

Integration of Transcriptome and Exome Genotyping Identifies Significant Variants with Autism Spectrum Disorder

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Table S1. List of significant SNPs at $p < 0.001$.

S.No.	CHR	SNP	BP	A1	F_A	F_U	A2	CHISQ	P	OR	SE	L95	U95
1	1	exm10307	6705944	T	0.08462	0.005682	C	12.36	0.0004376	16.18	1.051	2.061	127
2	1	exm2259679	11029478	T	0.3154	0.5057	G	11.08	0.0008721	0.4503	0.2416	0.2805	0.723
3	1	exm2264801	11938050	A	0.3154	0.5244	G	12.91	0.0003268	0.4178	0.2451	0.2584	0.6755
4	1	exm2250514	20717763	A	0.5923	0.3523	C	17.38	3.06E-05	2.671	0.2382	1.675	4.261
5	1	exm27957	21795388	A	0.3308	0.5227	G	11.18	0.0008289	0.4513	0.2398	0.282	0.7221
6	1	exm2268870	23198619	G	0.1231	0.3182	T	15.82	6.97E-05	0.3008	0.3122	0.1631	0.5546
7	1	exm39585	32149721	C	0.1308	0.02841	G	11.74	0.0006114	5.145	0.523	1.846	14.34
8	1	exm2265001	37254301	G	0.4615	0.267	A	12.44	0.0004207	2.353	0.2449	1.456	3.802
9	1	exm2264831	45460832	G	0.3	0.4943	A	11.66	0.0006398	0.4384	0.2436	0.272	0.7068
10	1	exm2264832	47309265	G	0.2462	0.4318	A	11.29	0.0007809	0.4296	0.2542	0.2611	0.7071
11	1	exm59762	53320274	G	0.2308	0.4602	T	17.03	3.68E-05	0.3519	0.2573	0.2125	0.5826
12	1	exm61147	54605320	G	0.2769	0.4773	C	12.59	0.0003876	0.4195	0.2474	0.2583	0.6811
13	1	exm65641	63999868	C	0.3952	0.2151	T	11.33	0.000762	2.384	0.2611	1.429	3.977
14	1	exm-rs6700896	66089782	T	0.2538	0.4659	C	14.33	0.0001531	0.39	0.2519	0.238	0.6389
15	1	exm-rs1892534	66105944	A	0.2385	0.4659	G	16.61	4.60E-05	0.359	0.2553	0.2176	0.5921
16	1	exm-rs4420065	66161461	T	0.2308	0.4602	C	17.03	3.68E-05	0.3519	0.2573	0.2125	0.5826
17	1	exm-rs12753193	66169679	G	0.2385	0.4483	A	14.24	0.0001607	0.3854	0.2561	0.2333	0.6367
18	1	exm69632	77685042	C	0.3308	0.1534	T	13.33	0.000261	2.728	0.2802	1.575	4.723
19	1	exm2268717	85213900	T	0.2077	0.4375	C	17.6	2.73E-05	0.337	0.2643	0.2008	0.5657
20	1	exm2268726	95276691	C	0.3231	0.5284	T	12.79	0.0003491	0.426	0.2408	0.2657	0.6828
21	1	exm2264886	108088171	A	0.2538	0.4489	G	12.25	0.0004641	0.4177	0.2522	0.2548	0.6847
22	1	exm-rs1933182	109999838	T	0.2308	0.4302	G	13.05	0.0003038	0.3973	0.2589	0.2392	0.66
23	1	exm2268738	111369934	T	0.3254	0.5345	C	12.93	0.000324	0.4201	0.2434	0.2607	0.677
24	1	exm83649	111957097	G	0.2923	0.4943	C	12.63	0.00038	0.4225	0.2448	0.2615	0.6827
25	1	exm83663	111957370	C	0	0.1364	G	19.24	1.16E-05	0	inf	0	nan
26	1	exm83704	111957693	G	0.2923	0.5057	A	14.02	0.0001807	0.4038	0.2448	0.2499	0.6523
27	1	exm2264891	112385547	A	0.2692	0.4773	G	13.62	0.0002241	0.4035	0.2487	0.2478	0.657

28	1	exm87717	117576522	T	0.01538	0.1307	A	13.25	0.0002728	0.1039	0.7469	0.02405	0.4493
29	1	exm2259802	150163390	C	0.07692	0.2159	T	10.92	0.0009509	0.3026	0.3767	0.1446	0.6332
30	1	exm95472	150940625	G	0.2462	0.09091	T	13.63	0.0002231	3.265	0.332	1.704	6.259
31	1	exm-rs267734	150951477	G	0.2462	0.08523	A	14.89	0.0001137	3.505	0.3381	1.807	6.799
32	1	exm95523	150958836	G	0.2769	0.08046	A	20.9	4.84E-06	4.377	0.3407	2.245	8.535
33	1	exm95850	151089888	C	0.05385	0.1818	A	11.01	0.0009057	0.2561	0.435	0.1092	0.6007
34	1	exm97215	151512895	G	0.1231	0.02273	A	12.33	0.0004468	6.035	0.5719	1.967	18.51
35	1	exm103508	153954646	T	0.07692	0	C	14	0.0001832	NA	NA	NA	NA
36	1	exm109473	156551248	A	0.06923	0	G	12.55	0.0003954	NA	NA	NA	NA
37	1	exm111298	157062739	G	0.1077	0.2784	C	13.33	0.0002614	0.3128	0.3291	0.1641	0.5963
38	1	exm112941	158576394	A	0	0.09091	C	12.47	0.0004135	0	inf	0	nan
39	1	exm113021	158587368	C	0	0.125	T	17.51	2.86E-05	0	inf	0	nan
40	1	exm113223	158623092	A	0	0.09091	T	12.47	0.0004135	0	inf	0	nan
41	1	exm113224	158623103	A	0	0.09091	G	12.47	0.0004135	0	inf	0	nan
42	1	exm113458	158669980	A	0.007692	0.1307	G	15.65	7.63E-05	0.05157	1.028	0.00687	0.3871
43	1	exm113678	158746678	C	0.06923	0.2045	T	10.91	0.000954	0.2893	0.3928	0.1339	0.6247
44	1	exm2259837	164733504	G	0.03077	0.1761	A	15.6	7.83E-05	0.1485	0.5451	0.05102	0.4322
45	1	exm121603	169391154	A	0.2846	0.4716	G	10.97	0.0009279	0.4458	0.2461	0.2752	0.7222
46	1	exm-rs17346452	172053287	C	0.2231	0.07955	T	12.75	0.0003552	3.322	0.3493	1.676	6.588
47	1	exm2265060	178518008	A	0.1231	0.2898	G	12.15	0.000491	0.344	0.3145	0.1857	0.6371
48	1	exm129362	182640864	C	0.07692	0.2216	T	11.64	0.000647	0.2927	0.3759	0.1401	0.6115
49	1	exm131467	186026474	T	0.5	0.3068	C	11.74	0.0006112	2.259	0.2398	1.412	3.615
50	1	exm2264936	190551418	G	0.3692	0.5625	A	11.19	0.0008229	0.4553	0.2369	0.2862	0.7243
51	1	exm2268805	195738953	G	0.6462	0.3678	T	23.07	1.56E-06	3.139	0.2416	1.955	5.039
52	1	exm134032	197070442	T	0.3385	0.5284	G	10.91	0.0009563	0.4566	0.2391	0.2858	0.7295
53	1	exm134043	197070697	C	0.3385	0.5284	T	10.91	0.0009563	0.4566	0.2391	0.2858	0.7295
54	1	exm-rs2786098	197325908	A	0.1077	0.2727	C	12.61	0.0003847	0.3218	0.3297	0.1687	0.6141
55	1	exm2265070	197359999	G	0.2923	0.5115	A	14.7	0.0001263	0.3945	0.2453	0.2439	0.638
56	1	exm2268809	198634625	C	0.2615	0.4655	T	13.16	0.0002854	0.4066	0.2509	0.2487	0.6649
57	1	exm2250517	207535246	A	0.3231	0.5795	C	19.74	8.87E-06	0.3463	0.2418	0.2155	0.5562
58	1	exm151013	222802376	G	0.3231	0.1591	A	11.4	0.0007357	2.523	0.2786	1.461	4.356

59	1	exm151047	222803204	G	0.3231	0.1591	A	11.4	0.0007357	2.523	0.2786	1.461	4.356
60	1	exm2260036	231326086	A	0.3538	0.5682	G	13.77	0.0002068	0.4162	0.2383	0.2609	0.664
61	1	exm159168	232568041	A	0.1154	0.01705	G	13.06	0.0003016	7.522	0.6438	2.13	26.57
62	1	exm2260055	239144913	G	0.2538	0.09659	A	13.53	0.0002352	3.182	0.3252	1.682	6.018
63	1	exm163482	240492734	A	0.3154	0.1534	G	11.35	0.0007545	2.542	0.2817	1.464	4.416
64	1	exm164066	242035382	T	0	0.1176	C	16.39	5.17E-05	0	inf	0	nan
65	1	exm168221	248569674	G	0	0.09659	A	13.3	0.0002661	0	inf	0	nan
66	2	exm2269013	4905977	T	0.5635	0.3563	C	12.71	0.0003638	2.332	0.2394	1.459	3.728
67	2	exm-rs6431805	6654714	C	0.08594	0.2443	T	12.73	0.0003607	0.2908	0.3609	0.1434	0.5899
68	2	exm-rs6741819	7147973	T	0.2	0.4602	C	22.27	2.37E-06	0.2932	0.2664	0.174	0.4942
69	2	exm2254476	11500314	C	0.3846	0.5795	A	11.37	0.0007484	0.4534	0.2363	0.2854	0.7205
70	2	exm174940	20173436	G	0.1	0.005682	A	15.24	9.49E-05	19.44	1.045	2.51	150.6
71	2	exm-rs2082871	20712300	G	0.1	0.3011	A	17.88	2.35E-05	0.2579	0.3354	0.1336	0.4976
72	2	exm179384	27260469	A	0.3692	0.1882	G	12.34	0.0004432	2.524	0.2674	1.495	4.264
73	2	exm2261254	32495471	A	0.4462	0.2414	C	14.13	0.0001702	2.532	0.25	1.551	4.133
74	2	exm2261261	37603801	G	0.6154	0.3466	A	21.74	3.12E-06	3.016	0.24	1.885	4.828
75	2	exm2265315	42180912	G	0.03846	0.1648	A	12.08	0.0005101	0.2028	0.4993	0.07621	0.5395
76	2	exm-rs13429458	43638838	C	0.1538	0.3409	A	13.55	0.0002322	0.3515	0.2905	0.1989	0.6212
77	2	exm190111	44021676	T	0	0.08046	C	10.96	0.0009286	0	inf	0	nan
78	2	exm190359	44099244	T	0	0.07955	C	10.84	0.0009951	0	inf	0	nan
79	2	exm195691	58316814	G	0.5846	0.3908	A	11.21	0.0008132	2.194	0.2363	1.381	3.486
80	2	exm2265168	86135154	G	0.4615	0.2727	A	11.67	0.0006345	2.286	0.2441	1.417	3.688
81	2	exm217591	102955468	A	0.5938	0.3807	C	13.5	0.000238	2.378	0.2377	1.492	3.789
82	2	exm-rs17483466	111797458	G	0.2077	0.07386	A	11.79	0.0005971	3.287	0.3603	1.622	6.66
83	2	exm221863	113539192	A	0.06154	0	T	11.12	0.0008533	NA	NA	NA	NA
84	2	exm2254482	115848781	T	0.3308	0.5284	C	11.83	0.0005832	0.4411	0.2399	0.2756	0.7059
85	2	exm2269311	120986872	T	0.1538	0.3864	C	19.73	8.91E-06	0.2888	0.2882	0.1641	0.508
86	2	exm-rs13420028	133188106	G	0.1077	0.267	T	11.9	0.0005625	0.3313	0.3303	0.1734	0.6328
87	2	exm-rs7567288	134434824	C	0.1538	0.3239	T	11.48	0.0007045	0.3796	0.2916	0.2143	0.6723
88	2	exm2269143	142707328	T	0.3492	0.5714	G	14.25	0.0001597	0.4024	0.2434	0.2498	0.6484
89	2	exm2263953	144092133	A	0.06154	0.2069	C	12.7	0.0003656	0.2514	0.4101	0.1125	0.5616

90	2	exm232550	152322095	A	0.1538	0.3295	T	12.15	0.0004901	0.3699	0.2912	0.209	0.6546
91	2	exm232595	152331418	C	0.1538	0.3295	G	12.15	0.0004901	0.3699	0.2912	0.209	0.6546
92	2	exm2265220	153891830	G	0.1328	0.3182	A	13.96	0.0001872	0.3282	0.3066	0.1799	0.5986
93	2	exm-rs10189160	157012321	G	0.5077	0.3059	A	12.57	0.0003913	2.34	0.2418	1.457	3.759
94	2	exm234189	157425931	C	0	0.07955	A	10.84	0.0009951	0	inf	0	nan
95	2	exm234888	159663599	C	0.3231	0.5455	T	14.93	0.0001113	0.3977	0.241	0.248	0.6379
96	2	exm235173	160086654	G	0.5154	0.3182	A	12.1	0.0005053	2.279	0.2387	1.427	3.639
97	2	exm239782	169824983	C	0.1077	0.01705	T	11.71	0.0006218	6.96	0.6474	1.957	24.76
98	2	exm249736	179914640	A	0.2538	0.08523	G	16.07	6.09E-05	3.652	0.3369	1.887	7.067
99	2	exm252043	189864080	A	0.2266	0.4091	G	11.13	0.0008501	0.4231	0.2609	0.2537	0.7056
100	2	exm2269194	192458747	C	0.4846	0.2727	T	14.52	0.0001385	2.507	0.2438	1.555	4.044
101	2	exm259986	207603234	G	0.1562	0.3409	T	13.03	0.0003063	0.358	0.2908	0.2025	0.633
102	2	exm2261158	208014898	T	0.1111	0.2917	C	13.94	0.0001886	0.3036	0.3304	0.1589	0.5801
103	2	exm2265268	212807645	A	0.2937	0.5123	G	13.95	0.0001881	0.3957	0.2509	0.242	0.6471
104	2	exm-rs7590720	216898658	G	0.4692	0.2784	A	11.82	0.0005846	2.291	0.2432	1.422	3.691
105	2	exm-rs16864755	224274622	A	0.1846	0.05114	G	13.85	0.0001984	4.201	0.4101	1.881	9.386
106	2	exm272457	228493211	A	0.2077	0.3977	G	12.47	0.0004132	0.3969	0.2655	0.2359	0.6679
107	2	exm278071	235950002	A	0.2077	0.07386	G	11.79	0.0005971	3.287	0.3603	1.622	6.66
108	2	exm278779	238244963	A	0.1385	0.3125	G	12.47	0.000414	0.3536	0.3015	0.1958	0.6385
109	2	exm278798	238247734	G	0.06923	0.2273	C	13.89	0.0001942	0.2529	0.3895	0.1179	0.5426
110	3	exm-rs2727943	1897973	T	0.03846	0.2184	C	19.84	8.44E-06	0.1432	0.4916	0.05462	0.3752
111	3	exm-rs6772112	11641535	C	0.04688	0.1818	T	12.34	0.0004439	0.2213	0.4616	0.08956	0.5469
112	3	exm291396	12875443	G	0.3615	0.5625	A	12.1	0.0005031	0.4404	0.2375	0.2765	0.7015
113	3	exm292458	14187449	G	0.6	0.3693	T	15.98	6.39E-05	2.562	0.2376	1.608	4.081
114	3	exm2269605	16237372	T	0	0.125	C	17.51	2.86E-05	0	inf	0	nan
115	3	exm294619	17053499	A	0.4615	0.2273	G	18.65	1.57E-05	2.914	0.2516	1.78	4.772
116	3	exm-rs17272796	17077268	C	0.4615	0.233	T	17.67	2.63E-05	2.822	0.2505	1.727	4.611
117	3	exm2261480	27614316	C	0.5	0.25	A	20.38	6.36E-06	3	0.2471	1.848	4.869
118	3	exm2269421	27615419	T	0.6	0.3807	C	14.43	0.0001458	2.44	0.237	1.534	3.883
119	3	exm299494	37574951	A	0.5154	0.3125	G	12.84	0.0003396	2.34	0.2393	1.464	3.74
120	3	exm302016	39161456	A	0.4538	0.2443	G	14.77	0.0001213	2.57	0.2486	1.579	4.184

121	3	exm302017	39161464	A	0.4538	0.2443	G	14.77	0.0001213	2.57	0.2486	1.579	4.184
122	3	exm302175	39180263	G	0.4453	0.2616	A	11.03	0.0008945	2.266	0.2484	1.392	3.687
123	3	exm2256022	42131415	A	0.4154	0.233	G	11.62	0.000651	2.34	0.2519	1.428	3.833
124	3	exm-rs4682869	42923964	C	0.4844	0.2931	T	11.52	0.0006878	2.266	0.2429	1.407	3.647
125	3	exm324348	53899276	T	0.06154	0.1989	C	11.67	0.0006335	0.2642	0.4109	0.1181	0.5911
126	3	exm2265460	64171993	A	0.3154	0.5227	G	13.08	0.0002982	0.4206	0.2417	0.2619	0.6754
127	3	exm330361	74334560	T	0.08462	0.2557	C	14.63	0.0001305	0.2691	0.3594	0.133	0.5443
128	3	exm334983	102157365	T	0.3154	0.1534	A	11.35	0.0007545	2.542	0.2817	1.464	4.416
129	3	exm334985	102157417	G	0.3154	0.1534	A	11.35	0.0007545	2.542	0.2817	1.464	4.416
130	3	exm2269497	102240202	T	0.5968	0.3916	C	11.98	0.0005388	2.3	0.2425	1.43	3.699
131	3	exm2265485	104640080	G	0.2231	0.4148	A	12.36	0.0004376	0.4051	0.2604	0.2432	0.6749
132	3	exm-rs10433406	124192674	A	0.02308	0.1307	C	11.14	0.0008469	0.1571	0.6255	0.04612	0.5354
133	3	exm2265501	125867617	G	0.3	0.4943	A	11.66	0.0006398	0.4384	0.2436	0.272	0.7068
134	3	exm2255707	134388550	A	0.5846	0.3864	G	11.8	0.0005936	2.235	0.2359	1.408	3.549
135	3	exm357173	147121751	T	0.08462	0.2356	C	11.97	0.0005413	0.2999	0.3622	0.1474	0.6099
136	3	exm363668	169518455	C	0.3385	0.5284	T	10.91	0.0009563	0.4566	0.2391	0.2858	0.7295
137	3	exm2269688	170171738	C	0.5615	0.3466	T	14.03	0.0001794	2.414	0.2373	1.516	3.845
138	3	exm2255870	183508590	G	0.08462	0.005682	A	12.36	0.0004376	16.18	1.051	2.061	127
139	3	exm367360	183508714	A	0.06154	0	G	11.12	0.0008533	NA	NA	NA	NA
140	3	exm376221	195935346	T	0	0.1023	C	14.13	0.0001709	0	inf	0	nan
141	4	exm380211	996165	A	0.1308	0.2955	G	11.61	0.0006554	0.3587	0.3082	0.1961	0.6563
142	4	exm382553	2306259	T	0.2385	0.08046	C	14.73	0.0001241	3.579	0.3465	1.815	7.057
143	4	exm389532	10079377	T	0	0.08523	C	11.65	0.0006418	0	inf	0	nan
144	4	exm-rs7442317	29903052	A	0.3692	0.1989	G	10.98	0.0009215	2.358	0.2621	1.411	3.942
145	4	exm404236	71346701	G	0.1846	0.358	C	11.04	0.0008912	0.4061	0.2754	0.2367	0.6967
146	4	exm2256737	78734563	A	0.3154	0.5284	G	13.78	0.000205	0.4111	0.2417	0.256	0.6603
147	4	exm408162	78987157	G	0.5615	0.3125	A	19.06	1.27E-05	2.818	0.2402	1.76	4.511
148	4	exm2269935	79625240	C	0.3538	0.5455	T	11.04	0.0008928	0.4563	0.2378	0.2863	0.7273
149	4	exm2265850	82318524	A	0.6077	0.4034	G	12.49	0.00041	2.291	0.2364	1.441	3.641
150	4	exm411960	88415636	C	0.6231	0.3864	G	16.77	4.22E-05	2.625	0.2382	1.646	4.187
151	4	exm411969	88416188	T	0.6231	0.3864	G	16.77	4.22E-05	2.625	0.2382	1.646	4.187

152	4	exm2265740	106922960	A	0.3077	0.5057	G	11.97	0.0005397	0.4343	0.2431	0.2697	0.6995
153	4	exm417605	107845794	T	0.1462	0.01705	C	18.68	1.55E-05	9.871	0.6331	2.854	34.14
154	4	exm419255	113352397	G	0.5077	0.2955	A	14.22	0.000163	2.459	0.241	1.533	3.944
155	4	exm419280	113352899	G	0.5077	0.2955	A	14.22	0.000163	2.459	0.241	1.533	3.944
156	4	exm2265770	147246721	A	0.3308	0.5284	G	11.83	0.0005832	0.4411	0.2399	0.2756	0.7059
157	4	exm2265806	183777997	A	0.5615	0.3295	G	16.44	5.03E-05	2.606	0.2387	1.632	4.16
158	5	exm2261915	3311493	T	0.06154	0.2102	C	13.18	0.0002831	0.2463	0.4092	0.1105	0.5493
159	5	exm-rs7729273	7228047	T	0.2154	0.04545	C	20.8	5.10E-06	5.765	0.4201	2.53	13.13
160	5	exm2266062	23020866	G	0.3462	0.5398	A	11.29	0.0007777	0.4514	0.2385	0.2829	0.7203
161	5	exm-rs2886725	37770836	A	0.04615	0.2216	G	18.35	1.84E-05	0.17	0.4557	0.06958	0.4152
162	5	exm451684	38955796	A	0.4462	0.2273	G	16.46	4.98E-05	2.739	0.252	1.672	4.488
163	5	exm452637	41033163	C	0.007692	0.1136	T	13.13	0.0002906	0.06047	1.032	0.008006	0.4567
164	5	exm452676	41048533	T	0.3538	0.1818	C	11.65	0.0006418	2.464	0.268	1.457	4.167
165	5	exm2266081	50057729	A	0.6077	0.4148	G	11.13	0.0008486	2.186	0.236	1.376	3.471
166	5	exm459265	70308262	T	0	0.09091	C	12.47	0.0004135	0	inf	0	nan
167	5	exm459568	70818150	G	0.1774	0.05357	C	11.53	0.0006842	3.81	0.4155	1.688	8.603
168	5	exm461037	73985215	G	0.1308	0.3352	A	16.74	4.28E-05	0.2983	0.3052	0.164	0.5427
169	5	exm464559	79950781	A	0.1953	0.4318	G	18.68	1.54E-05	0.3194	0.2699	0.1882	0.5421
170	5	exm2266097	86366246	G	0.06154	0.2045	A	12.42	0.0004247	0.255	0.41	0.1142	0.5696
171	5	exm466476	89979518	T	0.06154	0.2069	C	12.7	0.0003656	0.2514	0.4101	0.1125	0.5616
172	5	exm466624	90012379	A	0.1719	0.05172	G	11.56	0.0006745	3.805	0.4148	1.688	8.579
173	5	exm2270224	91840637	T	0.1462	0.3523	G	16.32	5.35E-05	0.3147	0.2942	0.1768	0.5602
174	5	exm-rs4869419	92567539	G	0.05385	0.1932	A	12.51	0.0004047	0.2377	0.4329	0.1017	0.5553
175	5	exm-rs17376456	93557702	G	0.1077	0.2614	A	11.2	0.0008173	0.3411	0.3309	0.1783	0.6524
176	5	exm-rs17418283	94154588	C	0.4154	0.2299	T	11.99	0.0005358	2.38	0.2533	1.449	3.91
177	5	exm468894	96503523	C	0.5769	0.3693	T	12.98	0.0003141	2.329	0.2365	1.465	3.701
178	5	exm468932	96513471	C	0.1905	0.4034	G	15.44	8.51E-05	0.348	0.274	0.2034	0.5954
179	5	exm2270091	96731630	T	0.3769	0.5739	C	11.6	0.0006579	0.4492	0.2366	0.2825	0.7143
180	5	exm-rs13355008	100695179	T	0.2	0.3765	C	10.92	0.0009491	0.4141	0.2704	0.2437	0.7035
181	5	exm2270231	103670162	T	0.03846	0.2045	C	17.77	2.49E-05	0.1556	0.4929	0.0592	0.4087
182	5	exm-rs1318772	112723567	G	0.04615	0.1932	A	14.22	0.0001622	0.2021	0.4595	0.08211	0.4974

183	5	exm2270111	112823998	T	0.5923	0.3636	C	15.74	7.28E-05	2.542	0.2375	1.596	4.05
184	5	exm472550	115428381	G	0.1923	0.05682	T	13.55	0.0002322	3.952	0.3944	1.825	8.562
185	5	exm479249	135287029	T	0.5308	0.3182	C	13.99	0.0001843	2.424	0.2389	1.518	3.871
186	5	exm2266014	140522425	A	0.5154	0.2955	G	15.22	9.58E-05	2.536	0.241	1.581	4.067
187	5	exm2266018	145270339	G	0.2923	0.5227	A	16.25	5.56E-05	0.3771	0.2449	0.2334	0.6094
188	5	exm493171	148206473	G	0.1615	0.3466	C	13.05	0.0003028	0.3632	0.2862	0.2073	0.6364
189	5	exm494951	149509446	T	0.1077	0.01136	C	14	0.0001827	10.5	0.7654	2.343	47.06
190	5	exm497540	150947390	T	0	0.1136	C	15.81	7.02E-05	0	inf	0	nan
191	5	exm2257065	156671437	T	0.03077	0.1667	G	14.2	0.0001643	0.1587	0.5471	0.05432	0.4638
192	5	exm2266139	167657421	A	0.2538	0.4602	G	13.62	0.0002233	0.399	0.252	0.2435	0.6538
193	5	exm-rs11249661	179277874	A	0.4308	0.25	G	11.11	0.0008605	2.27	0.2483	1.395	3.694
194	6	exm-rs675209	7102084	T	0.2154	0.4261	C	14.87	0.000115	0.3697	0.2622	0.2211	0.618
195	6	exm2266156	11477493	A	0.5538	0.3068	G	18.84	1.42E-05	2.805	0.2405	1.75	4.494
196	6	exm-rs16883019	19969638	C	0.02308	0.1307	T	11.14	0.0008469	0.1571	0.6255	0.04612	0.5354
197	6	exm2257690	23774487	A	0.6231	0.358	G	21.1	4.37E-06	2.965	0.2397	1.853	4.743
198	6	exm523653	27277051	T	0.1692	0.3466	C	11.9	0.0005617	0.384	0.2825	0.2208	0.6681
199	6	exm523713	27279852	C	0.2	0.05682	T	14.77	0.0001217	4.15	0.3926	1.923	8.958
200	6	exm524368	27925367	A	0.06154	0.2216	G	14.73	0.0001238	0.2303	0.4076	0.1036	0.5121
201	6	exm524507	28117331	T	0.007692	0.1591	C	19.98	7.84E-06	0.04097	1.025	0.005498	0.3054
202	6	exm-rs9257819	29360183	C	0.2308	0.5398	A	29.55	5.46E-08	0.2558	0.2573	0.1545	0.4235
203	6	exm-rs2022077	29361124	A	0.2344	0.5398	T	28.55	9.14E-08	0.261	0.2577	0.1575	0.4325
204	6	exm525841	29364615	T	0.2308	0.5398	G	29.55	5.46E-08	0.2558	0.2573	0.1545	0.4235
205	6	exm525845	29364643	C	0.2308	0.5398	T	29.55	5.46E-08	0.2558	0.2573	0.1545	0.4235
206	6	exm525853	29364815	G	0.2308	0.5398	C	29.55	5.46E-08	0.2558	0.2573	0.1545	0.4235
207	6	exm525854	29364835	G	0.2308	0.5465	T	30.5	3.34E-08	0.2489	0.2584	0.15	0.4131
208	6	exm525859	29364951	A	0.2266	0.5398	G	30.1	4.10E-08	0.2498	0.2597	0.1501	0.4155
209	6	exm-rs2073149	29365423	A	0.246	0.5795	T	33.14	8.57E-09	0.2367	0.2571	0.143	0.3918
210	6	exm-rs1028411	29367399	C	0.2308	0.5398	A	29.55	5.46E-08	0.2558	0.2573	0.1545	0.4235
211	6	exm-rs2394607	29369519	C	0.2538	0.5682	T	30.07	4.18E-08	0.2586	0.2525	0.1576	0.4241
212	6	exm-rs720497	29382433	G	0.3769	0.2045	C	11.07	0.0008752	2.353	0.2601	1.413	3.917
213	6	exm-rs7770592	29395747	A	0.1846	0.3693	C	12.37	0.0004369	0.3866	0.2748	0.2257	0.6625

214	6	exm-rs1233493	29458241	C	0.06154	0	T	11	0.0009126	NA	NA	NA	NA
215	6	exm-rs734960	29475142	A	0.07692	0.2159	G	10.92	0.0009509	0.3026	0.3767	0.1446	0.6332
216	6	exm-rs1592410	29483968	A	0.5538	0.3466	G	13.07	0.0003	2.34	0.2371	1.47	3.725
217	6	exm-rs724078	29489048	G	0.3385	0.5795	A	17.42	3.00E-05	0.3712	0.2402	0.2318	0.5943
218	6	exm-rs995185	29529137	A	0.1385	0.3125	T	12.47	0.000414	0.3536	0.3015	0.1958	0.6385
219	6	exm-rs926552	29548089	T	0.06154	0	C	11.12	0.0008533	NA	NA	NA	NA
220	6	exm526267	29598286	A	0	0.1047	G	14.25	0.00016	0	inf	0	nan
221	6	exm-rs2524005	29899677	T	0.1077	0.2701	C	12.24	0.0004682	0.3261	0.3305	0.1706	0.6232
222	6	exm-rs356971	29979797	C	0.07692	0.2216	A	11.64	0.000647	0.2927	0.3759	0.1401	0.6115
223	6	exm-rs165255	29989695	G	0.1452	0.3375	C	13.66	0.0002195	0.3333	0.3049	0.1834	0.6059
224	6	exm-rs166327	30002881	G	0.3538	0.5568	A	12.36	0.0004376	0.4359	0.2381	0.2733	0.695
225	6	exm-rs259938	30008003	C	0.2154	0.4023	G	11.9	0.0005613	0.4078	0.2635	0.2433	0.6835
226	6	exm-rs1150739	30031345	G	0.3538	0.5455	A	11.04	0.0008928	0.4563	0.2378	0.2863	0.7273
227	6	exm-rs1150735	30045199	T	0.2385	0.4205	C	10.99	0.0009173	0.4316	0.2563	0.2612	0.7132
228	6	exm-rs1264709	30056476	A	0.07692	0.2299	T	12.67	0.0003718	0.2792	0.3752	0.1338	0.5824
229	6	exm-rs2523734	30129676	G	0.1923	0.375	T	11.94	0.0005483	0.3968	0.2716	0.233	0.6757
230	6	exm-rs1264569	30365320	G	0.3306	0.142	A	14.39	0.0001483	2.985	0.2951	1.674	5.324
231	6	exm-rs3130654	30823075	G	0.2462	0.09659	C	12.44	0.000421	3.054	0.3264	1.611	5.791
232	6	exm-rs3130780	30874308	T	0.2462	0.07471	G	17.34	3.12E-05	4.044	0.353	2.025	8.077
233	6	exm-rs2253705	30900094	A	0.3462	0.125	G	21.38	3.76E-06	3.706	0.2931	2.086	6.583
234	6	exm-rs6933400	30907176	T	0.3077	0.1193	C	16.62	4.56E-05	3.28	0.3003	1.821	5.909
235	6	exm529258	30919878	C	0.3077	0.125	G	15.45	8.49E-05	3.111	0.2967	1.739	5.566
236	6	exm-rs3095150	30932532	G	0.375	0.5852	A	13.1	0.0002951	0.4252	0.2382	0.2666	0.6783
237	6	exm-rs13191258	30978717	T	0.01538	0.1322	C	13.45	0.0002451	0.1026	0.7469	0.02373	0.4435
238	6	exm-rs3871466	30983683	G	0.06154	0.2011	A	11.94	0.0005487	0.2604	0.4111	0.1164	0.5829
239	6	exm-rs3869096	30984404	C	0.06154	0.1932	A	10.94	0.0009398	0.2739	0.4119	0.1222	0.614
240	6	exm529509	30993567	T	0.07692	0.2184	G	11.2	0.0008182	0.2982	0.3768	0.1425	0.6242
241	6	exm-rs2517550	31008368	G	0.4	0.2159	A	12.21	0.0004766	2.421	0.2562	1.465	4
242	6	exm-rs3094188	31142245	G	0.3923	0.2159	T	11.28	0.0007834	2.344	0.2566	1.418	3.876
243	6	exm-rs6921663	31154620	C	0.09231	0.2384	T	10.92	0.000953	0.3249	0.3519	0.163	0.6476
244	6	exm-rs3132496	31208610	C	0.6	0.392	A	12.95	0.0003193	2.326	0.2364	1.464	3.697

245	6	exm-rs9264942	31274380	T	0.6	0.3693	C	15.98	6.39E-05	2.562	0.2376	1.608	4.081
246	6	exm-rs2523590	31327064	G	0.1538	0.4059	A	22.43	2.18E-06	0.2661	0.2889	0.1511	0.4689
247	6	exm-rs2523586	31327435	C	0.1308	0.3011	A	12.3	0.0004527	0.3491	0.3077	0.191	0.6381
248	6	exm-rs1063632	31378510	A	0.03077	0.1989	G	19	1.31E-05	0.1279	0.5418	0.04422	0.3699
249	6	exm530708	31379109	A	0.2615	0.4886	G	16.18	5.77E-05	0.3706	0.2501	0.227	0.6052
250	6	exm530736	31382882	A	0.2154	0.4659	C	20.38	6.35E-06	0.3147	0.2614	0.1885	0.5253
251	6	exm-rs10223421	31390055	T	0.2154	0.4659	G	20.38	6.35E-06	0.3147	0.2614	0.1885	0.5253
252	6	exm-rs11752262	31431757	G	0.1	0.2841	A	15.5	8.26E-05	0.28	0.3368	0.1447	0.5418
253	6	exm-rs2395029	31431780	G	0.01538	0.125	T	12.43	0.0004226	0.1094	0.7482	0.02524	0.474
254	6	exm-rs11759988	31432861	C	0.1	0.2614	T	12.51	0.0004049	0.314	0.339	0.1616	0.6102
255	6	exm-rs2516408	31463491	T	0.2154	0.4261	C	14.87	0.000115	0.3697	0.2622	0.2211	0.618
256	6	exm-rs6916394	31464050	C	0.5	0.3103	T	11.24	0.0008026	2.222	0.24	1.388	3.557
257	6	exm-rs4713468	31470875	A	0.5079	0.3046	T	12.7	0.0003654	2.357	0.2427	1.465	3.792
258	6	exm-rs2844498	31476854	A	0.5846	0.375	G	13.21	0.0002785	2.346	0.2365	1.476	3.729
259	6	exm-rs2246618	31478986	T	0.2154	0.4261	C	14.87	0.000115	0.3697	0.2622	0.2211	0.618
260	6	exm-rs9267673	31883679	T	0.05385	0.2386	C	18.98	1.32E-05	0.1816	0.4269	0.07864	0.4192
261	6	exm-rs7746553	31895973	G	0.1	0.3068	C	18.7	1.53E-05	0.251	0.3349	0.1302	0.484
262	6	exm-rs4151664	31920873	T	0.04615	0.2102	C	16.67	4.46E-05	0.1818	0.4571	0.07421	0.4453
263	6	exm-rs592229	31930441	G	0.2769	0.1136	T	13.33	0.0002607	2.987	0.3079	1.634	5.462
264	6	exm533591	31938412	T	0.04615	0.1761	G	11.88	0.0005659	0.2263	0.4625	0.09143	0.5603
265	6	exm-rs3130349	32147696	A	0.03077	0.1477	G	11.57	0.0006715	0.1832	0.5505	0.06226	0.5388
266	6	exm535099	32185796	T	0.007692	0.1023	C	11.49	0.0007015	0.06804	1.034	0.008963	0.5166
267	6	exm-rs13209234	32415975	A	0.03906	0.1648	G	11.79	0.0005957	0.2061	0.4994	0.07743	0.5484
268	6	exm-rs3135006	32667119	A	0.2154	0.08046	G	11.38	0.0007439	3.137	0.351	1.577	6.242
269	6	exm-rs2395296	32911814	A	0.2615	0.4659	G	13.27	0.00027	0.406	0.2503	0.2486	0.6631
270	6	exm-rs209473	32922908	C	0.6154	0.3636	A	19.02	1.29E-05	2.8	0.2389	1.753	4.472
271	6	exm-rs580962	32925692	G	0.3231	0.5852	A	20.61	5.63E-06	0.3383	0.242	0.2105	0.5436
272	6	exm-rs516535	32942302	C	0.3231	0.5852	T	20.61	5.63E-06	0.3383	0.242	0.2105	0.5436
273	6	exm-rs206777	32952546	C	0.3231	0.5568	T	16.46	4.97E-05	0.3799	0.2412	0.2367	0.6095
274	6	exm-rs206776	32953711	A	0.2462	0.4545	G	13.99	0.0001835	0.3918	0.2537	0.2383	0.6443
275	6	exm-rs188245	32955976	C	0.3615	0.1932	T	10.89	0.0009676	2.365	0.2642	1.409	3.969

276	6	exm-rs172276	32959770	A	0.3462	0.1761	T	11.58	0.0006675	2.476	0.2704	1.457	4.207
277	6	exm-rs206768	32961387	C	0.3538	0.1761	T	12.54	0.0003985	2.561	0.2698	1.509	4.347
278	6	exm-rs206767	32962420	G	0.3672	0.6047	T	16.55	4.73E-05	0.3794	0.2407	0.2367	0.6081
279	6	exm-rs206765	32964696	A	0.4538	0.2386	T	15.66	7.58E-05	2.651	0.2496	1.625	4.324
280	6	exm-rs6911639	32978178	C	0.3308	0.1648	T	11.45	0.0007147	2.505	0.2757	1.459	4.301
281	6	exm-rs443623	32996350	A	0.06923	0.2216	T	13.12	0.0002916	0.2613	0.3903	0.1216	0.5615
282	6	exm540479	34850826	C	0.01538	0.1364	G	14.08	0.0001756	0.09896	0.7457	0.02295	0.4268
283	6	exm545759	41310705	T	0	0.08523	C	11.65	0.0006418	0	inf	0	nan
284	6	exm-rs9395066	45095163	C	0.3615	0.5568	A	11.44	0.0007201	0.4507	0.2374	0.283	0.7177
285	6	exm556612	54805688	C	0.4692	0.2557	A	15.06	0.0001041	2.574	0.2465	1.588	4.172
286	6	exm556646	54806489	A	0.4692	0.2557	C	15.06	0.0001041	2.574	0.2465	1.588	4.172
287	6	exm2266221	79196788	A	0.2769	0.4659	G	11.27	0.0007869	0.439	0.2475	0.2703	0.7131
288	6	exm-rs4840086	100208438	G	0.6	0.3864	A	13.68	0.0002169	2.382	0.2367	1.498	3.788
289	6	exm568818	105609468	T	0	0.142	C	20.11	7.32E-06	0	inf	0	nan
290	6	exm-rs9374227	111283592	T	0.1	0.25	C	11.1	0.0008637	0.3333	0.3403	0.1711	0.6494
291	6	exm573638	116784797	A	0.007692	0.1337	G	16.08	6.09E-05	0.05022	1.029	0.006689	0.377
292	6	exm2270399	125576372	C	0.3462	0.5625	T	14.05	0.0001783	0.4118	0.2389	0.2578	0.6577
293	6	exm2257503	126248374	C	0.3308	0.5398	T	13.19	0.0002812	0.4214	0.24	0.2633	0.6746
294	6	exm581368	137482840	G	0.1	0.01136	A	12.6	0.0003855	9.667	0.7689	2.142	43.63
295	6	exm582318	139233946	T	0.06923	0	C	12.55	0.0003954	NA	NA	NA	NA
296	6	exm582791	142691549	C	0.09231	0.2386	A	11.02	0.0009031	0.3245	0.3508	0.1631	0.6453
297	6	exm583060	143092754	A	0.01538	0.1307	G	13.25	0.0002728	0.1039	0.7469	0.02405	0.4493
298	6	exm584047	145069600	A	0.07627	0	G	12.61	0.0003833	NA	NA	NA	NA
299	6	exm584803	147136244	A	0.5403	0.3333	G	12.54	0.0003988	2.351	0.2434	1.459	3.788
300	6	exm585864	150212003	T	0.05385	0.2898	C	27.09	1.94E-07	0.1395	0.4226	0.06093	0.3193
301	6	exm585866	150212034	A	0	0.07955	G	10.84	0.0009951	0	inf	0	nan
302	6	exm2270429	150525260	C	0.5769	0.358	T	14.48	0.0001417	2.446	0.2371	1.537	3.893
303	6	exm2262071	151327848	A	0.3308	0.5909	G	20.27	6.72E-06	0.3422	0.2414	0.2132	0.5492
304	6	exm-rs7747960	152791474	A	0.1032	0.259	C	11.23	0.0008064	0.3291	0.3423	0.1682	0.6437
305	7	exm-rs10488360	4411209	A	0.5769	0.3471	G	15.75	7.23E-05	2.565	0.2397	1.604	4.104
306	7	exm-rs10499504	17561583	G	0.007692	0.125	A	14.8	0.0001194	0.05426	1.029	0.007216	0.4081

307	7	exm-rs12155172	20994491	A	0.2538	0.09091	G	14.76	0.0001221	3.402	0.3307	1.779	6.505
308	7	exm608825	21901540	C	0.02344	0.1453	T	12.89	0.0003305	0.1411	0.623	0.04162	0.4785
309	7	exm611740	29519929	G	0.2385	0.08721	A	13.12	0.0002924	3.277	0.3397	1.684	6.378
310	7	exm-rs6974491	37374510	A	0.1613	0.04706	G	10.86	0.0009837	3.894	0.4368	1.654	9.167
311	7	exm618517	44874113	T	0.3065	0.5698	C	20.12	7.29E-06	0.3336	0.2483	0.2051	0.5428
312	7	exm2264260	46463342	C	0.1231	0.3409	A	19.01	1.30E-05	0.2713	0.3107	0.1476	0.4989
313	7	exm-rs1012036	52472450	T	0.1385	0.3663	C	19.58	9.66E-06	0.2781	0.2992	0.1547	0.4998
314	7	exm2266423	69006876	A	0.5385	0.3466	G	11.24	0.0007992	2.199	0.2367	1.383	3.498
315	7	exm-rs6943555	69806023	A	0.5476	0.2989	T	18.79	1.46E-05	2.84	0.2439	1.761	4.58
316	7	exm625784	73097654	T	0.5538	0.3636	C	10.96	0.000933	2.172	0.236	1.368	3.45
317	7	exm629018	76950686	A	0.01538	0.142	C	14.91	0.0001127	0.09438	0.7446	0.02193	0.4061
318	7	exm2270768	84709356	T	0.4	0.1761	C	18.96	1.34E-05	3.118	0.2668	1.848	5.261
319	7	exm-rs1767742	86625854	C	0.4769	0.2841	A	11.98	0.0005373	2.298	0.2424	1.429	3.695
320	7	exm2266441	87220886	G	0.6016	0.3977	A	12.33	0.0004459	2.286	0.2373	1.436	3.64
321	7	exm633222	91630620	T	0.5231	0.2898	G	17.13	3.50E-05	2.688	0.2417	1.674	4.318
322	7	exm633461	91712698	G	0.5154	0.2701	A	19.1	1.24E-05	2.874	0.2448	1.778	4.644
323	7	exm2264243	91726927	C	0.5231	0.2955	A	16.25	5.54E-05	2.615	0.2411	1.63	4.195
324	7	exm2266446	91974757	A	0.5538	0.3563	G	11.78	0.0005995	2.242	0.237	1.409	3.569
325	7	exm633881	92028039	C	0.5615	0.3636	A	11.84	0.0005787	2.241	0.2362	1.411	3.561
326	7	exm634427	92733975	A	0.007692	0.1149	G	13.31	0.0002641	0.05969	1.032	0.007903	0.4508
327	7	exm634435	92734051	T	0.007692	0.1023	C	11.49	0.0007015	0.06804	1.034	0.008963	0.5166
328	7	exm639333	99669802	G	0.02308	0.1364	A	11.93	0.000553	0.1496	0.6241	0.04403	0.5083
329	7	exm-rs7385804	100235970	C	0.2462	0.4716	A	16.2	5.70E-05	0.3659	0.2535	0.2226	0.6013
330	7	exm643074	100488658	C	0.2923	0.4943	G	12.63	0.00038	0.4225	0.2448	0.2615	0.6827
331	7	exm2266456	101288516	G	0.3	0.4886	A	11.01	0.0009056	0.4485	0.2437	0.2782	0.7231
332	7	exm2270664	106642123	T	0.2538	0.4483	C	12.13	0.0004951	0.4187	0.2527	0.2552	0.6871
333	7	exm649118	107002504	C	0.1	0.01136	T	12.6	0.0003855	9.667	0.7689	2.142	43.63
334	7	exm650406	107800936	T	0.09231	0.2701	C	15.04	0.0001053	0.2748	0.3478	0.139	0.5433
335	7	exm655800	128312463	G	0.1923	0.0625	C	12.14	0.0004943	3.571	0.3827	1.687	7.562
336	7	exm655815	128315882	A	0.2969	0.1337	C	12.06	0.0005153	2.735	0.296	1.531	4.886
337	7	exm655820	128317658	T	0.3	0.142	C	11.28	0.0007842	2.589	0.2885	1.47	4.557

338	7	exm655833	128323034	G	0.3	0.142	A	11.28	0.0007842	2.589	0.2885	1.47	4.557
339	7	exm657813	130008259	G	0.007692	0.1034	A	11.64	0.0006441	0.06718	1.034	0.008849	0.5101
340	7	exm-rs1106683	131453525	A	0.1846	0.05682	G	12.36	0.0004376	3.758	0.3964	1.728	8.174
341	7	exm-rs1106684	131453665	G	0.1846	0.06024	C	11.09	0.0008668	3.532	0.3969	1.623	7.689
342	7	exm-rs802568	145959243	G	0.1923	0.0625	T	12.14	0.0004943	3.571	0.3827	1.687	7.562
343	7	exm2266575	146020936	G	0.2538	0.09659	A	13.53	0.0002352	3.182	0.3252	1.682	6.018
344	7	exm2270806	157880211	C	0.05385	0.1905	T	12.03	0.000524	0.2419	0.4354	0.103	0.5678
345	8	exm2270814	4809686	C	0.5462	0.3353	T	13.39	0.000253	2.386	0.2396	1.492	3.816
346	8	exm680383	8560602	T	0.1484	0.3239	C	12.16	0.0004875	0.3639	0.2962	0.2036	0.6504
347	8	exm2273446	17503316	G	0	0.08523	T	11.65	0.0006418	0	inf	0	nan
348	8	exm695209	36767024	C	0.2462	0.4489	T	13.29	0.0002666	0.4009	0.2538	0.2438	0.6593
349	8	exm-rs9650315	57155598	T	0.1066	0.3077	G	16.17	5.79E-05	0.2683	0.3409	0.1376	0.5234
350	8	exm-rs6995588	61003897	T	0.01538	0.1379	C	14.29	0.0001569	0.09766	0.7458	0.02264	0.4212
351	8	exm2262509	62172668	A	0.2769	0.483	C	13.28	0.0002687	0.41	0.2473	0.2525	0.6658
352	8	exm-rs16933415	68497939	C	0.1615	0.04545	T	11.74	0.0006102	4.046	0.4333	1.731	9.459
353	8	exm2266637	70954335	A	0.1692	0.3466	G	11.9	0.0005617	0.384	0.2825	0.2208	0.6681
354	8	exm2270983	71164680	G	0.2308	0.4713	T	18.5	1.70E-05	0.3366	0.2577	0.2031	0.5577
355	8	exm2270985	73963866	T	0.02308	0.142	G	12.73	0.0003598	0.1427	0.6228	0.0421	0.4836
356	8	exm2270876	78530715	T	0.3231	0.5795	C	19.74	8.87E-06	0.3463	0.2418	0.2155	0.5562
357	8	exm2266647	79417222	G	0.5077	0.233	A	24.82	6.30E-07	3.396	0.2501	2.08	5.544
358	8	exm-rs6473383	83669120	A	0.09016	0.2531	G	12.35	0.000441	0.2925	0.3641	0.1433	0.597
359	8	exm713190	101648164	G	0.1846	0.3807	C	13.76	0.0002081	0.3683	0.2742	0.2152	0.6305
360	8	exm-rs16872085	105957540	G	0.2077	0.07386	A	11.79	0.0005971	3.287	0.3603	1.622	6.66
361	8	exm715065	107773675	C	0	0.08523	T	11.65	0.0006418	0	inf	0	nan
362	8	exm718494	123966085	A	0.03077	0.1591	G	13.15	0.0002877	0.1678	0.5481	0.05731	0.4913
363	8	exm719207	124658203	C	0.03077	0.1534	T	12.35	0.0004405	0.1752	0.5493	0.0597	0.5141
364	8	exm719236	124663987	G	0.02308	0.1534	C	14.36	0.0001507	0.1304	0.6204	0.03864	0.4398
365	8	exm2258655	129384895	C	0.6077	0.3693	A	17.05	3.63E-05	2.645	0.238	1.659	4.218
366	8	exm-rs1876201	139982997	A	0.2462	0.4602	G	14.71	0.0001253	0.383	0.2536	0.233	0.6296
367	8	exm724389	142367087	T	0.2769	0.1092	C	14.13	0.000171	3.124	0.3122	1.694	5.762
368	8	exm2266705	143310815	A	0.2769	0.4886	G	13.98	0.0001848	0.4008	0.2473	0.2468	0.6508

369	8	exm727185	144672047	T	0	0.09091	C	12.47	0.0004135	0	inf	0	nan
370	8	exm731612	145603114	C	0.2692	0.4545	A	10.95	0.0009379	0.4421	0.249	0.2714	0.7203
371	8	exm732031	145639726	T	0.3538	0.5747	C	14.54	0.0001371	0.4052	0.2391	0.2536	0.6475
372	9	exm734722	334337	G	0.4453	0.2045	A	20.23	6.86E-06	3.122	0.258	1.883	5.176
373	9	exm741237	18639300	A	0	0.07955	G	10.84	0.0009951	0	inf	0	nan
374	9	exm-rs1063192	22003367	C	0.1154	0.3068	T	15.69	7.46E-05	0.2947	0.3195	0.1575	0.5512
375	9	exm-rs564398	22029547	G	0.1231	0.3011	A	13.57	0.0002293	0.3257	0.3135	0.1762	0.6021
376	9	exm-rs7865618	22031005	G	0.1231	0.3011	A	13.57	0.0002293	0.3257	0.3135	0.1762	0.6021
377	9	exm-rs2157719	22033366	G	0.1231	0.3011	A	13.57	0.0002293	0.3257	0.3135	0.1762	0.6021
378	9	exm-rs1412829	22043926	C	0.1231	0.3011	T	13.57	0.0002293	0.3257	0.3135	0.1762	0.6021
379	9	exm-rs1889899	26789940	G	0.5462	0.3239	A	15.18	9.75E-05	2.512	0.2387	1.574	4.011
380	9	exm744049	27009100	C	0.1016	0.2529	T	11.03	0.0008978	0.334	0.3406	0.1713	0.6512
381	9	exm2266809	33426434	A	0.3385	0.5398	G	12.22	0.000472	0.4362	0.2392	0.273	0.6972
382	9	exm747610	34724241	A	0.3154	0.5057	C	11.04	0.0008925	0.4502	0.2421	0.2801	0.7236
383	9	exm748413	35295880	A	0	0.08621	C	11.79	0.000596	0	inf	0	nan
384	9	exm750210	35853517	T	0.07812	0.005747	C	11.01	0.0009074	14.66	1.056	1.852	116.1
385	9	exm-rs4745062	73784264	T	0.3231	0.523	C	12.08	0.0005087	0.4353	0.2413	0.2713	0.6985
386	9	exm-rs10869758	78965376	T	0.08462	0.2273	C	10.96	0.000933	0.3143	0.3629	0.1543	0.64
387	9	exm2271094	80515456	G	0.2538	0.4489	T	12.25	0.0004641	0.4177	0.2522	0.2548	0.6847
388	9	exm760409	92003679	T	0.2308	0.08621	C	12.33	0.0004457	3.18	0.341	1.63	6.204
389	9	exm2271111	94508700	T	0.5692	0.3636	C	12.76	0.0003532	2.312	0.2365	1.455	3.676
390	9	exm765802	100684757	G	0.4538	0.267	A	11.52	0.0006871	2.281	0.2451	1.411	3.687
391	9	exm-rs755109	100696203	C	0.4462	0.2614	T	11.38	0.0007423	2.277	0.2461	1.405	3.688
392	9	exm2262583	118869883	C	0.2308	0.4148	T	11.34	0.0007598	0.4233	0.2583	0.2551	0.7023
393	9	exm779307	125391127	T	0.1385	0.3466	C	16.91	3.92E-05	0.303	0.2993	0.1685	0.5447
394	9	exm779314	125391241	A	0.1154	0.3239	G	18.06	2.14E-05	0.2723	0.3183	0.1459	0.5082
395	9	exm779568	125512908	G	0	0.07955	T	10.84	0.0009951	0	inf	0	nan
396	9	exm-rs10818918	126860510	A	0.1	0.2614	G	12.51	0.0004049	0.314	0.339	0.1616	0.6102
397	9	exm2259238	139418260	A	0.5923	0.3977	G	11.34	0.000758	2.2	0.2357	1.386	3.492
398	9	exm799291	139634495	A	0.3077	0.142	G	12.26	0.0004619	2.684	0.2876	1.528	4.717
399	10	exm-rs3136618	6001696	A	0.5538	0.3409	G	13.82	0.000201	2.4	0.2375	1.507	3.823

400	10	exm807880	6002368	G	0.5538	0.3523	T	12.34	0.0004427	2.283	0.2367	1.435	3.63
401	10	exm809549	12046546	C	0.03846	0.1882	T	15.28	9.25E-05	0.1725	0.4965	0.06519	0.4565
402	10	exm811848	16877080	C	0	0.1023	G	14.13	0.0001709	0	inf	0	nan
403	10	exm2259561	16903080	C	0.01538	0.1534	T	16.6	4.61E-05	0.08623	0.7427	0.02011	0.3697
404	10	exm2249163	24489659	G	0.4385	0.2386	A	13.64	0.0002212	2.491	0.25	1.526	4.067
405	10	exm2259572	25620487	A	0.3308	0.5227	C	11.18	0.0008289	0.4513	0.2398	0.282	0.7221
406	10	exm2259581	31817905	T	0.1803	0.4091	C	17.46	2.93E-05	0.3178	0.281	0.1832	0.5512
407	10	exm823593	50183042	A	0.1538	0.3352	G	12.84	0.0003385	0.3606	0.2908	0.2039	0.6376
408	10	exm2271288	51503335	C	0.4048	0.2235	T	11.3	0.0007735	2.362	0.2585	1.423	3.921
409	10	exm2267104	63814914	A	0.06154	0.2045	G	12.42	0.0004247	0.255	0.41	0.1142	0.5696
410	10	exm2271409	66551141	G	0.06923	0.2102	T	11.64	0.0006463	0.2794	0.3919	0.1296	0.6024
411	10	exm2271410	67974590	T	0.1016	0.2647	C	12.4	0.0004296	0.314	0.3404	0.1612	0.6119
412	10	exm830729	71874784	T	0	0.08523	C	11.65	0.0006418	0	inf	0	nan
413	10	exm-rs10999409	72332440	C	0.5077	0.2955	T	14.22	0.000163	2.459	0.241	1.533	3.944
414	10	exm-rs588517	83153246	A	0.07692	0.2386	G	13.86	0.0001967	0.2659	0.3736	0.1278	0.553
415	10	exm840916	91468925	G	0.1562	0.3276	C	11.4	0.0007356	0.3801	0.2921	0.2144	0.6739
416	10	exm841012	91487649	T	0.1587	0.3393	A	12.14	0.0004929	0.3674	0.2932	0.2068	0.6528
417	10	exm841018	91488979	T	0.1562	0.3314	A	11.8	0.0005925	0.3736	0.2924	0.2106	0.6627
418	10	exm-rs1592051	93542186	T	0.3308	0.5398	C	13.19	0.0002812	0.4214	0.24	0.2633	0.6746
419	10	exm844300	97096357	T	0.1385	0.03409	C	11.27	0.0007883	4.554	0.4869	1.754	11.82
420	10	exm853997	105793750	C	0.2923	0.1193	T	14.38	0.0001496	3.049	0.3021	1.686	5.511
421	10	exm-rs7076938	115789375	C	0.4692	0.2841	T	11.09	0.0008693	2.228	0.2425	1.385	3.584
422	10	exm859987	121436286	T	0.06154	0.1932	C	10.94	0.0009398	0.2739	0.4119	0.1222	0.614
423	10	exm2267137	124942806	G	0.2063	0.05814	A	15.04	0.0001052	4.212	0.3932	1.949	9.104
424	10	exm863476	126715692	T	0.02308	0.1307	C	11.14	0.0008469	0.1571	0.6255	0.04612	0.5354
425	10	exm2249111	132139508	T	0.3308	0.5398	C	13.19	0.0002812	0.4214	0.24	0.2633	0.6746
426	11	exm881387	4791111	C	0.2154	0.07955	T	11.65	0.0006416	3.176	0.3509	1.597	6.319
427	11	exm2271580	5193410	C	0.1154	0.2955	T	14.18	0.0001664	0.311	0.3204	0.166	0.5828
428	11	exm888199	7727886	T	0.2308	0.4375	C	14.05	0.0001778	0.3857	0.2577	0.2328	0.6392
429	11	exm2249501	10019879	A	0.1846	0.0625	G	11.01	0.0009075	3.396	0.3848	1.598	7.22
430	11	exm890236	10019879	A	0.1846	0.0625	G	11.01	0.0009075	3.396	0.3848	1.598	7.22

431	11	exm2267252	10791983	A	0.05385	0.25	G	20.71	5.33E-06	0.1707	0.4258	0.07411	0.3933
432	11	exm-rs10741657	14914878	A	0.3	0.4943	G	11.66	0.0006398	0.4384	0.2436	0.272	0.7068
433	11	exm-rs2060793	14915310	A	0.3077	0.5	G	11.36	0.0007487	0.4444	0.2426	0.2763	0.715
434	11	exm2267156	19057767	A	0.375	0.5747	G	11.77	0.0006018	0.444	0.2384	0.2782	0.7085
435	11	exm2271472	20301930	T	0.2923	0.5341	C	17.82	2.43E-05	0.3603	0.245	0.2229	0.5824
436	11	exm2264446	31037514	C	0.03125	0.1534	A	12.08	0.0005107	0.178	0.5494	0.06065	0.5225
437	11	exm2271488	37700681	T	0.4692	0.2356	G	18.21	1.98E-05	2.868	0.2506	1.755	4.687
438	11	exm901458	43876698	T	0.2462	0.4375	C	11.94	0.0005501	0.4198	0.2541	0.2552	0.6907
439	11	exm904624	47270255	T	0.2385	0.4318	C	12.29	0.0004547	0.412	0.256	0.2495	0.6804
440	11	exm-rs7120118	47286290	C	0.2385	0.4205	T	10.99	0.0009173	0.4316	0.2563	0.2612	0.7132
441	11	exm2271498	47290984	G	0.2308	0.4432	T	14.77	0.0001213	0.3769	0.2576	0.2275	0.6245
442	11	exm2249889	47298360	G	0.2692	0.4716	A	12.92	0.0003244	0.4128	0.2488	0.2535	0.6722
443	11	exm904958	47354787	T	0.2231	0.4375	C	15.18	9.75E-05	0.3692	0.2598	0.2219	0.6142
444	11	exm905210	47431703	G	0.06154	0.1932	A	10.94	0.0009398	0.2739	0.4119	0.1222	0.614
445	11	exm2267177	47454701	A	0.2385	0.4318	G	12.29	0.0004547	0.412	0.256	0.2495	0.6804
446	11	exm910257	56756664	G	0.5769	0.3864	A	10.91	0.0009579	2.166	0.2355	1.365	3.436
447	11	exm929809	66083043	T	0	0.08235	C	11.23	0.0008049	0	inf	0	nan
448	11	exm936011	68840399	A	0.2923	0.1092	G	16.38	5.19E-05	3.37	0.3103	1.834	6.19
449	11	exm939470	72946204	T	0.3615	0.1875	C	11.73	0.0006153	2.454	0.2657	1.458	4.131
450	11	exm2271624	75756145	C	0.05385	0.2159	T	15.66	7.60E-05	0.2067	0.4296	0.08905	0.4797
451	11	exm942770	76751166	A	0.07692	0.2386	G	13.86	0.0001967	0.2659	0.3736	0.1278	0.553
452	11	exm2271539	92316799	G	0.5	0.2955	T	13.25	0.0002731	2.385	0.241	1.487	3.824
453	11	exm950371	101359750	A	0.06923	0.2216	G	13.12	0.0002916	0.2613	0.3903	0.1216	0.5615
454	11	exm950533	101832590	A	0.08462	0.005747	C	12.21	0.0004761	15.99	1.051	2.037	125.5
455	11	exm950535	101832608	C	0.08462	0.005682	T	12.36	0.0004376	16.18	1.051	2.061	127
456	11	exm950539	101832670	A	0.08462	0.005747	G	12.21	0.0004761	15.99	1.051	2.037	125.5
457	11	exm951212	102593248	T	0.2923	0.5057	C	14.02	0.0001807	0.4038	0.2448	0.2499	0.6523
458	11	exm2249527	103779025	G	0.3615	0.5625	A	12.1	0.0005031	0.4404	0.2375	0.2765	0.7015
459	11	exm2267223	109199040	G	0.2846	0.483	A	12.27	0.0004605	0.4259	0.246	0.263	0.6899
460	11	exm957388	114576626	T	0.1615	0.3294	A	10.88	0.0009714	0.3922	0.2888	0.2227	0.6908
461	11	exm-rs490592	116298367	T	0.3077	0.142	G	12.26	0.0004619	2.684	0.2876	1.528	4.717

462	11	exm962243	119045951	T	0	0.07955	C	10.84	0.0009951	0	inf	0	nan
463	11	exm-rs2126709	123595927	T	0.007692	0.108	C	12.3	0.0004519	0.06406	1.033	0.008461	0.485
464	11	exm-rs6590330	128311059	A	0.02308	0.1591	G	15.19	9.71E-05	0.1249	0.6194	0.03708	0.4204
465	11	exm-rs1128334	128328959	A	0.02344	0.1647	G	15.63	7.68E-05	0.1217	0.6197	0.03613	0.4101
466	11	exm2271658	132320394	T	0.1385	0.3068	C	11.78	0.0005992	0.3631	0.302	0.2009	0.6563
467	11	exm972168	134234269	G	0.06923	0	A	12.55	0.0003954	NA	NA	NA	NA
468	12	exm973199	668548	A	0	0.07955	G	10.84	0.0009951	0	inf	0	nan
469	12	exm977504	6562293	T	0.1846	0.358	C	11.04	0.0008912	0.4061	0.2754	0.2367	0.6967
470	12	exm977528	6562823	T	0.2231	0.4148	C	12.36	0.0004376	0.4051	0.2604	0.2432	0.6749
471	12	exm979034	6948468	C	0.2923	0.5057	T	14.02	0.0001807	0.4038	0.2448	0.2499	0.6523
472	12	exm979360	7015707	T	0.1615	0.04545	G	11.74	0.0006102	4.046	0.4333	1.731	9.459
473	12	exm2260138	8976780	T	0.1769	0.3523	C	11.46	0.0007112	0.3952	0.2788	0.2288	0.6826
474	12	exm2267321	12578786	G	0.5615	0.3693	A	11.16	0.0008367	2.187	0.2359	1.377	3.472
475	12	exm987235	14993882	A	0	0.09195	G	12.62	0.000382	0	inf	0	nan
476	12	exm2267418	15750391	G	0.06154	0.1989	A	11.67	0.0006335	0.2642	0.4109	0.1181	0.5911
477	12	exm988079	18649057	T	0.2154	0.4138	C	13.27	0.0002698	0.3889	0.2631	0.2322	0.6513
478	12	exm988131	18719972	G	0.03125	0.1488	T	11.36	0.00075	0.1845	0.5523	0.0625	0.5447
479	12	exm2271825	19028431	C	0.5469	0.3529	T	11.17	0.0008327	2.213	0.2393	1.384	3.537
480	12	exm989495	21713402	T	0.4766	0.2443	C	17.76	2.51E-05	2.816	0.2492	1.728	4.589
481	12	exm993136	32137512	G	0.1	0.25	C	11.1	0.0008637	0.3333	0.3403	0.1711	0.6494
482	12	exm2250923	39508651	T	0.5846	0.358	C	15.5	8.27E-05	2.524	0.2375	1.585	4.021
483	12	exm2271838	43258744	T	0.1154	0.2955	C	14.18	0.0001664	0.311	0.3204	0.166	0.5828
484	12	exm-rs17291650	51213433	G	0.05385	0.2045	A	14.06	0.0001771	0.2213	0.4312	0.09506	0.5153
485	12	exm1003138	51681903	T	0.2	0.05114	C	16.36	5.25E-05	4.639	0.4064	2.092	10.29
486	12	exm1003199	51707626	T	0.2077	0.06897	C	12.8	0.0003457	3.539	0.3691	1.717	7.296
487	12	exm1006180	53044267	T	0.4231	0.2386	C	11.75	0.000609	2.34	0.2506	1.432	3.823
488	12	exm1010338	55523587	A	0.4769	0.2784	T	12.75	0.0003566	2.363	0.2431	1.467	3.806
489	12	exm1010343	55523685	T	0.4769	0.2816	C	12.24	0.0004666	2.326	0.2434	1.443	3.748
490	12	exm1010354	55523860	C	0.4769	0.2784	A	12.75	0.0003566	2.363	0.2431	1.467	3.806
491	12	exm1010375	55524172	A	0.4769	0.2784	G	12.75	0.0003566	2.363	0.2431	1.467	3.806
492	12	exm1010442	55641075	G	0.4538	0.2614	A	12.29	0.0004552	2.348	0.2459	1.45	3.803

493	12	exm1010452	55641295	G	0.4538	0.2614	A	12.29	0.0004552	2.348	0.2459	1.45	3.803
494	12	exm1010453	55641328	A	0.4538	0.2614	G	12.29	0.0004552	2.348	0.2459	1.45	3.803
495	12	exm-rs12367822	57204160	T	0.3492	0.175	G	11.36	0.0007519	2.53	0.2797	1.462	4.376
496	12	exm2271850	69842643	C	0.2538	0.4432	T	11.6	0.0006612	0.4274	0.2523	0.2607	0.7008
497	12	exm2264475	70728679	C	0.6	0.4091	A	10.9	0.0009592	2.167	0.2357	1.365	3.439
498	12	exm2271753	72609368	C	0.3077	0.5227	T	14.1	0.0001738	0.4058	0.2427	0.2522	0.6529
499	12	exm2271867	108894909	C	0.3231	0.6118	T	24.58	7.15E-07	0.3029	0.2448	0.1874	0.4894
500	12	exm1035335	109826634	A	0.3	0.1207	C	15.1	0.0001019	3.122	0.3013	1.73	5.636
501	12	exm2259971	118889488	G	0.1692	0.3977	T	18.57	1.64E-05	0.3085	0.2801	0.1782	0.5341
502	12	exm1042101	119772991	C	0	0.1023	G	14.13	0.0001709	0	inf	0	nan
503	12	exm1047380	123466304	G	0.007692	0.1023	A	11.49	0.0007015	0.06804	1.034	0.008963	0.5166
504	12	exm1048951	124352505	A	0	0.1307	T	18.37	1.82E-05	0	inf	0	nan
505	12	exm1048970	124358121	G	0	0.1307	A	18.37	1.82E-05	0	inf	0	nan
506	12	exm1052962	132549264	T	0	0.08235	C	11.23	0.0008049	0	inf	0	nan
507	13	exm1056554	23824818	A	0.2692	0.1193	G	11.24	0.000801	2.719	0.3052	1.495	4.946
508	13	exm1060035	28626716	T	0	0.07955	C	10.84	0.0009951	0	inf	0	nan
509	13	exm1064919	40229891	A	0.5312	0.2907	G	17.8	2.46E-05	2.765	0.2441	1.714	4.462
510	13	exm1064923	40229957	A	0.5308	0.2955	T	17.32	3.16E-05	2.697	0.2412	1.681	4.328
511	13	exm1065549	41835039	C	0.06923	0.2159	T	12.37	0.0004353	0.2701	0.3911	0.1255	0.5813
512	13	exm2271966	81260479	T	0.5308	0.3239	C	13.22	0.0002777	2.362	0.2384	1.48	3.768
513	13	exm-rs2762111	94051114	A	0.3308	0.5341	G	12.5	0.0004068	0.4312	0.24	0.2694	0.6901
514	13	exm2267623	106266101	A	0.09483	0.2534	G	10.87	0.0009798	0.3086	0.3696	0.1496	0.6369
515	14	exm2272151	20818131	C	0.1077	0.2898	T	14.82	0.0001184	0.2958	0.3281	0.1555	0.5627
516	14	exm2264539	22974256	A	0.2	0.3977	C	13.58	0.0002289	0.3786	0.2679	0.2239	0.6401
517	14	exm1091429	24114483	C	0.007692	0.1023	T	11.49	0.0007015	0.06804	1.034	0.008963	0.5166
518	14	exm2251731	24901433	T	0.1	0.2898	C	16.28	5.46E-05	0.2723	0.3363	0.1409	0.5264
519	14	exm2267701	30312091	A	0.3692	0.5795	G	13.23	0.0002749	0.4247	0.2374	0.2667	0.6763
520	14	exm2260309	33956209	A	0.1077	0.2614	C	11.2	0.0008173	0.3411	0.3309	0.1783	0.6524
521	14	exm2272064	33979974	C	0.5615	0.3636	T	11.84	0.0005787	2.241	0.2362	1.411	3.561
522	14	exm2260328	48997206	C	0.2734	0.4651	T	11.41	0.000732	0.4328	0.2504	0.2649	0.707
523	14	exm1100197	50583083	T	0.04762	0.2176	G	16.85	4.05E-05	0.1797	0.4578	0.07328	0.4408

524	14	exm-rs1265879	50877983	A	0.3846	0.2011	G	12.43	0.0004216	2.482	0.2613	1.487	4.142
525	14	exm2272106	70591661	C	0.3154	0.5795	T	20.96	4.69E-06	0.3342	0.2428	0.2077	0.5379
526	14	exm-rs221901	71602226	G	0.5308	0.3125	A	14.78	0.0001208	2.489	0.2394	1.556	3.979
527	14	exml1112651	73440864	C	0.5462	0.3295	T	14.39	0.0001488	2.448	0.2382	1.535	3.905
528	14	exm2251917	73440864	C	0.5462	0.3295	T	14.39	0.0001488	2.448	0.2382	1.535	3.905
529	14	exml1113028	73727509	T	0.5	0.2898	G	14.04	0.000179	2.451	0.2416	1.526	3.936
530	14	exml1113341	73964964	T	0	0.1534	C	21.87	2.91E-06	0	inf	0	nan
531	14	exml1113345	73965778	A	0	0.07955	G	10.84	0.0009951	0	inf	0	nan
532	14	exml1113408	73985794	C	0	0.1307	G	18.37	1.82E-05	0	inf	0	nan
533	14	exml1114149	74428445	A	0.5231	0.3239	G	12.28	0.0004577	2.29	0.2383	1.435	3.653
534	14	exml1114232	74489695	T	0	0.1	G	13.55	0.0002319	0	inf	0	nan
535	14	exm-rs8014204	75322794	G	0.4538	0.25	A	13.91	0.0001914	2.493	0.2477	1.534	4.051
536	14	exm2251934	75347585	C	0.6231	0.3977	A	15.19	9.72E-05	2.503	0.2376	1.571	3.988
537	14	exml120001	89205265	C	0.03226	0.1647	T	12.97	0.0003169	0.169	0.5487	0.05767	0.4955
538	14	exm-rs17776811	90066451	A	0.3462	0.5455	C	11.95	0.0005455	0.4412	0.2385	0.2764	0.7041
539	14	exml121075	91739081	A	0.04615	0.233	G	20.07	7.47E-06	0.1593	0.4545	0.06538	0.3883
540	14	exm2252002	93138041	C	0.5692	0.358	T	13.5	0.0002388	2.37	0.2368	1.49	3.77
541	14	exml126941	100625902	C	0.5083	0.3125	T	10.99	0.0009157	2.275	0.2499	1.394	3.712
542	14	exml127228	100847707	A	0.1846	0.3864	G	14.47	0.0001421	0.3596	0.274	0.2102	0.6152
543	14	exm-rs730570	101142890	G	0.1692	0.3409	A	11.23	0.000803	0.3938	0.2828	0.2262	0.6856
544	14	exm2272147	104704722	C	0.5769	0.3352	T	17.75	2.53E-05	2.704	0.2388	1.694	4.318
545	15	exml144235	30018627	C	0.1328	0.3068	T	12.53	0.0003995	0.346	0.3075	0.1894	0.6322
546	15	exml169547	65235776	G	0.5308	0.3409	A	11.05	0.0008854	2.187	0.237	1.374	3.48
547	15	exml172611	68624396	A	0.04615	0.233	C	20.07	7.47E-06	0.1593	0.4545	0.06538	0.3883
548	15	exml172631	68628163	T	0	0.09091	C	12.47	0.0004135	0	inf	0	nan
549	15	exm-rs2472299	75033400	A	0.2308	0.4148	G	11.34	0.0007598	0.4233	0.2583	0.2551	0.7023
550	15	exm-rs2472304	75044238	A	0.5462	0.3182	G	16.01	6.31E-05	2.579	0.2392	1.614	4.121
551	15	exm2267788	75052994	A	0.3308	0.5795	G	18.56	1.65E-05	0.3586	0.241	0.2236	0.575
552	15	exm-rs1378942	75077367	T	0.5462	0.3352	G	13.61	0.0002245	2.386	0.2378	1.497	3.803
553	15	exm-rs6495122	75125645	C	0.4692	0.2784	A	11.82	0.0005846	2.291	0.2432	1.422	3.691
554	15	exml182735	81624768	C	0.1154	0.02273	T	11.02	0.0008999	5.609	0.5755	1.816	17.33

555	15	exml1183569	83499472	T	0	0.08523	C	11.65	0.0006418	0	inf	0	nan
556	15	exml1193919	101561275	T	0.1	0.005682	C	15.24	9.49E-05	19.44	1.045	2.51	150.6
557	16	exml1204207	2017804	G	0	0.07955	T	10.84	0.0009951	0	inf	0	nan
558	16	exml1204849	2070568	C	0.3923	0.2159	A	11.28	0.0007834	2.344	0.2566	1.418	3.876
559	16	exml1216236	8839954	A	0.5923	0.375	G	14.18	0.0001658	2.421	0.2368	1.522	3.852
560	16	exm2272419	10434389	C	0.1	0.2784	T	14.73	0.000124	0.288	0.3373	0.1487	0.5578
561	16	exm2252439	13090833	C	0.5769	0.3466	A	16.07	6.12E-05	2.571	0.2379	1.613	4.098
562	16	exm-rs153091	13253956	C	0.2462	0.09659	A	12.44	0.000421	3.054	0.3264	1.611	5.791
563	16	exml1222920	20441020	A	0.06923	0.2159	G	12.37	0.0004353	0.2701	0.3911	0.1255	0.5813
564	16	exml1223367	20748331	A	0.3615	0.1705	C	14.5	0.0001403	2.756	0.2711	1.62	4.688
565	16	exml1223535	20810266	C	0.2769	0.1023	T	15.69	7.45E-05	3.362	0.3167	1.807	6.254
566	16	exml1226195	23409440	A	0.1769	0.03409	G	17.78	2.48E-05	6.09	0.4747	2.402	15.44
567	16	exml1227682	24902299	G	0	0.07955	C	10.84	0.0009951	0	inf	0	nan
568	16	exm2252528	27113695	T	0.3154	0.517	C	12.4	0.0004302	0.4303	0.2416	0.268	0.6909
569	16	exm2252541	29043450	T	0.2923	0.483	G	11.31	0.0007729	0.4422	0.2448	0.2737	0.7145
570	16	exml1236395	31374535	G	0.5308	0.3125	C	14.78	0.0001208	2.489	0.2394	1.556	3.979
571	16	exm2225334	74481327	C	0.1077	0.005682	T	16.69	4.40E-05	21.12	1.042	2.74	162.8
572	16	exml1261911	81232564	T	0.1077	0.2784	G	13.33	0.0002614	0.3128	0.3291	0.1641	0.5963
573	17	exml1273421	648186	G	0.1538	0.3523	A	15.01	0.0001071	0.3343	0.2898	0.1894	0.59
574	17	exml1286675	7224921	G	0.06923	0.2159	C	12.37	0.0004353	0.2701	0.3911	0.1255	0.5813
575	17	exml1287293	7329134	A	0.3077	0.1193	G	16.62	4.56E-05	3.28	0.3003	1.821	5.909
576	17	exml1291491	8135444	G	0.1385	0.02841	C	13.03	0.0003069	5.496	0.5199	1.984	15.23
577	17	exml1291535	8138569	G	0.1385	0.02273	C	15.01	0.000107	6.911	0.5659	2.279	20.95
578	17	exml1291696	8166458	A	0.1385	0.03409	T	11.27	0.0007883	4.554	0.4869	1.754	11.82
579	17	exml1291833	8172506	G	0.2385	0.05114	T	23.09	1.55E-06	5.81	0.3993	2.656	12.71
580	17	exm2253321	8215927	T	0.1077	0.01724	C	11.53	0.0006845	6.879	0.6475	1.934	24.47
581	17	exml1292049	8224276	T	0.1769	0.3693	C	13.51	0.0002374	0.3671	0.2779	0.2129	0.6328
582	17	exml1312892	34077232	A	0.03846	0.1761	G	13.65	0.0002199	0.1871	0.4971	0.07061	0.4957
583	17	exm-rs16965350	36614563	T	0.1385	0.3182	C	13.17	0.0002842	0.3444	0.3011	0.1909	0.6214
584	17	exml1315705	36889559	T	0.2385	0.09659	C	11.38	0.0007428	2.929	0.3278	1.54	5.568
585	17	exml1315976	37054772	T	0.5154	0.3068	C	13.61	0.0002255	2.403	0.2398	1.502	3.844

586	17	exml1316097	37224211	T	0.1692	0.03409	C	16.43	5.06E-05	5.772	0.4767	2.267	14.69
587	17	exml1317944	38189659	T	0	0.09659	C	13.3	0.0002661	0	inf	0	nan
588	17	exml2252979	38243103	T	0	0.108	C	14.96	0.0001096	0	inf	0	nan
589	17	exml1338031	51901643	C	0.06154	0.1932	T	10.94	0.0009398	0.2739	0.4119	0.1222	0.614
590	17	exml1338036	51901703	C	0.05385	0.1875	G	11.75	0.000607	0.2466	0.4339	0.1054	0.5773
591	17	exml1339358	56270442	G	0.09231	0.01136	A	11.22	0.0008087	8.847	0.773	1.945	40.25
592	17	exml1348365	66364804	C	0.4692	0.2841	T	11.09	0.0008693	2.228	0.2425	1.385	3.584
593	17	exml1354846	73570718	G	0.1308	0.3068	C	13.01	0.0003106	0.3399	0.3072	0.1861	0.6207
594	17	exml1358102	74381555	A	0.3769	0.1724	G	16.18	5.76E-05	2.904	0.2702	1.71	4.932
595	17	exml1358104	74381567	G	0.0678	0.2529	A	16.38	5.17E-05	0.2148	0.4065	0.09684	0.4765
596	17	exml1358199	74387284	T	0.4692	0.2614	C	14.21	0.0001637	2.498	0.2456	1.544	4.043
597	17	exml1359079	74878259	A	0.1231	0.3693	G	23.29	1.39E-06	0.2397	0.3093	0.1307	0.4394
598	17	exml1360583	76433899	A	0.2769	0.108	G	14.48	0.0001417	3.165	0.3121	1.717	5.834
599	17	exml1364139	78272294	T	0.06154	0.2159	C	13.95	0.0001877	0.2381	0.4084	0.107	0.5302
600	17	exml-rs1046896	80685533	T	0.2538	0.4545	C	12.93	0.0003232	0.4082	0.252	0.2491	0.6691
601	17	exml1371159	81043175	T	0	0.108	G	14.96	0.0001096	0	inf	0	nan
602	18	exml-rs991014	42439886	A	0.3462	0.1591	G	14.4	0.0001475	2.798	0.2765	1.628	4.811
603	18	exml1391359	61654463	A	0.3462	0.5465	G	11.96	0.0005423	0.4393	0.2397	0.2746	0.7027
604	18	exml1392902	72343292	A	0	0.09412	T	12.92	0.0003243	0	inf	0	nan
605	19	exml1397560	830820	A	0.1308	0.01705	G	15.83	6.93E-05	8.676	0.6378	2.485	30.28
606	19	exml2253724	2079299	G	0.3462	0.5941	A	18.13	2.06E-05	0.3617	0.2416	0.2252	0.5808
607	19	exml-rs7248104	7224431	A	0.5615	0.3466	G	14.03	0.0001794	2.414	0.2373	1.516	3.845
608	19	exml1420079	8993018	A	0.1385	0.03409	G	11.27	0.0007883	4.554	0.4869	1.754	11.82
609	19	exml1420234	9003645	A	0.2769	0.09659	G	16.98	3.78E-05	3.582	0.3218	1.907	6.73
610	19	exml1422035	9086012	G	0.06154	0	T	11.12	0.0008533	NA	NA	NA	NA
611	19	exml2272761	9945354	C	0.2923	0.5227	T	16.25	5.56E-05	0.3771	0.2449	0.2334	0.6094
612	19	exml1423637	9968434	T	0.4923	0.2898	C	13.08	0.0002992	2.377	0.2416	1.48	3.816
613	19	exml1436482	15198441	T	0.04615	0.2102	G	16.67	4.46E-05	0.1818	0.4571	0.07421	0.4453
614	19	exml1436497	15198606	T	0.04615	0.2102	C	16.67	4.46E-05	0.1818	0.4571	0.07421	0.4453
615	19	exml1436499	15198631	A	0.2538	0.4489	C	12.25	0.0004641	0.4177	0.2522	0.2548	0.6847
616	19	exml1436508	15198751	C	0.04615	0.2102	T	16.67	4.46E-05	0.1818	0.4571	0.07421	0.4453

617	19	exm2272822	16808183	C	0.1769	0.4148	T	19.65	9.32E-06	0.3033	0.2761	0.1765	0.521
618	19	exm1440719	17036087	T	0.01538	0.1477	C	15.75	7.22E-05	0.09014	0.7436	0.02099	0.3872
619	19	exm1441188	17303774	T	0.6154	0.358	G	19.91	8.14E-06	2.87	0.2392	1.796	4.586
620	19	exm2272823	17958777	C	0.05385	0.1818	T	11.01	0.0009057	0.2561	0.435	0.1092	0.6007
621	19	exm1446569	19121084	C	0	0.08523	T	11.65	0.0006418	0	inf	0	nan
622	19	exm2260841	22522950	G	0.1231	0.358	A	21.54	3.47E-06	0.2517	0.3098	0.1372	0.462
623	19	exm2272797	48215633	C	0.2188	0.4034	T	11.51	0.0006935	0.4141	0.2633	0.2472	0.6938
624	19	exm1486034	48543906	C	0.07692	0.2216	G	11.64	0.000647	0.2927	0.3759	0.1401	0.6115
625	19	exm1487912	49206985	G	0.3462	0.5568	A	13.33	0.0002612	0.4214	0.2388	0.2639	0.6728
626	19	exm-rs504963	49208865	C	0.3231	0.5517	T	15.69	7.45E-05	0.3878	0.2417	0.2415	0.6227
627	19	exm1488777	49409026	A	0.06923	0	G	12.55	0.0003954	NA	NA	NA	NA
628	19	exm1494168	50905310	A	0	0.108	G	14.96	0.0001096	0	inf	0	nan
629	19	exm2253947	50912126	A	0	0.108	G	14.96	0.0001096	0	inf	0	nan
630	19	exm1494630	50971009	A	0	0.1307	C	18.37	1.82E-05	0	inf	0	nan
631	19	exm1497848	52223121	A	0.2615	0.4545	G	11.92	0.0005566	0.425	0.2505	0.2601	0.6944
632	19	exm1497888	52249672	A	0.5	0.3068	C	11.74	0.0006112	2.259	0.2398	1.412	3.615
633	19	exm-rs7507442	53278953	A	0.3615	0.6193	G	19.88	8.24E-06	0.3481	0.2396	0.2176	0.5567
634	19	exm1501784	54080067	C	0.06154	0.233	T	16.34	5.30E-05	0.2159	0.4062	0.09739	0.4787
635	19	exm-rs400322	55172578	A	0.2769	0.483	G	13.28	0.0002687	0.41	0.2473	0.2525	0.6658
636	19	exm1510830	56477710	T	0.4462	0.25	C	12.95	0.0003206	2.417	0.2479	1.487	3.928
637	19	exm1510859	56487603	A	0.5385	0.3352	G	12.67	0.0003725	2.314	0.2376	1.452	3.686
638	20	exm1517622	139456	A	0.1769	0.3636	G	12.81	0.0003447	0.3762	0.2782	0.2181	0.6489
639	20	exm1517629	139576	A	0.1769	0.3636	C	12.81	0.0003447	0.3762	0.2782	0.2181	0.6489
640	20	exm1517645	168728	T	0.1769	0.3864	A	15.7	7.43E-05	0.3414	0.2771	0.1983	0.5877
641	20	exm2254185	210061	A	0.2615	0.483	G	15.42	8.59E-05	0.3792	0.2502	0.2322	0.6191
642	20	exm-rs3761218	3776175	T	0.5846	0.3851	C	11.89	0.000563	2.248	0.2365	1.414	3.573
643	20	exm2272875	7482971	T	0.2846	0.4886	C	12.95	0.0003204	0.4164	0.246	0.2571	0.6743
644	20	exm-rs6056209	8836771	G	0.3923	0.5909	A	11.8	0.0005927	0.4469	0.2362	0.2813	0.71
645	20	exm-rs4141463	14747471	C	0.3125	0.5059	T	11.19	0.0008226	0.444	0.2447	0.2748	0.7173
646	20	exm2254184	20817745	G	0.3	0.5114	A	13.7	0.0002146	0.4095	0.2437	0.254	0.6602
647	20	exm1540821	37396120	G	0.6	0.392	A	12.95	0.0003193	2.326	0.2364	1.464	3.697

648	20	exm2268297	40783392	G	0.5769	0.3864	A	10.91	0.0009579	2.166	0.2355	1.365	3.436
649	20	exm-rs13038095	46425576	T	0.2154	0.0625	G	15.72	7.36E-05	4.118	0.3775	1.965	8.629
650	20	exm2260952	52019450	T	0.06923	0.2102	C	11.64	0.0006463	0.2794	0.3919	0.1296	0.6024
651	20	exm1554440	58576432	G	0	0.07955	A	10.84	0.0009951	0	inf	0	nan
652	20	exm2254385	61990939	A	0.2385	0.08523	G	13.75	0.0002093	3.361	0.3395	1.728	6.538
653	21	exm2254497	19220798	C	0.5846	0.3693	T	13.95	0.0001878	2.403	0.2368	1.511	3.823
654	21	exm-rs1475591	32440540	T	0.06923	0.2216	C	13.12	0.0002916	0.2613	0.3903	0.1216	0.5615
655	21	exm-rs2833256	32444485	A	0.04615	0.2069	G	16.15	5.86E-05	0.1855	0.458	0.07559	0.4551
656	21	exm1574967	44837555	G	0.0625	0.2093	A	12.64	0.0003783	0.2519	0.4104	0.1127	0.563
657	21	exm1576150	45564766	G	0.01538	0.1534	C	16.6	4.61E-05	0.08623	0.7427	0.02011	0.3697
658	21	exm1576957	45819296	C	0	0.1034	T	14.29	0.0001563	0	inf	0	nan
659	21	exm2272989	46334472	T	0.5692	0.3693	C	12.05	0.0005169	2.257	0.2361	1.421	3.585
660	22	exm1586012	19961730	A	0.007692	0.125	G	14.8	0.0001194	0.05426	1.029	0.007216	0.4081
661	22	exm2268401	20127554	G	0.2846	0.4886	A	12.95	0.0003204	0.4164	0.246	0.2571	0.6743
662	22	exm1596199	26695077	T	0.2308	0.4148	G	11.34	0.0007598	0.4233	0.2583	0.2551	0.7023
663	22	exm1598396	29913272	T	0.5615	0.358	C	12.55	0.000396	2.297	0.2366	1.445	3.652
664	22	exm1599866	30934816	T	0.1308	0.3125	C	13.72	0.0002117	0.331	0.3068	0.1814	0.6039
665	22	exm1606293	37906262	T	0.3308	0.1529	C	13.15	0.0002869	2.737	0.2831	1.572	4.768
666	22	exm-rs9607469	37919267	A	0.3	0.1307	G	13.27	0.00027	2.851	0.2944	1.601	5.076
667	22	exm1614469	43024271	C	0.007692	0.108	G	12.3	0.0004519	0.06406	1.033	0.008461	0.485
668	22	exm-rs9627183	48284514	A	0.007692	0.1023	G	11.49	0.0007015	0.06804	1.034	0.008963	0.5166
669	22	exm1622259	50752150	T	0.3538	0.1552	C	16.1	6.02E-05	2.981	0.2784	1.728	5.145
670	23	exm2268600	80201432	G	0.5465	0.2963	A	13.78	0.0002056	2.862	0.2871	1.63	5.025
671	23	exm2273280	95738501	C	0.4706	0.25	T	11.43	0.0007235	2.667	0.294	1.499	4.745
672	23	exm2273167	95794612	T	0.4353	0.2059	C	13.26	0.0002711	2.973	0.3047	1.636	5.402
673	23	exm1655810	122536945	A	0	0.1324	G	12.39	0.0004324	0	inf	0	nan
674	23	exm-rs5904726	146322623	G	0.1294	0.3529	A	13.36	0.0002577	0.2725	0.3696	0.1321	0.5624
675	23	exm1666749	153762634	A	0.03529	0.2206	G	14.14	0.0001698	0.1293	0.6231	0.03811	0.4384
676	24	exm-rs1865680	6868118	A	0	0.375	G	19.68	9.15E-06	0	inf	0	nan
677	24	exm-rs2032624	15026424	C	0	0.3421	A	16.42	5.07E-05	0	inf	0	nan
678	24	exm-rs2032658	15581983	G	0	0.3421	A	17.52	2.84E-05	0	inf	0	nan

679	24	exm-rs2032631	21867787	A	0.02273	0.375	G	16.86	4.02E-05	0.03876	1.063	0.004826	0.3113
680	25	exm1667537	91133892	G	0	0.08523	T	11.65	0.0006418	0	inf	0	nan
681	25	exm1667541	91134179	T	0	0.08523	G	11.65	0.0006418	0	inf	0	nan
682	26	exm2263340	8701	G	0.125	0.4713	A	20.17	7.09E-06	0.1603	0.4347	0.06837	0.3758

CHR: Chromosome; SNP: Illumina single nucleotide ID; BP: Base pair position at the respective chromosome as per GRCh37.p13; A1: Minor allele name; F_A: Frequency of minor allele in cases; F_U: Frequency of minor allele in controls; A2: Major allele name; CHISQ: Basic allelic test chi-square; P: *p*-value; OR: Odd ratio; SE: Standard error; L95: Lower bound of 95% confidence interval for odds ratio; U95: Upper bound of 95% confidence interval for odds ratio.

Table S2. The functional annotations of the most significant genes (p<0.0001) based on the DAVID 6.7 and Reactome.

ID	Gene Name	GAD_DISEASE	UP_SEQ_FEATURE
CD55	<i>CD55 molecule (Cromer blood group)(CD55)</i>	Birth Weight Leukemia Leukemia, Myeloid, Acute Precursor Cell Lymphoblastic Leukemia-Lymphoma,Breath Tests,Chorioamnionitis Fetal Membranes, Premature Rupture Infection of amniotic sac and membranes,Chorioamnionitis Fetal Membranes, Premature Rupture Infection of amniotic sac and membranes Obstetric Labor, Premature Pre-Eclampsia Premature Birth,Coronary Artery Disease,diabetes, type 1,Down Syndrome ,Lymphoma, Non-Hodgkin,macular degeneration,Meningeal Neoplasms meningioma,null,	chain:Complement decay-accelerating factor,compositionally biased region:Ser/Thr-rich,disulfide bond,domain:Sushi 1,domain:Sushi 2,domain:Sushi 3,domain:Sushi 4,glycosylation site:N-linked (GlcNAc...),helix,lipid moiety-binding region:GPI-anchor amidated serine,modified residue,propeptide:Removed in mature form,sequence conflict,sequence variant,signal peptide,splice variant,strand,turn,
CTR9	<i>CTR9 homolog, Paf1/RNA polymerase II complex component(CTR9)</i>	Coronary Disease,Osteoporosis,	chain:RNA polymerase-associated protein CTR9 homolog,compositionally biased region:Lys-rich,compositionally biased region:Poly-Gly,compositionally biased region:Poly-Lys,compositionally biased region:Ser-rich,modified residue,repeat:TPR 1,repeat:TPR 10,repeat:TPR 11,repeat:TPR 12,repeat:TPR 13,repeat:TPR 14,repeat:TPR 15,repeat:TPR 16,repeat:TPR 2,repeat:TPR 3,repeat:TPR 4,repeat:TPR 5,repeat:TPR 6,repeat:TPR 7,repeat:TPR 8,repeat:TPR 9,

H2AF
V *H2A histone*
family member
V(H2AFV)

chain:Histone H2A.v,cross-link:Glycyl lysine isopeptide
(Lys-Gly) (interchain with G-Cter in ubiquitin),modified
residue,sequence variant,

HCP5 *HLA complex P5*
(non-protein
coding)(HCP5) Acquired Immunodeficiency Syndrome|HIV Infections,Acquired
Immunodeficiency Syndrome|HIV Seropositivity,AIDS
progression,Drug Hypersensitivity|HIV Infections|[X]Human
immunodeficiency virus disease,drug-induced liver injury
(flucloxacillin),HIV Infections,HIV-1
control,Hypersensitivity,Lupus Erythematosus, Systemic,

chain:HLA class I histocompatibility antigen protein
P5,sequence conflict,sequence variant,

		Abortion, Spontaneous,Addison Disease Addison's disease,Addison Disease Addison's disease Autoimmune Diseases,Adenocarcinoma Adenosquamous carcinoma Carcinoma, Adenosquamous Carcinoma, Squamous Cell Cervical Neoplasm Squamous cell carcinoma Uterine Cervical Neoplasms,Adenocarcinoma Stomach Neoplasms,Arthritis, Juvenile Rheumatoid Chronic Childhood Arthritis,Arthritis, Rheumatoid Rheumatoid Arthritis Rheumatoid spondylitis Spondylitis, Ankylosing,Autoimmune Diseases Diabetes, Gestational Gestational diabetes mellitus ,Autoimmune Diseases Mixed Connective Tissue Disease,Behcet Syndrome,Behcet Syndrome Inflammatory bowel disease, NOS Inflammatory Bowel Diseases,Bile Duct Neoplasms Cholangiocarcinoma Cholangitis, Sclerosing,Breast Cancer,Brucellosis,Carcinoma, Squamous Cell Mouth Neoplasms Squamous cell carcinoma,Carcinoma Nasopharyngeal Neoplasms,Celiac disease,Celiac Disease Diabetes Mellitus, Insulin-Dependent Diabetes Mellitus, Type 1,Cervical Neoplasm Hypersensitivity Uterine Cervical Neoplasms,Cervical Neoplasm Papillomavirus Infections Tumor Virus Infections Uterine Cervical Neoplasms,Cholelithiasis,Chronic ulcerative colitis Colitis, Ulcerative,Chronic ulcerative colitis Colitis, Ulcerative Crohn Disease Crohn's disease Inflammatory bowel disease, NOS Inflammatory Bowel Diseases Peripheral Vascular Diseases,Colorectal Cancer,Diabetes Mellitus, Insulin-Dependent Diabetes Mellitus, Type 1,Diabetes Mellitus, Type 1,Giant Cell Arteritis Temporal Arteritis,Graves Disease Graves' Disease,HIV Infections [X]Human immunodeficiency virus disease,Inflammatory bowel disease, NOS Inflammatory Bowel Diseases,Lupus Erythematosus, Systemic Systemic lupus erythematosus,melanoma Uveal Neoplasms,Multiple Sclerosis,normal variation,Oral Submucous Fibrosis,Psoriasis,Rheumatoid spondylitis Spondylitis, Ankylosing,Type 2 Diabetes edema rosiglitazone,	
MICA	MHC class I polypeptide-related sequence A(MICA)		
ANXA9	annexin A9(ANXA9)	melanoma,	chain:Annexin A9,modified residue,repeat:Annexin 1,repeat:Annexin 2,repeat:Annexin 3,repeat:Annexin 4,sequence variant,

<i>BRD2</i>	<i>bromodomain containing 2(BRD2)</i>	Abortion, Spontaneous, Alzheimer's disease ,Asthma,Azoospermia,Heart Rate,Juvenile Myoclonic Epilepsy,Lupus Erythematosus, Systemic,null,photoparoxysmal response,Triglycerides,	chain:Bromodomain-containing protein 2,compositionally biased region:Arg/Lys-rich (highly basic),compositionally biased region:Glu/Ser-rich,compositionally biased region:Poly-Glu,compositionally biased region:Poly- Lys,compositionally biased region:Poly- Pro,compositionally biased region:Poly- Ser,compositionally biased region:Ser-rich,domain:Bromo 1,domain:Bromo 2,domain:ET,helix,modified residue,multigenesis site,sequence variant,short sequence motif:Nuclear localization signal,splice variant,turn,
<i>CDC1 4C</i>	<i>cell division cycle 14C, pseudogene(CDC 14C)</i>	Calcium,Cholesterol,Glucose,Heart Failure,Parkinson Disease,Platelet Aggregation,Sleep,Triglycerides,	
<i>CCDC 88C</i>	<i>coiled-coil domain containing 88C(CCDC88C)</i>	Body Mass Index,Insulin,Insulin Resistance,Waist Circumference,	chain:Protein Daple,modified residue,region of interest:DVL1-binding,sequence conflict,sequence variant,short sequence motif:PDZ-binding,splice variant,
<i>DOCK 8</i>	<i>dedicator of cytokinesis 8(DOCK8)</i>	Heart Failure,Platelet Count,Tobacco Use Disorder,	chain:Dedicator of cytokinesis protein 8,domain:DHR- 1,domain:DHR-2,modified residue,sequence conflict,sequence variant,splice variant,

<i>ITGA11</i>	<i>integrin subunit alpha 11(ITGA11)</i>	ADHD attention-deficit hyperactivity disorder,Attention Deficit Disorder with Hyperactivity,Cell Adhesion Molecules,Coronary Disease,Electrocardiography,lung cancer ,Psychomotor Performance,Survival,Tobacco Use Disorder,	chain:Integrin alpha-11,compositionally biased region:Poly-Arg,compositionally biased region:Poly-Leu,disulfide bond,domain:VWFA,glycosylation site:N-linked (GlcNAc...),mutagenesis site,repeat:FG-GAP 1,repeat:FG-GAP 2,repeat:FG-GAP 3,repeat:FG-GAP 4,repeat:FG-GAP 5,repeat:FG-GAP 6,repeat:FG-GAP 7,sequence variant,signal peptide,topological domain:Cytoplasmic,topological domain:Extracellular,transmembrane region,
<i>HLA-DMA</i>	<i>major histocompatibility complex, class II, DM alpha(HLA-DMA)</i>	Acquired Immunodeficiency Syndrome HIV Seropositivity,antiphospholipid syndrome,Arthritis, Rheumatoid,Body Composition,condyloma acuminata,Dermatitis, Contact ,Heart Rate,HIV,lupus erythematosus,Lupus Erythematosus, Systemic,measles,medicamentosa like dermatitis, trichloroethylene-induced,Multiple Sclerosis,multiple sclerosis; IgA nephropathy,normal variation,Psoriasis,rheumatoid arthritis,systemic lupus erythematosus,Type 2 Diabetes edema rosiglitazone,	chain:HLA class II histocompatibility antigen, DM alpha chain,disulfide bond,domain:Ig-like C1-type,glycosylation site:N-linked (GlcNAc...),helix,region of interest:Alpha-1,region of interest:Alpha-2,region of interest:Connecting peptide,sequence variant,signal peptide,strand,topological domain:Cytoplasmic,topological domain:Luminal,transmembrane region,turn,
<i>MGAT5B</i>	<i>mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetylglucosaminyltransferase, isozyme B(MGAT5B)</i>	Hemoglobin A, Glycosylated,Lipoproteins, LDL,Tobacco Use Disorder,Type 2 Diabetes edema rosiglitazone,	chain:Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase B,glycosylation site:N-linked (GlcNAc...),sequence variant,splice variant,topological domain:Cytoplasmic,topological domain:Luminal,transmembrane region,
<i>MTHFD1L</i>	<i>methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like(MTHFD1L)</i>	Acquired Immunodeficiency Syndrome Disease Progression,Alzheimer Disease,Alzheimer's Disease,Alzheimer's disease ,Aorta,Body Mass Index,Body Weight,Cleft Lip Cleft Palate Tooth Abnormalities,Coronary Artery Disease,Coronary Artery Disease Diabetes Mellitus, Type 1 Diabetic Nephropathies,Coronary Artery Disease Myocardial Infarction,Coronary Disease,neural tube defects ,Respiratory Function Tests,Stroke,Tunica Media,Type 2 Diabetes edema rosiglitazone,	chain:Monofunctional C1-tetrahydrofolate synthase, mitochondrial,compositionally biased region:Poly-Gly,modified residue,nucleotide phosphate-binding region:ATP,region of interest:Formyltetrahydrofolate synthetase,region of interest:Methylenetetrahydrofolate dehydrogenase and cyclohydrolase,sequence conflict,sequence variant,splice variant,transit peptide:Mitochondrion,

<i>MYO9B</i>	<i>myosin IXB(MYO9B)</i>	Celiac disease,celiac disease lupus erythematosus rheumatoid arthritis,Celiac Disease ,Celiac Disease Dermatitis Herpetiformis Inflammatory Bowel Diseases,Celiac Disease Down Syndrome,Colitis, Ulcerative Crohn Disease Inflammatory Bowel Diseases,coronary spastic angina,Crohn Disease,Crohn's disease ulcerative colitis,Diabetes Mellitus, Insulin-Dependent Diabetes Mellitus, Type 1,diabetes, type 1 ,Multiple Sclerosis,Schizophrenia,	chain:Myosin-IXb,domain:IQ 1,domain:IQ 2,domain:IQ 3,domain:IQ 4,domain:Myosin head-like,domain:Ras-associating,domain:Rho-GAP,modified residue,nucleotide phosphate-binding region:ATP,region of interest:Actin-binding,region of interest:Neck or regulatory domain,region of interest:Tail,sequence conflict,splice variant,zinc finger region:Phorbol-ester/DAG-type,
<i>OR12D2</i>	<i>olfactory receptor family 12 subfamily D member 2 (gene/pseudogene)(OR12D2)</i>	female preferences for male odors,Lipoproteins, VLDL,Lupus Erythematosus, Systemic,	chain:Olfactory receptor 12D2,disulfide bond,glycosylation site:N-linked (GlcNAc...),sequence variant,topological domain:Cytoplasmic,topological domain:Extracellular,transmembrane region,
<i>OR5V1</i>	<i>olfactory receptor family 5 subfamily V member 1(OR5V1)</i>	female preferences for male odors,HIV Infections [X]Human immunodeficiency virus disease,Lupus Erythematosus, Systemic,	chain:Olfactory receptor 12D3,chain:Olfactory receptor 5V1,disulfide bond,glycosylation site:N-linked (GlcNAc...),sequence conflict,sequence variant,topological domain:Cytoplasmic,topological domain:Extracellular,transmembrane region,
<i>PFAS</i>	<i>phosphoribosylformylglycinamidine synthase(PFAS)</i>	Tobacco Use Disorder,	
<i>RAET1E</i>	<i>retinoic acid early transcript 1E(RAET1E)</i>	normal variation,	chain:NKG2D ligand 4,compositionally biased region:Poly-Ser,disulfide bond,glycosylation site:N-linked (GlcNAc...),region of interest:MHC class I alpha-1 like,region of interest:MHC class I alpha-2 like,sequence conflict,sequence variant,signal peptide,splice variant,topological domain:Cytoplasmic,topological domain:Extracellular,transmembrane region,

<i>RNF144A</i>	<i>ring finger protein 144A(RNF144A)</i>	Amyotrophic Lateral Sclerosis,Body Fat Distribution,Cholesterol, LDL,Depressive Disorder, Major,Immunoglobulin E,Iron,longevity,Perphenazine,response to antipsychotic treatment,Schizophrenia,Stroke,Tobacco Use Disorder,	chain:Probable E3 ubiquitin-protein ligase RNF144A,helix,sequence variant,strand,transmembrane region,turn,zinc finger region:IBR-type,zinc finger region:RING-type 1; atypical,zinc finger region:RING-type 2; degenerate,
<i>SLC8A3</i>	<i>solute carrier family 8 member A3(SLC8A3)</i>	Cystic Fibrosis,Iron,Tobacco Use Disorder,	chain:Sodium/calcium exchanger 3,domain:Calx-beta 1,domain:Calx-beta 2,glycosylation site:N-linked (GlcNAc...),region of interest:Calmodulin-binding,repeat:Alpha-1,repeat:Alpha-2,sequence variant,signal peptide,splice variant,topological domain:Cytoplasmic,topological domain:Extracellular,transmembrane region,
<i>SFTA2</i>	<i>surfactant associated 2(SFTA2)</i>	Behcet Syndrome,Lupus Erythematosus, Systemic,	chain:Surfactant-associated protein 2,glycosylation site:N-linked (GlcNAc...),sequence variant,signal peptide,
<i>ZNF600</i>	<i>zinc finger protein 600(ZNF600)</i>	Phospholipids,	chain:Zinc finger protein 600,modified residue,sequence conflict,sequence variant,zinc finger region:C2H2-type 10,zinc finger region:C2H2-type 11; degenerate,zinc finger region:C2H2-type 12,zinc finger region:C2H2-type 13,zinc finger region:C2H2-type 14,zinc finger region:C2H2-type 15,zinc finger region:C2H2-type 16,zinc finger region:C2H2-type 17,zinc finger region:C2H2-type 18,zinc finger region:C2H2-type 19,zinc finger region:C2H2-type 1; degenerate,zinc finger region:C2H2-type 2,zinc finger region:C2H2-type 20,zinc finger region:C2H2-type 3,zinc finger region:C2H2-type 4,zinc finger region:C2H2-type 5,zinc finger region:C2H2-type 6,zinc finger region:C2H2-type 7,zinc finger region:C2H2-type 8,zinc finger region:C2H2-type 9,

ZKSC AN8	<p><i>zinc finger with KRAB and SCAN domains 8(ZKSCAN8)</i></p>	<p>chain:Zinc finger protein 192,domain:KRAB,domain:SCAN box,modified residue,sequence conflict,sequence variant,zinc finger region:C2H2-type 1,zinc finger region:C2H2-type 2,zinc finger region:C2H2-type 3,zinc finger region:C2H2-type 4,zinc finger region:C2H2-type 5,zinc finger region:C2H2-type 6,zinc finger region:C2H2-type 7,zinc finger region:C2H2-type 8,zinc finger region:C2H2-type 9,</p>
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