

Stable 1 peak promoter annotation

Column A: RefSeq_name: Refseq accession number of the nearest gene to a peak.

Column B: Symbol: Gene symbol.

Column C: Chr: The chromosome that the transcript lies in.

Column D: TSS: The start sites of the transcript.

Column E: TTS: The end sites of the transcript.

Column F: Strand: The strand of the transcript.

Column G: Chr:Start-End: Chr,Start and End of the peak

Column H: Length: Length of peak region.

Column I: Summit_position: Peak summit position related to the start position of peak region.

Column J: TagCounts_in_peak: Number of tags in peak region.

Column K: -10*LOG10(pvalue): -10*log10(pvalue) for the peak region (The cut-off is pvalue <=1e-04, then this value should be >=40).

Column L: Fold_enrichment: Fold enrichment for this region by sample comparisons (The peaks is sorted from high to low according to the fold enrichment value).

Column M: Peak_Classification: Peak classification.

Column N: Peak_to_TSS: The distance of peak center to TSS. ("- " indicates upstream to TSS, "+" indicates downstream to TSS).

Refseq_name	Symbol	Chr	TSS	TTS	Strand	Chr:Start-End	Length	Summit_p osition	TagCounts_ in peak	-10*LOG(p- value)	Fold_ enrichment	Peak_ Classification	Peak_to_T SS
NM_001242326	USP17L25	chr4	9326890	9328483	+	chr4:9325372-9326875	1504	695	47	108.16	11.61	promoter	-767
NM_001242330	USP17L27	chr4	9326890	9328483	+	chr4:9325372-9326875	1504	695	47	108.16	11.61	promoter	-767
NM_001242331	USP17L28	chr4	9326890	9328483	+	chr4:9325372-9326875	1504	695	47	108.16	11.61	promoter	-767
NM_001242332	USP17L29	chr4	9326890	9328483	+	chr4:9325372-9326875	1504	695	47	108.16	11.61	promoter	-767
NM_001242329	USP17L5	chr4	9326890	9328483	+	chr4:9325372-9326875	1504	695	47	108.16	11.61	promoter	-767
NM_001242327	USP17L24	chr4	9326890	9328483	+	chr4:9325372-9326875	1504	695	47	108.16	11.61	promoter	-767
NM_001256867	USP17L30	chr4	9326890	9328483	+	chr4:9325372-9326875	1504	695	47	108.16	11.61	promoter	-767
NM_001242328	USP17L26	chr4	9326890	9328483	+	chr4:9325372-9326875	1504	695	47	108.16	11.61	promoter	-767
NM_015640	SERBP1	chr1	67896123	67873492	-	chr1:67895559-67896284	726	272	26	105.38	10.69	promoter	202
NM_001018068	SERBP1	chr1	67896123	67873492	-	chr1:67895559-67896284	726	272	26	105.38	10.69	promoter	202
NM_001018067	SERBP1	chr1	67896123	67873492	-	chr1:67895559-67896284	726	272	26	105.38	10.69	promoter	202
NM_001018069	SERBP1	chr1	67896123	67873492	-	chr1:67895559-67896284	726	272	26	105.38	10.69	promoter	202
NM_001195581	ARL14EPL	chr5	115387162	115394827	+	chr5:115387105-115388577	1473	748	53	116.48	10.14	promoter	678
NR_136559	LOC100996335	chr22	21680925	21655548	-	chr22:21678242-21680335	2094	1574	75	177.98	10.12	promoter	1637
NR_077246	RPS14P3	chr1	19934300	19935138	+	chr1:19934540-19935257	718	289	23	84.79	10.11	promoter	598
NR_039624	MIR4426	chr16	61089670	61089610	-	chr16:61088922-61090415	1494	678	43	90.69	10	promoter	2
NM_002415	MIF	chr22	24236564	24237409	+	chr22:24236488-24237426	939	229	25	75.83	9.76	promoter	392
NR_132343	LINC01620	chr20	43093984	43080623	-	chr20:43094686-43095911	1226	665	37	78.65	9.76	promoter	-1314
NR_132342	LINC01620	chr20	43093984	43090402	-	chr20:43094686-43095911	1226	665	37	78.65	9.76	promoter	-1314
NR_027716	H2AFJ	chr12	14927269	14930936	+	chr12:14927333-14928284	952	289	37	103.71	9.4	promoter	539
NM_177925	H2AFJ	chr12	14927269	14930936	+	chr12:14927333-14928284	952	289	37	103.71	9.4	promoter	539
NR_108107	FAM230B	chr22	21521191	21546445	+	chr22:21521251-21522902	1652	1088	88	225.79	9.36	promoter	885
NM_153035	TCEANC2	chr1	54519244	54567321	+	chr1:54518291-54519305	1015	527	23	58.65	9.29	promoter	-447
NR_039942	MIR4781	chr1	54519751	54519827	+	chr1:54518291-54519305	1015	527	23	58.65	9.29	promoter	-954
NR_130900	TCEANC2	chr1	54519244	54578192	+	chr1:54518291-54519305	1015	527	23	58.65	9.29	promoter	-447
NM_001305066	TMEM59	chr1	54519111	54511158	-	chr1:54518291-54519305	1015	527	23	58.65	9.29	promoter	314
NM_001305049	TMEM59	chr1	54519246	54492353	-	chr1:54518291-54519305	1015	527	23	58.65	9.29	promoter	449
NM_001305052	TMEM59	chr1	54519246	54492353	-	chr1:54518291-54519305	1015	527	23	58.65	9.29	promoter	449
NM_001305051	TMEM59	chr1	54519246	54492353	-	chr1:54518291-54519305	1015	527	23	58.65	9.29	promoter	449
NM_001305050	TMEM59	chr1	54519111	54492353	-	chr1:54518291-54519305	1015	527	23	58.65	9.29	promoter	314
NM_001305043	TMEM59	chr1	54519111	54492353	-	chr1:54518291-54519305	1015	527	23	58.65	9.29	promoter	314
NM_004872	TMEM59	chr1	54519111	54492353	-	chr1:54518291-54519305	1015	527	23	58.65	9.29	promoter	314
NR_108061	VIM-AS1	chr10	17271984	17256237	-	chr10:17270813-17272391	1579	737	53	100.44	9.25	promoter	383
NM_003380	VIM	chr10	17270257	17279592	+	chr10:17270813-17272391	1579	737	53	100.44	9.25	promoter	1344
NR_038368	LINC00273	chr16	33962503	33961051	-	chr16:33962536-33964352	1817	668	498	1017.89	8.91	promoter	-940
NM_019058	DDIT4	chr10	74033676	74035794	+	chr10:74034374-74035740	1367	880	47	108.32	8.7	promoter	1380
NM_001679	ATP1B3	chr3	141595433	141645390	+	chr3:141595389-141596316	928	249	22	58.15	8.62	promoter	419
NM_001271606	BASP1	chr5	17216931	17276954	+	chr5:17217677-17218556	880	187	23	60.03	8.62	promoter	1185
NR_027253	LOC285696	chr5	17217531	17130136	-	chr5:17217677-17218556	880	187	23	60.03	8.62	promoter	-585
NM_006317	BASP1	chr5	17217669	17276954	+	chr5:17217677-17218556	880	187	23	60.03	8.62	promoter	447
NR_002182	NACAP1	chr8	102381120	102381823	+	chr8:102380871-102382210	1340	601	38	71.42	8.62	promoter	420
NM_030979	PABPC3	chr13	25670275	25672704	+	chr13:25670291-25672474	2184	727	80	196.74	8.62	promoter	1107
NR_047479	LINC00854	chr17	41381062	41373436	-	chr17:41381031-41382990	1960	1267	152	334.94	8.58	promoter	-948
NM_000291	PGK1	chrX	77359665	77382324	+	chrX:77359659-77360200	542	271	18	74.8	8.36	promoter	264
NR_106781	MIR6723	chr1	5677793	567704	-	chr1:569047-570097	1051	346	34	60.74	8.29	promoter	-1778
NR_128714	MIR3687-2	chr21	9826202	9826263	+	chr21:9825388-9827861	2474	811	1037	2757.09	8.26	promoter	422
NR_037458	MIR3687-1	chr21	9826202	9826263	+	chr21:9825388-9827861	2474	811	1037	2757.09	8.26	promoter	422
NR_037421	MIR3648-1	chr21	9825831	9826011	+	chr21:9825388-9827861	2474	811	1037	2757.09	8.26	promoter	793
NR_128711	MIR3648-2	chr21	9825831	9826011	+	chr21:9825388-9827861	2474	811	1037	2757.09	8.26	promoter	793
NR_132787	SNORA105A	chr5	21884562	21884678	+	chr5:21882138-21883997	1860	773	58	106.17	8.03	promoter	-1495
NR_132788	SNORA105B	chr5	21884562	21884678	+	chr5:21882138-21883997	1860	773	58	106.17	8.03	promoter	-1495
NM_005345	HSPA1A	chr6	31783290	31785719	+	chr6:31784305-31785760	1456	821	35	73.16	8.02	promoter	1742
NR_128710	MIR1244-4	chr2	232578023	232578105	+	chr2:232577226-232578457	1232	524	31	70.53	8.02	promoter	-182
NR_036262	MIR1244-2	chr2	232578023	232578105	+	chr2:232577226-232578457	1232	524	31	70.53	8.02	promoter	-182
NR_036263	MIR1244-3	chr2	232578023	232578105	+	chr2:232577226-232578457	1232	524	31	70.53	8.02	promoter	-182
NR_036052	MIR1244-1	chr2	232578023	232578105	+	chr2:232577226-232578457	1232	524	31	70.53	8.02	promoter	-182
NM_001012642	GRAMD2A	chr15	72490136	72452146	-	chr15:72491058-72492393	1336	543	52	89.43	7.94	promoter	-1589
NR_132980	SNORD141A	chr9	135895816	135895921	+	chr9:135894438-135896589	2152	655	373	1096.58	7.92	promoter	-303
NR_132981	SNORD141B	chr9	135895816	135895921	+	chr9:135894438-135896589	2152	655	373	1096.58	7.92	promoter	-303
NR_037688	ACTG1	chr17	79479892	79476996	-	chr17:79476456-79479796	3341	1637	160	180.67	7.84	promoter	1767
NM_001614	ACTG1	chr17	79479892	79476996	-	chr17:79476456-79479796	3341	1637	160	180.67	7.84	promoter	1767
NM_001199954	ACTG1	chr17	79479892	79476996	-	chr17:79476456-79479796	3341	1637	160	180.67	7.84	promoter	1767
NM_000581	GPX1	chr3	49396033	49394603	-	chr3:49395251-49396102	852	283	23	58.99	7.84	promoter	357
NM_201397	GPX1	chr3	49396033	49394603	-	chr3:49395251-49396102	852	283	23	58.99	7.84	promoter	357
NM_001329455	GPX1	chr3	49396033	49394603	-	chr3:49395251-49396102	852	283	23	58.99	7.84	promoter	357
NM_001329502	GPX1	chr3	49396033	49394603	-	chr3:49395251-49396102	852	283	23	58.99	7.84	promoter	357
NM_001329503	GPX1	chr3	49396033	49394603	-	chr3:49395251-49396102	852	283	23	58.99	7.84	promoter	357
NM_001675	ATF4	chr22	39916563	39918691	+	chr22:39917513-39918794	1282	814	31	81	7.44	promoter	1590
NM_182810	ATF4	chr22	39916568	39918691	+	chr22:39917513-39918794	1282	814	31	81	7.44	promoter	1585
NR_037427	MIR3654	chr7	132719675	132719619	-	chr7:132719295-132721264	1970	1121	98	197.12	7.18	promoter	-604
NM_145729	MRPL24	chr1	156710923	156707093	-	chr1:156711910-156713269	1360	651	41	74.88			

NM_002282	KRT83	chr12	52715182	52708084	-	chr12:52712717-52713843	1127	549	22	42.44	6.98	promoter	1903
NM_031369	HNRNPD	chr4	83295149	83274466	-	chr4:83294327-83295297	971	682	19	41.85	6.97	promoter	338
NM_002138	HNRNPD	chr4	83295149	83274466	-	chr4:83294327-83295297	971	682	19	41.85	6.97	promoter	338
NM_031370	HNRNPD	chr4	83295149	83274466	-	chr4:83294327-83295297	971	682	19	41.85	6.97	promoter	338
NM_001003810	HNRNPD	chr4	83295149	83274466	-	chr4:83294327-83295297	971	682	19	41.85	6.97	promoter	338
NR_132979	SNORD140	chr22	41469725	41469605	-	chr22:41470163-41470805	643	355	17	55.4	6.97	promoter	-758
NM_016255	FAM8A1	chr6	17600517	17611950	+	chr6:17601591-17602338	748	400	17	46.72	6.97	promoter	1447
NM_000992	RPL29	chr3	52029958	52027643	-	chr3:52027648-52028430	783	250	18	49.43	6.97	promoter	1920
NR_132380	LINC01596	chr4	190802669	190806022	+	chr4:190801764-190803110	1347	757	42	48.29	6.9	promoter	-233
NM_001256863	USP17L22	chr4	9269344	9270937	+	chr4:9269856-9271012	1157	426	43	49.05	6.9	promoter	1089
NM_001256861	USP17L20	chr4	9269344	9270937	+	chr4:9269856-9271012	1157	426	43	49.05	6.9	promoter	1089
NM_001256854	USP17L11	chr4	9217130	9218723	+	chr4:9217971-9218883	913	414	30	84.62	6.9	promoter	1296
NM_001256859	USP17L18	chr4	9217130	9218723	+	chr4:9217971-9218883	913	414	30	84.62	6.9	promoter	1296
NM_001256861	USP17L20	chr4	9217130	9218723	+	chr4:9217971-9218883	913	414	30	84.62	6.9	promoter	1296
NR_031696	MIR1283-2	chr19	54261485	54261572	-	chr19:54262611-54263365	755	286	17	42.09	6.9	promoter	1502
NR_030221	MIR516A2	chr19	54264386	54264476	+	chr19:54262611-54263365	755	286	17	42.09	6.9	promoter	-1399
NR_026673	RPL23P8	chr7	20866916	20867439	+	chr7:20866444-20867499	1056	638	24	49.98	6.82	promoter	55
NR_003573	ANXA2P2	chr9	33624222	33625532	+	chr9:33623852-33625578	1727	625	66	124.56	6.75	promoter	492
NR_126167	TMEMS-AS1	chr12	64215936	64202624	-	chr12:64215837-64217801	1965	1159	58	76.32	6.74	promoter	-882
NR_110014	KCCAT333	chr7	17414540	17506880	+	chr7:17414797-17415791	995	521	23	52.03	6.65	promoter	753
NR_110015	KCCAT333	chr7	17414540	17506880	+	chr7:17414797-17415791	995	521	23	52.03	6.65	promoter	753
NM_145016	GLYATL2	chr11	58611997	58601539	-	chr11:58612715-58613442	728	265	16	40.35	6.63	promoter	-1081
NM_001122634	CP51	chr2	211458078	211543832	+	chr2:211458550-211459605	1056	407	23	52.22	6.63	promoter	999
NM_024299	PPDPF	chr20	62152132	62153524	+	chr20:62153052-62153794	743	322	21	53.59	6.6	promoter	1290
NR_049831	MIR4444-2	chr3	75263626	75263699	+	chr3:75263232-75264797	1566	802	46	68.83	6.57	promoter	388
NR_039646	MIR4444-1	chr3	75263626	75263699	+	chr3:75263232-75264797	1566	802	46	68.83	6.57	promoter	388
NR_132980	SNORD141A	chr6	74228161	74227967	-	chr6:74227144-74228114	971	260	25	49.66	6.55	promoter	533
NR_132981	SNORD141B	chr6	74228161	74227967	-	chr6:74227144-74228114	971	260	25	49.66	6.55	promoter	533
NM_001402	EEF1A1	chr6	74230755	74225472	-	chr6:74228179-74229428	1250	660	35	78.75	6.53	promoter	1952
NR_132980	SNORD141A	chr6	74228161	74227967	-	chr6:74228179-74229428	1250	660	35	78.75	6.53	promoter	-642
NR_132981	SNORD141B	chr6	74228161	74227967	-	chr6:74228179-74229428	1250	660	35	78.75	6.53	promoter	-642
NM_001171805	PAPD7	chr5	6714717	6757161	+	chr5:6716323-6717053	731	324	18	53.54	6.51	promoter	1970
NM_006999	PAPD7	chr5	6714717	6757161	+	chr5:6716323-6717053	731	324	18	53.54	6.51	promoter	1970
NR_110795	LOC102723376	chr18	12074	15930	+	chr18:9881-10576	696	343	21	74.98	6.51	promoter	-1846
NM_001164771	SLC7A2	chr8	17396285	17428077	+	chr8:17394918-17396074	1157	722	22	40.39	6.51	promoter	-790
NM_003046	SLC7A2	chr8	17396285	17428077	+	chr8:17394918-17396074	1157	722	22	40.39	6.51	promoter	-790
NR_106951	MIR6891	chr6	31323093	31323000	-	chr6:31323637-31324723	1087	336	26	69.15	6.51	promoter	-1086
NM_005514	HLA-B	chr6	31325022	31321642	-	chr6:31323637-31324723	1087	336	26	69.15	6.51	promoter	843
NM_004501	HNRNPU	chr1	245027827	245013601	-	chr1:245026839-245027793	955	667	28	67.75	6.4	promoter	512
NM_031844	HNRNPU	chr1	245027827	245013601	-	chr1:245026839-245027793	955	667	28	67.75	6.4	promoter	512
NM_001256854	USP17L11	chr4	9250355	9251948	+	chr4:9251488-9255291	1104	444	28	46.24	6.33	promoter	1684
NM_001256859	USP17L18	chr4	9250355	9251948	+	chr4:9251488-9255291	1104	444	28	46.24	6.33	promoter	1684
NM_024541	C10orf76	chr10	103815932	103605355	-	chr10:103814101-103815093	993	544	22	42.91	6.2	promoter	1336
NM_024558	VCPKMT	chr14	50583297	50575349	-	chr14:50584225-50585444	1220	511	27	44.3	6.11	promoter	-1537
NR_049739	VCPKMT	chr14	50583297	50575349	-	chr14:50584225-50585444	1220	511	27	44.3	6.11	promoter	-1537
NR_049738	VCPKMT	chr14	50583297	50575349	-	chr14:50584225-50585444	1220	511	27	44.3	6.11	promoter	-1537
NM_001040662	VCPKMT	chr14	50583297	50575349	-	chr14:50584225-50585444	1220	511	27	44.3	6.11	promoter	-1537
NM_001256863	USP17L22	chr4	9259849	9261442	+	chr4:9260788-9261925	1138	661	32	48.64	6.09	promoter	1507
NM_001256854	USP17L11	chr4	9259849	9261442	+	chr4:9260788-9261925	1138	661	32	48.64	6.09	promoter	1507
NM_001256861	USP17L20	chr4	9259849	9261442	+	chr4:9260788-9261925	1138	661	32	48.64	6.09	promoter	1507
NR_033770	ROCK1P1	chr18	109064	122222	+	chr18:106065-112012	5948	2278	5822	2811.02	6.09	promoter	-26
NM_145232	CTU1	chr19	51611647	51600862	-	chr19:51613042-51613962	921	655	21	55.06	6.04	promoter	-1854
NM_139021	MAPK15	chr8	144798506	144804633	+	chr8:144798431-144799331	901	285	18	41.39	6.04	promoter	374
NR_049804	MIR5007	chr13	55748588	55748683	+	chr13:55746709-55747476	768	367	17	45.26	6.04	promoter	-1496
NM_001136265	IFFO2	chr1	19282826	19230773	-	chr1:19280347-19281406	1060	567	21	45.83	6.04	promoter	1950
NM_152459	C16orf89	chr16	5116146	5094122	-	chr16:5115888-5116618	731	443	16	42.71	6.04	promoter	-106
NM_001098514	C16orf89	chr16	5116146	5094122	-	chr16:5115888-5116618	731	443	16	42.71	6.04	promoter	-106
NM_001307937	COMMD9	chr11	36310999	36293841	-	chr11:36311130-36312290	1161	655	22	43.86	5.98	promoter	-710
NM_001307932	COMMD9	chr11	36310999	36293841	-	chr11:36311130-36312290	1161	655	22	43.86	5.98	promoter	-710
NM_014186	COMMD9	chr11	36310999	36293841	-	chr11:36311130-36312290	1161	655	22	43.86	5.98	promoter	-710
NM_001101653	COMMD9	chr11	36310999	36293841	-	chr11:36311130-36312290	1161	655	22	43.86	5.98	promoter	-710
NM_021103	TMSB10	chr2	85132762	85133799	+	chr2:85132925-85134109	1185	738	28	40.29	5.96	promoter	754
NM_199290	NACA2	chr17	59668563	59667793	-	chr17:59667612-59668959	1348	719	32	44.91	5.96	promoter	278
NM_001256894	USP17L15	chr4	9236110	9238060	+	chr4:9235216-9236884	1669	952	49	81.1	5.84	promoter	-61
NM_005022	PFN1	chr17	4825381	4848944	+	chr17:4851181-4851954	774	510	22	59.03	5.75	promoter	814
NR_030533	MIR675	chr11	2018061	2017988	-	chr11:2016330-2017531	1202	638	30	57.19	5.69	promoter	1131
NM_004291	CARTPT	chr5	71014989	71016875	+	chr5:71013002-71013862	861	373	19	40.28	5.61	promoter	-1558
NM_001353	AKR1C1	chr10	5500453	5020158	-	chr10:5006127-5007208	1082	462	22	44.24	5.6	promoter	1214
NM_014335	EID1	chr15	49170289	49172380	+	chr15:49170257-49171197	941	258	21	53.61	5.58	promoter	437
NR_132784	SNORA104	chr19	14733024	14733163	+	chr19:14732337-14733282	946	401	20	48.21	5.58	promoter	-215
NM_000700	ANXA1	chr9	75766646	75785310	+	chr9:75767614-75768480	867	541	18	43.54	5.58	promoter	1400
NM_013351	TBX21	chr17	45810609	45823485	+	chr17:45810530-45811578	1049	670	22	50.56	5.52	promoter	444
NR_046629	MYLK-AS2	chr3	123408490	123411254	+	chr3:123410089-123410731	643	363	15	42.75	5.44	promoter	1919
NM_001351365	NBPF19	chr1	148346791	146032541	-	chr1:148344038-148345804	1767	385	44	65.08	5.43	promoter	1871
NM_015383	NBPF14	chr1	148346756	148250248	-	chr1:148344038-148345804	1767	385	44	65.08	5.43	promoter	1836
NM_001351372	NBPF26	chr1	148346791	148002925	-	chr1:148344038-148345804	1767	385	44	65.08	5.43	promoter	1871
NM_001004717	OR4L1	chr14	20528203	20529142	+	chr14:20526665-20527710	1046	694	25	52.77	5.42	promoter	-1016
NM_001244706	CSAD	chr12	53558277	53551446	-	chr12:53557118-53558448	1331	884	36	61.64	5.33	promoter	495
NR_037415	MIR3620	chr1	228284963	228285042	+	chr1:228285405-228286918	1514	656	36	61.33	5.33	promoter	1198
NM_203379	ACSL5	chr10	114133915	114188138	+	chr10:114133065-114133877	813	268	19	49.44	5.31	promoter	-445
NM_203380	ACSL5	chr10	114135022	114188138	+	chr10:114133065-114133877	813	268	19	49.44	5.31	promoter	-1552
NR_132768	SNORA86	chr10	33190400	33190261	-	chr10:33189117-33190168	1052	423	25	55.81	5.27	promoter	758
NM_001018071	FRMPD2	chr10	49482941	49364601	-	chr10:49484210-49485							

NR_134513	AQP7	chr9	33402680	33384947	-	chr9:33402427-33403226	800	557	18	46.78	4.99	promoter	-146
NM_001170	AQP7	chr9	33402680	33384947	-	chr9:33402427-33403226	800	557	18	46.78	4.99	promoter	-146
NR_134515	AQP7	chr9	33402680	33384947	-	chr9:33402427-33403226	800	557	18	46.78	4.99	promoter	-146
NR_134514	AQP7	chr9	33402680	33384947	-	chr9:33402427-33403226	800	557	18	46.78	4.99	promoter	-146
NM_001318158	AQP7	chr9	33402680	33384947	-	chr9:33402427-33403226	800	557	18	46.78	4.99	promoter	-146
NM_001318157	AQP7	chr9	33402680	33384947	-	chr9:33402427-33403226	800	557	18	46.78	4.99	promoter	-146
NM_001318156	AQP7	chr9	33402680	33384947	-	chr9:33402427-33403226	800	557	18	46.78	4.99	promoter	-146
NR_106988	MIR7641-2	chr20	30596189	30596239	+	chr20:30595576-30596290	715	249	16	42.62	4.99	promoter	-257
NM_018263	ASXL2	chr2	26101385	25956621	-	chr2:26102586-26103582	997	518	23	40.69	4.99	promoter	-1698
NM_016141	DYNC1LI1	chr3	32612366	32567462	-	chr3:32609934-32611051	1118	589	23	43.27	4.93	promoter	1874
NM_001329135	DYNC1LI1	chr3	32612416	32567462	-	chr3:32609934-32611051	1118	589	23	43.27	4.93	promoter	1924
NR_046343	FAM90A7P	chr8	7431920	7421309	-	chr8:7430774-7432323	1550	768	49	45.8	4.87	promoter	372
NM_145255	MRPL10	chr17	45908907	45900637	-	chr17:45907054-45908118	1065	780	22	40.65	4.81	promoter	1322
NR_037575	MRPL10	chr17	45908907	45900637	-	chr17:45907054-45908118	1065	780	22	40.65	4.81	promoter	1322
NM_148887	MRPL10	chr17	45908907	45900637	-	chr17:45907054-45908118	1065	780	22	40.65	4.81	promoter	1322
NM_033413	LRRC46	chr17	45908992	45915079	+	chr17:45907054-45908118	1065	780	22	40.65	4.81	promoter	-1407
NM_001127644	GABRA1	chr5	161274939	161326965	+	chr5:161272796-161273951	1156	536	26	51.49	4.76	promoter	-1566
NM_001127643	GABRA1	chr5	161274684	161326965	+	chr5:161272796-161273951	1156	536	26	51.49	4.76	promoter	-1311
NM_000806	GABRA1	chr5	161274196	161326965	+	chr5:161272796-161273951	1156	536	26	51.49	4.76	promoter	-823
NR_002305	PDIAP3P1	chr1	146649429	146651528	+	chr1:146649303-146651317	2015	571	45	52.94	4.75	promoter	880
NM_006196	PCBP1	chr2	70314584	70316334	+	chr2:70315033-70316188	1156	381	28	47.81	4.73	promoter	1026
NR_033872	PCBP1-AS1	chr2	70314147	70189394	-	chr2:70315033-70316188	1156	381	28	47.81	4.73	promoter	-1463
NR_029704	MIR154	chr14	101526091	101526175	+	chr14:101524804-101525832	1029	451	24	44.83	4.72	promoter	-774
NR_030176	MIR496	chr14	101526909	101527011	+	chr14:101524804-101525832	1029	451	24	44.83	4.72	promoter	-1592
NM_033139	CALD1	chr7	134576150	134655480	+	chr7:134576836-134577670	835	248	20	40.15	4.67	promoter	1102
NM_033140	CALD1	chr7	134576150	134655480	+	chr7:134576836-134577670	835	248	20	40.15	4.67	promoter	1102
NM_002491	NDUF33	chr2	201936461	201950473	+	chr2:201937396-201938289	894	287	18	41.82	4.65	promoter	1381
NM_001257102	NDUF33	chr2	201936461	201950473	+	chr2:201937396-201938289	894	287	18	41.82	4.65	promoter	1381
NM_173822	FAM126B	chr2	201936394	201838440	-	chr2:201937396-201938289	894	287	18	41.82	4.65	promoter	-1448
NM_001321618	FAM126B	chr2	201936394	201838440	-	chr2:201937396-201938289	894	287	18	41.82	4.65	promoter	-1448
NM_001321629	FAM126B	chr2	201936394	201838440	-	chr2:201937396-201938289	894	287	18	41.82	4.65	promoter	-1448
NM_001321624	FAM126B	chr2	201936394	201838440	-	chr2:201937396-201938289	894	287	18	41.82	4.65	promoter	-1448
NM_001321623	FAM126B	chr2	201936394	201838440	-	chr2:201937396-201938289	894	287	18	41.82	4.65	promoter	-1448
NM_001321627	FAM126B	chr2	201936394	201838440	-	chr2:201937396-201938289	894	287	18	41.82	4.65	promoter	-1448
NM_001321619	FAM126B	chr2	201936351	201838440	-	chr2:201937396-201938289	894	287	18	41.82	4.65	promoter	-1491
NM_001321625	FAM126B	chr2	201936351	201838440	-	chr2:201937396-201938289	894	287	18	41.82	4.65	promoter	-1491
NM_001321622	FAM126B	chr2	201936351	201838440	-	chr2:201937396-201938289	894	287	18	41.82	4.65	promoter	-1491
NM_001321621	FAM126B	chr2	201936351	201838440	-	chr2:201937396-201938289	894	287	18	41.82	4.65	promoter	-1491
NM_001321628	FAM126B	chr2	201936351	201838440	-	chr2:201937396-201938289	894	287	18	41.82	4.65	promoter	-1491
NM_001321626	FAM126B	chr2	201936351	201838440	-	chr2:201937396-201938289	894	287	18	41.82	4.65	promoter	-1491
NR_039891	MIR3064	chr17	62496957	62496891	-	chr17:62496647-62498178	1532	954	41	45.27	4.56	promoter	-455
NR_039969	MIR5047	chr17	62497431	62497331	-	chr17:62496647-62498178	1532	954	41	45.27	4.56	promoter	19
NR_024217	SNAR-C2	chr19	48416307	48416427	+	chr19:48412320-48416311	3992	1266	195	54.63	4.45	promoter	-1992
NR_024220	SNAR-C1	chr19	48416307	48416427	+	chr19:48412320-48416311	3992	1266	195	54.63	4.45	promoter	-1992
NR_024219	SNAR-C5	chr19	48416307	48416427	+	chr19:48412320-48416311	3992	1266	195	54.63	4.45	promoter	-1992
NR_046416	USP17L9P	chr4	9360107	9361700	+	chr4:9360530-9361489	960	719	23	41.18	4.44	promoter	902
NR_024217	SNAR-C2	chr19	48432074	48432194	+	chr19:48428561-48431977	3417	1518	125	40.59	4.41	promoter	-1806
NR_024220	SNAR-C1	chr19	48432074	48432194	+	chr19:48428561-48431977	3417	1518	125	40.59	4.41	promoter	-1806
NR_024219	SNAR-C5	chr19	48432074	48432194	+	chr19:48428561-48431977	3417	1518	125	40.59	4.41	promoter	-1806
NR_106781	MIR6723	chr1	567793	567704	-	chr1:566032-567863	1832	645	40	44.38	4.35	promoter	846
NR_144485	RIC3	chr11	8190641	8114511	-	chr11:8190496-8191502	1007	486	26	53.72	4.27	promoter	-357
NM_001135109	RIC3	chr11	8190641	8127596	-	chr11:8190496-8191502	1007	486	26	53.72	4.27	promoter	-357
NM_001206671	RIC3	chr11	8190641	8127596	-	chr11:8190496-8191502	1007	486	26	53.72	4.27	promoter	-357
NM_001206672	RIC3	chr11	8190641	8127596	-	chr11:8190496-8191502	1007	486	26	53.72	4.27	promoter	-357
NM_001346690	RIC3	chr11	8190641	8127596	-	chr11:8190496-8191502	1007	486	26	53.72	4.27	promoter	-357
NM_001346691	RIC3	chr11	8190641	8127596	-	chr11:8190496-8191502	1007	486	26	53.72	4.27	promoter	-357
NM_001346692	RIC3	chr11	8190641	8127596	-	chr11:8190496-8191502	1007	486	26	53.72	4.27	promoter	-357
NM_001346693	RIC3	chr11	8190641	8127596	-	chr11:8190496-8191502	1007	486	26	53.72	4.27	promoter	-357
NM_001346694	RIC3	chr11	8190641	8127596	-	chr11:8190496-8191502	1007	486	26	53.72	4.27	promoter	-357
NM_024557	RIC3	chr11	8190641	8127596	-	chr11:8190496-8191502	1007	486	26	53.72	4.27	promoter	-357
NR_144484	RIC3	chr11	8190641	8127596	-	chr11:8190496-8191502	1007	486	26	53.72	4.27	promoter	-357
NR_144497	RIC3	chr11	8190641	8127596	-	chr11:8190496-8191502	1007	486	26	53.72	4.27	promoter	-357
NR_003284	PA2G4P4	chr3	156529810	156527059	-	chr3:156527130-156528857	1728	1134	45	57.44	4.24	promoter	1817
NM_001127605	LIPA	chr10	91011665	90973325	-	chr10:91011260-91012199	940	603	19	43.73	4.18	promoter	-64
NM_000235	LIPA	chr10	91011796	90973325	-	chr10:91011260-91012199	940	603	19	43.73	4.18	promoter	67
NM_001288979	LIPA	chr10	91011796	90973325	-	chr10:91011260-91012199	940	603	19	43.73	4.18	promoter	67
NR_004435	SNAR-A1	chr19	48421685	48421807	+	chr19:48421322-48425663	4342	2260	154	49.67	4.17	promoter	1807
NR_004436	SNAR-A2	chr19	48421685	48421807	+	chr19:48421322-48425663	4342	2260	154	49.67	4.17	promoter	1807
NR_004435	SNAR-A1	chr19	48437437	48437559	+	chr19:48436036-48438899	2864	2026	83	43.68	4.12	promoter	30
NR_004436	SNAR-A2	chr19	48437437	48437559	+	chr19:48436036-48438899	2864	2026	83	43.68	4.12	promoter	30
NM_015458	MTMR9	chr8	11141999	11185654	+	chr8:11142873-11143683	811	521	17	41	4.08	promoter	1278
NR_026999	LINC00265	chr7	39773166	39834222	+	chr7:39773461-39774404	944	563	20	40.09	4.06	promoter	766
NR_104189	SRGAP2-AS1	chr1	121139765	121102016	-	chr1:121139651-121140979	1329	873	39	41.25	3.83	promoter	-549
NM_004040	RHOB	chr2	20646831	20649204	+	chr2:20647035-20649051	2017	523	41	40.25	3.8	promoter	1211
NM_005324	H3F3B	chr17	73776016	73772514	-	chr17:73773649-73774864	1216	473	25	40.46	3.79	promoter	1760
NM_001303255	LRRC37A3	chr17	62915609	62850251	-	chr17:62915978-62918824	2847	1725	72	61.2	3.78	promoter	-1791
NM_199340	LRRC37A3	chr17	62915609	62850251	-	chr17:62915978-62918824	2847	1725	72	61.2	3.78	promoter	-1791
NR_073383	HSP90B2P	chr15	99797729	99800481	+	chr15:99797755-99799227	1473	887	43	42.66	3.78	promoter	761
NR_027084	FLJ36000	chr17	21904061	21913070	+	chr17:21904117-21907491	3375	2210	101	51.93	3.65	promoter	1742
NR_037962	RHO	chr1	228780393	228882416	+	chr1:228779601-228782424	2824	1801	107	84.69	3.52	promoter	619
NR_106988	MIR7641-2	chr1	228779635	228779585	-	chr1:228779601-228782424	2824	1801	107	84.69	3.52	promoter	-1377
NR_106988	MIR7641-2	chr1	228781866	228781816	-	chr1:228779601-228782424	2824	1801	107	84.69	3.52	promoter	854