

Table S4. High scoring genes with support of regulatory information.

Gene symbol	Score	Risk region (chr:start-end)	Linked TREs or eQTL (chr:start-end)	Implicated risk variant ¹	Reference of interaction ²	Distal gene?
<i>DRD2</i>	1420.9	chr11:113317745-113424042	chr11:113344860-113345010	rs61902807	ENCODE	No
<i>FGFR1</i>	926.8	chr8:38014429-38231314	chr8:38081200-38081350	rs6999796	ENCODE	Yes
	926.8	chr8:38014429-38231314	chr8:38226140-38226290	rs16887343	ENCODE	Yes
<i>MAPK3</i>	915.7	chr16:29923510-30018500	chr16:29986080-29986230	rs10871451	ENCODE	Yes
<i>STAR</i>	822.7	chr8:38014429-38231314	chr8:38014320-38014470	rs75168396	ENCODE	No
<i>CACNA1C</i>	597.1	chr12:2292690-2523772	chr12:2368640-2368790	rs10774035	ENCODE	No
<i>RAD51</i>	481.9	chr15:40566759-40602256	chr15:40569820-40569970	rs28676999	ENCODE	Yes
<i>PRKCD</i>	439.5	chr3:52638482-52960859	chr3:52721240-52721390	rs11177	ENCODE	Yes
	439.5	chr3:52638482-52960859	chr3:52744220-52744370	chr3:52744224-52744224	ENCODE	Yes
	439.5	chr3:52638482-52960859	chr3:52746520-52746670	rs4687644	ENCODE	Yes
	439.5	chr3:52638482-52960859	chr3:52755560-52755710	rs11130319	ENCODE	Yes
	439.5	chr3:52638482-52960859	chr3:52766600-52766750	rs2268027	ENCODE	Yes
	439.5	chr3:52638482-52960859	chr3:52826500-52826650	rs746694	ENCODE	Yes
	439.5	chr3:52638482-52960859	chr3:52864020-52864170	rs4687554	ENCODE	Yes
	439.5	chr3:52638482-52960859	chr3:52870600-52870750	rs4687663	ENCODE	Yes
<i>SREBF1</i>	388.5	chr17:17760789-18036283	chr17:17820860-17821010	chr17:17820998-17820998	ENCODE	Yes
	388.5	chr17:17760789-18036283	chr17:17847860-17848010	rs6502624	ENCODE	Yes
<i>OPN1LW</i>	359.6	chrX:153176959-153376436	chrX:153241340-153241490	rs4898374	ENCODE	Yes
<i>CD34</i>	346.3	chr1:207893266-208024062	chr1:207919840-207919990	rs2796264	ENCODE	Yes
	346.3	chr1:207893266-208024062	chr1:207992400-207992550	rs12123251	ENCODE	Yes
	346.3	chr1:207893266-208024062	chr1:208017040-208017190	rs2724394	ENCODE	Yes
<i>MECP2</i>	310.3	chrX:153176959-153376436	chrX:153265580-153265730	rs11795678	ENCODE	No
<i>CYP21A2</i>	299.8	chr6:31580539-31732547	chr6:31688080-31688230	rs116316082	ENCODE	No
<i>FES</i>	286.1	chr15:91412848-91429042	chr15:91423500-91423650	rs6224	ENCODE	No
<i>CHRNA4</i>	269.3	chr15:78785544-	chr15:78907320-	rs7177514	ENCODE	No

		78930510	78907470			
<i>PPARGCIA</i>	250.8	chr4:23348610-23443426	chr4:23355480-23355630	rs6834404	ENCODE	No
<i>FLNA</i>	246.1	chrX:153176959-153376436	chrX:153211620-153211770	rs762656	ENCODE	Yes
<i>GRIK3</i>	200.3	chr1:37093026-37194103	chr1:37162320-37162470	rs589249	ENCODE	No
	200.3	chr1:37093026-37194103	chr1:37164780-37164930	rs631416	ENCODE	No
<i>EPHX2</i>	192.7	chr8:27411100-27453579	chr8:27442080-27442230	rs73229090	ENCODE	No
	192.7	chr8:27411100-27453579	chr8:27453520-27453670	rs35236974	ENCODE	No
<i>HBEGF</i>	189.8	chr5:140024042-140222641	chr5:140024400-140024550	rs702399	ENCODE	Yes
	189.8	chr5:140024042-140222641	chr5:140024400-140024550	rs60115373	ENCODE	Yes
<i>PAM</i>	188.1	chr5:101581848-101871853	chr5:101630860-101631010	rs841921	ENCODE	Yes
<i>TPR</i>	185.0	chr1:186434518-186711910	chr1:186451940-186452090	rs3131554	ENCODE	Yes
<i>MCL1</i>	182.2	chr1:149998923-150226321	chr1:150152820-150152970	rs1105209	ENCODE	Yes
	182.2	chr1:149998923-150226321	chr1:150194840-150194990	rs11576997	ENCODE	Yes
<i>TAPI</i>	173.0	chr6:32014828-32609061	chr6:32430480-32430630	rs114664081	ENCODE	Yes
	173.0	chr6:32014828-32609061	chr6:32430480-32430630	rs116580588	ENCODE	Yes
<i>NMUR2</i>	167.7	chr5:151941138-152847217	chr5:152022020-152022170	rs17454953	ENCODE	Yes
<i>TIE1</i>	167.5	chr1:44029353-44248230	chr1:44083800-44083950	rs639929	ENCODE	Yes
<i>CCL22</i>	159.4	chr16:57021433-57040093	chr16:57040020-57040170	rs34218679	ENCODE	Yes
<i>NOTCH4</i>	151.4	chr6:32014828-32609061	chr6:32154880-32155030	rs115219661	ENCODE	No
<i>PJA2</i>	145.9	chr5:109030041-109209342	chr5:109047260-109047410	rs13153918	ENCODE	Yes
	145.9	chr5:109030041-109209342	chr5:109185320-109185470	rs12656712	ENCODE	Yes
<i>NISCH</i>	138.6	chr3:52638482-52960859	chr3:52833100-52833250	rs2535629	ENCODE	Yes
<i>ANK3</i>	135.1	chr10:62040118-62349324	chr10:62094060-62094210	rs991405	ENCODE	No
	135.1	chr10:62040118-62349324	chr10:62103140-62103290	rs2061488	ENCODE	No
	135.1	chr10:62040118-62349324	chr10:62103140-62103290	rs2061489	ENCODE	No
	135.1	chr10:62040118-62349324	chr10:62103140-62103290	rs4456215	ENCODE	No
	135.1	chr10:62040118-62349324	chr10:62320320-62320470	rs2068043	ENCODE	No
<i>ADD1</i>	129.7	chr4:2359807-	chr4:2392660-	rs9994065	ENCODE	Yes

		2404699	2392810			
<i>NEURL</i>	127.1	chr10:104423800-105059896	chr10:104786200-104786350	rs4917992	ENCODE	Yes
	127.1	chr10:104423800-105059896	chr10:104837720-104837870	rs1046411	ENCODE	Yes
	127.1	chr10:104423800-105059896	chr10:104856080-104856230	rs12412038	ENCODE	Yes
	127.1	chr10:104423800-105059896	chr10:104877200-104877350	rs79082900	ENCODE	Yes
	127.1	chr10:104423800-105059896	chr10:104945200-104945350	rs4917997	ENCODE	Yes
	127.1	chr10:104423800-105059896	chr10:104947400-104947550	rs10883843	ENCODE	Yes
	127.1	chr10:104423800-105059896	chr10:104949660-104949810	rs11191600	ENCODE	Yes
	127.1	chr10:104423800-105059896	chr10:104949660-104949810	rs11191601	ENCODE	Yes
	127.1	chr10:104423800-105059896	chr10:104951440-104951590	chr10:104951466-104951466	ENCODE	Yes
<i>HTR3B</i>	125.1	chr11:113317745-113424042	chr11:113317700-113317850	rs17601612	ENCODE	Yes
	125.1	chr11:113317745-113424042	chr11:113318820-113318970	rs4936272	ENCODE	Yes
<i>HCFC1</i>	122.0	chrX:153176959-153376436	chrX:153214460-153214610	rs201119463	ENCODE	No
<i>PRMT1</i>	116.7	chr19:50067508-50138023	chr19:50091400-50091550	rs10406941	ENCODE	Yes
<i>HLA-DQB1</i>	114.6	chr6:32014828-32609061	chr6:32165300-32165450	rs115344853	ENCODE	No
	114.6	chr6:32014828-32609061	chr6:32603380-32603530	rs111529210	ENCODE	No
	114.6	chr6:32014828-32609061	chr6:32603380-32603530	rs113008958	ENCODE	No
<i>SV2B</i>	107.8	chr15:91412848-91429042	chr15:91419340-91419490	chr15:91419432-91419432	ENCODE	Yes
<i>CTNNA1</i>	106.0	chr5:137598340-137948140	chr5:137652180-137652330	rs11740078	ENCODE	No
<i>AGER</i>	105.8	chr6:31580539-31732547	chr6:31692160-31692310	rs116193838	ENCODE	No
<i>MAPK11</i>	97.4	chr22:50162136-50321623	chr22:50244560-50244710	rs3788730	ENCODE	Yes
	97.4	chr22:50162136-50321623	chr22:50319900-50320050	rs10854860	ENCODE	Yes
<i>RANGAP1</i>	91.0	chr22:41429084-41637119	chr22:41434800-41434950	rs9611474	ENCODE	No
<i>DOCK4</i>	90.2	chr7:110843795-111092478	chr7:110917580-110917730	rs13239254	ENCODE	Yes
<i>GNL3</i>	89.9	chr3:52638482-52960859	chr3:52642440-52642590	rs3774365	ENCODE	No
<i>GCA</i>	88.6	chr2:162796517-162910223	chr2:162866140-162866290	rs2909448	ENCODE	Yes
<i>FLII</i>	87.9	chr17:17760789-18036283	chr17:17823100-17823250	rs9890341	ENCODE	Yes
	87.9	chr17:17760789-	chr17:17853780-	rs8078105	ENCODE	Yes

		18036283	17853930			
<i>FMR1</i>	85.7	chrX:147287097-147480725	chrX:147351240-147351390	rs59460742	ENCODE	Yes
<i>MLC1</i>	80.7	chr22:50162136-50321623	chr22:50309360-50309510	rs4074304	ENCODE	Yes
<i>CD46</i>	80.6	chr1:207893266-208024062	chr1:207981320-207981470	rs761276	ENCODE	No
<i>GRIN2A</i>	1385.0	chr16:9875513-9971728	chr16:9912515-9912659	rs11645219	FANTOM5	No
<i>SERPING1</i>	137.5	chr11:57369008-57681828	chr11:57371918-57372022	rs28362950	FANTOM5	No
<i>HLA-DQB1</i>	114.6	chr6:32014828-32609061	chr6:32576157-32576293	rs34811813	FANTOM5	No
	114.6	chr6:32014828-32609061	chr6:32590770-32591146	rs115195925	FANTOM5	No
	114.6	chr6:32014828-32609061	chr6:32590770-32591146	rs115553940	FANTOM5	No
<i>CD46</i>	80.6	chr1:207893266-208024062	chr1:207999163-207999611	rs12132780	FANTOM5	No
<i>SREBF1</i>	388.5	chr17:17760789-18036283	chr17:17958402-17958402	rs8082590	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17760789-17760789	rs8079321	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17762457-17762457	rs9911281	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17764061-17764061	rs35451946	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17764502-17764502	rs4924823	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17765655-17765655	rs12941039	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17767165-17767165	rs1889014	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17767767-17767767	rs9895335	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17767819-17767819	rs9895750	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17770355-17770355	rs11657074	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17770965-17770965	rs9907246	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17774118-17774118	rs9907287	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17774422-17774422	rs9908017	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17774568-17774568	rs9908299	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17776389-17776389	rs8080061	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17777245-17777245	rs12936037	GTE _{ex}	Yes
	388.5	chr17:17760789-18036283	chr17:17843378-17843378	rs11657845	GTE _{ex}	Yes
	388.5	chr17:17760789-	chr17:17891781-	rs7207821	GTE _{ex}	Yes

		18036283	17891781			
	388.5	chr17:17760789-18036283	chr17:17894750-17894750	rs62072048	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17896090-17896090	rs4368210	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17896205-17896205	rs4584886	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17896673-17896673	rs9912096	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17899839-17899839	rs4506969	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17902135-17902135	rs28537385	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17903505-17903505	chr17:17903505-17903505	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17906520-17906520	rs62072049	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17906564-17906564	rs62072050	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17913057-17913057	rs6502632	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17913504-17913504	rs7212167	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17915791-17915791	rs7223696	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17919749-17919749	rs9913277	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17924060-17924060	rs8079418	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17924868-17924868	rs9896837	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17926605-17926605	rs7215524	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17930253-17930253	rs2955378	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17932818-17932818	rs2955377	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17932931-17932931	rs7224047	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17939247-17939247	rs2955385	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17939573-17939573	rs2955384	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17940305-17940305	rs7503738	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17941037-17941037	rs6502633	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17942613-17942613	rs7406982	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17944349-17944349	rs2955380	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17945500-17945500	rs2955381	GTEEx	Yes
	388.5	chr17:17760789-	chr17:17946401-	rs2955357	GTEEx	Yes

		18036283	17946401			
388.5	chr17:17760789-18036283	chr17:17946730-17946730	rs2955359	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17947710-17947710	rs2955382	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17948716-17948716	rs2955354	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17948979-17948979	rs2955353	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17949789-17949789	rs7207461	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17949802-17949802	rs12948749	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17950001-17950001	rs12940282	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17952439-17952439	rs11652894	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17952868-17952868	rs4925135	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17953548-17953548	rs2955350	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17954728-17954728	rs8080602	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17954764-17954764	rs8080334	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17955344-17955344	rs6502634	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17960613-17960613	rs11650021	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17961349-17961349	rs2955368	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17961407-17961407	rs2955369	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17964717-17964717	rs2955356	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17966524-17966524	chr17:17966524-17966524	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17966945-17966945	rs2955370	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17967397-17967397	rs2955371	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17970229-17970229	rs2955372	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17972973-17972973	rs4643387	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17980671-17980671	rs12943914	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17983817-17983817	rs6502636	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17987285-17987285	rs2955351	GTEEx	Yes	
388.5	chr17:17760789-18036283	chr17:17990474-17990474	rs4506967	GTEEx	Yes	
388.5	chr17:17760789-	chr17:17992793-	rs4925138	GTEEx	Yes	

		18036283	17992793			
	388.5	chr17:17760789-18036283	chr17:17994332-17994332	rs12943202	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17995166-17995166	rs12950562	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17995619-17995619	rs2974998	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17997209-17997209	rs2230316	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:17997547-17997547	rs2974999	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18003648-18003648	rs854814	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18003845-18003845	rs854813	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18005073-18005073	rs721669	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18006421-18006421	rs854810	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18006539-18006539	rs854809	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18006634-18006634	rs854808	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18008447-18008447	rs712265	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18009028-18009028	rs2056842	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18009102-18009102	rs854762	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18010095-18010095	rs854763	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18011140-18011140	rs6826	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18011750-18011750	rs854764	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18012730-18012730	rs854765	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18012775-18012775	rs854766	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18016148-18016148	rs1101727	GTEEx	Yes
	388.5	chr17:17760789-18036283	chr17:18022039-18022039	rs854818	GTEEx	Yes
ARNTL	359.6	chr11:13288698-13350131	chr11:13288851-13288851	rs34560638	GTEEx	No
	359.6	chr11:13288698-13350131	chr11:13288885-13288885	rs61882109	GTEEx	No
	359.6	chr11:13288698-13350131	chr11:13291931-13291931	rs4146385	GTEEx	No
	359.6	chr11:13288698-13350131	chr11:13292864-13292864	rs2219998	GTEEx	No
	359.6	chr11:13288698-13350131	chr11:13294268-13294268	rs900144	GTEEx	No
	359.6	chr11:13288698-	chr11:13301875-	rs72867447	GTEEx	No

		13350131	13301875			
CYP2D6	275.3	chr22:42315790-42689370	chr22:42315790-42315790	rs763263	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42343091-42343091	rs6002555	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42361336-42361336	rs5996096	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42364057-42364057	rs4822076	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42603814-42603814	rs6002655	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42534148-42534148	rs2743449	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42534682-42534682	rs2743451	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42534864-42534864	rs35711087	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42537597-42537597	rs1800754	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42538103-42538103	rs3021083	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42540551-42540551	rs2743461	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42541349-42541349	rs5758605	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42542870-42542870	rs2142694	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42543288-42543288	rs2743462	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42547739-42547739	rs2743465	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42557710-42557710	rs5758619	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42566314-42566314	rs5758623	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42571028-42571028	rs760648	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42574830-42574830	rs2413684	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42579309-42579309	rs67588321	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42579520-42579520	rs2899355	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42592239-42592239	rs5751239	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42598951-42598951	rs5758645	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42600589-42600589	rs5751241	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42613485-42613485	rs5758653	GTE _x	No
	275.3	chr22:42315790-42689370	chr22:42618340-42618340	rs2143138	GTE _x	No
	275.3	chr22:42315790-	chr22:42622003-	rs5758659	GTE _x	No

		42689370	42622003			
	275.3	chr22:42315790-42689370	chr22:42623718-42623718	rs5758660	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42624445-42624445	rs5758661	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42636687-42636687	rs5758670	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42639645-42639645	rs5751250	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42640606-42640606	rs5751251	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42643039-42643039	rs5758677	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42648408-42648408	rs5751255	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42650323-42650323	rs68037805	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42650663-42650663	rs134866	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42652074-42652074	rs134869	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42652317-42652317	rs134870	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42652716-42652716	rs134871	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42657566-42657566	rs134873	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42662371-42662371	rs134877	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42664201-42664201	rs134879	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42670965-42670965	rs134882	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42675960-42675960	rs66607825	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42680800-42680800	rs86669	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42683343-42683343	rs134900	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42683997-42683997	rs134902	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42689140-42689140	rs80506	GTEEx	No
	275.3	chr22:42315790-42689370	chr22:42689370-42689370	rs134906	GTEEx	No
<i>HLA-DQB1</i>	114.6	chr6:32014828-32609061	chr6:32605982-32605982	chr6:32605982-32605982	GTEEx	No
	114.6	chr6:32014828-32609061	chr6:32586934-32586934	chr6:32586934-32586934	GTEEx	No
<i>HLA-DRB1</i>	107.4	chr6:32014828-32609061	chr6:32605982-32605982	chr6:32605982-32605982	GTEEx	No
	107.4	chr6:32014828-32609061	chr6:32586934-32586934	chr6:32586934-32586934	GTEEx	No

Notes:

1. Implicated risk variants refer to variants residing in the linked TREs or eQTL that are in strong LD ($r^2 > 0.5$) with schizophrenia GWAS signals.
2. Reference of transcriptional regulatory interactions between TREs or eQTL and their target genes are collected from ENCODE (THURMAN et al. 2012), FANTOM5 (ANDERSSON et al. 2014), and GTEx (blood tissue) (CONSORTIUM 2013).