	24	M	0.434	0.722	0	4E-06	0	208.16	gcggggcatCgacaaaagaa	m5C_19009
chr9	135894985	+	C	90	20	0.222	0	0	T	70	M	0.149	0.318	0	2E-15	0	59.485	gacaaaagaaCattgaaaaa	m5C_19015
chr9	135894986	+	C	90	28	0.311	0	0	T	62	M	0.225	0.413	0	1E-13	0	125.92	acaaaagaaCattgaaaaa	m5C_19007
chr9	135895009	+	C	173	93	0.538	0	0	C	93	M	0.463	0.61	0	0	0	861.67	gagaaggaggCtgcgatgatg	m5C_19038
chr9	135895012	+	C	153	56	0.366	0	0	T	97	M	0.294	0.445	0	0	0	329.09	aaggaggctgCtgaagaggga	m5C_19024
chr9	135895253	+	C	31	9	0.29	0	0	T	22	M	0.161	0.466	4E-13	1E-06	4E-13	18.015	aagctggtatCtccaagatg	m5C_19030
chr9	135895255	+	C	32	10	0.312	0	0	T	22	M	0.18	0.486	1E-14	2E-06	1E-14	25.084	gcttgatctCcaagaatggg	m5C_19021
chr9	136905268	-	C	32	23	0.719	0	0	C	23	M	0.546	0.844	0	8E-05	0	251.28	gaaggagaagCacaaaggaa	m5C_18913
chr9	139565125	+	C	60	46	0.767	0	0	C	46	M	0.646	0.856	0	7E-06	0	593.98	aggaatgagCgcgtccacg	m5C_18794
chr9	139620679	-	C	33	10	0.303	0	0	T	23	M	0.174	0.473	2E-14	2E-06	2E-14	23.982	tgtctggagCtggtagacc	m5C_18828
chr9	139621283	-	C	39	27	0.692	0	0	C	27	M	0.536	0.814	0	0.0001	0	289.32	acatcttggCattaggggc	m5C_18830
chr9	139621300	-	C	59	28	0.475	0	0	T	31	M	0.353	0.6	0	3E-07	0	197.49	gcttggtgctCgtgtcacat	m5C_18825
chr9	139621317	-	C	69	16	0.232	0	0	T	53	M	0.148	0.344	0	1E-10	0	47.385	cccttagaggCgttgacgtg	m5C_18833
chr9	139621325	-	C	67	20	0.299	0	0	T	47	M	0.202	0.417	0	7E-10	0	80.925	ggacacgtccCctagagggt	m5C_18834
chrM	247	-	C	215	62	0.288	0	0	T	153	M	0.232	0.352	0	0	0	287.62	tgcagattctCaattgtatt	m5C_23822
chrM	251	-	C	311	68	0.219	0	0	T	243	M	0.176	0.268	0	0	0	239.76	gcttggcagaCattcaattgt	m5C_24009
chrM	260	-	C	498	183	0.367	0	0	T	315	M	0.326	0.411	0	0	0	1194.2	tggaaagcggCtggcagaca	m5C_24070
chrM	263	-	C	601	170	0.283	0	0	T	431	M	0.248	0.32	0	0	0	844.29	gttgggaagCggctgtgcag	m5C_24134
chrM	275	-	C	556	124	0.223	0	0	T	432	M	0.19	0.259	0	0	0	472.16	gttatgatgCtgggtggaaa	m5C_24137

chrM	3276 +	C	49	33	0.673	0	0 C	33 M	0.534	0.788	0	2E-05	0	352.3	taaaactttaCagtcagaggt	m5C_23643
chrM	3288 +	C	47	36	0.766	0	0 C	36 M	0.628	0.864	0	3E-05	0	451.98	gtcagaggttCaattcttct	m5C_23541
chrM	6264 +	C	40	29	0.725	0	0 C	29 M	0.572	0.839	0	1E-05	0	331.56	tagtggaggcCggagcaggaa	m5C_23645
chrM	6461 -	C	35	22	0.629	0	0 C	22 M	0.463	0.768	0	6E-05	0	203.88	taggacggatCagacgaagag	m5C_23804
chrM	6466 -	C	92	44	0.478	0	0 T	48 M	0.379	0.579	0	2E-11	0	333.63	ggattaggaCggatcagacg	m5C_24087
chrM	6481 -	C	97	60	0.619	0	0 C	60 M	0.519	0.709	0	5E-10	0	622.95	agaaagaggaCtgcgtgatt	m5C_23799
chrM	6505 -	C	79	33	0.418	0	0 T	46 M	0.315	0.528	0	1E-09	0	208.07	gcagctaggaCttggagagat	m5C_24027
chrM	6511 -	C	66	38	0.576	0	0 C	38 M	0.456	0.688	0	1E-07	0	346.26	atgccagcagCtaggaactggg	m5C_23770
chrM	6514 -	C	47	13	0.277	0	0 T	34 M	0.169	0.418	0	1E-07	0	44.035	ggatgcagCagctaggaact	m5C_24030
chrM	6517 -	C	63	36	0.571	0	0 C	36 M	0.449	0.686	0	6E-08	0	323	atagtgatgcCagcagctagg	m5C_24126
chrM	6518 -	C	71	35	0.493	0	0 T	36 M	0.38	0.607	0	2E-09	0	266.03	tataggatgcCagcagctag	m5C_23878
chrM	6542 -	C	64	43	0.672	0	0 C	43 M	0.55	0.774	0	2E-07	0	472.99	gttaggttcCggtctgttag	m5C_23833
chrM	7638 -	C	113	24	0.212	0	0 T	89 M	0.147	0.297	0	0	0	70.6	ataagctcttCtatgataggg	m5C_24103
chrM	7641 -	C	134	28	0.209	0	0 T	106 M	0.149	0.285	0	0	0	83.278	gtgataagcttCtctatgata	m5C_24303
chrM	9134 -	C	35	20	0.571	0	0 C	20 M	0.409	0.72	0	4E-05	0	163.43	acagcgatttCtaggaatgc	m5C_23940
chrM	9143 -	C	36	21	0.583	0	0 C	21 M	0.422	0.729	0	5E-05	0	177.24	attaagggaCagcgatttct	m5C_23754
chrM	9146 -	C	38	23	0.605	0	0 C	23 M	0.447	0.744	0	8E-05	0	205.7	tggattaaggCgacagcgtatt	m5C_23932
chrM	9158 -	C	34	20	0.588	0	0 C	20 M	0.422	0.736	0	4E-05	0	168.89	aaaacgaggCttggattaag	m5C_24214
chrM	9308 -	C	41	27	0.659	0	0 C	27 M	0.505	0.784	0	7E-06	0	272.97	gaagggaaatCagctgcttag	m5C_24125
chrM	9330 -	C	47	32	0.681	0	0 C	32 M	0.538	0.796	0	2E-05	0	344.53	gtatggaggCgttatggagg	m5C_23965
chrM	9343 -	C	47	15	0.319	0	0 T	32 M	0.204	0.462	0	3E-07	0	61.186	gttagagggCtagtatggg	m5C_24185
chrM	9923 +	C	31	10	0.323	0	0 T	21 M	0.186	0.499	7E-15	2E-06	8E-15	26.273	gaagcccgccCctgatactgg	m5C_23685
chrM	11100 -	C	506	284	0.561	0	0 C	284 M	0.518	0.604	0	0	0	2940.7	atgattagttCtgggctgtg	m5C_23797
chrM	11247 -	C	128	48	0.375	0	0 T	80 M	0.296	0.461	0	1E-15	0	284.09	taaattaggtCgatggatagg	m5C_24010
chrM	11274 -	C	87	38	0.437	0	0 T	49 M	0.337	0.541	0	1E-10	0	256.44	ttatggagcCtaggggtgtg	m5C_23829
chrM	11275 -	C	75	23	0.307	0	0 T	52 M	0.214	0.418	0	4E-11	0	98.379	gtttaggagCtaggggtgt	m5C_24083
chrM	12584 -	C	65	26	0.4	0	0 T	39 M	0.29	0.521	0	6E-09	0	150.65	gagagagatCtagtttgaag	m5C_23746
chrM	13580 -	C	65	46	0.708	0	0 C	46 M	0.588	0.804	0	4E-07	0	540.99	agggagggatCgattgagata	m5C_23765
chrM	13591 -	C	57	33	0.579	0	0 C	33 M	0.45	0.698	0	9E-07	0	296.87	agggcgttgtCagggggatag	m5C_23825
chrM	13596 -	C	51	20	0.392	0	0 T	31 M	0.27	0.529	0	3E-08	0	108.11	gctataggcgCttgcaggga	m5C_24111
chrM	13598 -	C	46	23	0.5	0	0 CT	23 M	0.361	0.639	0	3E-06	0	166.15	gtgctataggCgcttgtcagg	m5C_23919
chrM	14161 -	C	76	33	0.434	0	0 T	43 M	0.329	0.546	0	1E-09	0	216.88	tgagattgtCgggggaatag	m5C_23830
chrM	14163 -	C	69	33	0.478	0	0 T	36 M	0.365	0.594	0	3E-08	0	240.69	attgagattgcCtgggggaat	m5C_23834
chrM	14682 -	C	124	31	0.25	0	0 T	93 M	0.182	0.333	0	0	0	112.89	gtagccgtgcCgagataatg	m5C_23910
chrM	14686 -	C	125	57	0.456	0	0 T	68 M	0.371	0.543	0	2E-14	0	423.28	gggttgatgcCgtgcgagaa	m5C_23836
chrM	14687 -	C	120	46	0.383	0	0 T	74 M	0.301	0.473	0	3E-14	0	277.14	tggttgatgcCgtgcgagaa	m5C_23982
chrM	14946 -	C	35	25	0.714	0	0 C	25 M	0.549	0.837	0	0.0001	0	274.72	gtgatggggCgattgagaa	m5C_23820
chrM	15315 -	C	36	20	0.556	0	0 C	20 M	0.396	0.705	0	4E-05	0	158.32	gctatgggtcCaataatgaag	m5C_24189
chrM	15324 -	C	34	12	0.353	0	0 T	22 M	0.215	0.521	0	5E-06	0	51.571	tggagtgctgcCtaggggtgca	m5C_23990
chrM	15467 -	C	1181	524	0.444	0	0 T	657 M	0.416	0.472	0	0	0	4355.3	gtgttaatgtCattaaggaga	m5C_23826
chrM	15498 -	C	811	423	0.522	0	0 C	423 M	0.487	0.556	0	0	0	4121.5	tctgggtcgcCtaggaagctt	m5C_23767
chrM	15501 -	C	658	426	0.647	0	0 C	426 M	0.61	0.683	0	0	0	5198.5	ttgtctgggtCgcttagggag	m5C_24230
chrM	15507 -	C	503	215	0.43	3	0.006 T	285 M	0.387	0.474	0	0	0	1665.4	gtataattgtCtgggtcgctt	m5C_23983
chrM	15522 -	C	80	51	0.637	0	0 C	51 M	0.528	0.734	0	2E-09	0	538.67	aaaggggtggCtagggataaa	m5C_24247
chrM	16440 -	C	36	18	0.5	0	0 CT	18 M	0.345	0.655	0	3E-05	0	124.11	aggagagtagCacttctgtgc	m5C_24296
chrX	1554623 -	C	35	15	0.429	0	0 T	20 M	0.28	0.591	0	1E-05	0	83.953	ctggagaagcCggggacaag	m5C_18676
chrX	1554624 -	C	39	18	0.462	0	0 T	21 M	0.316	0.614	0	3E-05	0	113.64	tctggagaagCcggtggacaa	m5C_18674
chrX	2641383 +	C	53	21	0.396	0	0 T	32 M	0.276	0.531	0	5E-08	0	115.87	gtggaggagcCcacaggaaag	m5C_18681
chrX	2641384 +	C	49	16	0.327	0	0 T	33 M	0.212	0.466	0	4E-07	0	67.863	tggaggcagcCacagggaaga	m5C_18686
chrX	5301641 +	C	38	20	0.526	0	0 C	20 M	0.373	0.675	0	4E-05	0	149.03	gggtcgggattCctgtgtatgc	m5C_18701
chrX	5301642 +	C	41	13	0.317	0	0 T	28 M	0.196	0.47	0	1E-07	0	50.868	gggtcgggattCtgtgtatgca	m5C_18708
chrX	10096686 +	C	42	27	0.643	0	0 C	27 M	0.492	0.77	0	7E-06	0	265.5	agcttggagtaCacggaggagg	m5C_18762
chrX	10096688 +	C	37	8	0.216	0	0 T	29 M	0.114	0.372	1E-10	7E-07	1E-10	9.1227	ctggagtaacaCggaggaggag	m5C_18763
chrX	10096701 +	C	40	23	0.575	0	0 C	23 M	0.422	0.715	0	3E-06	0	194.1	aggagaggggtCcttggatagg	m5C_18758
chrX	10096702 +	C	39	22	0.564	0	0 C	22 M	0.41	0.707	0	6E-05	0	180.29	ggaggagggtCtggagtgga	m5C_18765
chrX	17168035 -	C	65	20	0.308	0	0 T	45 M	0.209	0.428	0	7E-10	0	83.548	atttgattgcCaatgcaagt	m5C_19068
chrX	18693030 -	C	91	59	0.648	0	0 C	59 M	0.546	0.739	0	4E-10	0	644.35	ccagtggaacCatagccgtaa	m5C_19307
chrX	18693031 -	C	93	67	0.72	0	0 C	67 M	0.622	0.801	0	1E-09	0	833.31	cccagtggaacCatagccgta	m5C_19308
chrX	18693039 -	C	103	77	0.748	0	0 C	77 M	0.656	0.822	0	4E-10	0	1010	gttcgagcccCagtggaacca	m5C_19311
chrX	18693040 -	C	103	77	0.748	0	0 C	77 M	0.656	0.822	0	4E-10	0	1010	gggtcggagCcgatgggaacc	m5C_19312
chrX	18693041 -	C	107	70	0.654	0	0 C	70 M	0.56	0.738	0	1E-10	0	784.21	gggttcgagcCccagtggaac	m5C_19314
chrX	18693042 -	C	103	69	0.67	0	0 C	69 M	0.574	0.753	0	1E-10	0	792.69	tgggttcgagCccagtggaag	m5C_19313
chrX	18693046 -	C	98	64	0.653	0	0 C	64 M	0.555	0.74	0	9E-10	0	709.96	gtctgggtgtCgagcccgatg	m5C_19304
chrX	18693062 -	C	135	43	0.319	0	0 T	92 M	0.246	0.401	0	0	0	211.46	gctttacacCagaaaggtcct	m5C_19294
chrX	18693064 -	C	113	49	0.434	0	0 T	64 M	0.346	0.526	0	7E-14	0	339.01	ctgtttacaCgcgaagggc	m5C_19291
chrX	18693066 -	C	111	32	0.288	0	0 T	79 M	0.212	0.379	0	2E-16	0	135.82	gtctgtttaCagcgagaagg	m5C_19298
chrX	18693071 -	C	95	51	0.537	0	0 C	51 M	0.437	0.634	0	9E-11	0	445.84	atcacgtctgtCttacacgca	m5C_19299
chrX	18693074 -	C	99	55	0.556	0	0 C	55 M	0.457	0.65	0	2E-10	0	503.16	gttatcacgtCtgtttacac	m5C_19309
chrX	18693077 -	C	104	28	0.269	0	0 T	76 M	0.193	0.362	0	2E-15	0	108.27	gtggtatcacCgtctgttta	m5C_19305
chrX	18693079 -	C	104	29	0.279	0	0 T	75 M	0.202	0.372	0	3E-15	0	117	tagtgggttatCacgtctgctt	m5C_19310
chrX	18693096 -	C	112	28	0.25	0	0 T	84 M	0.179	0.338	0	0	0	100.24	gttaggggtCatagtgttagt	m5C_19300
chrX	18693097 -	C	61	24	0.393	0	0 T	37 M	0.281	0.519	0	3E-09	0	134.73	cttagaggttCatagtgttag	m5C_19306
chrX	30156371 +	C	61	29	0.475	0	0 T	32 M	0.355	0.598	0	1E-08	0	206.08	tgaaaagaatCtagcatttat	m5C_19117
chrX	34234109 +	C	46	18	0.391	0	0 T	28 M	0.264	0.535	0	8E-07	0	95.015	tgagcagaaCaggctctgga	m5C_19141
chrX	34234114 +	C	78	25	0.321	0	0 T	53 M	0.227	0.43	0	9E-11	0	113.74	agtaacaggtCtgttagcttc	m5C_19132
chrX	34234139 +	C	84	21	0.25	0	0 T	63 M	0.17	0.352	0	3E-13	0	71.283	atgtctggggCtgcattcatg	m5C_19140
chrX	34234146 +	C	69	23	0.333	0	0 T	46 M	0.234	0.451	0	2E-09	0	107.41	gggtctcatgCatgccaaggt	m5C_19133
chrX	50374827 +	C	38	28	0.737	0	0 C	28 M	0.58	0.85	0	0.0002	0	324.75	ggctaggattCggcgctttca	m5C_19328
chrX	50374832 +	C	32	22	0.688	0	0 C	22 M	0.514	0.82	0	6E-05	0	226.31	gggttcgggtCtttcaaaaa	m5C_19331
chrX	53423442 -	C	53	33	0.623	0	0 C	33 M	0.488	0.741	0	9E-07	0</			

chrX	64956736	+	C	47	15	0.319	0	0	T	32	M	0.204	0.462	0	3E-07	0	61.186	gaaggaggagCtgatggagag	m5C_19398
chrX	67580924	+	C	38	23	0.605	0	0	C	23	M	0.447	0.744	0	8E-05	0	205.7	aaggcctggCtgaggaggt	m5C_19470
chrX	67580942	+	C	37	11	0.297	0	0	T	26	M	0.175	0.458	1E-15	3E-06	2E-15	28.551	agtgatgatCtcaactgatt	m5C_19471
chrX	67580944	+	C	31	14	0.452	0	0	T	17	M	0.292	0.622	0	9E-06	0	81.652	tgagtattctCaactgattg	m5C_19476
chrX	70516821	+	C	39	10	0.256	0	0	T	29	M	0.146	0.411	1E-13	2E-06	1E-13	18.775	accgcaacatCaaggagctc	m5C_19611
chrX	70516840	+	C	75	48	0.64	0	0	C	48	M	0.527	0.739	0	3E-08	0	505.92	tcgtgagaagCtggaagatga	m5C_19622
chrX	80370383	-	C	32	23	0.719	0	0	C	23	M	0.546	0.844	0	8E-05	0	251.28	agaaagaaaCaggagatgga	m5C_19722
chrX	102841797	+	C	102	42	0.412	0	0	T	60	M	0.321	0.509	0	3E-13	0	269.77	aaaggaaagCagagagtgag	m5C_19750
chrX	102841901	+	C	44	15	0.341	0	0	T	29	M	0.219	0.489	0	3E-07	0	65.627	agagggaagCcaagagatga	m5C_19747
chrX	108297350	+	C	57	30	0.526	0	0	C	30	M	0.399	0.65	0	5E-07	0	239.51	aagaattttCgcgaaggccc	m5C_20350
chrX	108297352	+	C	76	42	0.553	0	0	C	42	M	0.441	0.659	0	9E-09	0	370.44	gaatttttcCgaaggccgc	m5C_20311
chrX	108297358	+	C	117	62	0.53	0	0	C	62	M	0.44	0.618	0	1E-12	0	545.56	ttcgcgaaggCccgcgcggg	m5C_20325
chrX	108297359	+	C	130	91	0.7	0	0	C	91	M	0.616	0.772	0	5E-13	0	1121.9	tcgcgaaggCcggcgcgggt	m5C_20321
chrX	108297360	+	C	131	70	0.534	0	0	C	70	M	0.449	0.618	0	1E-14	0	628.84	cgcgaaggCcggcgcggg	m5C_20300
chrX	108297362	+	C	132	86	0.652	0	0	C	86	M	0.567	0.727	0	2E-13	0	975.22	cgaaggccgcgggcgggt	m5C_20343
chrX	108297365	+	C	154	116	0.753	0	0	C	116	M	0.68	0.815	0	7E-14	0	1576.5	agcccccgcgcgggtgtgat	m5C_20290
chrX	111904912	+	C	41	11	0.268	0	0	T	30	M	0.157	0.419	6E-15	4E-08	7E-15	24.554	tgagtgtctCaattgattg	m5C_19992
chrX	118975164	-	C	36	26	0.722	0	0	C	26	M	0.56	0.842	0	0.0001	0	291.24	aagaaaaaCaagagaga	m5C_19945
chrX	125715081	+	C	206	58	0.282	0	0	T	148	M	0.225	0.347	0	0	0	260.5	aggaaggatgcgcgaaggccg	m5C_19961
chrX	125715083	+	C	188	92	0.489	0	0	T	96	M	0.419	0.56	0	0	0	770.66	gaaggatgcCgaaggccgga	m5C_19963
chrX	125715089	+	C	107	56	0.523	0	0	C	56	M	0.43	0.616	0	1E-11	0	481.12	tcgcgaaggCcggaacgcg	m5C_19969
chrX	125715090	+	C	90	53	0.589	0	0	C	53	M	0.486	0.685	0	3E-09	0	514.77	gcgcgaaggCggaacgcgg	m5C_19964
chrX	125715238	+	C	42	19	0.452	0	0	T	23	M	0.312	0.601	0	1E-06	0	118.65	gagtcccccCccggcgga	m5C_19968
chrX	125715239	+	C	48	20	0.417	0	0	T	28	M	0.288	0.557	0	1E-06	0	115.4	agtcccccCcggcgggaa	m5C_19957
chrX	125715240	+	C	58	22	0.379	0	0	T	36	M	0.266	0.508	0	7E-08	0	116.88	gtcccccccCggcggtgaac	m5C_19959
chrX	125715243	+	C	87	45	0.517	0	0	C	45	M	0.414	0.619	0	6E-10	0	372.37	cccccccgcCgggaacggg	m5C_19960
chrX	125715250	+	C	150	86	0.573	0	0	C	86	M	0.493	0.65	0	1E-14	0	848.52	cggcggaCaaggagggag	m5C_19962
chrX	125715261	+	C	143	32	0.224	0	0	T	111	M	0.163	0.299	0	0	0	104.45	gggagagagCgggaacccaa	m5C_19970
chrX	125715268	+	C	56	18	0.321	0	0	T	38	M	0.214	0.452	0	2E-08	0	77.043	agggcggaacCaagaagcgg	m5C_19958
chrX	128788242	+	C	66	26	0.394	0	0	T	40	M	0.285	0.515	0	6E-09	0	148.21	ggcggtggaCacgcggcga	m5C_20112
chrX	128788249	+	C	65	28	0.431	0	0	T	37	M	0.318	0.552	0	1E-08	0	177.85	ggacacgcggCgcacacctgt	m5C_20108
chrY	10036071	+	C	217	57	0.263	0	0	T	160	M	0.209	0.325	0	0	0	237.82	aagggcaccaCaggaaggga	m5C_23038
chrY	10036083	+	C	68	37	0.544	0	0	C	37	M	0.427	0.657	0	8E-08	0	315.66	aggaaggagCctgcactta	m5C_23142
chrY	10036084	+	C	51	14	0.275	0	0	T	37	M	0.171	0.409	0	3E-09	0	47.92	ggagrggagCtgacacttaa	m5C_23043
chrY	10036260	-	C	89	69	0.775	0	0	C	69	M	0.678	0.85	0	3E-08	0	935.95	ttgggggtcgCgtaactagt	m5C_23178
chrY	10036584	+	C	82	48	0.585	0	0	C	48	M	0.477	0.686	0	1E-09	0	458.16	tagtgaggccCttggatcgc	m5C_23116
chrY	10036591	+	C	67	39	0.582	0	0	C	39	M	0.463	0.693	0	1E-07	0	360.9	gcccttgatCggccccgcg	m5C_23099
chrY	10036595	+	C	50	35	0.7	0	0	C	35	M	0.562	0.809	0	1E-06	0	393.75	ttgatcggcCccgcgggtc	m5C_23032
chrY	10037757	+	C	105	31	0.295	0	0	T	74	M	0.216	0.388	0	7E-15	0	134.21	caaatggacCttgatgact	m5C_23140
chrY	10037766	+	C	2263	826	0.365	1	0	T	1436	M	0.346	0.385	0	0	0	5708.7	ccttgatgaCtttagcgg	m5C_23108
chrY	10037773	+	C	3520	1402	0.399	3	0.001	T	2115	M	0.383	0.415	0	0	0	10727	tgacttttagCggggatcac	m5C_23105
chrY	10037781	+	C	3653	1409	0.386	0	0	T	2244	M	0.37	0.402	0	0	0	10428	agcggtggaCactcggtcc	m5C_23069
chrY	10037783	+	C	3703	1476	0.399	1	0	T	2226	M	0.383	0.415	0	0	0	11307	cggggatcaCtcggctctg	m5C_23137
chrY	10037785	+	C	3687	1459	0.396	0	0	T	2228	M	0.38	0.412	0	0	0	11090	gggatcaactCggctctctg	m5C_23055
chrY	10037788	+	C	3674	1498	0.408	1	0	T	2175	M	0.392	0.424	0	0	0	11746	gatcatcggCicctgcgtg	m5C_23087
chrY	10037790	+	C	3449	1432	0.415	2	0.001	T	2015	M	0.399	0.432	0	0	0	11430	tcactcggtCctgcgtgat	m5C_23083
chrY	10037794	+	C	3419	1313	0.384	3	0.001	T	2103	M	0.368	0.401	0	0	0	9668.8	tcggctctctCgtgatgaag	m5C_23056
chrY	10037809	+	C	2917	1161	0.398	0	0	T	1756	M	0.38	0.416	0	0	0	8832.7	atgaagaatCagctagtgt	m5C_23155
chrY	10037812	+	C	2814	1094	0.389	0	0	T	1720	M	0.371	0.407	0	0	0	8115.8	aagaatgcagCtagctggag	m5C_23074
chrY	10037816	+	C	2599	884	0.34	1	0	T	1714	M	0.322	0.359	0	0	0	5698.1	atgcagctagCtgtggaatt	m5C_23076
chrY	10037838	+	C	1285	685	0.533	0	0	C	685	M	0.506	0.56	0	0	0	6928.6	atgtgaattCaggacacatt	m5C_23054
chrY	10037843	+	C	1090	664	0.609	0	0	C	664	M	0.58	0.638	0	0	0	7700.7	aattcagggaCacattgatca	m5C_23163
chrY	10037845	+	C	859	539	0.627	0	0	C	539	M	0.595	0.659	0	0	0	6410.2	ttgcaggacaCattgatcatc	m5C_23094
chrY	10037852	+	C	687	495	0.721	0	0	C	495	M	0.686	0.753	0	0	0	6789.5	acacattgatCattgcacatt	m5C_23107
chrY	10037916	+	C	34	27	0.794	0	0	C	27	M	0.632	0.897	0	0.0001	0	341.29	ctgagctttgCttgcaatca	m5C_23037