Table S1. Lead variants of the GWAS analyses for diabetic retinopathy (n=14,584)

chrom	pos	ref	alt	rsids	nearest_genes	most_severe	info	fin_enrichment	maf	maf_cases	maf_controls	beta	pval
6	32695467	CAG	C	rs111953004,rs9280092	HLA-DQB1	intergenic	0.996293	1.150746968822170	0.1201	0.1769	0.116	0.5532	2.146E-160
10	122454932	G	T	rs10490924	ARMS2	missense	0.999816	1.1291066942203500	0.2435	0.2736	0.2414	0.1802	6.858E-33
6	25973043	T	C	rs201543396	TRIM38	intron	0.987339	33.25815113156890	0.01096	0.01713	0.01052	0.5645	4.626E-19
1	113834946	A	G	rs2476601	PTPN22	missense	0.999595	0.9472066890874480	0.8514	0.8364	0.8525	-0.1375	2.709E-14
1	196695521	C	T	rs10922098	CFH	intron	0.999453	0.8812178780215200	0.563	0.5452	0.5643	-0.0849	5.191E-11
6	25385158	T	A	rs545522622	LRRC16A	intron	0.977396	36.39704471310690	0.01036	0.01436	0.01008	0.405	3.499E-10
10	112995025	T	C	rs35198068	TCF7L2	intron	0.99563	0.6771486572655200	0.2011	0.2157	0.2001	0.094	4.682E-09
19	41441720	A	C	rs7260507	ATP5SL	upstream gene	0.98438	0.8485412594500120	0.3785	0.3636	0.3796	-0.0763	1.045E-08
6	24319889	T	C		DCDC2	intron	0.685218	1000000	0.003632	0.005465	0.0035	0.7468	1.163E-08
7	93289005	T	C	rs529729969	VPS50	intron	0.876415	0.12483796296296300	0.0006448	0.00143	0.0005881	1.7447	2.106E-08
11	2160994	A	T	rs689	INS,INS-IGF2	splice region	0.982735	1.1086562240544200	0.7908	0.8031	0.7899	0.0888	2.624E-08
6	36448782	A	C		KCTD20	intron	0.80607	1000000	0.003839	0.005598	0.003712	0.6301	9.777E-08
1	36471456	G	A	rs776379864	CSF3R	missense	0.966821	10.92314335060450	0.001456	0.002554	0.001376	0.9842	1.139E-07
6	7267798	C	T	rs11243147	SSR1	downstream gene	0.981201	1.1792389009870400	0.5604	0.5742	0.5594	0.0686	1.415E-07
3	167364140	G	T	rs4546147	ZBBX	intron	0.986574	0.7404835101833830	0.3674	0.3545	0.3683	-0.0685	3.049E-07
12	111140929	C	T	rs55971330	CUX2	intron	0.985529	2.604198268647350	0.08409	0.07587	0.08468	-0.119	3.814E-07
3	23252697	A	G	rs4858066	UBE2E2	intron	0.998666	1.1489451700066600	0.3532	0.3672	0.3522	0.0667	6.694E-07
19	49198540	C	T	rs574023746	TRPM4	intron	0.974382	6.860451603313380	0.02553	0.02923	0.02527	0.2054	8.614E-07
17	66606500	G	A	rs181072797	PRKCA	intron	0.95633	0.4439327634167850	0.01078	0.008192	0.01097	-0.3143	8.618E-07
12	55991020	G	A	rs705699	RAB5B	non coding transcript exon	0.990211	0.9290176028939010	0.3852	0.3995	0.3841	0.0649	9.179E-07
7	50531824	A	G	rs1018175784	DDC,FIGNL1	non coding transcript exon	0.911508	1000000	0.000118	0.0004976	0.00009061	3.3586	0.000001009
3	99132850	T	C	rs960729525	DCBLD2	intergenic	0.94236	28.160115606936400	0.005124	0.006963	0.004991	0.4626	0.000001076
13	97714040	T	C	rs181777463	IPO5	intergenic	0.813585	0.03819444444444440	0.0007208	0.001404	0.0006715	1.4216	0.000001171
2	223997421	T	C	rs536474853	SERPINE2	intron	0.825995	0.19487197928653600	0.0005106	0.001169	0.0004631	1.6123	0.000001272
2	222214897	C	T	rs201460657	PAX3	intron	0.921711	0.17566742062771400	0.0005239	0.001186	0.0004761	1.534	0.00000133
17	3964877	T	C	rs2676275	ATP2A3	upstream gene	0.972034	1.803599103426190	0.1449	0.1531	0.1443	0.0879	0.00000215
8	110698058	A	G		KCNV1	intergenic	0.8073	21.809551208285400	0.001621	0.002644	0.001548	0.8662	0.000002416
8	108931152	C	T	rs902290858	TMEM74	intron	0.930804	9.323156682027650	0.001192	0.002114	0.001125	0.9535	0.000002466
8	109977471	A	C	rs545672991	KCNV1	upstream gene	0.955844	1.678587235549260	0.001104	0.002025	0.001037	0.9742	0.000002503
11	97634667	C	T		JRKL	intergenic	0.605699	1000000	0.001458	0.002277	0.001399	1.0779	0.000002648
14	80709454	T	C	rs193193673	CEP128	intron	0.724684	0	0.0002426	0.0005988	0.0002169	2.8609	0.000002668
8	69790735	T	G	rs182445894	SLCO5A1	intron	0.985575	0.7371383001484730	0.005726	0.007842	0.005574	0.4026	0.000002876
17	30638262	T	C	rs893835626	TBC1D29	intron	0.783734	1000000	0.0004559	0.001	0.0004166	1.7464	0.000002899
10	59661283	G	T	rs748611382	SLC16A9	intron	0.836272	0.6683790892651650	0.002263	0.003419	0.002179	0.7133	0.000003178
18	24961722	T	G	rs11083103	ZNF521	intron	0.992089	0.744416844845462	0.3606	0.3735	0.3597	0.0624	0.00000318
7	70480178	GA	G	rs1056909333	AUTS2	intron	0.819825	4.678653624856160	0.0006752	0.001329	0.000628	1.3705	0.000003246
13	95272583	A	T	rs541509246	ABCC4	intron	0.95465	1.8740057636887600	0.0009657	0.001711	0.0009119	1.0774	0.000003364
4	100975596	G	T	rs150479353	PPP3CA	intergenic	0.968997	0.4924898552480160	0.01436	0.01146	0.01457	-0.2556	0.000003464
X	14978050	T	C		MOSPD2	non coding transcript exon	0.677186	1000000	0.0006689	0.001529	0.0006069	1.1685	0.000003568
9	34834137	A	G	rs146266330	FAM205C	non coding transcript exon	0.958572	1.1871732090145600	0.03669	0.04183	0.03632	0.1609	0.000003605
15	77975512	T	C	rs12901288	TBC1D2B	upstream gene	0.976724	0.554153031011376	0.07461	0.08119	0.07414	0.1144	0.000003742
2	169026835	AGT	A	rs953310741	ABCB11	intron	0.982933	6.240783410138250	0.002208	0.003646	0.002104	0.6346	0.000003895
8	734986	GC	G	rs548222351	ERICH1	intron	0.905346	0.8508776526067590	0.001273	0.002197	0.001207	0.9126	0.000003901
1	118569060	G	A	rs533296304	TBX15	intergenic	0.931345	4.840401714322270	0.004901	0.006682	0.004773	0.4428	0.000003993
1	113318163	T	C	rs181871363	MAGI3	intergenic	0.985489	10.606100983182900	0.04794	0.05314	0.04756	0.1399	0.000004098
4	175021664	A	G		ADAM29	downstream gene	0.82461	1000000	0.0002328	0.0006257	0.0002044	2.4799	0.000004225
8	2147282	G	A		MYOM2	intron	0.990215	15.592635212888400	0.002194	0.003508	0.0021	0.6409	0.000004405
7	131464057	T	C	rs1012757241	MKLN1	intron	0.762772	1000000	0.0004074	0.0008621	0.0003746	1.9129	0.000004596
7	55367905	A	G		LANCL2	intron	0.673138	0	0.0003682	0.000848	0.0003336	1.9848	0.000004604
1	52888638	A	G	rs184003309	ZYG11A	intron	0.954666	32.20099731492140	0.009482	0.01155	0.009333	0.3162	0.000004753
9	72316455	T	A	rs744061	ZFAND5	intron	0.998298	1.3391891572498200	0.4904	0.5034	0.4895	0.0584	0.000005369
8	108239300	A	G	rs183201793	EIF3E	intron	0.879047	0.5898827481105960	0.001493	0.002462	0.001423	0.8293	0.000005625
17	78236644	G	A		TMEM235	intron	0.734076	1000000	0.0004113	0.000881	0.0003774	1.8685	0.000005659
12	28918134	C	T	rs111389807	FAR2	intergenic	0.620003	0.34859018926226300	0.0003218	0.0007142	0.0002935	2.3313	0.00000577
11	63010009	G	A	rs72933464	SLC22A8	intron	0.976151	1.5687623979453300	0.05493	0.04918	0.05535	-0.1296	0.000005837
17	56705934	G	A	rs181866253	C17orf67	intergenic	0.956705	0.37533027395355300	0.002505	0.003704	0.002419	0.613	0.000006029
12	14087348	T	C	rs187059341	GRIN2B	intergenic	0.9903	2.083044982698960	0.01261	0.01549	0.0124	0.2615	0.000006196
8	94832855	C	T	rs12155666	INTS8	intron	0.99908	1.0977200577200600	0.4836	0.4709	0.4845	-0.058	0.000006422
17	31621737	G	A		RAB11FIP4	intron	0.906889	6.238341968911920	0.0003543	0.0008562	0.0003181	1.7819	0.000006483
15	57397174	T	C	rs1664446	CGNL1	intron	0.998277	1.0731534606448800	0.4467	0.4596	0.4458	0.0582	0.000006622
1	163690290	T	A	rs184075501	NUF2	intergenic	0.94666	1.4946027633851500	0.009917	0.01272	0.009715	0.2966	0.000006697
20	1570918	T	C	rs41297640	RP4-576H24.4,SIRPB1	missense	0.972769	0.40239058613905500	0.01188	0.01487	0.01166	0.2687	0.000006712
5	65458953	G	A	rs78221622	ADAMTS6	intron	0.882877	0.217746799812345	0.003749	0.005371	0.003632	0.5017	0.000006999
2	54389533	CA	C		C2orf73	intergenic	0.930889	1000000	0.002636	0.00402	0.002537	0.5863	0.00000726
21	42431928	T	C	rs12482947	UBASH3A	intron	0.991283	0.9308095269470540	0.5783	0.5905	0.5774	0.0586	0.000007271
17	30023572	A	T		EFCAB5	intron	0.786737	1000000	0.00045	0.0009645	0.0004129	1.6643	0.000007496
9	11668046	C	G	rs536499783	TYRP1	intergenic	0.689556	1000000	0.002443	0.003584	0.002361	0.7032	0.000007548
12	114974798	T	A		TBX3	regulatory region	0.819672	1000000	0.001902	0.002952	0.001827	0.7426	0.000007642
9	122118276	C	G	rs78248304	TTLL11	downstream gene	0.948738	0.20076354351358400	0.005271	0.00697	0.005148	0.41	0.000008052
1	29145312	G	A	rs188206323	SRSF4	intron	0.614891	1000000	0.001186	0.001937	0.001131	1.0824	0.000008085
14	89491696	G	A	rs76267172	FOXN3	intron	0.95366	0.29426141362792100	0.003345	0.004583	0.003256	0.5278	0.00000809
8	15659942	T	A	rs547624384	TUSC3	intron	0.944002	0.13541875375676200	0.001466	0.002511	0.00139	0.7773	0.000008333
8	106653569	A	C		OXR1	intron	0.946744	1000000	0.001075	0.00204	0.001005	0.8963	0.000008694

11	18916431	A	G	rs555340325	MRGPRX1	intergenic	0.901368	0.07244977334298970	0.001533	0.002482	0.001465	0.799	0.000008817
2	2269288	C	T	rs749344628	MYT1L	intron	0.867523	0	0.000648	0.001237	0.0006055	1.3175	0.000008838
18	28830153	T	G	rs79306715	CDH2	intergenic	0.987192	0.40647292933844000	0.002866	0.004359	0.002758	0.5361	0.000008986
15	38409925	G	T	rs12907757	FAM98B	intergenic	0.990505	0.8618033281245720	0.02974	0.03403	0.02943	0.1681	0.000009085
3	11499936	C	G	rs13326352	ATG7	intron	0.987888	0.8579167153839800	0.3513	0.3647	0.3503	0.06	0.000009161
21	36063678	C	A	rs530988874	SETD4	intron	0.958841	0.5673313445334170	0.001731	0.002895	0.001647	0.7028	0.00000959
13	36668029	A	G	rs117636209	SERTM1	intergenic	0.942882	0.8308878279532220	0.00623	0.008254	0.006084	0.3703	0.000009665
12	47947535	A	G	rs959194560	VDR	upstream gene	0.820463	1000000	0.0002481	0.000631	0.0002205	2.3133	0.000009902
12	48459721	C	T	rs534898754	ANP32D	intergenic	0.873569	3.1203223949337900	0.0002315	0.0006181	0.0002036	2.312	0.000009928
2	240631677	A	G		GPR35	downstream gene	0.897816	1000000	0.002424	0.003689	0.002332	0.6104	0.000009936
8	107407874	G	T		ANGPT1	intron	0.929088	1000000	0.001221	0.002178	0.001152	0.8523	0.000009977
19	48089924	G	A	rs185376650	PLA2G4C	intron	0.959599	1.3693620365432700	0.005834	0.007639	0.005704	0.3842	0.00001024
7	148187507	C	T	rs77422637	CNTNAP2	intron	0.990163	0.5319920805171770	0.06398	0.06996	0.06355	0.1164	0.00001063
2	35320093	ATT	A	rs927987157	CRIM1	intergenic	0.908074	4.6631185270425800	0.0004163	0.0008996	0.0003815	1.6336	0.00001067
3	134790201	G	A		EPHB1	intron	0.604369	1000000	0.0002509	0.0006234	0.000224	2.5425	0.00001082
9	38579249	A	G	rs2993203	ANKRD18A	intron	0.922526	0.847825445513943	0.0698	0.07517	0.06942	0.1156	0.00001099
15	32624514	A	G	rs558809168	ARHGAP11A	intron	0.897211	1.7838595334267600	0.006832	0.008477	0.006713	0.3692	0.00001121
8	112104652	G	A		CSMD3	intergenic	0.856168	22.021511627907000	0.001557	0.002526	0.001487	0.7899	0.00001126
1	7470867	C	G	rs74844902	CAMTA1	intron	0.997178	0.23671987451909700	0.00821	0.01015	0.00807	0.3177	0.00001186
10	128942170	T	G	rs542015470	MGMT	intergenic	0.982584	10.887406508995400	0.002962	0.004131	0.002878	0.5438	0.00001189
21	45875107	A	G	rs882668	PCBP3	intron	0.998124	1.0094413665226200	0.5914	0.5792	0.5923	-0.0574	0.0000119
14	24657710	G	A	rs147187996	GZMB	non coding transcript exon	0.981267	0.650067165611207	0.005399	0.007078	0.005278	0.3917	0.00001206
7	80998413	G	A	rs10260680	SEMA3C	intergenic	0.982689	0.8081891336594420	0.2076	0.2176	0.2069	0.0698	0.00001214
7	138196840	G	A	rs568482025	AKR1D1	regulatory region	0.889414	3.019109699704720	0.007912	0.009678	0.007784	0.3424	0.00001225
X	151347744	A	T	rs906452932	VMA21	intergenic	0.802271	1000000	0.001292	0.002423	0.00121	0.7309	0.00001268
6	119593623	G	T	rs116919772	MAN1A1	intergenic	0.991687	1.989208477441810	0.06858	0.07447	0.06815	0.1115	0.0000128
1	208972678	C	G	rs571919280	CAMK1G	non coding transcript exon	0.874854	0	0.0008877	0.001602	0.0008361	1.0638	0.00001283
X	112237845	C	G	rs748575336	TRPC5	intergenic	0.931417	0.44479289940828400	0.0005425	0.001255	0.000491	1.1432	0.00001305
11	75001886	G	A	rs17245026	NEU3	intron	0.990944	0.6939200706022820	0.04077	0.04489	0.04048	0.1428	0.00001322
14	97438758	G	A		VRK1	intergenic	0.785243	1000000	0.000383	0.000794	0.0003533	1.8974	0.0000133
1	111867816	A	G	rs74692935	KCND3	intron	0.988	0.7569240394606010	0.006815	0.00863	0.006684	0.3452	0.0000144
19	54542652	T	C	rs151023716	KIR3DX1	splice region	0.932755	1.8202689721421700	0.001876	0.002935	0.0018	0.6813	0.00001447
12	115486317	T	A	rs73206280	MED13L	intergenic	0.974502	1.34575260804769	0.07093	0.06404	0.07142	-0.1106	0.00001451
2	105759472	T	TAT	rs144136010	NCK2	intron	0.989136	1.0232811494627400	0.952	0.9468	0.9523	-0.131	0.00001461
17	43361468	C	A	rs117431832	ARL4D	upstream gene	0.946189	0.16902302243211300	0.004735	0.006478	0.004609	0.4157	0.00001497
22	24005096	G	A	rs5751792	CABIN1	non coding transcript exon	0.976388	1.0668042985855500	0.5806	0.5932	0.5797	0.0569	0.00001499
3	109831108	G	A	rs188637200	DPPA4	intergenic	0.710682	0.13553809976484700	0.0001014	0.0003389	0.00008426	4.2193	0.00001541
5	105933589	C	G	rs138508964	EFNA5	intergenic	0.913479	0.8311469121595700	0.001202	0.002028	0.001142	0.8677	0.00001551
8	3067148	C	A	rs763007714	CSMD1	intron	0.947301	4.678756476683940	0.001261	0.002152	0.001197	0.8279	0.00001591
21	31405492	G	T	rs138234190	TIAM1	intron	0.928536	3.585480722213850	0.09681	0.08935	0.09735	-0.0972	0.00001608
2	34313104	A	C	rs166063	FAM98A	intergenic	0.992415	1.0014227866945600	0.9497	0.9443	0.9501	-0.1267	0.00001609
6	156620163	T	C	rs915081598	ARID1B	intergenic	0.909939	0	0.0002172	0.00056	0.0001925	2.3712	0.00001634
4	181673409	C	T	rs184856032	TENM3	intergenic	0.959878	1.1366257733039700	0.007064	0.009172	0.006911	0.3365	0.00001642
2	209373939	G	A	rs9752306	MAP2	intergenic	0.996043	0.9551537745208230	0.4878	0.5	0.487	0.0554	0.00001643
16	73630418	T	A	rs922647	ZFHX3	intergenic	0.991468	1.0618412621492900	0.8952	0.8868	0.8958	-0.0906	0.00001663
10	28345042	T	C	rs141759774	MPP7	upstream gene	0.981369	5.449547256221600	0.04618	0.05101	0.04583	0.1331	0.00001666
9	10736241	G	A	rs935712333	PTPRD	intergenic	0.864966	1000000	0.003163	0.004585	0.00306	0.5253	0.00001685
2	75505768	C	T	rs547791529	EVA1A	intron	0.978238	3.149505526468880	0.001612	0.002591	0.001542	0.718	0.0000171
10	18212042	C	T	rs955592087	CACNB2	intron	0.949713	1000000	0.002203	0.003274	0.002126	0.6211	0.00001711
5	86522306	A	G	rs530216351	COX7C	intergenic	0.923205	0	0.0008692	0.001674	0.0008112	0.9826	0.00001718
18	24149929	G	A	rs538343675	CABYR	intron	0.946194	1.9487197928653600	0.0007901	0.001518	0.0007376	1.043	0.00001737
22	45132769	G	T	rs11704695	NUP50	downstream gene	0.974224	2.0168059408128500	0.01913	0.01566	0.01938	-0.2064	0.0000174
5	63286696	C	A	rs771154012	IPO11	intergenic	0.891546	1.3869333846252500	0.000917	0.001609	0.000867	1.0231	0.00001741
7	108830425	C	T	rs78117583	DNAJB9	intergenic	0.973315	3.022645689847660	0.03616	0.04063	0.03584	0.1496	0.00001777
4	57549766	C	T	rs530099211	IGFBP7	intergenic	0.782077	1000000	0.002021	0.002946	0.001954	0.7215	0.00001791
6	141513173	T	C	rs945703121	NMBR	intergenic	0.732107	1000000	0.00071	0.00126	0.0006703	1.3127	0.00001809
2	145281856	A	G	rs527287382	ZEB2	intergenic	0.95192	0.779217040875072	0.000349	0.0009124	0.0003083	1.5228	0.00001809
9	118568243	C	T	rs569307646	BRINP1	intergenic	0.9485	1.1496179966044100	0.002016	0.003113	0.001937	0.6419	0.00001819
18	56414687	A	G	rs72938948	TXNL1	intergenic	0.909708	0.3465030047308530	0.001012	0.001788	0.0009565	0.9366	0.00001826
22	20648599	A	T	rs853109	PI4KA	intron	0.99037	0.8744122754291060	0.5038	0.5162	0.5029	0.0553	0.00001827
13	97025997	A	G	rs9556658	OXGR1	intergenic	0.996554	0.9395652137736590	0.113	0.1207	0.1124	0.0867	0.00001832
15	94285521	T	TG		MCTP2	intron	0.654523	0	0.0002244	0.0005807	0.0001986	2.4853	0.00001865
4	163079077	C	T	rs145034465	NAF1	intergenic	0.888129	1.274604678669110	0.03368	0.0296	0.03397	-0.1619	0.00001867
13	28692502	A	AT	rs59365303,rs397953574	SLC46A3	intergenic	0.975862	1.178261091366670	0.1864	0.1966	0.1857	0.0712	0.00001888
15	27810608	A	ATT	rs111964420,rs38638255	OCA2	intron	0.998608	0.7176248407958700	0.3789	0.3673	0.3797	-0.0566	0.0000189
15	88070468	A	C	rs113092308	NTRK3	intron	0.99081	0	0.000667	0.001372	0.0006161	1.0991	0.00001892
6	143944090	G	C	rs541359813	PLAGL1	intron	0.782308	1000000	0.0005735	0.001054	0.0005388	1.4537	0.00001907
6	167843108	G	T		MLLT4	intron	0.80403	1000000	0.0004417	0.0009005	0.0004086	1.6086	0.00001927
10	127799461	A	G	rs527718626	FOXI2	intergenic	0.975962	5.252302365839590	0.01147	0.01419	0.01127	0.2594	0.00001938
2	144345635	C	A	rs570993510	GTDC1	intergenic	0.901	0.14873061616577500	0.0005138	0.001136	0.0004689	1.3022	0.00001949
10	103422950	C	T	rs140622243	PDCD11	intron	0.927679	1.4476204175571300	0.003294	0.004518	0.003206	0.5066	0.0000204
3	194298612	C	T	rs140296302	CPN2	intron	0.945046	0.4648719035794320	0.008973	0.011	0.008826	0.3014	0.00002052
3	117883653	C	T	rs9881641	LSAMP	intron	0.996261	1.1025086077842600	0.7583	0.7687	0.7575	0.064	0.00002058
8	55440002	A	G	rs117488844	XKR4	intron	0.978031	0.6008477607823360	0.03194	0.03574	0.03167	0.1575	0.00002081
15	27093341	A	C	rs188607399	GABRG3	intron	0.833537	0.10751557477877900	0.0006583	0.001266	0.0006145	1.219	0.00002101

3	190082124	T	C	rs6791047	P3H2	intron	0.996251	1.2383819956597300	0.2431	0.2531	0.2424	0.0637	0.00002105
14	94577381	G	A		SERPINA5	intron	0.80613	1000000	0.002015	0.003004	0.001943	0.6878	0.00002106
8	93129302	A	G	rs140447551	TRIQK	downstream gene	0.914413	0.781486554682431	0.009662	0.00733	0.00983	-0.2967	0.00002116
14	101145930	C	G	rs184852490	RTL1	upstream gene	0.82829	1000000	0.001327	0.002038	0.001276	0.8741	0.00002164
2	25155553	C	T	rs57457259	EFR3B	3 prime UTR	0.999501	0.6663330671681270	0.2287	0.24	0.2278	0.0647	0.00002179
16	19330492	C	T		CLEC19A	intergenic	0.885158	1000000	0.0008245	0.00145	0.0007794	1.0844	0.00002186
11	29779073	A	G	rs146071559	KCNA4	intron	0.931099	0.5028954304168680	0.00155	0.002451	0.001485	0.7406	0.00002215
3	143814142	C	T	rs80199037	SLC9A9	intron	0.98138	1.4894131185270400	0.03608	0.03201	0.03637	-0.1473	0.00002231
7	69232847	GA	G	rs150386894	AUTS2	intron	0.982914	0.12048854482686500	0.007708	0.01005	0.007539	0.3109	0.00002246
1	3288372	C	T		PRDM16	intron	0.848295	1000000	0.001835	0.002695	0.001773	0.7206	0.00002257
14	78342188	A	G	rs570895017	NRXN3	intron	0.91123	1000000	0.008064	0.009881	0.007933	0.322	0.00002289
16	67731867	C	T	rs140139712	RANBP10	intron	0.897258	0.07256563709148360	0.0005882	0.001163	0.0005467	1.2602	0.00002295
1	5483409	C	A	rs543058066	NPHP4	intergenic	0.912568	0.6238204833141540	0.0008396	0.001479	0.0007934	1.0568	0.0000231
9	114108777	A	T	rs559769966	KIF12	regulatory region	0.932119	0.15602305475504300	0.001199	0.00193	0.001146	0.8607	0.00002323
4	65894309	G	A	rs114854424	EPHA5	intergenic	0.9443	1.1407388685285800	0.005518	0.007307	0.005388	0.376	0.00002331
18	12428641	C	T	rs76431133	PRELID3A	intron	0.98069	1.0297822024683000	0.04071	0.03633	0.04103	-0.1388	0.00002332
4	154330877	C	T	rs138153802	DCHS2	intron	0.963144	121.74020737327200	0.01136	0.01359	0.0112	0.264	0.00002341
5	74872153	T	G		FAM169A	downstream gene	0.817004	1000000	0.0009129	0.001534	0.0008681	1.0682	0.00002356
9	84561242	G	A	rs13297774	NTRK2	intergenic	0.969983	0.3987341772151900	0.005436	0.007103	0.005316	0.3776	0.00002363
19	20382532	C	A		ZNF737	intron	0.920585	1000000	0.00008695	0.0003204	0.0000701	3.9717	0.00002377
17	40518905	C	T	rs645991	TNS4	intron	0.978279	0.947268640221152	0.4328	0.423	0.4335	-0.0553	0.00002389
6	23677168	G	C	rs556001254	NRSN1	intergenic	0.973257	37.07942464040030	0.01206	0.01498	0.01185	0.2487	0.0000239
1	56558705	C	T	rs192339980	PLPP3	intron	0.946268	9.357307249712310	0.001847	0.002905	0.001771	0.6548	0.00002455
17	16816781	C	A	rs149244542	RP11-219A15.1	downstream gene	0.907333	0.41123313261752800	0.004403	0.002956	0.004507	-0.4362	0.00002458
11	34806716	T	TC	rs537597322	APIP	intergenic	0.947462	2.433523253529430	0.007107	0.00889	0.006978	0.3355	0.00002459
5	52509424	C	G	rs189361882	ITGA1	intergenic	0.719041	0	0.0003696	0.0007686	0.0003408	1.8536	0.00002468
4	122017545	A	G	rs4833242	TRPC3	regulatory region	0.994207	0.8469221912227090	0.4133	0.4011	0.4141	-0.0553	0.00002479
6	6375559	G	A	rs550252718	F13A1	intron	0.957798	1.4772293427870200	0.003587	0.00505	0.003482	0.4627	0.00002489
10	3777031	T	C	rs75254297	KLF6	3 prime UTR	0.846547	0.23320676681930000	0.003048	0.00449	0.002944	0.5245	0.00002494
11	117931086	G	GA(	rs544606424	TMPRSS13	upstream gene	0.99173	1.0142928292737800	0.554	0.5412	0.5549	-0.0545	0.00002503
4	137634260	G	C	rs79024220	PCDH18	intergenic	0.986404	1.1688122026827700	0.2302	0.2403	0.2294	0.0646	0.0000254
11	25720055	G	A	rs546998652	ANO3	intergenic	0.84323	0.49673202614379100	0.0006007	0.001119	0.0005633	1.3231	0.00002554
19	2525346	C	G		GNG7	intron	0.968516	28.126297577854700	0.002828	0.003939	0.002748	0.5353	0.00002561
7	82780	T	G	rs112792677	FAM20C	intron	0.886749	0.3900402993667240	0.001239	0.002135	0.001174	0.8269	0.00002573
7	29056073	G	A	rs187455892	CPVL	intron	0.947329	18.714614499424600	0.001166	0.001921	0.001111	0.8548	0.00002578
4	35479756	C	A	rs73238926	ARAP2	intergenic	0.963682	0.5191901746305890	0.0007137	0.00138	0.0006657	1.0745	0.00002579
3	60442704	T	C	rs551437420	FHIT	intron	0.875156	1.3770869314910800	0.00144	0.002371	0.001373	0.7637	0.00002694
22	28865171	C	T	rs5762870	ZNRF3	regulatory region	0.997454	1.1905520910952100	0.3548	0.3655	0.3541	0.0564	0.00002711
4	150611686	C	T	rs182216281	LRBA	intron	0.908187	3.508496543778800	0.003551	0.004893	0.003454	0.4785	0.00002727
7	9611587	G	A	rs7792428	NXPH1	upstream gene	0.974582	1.0510055019290300	0.8202	0.8107	0.8209	-0.0707	0.00002763
15	96261017	T	G	rs28619536	NR2F2	intron	0.900563	0.2228720756595320	0.0008953	0.001555	0.0008476	1.005	0.00002764
15	91092279	C	G		SV2B	intergenic	0.988275	20.154864709268900	0.003984	0.00543	0.00388	0.433	0.00002816
19	7903499	A	C	rs527488572	MAP2K7	non coding transcript exon	0.88607	1000000	0.0006255	0.001234	0.0005816	1.1895	0.00002862
X	83591605	T	A	rs760437155	POU3F4	intergenic	0.853788	0.5747432483834160	0.0001122	0.0004405	0.00008854	2.9442	0.0000288
6	146171187	G	C	rs571776826	GRM1	intron	0.906961	1000000	0.0005235	0.001016	0.000488	1.3642	0.00002892
6	144481772	A	C		UTRN	intron	0.889435	1000000	0.0005387	0.001039	0.0005026	1.3552	0.00002896
12	122239468	A	G	rs138439395	RP11-512M8.5,VPS33A	intron	0.821093	3.1433546140452700	0.001307	0.002082	0.001251	0.8536	0.00002905
12	61055592	A	G	rs186627445	FAM19A2	intergenic	0.986779	0.5467080469962310	0.005595	0.003935	0.005715	-0.3657	0.00002906
X	12451572	A	G	rs183412527	FRMPD4	intron	0.922	0.24282945736434100	0.0004721	0.001118	0.0004255	1.1583	0.00002909
6	105649111	G	A	rs181370604	PREP	intergenic	0.765702	1000000	0.0008363	0.0002701	0.0008771	-1.0867	0.00002949
4	96127227	T	C	rs955402507	PDHA2	intergenic	0.607991	0	0.0001512	0.0004037	0.0001329	3.388	0.00002954
1	39566856	A	T		PABPC4	intron	0.957064	1000000	0.0003365	0.0007892	0.0003038	1.6293	0.00002973
17	1660183	GAGC	G		PRPF8	intron	0.892241	0.7234506428109260	0.009116	0.006806	0.009283	-0.3041	0.00002975
3	112133056	A	G	rs142548681	GCSAM	intron	0.91529	0.6782058021075820	0.001179	0.001897	0.001127	0.8662	0.00003004
11	30376843	T	C	rs150134971	MPPED2	intergenic	0.975888	0.5775050078847550	0.00158	0.002506	0.001514	0.6997	0.00003058
11	61912914	G	T	rs117324079	RAB3IL1	intron	0.959937	0.6987067648755980	0.01454	0.01767	0.01431	0.2257	0.00003071
11	131947229	G	A	rs531230486	NTM	intron	0.91762	5.454401611047180	0.002122	0.003206	0.002043	0.6139	0.00003076
2	146072959	C	T	rs1012909876	ZEB2	intergenic	0.889918	1.5602305475504300	0.0004115	0.0009692	0.0003712	1.4091	0.00003088
7	116203932	A	T	rs13233347	TES	intergenic	0.947625	1.690691242056140	0.03254	0.03644	0.03226	0.1546	0.0000312
3	173456574	T	G	rs545980792	NLGN1	intron	0.942868	0.6560474834958510	0.0008974	0.001654	0.0008428	0.9386	0.00003129
12	31334756	TAAG	T	rs34565691,rs35692772	FAM60A	intergenic	0.981719	0.9337740336475830	0.2636	0.2735	0.2629	0.0613	0.00003143
11	116163476	T	A	rs1035545166	BUD13	intergenic	0.927356	9.360967184801380	0.0006296	0.001203	0.0005881	1.183	0.00003143
2	47068946	G	A		C2orf61,RP11-761B3.1,7	intron	0.863905	1000000	0.0002046	0.0005044	0.000183	2.4844	0.00003162
2	220336654	A	C		SLC4A3	intron	0.943326	1000000	0.004475	0.005869	0.004374	0.4179	0.00003179
3	190877971	C	T	rs13323015	GMNC	intron	0.98242	0.9594613019894040	0.4527	0.4415	0.4535	-0.054	0.00003184
3	160072822	T	A	rs149039449	IL12A	intron	0.792094	0.2968381829141320	0.0008677	0.001499	0.0008221	1.0614	0.00003208
11	35408784	C	A	rs140412290	SLC1A2	intron	0.977006	12.015349126075800	0.0115	0.01376	0.01134	0.2554	0.00003209
X	32977931	A	G		DMD	intron	0.737235	-1	0.000719	0.001477	0.0006643	0.9868	0.00003233
3	169678781	C	T	rs182040511	MECOM	intergenic	0.948915	0.3829621866057440	0.003039	0.004327	0.002946	0.5025	0.00003246
1	238433979	C	T	rs77873003	MTRNR2L11	intergenic	0.975882	1.0578010888891700	0.03942	0.04385	0.0391	0.1383	0.00003256
1	246537386	G	A	rs138797980	TFB2M	downstream gene	0.975291	4.049934082863030	0.02812	0.03192	0.02785	0.1625	0.00003276
1	184123700	A	G		TSEN15	intergenic	0.710065	1000000	0.0003657	0.0007184	0.0003402	1.9492	0.0000331
10	106725880	G	A	rs911823257	SORCS1	intron	0.97693	1000000	0.007367	0.005426	0.007507	-0.3177	0.00003346
1	81767190	C	T		ADGRL2	intron	0.652973	1000000	0.001569	0.002315	0.001515	0.8588	0.00003358
9	77615441	A	G	rs17063807	GNA14	intron	0.988302	1.5291683283045300	0.2629	0.2724	0.2622	0.0608	0.00003359

10	19526897	C	T	rs117784946	MALRD1	intron	0.887599	0.17509557136975800	0.002319	0.001239	0.002397	-0.6119	0.00003372
19	531208	C	T	rs185151998	CDC34	upstream gene	0.943443	6.990811744386870	0.01943	0.01641	0.01965	-0.2	0.0000338
1	53951112	C	T	rs190711408	LRRC42	intron	0.959615	1000000	0.0005936	0.001225	0.000548	1.147	0.00003419
10	77983410	C	T	rs188194365	POLR3A	intron	0.955566	1.0018288673352000	0.002779	0.004009	0.002691	0.5205	0.00003424
18	63882479	G	A	rs981351340	SERPINB2	intron	0.643155	1000000	0.001614	0.00239	0.001558	0.8509	0.00003439
15	26228360	G	A	rs754673565	GABRB3	intergenic	0.914187	11.228768699654800	0.004532	0.002973	0.004645	-0.4245	0.00003451
7	72407381	C	T	rs79740942	CALN1	intron	0.977546	8.421576524741080	0.007189	0.009126	0.007049	0.319	0.00003466
7	125833484	G	T		GRM8	intergenic	0.73309	1000000	0.005745	0.007217	0.005639	0.4139	0.00003474
9	92170540	T	C	rs77401124	IARS	upstream gene	0.970801	0.781153112931927	0.02723	0.02316	0.02753	-0.1667	0.00003489
3	7330848	C	G	rs7621537	GRM7	intron	0.942296	1.0207702849855100	0.6329	0.6227	0.6337	-0.0567	0.00003494
X	117589451	C	T	rs187730387	KLHL13	intergenic	0.963753	2.569505178365940	0.02316	0.02792	0.02281	0.1455	0.00003502
9	2348256	C	T	rs12378747	SMARCA2	intergenic	0.961422	0.6448553628824250	0.02648	0.03053	0.02618	0.167	0.00003541
3	144994996	T	C	rs983231847	C3orf58	intergenic	0.664619	1000000	0.0003333	0.0006667	0.0003092	2.0725	0.00003542
8	139738125	C	G	rs77980507	TRAPPC9	intron	0.92476	0.21773707675623600	0.001348	0.002188	0.001287	0.7746	0.00003556
8	4026924	CAAC	C	rs148736073,rs61192854	CSMD1	intron	0.975695	0.8956693559504510	0.1128	0.1196	0.1123	0.0849	0.00003557
7	74400677	G	A		CLIP2	intron	0.979262	0	0.001355	0.002285	0.001288	0.7338	0.00003582
14	71646366	C	T	rs376990979	SIPA1L1	intron	0.907345	3.1379710144927500	0.0006888	0.001301	0.0006447	1.113	0.00003616
4	152283423	C	T		FBXW7	intergenic	0.930635	1000000	0.0036	0.005026	0.003497	0.4582	0.00003616
17	80454269	G	A	rs11652184	NPTX1	non coding transcript exon	0.888771	0.24948216340621400	0.001593	0.002513	0.001527	0.7158	0.00003637
1	70689070	T	G	rs1889602	PTGER3	intergenic	0.995679	0.7222998599297550	0.2105	0.2017	0.2112	-0.0652	0.00003637
X	145846624	G	A	rs187946175	TMEM257	intergenic	0.836625	1.1507668711656400	0.000875	0.001627	0.0008207	0.8804	0.00003643
10	129779307	G	A	rs183318019	MGMT	intergenic	0.879416	0.28791714614499400	0.003014	0.001879	0.003096	-0.5203	0.00003644
2	28424783	G	A	rs55870117	FOSL2	upstream gene	0.985197	1.0851847684823900	0.3175	0.3278	0.3167	0.0573	0.00003657
19	34304658	G	T		KIAA0355	intron	0.682579	1000000	0.001702	0.002493	0.001645	0.7948	0.00003685
14	23823746	T	C	rs150428698	DHRS4	downstream gene	0.916669	0.8237533394138160	0.01639	0.01908	0.0162	0.2182	0.00003692
9	9391545	C	T	rs548664681	PTPRD	intron	0.954646	34.32430875576040	0.00635	0.008431	0.006199	0.336	0.00003718
2	51258670	CTG	C	rs759611290	NRXN1	intron	0.985249	0.6228242074927950	0.0007302	0.001299	0.0006891	1.0785	0.00003742
6	168483449	A	G	rs62424593	SMOC2	intron	0.811105	0.5186996547756040	0.0003667	0.0007782	0.000337	1.6953	0.00003767
20	44332569	G	A	rs188673551	R3HDML	upstream gene	0.969689	6.238204833141540	0.001064	0.001822	0.001009	0.8527	0.00003824
3	26796379	C	T	rs17224781	LRRC3B	intergenic	0.958089	0.4426866359447010	0.02442	0.02807	0.02415	0.1736	0.00003838
1	69968622	G	A	rs192676134	LRRC7	intron	0.943403	0.12012857459543300	0.002335	0.003644	0.002241	0.5512	0.00003872
1	161106269	C	T	rs534808265	PFDN2	intron	0.983391	132.56185270425800	0.0211	0.01752	0.02135	-0.1876	0.00003876
13	49297349	C	A	rs182995158	CDADC1	downstream gene	0.915558	0.5201496833621190	0.001046	0.001737	0.0009961	0.8937	0.00003909
6	2959091	G	A	rs182269539	SERPINB6	intron	0.921607	1000000	0.004932	0.006594	0.004812	0.3906	0.00003914
8	14037661	T	G	rs11990781	SGCZ	intergenic	0.966638	0.879386058485521	0.2389	0.249	0.2382	0.0629	0.00003915
22	29552513	C	T	rs55752411	THOC5	intron	0.998133	0.7815992495883370	0.1457	0.1537	0.1451	0.0747	0.00003947
15	62440143	C	T	rs191031804	TLN2	intron	0.952128	0.10071354244091000	0.001709	0.002773	0.001632	0.6506	0.00003949
4	150007283	G	A	rs746090308	DCLK2	intergenic	0.945297	1000000	0.003286	0.004601	0.003191	0.4762	0.00003968
4	141398119	G	T	rs562535932	ZNF330	intergenic	0.948735	2.6788188716595200	0.002995	0.004085	0.002917	0.5111	0.00003969
15	89914492	G	A	rs191590133	ARPIN	upstream gene	0.917931	3.7525865946918600	0.02407	0.02047	0.02434	-0.1813	0.00003974
7	132735193	A	G	rs181000660	CHCHD3	intergenic	0.944313	0.12483592400690800	0.001419	0.002205	0.001362	0.7533	0.00003991
4	55220792	A	T	rs371941069	KDR	upstream gene	0.967127	2.549354204088620	0.004214	0.005729	0.004105	0.4142	0.00003992
12	47264923	T	C		PCED1B	intron	0.816364	1000000	0.0001934	0.0005922	0.0001647	2.0581	0.0000404
2	197217361	A	G	rs145531842	AC013264.1,ANKRD44	intron	0.773505	0.5504298382183710	0.0007165	0.001247	0.0006782	1.2028	0.00004066
2	4890702	G	C	rs10208594	SOX11	intergenic	0.998359	1.0622896891068200	0.741	0.7504	0.7403	0.0604	0.00004085
10	17281296	TAGT	T	rs200217406	ST8SIA6	intergenic	0.949989	0.6014433752775720	0.005872	0.007454	0.005757	0.3584	0.00004104
6	95352469	A	C	rs924978920	MANEA	intergenic	0.852421	-1	0.0006861	0.001236	0.0006464	1.1664	0.00004104
13	111576501	C	T	rs753954886	TEX29	intergenic	0.938573	12.47180667433830	0.001934	0.002897	0.001864	0.6314	0.00004115
7	126739661	C	A		GRM8	intron	0.748961	1000000	0.006021	0.007495	0.005915	0.3964	0.00004118
2	229779801	C	A	rs80305756	TRIP12	intron	0.910828	0	0.000373	0.0008442	0.0003389	1.5261	0.0000412
1	218751381	C	A		TGFB2	intergenic	0.881139	1000000	0.001805	0.002626	0.001746	0.691	0.00004129
14	76734848	C	T		VASH1	intron	0.989799	1000000	0.00092	0.001755	0.0008598	0.8692	0.00004139
19	14083437	G	A	rs566240879	C19orf67	intron	0.910141	0.22309592424866200	0.0009128	0.001554	0.0008665	0.9666	0.00004142
9	137355775	G	A	rs77851732	EXD3	intron	0.822579	0.4444158958547450	0.03334	0.03691	0.03308	0.1616	0.00004143
17	60794929	A	G	rs185080871	BCAS3	intron	0.936091	2.6791820930955500	0.009135	0.0113	0.008979	0.2846	0.00004199
1	38461511	T	A	rs113461897	RRAGC	intergenic	0.948236	0.5385447612809660	0.01263	0.0153	0.01243	0.2403	0.00004209
3	3479559	C	T	rs114036028	SUMF1	intron	0.905513	0.45168714503136700	0.002724	0.003861	0.002642	0.535	0.00004214
17	34440850	G	C	rs117108151	CCL1	intergenic	0.986856	4.695029258943470	0.02854	0.0324	0.02826	0.1584	0.0000422
16	82663172	C	T	rs79492375	CDH13	intron	0.984641	1.1476289485196900	0.101	0.1084	0.1004	0.0876	0.00004228
5	95188008	C	T	rs145659358	MCTP1	intron	0.984839	1.6418169372005100	0.05913	0.05355	0.05954	-0.1127	0.00004251
19	9855603	G	A	rs193179342	OLFM2	intron	0.967246	75.41463414634150	0.01049	0.01281	0.01033	0.2623	0.00004256
12	15029679	C	T		PDE6H	intergenic	0.880816	0	0.000246	0.0006482	0.000217	1.8969	0.00004264
9	80423173	CA	C		TLE4	intergenic	0.992222	1000000	0.001285	0.002077	0.001228	0.7679	0.00004269
6	129611749	T	C	rs7753754	ARHGAP18	intron	0.992992	1.070421312236570	0.379	0.3887	0.3783	0.0543	0.00004295
7	71729804	G	A	rs138705771	WBSCR17	intergenic	0.976268	1.4734201856843400	0.0557	0.05039	0.05608	-0.1163	0.000043
8	65240268	A	G	rs4448317	ARMC1	intergenic	0.991413	0.990250265433035	0.7003	0.6903	0.701	-0.0575	0.00004304
9	30530718	C	A	rs574478773	ACO1	intron	0.938883	0.2528535439927850	0.001671	0.002573	0.001606	0.6818	0.00004316
11	77148981	G	A	rs190124410	MYO7A	intron	0.654923	0.38981588032220900	0.0001185	0.0003523	0.0001016	3.5857	0.00004321
16	50728860	T	C	rs72796367	NOD2	intron	0.981268	2.2311101311873000	0.04816	0.04268	0.04855	-0.125	0.00004334
2	62408232	A	C	rs6717002	TMEM17	regulatory region	0.97517	1.0787614012501400	0.3849	0.3713	0.3858	-0.0548	0.00004352
19	10692780	C	G	rs779789066	ILF3	downstream gene	0.950787	13.409666283084000	0.01153	0.01398	0.01136	0.2507	0.00004366
9	126279820	TGA	T	rs35838010,rs71493838,	MVB12B	upstream gene	0.996001	0.7426023343744860	0.09473	0.08717	0.09528	-0.0905	0.0000437
18	22148618	C	T	rs138159730	GATA6	intergenic	0.832735	10.921128382268300	0.003213	0.004401	0.003127	0.5123	0.00004381
22	41913468	G	A	rs141336766	SHISA8	intron	0.99359	0.22711029604401400	0.003094	0.004475	0.002994	0.4703	0.00004388
12	60430028	A	C	rs73125246	SLC16A7	intergenic	0.97716	0.7796488198042600	0.008335	0.006242	0.008487	-0.2954	0.00004394

7	103239399	A	C	rs561481774	PMPCB	intron	0.993185	9.122895622895620	0.01659	0.01368	0.0168	-0.2068	0.00004395
4	26503031	A	G	rs2171754	CCKAR	intergenic	0.997689	0.7773067593780250	0.2672	0.2565	0.268	-0.0595	0.00004403
5	102868347	T	G	rs112407725	PAM	intron	0.96434	0.36464571697732300	0.004454	0.005929	0.004348	0.4029	0.00004459
3	196418829	C	G	rs4916494	UBXN7	intron	0.988454	0.9936961346930290	0.967	0.9706	0.9667	0.1473	0.0000447
10	79790827	C	A		NUTM2E	intron	0.937475	1000000	0.005543	0.007163	0.005426	0.3674	0.00004474
1	182440497	C	T	rs148212790	RGSL1	intron	0.964896	17.168876080691600	0.007104	0.008963	0.00697	0.3194	0.00004491
19	8603636	C	T	rs74758686	ADAMTS10	intron	0.91923	3.1173762945914800	0.01089	0.01293	0.01074	0.2662	0.00004514
3	28606412	G	C	rs11923408	RBMS3,RP11-9J18.1	intron	0.926384	0.9726107213849240	0.2967	0.2864	0.2974	-0.0594	0.00004516
2	172931344	G	A	rs77882306	RAPGEF4	intron	0.935334	0.5046249109540250	0.003553	0.004741	0.003467	0.4656	0.00004539
6	132756409	A	G	rs893732636	VNN 2.00	intron	0.650904	0.5197545070962790	0.0004714	0.0008653	0.000443	1.6553	0.00004543
12	71058598	G	T	rs184188109	TSPAN8	intron	0.914732	0.3465030047308530	0.0006225	0.001205	0.0005805	1.147	0.00004593
4	66959382	A	C	rs116035446	CENPC	intergenic	0.993658	0.6170946010740320	0.01581	0.01342	0.01599	-0.2088	0.00004648
X	16715663	T	C		CTPS2	upstream gene	0.757411	1000000	0.0006813	0.001494	0.0006226	0.9163	0.00004676
9	135482479	T	C	rs534235071	PPP1R26	intron	0.894844	1000000	0.003333	0.004478	0.00325	0.4889	0.00004746
X	155598637	G	A	rs183881096	TMLHE	intron	0.815893	0.3580533596837950	0.0004228	0.0009834	0.0003823	1.275	0.00004763
12	82054599	T	C	rs61933746	CCDC59	intergenic	0.996729	0.5557272571180400	0.01976	0.02304	0.01952	0.1873	0.00004782
19	1035573	T	G		CNN2	intron	0.700122	0	0.0001882	0.0004917	0.0001663	2.5499	0.0000479
11	123278543	T	C	rs181894815	GRAMD1B	intergenic	0.84886	1000000	0.001598	0.002544	0.00153	0.7057	0.00004795
6	39243154	G	A	rs145164634	KCNK5	intergenic	0.950416	1.820228494623660	0.006541	0.008247	0.006418	0.3354	0.00004799
15	87509869	T	C	rs138332122	NTRK3	intron	0.893742	0.04453394706559260	0.001015	0.001745	0.0009624	0.8874	0.00004806
2	211829564	C	A	rs910061482	ERBB4	intron	0.791746	1000000	0.0008619	0.001476	0.0008176	1.0537	0.00004831
17	48030560	C	T	rs542158473	COPZ2	intron	0.956085	0.20104680945840600	0.0009193	0.001522	0.0008758	0.9499	0.00004848
2	235352346	G	A	rs191435076	AGAP1	intergenic	0.872651	0.2447420466745780	0.001219	0.002121	0.001154	0.7856	0.00004848
14	92468164	C	T	rs186085385	SLC24A4	intron	0.815499	46.80483592400690	0.004014	0.005242	0.003926	0.4637	0.00004854
6	130878057	T	C	rs145997698	EPB41L2	intron	0.691915	0	0.0005596	0.001003	0.0005276	1.4338	0.00004869
18	13516687	G	A	rs190118591	LDLRAD4	intron	0.863989	0.5323332117095630	0.0009526	0.001618	0.0009046	0.9451	0.00004871
20	23708518	C	T	rs140117599	CST4	downstream gene	0.943178	0.05198504027617950	0.0008333	0.001563	0.0007806	0.9379	0.00004921
17	48573040	G	A	rs542996712	HOXB3	intron	0.959621	0.21515494411688800	0.0009156	0.001517	0.0008722	0.9478	0.00004985
4	134482423	C	CT	rs201136779	PABPC4L	intergenic	0.984957	1.5905475893433400	0.03996	0.04488	0.0396	0.1331	0.00004996
3	153461958	A	G	rs533446523	RAP2B	intron	0.869719	0.38960011507479900	0.000539	0.001103	0.0004983	1.2316	0.00005006
8	140377914	C	T	rs527780961	TRAPPC9	intron	0.83419	0.20854997111496200	0.0005083	0.001032	0.0004705	1.318	0.00005008
11	387673	C	T	rs550085047	PKP3	upstream gene	0.772924	0.3019666833806900	0.0005556	0.001065	0.0005189	1.3144	0.00005088
9	39151292	T	C	rs10974175	CNTNAP3	intron	0.825015	1.5207516721806700	0.04354	0.04786	0.04323	0.1396	0.00005113
5	153047583	GC	G	rs200338415	GRIA1	intron	0.954352	0.24335232535294300	0.005209	0.006855	0.00509	0.3699	0.00005115
12	4080024	T	C	rs75538199	CCND2	intergenic	0.997288	1.5254643740052200	0.06573	0.05973	0.06616	-0.1053	0.00005125
9	116874535	T	C	rs79245839	ASTN2	intron	0.968789	0.12394078878543800	0.003015	0.004147	0.002933	0.4922	0.00005128
2	113072705	C	G	rs188407486	IL1F10	splice region	0.835481	0.21499146859251600	0.0005592	0.001137	0.0005175	1.2198	0.00005137
5	1354733	C	T		CLPTM1L	intergenic	0.789496	1000000	0.0002852	0.0007253	0.0002535	1.7411	0.00005153
15	34588734	G	A	rs12441187	GOLGA8B	upstream gene	0.999155	1.1142579693420500	0.5605	0.5735	0.5595	0.0524	0.00005174
X	108772677	G	C		IRS4	intergenic	0.912681	0	0.001399	0.002327	0.001332	0.6386	0.00005192
1	171786407	T	G	rs79133693	METTL13	intron	0.970447	1.0887672304233100	0.008002	0.009844	0.007869	0.2985	0.00005192
7	21854744	C	T		DNAH11	intron	0.794366	1000000	0.0003346	0.0007385	0.0003055	1.7315	0.00005203
5	113457361	C	T	rs186525850	MCC	intron	0.923608	0.44856507440793100	0.008705	0.01054	0.008572	0.2928	0.00005232
12	6693611	G	A	rs147914326	PIANP	upstream gene	0.922224	0.8866489865385640	0.01441	0.01216	0.01457	-0.225	0.00005249
11	95638556	A	T	rs146054691	FAM76B	intergenic	0.883353	0	0.00077	0.001381	0.0007259	1.0428	0.0000527
11	132959394	G	C		OPCML	intron	0.90521	1000000	0.004065	0.002612	0.00417	-0.441	0.00005313
4	149167013	C	T	rs192504379	RP11-526A4.1	intron	0.950262	2.4269174182818400	0.003059	0.004314	0.002969	0.4832	0.00005396
11	92564579	T	C	rs149937921	FAT3	intron	0.972046	2.84348409212467	0.06828	0.06173	0.06875	-0.1052	0.00005407
1	112411859	C	T	rs748304538	CTTNBP2NL	intron	0.982158	31.192396313364100	0.003464	0.004695	0.003375	0.4525	0.00005409
3	100745228	C	T	rs771511466	TFG	intron	0.974449	5.9890300230946900	0.005904	0.007498	0.005789	0.3461	0.00005471
5	124309406	A	G		ZNF608	intron	0.833982	1000000	0.0005118	0.0009983	0.0004767	1.3464	0.00005515
14	69229619	C	G	rs12886715	EXD2	intron	0.996424	0.9813518355012670	0.3312	0.341	0.3304	0.0551	0.0000554
11	106872179	T	C	rs562868444	GUCY1A2	intron	0.943468	0.09597449182941410	0.001379	0.002237	0.001317	0.73	0.00005559
8	127095706	C	T	rs902041617	POU5F1B	downstream gene	0.894634	1000000	0.001281	0.002017	0.001227	0.7969	0.00005565
2	153457666	A	C	rs73972939	RPRM	intron	0.993474	0.8005615901869500	0.04963	0.0445	0.05	-0.1199	0.00005601
6	96192741	C	A		FUT9	intron	0.852805	1000000	0.000569	0.001072	0.0005327	1.2565	0.00005636
X	40338527	C	T		BCOR	intergenic	0.928288	23.538211382113800	0.005064	0.003129	0.005203	-0.3162	0.00005663
10	26367489	G	A	rs572160777	GAD2	intergenic	0.932256	0.275011845935152	0.0007773	0.001444	0.0007291	0.9816	0.00005678
16	76373476	A	G	rs78529051	CNTNAP4	intron	0.962989	0.2727226941543830	0.01149	0.01415	0.0113	0.245	0.000057
3	18216293	A	G	rs187784206	TBC1D5	intron	0.976499	26.15874855156430	0.008847	0.00685	0.008992	-0.2805	0.0000571
10	49458075	CTTT/	C	rs557687404	ERCC6	3 prime UTR	0.76828	9.350604490500860	0.0002044	0.0005231	0.0001814	2.3209	0.00005755
6	3676798	G	A	rs187338773	PXDC1	intergenic	0.909385	9.35385500575374	0.001835	0.00287	0.001761	0.6336	0.00005776
12	13562499	G	A	rs201725673	GRIN2B	3 prime UTR	0.850038	37.401611047180700	0.002418	0.003424	0.002346	0.5806	0.00005849
16	2313478	A	C	rs149620152	ABCA3	intron	0.97109	1.588547815820540	0.1176	0.11	0.1182	-0.0815	0.00005864
2	227663628	G	A	rs55821295	SLC19A3	intergenic	0.972942	0.8262779137738960	0.297	0.3085	0.2962	0.0571	0.00005878
3	148097506	T	C	rs138007650	ZIC1	intron	0.951673	0.8347399217936820	0.003956	0.005311	0.003858	0.4239	0.000059
5	109969088	T	G	rs148035664	MAN2A1	intergenic	0.96683	0.1495872186256460	0.004047	0.005503	0.003942	0.4124	0.00005911
6	147042563	G	GA	rs989524461	STXBP5	intron	0.816358	1.8032786885245900	0.0008123	0.00141	0.0007692	1.0354	0.00005915
22	43762177	A	T	rs151116284	EFCAB6	intron	0.981656	3.71763872282007	0.02363	0.02041	0.02387	-0.1716	0.00005935
10	119563	C	T		ZMYND11	intergenic	0.845074	0.09437877044321230	0.0005008	0.001057	0.0004606	1.2626	0.00005957
11	34110856	C	T	rs187217282	NAT10	intron	0.942086	1000000	0.005864	0.007478	0.005748	0.3503	0.00005972
8	121323372	G	A	rs13265178	HAS2	intergenic	0.997011	1.006189521769750	0.3534	0.344	0.3541	-0.054	0.00005975
6	170187695	C	G	rs139637431	DLL1	intergenic	0.950935	84.13808975834290	0.006169	0.004516	0.006288	-0.3375	0.00005988
11	57557921	C	T	rs79462097	UBE2L6	intron	0.98981	3.645799241984350	0.06424	0.05819	0.06468	-0.1082	0.0000599
10	13852412	A	T	rs186255870	FRMD4A	intron	0.894633	2.077956989247310	0.00173	0.002752	0.001656	0.6446	0.00005994

16	58589003	C	T	rs113479751	CNOT1	intron	0.985536	0.30177590699539000	0.005476	0.007379	0.005339	0.3489	0.00006001
8	52960413	C	T	rs923625917	NPBWR1	intergenic	0.970247	7.793440736478710	0.001081	0.001779	0.001031	0.833	0.00006006
9	7346950	C	A		KDM4C	intergenic	0.699436	1000000	0.000499	0.0009723	0.0004649	1.4498	0.00006007
4	189762969	C	T	rs6816277	FRG1	intergenic	0.998084	-1	0.5715	0.5834	0.5707	0.0522	0.0000602
11	7627409	G	A	rs145187200	PPFIBP2	intron	0.970959	0.5327985763964360	0.0219	0.01904	0.0221	-0.1782	0.00006031
12	32311558	C	T	rs183537774	BICD1	intron	0.947465	4.370161290322580	0.004557	0.006153	0.004442	0.3905	0.00006044
16	25765598	A	G	rs12325368	HS3ST4	intron	0.999762	0.9186338489007590	0.4704	0.4823	0.4695	0.0514	0.00006065
3	25613787	TA	T	rs528598032	TOP2B	intron	0.950535	1.9891720683559200	0.003662	0.005065	0.003561	0.436	0.00006078
1	213192622	G	A	rs181363272	RPS6KC1	intron	0.968049	1000000	0.001495	0.002341	0.001433	0.6958	0.00006081
9	70056003	A	G	rs1023272819	MAMDC2	intron	0.842176	1000000	0.0006846	0.001202	0.0006473	1.1506	0.00006174
2	176279116	G	GT	rs200032230	MTX2	intron	0.641413	0.05631150781266260	0.0000425	0.0002006	0.00003116	5.8201	0.00006185
14	75711263	T	A		TTLL5	non coding transcript exon	0.852656	1000000	0.001167	0.001933	0.001112	0.8262	0.00006186
22	17651500	G	A	rs188141384	BCL2L13	intron	0.93017	18.857142857142900	0.001069	0.001845	0.001013	0.8271	0.000062
6	163878113	C	A		QKI	intergenic	0.793404	1000000	0.0001873	0.0004727	0.0001668	2.4537	0.00006207
19	14979904	C	G	rs189175700	SLC1A6	5 prime UTR	0.974501	1.0750507099391500	0.01214	0.009617	0.01232	-0.2401	0.00006232
1	87627137	C	T	rs116475498	LMO4	intergenic	0.995713	1.2044145970706000	0.06204	0.06704	0.06168	0.1066	0.00006247
20	53106082	T	G		TSHZ2	intron	0.834852	1000000	0.000549	0.001044	0.0005133	1.2776	0.00006256
9	33618367	A	G	rs754909627	TRBV20OR9-2	missense	0.783706	1000000	0.0006606	0.001217	0.0006204	1.1626	0.00006285
14	41507138	G	T	rs116945624	LRFN5	intergenic	0.994922	0.3779641193004960	0.0155	0.01842	0.01529	0.2083	0.00006288
12	9134334	C	T		PZP	upstream gene	0.940326	9.355581127733030	0.00197	0.00292	0.001902	0.6064	0.00006309
11	58797916	T	A	rs146865331	GLYATL2	upstream gene	0.991507	69.50545921644190	0.05284	0.04729	0.05324	-0.1186	0.00006317
4	15202839	G	A	rs35277028	CPEB2	intron	0.999324	1.9287180170364300	0.1334	0.1402	0.1329	0.0756	0.00006332
15	60105957	A	G	rs72739977	FOXB1	intron	0.87572	0.23993095512082900	0.0004357	0.0009103	0.0004015	1.389	0.00006384
12	8620477	A	G		AICDA	intergenic	0.9027	1000000	0.0003864	0.0007782	0.0003581	1.5571	0.00006412
7	26620503	C	T	rs140038667	SKAP2	regulatory region	0.87348	0.2437302101324120	0.00157	0.002492	0.001504	0.6946	0.0000646