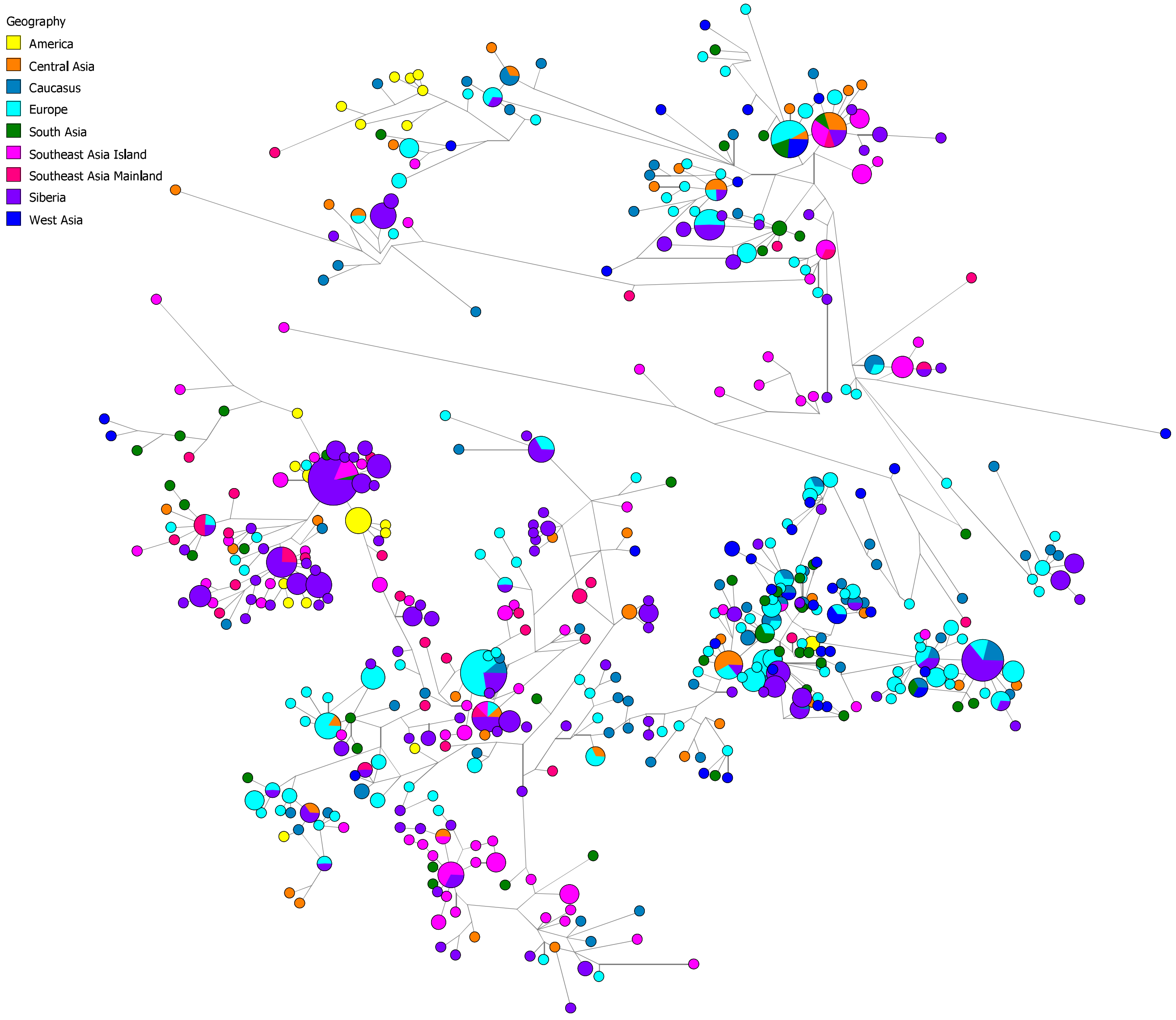
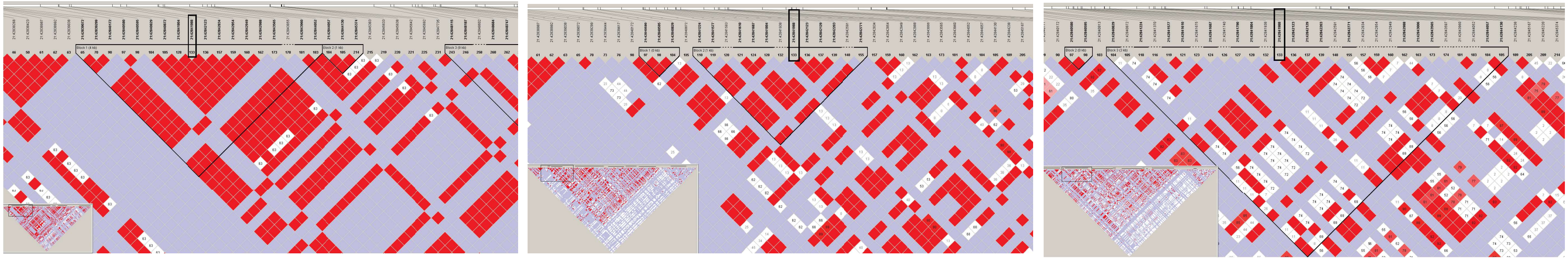
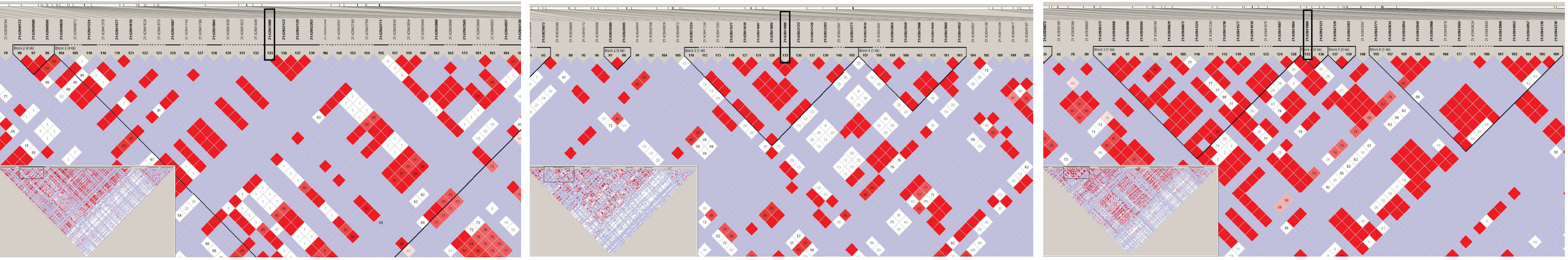
Supplementary Figure 1

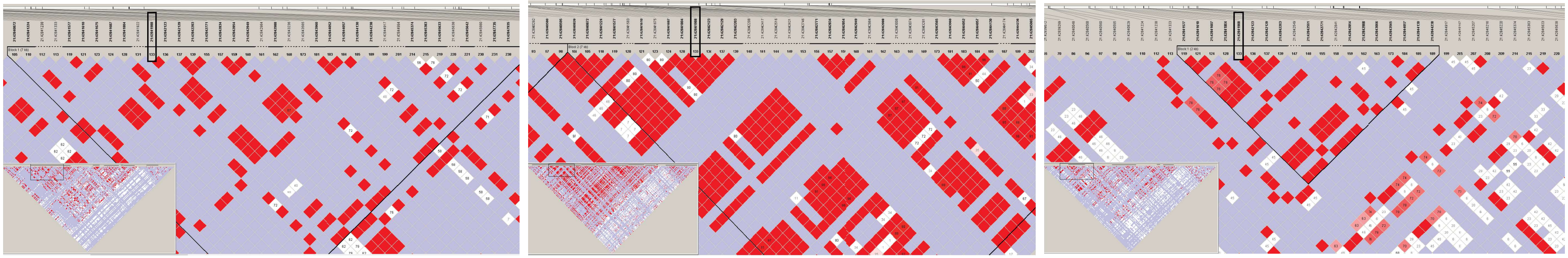




AMERICA CENTRAL ASIA CAUCASUS



EUROPE SOUTH ASIA SOUTHEAST ASIA ISLAND



SOUTHEAST ASIA MAINLAND SIBERIA WEST ASIA

Supplementary Figure 2

Supplementary Figure 3

Supplementary Table 1. The details of SNPs observed in TMPRSS2 gene. MAF- Minor Allale Frequency, AMR-America, CA-Central Asia, CAU-Caucasus, EU-Europe, SA-South Asia, SEAI-Southeast Asia Island, SEAM-Southeast Asia Mainland SIB-Siberia, WA-West Asia.

S. No.	rs number	Build 37	Build 38	Ref. Allele	Alt. Allele	Functional Consequence	Total MAF	AMR MAF	CA MAF	CAU MAF	EU MAF	SA MAF	SEAI MAF	SEAM MAF	SIB MAF	WA MAF
1	rs547758146	42836222	41464295	A	C	downstream_gene_variant	0	0	0	0	0.0198	0	0	0	0	0
2	rs1308901935	42836290	41464363	C	T	downstream_gene_variant	0	0	0	0	0	0	0	0	0	0
3	rs559811756	42836341	41464414	A	G	downstream_gene_variant	0	0	0	0	0	0	0	0	0	0
4	rs8129769	42836344	41464417	A	G	downstream_gene_variant	0	0	0	0	0	0	0	0	0	0
5	rs553400003	42836389	41464462	A	G	downstream_gene_variant	0	0	0	0	0	0	0	0	0	0
6	rs768729764	42836417	41464490	T	C	downstream_gene_variant	0	0	0	0	0	0	0	0	0	0
7	-	42836476	41464549	A	G	downstream_gene_variant	0.3462	0.3462	0.2292	0.2179	0.2277	0.32	0.3444	0.4167	0.4583	0.05
8	rs76000363	42836477	41464550	A	G	downstream_gene_variant	0.07692	0.07692	0.0833	0.07692	0.1683	0.06	0.02222	0.08333	0.06019	0.025
9	-	42836485	41464558	A	G	3_prime_UTR_variant	0	0	0	0	0	0	0	0	0.00463	0
10	-	42836496	41464569	T	C	3_prime_UTR_variant	0.3462	0.3462	0.2292	0.2179	0.2277	0.32	0.3333	0.4167	0.463	0.075
11	rs929663872	42836594	41464667	C	G	3_prime_UTR_variant	0	0	0	0	0	0	0	0	0	0
12	rs185078457	42836613	41464686	T	C	3_prime_UTR_variant	0	0	0.0208	0	0.0099	0	0	0	0	0
13	-	42836664	41464737	C	T	3_prime_UTR_variant	0.03846	0.03846	0	0	0	0	0	0	0	0
14	rs112657409	42836672	41464745	T	C	3_prime_UTR_variant	0	0	0	0.01282	0.005	0	0.04444	0.08333	0.03241	0
15	rs2838038	42836685	41464758	T	A	3_prime_UTR_variant	0.07692	0.07692	0.0833	0.07692	0.1683	0.06	0.02222	0.08333	0.06019	0.025
16	rs377038375	42836701	41464774	C	T	3_prime_UTR_variant	0	0	0	0	0	0	0.06667	0	0	0
17	-	42836729	41464802	A	G	3_prime_UTR_variant	0.4231	0.4231	0.1458	0.141	0.0594	0.24	0.4444	0.4722	0.3981	0.025
18	-	42836751	41464824	T	A	3_prime_UTR_variant	0.3462	0.3462	0.2292	0.2179	0.2277	0.32	0.3444	0.4167	0.4583	0.05
19	-	42836873	41464946	G	A	3_prime_UTR_variant	0	0	0	0	0	0	0	0	0	0
20	rs117652812	42836891	41464964	T	C	3_prime_UTR_variant	0	0	0.0417	0.01282	0.0099	0	0.05556	0	0.02315	0
21	-	42836921	41464994	A	G	3_prime_UTR_variant	0	0	0	0	0.005	0	0	0	0	0
22	rs17001042	42836967	41465040	A	G	3_prime_UTR_variant	0	0	0	0	0	0.02	0.07778	0.02778	0	0
23	rs572422499	42836971	41465044	T	C	3_prime_UTR_variant	0	0	0	0.01282	0	0	0	0	0	0
24	rs11910678	42836986	41465059	C	T	3_prime_UTR_variant	0	0	0	0.01282	0.005	0	0.05556	0.08333	0.03241	0
25	rs183418223	42837069	41465142	A	G	3_prime_UTR_variant	0	0	0	0	0	0	0	0	0	0
26	rs1453389785	42837277	41465350	T	C	3_prime_UTR_variant	0	0	0	0	0	0.02	0	0	0	0
27	rs377348479	42837392	41465465	A	G	3_prime_UTR_variant	0	0	0	0	0	0	0.01111	0.02778	0	0
28	rs75317729	42837502	41465575	C	T	3_prime_UTR_variant	0	0	0	0	0	0	0	0	0	0

29	rs771633249	42837518	41465591	T	C	3_prime_UTR_variant	0	0	0	0	0	0	0	0	0	0
30	rs370421631	42837531	41465604	A	G	3_prime_UTR_variant	0	0	0	0	0	0	0.01111	0	0	0
31	rs77675406	42837534	41465607	A	G	3_prime_UTR_variant	0.07692	0.07692	0.0833	0.07692	0.1683	0.06	0.02222	0.08333	0.06019	0.025
32	rs542458473	42837636	41465709	C	G	3_prime_UTR_variant	0	0	0	0	0	0.04	0	0	0	0
33	rs12627374	42837691	41465764	T	C	3_prime_UTR_variant	0	0	0.0625	0.05128	0.0149	0.12	0.3	0.05556	0.05556	0
34	rs567103273	42837751	41465824	G	A	3_prime_UTR_variant	0	0	0	0	0	0	0	0	0	0
35	rs372405355	42837754	41465827	C	T	3_prime_UTR_variant	0	0	0	0	0	0	0.06667	0	0	0
36	rs996615575	42837756	41465829	C	G	3_prime_UTR_variant	0	0	0	0	0	0	0.01111	0	0	0
37	rs62217525	42837848	41465921	T	C	3_prime_UTR_variant	0	0	0.0208	0.07692	0.0446	0	0	0	0.00463	0.2
38	rs146564124	42837861	41465934	T	C	3_prime_UTR_variant	0	0	0	0.01282	0.0198	0	0	0	0.00463	0
39	rs780868244	42837913	41465986	G	A	3_prime_UTR_variant	0	0	0	0	0	0	0.02222	0	0	0
40	rs77996454	42837928	41466001	A	G	3_prime_UTR_variant	0	0	0	0	0	0	0	0	0	0
41	rs374981614	42838036	41466109	A	G	3_prime_UTR_variant	0	0	0	0	0	0	0.06667	0	0	0
42	rs118028230	42838104	41466177	C	G	intron_variant	0	0	0	0.01282	0.005	0	0.04444	0.08333	0.03241	0
43	rs369092228	42838114	41466187	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
44	rs73905370	42838138	41466211	T	A	intron_variant	0.07692	0.07692	0.0833	0.07692	0.1683	0.06	0.02222	0.08333	0.06019	0.025
45	rs55896064	42838198	41466271	A	G	intron_variant	0.07692	0.07692	0.0833	0.07692	0.1683	0.06	0.02222	0.08333	0.06019	0.025
46	rs57474639	42838268	41466341	T	C	intron_variant	0.07692	0.07692	0.0833	0.07692	0.1683	0.06	0.02222	0.08333	0.06019	0.025
47	rs79971314	42838269	41466342	A	G	intron_variant	0	0	0	0	0	0.02	0.06667	0.02778	0	0.05
48	rs73372161	42838279	41466352	A	G	intron_variant	0	0	0	0	0	0.02	0	0.02778	0	0.05
49	rs370634518	42838411	41466484	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0
50	rs61459778	42838423	41466496	G	C	intron_variant	0.07692	0.07692	0.0833	0.07692	0.1683	0.08	0.1	0.1111	0.06019	0.075
51	rs145024812	42838456	41466529	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
52	rs377591443	42838514	41466587	C	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
53	rs115975538	42838629	41466702	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0
54	rs118133613	42838665	41466738	A	G	intron_variant	0	0	0	0	0.005	0	0	0	0	0
55	rs143595083	42838707	41466780	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
56	rs148038688	42838711	41466784	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
57	rs546913068	42838803	41466876	G	C	intron_variant	0	0	0	0	0	0	0	0	0.00926	0
58	-	42838860	41466933	T	A	intron_variant	0	0	0	0	0	0	0	0.02778	0	0
59	rs534326511	42838913	41466986	T	C	intron_variant	0	0	0	0	0	0	0	0	0.00926	0
60	rs1033026879	42838937	41467010	A	C	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
61	rs73905371	42838987	41467060	G	C	intron_variant	0.07692	0.07692	0.0833	0.07692	0.1683	0.06	0.02222	0.08333	0.06019	0.025
62	rs73372163	42838992	41467065	A	G	intron_variant	0.07692	0.07692	0.0833	0.07692	0.1683	0.08	0.1	0.1111	0.06019	0.075
63	rs73372166	42839038	41467111	A	G	intron_variant	0.07692	0.07692	0.0833	0.07692	0.1683	0.08	0.1	0.1111	0.06019	0.075

64	rs113562865	42839044	41467117	T	C	intron_variant	0	0	0	0	0	0.02	0	0.02778	0	0.05
65	-	42839072	41467145	G	T	intron_variant	0.4231	0.4231	0.1458	0.141	0.0594	0.24	0.4556	0.4722	0.4028	0.025
66	-	42839196	41467269	G	A	intron_variant	0	0	0	0	0	0	0.03333	0	0	0
67	rs368452629	42839233	41467306	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
68	rs981602772	42839261	41467334	T	A	intron_variant	0	0	0	0	0.005	0	0	0	0	0
69	rs371583992	42839278	41467351	G	T	intron_variant	0	0	0	0	0	0	0	0	0	0
70	-	42839299	41467372	C	G	intron_variant	0.4231	0.4231	0.0833	0.07692	0.0396	0.12	0.2	0.3333	0.3102	0.025
71	-	42839361	41467434	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
72	rs73372168	42839362	41467435	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
73	rs910388295	42839444	41467517	G	C	intron_variant	0	0	0.0208	0	0.0099	0	0	0	0.00463	0
74	rs192955773	42839545	41467618	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
75	rs961773771	42839588	41467661	G	C	intron_variant	0	0	0	0	0	0	0	0	0	0
76	rs1429823013	42839617	41467690	G	C	intron_variant	0	0	0.0208	0	0	0	0	0	0	0
77	rs183984610	42839626	41467699	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
78	rs142750000	42839661	41467734	T	C	splice_region_variant,synonymous_variant	0	0	0	0	0.005	0	0	0	0	0
79	rs374377315	42839784	41467857	T	C	synonymous_variant	0	0	0	0	0.005	0	0	0	0	0
80	rs147359020	42839865	41467938	A	G	intron_variant	0	0	0	0	0	0.04	0.01111	0	0.00463	0
81	rs1016428148	42839900	41467973	G	C	intron_variant	0	0	0	0	0	0	0	0	0	0
82	rs139015396	42839982	41468055	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
83	rs149855493	42839993	41468066	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
84	rs1014364281	42839999	41468072	G	C	intron_variant	0	0	0	0	0	0	0	0	0	0
85	rs144823388	42840029	41468102	T	A	intron_variant	0	0	0	0	0	0	0	0	0	0
86	rs191394761	42840048	41468121	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0.05
87	rs76315847	42840130	41468203	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
88	rs146605032	42840168	41468241	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
89	rs1017698498	42840171	41468244	T	C	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
90	rs743542	42840172	41468245	A	G	intron_variant	0.2692	0.2692	0.2083	0.1154	0.1287	0.18	0.3889	0.25	0.213	0
91	rs190618812	42840187	41468260	A	G	intron_variant	0	0	0	0	0	0	0	0.02778	0.00463	0
92	-	42840267	41468340	A	G	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
93	rs572963642	42840292	41468365	C	G	intron_variant	0	0	0	0	0	0	0	0	0.00926	0
94	rs148125094	42840394	41468467	T	C	missense_variant	0	0	0	0	0	0	0	0	0	0
95	rs375874663	42840504	41468577	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
96	rs73372170	42840568	41468641	G	C	intron_variant	0	0	0	0	0	0.02	0.06667	0.02778	0	0.05
97	COSV59827297	42840580	41468653	T	C	intron_variant	0.07692	0.07692	0.3542	0.2308	0.3218	0.34	0.3444	0.25	0.3843	0.025
98	-	42840595	41468668	G	C	intron_variant	0.07692	0.07692	0.3542	0.2308	0.3218	0.34	0.3444	0.25	0.3843	0.025

99	rs143672898	42840655	41468728	T	C	intron_variant	0	0	0	0	0	0.02	0	0	0	0
100	rs748580091	42840740	41468813	T	A	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
101	rs146797606	42840758	41468831	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
102	rs573343651	42840760	41468833	C	A	intron_variant	0	0	0	0	0	0.02	0	0.02778	0	0
103	rs1443771075	42840813	41468886	T	C	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
104	rs7283324	42840829	41468902	T	C	intron_variant	0.3462	0.3462	0.3125	0.2179	0.3267	0.24	0.4667	0.4167	0.3056	0.075
105	-	42840872	41468945	T	C	intron_variant	0.4231	0.4231	0.0625	0.02564	0.0297	0.12	0.1667	0.3333	0.3102	0
106	rs150382508	42841054	41469127	C	A	intron_variant	0	0	0	0	0	0	0	0	0	0
107	rs115774576	42841073	41469146	A	T	intron_variant	0	0	0	0	0	0	0	0	0	0
108	rs114549926	42841128	41469201	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
109	rs376403654	42841168	41469241	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
110	rs7279603	42841224	41469297	C	T	intron_variant	0	0	0.3333	0.3077	0.2475	0.22	0.2889	0.2222	0.1991	0.375
111	rs971603670	42841234	41469307	C	G	intron_variant	0	0	0	0	0	0	0.03333	0	0	0
112	rs7278739	42841238	41469311	A	G	intron_variant	0	0	0	0	0	0.02	0.07778	0.02778	0	0.05
113	rs7278627	42841333	41469406	A	C	intron_variant	0	0	0	0	0	0.02	0	0.02778	0	0.05
114	rs149109132	42841334	41469407	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
115	rs374608719	42841359	41469432	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
116	rs185416185	42841370	41469443	T	C	intron_variant	0	0	0	0.01282	0.0099	0	0	0	0	0
117	rs146052428	42841445	41469518	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
118	rs370663590	42841554	41469627	G	C	intron_variant	0	0	0	0	0	0	0	0	0	0
119	rs2070793	42841577	41469650	G	A	intron_variant	0	0	0.3333	0.3077	0.2475	0.22	0.2889	0.2222	0.1991	0.375
120	rs117898838	42841583	41469656	A	G	intron_variant	0	0	0.0208	0	0	0	0	0	0.00463	0
121	rs2070792	42841610	41469683	A	G	intron_variant	0	0	0.3333	0.3077	0.2475	0.22	0.2889	0.2222	0.1991	0.375
122	-	42841629	41469702	C	A	intron_variant	0	0	0	0	0.005	0	0	0	0	0
123	rs2070791	42841675	41469748	G	C	intron_variant	0	0	0	0.01282	0.005	0	0.04444	0.08333	0.03241	0
124	rs2070790	42841687	41469760	C	G	intron_variant	0	0	0.3333	0.3077	0.2475	0.2	0.2889	0.1944	0.1991	0.325
125	rs373678323	42841694	41469767	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
126	rs142769034	42841740	41469813	T	C	intron_variant	0	0	0	0.01282	0.0099	0	0	0	0	0
127	rs111572592	42841790	41469863	A	G	intron_variant	0	0	0	0.05128	0.005	0	0	0	0	0
128	rs2070789	42841804	41469877	T	C	intron_variant	0.3462	0.3462	0.3125	0.2179	0.3267	0.24	0.4667	0.4167	0.3056	0.075
129	rs1461069953	42841830	41469903	C	T	intron_variant	0	0	0	0	0.005	0	0	0	0	0
130	rs141603473	42841910	41469983	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0
131	rs542946711	42841922	41469995	G	A	intron_variant	0	0	0	0	0.0099	0	0	0.02778	0	0
132	rs113564116	42841938	41470011	C	T	intron_variant	0	0	0.0208	0.01282	0.0297	0	0	0	0	0
133	rs2070788	42841988	41470061	G	A	intron_variant	0.3462	0.3462	0.3542	0.4744	0.4257	0.44	0.3222	0.3889	0.4954	0.4

134	rs139432971	42842046	41470119	G	C	intron_variant	0	0	0	0	0	0	0	0	0	0
135	rs189832305	42842079	41470152	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
136	-	42842123	41470196	A	C	intron_variant	0.3462	0.3462	0.3542	0.4744	0.4257	0.44	0.2444	0.3889	0.4954	0.4
137	rs2070787	42842129	41470202	G	T	intron_variant	0	0	0.3333	0.3077	0.2475	0.2	0.2778	0.1944	0.1991	0.325
138	rs376499029	42842152	41470225	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
139	rs2070786	42842203	41470276	C	T	intron_variant	0	0	0.3333	0.3077	0.2475	0.2	0.2889	0.1944	0.1991	0.325
140	rs758426874	42842208	41470281	A	G	intron_variant	0	0	0	0	0	0	0	0	0.00926	0
141	-	42842417	41470490	G	A	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
142	rs547168890	42842451	41470524	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
143	rs373469999	42842492	41470565	C	G	intron_variant	0	0	0	0	0	0	0	0	0	0
144	rs1406734513	42842516	41470589	A	C	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
145	rs78503214	42842543	41470616	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
146	-	42842546	41470619	T	C	intron_variant	0	0	0	0	0.005	0	0	0	0	0
147	rs749103473	42842549	41470622	A	T	intron_variant	0	0	0	0	0	0	0	0	0	0.025
148	rs61735794	42842591	41470664	T	C	synonymous_variant	0	0	0.0208	0.01282	0.0248	0.02	0.01111	0	0	0.05
149	-	42842621	41470694	C	T	synonymous_variant	0	0	0	0	0	0	0	0	0.00463	0
150	rs61735795	42842623	41470696	A	G	missense_variant	0	0	0	0	0	0	0	0	0	0
151	rs143712818	42842705	41470778	T	G	intron_variant	0	0	0	0	0	0	0	0	0	0
152	rs573482152	42842740	41470813	A	T	intron_variant	0	0	0	0	0.005	0	0	0	0	0
153	rs1160357228	42842746	41470819	T	C	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
154	-	42842759	41470832	A	C	intron_variant	0	0	0	0	0.005	0	0	0	0	0
155	rs28524972	42842771	41470844	G	C	intron_variant	0	0	0.3333	0.2949	0.2376	0.2	0.2778	0.1944	0.1991	0.325
156	-	42842823	41470896	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0
157	-	42842834	41470907	T	C	intron_variant	0.4231	0.4231	0.0625	0.02564	0.0297	0.12	0.2	0.3333	0.3102	0
158	rs544946928	42842841	41470914	T	C	intron_variant	0	0	0	0	0	0.02	0	0	0	0.025
159	-	42842854	41470927	C	A	intron_variant	0.4231	0.4231	0.0625	0.02564	0.0297	0.14	0.2	0.3611	0.3102	0.05
160	-	42842949	41471022	T	C	intron_variant	0.4231	0.4231	0.0625	0.02564	0.0297	0.12	0.2	0.3333	0.3102	0
161	rs1000072663	42842984	41471057	G	A	intron_variant	0	0	0	0	0	0	0	0.02778	0.00463	0
162	rs9305744	42842988	41471061	A	G	intron_variant	0.3462	0.3462	0.3125	0.2308	0.3366	0.24	0.4667	0.4167	0.3056	0.075
163	rs35050484	42843006	41471079	A	G	intron_variant	0	0	0.0625	0.0641	0.0297	0	0	0	0.00463	0.05
164	rs372665499	42843031	41471104	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
165	rs1198022001	42843074	41471147	G	C	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
166	rs375719922	42843078	41471151	C	T	intron_variant	0	0	0	0	0	0	0.02222	0	0	0
167	rs142834250	42843107	41471180	G	T	intron_variant	0	0	0	0	0	0	0	0	0	0
168	rs370896169	42843236	41471309	C	T	intron_variant	0	0	0	0	0	0	0	0.02778	0	0

169	rs952726028	42843281	41471354	C	T	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
170	rs1016288269	42843352	41471425	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
171	rs377410798	42843419	41471492	C	G	intron_variant	0	0	0	0	0	0	0	0	0	0
172	rs187052796	42843532	41471605	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
173	rs467375	42843565	41471638	A	G	intron_variant	0.07692	0.07692	0.2917	0.4487	0.396	0.42	0.05556	0.02778	0.1806	0.45
174	-	42843597	41471670	T	C	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
175	rs1015613248	42843624	41471697	T	C	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
176	rs116511699	42843655	41471728	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
177	rs370478006	42843703	41471776	T	A	intron_variant	0	0	0	0	0	0	0	0	0	0
178	COSV59828007	42843855	41471928	C	G	missense_variant	0.03846	0.03846	0	0	0	0	0	0	0	0
179	rs201320664	42843935	41472008	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
180	rs187078345	42843940	41472013	A	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
181	COSV59823391	42843960	41472033	A	G	intron_variant	0.4231	0.4231	0.0625	0.02564	0.0297	0.12	0.2	0.3333	0.2917	0
182	rs937260183	42844014	41472087	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
183	COSV59821944	42844052	41472125	T	G	intron_variant	0.4231	0.4231	0.0625	0.02564	0.0297	0.12	0.2	0.3333	0.287	0
184	COSV59824040	42844057	41472130	G	A	intron_variant	0.3462	0.3462	0.3542	0.4744	0.4257	0.46	0.2556	0.3611	0.4954	0.45
185	rs7364088	42844130	41472203	A	G	intron_variant	0.3462	0.3462	0.3333	0.2564	0.3465	0.24	0.4667	0.4167	0.3102	0.075
186	rs182254633	42844168	41472241	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
187	rs146957681	42844174	41472247	T	C	intron_variant	0	0	0	0	0	0	0	0	0.00926	0
188	rs76135088	42844202	41472275	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
189	rs28548447	42844238	41472311	A	G	intron_variant	0	0	0.3333	0.2949	0.2475	0.22	0.2111	0.1944	0.1991	0.325
190	rs375524422	42844257	41472330	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
191	rs114844880	42844262	41472335	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
192	rs79065748	42844498	41472571	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0
193	rs986882653	42844642	41472715	G	C	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
194	rs116606027	42844713	41472786	A	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
195	rs368644630	42844733	41472806	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
196	rs112980967	42844765	41472838	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
197	rs184164037	42844780	41472853	C	T	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
198	-	42844870	41472943	A	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
199	rs73372182	42844917	41472990	A	C	intron_variant	0	0	0	0	0	0.02	0	0.02778	0	0.05
200	rs143097165	42844925	41472998	A	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
201	rs766846682	42844994	41473067	T	C	intron_variant	0	0	0	0	0	0	0	0.02778	0	0
202	rs117827300	42845065	41473138	A	G	intron_variant	0	0	0	0	0.0198	0	0	0	0.06019	0
203	rs188514624	42845101	41473174	C	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0

204	rs374689537	42845160	41473233	T	C	intron_variant	0	0	0	0	0	0	0.06667	0	0	0
205	rs73230068	42845167	41473240	C	G	intron_variant	0	0	0.0208	0.05128	0.0248	0.02	0	0	0	0.05
206	rs990674063	42845180	41473253	T	C	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
207	rs75168613	42845207	41473280	A	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0.05
208	rs113288437	42845216	41473289	G	T	intron_variant	0	0	0	0	0	0	0.01111	0	0	0.05
209	rs140141551	42845220	41473293	A	C	intron_variant	0	0	0	0.02564	0.0248	0	0	0	0	0.025
210	rs774049600	42845257	41473330	T	C	synonymous_variant	0	0	0	0	0	0	0	0	0	0
211	rs143291395	42845260	41473333	A	G	synonymous_variant	0	0	0	0	0	0	0	0	0	0
212	rs113436669	42845278	41473351	A	G	synonymous_variant	0	0	0	0	0	0	0	0	0	0
213	rs2298658	42845359	41473432	T	C	synonymous_variant	0	0	0	0	0	0	0	0	0.02315	0
214	rs2298659	42845374	41473447	A	G	synonymous_variant	0.3462	0.3462	0.25	0.1795	0.3168	0.16	0.1667	0.3333	0.2454	0.075
215	rs17854725	42845383	41473456	G	A	synonymous_variant	0.3462	0.3462	0.4375	0.4744	0.4703	0.48	0.1444	0.2222	0.3426	0.35
216	rs756848444	42845471	41473544	A	G	intron_variant	0	0	0	0	0.005	0	0	0	0	0
217	rs377496737	42845489	41473562	T	C	intron_variant	0	0	0	0	0.005	0	0	0	0	0
218	rs113928389	42845559	41473632	A	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
219	rs2298660	42845633	41473706	T	C	intron_variant	0.3462	0.3462	0.2083	0.1538	0.2822	0.16	0.1667	0.3611	0.2454	0.075
220	rs55964536	42845638	41473711	T	C	intron_variant	0.07692	0.07692	0.2708	0.4615	0.4158	0.42	0.04444	0.02778	0.1852	0.4
221	rs2298661	42845642	41473715	A	C	intron_variant	0.3462	0.3462	0.3125	0.2436	0.3119	0.22	0.4667	0.4167	0.3102	0.025
222	rs1039732893	42845655	41473728	A	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
223	-	42845658	41473731	C	G	intron_variant	0	0	0	0	0	0	0	0	0	0
224	rs950562638	42845665	41473738	A	G	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
225	rs559830930	42845692	41473765	G	A	intron_variant	0.03846	0.03846	0	0	0	0	0	0	0	0
226	rs374850529	42845705	41473778	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
227	rs77511690	42845740	41473813	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
228	rs368994585	42845816	41473889	A	G	intron_variant	0	0	0	0	0	0	0.07778	0	0	0
229	rs371053759	42845834	41473907	T	G	intron_variant	0	0	0	0	0	0	0	0	0	0
230	-	42845880	41473953	T	G	intron_variant	0	0	0	0	0	0	0	0.02778	0	0
231	rs3787946	42847735	41475808	C	G	intron_variant	0.3462	0.3462	0.3125	0.2436	0.3119	0.18	0.4778	0.4167	0.3102	0.025
232	rs374510753	42847763	41475836	T	C	intron_variant	0	0	0	0	0	0	0.02222	0	0	0
233	rs180784757	42847764	41475837	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
234	rs375615614	42847773	41475846	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
235	rs371965055	42847798	41475871	T	C	intron_variant	0	0	0	0	0	0.02	0	0	0	0
236	rs117888036	42847846	41475919	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
237	rs368735421	42847909	41475982	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
238	rs66575656	42847935	41476008	T	C	intron_variant	0	0	0.3542	0.2692	0.2426	0.22	0.2222	0.1944	0.1944	0.275

239	rs1310846114	42848016	41476089	T	C	intron_variant	0	0	0	0	0	0	0	0	0.00926	0
240	rs189425119	42848017	41476090	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
241	-	42848038	41476111	C	A	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
242	rs80027429	42848096	41476169	A	G	intron_variant	0	0	0	0.03846	0.0099	0	0	0	0	0
243	-	42848115	41476188	G	C	intron_variant	0.4231	0.4231	0.0625	0.02564	0.0297	0.12	0.1778	0.3333	0.3102	0
244	rs367879274	42848178	41476251	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
245	rs8129582	42848183	41476256	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
246	-	42848187	41476260	C	T	intron_variant	0.07692	0.07692	0.375	0.2692	0.3416	0.36	0.2778	0.2222	0.3796	0.075
247	rs62217527	42848219	41476292	T	C	intron_variant	0	0	0.0208	0.1026	0.0842	0.02	0	0	0.00926	0.175
248	rs112213575	42848274	41476347	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
249	rs527284833	42848324	41476397	G	A	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
250	COSV59826599	42848363	41476436	A	C	intron_variant	0	0	0	0	0	0.02	0	0	0	0
251	rs113034290	42848371	41476444	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
252	rs111383922	42848398	41476471	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
253	rs75756279	42848457	41476530	T	C	intron_variant	0	0	0	0.03846	0.0099	0	0	0	0	0
254	rs200615061	42848494	41476567	C	A	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
255	rs74423429	42848579	41476652	A	G	intron_variant	0	0	0.0417	0.01282	0.0347	0	0	0	0	0
256	rs1043973308	42848580	41476653	G	A	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
257	rs375891843	42848591	41476664	G	T	intron_variant	0	0	0	0	0.005	0	0	0	0	0
258	-	42848602	41476675	C	T	intron_variant	0.03846	0.03846	0	0	0	0	0	0	0	0
259	rs1303041038	42848640	41476713	A	C	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
260	rs9985159	42848684	41476757	T	C	intron_variant	0.3462	0.3462	0.3125	0.2436	0.3119	0.24	0.4778	0.4444	0.3102	0.075
261	rs148136016	42848689	41476762	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
262	rs113506821	42848747	41476820	T	C	intron_variant	0.07692	0.07692	0.1042	0.07692	0.0891	0.04	0	0	0.1343	0
263	rs931996263	42848765	41476838	C	T	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
264	rs118108663	42848819	41476892	T	C	intron_variant	0	0	0	0	0	0	0	0	0.03704	0
265	rs76973757	42848821	41476894	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
266	-	42848835	41476908	T	C	intron_variant	0.07692	0.07692	0.375	0.2692	0.3416	0.36	0.3444	0.2222	0.3796	0.075
267	rs1380427461	42848924	41476997	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0.025
268	rs375837256	42848951	41477024	G	A	intron_variant	0	0	0	0	0	0	0.03333	0	0	0
269	-	42849089	41477162	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0.025
270	-	42849097	41477170	G	A	intron_variant	0.07692	0.07692	0.3958	0.2692	0.3515	0.36	0.3444	0.2222	0.3796	0.075
271	rs886737856	42849102	41477175	T	C	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
272	-	42849137	41477210	T	C	intron_variant	0.07692	0.07692	0.3958	0.2692	0.3515	0.36	0.3444	0.2222	0.3796	0.075
273	rs150633108	42849163	41477236	T	C	intron_variant	0	0	0	0	0	0.04	0.01111	0	0.00463	0

274	rs58978895	42849228	41477301	T	C	intron_variant	0	0	0	0	0	0.06	0.02222	0.02778	0	0.05
275	-	42849242	41477315	C	T	intron_variant	0.07692	0.07692	0.3958	0.2821	0.3515	0.36	0.3444	0.2222	0.3796	0.075
276	-	42849258	41477331	C	T	intron_variant	0.07692	0.07692	0.3958	0.2821	0.3515	0.36	0.3444	0.2222	0.3796	0.075
277	rs561179495	42849383	41477456	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
278	rs144576889	42849576	41477649	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
279	rs565720190	42849702	41477775	A	G	intron_variant	0	0	0	0	0	0.02	0	0	0	0
280	-	42849773	41477846	A	C	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
281	-	42849781	41477854	A	C	intron_variant	0	0	0	0.01282	0.005	0	0	0	0.00463	0
282	-	42849783	41477856	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
283	rs548267325	42849802	41477875	A	G	intron_variant	0	0	0	0	0.005	0	0	0	0	0
284	rs61325328	42849821	41477894	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
285	-	42849893	41477966	A	G	intron_variant	0	0	0	0	0	0	0	0.02778	0	0
286	rs576215861	42849909	41477982	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0
287	rs953081299	42849917	41477990	T	C	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
288	rs1259681953	42849918	41477991	A	G	intron_variant	0	0	0	0	0	0.02	0	0	0	0
289	-	42849929	41478002	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
290	rs115967323	42849951	41478024	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
291	-	42850038	41478111	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0.025
292	rs9636988	42850045	41478118	C	T	intron_variant	0.2692	0.2692	0.3333	0.2564	0.2475	0.24	0.2222	0.1667	0.1944	0.275
293	-	42850051	41478124	T	G	intron_variant	0	0	0	0	0	0	0	0	0	0.025
294	rs4818239	42850075	41478148	C	T	intron_variant	0.07692	0.07692	0.2708	0.4487	0.4158	0.4	0.04444	0.08333	0.1759	0.325
295	rs116170128	42850110	41478183	C	A	intron_variant	0	0	0.0208	0.01282	0.0347	0.02	0.01111	0	0	0.05
296	rs543337196	42850238	41478311	T	C	intron_variant	0	0	0	0	0	0.02	0	0	0	0
297	rs139816990	42850239	41478312	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
298	rs9983330	42850253	41478326	G	A	intron_variant	0.07692	0.07692	0.3333	0.2692	0.3168	0.18	0.4778	0.3889	0.3194	0.025
299	-	42850281	41478354	T	C	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
300	rs116577479	42850370	41478443	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
301	-	42850549	41478622	G	A	intron_variant	0	0	0	0	0	0	0	0	0.00926	0
302	rs1339402659	42850749	41478822	G	T	intron_variant	0	0	0	0	0	0	0	0.02778	0	0
303	rs374961008	42850870	41478943	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
304	rs73372191	42850882	41478955	T	A	intron_variant	0	0	0	0	0	0.06	0.02222	0.02778	0	0.05
305	rs9974995	42850911	41478984	T	C	intron_variant	0.2692	0.2692	0.3333	0.2692	0.2475	0.24	0.2222	0.1667	0.1852	0.25
306	rs766178676	42850916	41478989	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0.025
307	rs893281455	42850933	41479006	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0.025
308	-	42850957	41479030	T	C	intron_variant	0	0	0	0.01282	0	0	0	0	0	0

309	rs73372193	42850966	41479039	C	A	intron_variant	0	0	0	0	0	0.06	0.02222	0.02778	0	0.05
310	rs9974933	42850977	41479050	G	A	intron_variant	0.2692	0.2692	0.3333	0.2692	0.2475	0.24	0.2222	0.1944	0.1852	0.25
311	rs9975014	42851006	41479079	G	A	intron_variant	0.2692	0.2692	0.3333	0.2692	0.2475	0.24	0.2222	0.1944	0.1852	0.25
312	rs141788162	42851134	41479207	A	G	synonymous_variant	0	0	0	0	0.0198	0	0	0	0.05556	0
313	rs201661208	42851135	41479208	A	G	missense_variant	0	0	0	0	0	0	0	0	0	0.025
314	rs112247445	42851257	41479330	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
315	rs377385043	42851258	41479331	G	A	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
316	rs112985398	42851268	41479341	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
317	rs145292327	42851303	41479376	G	A	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
318	-	42851310	41479383	A	G	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
319	rs538022064	42851370	41479443	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
320	rs117432315	42851374	41479447	A	G	intron_variant	0	0	0.0208	0	0	0	0	0	0	0
321	rs137871202	42851376	41479449	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
322	rs199575615	42851419	41479492	G	A	intron_variant	0	0	0	0	0	0	0	0	0.00926	0
323	rs117941520	42851423	41479496	A	G	intron_variant	0	0	0	0	0	0.02	0	0	0.00463	0
324	rs915823	42851454	41479527	C	A	intron_variant	0.07692	0.07692	0.25	0.1795	0.2871	0.08	0.1778	0.3333	0.2546	0.05
325	-	42851575	41479648	G	T	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
326	-	42851578	41479651	A	C	intron_variant	0	0	0.0208	0	0	0	0	0	0	0
327	-	42851588	41479661	G	C	intron_variant	0	0	0	0	0	0	0.03333	0	0	0
328	rs184380117	42851644	41479717	A	G	intron_variant	0	0	0.0417	0	0	0	0	0	0.02778	0
329	rs553747026	42851723	41479796	G	A	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
330	rs1368879178	42851727	41479800	G	A	intron_variant	0	0	0	0	0	0	0	0	0.01852	0
331	rs1051561804	42851731	41479804	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
332	rs875393	42851815	41479888	A	G	intron_variant	0	0	0.1458	0.07692	0.1139	0.04	0.1222	0.1944	0.1944	0.025
333	rs184764113	42851826	41479899	A	G	intron_variant	0	0	0	0	0	0	0.03333	0	0	0
334	rs372876361	42851846	41479919	T	G	intron_variant	0	0	0	0	0	0	0.02222	0	0	0
335	-	42851931	41480004	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
336	rs149601802	42851965	41480038	T	C	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
337	rs967358213	42852025	41480098	T	C	intron_variant	0	0	0	0	0	0.02	0	0	0	0
338	rs734055	42852170	41480243	A	T	intron_variant	0	0	0	0	0.005	0	0	0	0	0
339	rs1035659632	42852258	41480331	G	T	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
340	rs34561135	42852311	41480384	A	G	intron_variant	0	0	0.0417	0.05128	0.0891	0.04	0	0	0.02315	0.025
341	rs373852195	42852316	41480389	A	G	intron_variant	0	0	0	0	0.0149	0	0.06667	0	0	0
342	rs734056	42852320	41480393	A	C	intron_variant	0.07692	0.07692	0.2708	0.4231	0.4059	0.4	0.04444	0.05556	0.1713	0.35
343	rs186734573	42852365	41480438	T	C	intron_variant	0	0	0	0	0.0099	0	0	0	0	0

344	rs79397218	42852382	41480455	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
345	rs61735789	42852435	41480508	A	G	synonymous_variant	0	0	0.0208	0.01282	0.0099	0	0	0	0	0
346	rs12329760	42852497	41480570	T	C	missense_variant	0.07692	0.07692	0.3333	0.2821	0.3168	0.18	0.4444	0.3056	0.3194	0.05
347	-	42852545	41480618	A	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
348	rs378501	42852591	41480664	G	A	intron_variant	0	0	0	0	0	0	0.05556	0.1111	0	0
349	rs1601575263	42852673	41480746	A	C	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
350	rs1181456418	42852722	41480795	T	C	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
351	rs370654859	42852797	41480870	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
352	-	42852847	41480920	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
353	rs866828358	42852904	41480977	T	C	intron_variant	0	0	0.0208	0	0	0	0	0	0	0
354	rs935832638	42852907	41480980	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
355	rs112209215	42852922	41480995	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
356	rs75833467	42852952	41481025	A	G	intron_variant	0	0	0	0.03846	0.0347	0	0	0	0.00463	0.05
357	-	42853026	41481099	C	T	intron_variant	0.03846	0.03846	0	0	0	0	0	0	0	0
358	rs370641046	42853045	41481118	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0.025
359	rs4290734	42853083	41481156	G	A	intron_variant	0.07692	0.07692	0.2708	0.4231	0.4059	0.4	0.04444	0.05556	0.1713	0.375
360	rs1244375280	42853121	41481194	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
361	rs1569018086	42853239	41481312	T	C	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
362	rs149708827	42853243	41481316	T	G	intron_variant	0	0	0	0	0	0	0.04444	0	0	0
363	-	42853301	41481374	A	G	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
364	rs544784789	42853341	41481414	G	A	intron_variant	0	0	0	0	0	0.02	0	0	0	0
365	rs1312825450	42853470	41481543	C	T	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
366	rs952095916	42853500	41481573	A	T	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
367	rs200072801	42854102	41482175	G	A	intron_variant	0	0	0	0	0	0	0	0.02778	0	0
368	-	42854118	41482191	G	T	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
369	rs111620846	42854144	41482217	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0
370	rs2276205	42854203	41482276	G	A	intron_variant	0	0	0.1875	0.1026	0.1287	0.04	0.1222	0.1667	0.2546	0.025
371	rs578103765	42854205	41482278	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
372	rs144033559	42854343	41482416	C	G	intron_variant	0	0	0	0	0	0	0	0	0	0
373	rs118134524	42854376	41482449	A	G	intron_variant	0	0	0	0	0	0	0	0.02778	0.00463	0
374	rs527489879	42854400	41482473	C	T	intron_variant	0	0	0	0	0	0	0	0.02778	0	0
375	rs930977615	42854436	41482509	C	T	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
376	rs112753686	42854460	41482533	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
377	rs900993466	42854525	41482598	C	T	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
378	-	42854637	41482710	C	G	intron_variant	0	0	0	0	0	0.02	0	0	0	0

379	rs34783969	42854638	41482711	T	A	intron_variant	0.07692	0.07692	0.2708	0.4231	0.401	0.4	0.04444	0.05556	0.1713	0.375
380	rs980528078	42854659	41482732	C	G	intron_variant	0	0	0	0	0	0	0	0	0	0
381	rs1309520200	42854715	41482788	T	C	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
382	rs544657781	42854830	41482903	C	A	intron_variant	0	0	0	0	0	0	0	0	0	0
383	rs554462605	42854914	41482987	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
384	-	42854923	41482996	A	C	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
385	rs143818732	42855131	41483204	C	T	intron_variant	0	0	0	0.07692	0.0099	0	0	0	0	0
386	-	42855215	41483288	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
387	rs9977234	42855564	41483637	T	G	intron_variant	0.2692	0.2692	0.2917	0.2436	0.2376	0.24	0.2222	0.2222	0.1343	0.25
388	rs9980225	42855798	41483871	C	T	intron_variant	0.07692	0.07692	0.1042	0.1154	0.1634	0.04	0.02222	0.08333	0.05093	0
389	rs75430506	42855856	41483929	A	G	intron_variant	0	0	0.0208	0	0.005	0	0	0.05556	0.01852	0
390	rs1230739206	42855862	41483935	A	C	intron_variant	0	0	0	0	0.005	0	0	0	0	0
391	-	42856048	41484121	A	C	intron_variant	0.1538	0.1538	0.3542	0.2692	0.2673	0.36	0.4222	0.3889	0.463	0.275
392	rs182231135	42856065	41484138	C	T	intron_variant	0.03846	0.03846	0	0	0	0	0	0	0	0
393	rs141091900	42856099	41484172	C	G	intron_variant	0	0	0.0417	0	0.0099	0	0	0	0.01852	0
394	-	42856116	41484189	A	G	intron_variant	0.4231	0.4231	0.0625	0.02564	0.0297	0.12	0.1889	0.3889	0.3102	0
395	rs146865760	42856216	41484289	T	C	intron_variant	0	0	0	0	0.0149	0	0	0	0	0
396	rs139222305	42856338	41484411	T	C	intron_variant	0	0	0	0.02564	0.0099	0	0	0	0	0.025
397	rs372976235	42856379	41484452	C	G	intron_variant	0	0	0	0	0	0	0	0	0	0
398	rs541215881	42856397	41484470	A	G	intron_variant	0.03846	0.03846	0	0	0	0	0	0	0	0
399	rs56066678	42856479	41484552	T	C	intron_variant	0.2692	0.2692	0.2917	0.2436	0.2376	0.32	0.2556	0.2222	0.1528	0.325
400	rs2838039	42856544	41484617	C	T	intron_variant	0.07692	0.07692	0.375	0.3077	0.3317	0.16	0.4444	0.3333	0.3657	0.05
401	rs147054075	42856619	41484692	A	G	intron_variant	0	0	0	0	0	0.02	0	0	0	0
402	rs549990870	42856711	41484784	G	A	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
403	rs138164084	42856742	41484815	T	G	intron_variant	0	0	0	0	0	0	0	0	0	0
404	-	42856756	41484829	G	A	intron_variant	0.4231	0.4231	0.0625	0.02564	0.0297	0.12	0.1889	0.3889	0.3102	0
405	-	42856774	41484847	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
406	rs79243099	42856901	41484974	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0
407	-	42856949	41485022	T	C	intron_variant	0.4231	0.4231	0.0625	0.02564	0.0297	0.12	0.1889	0.3889	0.3102	0
408	rs149551068	42856975	41485048	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0
409	rs762602293	42857262	41485335	G	T	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
410	-	42857302	41485375	T	C	intron_variant	0.4231	0.4231	0.0625	0.02564	0.0297	0.18	0.2111	0.4167	0.3056	0.05
411	rs9983252	42857322	41485395	G	C	intron_variant	0.07692	0.07692	0.375	0.3077	0.3317	0.16	0.4444	0.3333	0.3704	0.05
412	-	42857444	41485517	C	T	intron_variant	0.4231	0.4231	0.0625	0.02564	0.0297	0.18	0.2222	0.4167	0.3056	0.05
413	rs4818242	42857557	41485630	T	C	intron_variant	0.1923	0.1923	0	0	0	0	0	0	0.00463	0

414	rs11702475	42857568	41485641	T	C	intron_variant	0.07692	0.07692	0.2708	0.4231	0.396	0.42	0.04444	0.05556	0.1713	0.4
415	-	42857642	41485715	T	C	intron_variant	0	0	0	0	0	0	0.02222	0	0	0
416	rs2257202	42857715	41485788	C	T	intron_variant	0.2692	0.2692	0.2917	0.2436	0.2426	0.24	0.2222	0.1944	0.1528	0.25
417	rs746347660	42857750	41485823	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0.05
418	rs118108194	42857755	41485828	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
419	rs1043408573	42857809	41485882	T	C	intron_variant	0	0	0.0208	0	0	0	0	0	0	0
420	rs752423992	42857830	41485903	T	C	intron_variant	0	0	0	0	0.005	0	0	0	0	0
421	rs1262043781	42857893	41485966	G	A	intron_variant	0	0	0.0208	0	0	0	0	0	0	0
422	rs62217531	42857901	41485974	T	C	intron_variant	0.07692	0.07692	0.2292	0.3974	0.3861	0.46	0.06667	0.08333	0.1667	0.375
423	rs1601579713	42857940	41486013	T	G	intron_variant	0	0	0	0	0.005	0	0	0	0	0
424	rs144052153	42857954	41486027	G	T	intron_variant	0	0	0	0	0	0	0	0	0.02315	0
425	rs2298857	42857981	41486054	A	G	intron_variant	0.2692	0.2692	0.2917	0.2436	0.2426	0.3	0.2444	0.2222	0.1528	0.35
426	-	42857985	41486058	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
427	-	42858054	41486127	C	G	intron_variant	0	0	0	0	0	0	0	0	0	0
428	rs572593241	42858080	41486153	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0.025
429	rs182791541	42858096	41486169	T	A	intron_variant	0	0	0	0	0	0	0	0	0	0.025
430	rs539934676	42858142	41486215	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0.025
431	-	42858367	41486440	T	C	intron_variant	0.3077	0.3077	0.2917	0.4231	0.4109	0.42	0.2889	0.4167	0.4491	0.375
432	rs752183643	42858375	41486448	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
433	rs564834372	42858408	41486481	C	G	intron_variant	0	0	0	0	0.005	0	0	0	0	0
434	rs139467735	42858441	41486514	T	G	intron_variant	0	0	0	0	0	0	0	0	0	0.025
435	rs546775580	42858460	41486533	T	C	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
436	rs182336392	42858499	41486572	G	A	intron_variant	0	0	0	0	0.005	0	0	0	0	0
437	rs149676870	42858520	41486593	T	C	intron_variant	0.2692	0.2692	0	0	0	0	0	0	0	0
438	-	42858549	41486622	A	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
439	rs779138284	42858594	41486667	T	C	intron_variant	0	0	0	0	0.005	0	0	0	0	0
440	rs193122175	42858697	41486770	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
441	rs364289	42858865	41486938	A	G	intron_variant	0.2692	0.2692	0.2917	0.2308	0.2376	0.3	0.2778	0.3056	0.1528	0.35
442	-	42858868	41486941	G	A	intron_variant	0.03846	0.03846	0	0	0	0	0	0	0	0
443	rs370363307	42858874	41486947	T	A	intron_variant	0	0	0	0	0	0	0.03333	0.02778	0.00926	0
444	rs149226336	42858936	41487009	G	C	intron_variant	0	0	0	0.01282	0.005	0	0.03333	0.02778	0.03241	0
445	rs903787356	42858958	41487031	C	T	intron_variant	0	0	0.0208	0	0	0	0	0	0	0
446	-	42858990	41487063	C	G	intron_variant	0	0	0	0	0	0	0.02222	0	0	0
447	rs79468500	42858995	41487068	G	T	intron_variant	0	0	0.0208	0.01282	0.0347	0.02	0.01111	0	0	0.025
448	rs80275470	42859054	41487127	A	G	intron_variant	0	0	0	0	0.0198	0	0	0	0	0

449	rs365025	42859067	41487140	C	G	intron_variant	0.3462	0.3462	0.4792	0.3846	0.3713	0.3	0.3222	0.3611	0.3194	0.1
450	rs193067129	42859193	41487266	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
451	rs365724	42859222	41487295	C	G	intron_variant	0.3462	0.3462	0.4792	0.3718	0.3713	0.3	0.3222	0.3611	0.3194	0.1
452	rs188508398	42859319	41487392	C	G	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
453	rs372400372	42859325	41487398	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
454	-	42859604	41487677	G	A	intron_variant	0.4231	0.4231	0.0625	0.02564	0.0297	0.12	0.1667	0.3333	0.287	0
455	-	42859670	41487743	T	C	intron_variant	0.4231	0.4231	0.0625	0.02564	0.0297	0.12	0.2222	0.3333	0.287	0
456	rs375760	42859686	41487759	T	G	intron_variant	0.2692	0.2692	0.2917	0.2308	0.2376	0.26	0.2444	0.2778	0.1528	0.25
457	rs147063811	42859733	41487806	T	A	intron_variant	0	0	0	0	0	0	0	0	0	0
458	rs415918	42859876	41487949	T	C	intron_variant	0.3462	0.3462	0.4792	0.3718	0.3713	0.3	0.3222	0.3611	0.3194	0.1
459	rs141888586	42859971	41488044	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
460	-	42859999	41488072	T	C	intron_variant	0	0	0	0	0	0.02	0	0	0	0
461	rs528451616	42860109	41488182	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
462	rs56136037	42860136	41488209	T	G	intron_variant	0	0	0.0417	0	0.0545	0.02	0	0	0.00463	0
463	rs761668242	42860295	41488368	T	C	intron_variant	0	0	0	0	0	0	0	0.02778	0	0
464	rs371531071	42860299	41488372	T	C	intron_variant	0	0	0	0	0	0	0.02222	0	0	0
465	rs422471	42860307	41488380	T	C	intron_variant	0.3462	0.3462	0.4792	0.3718	0.3762	0.3	0.3222	0.3611	0.3194	0.1
466	COSV59827512	42860336	41488409	T	C	missense_variant	0	0	0	0	0.005	0	0	0	0	0
467	rs386416	42860485	41488558	C	G	intron_variant	0.3462	0.3462	0.4792	0.3718	0.3713	0.3	0.3222	0.3611	0.3194	0.1
468	rs187290362	42860488	41488561	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0.05
469	rs3819138	42860494	41488567	G	C	intron_variant	0.07692	0.07692	0.1042	0.1154	0.1683	0.02	0.03333	0.05556	0.05093	0
470	rs536039173	42860514	41488587	T	G	intron_variant	0	0	0.0208	0.01282	0.005	0	0	0	0	0
471	rs555995855	42860520	41488593	C	T	intron_variant	0	0	0	0	0	0.06	0	0	0	0
472	rs117696554	42860532	41488605	A	G	intron_variant	0	0	0.0208	0.01282	0.0248	0.02	0.01111	0	0	0.025
473	rs3787947	42860593	41488666	T	C	intron_variant	0.07692	0.07692	0.4167	0.3333	0.3366	0.18	0.4222	0.2778	0.3611	0.1
474	rs910522814	42860603	41488676	T	C	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
475	-	42860648	41488721	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0.025
476	rs139305247	42860655	41488728	T	C	intron_variant	0.07692	0.07692	0.0417	0.01282	0.0347	0	0	0	0.01389	0
477	rs1210853029	42860713	41488786	T	C	intron_variant	0	0	0	0	0.005	0	0	0	0	0
478	rs423596	42860809	41488882	T	C	intron_variant	0	0	0.1042	0.0641	0.0545	0.14	0.2333	0.25	0.125	0.075
479	-	42860838	41488911	T	G	intron_variant	0	0	0	0	0.005	0	0	0	0	0
480	rs145996484	42860853	41488926	G	C	intron_variant	0	0	0	0	0	0	0	0	0	0
481	rs1230361255	42860887	41488960	A	G	intron_variant	0	0	0	0	0	0	0	0	0.00926	0
482	rs532082574	42861129	41489202	G	C	intron_variant	0	0	0	0	0	0	0	0	0	0
483	-	42861143	41489216	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0

484	rs2298664	42861181	41489254	C	G	intron_variant	0.07692	0.07692	0.4167	0.3462	0.3416	0.18	0.4556	0.3056	0.3935	0.1
485	rs1191882308	42861203	41489276	A	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
486	rs1426886770	42861289	41489362	T	G	intron_variant	0	0	0.0208	0	0	0	0	0	0	0
487	rs429442	42861332	41489405	T	C	intron_variant	0.2692	0.2692	0.2917	0.2308	0.2426	0.32	0.2667	0.3056	0.1528	0.325
488	rs151152524	42861368	41489441	C	A	intron_variant	0	0	0	0	0	0	0	0	0	0
489	rs768426172	42861473	41489546	T	C	missense_variant	0	0	0	0	0	0	0.02222	0	0	0
490	rs190265904	42861476	41489549	A	G	missense_variant	0	0	0	0	0	0	0	0	0.01389	0
491	rs144948620	42861545	41489618	A	G	intron_variant	0	0	0	0	0.0149	0	0	0	0	0
492	rs371894730	42861591	41489664	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
493	rs373622147	42861764	41489837	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
494	rs141764184	42861794	41489867	A	G	intron_variant	0	0	0	0	0	0	0.08889	0	0	0
495	rs199704982	42861935	41490008	T	C	intron_variant	0	0	0	0	0	0	0	0	0.02315	0
496	rs192666663	42861936	41490009	A	G	intron_variant	0	0	0	0	0	0	0	0.02778	0	0
497	rs147099383	42861959	41490032	C	T	intron_variant	0	0	0.0833	0.07692	0.0297	0.1	0.3333	0.08333	0.06481	0
498	rs11911394	42862275	41490348	C	T	intron_variant	0.07692	0.07692	0.4167	0.3333	0.3366	0.24	0.4556	0.3056	0.3611	0.175
499	rs189040987	42862333	41490406	C	G	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
500	rs561412657	42862367	41490440	G	A	intron_variant	0	0	0	0	0.005	0	0	0	0	0
501	rs192259532	42862416	41490489	T	G	intron_variant	0	0	0	0	0	0	0	0	0	0
502	rs1315753045	42862485	41490558	G	T	intron_variant	0	0	0	0	0	0	0.03333	0	0	0
503	rs928871	42862531	41490604	T	C	intron_variant	0.07692	0.07692	0.4167	0.3333	0.3366	0.24	0.4778	0.3056	0.3611	0.175
504	rs1266169667	42862605	41490678	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
505	-	42862676	41490749	G	A	intron_variant	0	0	0.0208	0	0	0	0	0	0	0
506	rs370823400	42862693	41490766	A	G	intron_variant	0	0	0	0	0	0	0.06667	0	0	0
507	rs116865960	42862768	41490841	A	G	intron_variant	0	0	0.0208	0	0.0149	0	0	0	0	0.025
508	rs528452414	42862848	41490921	C	A	intron_variant	0	0	0	0.01282	0.0099	0	0	0	0	0
509	rs115596471	42862869	41490942	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
510	rs149173609	42862892	41490965	T	C	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
511	rs184365262	42862918	41490991	T	C	intron_variant	0	0	0	0	0.005	0	0	0	0	0
512	-	42862924	41490997	A	G	intron_variant	0	0	0	0	0.005	0	0	0	0.00463	0
513	rs570544092	42862927	41491000	T	C	intron_variant	0	0	0	0	0.005	0	0	0	0.00463	0
514	rs6517669	42862936	41491009	G	A	intron_variant	0.07692	0.07692	0.4167	0.3333	0.3366	0.24	0.4556	0.3056	0.3611	0.175
515	rs1404996705	42862969	41491042	C	T	intron_variant	0	0	0	0	0.005	0	0	0	0	0
516	rs187208295	42863008	41491081	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0.025
517	rs117656646	42863050	41491123	C	T	intron_variant	0	0	0	0.01282	0.0297	0.02	0	0	0	0.025
518	rs143270468	42863127	41491200	A	G	intron_variant	0	0	0	0	0.005	0	0	0	0	0

519	rs148304071	42863169	41491242	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
520	-	42863178	41491251	A	G	intron_variant	0.4231	0.4231	0.0625	0.03846	0.0347	0.12	0.1889	0.3611	0.3148	0
521	rs140458174	42863219	41491292	A	G	intron_variant	0	0	0	0	0	0	0	0	0.00926	0
522	-	42863238	41491311	G	C	intron_variant	0	0	0	0	0	0	0	0	0	0.025
523	rs374771570	42863251	41491324	C	T	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
524	rs866824112	42863293	41491366	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
525	rs145570856	42863294	41491367	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
526	rs35899679	42863320	41491393	A	C	intron_variant	0.07692	0.07692	0.2292	0.3846	0.3861	0.38	0.03333	0.05556	0.1667	0.475
527	rs562045100	42863321	41491394	A	G	intron_variant	0	0	0.0208	0	0	0	0	0	0.02778	0
528	-	42863326	41491399	A	G	intron_variant	0.3462	0.3462	0.2917	0.4231	0.4208	0.5	0.2889	0.4167	0.4815	0.475
529	rs35041537	42863369	41491442	T	C	intron_variant	0.07692	0.07692	0.2292	0.3974	0.3861	0.38	0.1	0.05556	0.1667	0.475
530	rs115429336	42863461	41491534	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
531	rs1056841585	42863507	41491580	A	T	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
532	-	42863608	41491681	A	G	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
533	-	42863650	41491723	C	T	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
534	-	42863685	41491758	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
535	rs10154090	42863723	41491796	A	T	intron_variant	0.07692	0.07692	0.4167	0.3205	0.3218	0.18	0.4222	0.2778	0.338	0.1
536	rs73357642	42863750	41491823	A	G	intron_variant	0	0	0	0	0	0.06	0.03333	0.02778	0	0.075
537	rs391099	42863779	41491852	C	T	intron_variant	0.3077	0.3077	0.2917	0.2436	0.2574	0.32	0.2889	0.3056	0.1759	0.35
538	rs73357644	42863827	41491900	T	C	intron_variant	0	0	0	0	0	0.06	0.04444	0.02778	0	0.075
539	rs750532727	42863870	41491943	C	T	intron_variant	0	0	0	0	0	0	0	0	0.01389	0
540	-	42863922	41491995	C	G	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
541	-	42863925	41491998	A	C	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
542	rs142659685	42863949	41492022	T	C	intron_variant	0	0	0	0.01282	0.005	0	0.03333	0.02778	0.03241	0
543	rs9305745	42864074	41492147	T	C	intron_variant	0.07692	0.07692	0.4167	0.3205	0.3218	0.18	0.4222	0.2778	0.3333	0.1
544	rs886331524	42864155	41492228	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
545	rs392370	42864166	41492239	C	A	intron_variant	0.2692	0.2692	0.2917	0.2436	0.2574	0.32	0.2889	0.3056	0.1852	0.35
546	rs1311837486	42864175	41492248	G	A	intron_variant	0	0	0.0208	0	0	0	0	0	0	0
547	rs79617378	42864217	41492290	C	A	intron_variant	0	0	0	0.01282	0.0099	0	0	0	0.00463	0.025
548	rs771632181	42864269	41492342	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
549	rs374261644	42864398	41492471	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
550	rs886382727	42864457	41492530	G	C	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
551	rs746668285	42864515	41492588	C	A	intron_variant	0	0	0	0	0	0	0	0	0	0
552	-	42864520	41492593	C	A	intron_variant	0	0	0	0	0	0	0	0	0	0
553	rs551122576	42864687	41492760	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0

554	rs2838040	42864692	41492765	G	A	intron_variant	0.07692	0.07692	0.4167	0.3205	0.3168	0.18	0.4889	0.2778	0.3333	0.125
555	-	42864743	41492816	A	G	intron_variant	0.2692	0.2692	0.3125	0.4487	0.4257	0.5	0.2556	0.4167	0.4907	0.475
556	rs536023174	42864747	41492820	T	C	intron_variant	0	0	0	0	0	0.02	0	0	0	0
557	rs401371	42864812	41492885	C	G	intron_variant	0.1923	0.1923	0.25	0.2179	0.2228	0.24	0.2444	0.2778	0.1574	0.225
558	rs144988776	42864871	41492944	T	C	intron_variant	0	0	0	0	0.0149	0	0.06667	0	0	0
559	-	42864927	41493000	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0.025
560	rs373940448	42864947	41493020	T	G	intron_variant	0	0	0	0	0	0	0	0	0	0
561	rs147138431	42865014	41493087	A	C	intron_variant	0	0	0	0.01282	0.0099	0	0	0	0	0
562	rs368086767	42865035	41493108	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
563	-	42865047	41493120	C	T	intron_variant	0.3462	0.3462	0.1458	0.03846	0.0446	0.12	0.1889	0.5	0.4398	0
564	-	42865151	41493224	T	C	intron_variant	0.2692	0.2692	0.5	0.3718	0.3465	0.34	0.3444	0.3611	0.3426	0.125
565	rs375827195	42865216	41493289	G	A	intron_variant	0	0	0	0	0	0	0.01111	0	0	0.05
566	rs186185630	42865275	41493348	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
567	-	42865283	41493356	G	A	intron_variant	0	0	0	0	0.005	0.02	0	0	0	0
568	-	42865300	41493373	G	A	intron_variant	0	0	0	0	0.005	0	0	0	0	0
569	-	42865324	41493397	G	A	intron_variant	0.1538	0.1538	0.3542	0.2821	0.2871	0.46	0.4444	0.3333	0.4815	0.35
570	rs1180926833	42865398	41493471	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
571	rs377011212	42865555	41493628	T	C	intron_variant	0	0	0	0	0	0	0.02222	0	0	0
572	rs566903241	42865789	41493862	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
573	rs549801931	42865820	41493893	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
574	rs1601585975	42865828	41493901	G	C	intron_variant	0	0	0	0	0	0	0	0	0	0
575	rs2838041	42865906	41493979	C	G	intron_variant	0	0	0.0833	0.07692	0.0198	0.04	0	0	0.00926	0.05
576	rs1000568527	42866068	41494141	G	C	intron_variant	0	0	0	0	0	0	0	0	0	0
577	rs376235035	42866099	41494172	T	C	intron_variant	0	0	0	0	0.0198	0	0	0	0.0463	0
578	rs2838042	42866107	41494180	C	T	intron_variant	0.07692	0.07692	0.3333	0.2051	0.2327	0.18	0.4444	0.25	0.1343	0.25
579	rs923545665	42866226	41494299	C	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
580	rs373196115	42866232	41494305	A	G	intron_variant	0	0	0	0	0	0	0	0.05556	0	0
581	rs750152865	42866245	41494318	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
582	rs3787950	42866296	41494369	C	T	synonymous_variant	0	0	0.125	0.1538	0.0693	0.22	0.4	0.2222	0.06481	0.175
583	rs61735792	42866332	41494405	A	G	synonymous_variant	0	0	0	0.01282	0.0099	0	0	0	0	0
584	rs201679623	42866388	41494461	C	A	missense_variant	0	0	0	0.01282	0	0	0	0	0.00463	0
585	rs138651919	42866399	41494472	A	G	missense_variant	0	0	0	0	0	0	0	0	0	0
586	rs199824558	42866422	41494495	A	G	synonymous_variant	0	0	0	0	0	0.02	0	0	0	0
587	rs201093031	42866423	41494496	G	A	missense_variant	0	0	0	0	0	0	0.01111	0	0	0
588	rs61735791	42866439	41494512	T	C	missense_variant	0	0	0	0	0.005	0	0	0	0	0.025

589	rs141685390	42866440	41494513	C	G	synonymous_variant	0	0	0	0	0	0	0.01111	0	0	0
590	rs61735790	42866468	41494541	C	T	missense_variant	0	0	0	0	0	0	0	0	0	0
591	rs368773451	42866553	41494626	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
592	rs368625065	42866644	41494717	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
593	rs547701911	42866723	41494796	C	T	intron_variant	0	0	0	0	0.005	0	0	0	0	0
594	-	42866725	41494798	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
595	rs374203194	42866726	41494799	A	G	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
596	rs569947342	42866868	41494941	T	C	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
597	-	42866884	41494957	A	T	intron_variant	0.03846	0.03846	0	0	0	0	0	0	0	0
598	rs927713682	42866888	41494961	T	C	intron_variant	0	0	0	0	0	0	0	0	0.00926	0
599	-	42866891	41494964	A	G	intron_variant	0	0	0	0	0	0	0	0.02778	0	0
600	rs1007596550	42866974	41495047	A	G	intron_variant	0	0	0	0	0	0	0.03333	0	0	0
601	rs190899605	42867015	41495088	C	T	intron_variant	0	0	0.0208	0	0	0.02	0	0	0	0
602	-	42867175	41495248	A	T	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
603	-	42867179	41495252	T	C	intron_variant	0.03846	0.03846	0	0	0	0	0	0	0	0
604	rs1307770905	42867237	41495310	G	T	intron_variant	0	0	0	0	0	0	0	0.02778	0	0
605	rs558991814	42867326	41495399	C	G	intron_variant	0	0	0	0	0.005	0	0	0	0	0
606	rs530471976	42867424	41495497	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
607	rs114911304	42867425	41495498	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
608	rs775158277	42867499	41495572	C	T	intron_variant	0	0	0	0.02564	0	0	0	0	0	0.025
609	rs58146697	42867667	41495740	C	T	intron_variant	0	0	0.0208	0.01282	0.0248	0.06	0.01111	0.05556	0.03704	0
610	-	42867719	41495792	T	C	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
611	rs372453344	42867735	41495808	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
612	rs142425263	42867756	41495829	A	C	intron_variant	0	0	0	0	0	0	0	0	0.01389	0
613	rs184876485	42867990	41496063	G	A	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
614	rs370530303	42868060	41496133	T	C	intron_variant	0	0	0	0	0	0	0.04444	0	0	0
615	rs55760462	42868206	41496279	C	T	intron_variant	0.03846	0.03846	0.2083	0.2179	0.1881	0.06	0.04444	0.02778	0.1296	0.15
616	-	42868299	41496372	G	A	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
617	rs144276163	42868411	41496484	G	T	intron_variant	0	0	0	0	0	0	0	0	0	0
618	rs914184	42868641	41496714	A	G	intron_variant	0	0	0.0208	0	0	0	0.01111	0	0.00926	0
619	rs78217567	42868655	41496728	C	T	intron_variant	0	0	0.0417	0	0.0446	0.02	0	0	0.00463	0
620	-	42868820	41496893	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
621	rs34256269	42868876	41496949	A	G	intron_variant	0	0	0.1667	0.1026	0.1485	0.18	0.1111	0.05556	0.0463	0.1
622	COSV59828093	42868888	41496961	C	T	intron_variant	0.3462	0.3462	0.3542	0.4487	0.495	0.34	0.4778	0.4444	0.4398	0.4
623	-	42868905	41496978	C	T	intron_variant	0	0	0	0	0	0	0.01111	0	0	0

624	rs573213706	42868957	41497030	A	G	intron_variant	0	0	0	0	0.005	0	0	0	0	0
625	-	42868992	41497065	C	T	intron_variant	0	0	0	0	0.0099	0	0	0	0	0
626	rs34983238	42868997	41497070	C	A	intron_variant	0	0	0.0833	0.1538	0.0743	0.08	0	0	0.01389	0.25
627	-	42869028	41497101	G	A	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
628	-	42869063	41497136	A	G	intron_variant	0.3462	0.3462	0.1875	0.3462	0.3564	0.16	0.3889	0.3889	0.3889	0.3
629	-	42869080	41497153	C	T	intron_variant	0	0	0	0	0.005	0	0	0	0	0
630	rs924332623	42869283	41497356	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0
631	rs1003030	42869606	41497679	G	A	intron_variant	0	0	0.25	0.141	0.1188	0.24	0.2333	0.2222	0.1389	0.2
632	rs184859933	42869637	41497710	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
633	rs56695953	42869735	41497808	A	G	intron_variant	0.2308	0.2308	0.0208	0.1923	0.1386	0.04	0.03333	0.02778	0.05556	0.175
634	rs148901354	42869772	41497845	T	C	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
635	rs367885466	42869836	41497909	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
636	rs181592444	42869927	41498000	T	C	intron_variant	0	0	0	0	0	0	0.01111	0.02778	0	0
637	rs115968373	42869938	41498011	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
638	rs186510586	42870205	41498278	C	T	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
639	-	42870211	41498284	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
640	rs11701576	42870262	41498335	G	A	intron_variant	0	0	0.25	0.141	0.1188	0.24	0.2333	0.2222	0.1389	0.2
641	rs780560155	42870392	41498465	A	G	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
642	rs138661151	42870421	41498494	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
643	rs150715708	42870450	41498523	T	C	intron_variant	0	0	0	0.01282	0	0	0	0	0.00463	0
644	rs557714443	42870451	41498524	A	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
645	rs3761373	42870522	41498595	T	C	intron_variant	0	0	0.25	0.141	0.1188	0.24	0.2333	0.2222	0.1389	0.2
646	rs940625478	42870890	41498963	G	T	intron_variant	0	0	0	0	0.005	0	0	0	0	0
647	rs913523407	42870902	41498975	A	G	intron_variant	0	0	0.0208	0	0	0	0	0	0	0
648	rs422761	42870993	41499066	A	G	intron_variant	0.3846	0.3846	0.0833	0.02564	0.0693	0.26	0.2	0.3056	0.2778	0.075
649	-	42871051	41499124	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
650	rs1233077154	42871073	41499146	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
651	rs939814881	42871083	41499156	T	C	intron_variant	0	0	0	0	0.005	0	0	0	0	0
652	rs389001	42871131	41499204	G	A	intron_variant	0.3846	0.3846	0.0833	0.02564	0.0693	0.26	0.2	0.3056	0.2778	0.075
653	rs931406088	42871153	41499226	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
654	rs534034788	42871213	41499286	A	G	intron_variant	0	0	0	0	0	0.02	0	0	0	0
655	rs2838043	42871220	41499293	T	C	intron_variant	0.2308	0.2308	0.0208	0.1923	0.1386	0.04	0.03333	0.02778	0.05556	0.175
656	rs187648498	42871225	41499298	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
657	rs372249693	42871227	41499300	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
658	rs149424945	42871251	41499324	T	C	intron_variant	0	0	0	0	0	0	0	0.02778	0	0

659	rs3761374	42871273	41499346	C	T	intron_variant	0	0	0.1667	0.1026	0.1485	0.18	0.1222	0.05556	0.0463	0.1
660	rs1418216524	42871415	41499488	G	A	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
661	rs190673599	42871481	41499554	T	A	intron_variant	0	0	0	0	0	0	0	0	0	0
662	rs183722985	42871662	41499735	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
663	rs573044175	42871680	41499753	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
664	-	42871776	41499849	C	T	intron_variant	0.03846	0.03846	0	0	0	0	0	0	0	0
665	rs188198121	42871792	41499865	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
666	rs571275590	42871867	41499940	G	A	intron_variant	0	0	0	0	0	0.02	0	0	0	0
667	rs78528160	42871921	41499994	A	T	intron_variant	0	0	0	0	0	0	0	0	0	0
668	-	42871941	41500014	G	C	intron_variant	0.1154	0.1154	0.1667	0.1538	0.2178	0.14	0.3556	0.3611	0.338	0.125
669	rs144318842	42872059	41500132	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
670	rs556371948	42872119	41500192	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0.025
671	rs374881231	42872302	41500375	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
672	rs148719900	42872315	41500388	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0
673	rs142296178	42872342	41500415	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
674	rs527416684	42872354	41500427	A	G	intron_variant	0	0	0	0	0	0.04	0	0	0	0
675	-	42872372	41500445	A	G	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
676	rs986686535	42872391	41500464	T	C	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
677	rs151248079	42872429	41500502	T	A	intron_variant	0	0	0	0	0	0	0	0	0	0
678	rs115266855	42872559	41500632	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
679	rs114027875	42872658	41500731	T	A	intron_variant	0	0	0	0	0	0	0	0	0	0
680	rs2187238	42872751	41500824	C	T	intron_variant	0.2308	0.2308	0.0208	0.1923	0.1386	0.06	0.03333	0.02778	0.05556	0.175
681	rs112416131	42872793	41500866	A	G	intron_variant	0	0	0	0	0.005	0	0	0	0	0
682	-	42872897	41500970	G	C	intron_variant	0.1154	0.1154	0.1667	0.1538	0.2178	0.14	0.3556	0.3611	0.338	0.125
683	rs1343871927	42872949	41501022	A	G	intron_variant	0.03846	0.03846	0	0	0	0	0	0	0	0
684	rs73903404	42872955	41501028	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
685	-	42872956	41501029	C	T	intron_variant	0	0	0	0	0	0	0	0.02778	0	0
686	-	42873008	41501081	C	T	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
687	rs972527688	42873213	41501286	A	T	intron_variant	0	0	0	0	0	0	0	0	0	0
688	rs530009764	42873243	41501316	C	T	intron_variant	0	0	0	0	0.005	0	0	0	0	0
689	rs371046741	42873258	41501331	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
690	rs147620204	42873274	41501347	C	G	intron_variant	0	0	0	0	0	0	0	0	0	0
691	rs552447029	42873362	41501435	G	C	intron_variant	0	0	0	0	0	0	0	0	0	0
692	rs1003304387	42873400	41501473	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
693	rs962596107	42873604	41501677	C	G	intron_variant	0	0	0	0	0	0	0	0	0	0

694	rs9980693	42873605	41501678	A	G	intron_variant	0	0	0.1667	0.1026	0.1535	0.16	0.1222	0.05556	0.0463	0.1
695	rs73903405	42873700	41501773	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0
696	rs145877432	42873827	41501900	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
697	-	42873984	41502057	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
698	-	42874065	41502138	A	G	intron_variant	0	0	0.0208	0	0	0	0	0	0	0
699	rs968067353	42874098	41502171	A	G	intron_variant	0	0	0	0	0	0	0	0.02778	0	0
700	rs377403765	42874104	41502177	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
701	rs149270377	42874184	41502257	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
702	rs143460343	42874270	41502343	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
703	rs141583878	42874306	41502379	A	G	intron_variant	0	0	0	0.01282	0	0	0	0	0	0
704	rs567302726	42874338	41502411	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
705	-	42874368	41502441	G	A	intron_variant	0.03846	0.03846	0	0	0.005	0	0	0	0	0
706	-	42874384	41502457	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
707	rs536147878	42874513	41502586	A	G	intron_variant	0	0	0	0	0.005	0	0	0	0	0
708	rs992437148	42874535	41502608	T	C	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
709	rs146385718	42874559	41502632	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
710	rs531756387	42874831	41502904	T	G	intron_variant	0	0	0.0208	0	0	0	0.01111	0	0	0
711	rs139700775	42874841	41502914	C	T	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
712	-	42874844	41502917	T	C	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
713	rs9984012	42875004	41503077	T	C	intron_variant	0	0	0.1667	0.1026	0.1535	0.16	0.1222	0.05556	0.0463	0.1
714	rs142914234	42875089	41503162	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
715	rs1308693805	42875131	41503204	T	C	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
716	-	42875190	41503263	A	G	intron_variant	0	0	0	0	0.005	0	0	0	0	0
717	rs420737	42875404	41503477	G	A	intron_variant	0.3846	0.3846	0.0833	0.02564	0.0693	0.26	0.2444	0.2778	0.2778	0.075
718	rs146120690	42875620	41503693	A	G	intron_variant	0	0	0	0	0	0	0.08889	0	0	0
719	rs74749793	42875652	41503725	T	G	intron_variant	0	0	0.25	0.141	0.1188	0.24	0.1889	0.1944	0.1389	0.2
720	rs1033407344	42875668	41503741	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0
721	rs373052874	42875816	41503889	C	G	intron_variant	0	0	0	0	0	0	0.05556	0	0	0
722	rs763295257	42875832	41503905	A	G	intron_variant	0	0	0	0	0.0099	0	0	0	0.00926	0
723	-	42875847	41503920	T	G	intron_variant	0	0	0	0	0	0	0	0	0	0
724	rs1381741328	42875859	41503932	T	C	intron_variant	0	0	0	0	0.005	0	0	0	0	0
725	-	42876060	41504133	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0.025
726	rs575313753	42876148	41504221	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
727	-	42876162	41504235	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0.025
728	rs7277080	42876400	41504473	T	C	intron_variant	0.03846	0.03846	0.3125	0.3846	0.3069	0.14	0.04444	0.02778	0.1435	0.325

729	rs756657861	42876412	41504485	A	G	intron_variant	0	0	0	0	0.0099	0	0	0	0.00926	0
730	rs395584	42876447	41504520	C	T	intron_variant	0.3846	0.3846	0.0833	0.02564	0.0693	0.26	0.2444	0.2778	0.2778	0.075
731	rs8129713	42876598	41504671	C	T	intron_variant	0.2308	0.2308	0.0208	0.1923	0.1337	0.06	0.03333	0.05556	0.05556	0.175
732	-	42876599	41504672	T	C	intron_variant	0	0	0	0	0	0.02	0	0	0	0
733	-	42876684	41504757	C	G	intron_variant	0	0	0	0	0	0	0	0	0	0
734	rs1027558002	42876698	41504771	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
735	rs1014761397	42876720	41504793	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
736	-	42876757	41504830	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
737	rs374886738	42876786	41504859	C	A	intron_variant	0	0	0	0	0	0	0	0	0	0
738	rs368411333	42876791	41504864	T	A	intron_variant	0	0	0	0	0	0	0	0	0	0
739	rs73357663	42876845	41504918	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
740	rs1045511841	42876921	41504994	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0.025
741	-	42876949	41505022	T	C	intron_variant	0	0	0	0	0	0	0	0	0.00463	0
742	rs145728087	42877028	41505101	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0
743	rs148499598	42877041	41505114	C	T	intron_variant	0	0	0	0	0.0099	0	0	0	0.00463	0
744	-	42877167	41505240	C	A	intron_variant	0	0	0	0	0	0.02	0	0	0	0
745	rs186418926	42877262	41505335	A	G	intron_variant	0	0	0.0208	0	0.0099	0	0	0	0	0
746	rs74605993	42877274	41505347	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
747	-	42877307	41505380	G	C	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
748	rs75373173	42877382	41505455	C	T	intron_variant	0	0	0.0417	0.07692	0.1584	0.04	0	0	0.02315	0.025
749	rs377054370	42877408	41505481	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
750	-	42877414	41505487	G	A	intron_variant	0	0	0	0	0	0.02	0	0	0	0
751	rs147630170	42877432	41505505	G	C	intron_variant	0	0	0	0	0	0	0	0	0	0
752	-	42877453	41505526	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
753	rs73357664	42877469	41505542	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
754	rs548025657	42877481	41505554	A	G	intron_variant	0	0	0	0	0	0.02	0	0	0	0
755	-	42877542	41505615	C	A	intron_variant	0.1154	0.1154	0.2917	0.2308	0.3564	0.32	0.4667	0.4722	0.3843	0.2
756	rs936471151	42877574	41505647	A	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
757	rs183758144	42877588	41505661	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
758	rs115129572	42877673	41505746	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
759	rs191526916	42877747	41505820	T	C	intron_variant	0	0	0	0	0.0149	0	0	0	0.00463	0
760	-	42878111	41506184	A	G	intron_variant	0	0	0	0	0.005	0	0	0	0	0
761	rs866793401	42878114	41506187	A	T	intron_variant	0	0	0	0	0	0	0	0	0	0.025
762	rs28360562	42878126	41506199	C	A	intron_variant	0	0	0.0833	0.1667	0.0743	0.08	0	0	0.01389	0.25
763	-	42878274	41506347	C	T	intron_variant	0	0	0	0	0	0	0	0	0.00463	0

764	rs144458055	42878469	41506542	T	G	intron_variant	0	0	0	0	0	0	0	0	0	0
765	-	42878471	41506544	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
766	rs151189718	42878478	41506551	T	C	intron_variant	0	0	0	0	0	0	0	0	0	0
767	rs746727496	42878493	41506566	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0.025
768	rs114641598	42878507	41506580	C	T	intron_variant	0	0	0	0	0	0	0	0	0	0
769		42878611	41506684	T	C	intron_variant	0.2308	0.2308	0.0208	0.1923	0.1337	0.04	0.03333	0.05556	0.05556	0.175
770	rs55704664	42878612	41506685	C	T	intron_variant	0	0	0	0.01282	0.0198	0.02	0.05556	0.05556	0.03704	0.025
771	rs75200570	42878626	41506699	C	G	intron_variant	0	0	0	0	0	0	0	0	0	0
772	rs538465291	42878710	41506783	A	C	intron_variant	0	0	0	0	0	0	0	0	0	0
773	rs150314077	42878761	41506834	T	C	intron_variant	0	0	0	0	0.005	0	0	0	0	0
774	rs538226704	42878941	41507014	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
775	rs149021153	42878991	41507064	G	A	intron_variant	0	0	0	0	0	0	0	0	0	0
776	-	42879072	41507145	C	G	intron_variant	0	0	0	0	0	0	0	0	0	0
777	rs1601595157	42879098	41507171	T	C	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
778	rs912134074	42879182	41507255	T	G	intron_variant	0	0	0	0	0	0	0	0	0	0
779	rs145900878	42879197	41507270	T	A	intron_variant	0	0	0	0	0	0	0	0	0	0
780	rs968128742	42879236	41507309	A	C	intron_variant	0	0	0	0.03846	0.0099	0	0	0	0	0
781	rs138498737	42879283	41507356	T	G	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
782	-	42879356	41507429	A	G	intron_variant	0	0	0	0	0	0	0	0	0	0
783	rs57161767	42879403	41507476	T	A	intron_variant	0.03846	0.03846	0.2917	0.2436	0.2475	0.06	0.04444	0.02778	0.1296	0.1
784	rs112467088	42879473	41507546	C	T	intron_variant	0	0	0	0	0	0.02	0	0	0	0
785	rs578020496	42879604	41507677	A	C	intron_variant	0	0	0.1667	0.08974	0.1535	0.16	0.1222	0.05556	0.0463	0.1
786	rs73230088	42879688	41507761	A	G	intron_variant	0	0	0	0	0	0	0	0.02778	0	0
787	rs573736906	42879690	41507763	A	G	intron_variant	0	0	0	0	0	0	0	0.02778	0	0
788	rs1038320368	42879705	41507778	T	A	intron_variant	0	0	0	0	0	0.02	0	0	0	0
789	-	42879709	41507782	C	G	intron_variant	0	0	0	0	0	0	0	0	0	0
790	-	42879724	41507797	A	G	intron_variant	0.2308	0.2308	0.0208	0.1923	0.1238	0.04	0.03333	0.05556	0.05556	0.175
791	rs8126497	42879747	41507820	C	T	intron_variant	0	0	0	0	0	0	0.01111	0	0	0
792	rs371055210	42879841	41507914	T	G	intron_variant	0	0	0	0	0	0	0	0	0	0
793	rs1031142674	42879909	41507982	A	C	missense_variant	0.03846	0.03846	0.3958	0.4103	0.3267	0.14	0.04444	0.02778	0.1435	0.35
794	rs75603675	42879910	41507983	G	C	missense_variant	0	0	0	0	0.0099	0	0	0	0	0
795	rs200291871	42880296	41508369	C	G	upstream_gene_variant	0	0	0	0	0	0	0	0	0	0

Supplementary Table 2: Geographic region and numbers of samples examined in this study

Geographic Region	**Number of Samples (N)**
America	13
Central Asia	24
Caucasus	39
Europe	101
South Asia:- *Indo-European* *Dravidian* *Austroasiatic*	25 18 4 3
SEAM (Southeast Asia Mainland)	18
SEAI (Southeast Asia Island)	45
Siberia	108
West Asia	20

Supplementary Table 3a. Distribution of major haplotypes of TMPRSS2 gene among the world population.

Haplotype No.	**AMR**	**SIB**	**CA**	**EUR**	**SEAI**	**SEAM**	**SA**	**CAU**	**WA**
Hap_34	0	2	3	0	3	1	1	0	0
Hap_48	0	0	1	5	0	0	2	0	3
Hap_75	0	4	0	12	0	0	0	2	0
Hap_98	0	9	0	2	0	0	0	3	0
Hap_260	0	17	0	0	3	0	1	0	0

Supplementary Table 3b. Frequency of haplotypes present in South Asia, among studied groups

Haplotypes	AMR	SIB	CA	EUR	SEAI	SEAM	SA	CAU	WA	Total	AMR	SIB	CA	EUR	SEAI	SEAM	SA	CAU	WA
Hap_34	0	2	3	0	3	1	1	0	0	10	-	0.200	0.300	-	0.300	0.100	0.100	-	-
Hap_48	0	0	1	5	0	0	2	0	3	11	-	-	0.091	0.455	-	-	0.182	-	0.273
Hap_78	0	0	0	0	0	0	1	1	1	3	-	-	-	-	-	-	0.333	0.333	0.333
Hap_112	0	0	0	0	0	0	1	1	0	2	-	-	-	-	-	-	0.500	0.500	-
Hap_219	0	0	0	1	0	0	2	0	0	3	-	-	-	0.333	-	-	0.667	-	-
Hap_245	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_246	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_247	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_248	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_249	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_250	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_251	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_252	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_253	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_254	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_255	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_256	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_257	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_258	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_259	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_260	0	17	0	0	3	0	1	0	0	21	-	0.810	-	-	0.143	-	0.048	-	-
Hap_261	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_262	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_263	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_264	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_265	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_266	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_267	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_268	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_269	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_270	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_271	0	0	0	0	0	0	2	0	0	2	-	-	-	-	-	-	1	-	-
Hap_272	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_273	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_274	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_275	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_276	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_277	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_278	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_279	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_280	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_281	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_282	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_283	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_284	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_285	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-
Hap_286	0	0	0	0	0	0	1	0	0	1	-	-	-	-	-	-	1	-	-

Supplementary Table 4a. Statewise allele frequency of studied SNP for the association

State	Population Groups	Sanple Size(N)	rs2070788(G)	rs734056(A)	rs12329760(T)	rs2276205(G)	rs3787950(C)	Refrences
Arunanchal Pradesh	Nyshi_Bom_Mro_Oraon	28	0.2143	0.125	0.3214	0.05357	0.1607	present study
Bihar	Brahmin Bihar	8	0.5	0.4375	0.3125	0.125	0.0625	present study
Gujarat	Gujarati and Brahmin_Guj	121	0.4835	0.5	0.1694	0.03719	0.2521	1000 Genome
Haryana	Ror and Brahmin_Har	18	0.3056	0.3056	0.3333	0.1471	0.1765	Pathak et al. 2018
Jharkhand	Santhal and Oraon	51	0.3137	0.2059	0.3431	0.01961	0.2843	present study
Kerala	Cochin_Jews	8	0.25	0.1875	0.0625	0	0	present study
Meghalaya	Garo and Khasi	16	0.4062	0	0.1562	0.09375	0.1875	Tatte et al. 2019 and present study
Rajasthan	Gujjar	15	0.4	0.3667	0.3667	0.1	0.2	Pathak et al. 2018
Tamilnadu	Brahmins_TN	15	0.4333	0.4667	0.3	0.06667	0.2667	1000 Genome and present study
Tripura	Tripuri	20	0.3	0.05	0.175	0.1	0.025	present study
Uttar Pradesh	Brahmins and Kshatriya	89	0.483	0.4494	0.2303	0.0618	0.1818	present study
West Bengal	Bengali and Brahmin_WB	19	0.4737	0.4211	0.1579	0.07895	0.2105	present study
Maharashtra	Maratha and Mumbai Jews	13	0.3846	0.3077	0.3462	0.1154	0.2308	Chaubey et al. 2017 and present study
Manipur	Manipuri Brahmin	29	0.475	0.2895	0.25	0.1	0.2	present study

Supplementary Table 4b. Statewise epidemiological data of cases, deaths and CFR.

	(June_2021)			**(July_2021)**			**(August_2021)**		
State	**Cases**	**Death**	**CFR**	**Cases**	**Death**	**CFR**	**Cases**	**Death**	**CFR**
Arunanchal Pradesh	30850	138	0.004473258	41646	197	0.004730346	50070	242	0.00483323
Bihar	716296	9466	0.013215207	723695	9625	0.013299802	725192	9646	0.01330131
Gujarat	819376	9985	0.012186103	824384	10074	0.012220033	825045	10077	0.01221388
Haryana	765096	8904	0.011637755	769417	9578	0.012448386	770079	9649	0.01252988
Jharkhand	343065	5082	0.014813519	346533	5120	0.014774928	347392	5130	0.01476718
Kerala	2702823	10804	0.003997302	3117083	15025	0.004820212	3552525	17747	0.0049956
Meghalaya	41100	714	0.017372263	56052	926	0.016520374	69171	1163	0.0168134
Rajasthan	949008	8799	0.009271787	953257	8947	0.009385717	953827	8954	0.00938745
Tamilnadu	2324597	28906	0.012434844	2528806	33606	0.013289276	2575308	34317	0.0133254
Tripura	58521	604	0.010321081	72860	722	0.009909415	80211	770	0.00959968
Uttar Pradesh	1701668	21667	0.012732801	1707655	22705	0.013296011	1708772	22773	0.01332711
West Bengal	1452987	16731	0.0115149	1515599	17970	0.011856698	1533803	18229	0.01188484
Maharashtra	5887853	106367	0.018065499	6189257	126560	0.020448335	6353328	133996	0.02109068
Manipur	58768	944	0.016063164	81560	1340	0.016429622	104324	1650	0.01581611

Supplementary Table 5. Results of the tests performed for statistical significance.

Observation	**Linear regression analysis parameters**			
rs2070788	**R^2**	**p-value**	**Effect size (β)**	**Std. Error (S_e)**
June 2021_CFR	0.338	0.029	0.582	0.080467
July 2021_CFR	0.310	0.039	0.557	0.082181
August 2021_CFR	0.289	0.047	0.537	0.083416

Observation	**Linear regression analysis parameters**			
rs734056	**R^2**	**p-value**	**Effect size (β)**	**Std. Error (S_e)**
June 2021_CFR	0.011	0.720	0.105	0.165511
July 2021_CFR	0.028	0.570	0.166	0.164118
August 2021_CFR	0.026	0.580	0.162	0.164237

Observation	**Linear regression analysis parameters**			
rs12329760	**R^2**	**p-value**	**Effect size (β)**	**Std. Error (S_e)**
June 2021_CFR	0.056	0.417	0.236	0.095090
July 2021_CFR	0.079	0.330	0.281	0.093903
August 2021_CFR	0.081	0.324	0.284	0.093807

Observation	**Linear regression analysis parameters**			
rs2276205	**R^2**	**p-value**	**Effect size (β)**	**Std. Error (S_e)**
June 2021_CFR	0.183	0.127	0.428	0.038890
July 2021_CFR	0.190	0.120	0.435	0.038743
August 2021_CFR	0.184	0.126	0.429	0.038880

Observation	**Linear regression analysis parameters**			
rs3787950	**R^2**	**p-value**	**Effect size (β)**	**Std. Error (S_e)**
June 2021_CFR	0.265	0.060	0.515	0.077517
July 2021_CFR	0.278	0.053	0.527	0.076816
August 2021_CFR	0.280	0.052	0.529	0.076711

Supplementary Table 6: Aggregate haplotypes frequency carrying rs2070788 (G allele).

	AMR	CA	CAU	EUR	SA	SEAI	SEAM	SIB	WA
Haplotype Freq.	0.654	0.354	0.474	0.426	0.560	0.322	0.389	0.486	0.6

Supplementary Table 7 | rs2070788 frequency from gnomAD and 1000 genome database.

Region	**gnomAD**		**1000 genome**	
	Ref. Allele (G)	**Alt. Allele (A)**	**Ref. Allele (G)**	**Alt. Allele (A)**
African	0.3035	0.6965	0.2738	0.7262
East Asian	0.3482	0.6518	0.3562	0.6438
Europe	0.467	0.5330	0.4642	0.5358
American	0.5039	0.4961	0.494	0.506
South Asian	0.444	0.5560	0.466	0.534