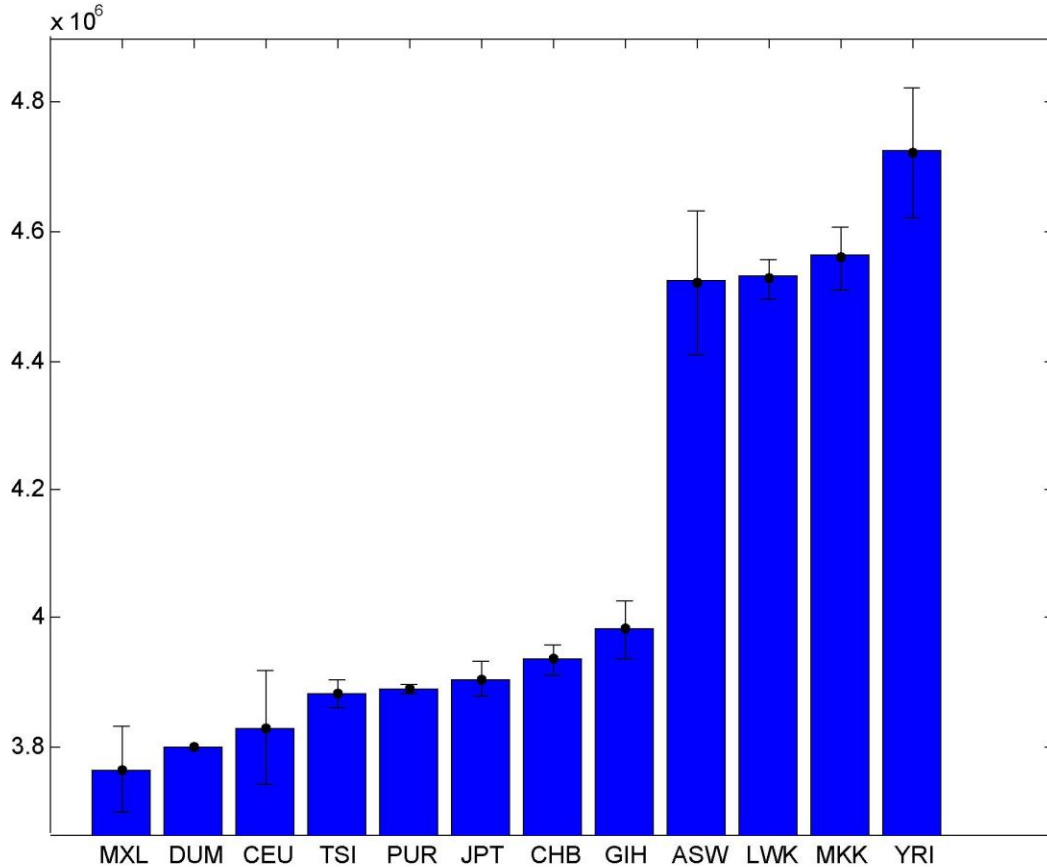


Supplementary Materials



Supplementary Figure 1: Number of variants in Tianjiao1 and CGI diversity panel individuals. Individuals in the diversity panel were grouped by populations. The mean number of variants and standard deviation for each population is shown. Population code: DUM: Tianjiao1; CHB: Han Chinese; JPT: Japanese; GIH: Gujarati; PUR: Puerto Rican; MXL: Mexican-American; TSI: Tuscan; CEU: Utah residents (CEPH) with Northern and Western European ancestry; MKK: Maasai; ASW: African-American; YRI: Yoruba; LWK: Luhya.

Supplementary Table 1. Overlap of DU and Buryat Mongolian selection candidate regions at $p < 0.02$ level in iHS and/or XP-EHH selection scans

Chr	200KB Region	Gene List	DU Mongolian	p	Buryat Mongolian	p
chr1	377	SLC44A5	iHS	0.0008	iHS	0.0148
chr1	403	No Gene	XP-EHH	0.0012	XP-EHH	0.0062
chr1	569	MAGI3	iHS	0.0145	iHS	0.0003
chr1	596	WARS2,TBX15	iHS	0.0112	iHS	0.0009
chr1	894	XPR1	iHS	0.012	iHS	0.0167
chr2	58	GREB1,NTSR2	XP-EHH	0.0072	XP-EHH	0.0093
chr2	416	No Gene	iHS	0.0025	iHS	0.0011
chr2	429	ST3GAL5,ATOH8	iHS	-	iHS	0.0146
			XP-EHH	0.019	XP-EHH	0.0052
chr2	539	SLC5A7,LOC729121,RGPD4	iHS	0.0196	iHS	0.001
chr2	541	SULT1C2,SULT1C3,SULT1C4	iHS	0.0013	iHS	0.0002
chr2	589	No Gene	XP-EHH	0.0051	XP-EHH	0.013
chr2	687	THSD7B	XP-EHH	0.0109	iHS	0.0108
chr2	769	No Gene	iHS	0.015	iHS	0.0026
chr2	891	PDE11A	iHS	-	iHS	0.0096
			XP-EHH	0.0149	XP-EHH	0.0027
chr2	893	PDE11A,OSBPL6,RBM45	iHS	0.0049	iHS	0.0018
			XP-EHH	-	XP-EHH	0.0197
chr2	948	COL5A2	iHS	0.0027	XP-EHH	0.0085
chr2	950	WDR75,SLC40A1	iHS	0.0187	iHS	0.0032
chr2	1020	RAPH1,ABI2	iHS	0.0134	iHS	0.0195
chr2	1142	WDR69,SPHKAP	XP-EHH	0.0192	XP-EHH	0.018
chr3	327	MAGI1	iHS	0.0159	iHS	0.0036
chr3	564	PHLDB2,PLCXD2,CD96	iHS	0.0123	iHS	0.004
chr3	828	No Gene	iHS	0.0108	iHS	0.0111
chr3	829	No Gene	iHS	0.003	iHS	0.0033
chr3	873	NLGN1	iHS	0.0097	iHS	0.0067
chr4	82	LDB2	iHS	0.0163	iHS	0.0169
chr4	130	TBC1D19,RBPJ,CCKAR	XP-EHH	0.0032	iHS	0.0163

chr4	170	No Gene	iHS	0.0058	iHS	0.0075
chr4	304	No Gene	iHS	0.0069	iHS	0.0111
chr4	481	UNC5C,BMPR1B	XP-EHH	0.0196	XP-EHH	0.0047
chr4	614	TMEM155,CCNA2,EXOSC9,ANXA5,LOC100192379,BBS7	XP-EHH	0.0061	iHS	0.0083
chr4	719	INPP4B	iHS	0.005	iHS	0.0027
chr4	720	No Gene	iHS	0.0101	iHS	0.0173
chr4	722	GAB1	iHS	0.0007	iHS	0.0022
chr4	793	No Gene	iHS	0.0018	iHS	0.0005
chr4	803	No Gene	iHS	0.0083	iHS	0.0109
chr4	846	DDX60,ANXA10	iHS	0.004	XP-EHH	0.0163
chr5	544	No Gene	iHS	0.0114	iHS	0.0179
chr5	562	MCC	iHS	0.0042	iHS	0.0046
chr5	674	NEUROG1,CXCL14,C5orf20,TIFAB	XP-EHH	0.0018	XP-EHH	0.0186
			iHS	0.0198	iHS	0.0165
chr5	678	TRPC7	XP-EHH	0.0189	XP-EHH	0.0176
chr5	739	FBXO38,HTR4	XP-EHH	0.0139	XP-EHH	0.0078
chr6	48	No Gene	iHS	0.0185	iHS	0.0131
chr6	133	ABT1,BTN1A1,HMGNA4,ZNF322A	iHS	0.0051	iHS	0.011
chr6	174	ANKS1A,UHRF1BP1,SNRPC,TAF11	XP-EHH	0.0156	XP-EHH	0.0028
chr6	239	OPN5,C6orf138	iHS	0.0108	iHS	0.0007
chr6	313	KHDRBS2	iHS	0.0182	iHS	0.0093
chr6	350	BAI3	iHS	0.007	iHS	0.0057
chr6	417	No Gene	iHS	0.0035	iHS	0.0071
chr6	629	No Gene	iHS	0.0038	iHS	0.0051
chr7	40	GLCCI1,ICA1	XP-EHH	0.0007	XP-EHH	0.0079
chr7	71	DGKB	XP-EHH	0.0045	XP-EHH	0.0067
chr7	393	MAGI2	XP-EHH	0.0159	XP-EHH	0.016
chr7	400	CD36	XP-EHH	0.0025	XP-EHH	0.0007
chr7	493	MYH16,ARPC1A	iHS	0.0112	iHS	-
			XP-EHH	0.0132	XP-EHH	0.0102
chr7	675	FAM180A,SLC13A4,PL-5283	XP-EHH	0.0038	XP-EHH	0.0008
chr8	22	CSMD1	XP-EHH	0.0036	XP-EHH	0.0189
chr8	658	No Gene	XP-EHH	0.0157	XP-EHH	0.001
chr10	20	No Gene	XP-EHH	0.007	iHS	0.0194

chr10	286	No Gene	iHS	0.0141	iHS	0.0012
			XP-EHH	-	XP-EHH	0.0153
chr10	295	No Gene	iHS	0.0174	iHS	0.0147
chr10	376	KIAA0913,NDST2,FUT11,SEC24C,CHCHD1,PLAU,C10orf55,CAMK2G	iHS	0.0147	iHS	0.0178
chr10	473	EXOC6	iHS	0.0122	iHS	0.0184
chr10	474	EXOC6,CYP26A1,CYP26C1	iHS	0.0062	iHS	0.0019
chr10	475	MYOF	iHS	0.0031	iHS	0.0076
chr10	563	NCRNA00081,PDCD4,SHOC2	XP-EHH	0.0046	XP-EHH	0.0002
chr10	564	ADRA2A	XP-EHH	0.0136	XP-EHH	0.0001
chr10	609	No Gene	iHS	-	iHS	0.0197
			XP-EHH	0.0126	XP-EHH	0.0026
chr11	199	No Gene	iHS	0.0052	iHS	0.007
chr11	221	ALX4,EXT2	XP-EHH	0.012	XP-EHH	0.019
chr11	340	SAPS3	iHS	0.0024	iHS	0.0028
chr12	53	STYK1,MAGOHB,KLRA1,CSDA	XP-EHH	0.0194	XP-EHH	0.0109
chr12	163	FGD4,YARS2,DNM1L	iHS	0.0189	iHS	0.0162
chr12	225	SLC38A2	XP-EHH	0.002	XP-EHH	0.0012
chr12	226	No Gene	XP-EHH	0.009	XP-EHH	0.0091
chr13	152	C13orf26	XP-EHH	0.0013	XP-EHH	0.0128
chr13	302	No Gene	iHS	0.013	iHS	0.0155
chr13	483	MBNL2	XP-EHH	0.0095	XP-EHH	0.0002
chr13	519	No Gene	iHS	0.0078	iHS	0.013
chr14	313	KCNH5,RHOJ	iHS	-	iHS	0.0131
			XP-EHH	0.0014	XP-EHH	0.0022
chr14	343	WDR22,EXDL2,GALNTL1	iHS	0.0004	iHS	0.0013
chr14	434	No Gene	iHS	0.0118	iHS	0.0192
chr15	135	KIAA0574,APBA2	XP-EHH	0.0005	XP-EHH	0.0145
chr15	160	AVEN,C15orf24,CHRM5,PGBD4	XP-EHH	0.0011	XP-EHH	0.0081
chr15	206	TGM5,TGM7,CCNDBP1,EPB42,TMEM62	iHS	0.0067	iHS	0.012
chr15	217	C15orf21,SPATA5L1,SLC30A4,GATM,C15orf48	iHS	0.0163	iHS	0.0072
chr15	329	LBXCOR1,MAP2K5	iHS	0.0117	iHS	0.006
chr15	432	NTRK3	iHS	0.0193	iHS	0.0144
chr16	149	DOC2A,PPP4C,ASPHD1,TMEM219,FAM57B,FLJ25404,TAOK2,KCTD13,SEZ6L2,ALDOA,HIRIP	iHS	0.0034	iHS	0.0042

		3,INO80E				
chr16	321	No Gene	iHS	0.0002	iHS	0.0052
chr16	403	MPHOSPH6,HSD17B2,SDR42E1	XP-EHH	0.0141	XP-EHH	0.017
chr20	0	C20orf96,DEFB127,DEFB128,DEFB132,DEFB129,DEFB125,DEFB126	XP-EHH	0.0062	XP-EHH	0.0018
chr20	167	GDF5,UQCC,CEP250,ERGIC3	iHS	0.0021	iHS	0.0113
chr20	293	No Gene	XP-EHH	0.0009	XP-EHH	0.0121
chr21	79	No Gene	XP-EHH	0.0112	iHS	0.0052
chr21	208	FAM3B,TMPRSS2,MX1,MX2	XP-EHH	0.0006	XP-EHH	0.0059
chr22	242	BRD1	iHS	-	iHS	0.0053
			XP-EHH	0.0031	XP-EHH	0.0015

Supplementary Table 2. Overlap of Tibetan and Mongolian selection candidate regions at p < 0.02 level in iHS and/or XP-EHH selection scans

Chr	200KB Region	Gene List	DU Mongolian	p	Buryat Mongolian	p	TTR Tibetan	p	Maduo Tibetan	p
chr1	117	TCEA3,ZNF436,HNRNPR,C1orf213	iHS	0.0079					iHS	0.0141
chr1	251	AGBL4,ELAVL4			iHS	0.0032	iHS	0.0139	iHS	0.0083
							XP-EHH	0.0124		
chr1	252	ELAVL4	iHS	0.0143			XP-EHH	0.0136		
chr1	254	FAF1	iHS	0.0028			XP-EHH	0.0165		
chr1	377	SLC44A5	iHS	0.0008	iHS	0.0148	XP-EHH	0.0081		
chr1	411	LPHN2			iHS	0.0117	iHS	0.0128		
chr1	569	MAGI3	iHS	0.0145	iHS	0.0003	iHS	0.0124		
chr1	767	GBAP,PKLR ^b ,C1orf104,SCAMP3,MTX1,GBA,HCN3,TRIM46,KRTCAP2,FDPS,MUC1,C1orf2,CLK2,THBS3,ASH1L,RUSC1	iHS	0.0092			iHS	0.0043	iHS	0.02
chr1	799	DUSP12,FCGR3B,FCRLA,LOC641311,FCGR2B,FCRLB,HSPA7,FCGR2C	iHS	0.0093			iHS	0.0068		
chr1	890	FAM163A,TOR1AIP2,IFRG15,CEP350,TOR1AIP1	iHS	0.0095			iHS	0.0142	iHS	0.0035
chr1	894	XPR1	iHS	0.012	iHS	0.0167			iHS	0.0135
chr1	898	CACNA1E	XP-EHH	0.0039					iHS	0.0095
chr1	1026	PFKFB2,C4BPB,C4BPA,FCAMR,YOD1,C1orf116			iHS	0.0073			iHS	0.0115
chr1	1070	USH2A	XP-EHH	0.0089					XP-EHH	0.0131
chr1	1124	ITPKB,C1orf95			XP-EHH	0.0039			XP-EHH	0.0064
chr2	88	VSNL1,SMC6,GEN1	iHS	0.0013			XP-EHH	0.0129	iHS	0.0023
chr2	162	BIRC6	XP-EHH	0.0117					XP-EHH	0.0122
chr2	163	BIRC6,TTC27	XP-EHH	0.0066					XP-EHH	0.0062
chr2	231	PRKCE,EPAS1 ^b	XP-EHH	0.0069					XP-EHH	0.0015
chr2	236	C2orf61,CALM2			XP-EHH	0.016			XP-EHH	0.0079
chr2	342	PLEK,APLF,CNRIP1,FBXO48	iHS	0.0057			iHS	0.0145		
chr2	430	PTCD3,POLR1A			iHS	0.0081	XP-EHH	0.0027		

					XP-EHH	0.01				
chr2	522	LOC150568	XP-EHH	0.0015					XP-EHH	0.0066
chr2	541	SULT1C3,SULT1C2,SULT1C4	iHS	0.0013	iHS	0.0002			iHS	0.0105
chr2	544	EDAR,CCDC138	iHS	0.0035			iHS	0.0164		
chr2	772	GALNT13	iHS	0.01					iHS	0.0073
chr2	793	CCDC148,UPP2			iHS	0.0128	iHS	0.0172		
chr2	838	XIRP2	XP-EHH	0.0134					XP-EHH	0.0087
chr2	891	PDE11A	XP-EHH	0.0149	iHS	0.0096	XP-EHH	0.0101		
					XP-EHH	0.0027				
chr2	916	DNAJC10	XP-EHH	0.0003					XP-EHH	0.0022
chr2	951	PMS1,ORMDL1,ANKAR,OSGEPL1,ASNSD1			iHS	0.0118	XP-EHH	0.0036	iHS	0.0118
chr2	1020	RAPH1,ABI2	iHS	0.0134	iHS	0.0195	iHS	0.0117		
chr2	1094	C2orf62,GPBAR1,SLC11A1,TMBIM1,PNKD,CTDSP1,AAMP,ARPC2,VIL1	iHS	0.019			iHS	0.0168	iHS	0.0056
chr2	1095	USP37,RQCD1,PLCD4,VIL1			iHS	0.0181	iHS	0.0099		
chr3	62	PPARG,TSEN2,MKRN2	iHS	0.0071			iHS	0.0148	iHS	0.0178
chr3	127	RARB			XP-EHH	0.0038	XP-EHH	0.0006		
chr3	242	PLXNB1,CCDC51,ATRIP,TREX1,PFKFB4,FBXW12,UCN2,CCDC72,SHISA5,COL7A1	iHS	0.0053					iHS	0.0031
chr3	327	MAGI1	iHS	0.0159	iHS	0.0036			iHS	0.0114
chr3	490	EPHA6			iHS	0.0004			iHS	0.0168
chr3	543	BBX			iHS	0.0029	iHS	0.0028		
chr3	551	MORC1			iHS	0.0122			iHS	0.0121
chr3	552	DPPA2,DPPA4	iHS	0.0024					iHS	0.0082
chr3	579	ZBTB20	iHS	0.0019			iHS	0.0135	iHS	0.0037
chr3	789	TIPARP	iHS	0.0126					iHS	0.013
chr3	793	VEPH1,PTX3,C3orf55			XP-EHH	0.0069			XP-EHH	0.0107
chr3	813	OTOL1	iHS	0.0189					iHS	0.0126
chr3	844	SERPINI1,WDR49,PDCD10			iHS	0.0159	iHS	0.0019	iHS	0.0196

chr4	99	SLIT2	iHS	0.0166					iHS	0.0086
chr4	107	NCRNA00099,KCNIP4	iHS	0.0152			iHS	0.0027	iHS	0.0007
chr4	206	LIMCH1	iHS	0.0157			iHS	0.0089		
chr4	207	PHOX2B			iHS	0.0185	iHS	0.0033		
chr4	481	UNC5C,BMPR1B	XP-EHH	0.0196	XP-EHH	0.0047	XP-EHH	0.0111		
chr4^a	614	TMEM155,CCNA2,EXOSC9,ANXA5,LOC100192379,BBS7	XP-EHH	0.0061	iHS	0.0083	iHS	0.0179	iHS	0.0044
									XP-EHH	0.004
chr4	615	TRPC3,BBS7			iHS	0.0153			iHS	0.0029
									XP-EHH	0.0027
chr4	718	INPP4B			iHS	0.0102	iHS	0.0105	iHS	0.0175
chr4	719	INPP4B	iHS	0.005	iHS	0.0027	iHS	0.0051	iHS	0.0053
chr4	721	USP38	iHS	0.0005			iHS	0.0053	iHS	0.0025
chr4	722	GAB1	iHS	0.0007	iHS	0.0022	iHS	0.0192		
chr4	743	EDNRA ^c ,TMEM184C,LOC90826			iHS	0.0121			iHS	0.0118
									XP-EHH	0.0078
chr4	792	GRIA2	iHS	0.0016			iHS	0.0152		
chr4	802	RAPGEF2	iHS	0.002			iHS	0.0055	iHS	0.0005
chr5	135	CDH9	iHS	0.0192					iHS	0.0197
chr5	216	ZNF131,HMGCS1,MGC42105			iHS	0.018			iHS	0.0156
chr5	323	ADAMTS6	iHS	0.0063					iHS	0.0155
chr5	501	ST8SIA4	XP-EHH	0.0129			iHS	0.0067		
chr5	562	MCC	iHS	0.0042	iHS	0.0046	iHS	0.0017	iHS	0.0027
									XP-EHH	0.0063
									XP-EHH	0.0164
chr6	133	ABT1,BTN1A1,HMG4,ZNF322A	iHS	0.0051	iHS	0.011	iHS	0.0046		
chr6	157	HCP5,MICA,HLA-B,MICB,HCG26			iHS	0.0095	iHS	0.0069	iHS	0.0074
chr6	162	BTNL2,HLA-DRA,C6orf10,HLA-DRB5	iHS	0.0123			iHS	0.0098		
chr6	238	CD2AP,GPR111,GPR115			iHS	0.0067			iHS	0.001
chr6	239	OPN5,C6orf138	iHS	0.0108	iHS	0.0007			iHS	0.0152
chr6	313	KHDRBS2	iHS	0.0182	iHS	0.0093	iHS	0.0136		

chr6	400	HMGN3	iHS	0.0175					iHS	0.0199
chr6	418	UBE2CBP	iHS	0.0115			iHS	0.0073		
chr6	544	LACE1,FOXO3	iHS	0.0075			iHS	0.0037		
chr6	596	ASF1A,FAM184A,MCM9	iHS	0.0109			iHS	0.0098	iHS	0.003
chr6	724	UTRN			XP-EHH	0.0137			XP-EHH	0.0132
chr6	725	UTRN			XP-EHH	0.0031			XP-EHH	0.0005
chr7	19	SDK1			iHS	0.0048	XP-EHH	0.0119		
chr7	101	MACC1,ITGB8	XP-EHH	0.0172					XP-EHH	0.0042
chr7	189	EPDR1,TXNDC3,SFRP4	XP-EHH	0.0002					XP-EHH	0.0069
chr7	325	GUSB,VKORC1L1,ASL	iHS	0.0071					iHS	0.0057
chr7	412	PCLO			iHS	0.009			XP-EHH	0.0032
chr7	562	LOC401397,GPR85	iHS	0.0009					iHS	0.0059
chr7	645	NRF1			iHS	0.0077			iHS	0.0164
chr7	646	UBE2H			iHS	0.0134	iHS	0.0139		
chr7	664	EXOC4	iHS	0.0115					iHS	0.0139
chr7	711	TRPV6,C7orf34,EPHB6,KEL,TRPV5	iHS	0.0057			iHS	0.0036	iHS	0.0054
chr9	139	LINGO2	XP-EHH	0.0071					iHS	0.0171
chr9	359	MAMDC2	XP-EHH	0.0034			iHS	0.019	XP-EHH	0.0025
			iHS	0.0148					iHS	0.0116
chr9	451	NXNL2,SPIN1			iHS	0.02	iHS	0.0133	iHS	0.0167
chr9	478	BARX1	XP-EHH	0.0033					XP-EHH	0.0072
chr9	479	PTPDC1	XP-EHH	0.0042					XP-EHH	0.0053
chr9	627	DENND1A	iHS	0.0033			iHS	0.0009		
chr9	649	CIZ1,NAIF1,LCN2,C9orf16,LOC389791,SLC25A25,PTGES2	iHS	0.0088			iHS	0.0158		
chr10	19	KLF6	XP-EHH	0.0179					XP-EHH	0.0028
chr10	84	RSU1,CUBN			XP-EHH	0.011			XP-EHH	0.0125
chr10	128	GPR158	iHS	0.02			XP-EHH	0.0118		
chr10	271	MBL2			XP-EHH	0.0024			XP-EHH	0.0198
chr10	276	PCDH15			iHS	0.0125	iHS	0.0176		
chr10	397	RPS24,POLR3A	XP-EHH	0.0149					XP-EHH	0.0148
chr10	454	LIPA,CH25H	iHS	0.009			iHS	0.0179		

chr10	475	MYOF	iHS	0.0031	iHS	0.0076	iHS	0.011	iHS	0.0143
chr10	563	NCRNA00081,PDCD4,SHOC2	XP-EHH	0.0046	XP-EHH	0.0002	XP-EHH	0.0035		
chr10	675	C10orf125,PRAP1,CALY,ECHS1,CYP2E1 ^b ,SPRN,PAOX,MTG1,LOC619207	iHS	0.0045					iHS	0.0148
			XP-EHH	0.0017						
chr10	676	FRG2B,SYCE1,DUX4,CYP2E1 ^b ,LOC728410,LOC653544,LOC653545,LOC653543	XP-EHH	0.0026					XP-EHH	0.0074
chr11	218	HSD17B12	iHS	0.0096			iHS	0.0104		
chr11	221	ALX4,EXT2	XP-EHH	0.012	XP-EHH	0.019			XP-EHH	0.0178
chr11	283	APLNR,LRRC55			iHS	0.015			iHS	0.0183
									XP-EHH	0.0112
chr11	284	P2RX3,PRG3,SLC43A3,RTN4RL2,SSRP1,TNKS1BP1,PRG2			iHS	0.0127			iHS	0.0101
chr11	544	C11orf87			XP-EHH	0.0154			XP-EHH	0.0102
chr12	5	ERC1	iHS	0.0005			iHS	0.0122		
							XP-EHH	0.0086		
chr12	46	PZP,LOC642846	XP-EHH	0.0091			iHS	0.0131	iHS	0.0107
chr12	61	BCL2L14,LOH12CR2,LRP6,MANSC1	XP-EHH	0.0059			iHS	0.0047	iHS	0.0028
									XP-EHH	0.0118
chr12	211	ADAMTS20	iHS	0.0192			XP-EHH	0.0175		
			XP-EHH	0.0119						
chr12	212	PUS7L,IRAK4,TWF1,TMEM117	iHS	0.0029			XP-EHH	0.0178		
			XP-EHH	0.013						
chr12	265	GTSF1,COPZ1,NCKAP1L,ITGA5,ZNF385A,GPR84	iHS	0.0047			iHS	0.0198		
chr12	470	FGD6,VEZT	XP-EHH	0.0092					XP-EHH	0.0079
chr12	489	ANKS1B	iHS	0.0153					iHS	0.0173
chr12	594	CCDC64	XP-EHH	0.0029					XP-EHH	0.0048
chr13	330	PCDH9	iHS	0.0065			iHS	0.0172		
chr13	426	SLITRK6			iHS	0.014			iHS	0.0147
chr13	504	NALCN,ITGBL1	XP-EHH	0.0102					XP-EHH	0.0195
chr14	344	ERH,SLC39A9,GALNTL1	iHS	0.001					iHS	0.0151

chr14	383	TMEM63C,KIAA1737,ZDHHC22	XP-EHH	0.0133					XP-EHH	0.012
chr15	145	TRPM1,MTMR10,MTMR15	iHS	0.0017			iHS	0.008		
chr15	206	TGM5,TGM7,CCNDBP1,EPB42,TMEM62	iHS	0.0067	iHS	0.012	iHS	0.01		
chr15	217	C15orf21,SPATA5L1,SLC30A4,GATM,C15orf48	iHS	0.0163	iHS	0.0072	iHS	0.0031		
			iHS	0.0163			XP-EHH	0.0037		
chr15	309	DAPK2,HERC1	iHS	0.0068			iHS	0.0026		
chr15	310	DAPK2,SNX1,FAM96A	iHS	0.0049			iHS	0.0013		
chr15	311	CSNK1G1,SNX1,SNX22,PPIB	iHS	0.0037			iHS	0.004		
chr15	329	LBXCOR1,MAP2K5	iHS	0.0117	iHS	0.006	iHS	0.0025	iHS	0.0018
chr15	456	RGMA,CHD2	iHS	0.003			iHS	0.0061	iHS	0.0036
chr16	8	HN1L,IGFALS,SPSB3,EME2,NUBP2,M RPS34,NME3,IFT140,HAGH,MAPK8IP 3,CRAMP1L			XP-EHH	0.0016			XP-EHH	0.0001
chr16	23	ROGDI,C16orf71,ANKS3,NUDT16L1,N- PAC,ZNF500,SEPT12,FAM100A,MGR N1	iHS	0.0135			iHS	0.0132		
chr16	78	NDE1,MYH11,KIAA0430	XP-EHH	0.0018					XP-EHH	0.0035
chr16	154	BCL7C,STX1B,NCRNA00095,ZNF646, CTF1,FBXL19,HSD3B7,ORAI3,ZNF668 ,SETD1A,STX4	iHS	0.0156			XP-EHH	0.012		
chr16	260	RBL2,AKTIP,RPGRIP1L			XP-EHH	0.0082	iHS	0.018		
chr16	408	CDH13			XP-EHH	0.0035			XP-EHH	0.0173
chr16	443	PRDM7,GAS8,DBNDD1,C16orf3			iHS	0.0015			iHS	0.006
chr17	99	AKAP10,SPECC1	iHS	0.006			iHS	0.0014		
chr17	100	SPECC1,CCDC144C	iHS	0.0016			iHS	0.0009		
chr17	121	SEZ6,PIPOX,DHRS13,ERAL1,FLOT2,P HF12			iHS	0.0074	iHS	0.0127		
chr20	95	LOC100130264,SLC24A3			iHS	0.0149	iHS	0.0181	iHS	0.0068
chr20	112	FOXA2			iHS	0.0037			iHS	0.0099
chr20	166	FAM83C,EIF6,UQCC,PROCR,MMP24	iHS	0.0082			iHS	0.0111	iHS	0.0019
chr20	167	UQCC,GDF5,CEP250,ERGIC3	iHS	0.0021	iHS	0.0113	iHS	0.0015	iHS	0.0022
chr20	170	SCAND1,PHF20,EPB41L1,C20orf152	iHS	0.0001					iHS	0.0024
chr20	185	DHX35,FAM83D			XP-EHH	0.0134			iHS	0.0143

chr20	240	TMEM189, TMEM189-UBE2V1, SNAI1, UBE2V1, RNF114	XP-EHH	0.0063					XP-EHH	0.0099
chr21	221	C21orf33, AGPAT3, TRAPPC10, PWP2			XP-EHH	0.02			iHS	0.0172
chr22	86	DGCR6, PRODH, DGCR5, DGCR9	iHS	0.014			iHS	0.012		
chr22	174	APOL4, APOL2, APOL3, APOL1	iHS	0.0026					iHS	0.0172

^a Candidate regions that are identified in all four populations are in bold.

^b Highlighted as high-altitude selection candidates in Tibetans (Simonson et al. 2010; Yi et al. 2010; Wuren et al. submitted) and exclusively in DU Mongolians

^c Highlighted as high-altitude selection candidates in Tibetans (Simonson et al. 2010) and Buryat Mongolians, but not DU Mongolians

Supplementary Table 3: Top 2% of PBS selection candidate regions identified in DU Mongolians

Chr	200 KB region	Gene list	p
chr4	345	UGT2B17,UGT2B15,TMPRSS11E2,TMPRSS11E	0.0001
chr8	453	No genes in this region	0.0001
chr1	1049	SLC30A1,NEK2,LPGAT1	0.0002
chr9	149	No genes in this region	0.0003
chr6	623	NKAIN2	0.0004
chr2	790	ACVR1C,CYTIP	0.0004
chr11	179	LDLRAD3	0.0005
chr12	214	TMEM117	0.0006
chr7	247	No genes in this region	0.0007
chr12	579	TESC,FBXW8,HRK	0.0007
chr21	82	C21orf34	0.0008
chr12	500	SLC5A8,ANO4,UTP20	0.0009
chr1	579	VANGL1	0.0010
chr6	581	FRK	0.0010
chr6	224	SUPT3H	0.0011
chr2	395	REG1B,REG3G	0.0012
chr8	82	No genes in this region	0.0013
chr9	374	ANXA1	0.0013
chr5	311	No genes in this region	0.0014
chr15	421	No genes in this region	0.0015
chr14	139	No genes in this region	0.0016
chr17	305	CCDC46	0.0016
chr4	301	No genes in this region	0.0017
chr4	735	ZNF827	0.0018
chr7	395	No genes in this region	0.0019
chr9	504	COL15A1,TGFBR1	0.0019
chr18	331	No genes in this region	0.0020

chr3	720	PCOLCE2,PAQR9,TRPC1	0.0021
chr16	112	LOC23117,LOC100132247,LOC100190986,LOC653786	0.0022
chr16	107	IGSF6,IMAA,METTLL9,OTOA	0.0022
chr15	308	FBXL22,HERC1,USP3	0.0023
chr2	525	MRPS9	0.0024
chr11	305	RPLP0P2,C11orf66,SYT7	0.0025
chr11	354	NADSYN1,KRTAP5-10,KRTAP5-7,KRTAP5-8,DHCR7,KRTAP5-11,KRTAP5-9	0.0025
chr17	45	NTN1,STX8	0.0026
chr2	587	No genes in this region	0.0027
chr2	19	No genes in this region	0.0028
chr2	894	OSBPL6	0.0028
chr15	307	USP3,CA12	0.0029
chr3	12	CNTN4	0.0030
chr12	61	BCL2L14,LOH12CR2,LRP6,MANSC1	0.0031
chr9	478	BARX1	0.0031
chr18	347	No genes in this region	0.0032
chr7	268	No genes in this region	0.0033
chr10	315	C10orf107	0.0034
chr22	123	MYO18B	0.0034
chr13	125	ATP8A2	0.0035
chr6	504	SIM1	0.0036
chr2	854	MYO3B	0.0037
chr4	726	GYP A	0.0037
chr19	101	ZNF826,LOC284441	0.0038
chr2	260	No genes in this region	0.0039
chr8	16	CSMD1	0.0040
chr8	509	YWHAZ,PABPC1	0.0040
chr15	401	FAM154B,EFTUD1	0.0041
chr2	231	PRKCE,EPAS1	0.0042
chr5	612	PRDM6,PPIC	0.0043

chr3	849	No genes in this region	0.0043
chr20	217	SYS1,WFDC2,SYS1-DBNDD2,PIGT,DBNDD2,SPINT3,SDC4,TP53TG5,WFDC6	0.0044
chr20	308	PRIC285,C20orf195,EEF1A2,RTEL1,C20orf149,SRMS,PTK6,GMEB2,TNFRSF6B,STMN3	0.0045
chr5	710	FGF1,ARHGAP26	0.0046
chr15	254	ONECUT1	0.0046
chr13	462	No genes in this region	0.0047
chr13	461	GPC5	0.0048
chr3	61	PPARG,GSTM1L,SYN2	0.0049
chr16	119	PRKCB	0.0049
chr7	36	COL28A1,C1GALT1	0.0050
chr1	813	PBX1	0.0051
chr14	383	TMEM63C,KIAA1737,ZDHHC22	0.0052
chr6	844	SMOC2	0.0052
chr13	501	No genes in this region	0.0053
chr3	571	GTPBP8,C3orf17	0.0054
chr3	623	PTPLB,ADCY5	0.0055
chr12	569	No genes in this region	0.0055
chr13	504	NALCN,ITGBL1	0.0056
chr12	633	No genes in this region	0.0057
chr12	68	GRIN2B	0.0058
chr13	168	No genes in this region	0.0058
chr1	805	DDR2,C1orf110,HSD17B7	0.0059
chr1	1198	FH,KMO	0.0060
chr5	691	LRRTM2,SIL1,CTNNA1	0.0061
chr4	788	No genes in this region	0.0061
chr5	86	BASP1	0.0062
chr11	429	CCDC81,ME3	0.0063
chr2	897	CCDC141	0.0064
chr2	84	No genes in this region	0.0064
chr3	850	C3orf50	0.0065

chr1	295	JUN	0.0066
chr15	436	HAPLN3,ACAN,MFGE8	0.0067
chr20	286	ZNF831,EDN3	0.0067
chr17	75	PMP22,TEKT3	0.0068
chr6	607	C6orf170	0.0069
chr16	53	FAM18A,TEKT5,NUBP1	0.0070
chr12	311	DPY19L2	0.0070
chr11	399	No genes in this region	0.0071
chr11	117	No genes in this region	0.0072
chr10	402	ZMIZ1,LOC283050	0.0073
chr5	751	ZNF300,TNIP1,GPX3	0.0073
chr1	1024	MAPKAPK2,RASSF5,DYRK3,LGTN	0.0074
chr7	43	NXPH1	0.0075
chr5	168	ADAMTS12	0.0076
chr1	1071	USH2A	0.0076
chr11	473	SESN3	0.0077
chr13	131	GPR12	0.0078
chr2	685	No genes in this region	0.0079
chr3	436	CHMP2B,POU1F1	0.0079
chr3	852	MDS1	0.0080
chr2	885	No genes in this region	0.0081
chr12	69	GRIN2B	0.0082
chr1	1048	RD3,TRAF5	0.0082
chr1	992	FAM58B,NR5A2	0.0083
chr7	378	HSPB1,YWHAG,FLJ37078	0.0084
chr3	967	FGF12	0.0085
chr8	639	No genes in this region	0.0085
chr16	133	No genes in this region	0.0086
chr3	708	CLSTN2	0.0087
chr13	238	ITM2B,RB1	0.0088

chr7	377	TMEM120A,MDH2,SNORA14A,STYXL1,POR	0.0088
chr2	519	No genes in this region	0.0089
chr5	68	DNAH5	0.0090
chr4	142	No genes in this region	0.0091
chr4	113	No genes in this region	0.0091
chr20	288	PHACTR3	0.0092
chr15	232	FBN1,DUT	0.0093
chr5	7	SLC6A3,LPCAT1	0.0094
chr7	516	RELN	0.0094
chr8	657	ASAP1	0.0095
chr14	218	No genes in this region	0.0096
chr4	308	No genes in this region	0.0097
chr7	148	LOC646762	0.0097
chr15	200	PLA2G4E,EHD4,PLA2G4D	0.0098
chr3	624	MYLK	0.0099
chr1	211	GUCA2B	0.0100
chr1	68	PRAMEF21,PDPN,PRAMEF20	0.0100
chr7	348	AUTS2	0.0101
chr2	672	No genes in this region	0.0102
chr11	400	No genes in this region	0.0103
chr2	18	ALLC,RPS7,COLEC11	0.0103
chr3	10	CNTN4	0.0104
chr6	845	No genes in this region	0.0105
chr15	352	ARIH1,HEXA,TMEM202	0.0106
chr5	149	No genes in this region	0.0106
chr3	975	No genes in this region	0.0107
chr5	733	STK32A,DPYSL3	0.0108
chr13	348	ATXN8OS	0.0109
chr2	1159	ARMC9,B3GNT7	0.0109
chr6	149	HCG4,HLA-F,HLA-G,HCG2P7,IFITM4P,HLA-H	0.0110

chr15	351	BRUNOL6,PARP6,PKM2,SENP8,GRAMD2	0.0111
chr3	9	No genes in this region	0.0112
chr18	99	TTC39C,CABYR,OSBPL1A	0.0112
chr4	34	KIAA0232,TBC1D14	0.0113
chr20	255	TSHZ2	0.0114
chr17	119	SDF2,ALDOC,SLC13A2,FOXN1,FLJ25006,KIAA0100,PIGS,UNC119,SPAG5,LOC645851	0.0115
chr17	95	LOC400581,B9D1,EPN2	0.0115
chr8	481	C8orf37,PLEKHF2	0.0116
chr2	300	No genes in this region	0.0117
chr2	859	METTLL8,C2orf37	0.0118
chr3	30	No genes in this region	0.0118
chr2	555	RGPD7,RGPD5,BUB1	0.0119
chr7	759	XRCC2	0.0120
chr2	855	MYO3B	0.0121
chr6	14	FAM136B,SERPINB6,NQO2,SERPINB9	0.0121
chr7	66	No genes in this region	0.0122
chr1	421	PRKACB,TTLL7	0.0123
chr22	162	LARGE	0.0124
chr9	67	No genes in this region	0.0124
chr1	235	CYP4Z2P,CYP4B1,CYP4A11	0.0125
chr18	44	KIAA0802	0.0126
chr13	167	RFC3	0.0127
chr8	265	ST18	0.0127
chr15	126	GABRG3	0.0128
chr6	608	GJA1,C6orf170	0.0129
chr22	196	MKL1	0.0130
chr9	377	No genes in this region	0.0130
chr13	237	SUCLA2,NUDT15,MED4	0.0131
chr11	250	LOC441601	0.0132
chr10	365	CDH23,C10orf54	0.0133

chr6	5	No genes in this region	0.0133
chr13	152	C13orf26	0.0134
chr2	70	No genes in this region	0.0135
chr20	69	SEL1L2,MACROD2	0.0136
chr4	196	C4orf34,UGDH,UBE2K	0.0136
chr14	177	BRMS1L	0.0137
chr15	405	RPS17,AP3B2,CPEB1	0.0138
chr1	1209	AKT3	0.0139
chr2	799	WDSUB1,BAZ2B	0.0139
chr13	427	No genes in this region	0.0140
chr3	705	CLSTN2	0.0141
chr8	586	No genes in this region	0.0142
chr21	196	No genes in this region	0.0142
chr6	381	SENP6,FILIP1	0.0143
chr8	32	AGPAT5,MCPH1,ANGPT2	0.0144
chr20	95	LOC100130264,SLC24A3	0.0145
chr15	239	ATP8B4	0.0145
chr22	195	ADSL,TNRC6B,SGSM3,MKL1	0.0146
chr18	315	No genes in this region	0.0147
chr15	425	AGBL1	0.0148
chr1	721	ITGA10,ANKRD35,RBM8A,PEX11B,GNRHR2,LIX1L,RNF115,PIAS3,NUDT17,POLR3C	0.0148
chr14	292	No genes in this region	0.0149
chr1	1174	ACTN2,HEATR1	0.0150
chr3	54	SLC6A11	0.0151
chr2	856	GAD1,MYO3B,SP5	0.0151
chr15	136	KIAA0574,NDNL2	0.0152
chr22	203	SREBF2,LOC339674,CENPM,NAGA,SEPT3,TNFRSF13C,WBP2NL	0.0153
chr11	660	OPCML	0.0154
chr1	310	INADL	0.0154
chr7	111	RAPGEF5	0.0155

chr8	619	ZHX2	0.0156
chr16	41	No genes in this region	0.0157
chr15	234	CEP152,EID1,SHC4	0.0157
chr20	209	TOX2	0.0158
chr13	197	No genes in this region	0.0159
chr6	693	KIAA1244,HEBP2	0.0160
chr10	190	ZNF248	0.0160
chr7	330	TYW1,C7orf42,SBDS	0.0161
chr6	497	FBXL4	0.0162
chr10	192	LOC100129055,ZNF37A	0.0162
chr15	446	RCCD1,MAN2A2,UNC45A,FURIN,FES,HDDC3,VPS33B,PRC1	0.0163
chr14	420	No genes in this region	0.0164
chr10	182	No genes in this region	0.0165
chr5	166	No genes in this region	0.0165
chr4	481	UNC5C,BMP1B	0.0166
chr5	818	No genes in this region	0.0167
chr12	312	TMEM5,SRGAP1	0.0168
chr22	104	VPREB1	0.0168
chr11	200	LRRC4C	0.0169
chr9	11	No genes in this region	0.0170
chr4	355	C4orf40,CSN3,ODAM,CSN1S2B,C4orf7	0.0171
chr12	600	CAMKK2,P2RX7,P2RX4	0.0171
chr2	510	IL1R2,IL1RL2,IL1R1	0.0172
chr17	152	RFFL,AMAC1,SLFN5,FNDC8,UNC45B,NLE1,RAD51L3	0.0173
chr10	454	LIPA,CH25H	0.0174
chr9	124	No genes in this region	0.0174
chr22	89	CDC45L,C22orf39,UFD1L,LOC150185,CLDN5,MRPL40	0.0175
chr10	54	No genes in this region	0.0176
chr12	19	PARP11	0.0177
chr9	679	NCRNA00094,WDR5,BRD3,VAV2	0.0177

chr2	1124	FAM124B	0.0178
chr2	847	SPC25,NOSTRIN,ABCB11,G6PC2	0.0179
chr2	1167	NGEF,GIGYF2,UNQ830	0.0180
chr17	48	GAS7,GLP2R,DHRS7C,RCVRN	0.0180
chr8	52	C8orf74,UNQ9391,RP1L1	0.0181
chr13	198	No genes in this region	0.0182
chr10	272	No genes in this region	0.0183
chr22	202	CCDC134,SREBF2,NHP2L1,MEI1,FLJ23584	0.0183
chr7	466	TFPI2,GNG11,GNGT1	0.0184
chr12	164	PKP2,YARS2	0.0185
chr7	40	GLCCI1,ICA1	0.0186
chr10	40	GATA3,FLJ45983,TAF3	0.0186
chr3	853	MDS1	0.0187
chr13	232	No genes in this region	0.0188
chr16	386	WWOX	0.0189
chr13	405	No genes in this region	0.0189
chr18	259	No genes in this region	0.0190
chr12	437	KITLG	0.0191
chr9	413	No genes in this region	0.0192
chr16	108	OTOA,LOC100190986,LOC730092	0.0192
chr12	632	No genes in this region	0.0193
chr6	403	ELOVL4,TTK	0.0194
chr15	270	NEDD4,RFX7	0.0195
chr11	359	CLPB,PDE2A	0.0195
chr5	263	No genes in this region	0.0196
chr19	305	NLRP11,NLRP13,NLRP4,NLRP8	0.0197
chr1	984	PTPRC	0.0198
chr1	1210	AKT3	0.0198
chr15	350	SENPA8,MYO9A	0.0199
chr9	127	No genes in this region	0.0200

Supplementary Table 4: Top 2% of selection candidate genes identified in the MR analysis in DU Mongolians

Gene	Chr	Begin	End	nSNP	nTail SNPs 05	nTail SNPs 01	nTail SNPs 005	MR05	MR01	MR005	P05	P01	P005
CUL2	chr10	35328811	35429300	12	11	7	0	13.91	25.8	0	1	0.998	0
GFPT1	chr2	69390408	69477886	13	11	0	0	12.84	0	0	1	0	0
KISS1	chr1	202416091	202442242	11	9	6	1	12.42	24.12	6.32	1	0.998	0.948
LCE1E	chr1	151015376	151037525	11	9	6	4	12.42	24.12	25.27	1	0.998	0.995
NET1	chr10	5434517	5500426	16	13	13	13	12.33	35.93	56.47	0.999	1	1
VPS13C	chr15	59921881	60149939	24	19	12	10	12.02	22.11	28.96	0.999	0.997	0.997
GLIPR1L2	chr12	74061155	74114087	14	11	10	10	11.93	31.59	49.64	0.999	1	1
KLK8	chr19	56181075	56206770	12	9	5	5	11.38	18.43	28.96	0.999	0.995	0.997
LCE1F	chr1	151005471	151025828	12	9	6	4	11.38	22.11	23.17	0.999	0.997	0.992
XRN2	chr20	21221941	21328463	16	12	11	8	11.38	30.4	34.75	0.999	0.999	0.998
LOC92973	chr9	35840270	35865515	11	8	3	3	11.04	12.06	18.95	0.998	0.982	0.989
NDUFS2	chr1	159425728	159460808	11	8	2	0	11.04	8.04	0	0.998	0.962	0
OR5B3	chr11	57916513	57937458	11	8	8	8	11.04	32.16	50.55	0.998	1	1
SLC30A6	chr2	32234436	32310313	11	8	8	3	11.04	32.16	18.95	0.998	1	0.989
SYCE1	chr10	135207394	135242866	22	16	15	3	11.04	30.15	9.48	0.998	0.999	0.969
ZNF148	chr3	126417202	126586888	31	22	1	0	10.77	1.43	0	0.998	0.819	0
BLVRA	chr7	43754796	43823466	10	7	3	2	10.62	13.27	13.9	0.998	0.986	0.981
IFNGR2	chr21	33687071	33741698	10	7	5	3	10.62	22.11	20.85	0.998	0.997	0.991
ST3GAL5	chr2	85909781	85979668	20	14	11	11	10.62	24.32	38.23	0.998	0.998	0.999
C16orf73	chr16	1813989	1872103	22	15	6	0	10.35	12.06	0	0.998	0.982	0
C12orf51	chr12	111072493	111238421	21	14	13	13	10.12	27.38	43.02	0.997	0.999	0.999
CD46	chr1	205982024	206045481	12	8	7	4	10.12	25.8	23.17	0.997	0.998	0.992
CDC16	chr13	114008463	114066252	12	8	3	1	10.12	11.06	5.79	0.997	0.978	0.942
GRK4	chr4	2925140	3022272	27	18	4	3	10.12	6.55	7.72	0.997	0.951	0.963
IPO7	chr11	9352779	9433651	15	10	10	10	10.12	29.48	46.33	0.997	0.999	1

MDH2	chr7	75505328	75543866	12	8	7	4	10.12	25.8	23.17	0.997	0.998	0.992
SLC28A2	chr15	43321725	43365425	24	16	0	0	10.12	0	0	0.997	0	0
SFRS2B	chr11	94429703	94454036	14	9	3	2	9.76	9.48	9.93	0.997	0.973	0.97
TRPC2	chr11	3594289	3625365	14	9	5	4	9.76	15.79	19.86	0.997	0.99	0.99
AFF4	chr5	132228969	132337253	11	7	4	4	9.66	16.08	25.27	0.996	0.991	0.995
C4orf10	chr4	2897075	2932591	11	7	1	0	9.66	4.02	0	0.996	0.915	0
CPOX	chr3	99770979	99805131	11	7	4	2	9.66	16.08	12.64	0.996	0.991	0.978
KIAA1377	chr11	101280955	101387003	22	14	0	0	9.66	0	0	0.996	0	0
SIM1	chr6	100933470	101028272	33	21	16	16	9.66	21.44	33.7	0.996	0.997	0.998
SR140	chr3	144193061	144272257	22	14	2	1	9.66	4.02	3.16	0.996	0.915	0.902
SSTR4	chr20	22954056	22975314	11	7	4	3	9.66	16.08	18.95	0.996	0.991	0.989
TFAP2D	chr6	50779215	50858705	11	7	7	4	9.66	28.14	25.27	0.996	0.999	0.995
ZNF37A	chr10	38413280	38462284	11	7	1	1	9.66	4.02	6.32	0.996	0.915	0.948
MCCC2	chr5	70908870	71000286	24	15	4	2	9.49	7.37	5.79	0.996	0.956	0.942
TUBAL3	chr10	5415060	5446793	16	10	10	10	9.49	27.64	43.44	0.996	0.999	0.999
GOLT1A	chr1	202423910	202459843	13	8	5	0	9.34	17.01	0	0.996	0.993	0
NGDN	chr14	22998737	23027242	13	8	3	0	9.34	10.21	0	0.996	0.975	0
TFPI2	chr7	93343680	93368001	13	8	7	7	9.34	23.81	37.42	0.996	0.998	0.999
GJB6	chr13	19684100	19714534	10	6	2	1	9.11	8.84	6.95	0.995	0.967	0.955
GOLPH3L	chr1	148875324	148946296	20	12	10	3	9.11	22.11	10.43	0.995	0.997	0.972
GOSR2	chr17	42345484	42383732	20	12	2	1	9.11	4.42	3.48	0.995	0.925	0.907
HUS1	chr7	47960307	47995771	10	6	5	5	9.11	22.11	34.75	0.995	0.997	0.998
NOP14	chr4	2899461	2944916	10	6	1	0	9.11	4.42	0	0.995	0.925	0
TAS2R49	chr12	11029827	11051741	10	6	0	0	9.11	0	0	0.995	0	0
ZNF554	chr19	2760871	2797733	10	6	6	5	9.11	26.53	34.75	0.995	0.999	0.998
ZNF555	chr19	2782481	2815035	10	6	6	5	9.11	26.53	34.75	0.995	0.999	0.998
DIXDC1	chr11	111303136	111408517	12	7	2	0	8.85	7.37	0	0.994	0.956	0
KPNA5	chr6	117099059	117179723	12	7	6	6	8.85	22.11	34.75	0.994	0.997	0.998
ZNF787	chr19	61280543	61334461	12	7	5	0	8.85	18.43	0	0.994	0.995	0
ZNF829	chr19	42064092	42109030	12	7	2	0	8.85	7.37	0	0.994	0.956	0
BDP1	chr5	70777197	70909405	26	15	1	0	8.76	1.7	0	0.994	0.833	0

DEPDC1B	chr5	59918495	60041713	14	8	5	5	8.67	15.79	24.82	0.994	0.99	0.994
GLUL	chr1	180608291	180637573	14	8	0	0	8.67	0	0	0.994	0	0
GOLSYN	chr8	110645580	110783196	42	24	19	14	8.67	20.01	23.17	0.994	0.996	0.992
RNF212	chr4	1045268	1107582	21	12	4	0	8.67	8.42	0	0.994	0.966	0
RWDD1	chr6	116989275	117031129	14	8	8	8	8.67	25.27	39.71	0.994	0.998	0.999
TEDDM1	chr1	180623874	180646374	14	8	1	1	8.67	3.16	4.96	0.994	0.892	0.931
FOXJ3	chr1	42404796	42583490	23	13	2	0	8.58	3.85	0	0.994	0.912	0
HICE1	chr19	17011570	17057343	16	9	2	1	8.54	5.53	4.34	0.993	0.941	0.921
UMPS	chr3	125921902	125956730	16	9	4	0	8.54	11.06	0	0.993	0.978	0
FDX1	chr11	109795803	109850815	27	15	9	9	8.43	14.74	23.17	0.993	0.988	0.992
GBF1	chr10	103985298	104142639	18	10	1	1	8.43	2.46	3.86	0.993	0.866	0.913
GSTA4	chr6	52940705	52978137	18	10	9	8	8.43	22.11	30.89	0.993	0.997	0.998
FRRS1	chr1	99936846	100013937	31	17	14	6	8.32	19.97	13.45	0.993	0.996	0.981
ARNT	chr1	149038809	149125810	11	6	3	2	8.28	12.06	12.64	0.991	0.982	0.978
C12orf30	chr12	110938875	111040980	11	6	5	5	8.28	20.1	31.59	0.991	0.996	0.998
C15orf42	chr15	87909821	87982257	22	12	0	0	8.28	0	0	0.991	0	0
CCL4	chr17	31445332	31467127	11	6	4	3	8.28	16.08	18.95	0.991	0.991	0.989
CDRT4	chr17	15270062	15321650	22	12	4	4	8.28	8.04	12.64	0.991	0.962	0.978
FAM55C	chr3	102970718	103039763	11	6	1	1	8.28	4.02	6.32	0.991	0.915	0.948
HMSD	chr18	59757567	59788625	11	6	0	0	8.28	0	0	0.991	0	0
LOC285194	chr3	117901324	117928575	22	12	3	3	8.28	6.03	9.48	0.991	0.947	0.969
NSL1	chr1	210956117	211041762	22	12	0	0	8.28	0	0	0.991	0	0
OR1S1	chr11	57728792	57749770	11	6	2	1	8.28	8.04	6.32	0.991	0.962	0.948
RBP5	chr12	7157553	7182733	11	6	1	0	8.28	4.02	0	0.991	0.915	0
TCL1B	chr14	95212515	95238720	11	6	4	4	8.28	16.08	25.27	0.991	0.991	0.995
TMEM155	chr4	122889534	122915790	11	6	4	3	8.28	16.08	18.95	0.991	0.991	0.989
VAMP8	chr2	85648158	85672667	11	6	6	6	8.28	24.12	37.91	0.991	0.998	0.999
ZNF143	chr11	9429088	9516647	11	6	5	5	8.28	20.1	31.59	0.991	0.996	0.998
MKL1	chr22	39126237	39372636	24	13	8	8	8.22	14.74	23.17	0.991	0.988	0.992
HLA-G	chr6	29892734	29916878	13	7	4	3	8.17	13.61	16.04	0.991	0.987	0.986
OR4B1	chr11	48184937	48205867	13	7	4	2	8.17	13.61	10.69	0.991	0.987	0.973

SRD5A2	chr2	31593159	31669544	13	7	4	4	8.17	13.61	21.38	0.991	0.987	0.991
UBE2D3	chr4	103926216	104019473	13	7	0	0	8.17	0	0	0.991	0	0
VAMP5	chr2	85655041	85684022	13	7	6	6	8.17	20.41	32.08	0.991	0.996	0.998
C11orf49	chr11	46904826	47152507	28	15	2	2	8.13	3.16	4.96	0.991	0.892	0.931
ADPGK	chr15	70820760	70873179	15	8	6	6	8.09	17.69	27.8	0.99	0.994	0.997
C9orf127	chr9	35809221	35854844	15	8	2	2	8.09	5.9	9.27	0.99	0.945	0.968
CLIP2	chr7	73331740	73468209	15	8	5	5	8.09	14.74	23.17	0.99	0.988	0.992
ITCH	chr20	32404722	32572858	15	8	2	0	8.09	5.9	0	0.99	0.945	0
FLYWCH1	chr16	2891980	2951210	17	9	7	7	8.04	18.21	28.62	0.99	0.995	0.997
MYO18A	chr17	24414653	24541533	17	9	5	0	8.04	13.01	0	0.99	0.985	0
TDH	chr8	11224555	11273371	17	9	4	2	8.04	10.41	8.18	0.99	0.976	0.964
DHCR7	chr11	70813104	70847125	19	10	9	8	7.99	20.95	29.26	0.99	0.997	0.997
LCMT1	chr16	25020547	25107052	19	10	4	1	7.99	9.31	3.66	0.99	0.972	0.91
SREBF2	chr22	40549051	40642321	19	10	7	6	7.99	16.29	21.95	0.99	0.993	0.992
CPEB1	chr15	80999005	81123783	23	12	12	10	7.92	23.07	30.22	0.99	0.998	0.998
OAS3	chr12	111850631	111905438	27	14	8	6	7.87	13.1	15.44	0.989	0.985	0.985
SPSB4	chr3	142243432	142360143	27	14	5	4	7.87	8.19	10.3	0.989	0.965	0.972
SFRS8	chr12	130751587	130860235	29	15	9	6	7.85	13.72	14.38	0.989	0.988	0.983
NOS2	chr17	23097919	23161682	31	16	11	9	7.83	15.69	20.18	0.989	0.99	0.991
C9orf91	chr9	116403526	116458524	33	17	2	0	7.82	2.68	0	0.989	0.876	0
POLN	chr4	2033442	2210756	35	18	2	1	7.81	2.53	1.99	0.989	0.871	0.878
DOCK3	chr3	50677675	51406669	74	38	26	3	7.79	15.54	2.82	0.989	0.99	0.897
ART1	chr11	3612936	3652222	16	8	8	6	7.59	22.11	26.06	0.986	0.997	0.996
ATF7IP2	chr16	10420225	10494996	24	12	0	0	7.59	0	0	0.986	0	0
C1orf201	chr1	24546075	24610536	18	9	7	7	7.59	17.2	27.03	0.986	0.994	0.996
CCDC15	chr11	124319226	124426595	16	8	1	1	7.59	2.76	4.34	0.986	0.878	0.921
CLEC2A	chr12	9947092	9986247	22	11	3	3	7.59	6.03	9.48	0.986	0.947	0.969
DIO2	chr14	79723621	79758278	10	5	2	1	7.59	8.84	6.95	0.986	0.967	0.955
FBXL4	chr6	99418321	99512570	22	11	7	7	7.59	14.07	22.11	0.986	0.988	0.992
GARNL1	chr14	35067308	35358183	28	14	9	8	7.59	14.21	19.86	0.986	0.988	0.99
GP5	chr3	195586838	195611284	10	5	1	1	7.59	4.42	6.95	0.986	0.925	0.955

KLK7	chr19	56161540	56188962	12	6	4	4	7.59	14.74	23.17	0.986	0.988	0.992
LASS5	chr12	48799847	48857364	12	6	0	0	7.59	0	0	0.986	0	0
LOC100129055	chr10	38494604	38553278	12	6	4	0	7.59	14.74	0	0.986	0.988	0
LOC100192379	chr4	122895189	122917412	12	6	3	3	7.59	11.06	17.38	0.986	0.978	0.987
LPXN	chr11	58040919	58109910	10	5	1	1	7.59	4.42	6.95	0.986	0.925	0.955
LRP11	chr6	150171624	150237173	16	8	0	0	7.59	0	0	0.986	0	0
MND1	chr4	154475250	154565693	14	7	1	1	7.59	3.16	4.96	0.986	0.892	0.931
NPAL3	chr1	24604831	24682059	26	13	3	1	7.59	5.1	2.67	0.986	0.937	0.894
NUP98	chr11	3642815	3785468	28	14	14	12	7.59	22.11	29.79	0.986	0.997	0.998
PDS5A	chr4	39490877	39665971	20	10	2	0	7.59	4.42	0	0.986	0.925	0
PTGES	chr9	131530436	131565165	12	6	0	0	7.59	0	0	0.986	0	0
SCRN3	chr2	174958712	175011974	12	6	0	0	7.59	0	0	0.986	0	0
SCUBE3	chr6	35280167	35336587	10	5	3	1	7.59	13.27	6.95	0.986	0.986	0.955
TMEM63B	chr6	44193353	44241234	12	6	4	4	7.59	14.74	23.17	0.986	0.988	0.992
TOP1P2	chr22	23480467	23501986	10	5	2	1	7.59	8.84	6.95	0.986	0.967	0.955
WASL	chr7	123099232	123186352	30	15	5	3	7.59	7.37	6.95	0.986	0.956	0.955
ZFC3H1	chr12	70279648	70354016	16	8	2	1	7.59	5.53	4.34	0.986	0.941	0.921
ZNF345	chr19	42023106	42072310	10	5	2	1	7.59	8.84	6.95	0.986	0.967	0.955
ZNF420	chr19	42251221	42322491	12	6	1	1	7.59	3.69	5.79	0.986	0.907	0.942
ZNF558	chr19	8771381	8804565	12	6	3	2	7.59	11.06	11.58	0.986	0.978	0.976
CNNM2	chr10	104658103	104838230	35	17	6	0	7.37	7.58	0	0.986	0.96	0
KITLG	chr12	87400697	87508369	31	15	13	11	7.34	18.55	24.66	0.986	0.995	0.994
ABCA6	chr17	64576441	64659610	29	14	10	9	7.33	15.25	21.57	0.986	0.99	0.992
ADD1	chr4	2805381	2911587	25	12	10	5	7.29	17.69	13.9	0.986	0.994	0.981
MAPKAPK2	chr1	204914911	204984249	25	12	9	9	7.29	15.92	25.02	0.986	0.991	0.994
VPS13B	chr8	100084669	100968984	96	46	16	8	7.27	7.37	5.79	0.985	0.956	0.942
BIRC6	chr2	32425599	32707469	23	11	9	7	7.26	17.3	21.15	0.985	0.994	0.991
OPALIN	chr10	98082964	98119082	23	11	2	0	7.26	3.85	0	0.985	0.912	0
ISCA1L	chr5	62096952	62118926	21	10	3	3	7.23	6.32	9.93	0.985	0.949	0.97
CREM	chr10	35445806	35551892	19	9	0	0	7.19	0	0	0.985	0	0
GATAD2A	chr19	19347641	19490741	19	9	1	0	7.19	2.33	0	0.985	0.86	0

PMFBP1	chr16	70700498	70773525	19	9	7	7	7.19	16.29	25.61	0.985	0.993	0.996
CCDC64	chr12	118902030	119026682	17	8	8	8	7.14	20.81	32.71	0.984	0.997	0.998
GPX3	chr5	150370191	150398747	17	8	5	2	7.14	13.01	8.18	0.984	0.985	0.964
LGTN	chr1	204821597	204862527	17	8	2	1	7.14	5.2	4.09	0.984	0.938	0.917
LOC100130958	chr16	75780849	75814477	17	8	0	0	7.14	0	0	0.984	0	0
ZNF578	chr19	57638640	57721943	32	15	10	0	7.11	13.82	0	0.984	0.988	0
GLCCI1	chr7	7964947	8105234	47	22	14	12	7.1	13.17	17.74	0.984	0.985	0.988
LMNB1	chr5	126130731	126210608	15	7	2	2	7.08	5.9	9.27	0.984	0.945	0.968
LOC286238	chr9	90441913	90466895	15	7	7	6	7.08	20.64	27.8	0.984	0.996	0.997
MTMR12	chr5	32252867	32358871	15	7	1	0	7.08	2.95	0	0.984	0.885	0
RHBDL3	chr17	27607307	27685793	15	7	1	1	7.08	2.95	4.63	0.984	0.885	0.926
SLFN14	chr17	30889256	30919223	15	7	4	4	7.08	11.79	18.53	0.984	0.981	0.988
THBD	chr20	22964269	22988301	15	7	3	3	7.08	8.84	13.9	0.984	0.967	0.981
PCNX	chr14	70433874	70661852	28	13	5	1	7.05	7.9	2.48	0.983	0.961	0.89
AASDH	chr4	56889213	56958395	13	6	0	0	7.01	0	0	0.982	0	0
AP4E1	chr15	48978237	49095389	13	6	4	3	7.01	13.61	16.04	0.982	0.987	0.986
C10orf10	chr10	44781714	44804336	13	6	1	1	7.01	3.4	5.35	0.982	0.9	0.937
C2orf63	chr2	55243187	55323203	13	6	5	5	7.01	17.01	26.73	0.982	0.993	0.996
CXCL1	chr4	74943972	74965817	13	6	0	0	7.01	0	0	0.982	0	0
EPB41L5	chr2	120477138	120663165	26	12	1	0	7.01	1.7	0	0.982	0.833	0
MAPKAPK5	chr12	110754661	110825611	13	6	5	5	7.01	17.01	26.73	0.982	0.993	0.996
NR1D2	chr3	23951809	24006241	13	6	2	2	7.01	6.8	10.69	0.982	0.953	0.973
PPP3R1	chr2	68249492	68343155	13	6	4	0	7.01	13.61	0	0.982	0.987	0
STK17A	chr7	43579216	43643503	13	6	1	0	7.01	3.4	0	0.982	0.9	0
TYSND1	chr10	71557738	71586502	13	6	4	3	7.01	13.61	16.04	0.982	0.987	0.986
BANP	chr16	86532538	86678425	50	23	12	10	6.98	10.61	13.9	0.982	0.977	0.981
ACER3	chr11	76239564	76422498	37	17	13	13	6.97	15.54	24.42	0.982	0.99	0.994
MC2R	chr18	13862042	13915535	24	11	0	0	6.96	0	0	0.982	0	0
GTF2F2	chr13	44582630	44766239	35	16	0	0	6.94	0	0	0.982	0	0
HAGH	chr16	1789104	1827196	11	5	1	1	6.9	4.02	6.32	0.981	0.915	0.948

KCTD20	chr6	36508521	36576293	11	5	0	0	6.9	0	0	0.981	0	0
MANBAL	chr20	35341464	35389077	11	5	0	0	6.9	0	0	0.981	0	0
NR1I3	chr1	159456079	159484624	11	5	2	2	6.9	8.04	12.64	0.981	0.962	0.978
SETD2	chr3	47022903	47190471	11	5	5	0	6.9	20.1	0	0.981	0.996	0
TIGD2	chr4	90242990	90265075	11	5	2	0	6.9	8.04	0	0.981	0.962	0
TMEM209	chr7	129581790	129642574	11	5	5	3	6.9	20.1	18.95	0.981	0.996	0.989
UBE2L6	chr11	57065704	57102029	11	5	5	5	6.9	20.1	31.59	0.981	0.996	0.998
MYH15	chr3	109571905	109740859	53	24	19	14	6.87	15.85	18.36	0.981	0.991	0.988
CAPS2	chr12	73946025	74020103	20	9	7	2	6.83	15.48	6.95	0.981	0.99	0.955
CPA4	chr7	129710229	129761250	20	9	4	3	6.83	8.84	10.43	0.981	0.967	0.972
PPP2R1A	chr19	57375002	57431482	20	9	6	2	6.83	13.27	6.95	0.981	0.986	0.955
YAF2	chr12	40827173	40928317	20	9	6	3	6.83	13.27	10.43	0.981	0.986	0.972
PIWIL3	chr22	23435000	23510683	29	13	8	7	6.8	12.2	16.78	0.981	0.983	0.987
C5orf45	chr5	179186871	179228446	18	8	1	1	6.75	2.46	3.86	0.98	0.866	0.913
GLCE	chr15	67230026	67361598	27	12	4	0	6.75	6.55	0	0.98	0.951	0
HMHB1	chr5	143161918	143190477	18	8	6	6	6.75	14.74	23.17	0.98	0.988	0.992
METT5D1	chr11	28076373	28321630	27	12	0	0	6.75	0	0	0.98	0	0
PBLD	chr10	69702422	69772690	18	8	0	0	6.75	0	0	0.98	0	0

MR_Factor: multiple regression factor; P: empirical p-value, aka transformed rank metric; the 05, 01, and 005 suffixes refer to the alpha value used to identify regression residuals outside the respective central portion of the distribution.

Supplementary Table 5: Stepwise linear regression analysis of [Hb] and Tibetan high-altitude selection candidate gene haplotypes in 26 female DU Mongolians

Predictor	In Model	p	beta
<i>Age</i>	0	0.06	0.03
<i>EGLN1</i>	0	0.97	-0.02
<i>HIF1AN</i>	0	0.65	-0.23
<i>NOS1</i>	0	0.25	0.48
<i>MCC</i>	0	0.57	-0.25
<i>CYP17A1</i>	0	0.14	-0.85
<i>EPAS1</i>	0	1.00	0.00
<i>HFE</i>	0	0.99	0.00
<i>HMOX2</i>	0	0.53	0.33
<i>PKLR</i>	0	0.79	0.15
<i>PPARA</i>	0	0.53	0.38
<i>PPARG</i>	0	0.31	-0.58

Supplementary Table 6: Key variants for Tianjiao1 mtDNA and Y-chromosome haplogroup assignments

Marker	Rs number	Position ^a	Variation ^b	Reference	Mongolian	Haplogroup
<u>mtDNA</u>						
769	rs2853519	769	G->A	G	G	L3
1018	rs2856982	1018	A->G	G	G	L3
10873	rs2857284	10873	C->T	T	T	N
10398	rs2853826	10398	A->G	A	A	N
12705	rs2854122	12705	C->T	C	C	R
16223	rs2853513	16223	C->T	C	C	R
73	rs3087742	73	G->A	A	A	R0
11719	rs2853495	11719	A->G	G	G	R0
14766	rs3135031	14766	T->C	C	C	HV
2706	rs2854128	2706	A->G	A	A	H
7028	rs2015062	7028	C->T	C	C	H
13708	rs28359178	13708	A->G	G	A	H18
14364	-	14364	G->A	G	A	H18
<u>Y-chromosome</u>						
P69	rs7892898	14926420	G->A	G	A	P
P240	rs6530605	14598808	T->C	T	C	P
P244	rs2740981	14433100	G->A	G	A	P
Page83	rs13305774	14898094	A->G	A	G	P
M242	rs8179021	15018582	C->T	C	T	Q
P36.2	-	14496441	G->T	G	T	Q1
L232	-	17516095	G->A	G	A	Q1
L472	rs35724598	7014317	G->C	G	C	Q1a
L528	-	18029008	T->C	T	C	Q1a3
M120	-	21907394	T->C	T	C	Q1a1
M265	rs3212294	15030650	C->A	C	A	Q1a1

^a Position is relative to the revised Cambridge Reference Sequence (rCRS) and to GRCh37 for the mtDNA and Y-chromosome, respectively; ^b Ancestral allele -> derived allele.

Supplemental Table 7: SIFT prediction for the effect of Tianjiao1-specific SNVs.

Chr	Type	Start	End	Var Seq	Ref Seq	Effect	Gene	AA Sub	SIFT Prediction
chr1	SNV	878184	878184	T	C	Nonsynonymous	SAMD11	P345S	TOLERATED
chr1	SNV	13182995	13182995	C	G	Nonsynonymous	LOC440563		
chr1	SNV	16054156	16054156	C	A	Nonsynonymous	PLEKHM2	Q510P	TOLERATED
chr1	SNV	17409046	17409046	A	C	Nonsynonymous	PADI2	E384D	TOLERATED
chr1	SNV	21042129	21042129	T	C	Nonsynonymous	KIF17	V79I	DAMAGING
chr1	SNV	22924345	22924345	A	G	Nonsynonymous	EPHA8	V703I	TOLERATED
chr1	SNV	29138936	29138936	T	C	Nonsynonymous	OPRD1	P14L	TOLERATED
chr1	SNV	36556854	36556854	G	A	Nonsynonymous	ADPRHL2	Y74C	TOLERATED
chr1	SNV	38352592	38352592	T	C	Nonsynonymous	INPP5B	E447K	TOLERATED
chr1	SNV	39340828	39340828	T	C	Nonsynonymous	GJA9	V315I	TOLERATED
chr1	SNV	41483638	41483638	G	T	Nonsynonymous	LOC100507178	K209T	TOLERATED
chr1	SNV	43108240	43108240	G	A	Nonsynonymous	CCDC30	I579V	TOLERATED
chr1	SNV	44458021	44458021	C	G	Nonsynonymous	CCDC24	L88F	TOLERATED
chr1	SNV	46976776	46976776	A	G	Nonsynonymous	DMBX1	S168N	TOLERATED
chr1	SNV	150955830	150955830	T	C	Nonsynonymous	ANXA9	T31I	TOLERATED
chr1	SNV	151259861	151259861	C	T	Nonsynonymous	ZNF687		Not scored
chr1	SNV	152191190	152191190	C	T	Nonsynonymous	HRNR	Q972R	TOLERATED
chr1	SNV	158150923	158150923	A	C	Nonsynonymous	CD1D	A11E	DAMAGING
chr1	SNV	158590141	158590141	A	C	Nonsynonymous	SPTA1	R2076L	TOLERATED
chr1	SNV	158590144	158590144	T	A	Nonsynonymous	SPTA1	I2075N	DAMAGING
chr1	SNV	160783582	160783582	T	G	Nonsynonymous	LY9	G204V	DAMAGING
chr1	SNV	161753858	161753858	G	A	Nonsynonymous	ATF6	D109G	TOLERATED
chr1	SNV	163325234	163325234	A	G	Nonsynonymous	NUF2	R457K	TOLERATED
chr1	SNV	165648771	165648771	T	C	Nonsynonymous	ALDH9A1	G280R	DAMAGING
chr1	SNV	172002248	172002248	T	A	Nonsynonymous	DNM3	Y231F	TOLERATED
chr1	SNV	205156703	205156703	A	G	Nonsynonymous	DSTYK	A166V	TOLERATED
chr1	SNV	206652371	206652371	A	G	Nonsynonymous	IKBKE	V360I	TOLERATED
chr1	SNV	207643193	207643193	A	G	Nonsynonymous	CR2	R324H	TOLERATED

chr1	SNV	208218070	208218070	A	C	Nonsynonymous	PLXNA2	M1219I	DAMAGING
chr1	SNV	213032071	213032071	A	G	Nonsynonymous	FLVCR1	A93T	TOLERATED
chr1	SNV	228540735	228540735	A	C	Nonsynonymous	OBSCN	H6211Q	TOLERATED
chr1	SNV	229730829	229730829	A	C	Nonsynonymous	TAF5L	D329Y	TOLERATED
chr1	SNV	235299029	235299029	T	C	Nonsynonymous	RBM34	V311M	DAMAGING
chr1	SNV	247076557	247076557	C	T	Nonsynonymous	AHCTF1	N187S	TOLERATED
chr10	SNV	85968116	85968116	A	G	Nonsynonymous	CDHR1	V384I	TOLERATED
chr10	SNV	85984866	85984866	C	G	Nonsynonymous	LRIT2	L39V	TOLERATED
chr10	SNV	87373271	87373271	T	C	Nonsynonymous	GRID1	A832T	DAMAGING
chr10	SNV	99342169	99342169	C	G	Nonsynonymous	ANKRD2	R278T	TOLERATED
chr10	SNV	104123091	104123091	A	G	Nonsynonymous	GBF1	R651Q	TOLERATED
chr10	SNV	105238645	105238645	T	C	Nonsynonymous	CALHM3	A49T	TOLERATED
chr10	SNV	133058581	133058581	A	G	Nonsynonymous	TCERG1L	P266L	DAMAGING
chr10	SNV	135102420	135102420	G	C	Nonsynonymous	TUBGCP2	E489Q	TOLERATED
chr10	SNV	135195116	135195116	G	A	Nonsynonymous	PAOX	D274G	DAMAGING
chr11	SNV	598457	598457	T	C	Nonsynonymous	PHRF1	R327C	DAMAGING
chr11	SNV	5255266	5255266	C	A	Nonsynonymous	HBD	S90R	DAMAGING *
chr11	SNV	7982354	7982354	A	G	Nonsynonymous	NLRP10	P269S	TOLERATED
chr11	SNV	12316041	12316041	A	G	Nonsynonymous	MICALCL	V355I	TOLERATED
chr11	SNV	18743487	18743487	G	C	Nonsynonymous	IGSF22	E71Q	TOLERATED
chr11	SNV	35338975	35338975	C	G	Nonsynonymous	SLC1A2	R36G	DAMAGING
chr11	SNV	44079938	44079938	A	G	Nonsynonymous	ACCSL	E467K	TOLERATED
chr11	SNV	49207245	49207245	A	G	Nonsynonymous	FOLH1	L268F	DAMAGING
chr11	SNV	49229874	49229874	T	C	Nonsynonymous	FOLH1	G30S	TOLERATED
chr11	SNV	56000040	56000040	G	A	Nonsynonymous	OR5T2	C208R	DAMAGING
chr11	SNV	62299095	62299095	T	G	Nonsynonymous	AHNAK	P932T	TOLERATED
chr11	SNV	62365580	62365580	T	C	Nonsynonymous	MTA2	V136M	TOLERATED
chr11	MNP	62417239	62417242	AGGT	GACG	Nonsynonymous	INTS5		
chr11	SNV	66633792	66633792	T	C	Nonsynonymous	PC	V351M	DAMAGING
chr11	SNV	67163780	67163780	A	G	Nonsynonymous	RAD9A	V261I	TOLERATED
chr11	SNV	72421459	72421459	T	C	Nonsynonymous	ARAP1	D218N	TOLERATED
chr11	SNV	93469364	93469364	G	T	Nonsynonymous	TAF1D	K267T	TOLERATED

chr11	SNV	119183298	119183298	T	C	Nonsynonymous	MCAM	R267H	TOLERATED
chr12	SNV	980497	980497	G	A	Nonsynonymous	WNK1	I736V	TOLERATED
chr12	SNV	995173	995173	A	T	Nonsynonymous	WNK1	S908T	TOLERATED
chr12	SNV	8672931	8672931	A	G	Nonsynonymous	CLEC4D		Not scored
chr12	SNV	10978472	10978472	C	T	Nonsynonymous	TAS2R10	I133V	TOLERATED
chr12	SNV	25257327	25257327	A	G	Nonsynonymous	LRMP	R360H	DAMAGING
chr12	SNV	64823860	64823860	T	A	Nonsynonymous	XPOT		Not scored
chr12	SNV	72024726	72024726	T	G	Nonsynonymous	ZFC3H1	P1160Q	DAMAGING
chr12	SNV	111748390	111748390	G	A	Nonsynonymous	CUX2	T602A	DAMAGING
chr12	SNV	111923534	111923534	G	C	Nonsynonymous	ATXN2	V974L	TOLERATED
chr12	SNV	113549898	113549898	G	T	Nonsynonymous	RASAL1	E456A	TOLERATED
chr12	SNV	114386754	114386754	T	C	Nonsynonymous	RBM19	R387Q	TOLERATED
chr12	SNV	123107112	123107112	G	A	Nonsynonymous	KNTC1	N2158S	TOLERATED
chr12	SNV	128899835	128899835	G	A	Nonsynonymous	TMEM132C	K215R	TOLERATED
chr12	SNV	132512674	132512674	A	T	Nonsynonymous	EP400	L1660Q	TOLERATED
chr13	SNV	35685074	35685074	C	T	Nonsynonymous	NBEA	I654T	TOLERATED
chr13	SNV	46656622	46656622	A	G	Nonsynonymous	CPB2	P113L	TOLERATED
chr13	SNV	96555164	96555164	T	C	Nonsynonymous	UGGT2	E816K	TOLERATED
chr13	SNV	109793571	109793571	G	A	Nonsynonymous	MYO16		Not scored
chr14	SNV	21899028	21899028	T	C	Nonsynonymous	CHD8	A259T	TOLERATED
chr14	SNV	23885038	23885038	C	T	Nonsynonymous	MYH7	T1653A	TOLERATED
chr14	SNV	24538140	24538140	A	G	Nonsynonymous	LRRC16B	S369N	TOLERATED
chr14	SNV	24615789	24615789	G	A	Nonsynonymous	PSME2	M1T	DAMAGING
chr14	SNV	24883915	24883915	T	C	Nonsynonymous	NYNRIN	P987L	DAMAGING *
chr14	SNV	59988313	59988313	A	G	Nonsynonymous	C14orf38	R693W	TOLERATED
chr14	SNV	60581449	60581449	G	A	Nonsynonymous	C14orf135	M7V	TOLERATED
chr14	SNV	62014512	62014512	A	G	Nonsynonymous	PRKCH	E605K	DAMAGING
chr14	SNV	65519973	65519973	G	A	Nonsynonymous	FNTB	M325V	TOLERATED
chr14	SNV	102467378	102467378	G	A	Nonsynonymous	DYNC1H1	R1388G	TOLERATED
chr14	SNV	105413494	105413494	A	G	Nonsynonymous	AHNAK2	A2765V	TOLERATED
chr14	MNP	105413516	105413517	GC	CG	Nonsynonymous	AHNAK2		
chr14	SNV	105416270	105416270	C	T	Nonsynonymous	AHNAK2	K1840E	TOLERATED

chr14	MNP	105416384	105416385	CA	TG	Nonsynonymous	AHNAK2		
chr14	SNV	105416505	105416505	T	C	Nonsynonymous	AHNAK2	M1761I	TOLERATED
chr14	SNV	105416541	105416541	G	C	Nonsynonymous	AHNAK2	L1749F	TOLERATED
chr15	SNV	22368810	22368810	G	C	Nonsynonymous	LOC727924	P79A	DAMAGING
chr15	SNV	22743326	22743326	A	G	Nonsynonymous	GOLGA6L1	E571K	TOLERATED
chr15	SNV	22743347	22743347	A	G	Nonsynonymous	GOLGA6L1	E578K	TOLERATED
chr15	SNV	40462304	40462304	G	C	Nonsynonymous	BUB1B	P74R	DAMAGING
chr15	SNV	40632155	40632155	T	C	Nonsynonymous	C15orf52	R69K	TOLERATED
chr15	SNV	42133075	42133075	A	G	Nonsynonymous	JMJD7	R339Q	TOLERATED
chr15	SNV	48717652	48717652	C	T	Nonsynonymous	FBN1	N2456S	TOLERATED
chr16	SNV	847859	847859	T	G	Nonsynonymous	CHTF18	D938Y	DAMAGING
chr16	SNV	3022997	3022997	A	C	Nonsynonymous	PAQR4	R486L	DAMAGING
chr16	SNV	3070438	3070438	T	G	Nonsynonymous	TNFRSF12A	V14L	TOLERATED
chr16	SNV	12996291	12996291	C	G	Nonsynonymous	SHISA9	D165H	DAMAGING
chr16	SNV	22360643	22360643	T	C	Nonsynonymous	CDR2	A155T	TOLERATED
chr16	SNV	68398925	68398925	A	G	Nonsynonymous	SMPD3	P465L	TOLERATED
chr16	SNV	69752348	69752348	C	T	Nonsynonymous	NQO1		Not scored
chr16	SNV	88804443	88804443	T	C	Nonsynonymous	FAM38A	G307S	TOLERATED
chr17	SNV	263145	263145	T	C	Nonsynonymous	C17orf97	R171S	TOLERATED
chr17	SNV	4349487	4349487	A	G	Nonsynonymous	SPNS3	V56I	DAMAGING
chr17	SNV	7246852	7246852	T	C	Nonsynonymous	ACAP1	R167W	DAMAGING
chr17	SNV	8296520	8296520	A	G	Nonsynonymous	RNF222	T87M	TOLERATED
chr17	SNV	15142830	15142830	G	C	Nonsynonymous	PMP22	G93R	DAMAGING
chr17	SNV	17106166	17106166	T	C	Nonsynonymous	PLD6	S225N	DAMAGING *
chr17	SNV	39913725	39913725	T	C	Nonsynonymous	JUP	R663H	DAMAGING *
chr17	SNV	42988801	42988801	T	C	Nonsynonymous	GFAP	M310I	TOLERATED
chr17	SNV	48753779	48753779	T	A	Nonsynonymous	ABCC3	N1070Y	DAMAGING
chr17	SNV	56277147	56277147	C	T	Nonsynonymous	EPX	V510A	DAMAGING
chr17	SNV	56544322	56544322	A	G	Nonsynonymous	HSF5	S315F	DAMAGING
chr17	SNV	58121201	58121201	A	C	Nonsynonymous	HEATR6	C1090F	TOLERATED
chr17	SNV	58303550	58303550	T	C	Nonsynonymous	USP32	G428R	TOLERATED

chr17	SNV	72954840	72954840	T	G	Nonsynonymous	C17orf28	L162M	DAMAGING
chr17	SNV	74383132	74383132	A	G	Nonsynonymous	SPHK1	R293H	TOLERATED
chr18	SNV	3134744	3134744	C	T	Nonsynonymous	MYOM1	K763R	TOLERATED
chr18	SNV	29339873	29339873	A	G	Nonsynonymous	MCART2	P261L	TOLERATED
chr18	SNV	33736484	33736484	C	T	Nonsynonymous	ELP2	L439S	DAMAGING
chr18	SNV	44559927	44559927	A	C	Nonsynonymous	KATNAL2	R570I	TOLERATED
chr19	SNV	4847711	4847711	C	G	Nonsynonymous	PLIN3	L276V	TOLERATED
chr19	SNV	7696633	7696633	A	G	Nonsynonymous	PCP2	P118L	TOLERATED
chr19	SNV	8615202	8615202	T	C	Nonsynonymous	MYO1F	G360R	TOLERATED
chr19	SNV	9048845	9048845	T	C	Nonsynonymous	MUC16	G10929E	Not Predicted
chr19	SNV	14273649	14273649	T	C	Nonsynonymous	LPHN1	V327I	DAMAGING *
chr19	SNV	22156512	22156512	G	C	Nonsynonymous	ZNF208	E442Q	TOLERATED
chr19	SNV	35837547	35837547	A	G	Nonsynonymous	CD22	G831R	TOLERATED
chr19	SNV	36350384	36350384	A	C	Nonsynonymous	KIRREL2	T175N	TOLERATED
chr19	SNV	38102446	38102446	C	T	Nonsynonymous	ZNF540	S89P	TOLERATED
chr19	SNV	39597600	39597600	A	G	Nonsynonymous	PAPL	R376Q	TOLERATED
chr19	SNV	40354519	40354519	T	C	Nonsynonymous	FCGBP	R5317Q	TOLERATED
chr19	SNV	41355733	41355733	T	G	Nonsynonymous	CYP2A6	F111L	TOLERATED
chr19	SNV	44006363	44006363	T	C	Nonsynonymous	PHLDB3	G96R	TOLERATED
chr19	SNV	44417682	44417682	T	C	Nonsynonymous	ZNF45	G636R	DAMAGING
chr19	SNV	47920111	47920111	T	C	Nonsynonymous	MEIS3	V99I	DAMAGING
chr19	SNV	51650550	51650550	G	C	Nonsynonymous	SIGLEC7	N306K	TOLERATED
chr19	SNV	52034159	52034159	A	G	Nonsynonymous	SIGLEC6	P161L	TOLERATED
chr19	SNV	52034175	52034175	C	G	Nonsynonymous	SIGLEC6	L156V	TOLERATED
chr19	SNV	55401040	55401040	A	G	Nonsynonymous	FCAR	T129T	TOLERATED
chr19	SNV	55738797	55738797	A	G	Nonsynonymous	TMEM86B	P145S	TOLERATED
chr19	SNV	57060489	57060489	T	C	Nonsynonymous	ZFP28	P229L	TOLERATED
chr2	SNV	10717763	10717763	G	C	Nonsynonymous	NOL10	R599T	TOLERATED
chr2	SNV	21230333	21230333	T	C	Nonsynonymous	APOB	R3136H	TOLERATED
chr2	SNV	24516570	24516570	C	G	Nonsynonymous	ITSN2	F570L	TOLERATED
chr2	MNP	26537362	26537363	CA	GG	Nonsynonymous	GPR113		

chr2	SNV	29274645	29274645	T	C	Nonsynonymous	FAM179A	R916W	TOLERATED
chr2	SNV	73868638	73868638	A	G	Nonsynonymous	NAT8	P40S	TOLERATED
chr2	SNV	113326338	113326338	T	G	Nonsynonymous	POLR1B	A645S	TOLERATED
chr2	SNV	160807986	160807986	A	C	Nonsynonymous	PLA2R1	W1135C	DAMAGING
chr2	SNV	171319953	171319953	T	C	Nonsynonymous	MYO3B	R935W	DAMAGING
chr2	SNV	189599490	189599490	A	G	Nonsynonymous	DIRC1	A53V	Not Predicted
chr2	SNV	216240027	216240027	T	C	Nonsynonymous	FN1	G1933S	DAMAGING
chr2	SNV	217234673	217234673	T	A	Nonsynonymous	MARCH4	V104E	TOLERATED
chr2	SNV	223423385	223423385	C	T	Nonsynonymous	SGPP2	L323S	TOLERATED
chr2	SNV	224746659	224746659	C	T	Nonsynonymous	WDFY1		
chr2	SNV	242312656	242312656	G	A	Nonsynonymous	FARP2	H45R	TOLERATED
chr20	SNV	1293237	1293237	T	C	Nonsynonymous	FKBP1A	R185Q	DAMAGING
chr20	SNV	2638855	2638855	T	C	Nonsynonymous	NOP56	P567L	DAMAGING *
chr20	SNV	5093667	5093667	C	G	Nonsynonymous	C20orf30	P3R	DAMAGING *
chr20	SNV	37580397	37580397	A	G	Nonsynonymous	FAM83D	R361Q	TOLERATED
chr20	SNV	55206895	55206895	G	A	Nonsynonymous	TFAP2C	Q190R	TOLERATED
chr20	SNV	62737344	62737344	G	C	Nonsynonymous	NPBWR2	V281L	TOLERATED
chr22	SNV	30403188	30403188	G	C	Nonsynonymous	MTMR3	L117V	DAMAGING
chr22	SNV	38051336	38051336	A	G	Nonsynonymous	SH3BP1		Not scored
chr22	SNV	44064859	44064859	C	T	Nonsynonymous	EFCAB6	I569M	TOLERATED
chr3	SNV	9754227	9754227	C	G	Nonsynonymous	CPNE9	G127A	TOLERATED
chr3	SNV	10452482	10452482	C	G	Nonsynonymous	ATP2B2	P73A	TOLERATED
chr3	SNV	11421450	11421450	C	G	Nonsynonymous	ATG7	R627P	DAMAGING
chr3	SNV	39178730	39178730	A	C	Nonsynonymous	TTC21A	A1109D	TOLERATED
chr3	MNP	44328999	44329000	AT	GA	Nonsynonymous	C3orf77		
chr3	SNV	47742774	47742774	G	T	Nonsynonymous	SMARCC1	K387Q	TOLERATED
chr3	SNV	75787273	75787273	T	G	Nonsynonymous	ZNF717	H494N	DAMAGING
chr3	SNV	87325581	87325581	T	G	Nonsynonymous	POU1F1	T11N	TOLERATED
chr3	SNV	97869037	97869037	G	C	Nonsynonymous	OR5H14	Q270E	TOLERATED
chr3	SNV	108298489	108298489	C	T	Nonsynonymous	KIAA1524	H199R	DAMAGING
chr3	SNV	108363395	108363395	A	G	Nonsynonymous	DZIP3	R509K	TOLERATED

chr3	SNV	121575926	121575926	A	G	Nonsynonymous	EAF2	R136K	TOLERATED
chr3	SNV	128603562	128603562	T	C	Nonsynonymous	ACAD9	P73S	TOLERATED
chr3	SNV	140997267	140997267	G	C	Nonsynonymous	ACPL2	P55A	TOLERATED
chr3	SNV	145841930	145841930	T	C	Nonsynonymous	PLOD2	V66M	DAMAGING
chr3	SNV	149469216	149469216	A	G	Nonsynonymous	COMMD2	L68F	DAMAGING
chr3	SNV	154056041	154056041	A	G	Nonsynonymous	GPR149	A548V	DAMAGING *
chr3	SNV	160143869	160143869	C	T	Nonsynonymous	SMC4	I829T	TOLERATED
chr3	SNV	168802737	168802737	A	G	Nonsynonymous	MECOM	A1104V	DAMAGING
chr4	SNV	1657045	1657045	A	G	Nonsynonymous	FAM53A	S181L	DAMAGING
chr4	SNV	2073872	2073872	A	G	Nonsynonymous	HAUS3	P572S	TOLERATED
chr4	SNV	2460932	2460932	T	C	Nonsynonymous	LOC402160	R213C	DAMAGING
chr4	SNV	5843059	5843059	C	T	Nonsynonymous	CRMP1	I377V	TOLERATED
chr4	SNV	7780516	7780516	T	C	Nonsynonymous	AFAP1	A540T	TOLERATED
chr4	SNV	25379167	25379167	G	A	Nonsynonymous	ANAPC4	T40A	TOLERATED
chr4	SNV	55141095	55141095	T	C	Nonsynonymous	PDGFRA	P341S	DAMAGING *
chr4	SNV	75937929	75937929	A	G	Nonsynonymous	PARM1	S113N	DAMAGING
chr4	SNV	85687053	85687053	C	T	Nonsynonymous	WDFY3	I1700V	TOLERATED
chr4	SNV	102984248	102984248	G	T	Nonsynonymous	BANK1	L722R	DAMAGING
chr4	SNV	129873940	129873940	G	A	Nonsynonymous	SCLT1		Not scored
chr4	SNV	153691825	153691825	T	C	Nonsynonymous	TIGD4	R111H	TOLERATED
chr4	SNV	187078781	187078781	A	C	Nonsynonymous	FAM149A	P213T	TOLERATED
chr5	SNV	14713075	14713075	T	C	Nonsynonymous	ANKH	G425S	DAMAGING
chr5	SNV	56777648	56777648	A	G	Nonsynonymous	ACTBL2	A296V	Not Predicted
chr5	SNV	74096792	74096792	A	C	Nonsynonymous	FAM169A	G339V	TOLERATED
chr5	SNV	111576498	111576498	C	T	Nonsynonymous	EPB41L4A	T269A	DAMAGING
chr5	SNV	115177216	115177216	T	G	Nonsynonymous	ATG12	P59T	DAMAGING
chr5	SNV	115783100	115783100	A	G	Nonsynonymous	SEMA6A	R785W	DAMAGING
chr5	SNV	130928107	130928107	T	C	Nonsynonymous	RAPGEF6	V134M	TOLERATED
chr5	SNV	140347339	140347339	G	T	Nonsynonymous	PCDHAC1	S330A	TOLERATED
chr5	SNV	169689733	169689733	T	G	Nonsynonymous	LCP2		Not scored
chr6	SNV	5187181	5187181	C	G	Nonsynonymous	LYRM4	H81D	TOLERATED

chr6	SNV	26413895	26413895	T	C	Nonsynonymous	BTN3A1	T506M	DAMAGING
chr6	SNV	29142182	29142182	C	T	Nonsynonymous	OR2J2_DUP_07	M257T	DAMAGING
chr6	SNV	30954338	30954338	T	C	Nonsynonymous	MUC21_DUP_06		Not scored
chr6	SNV	32064893	32064893	A	T	Nonsynonymous	TNXB_DUP_10	Q246L	TOLERATED
chr6	SNV	76063261	76063261	T	C	Nonsynonymous	FILIP1	R208Q	TOLERATED
chr6	SNV	83900563	83900563	C	T	Nonsynonymous	PGM3	I85V	TOLERATED
chr6	SNV	93967964	93967964	C	G	Nonsynonymous	EPHA7	P655A	DAMAGING
chr6	SNV	129634117	129634117	T	G	Nonsynonymous	LAMA2	G1096C	DAMAGING
chr6	SNV	159173006	159173006	T	C	Nonsynonymous	SYTL3	R361C	DAMAGING
chr6	SNV	159178375	159178375	G	A	Nonsynonymous	SYTL3	T424A	TOLERATED
chr6	SNV	168315362	168315362	G	A	Nonsynonymous	MLLT4	Y741C	TOLERATED
chr7	SNV	4839385	4839385	T	C	Nonsynonymous	RADIL	A971T	TOLERATED
chr7	SNV	21469852	21469852	T	C	Nonsynonymous	SP4	R357C	DAMAGING
chr7	SNV	27147898	27147898	T	G	Nonsynonymous	HOXA3	P323Q	DAMAGING
chr7	SNV	27147926	27147926	G	C	Nonsynonymous	HOXA3	A314P	TOLERATED
chr7	SNV	42005922	42005922	C	T	Nonsynonymous	GLI3	S917G	TOLERATED
chr7	SNV	47409150	47409150	A	G	Nonsynonymous	TNS3	P365S	TOLERATED
chr7	SNV	51152907	51152907	A	G	Nonsynonymous	COBL	P351L	DAMAGING
chr7	SNV	63679749	63679749	C	T	Nonsynonymous	ZNF735		
chr7	SNV	70242155	70242155	A	G	Nonsynonymous	AUTS2		Not scored
chr7	SNV	87174186	87174186	A	G	Nonsynonymous	ABCB1	R673C	TOLERATED
chr7	SNV	99753020	99753020	C	G	Nonsynonymous	C7orf43	P104R	DAMAGING *
chr7	SNV	100470912	100470912	T	C	Nonsynonymous	TRIP6	T473I	DAMAGING
chr7	SNV	100731797	100731797	G	A	Nonsynonymous	TRIM56	T402A	TOLERATED
chr7	SNV	107720227	107720227	A	G	Nonsynonymous	LAMB4	S569L	TOLERATED
chr7	SNV	142563850	142563850	T	G	Nonsynonymous	EPHB6	R413L	TOLERATED
chr7	SNV	156976575	156976575	A	C	Nonsynonymous	UBE3C	A332D	TOLERATED
chr8	SNV	27145141	27145141	A	G	Nonsynonymous	TRIM35	R470W	TOLERATED
chr8	SNV	59410841	59410841	G	A	Nonsynonymous	CYP7A1	C90R	TOLERATED

chr8	SNV	88886001	88886001	G	A	Nonsynonymous	DCAF4L2	S67P	DAMAGING
chr9	SNV	35711280	35711280	C	G	Nonsynonymous	TLN1	L1331V	TOLERATED
chr9	SNV	114341165	114341165	G	C	Nonsynonymous	PTGR1	D65H	DAMAGING
chr9	SNV	131469059	131469059	A	G	Nonsynonymous	PKN3	R160Q	DAMAGING
chr9	SNV	139752710	139752710	A	G	Nonsynonymous	MAMDC4	G886R	TOLERATED
chr9	SNV	139960719	139960719	T	C	Nonsynonymous	C9orf140	G227S	TOLERATED
chr9	SNV	141015292	141015292	G	A	Nonsynonymous	CACNA1B	T1344A	TOLERATED
chrX	SNV	35966493	35966493	A	G	Nonsynonymous	CXorf22	V194M	DAMAGING
chrX	SNV	49963354	49963354	G	A	Nonsynonymous	AKAP4		Not scored
chrX	SNV	150869437	150869437	C	G	Nonsynonymous	PRRG3		Not scored
chr1	SNV	152283380	152283380	A	G	Stop gained	FLG	Q1328*	N/A
chr10	SNV	74994624	74994624	T	C	Stop gained	FAM149B1	R468*	N/A
chr19	SNV	48789663	48789663	G	C	Stop gained	ZNF114	S261*	N/A
chr6	SNV	97597763	97597763	A	G	Stop gained	MIR548H3	Q1206*	N/A
chr9	SNV	103275606	103275606	T	G	Stop gained	TMEFF1	G113*	N/A
chr5	SNV	148697504	148697504	T	G	Splice donor	AFAP1L1		
chr12	SNV	102542007	102542007	A	G	Splice acceptor	C12orf48		
chr9	SNV	127662827	127662827	A	C	Splice acceptor	GOLGA1		

DAMAGING *: Low confidence prediction.

Supplemental Table 8: SIFT prediction for the effect of Tianjiao1-specific Indels.

Chr	Type	Start	End	Var Seq	Ref Seq	Effect	Gene	NMD ^a	Indel location
chr1	nucleotide_deletion	62579839	62579841	-	GAG	inframe	INADL	NO	98%
chr10	nucleotide_insertion	124921830	124921830	AAG	-	inframe	BUB3	YES	67%
chr11	complex_substitution	309147	309148	GGTCC	CG	inframe	IFITM2		
chr11	nucleotide_insertion	64337176	64337176	ATG	-	inframe	SLC22A11	NO	87%
chr12	nucleotide_deletion	118506328	118506333	-	TCCTCC	inframe	VSIG10	YES	87%
chr15	nucleotide_insertion	49284783	49284783	TTC	-	inframe	SECISBP2L	NO	89%
chr18	nucleotide_deletion	28649002	28649004	-	CCT	inframe	DSC2	NO	87%
chr19	nucleotide_insertion	36002422	36002422	CTGCTGC TG	-	inframe	DMKN	NO	57%
chr2	nucleotide_insertion	133403084	133403084	AAG	-	inframe	GPR39	NO	93%
chr3	nucleotide_deletion	46751086	46751088	-	AAG	inframe	TMIE	NO	80%
chr4	nucleotide_deletion	3494840	3494842	-	CAG	inframe	DOK7	NO	74%
chr4	nucleotide_deletion	42145560	42145562	-	CTC	inframe	BEND4	YES	45%
chr4	nucleotide_deletion	88536883	88536900	-	TAGCAGT GACAGCA GCAA	inframe	DSPP	NO	79%
chr9	nucleotide_insertion	100092982	100092982	AGGAGG	-	inframe	C9orf174	NO	56%
chr9	nucleotide_deletion	125618125	125618127	-	TTC	inframe	RC3H2	YES	70%
chr9	nucleotide_deletion	134019968	134019973	-	CACCCC	inframe	NUP214	YES	25%
chr9	nucleotide_deletion	135203945	135203947	-	TAA	inframe	SETX	YES	38%
chr1	nucleotide_insertion	90178768	90178768	A	-	frameshift	LRRC8C	NO	26%
chr1	nucleotide_insertion	182812483	182812483	A	-	frameshift	DHX9	YES	4%
chr1	nucleotide_deletion	196928052	196928053	-	AT	frameshift	CFHR2	NO	80%
chr11	nucleotide_insertion	4567095	4567095	T	-	frameshift	OR52M1	N/A	71%
chr11	nucleotide_insertion	67412231	67412231	AC	-	frameshift	ACY3	NO	0%
chr12	nucleotide_deletion	57005751	57005752	-	GA	frameshift	BAZ2A	YES	24%
chr15	nucleotide_insertion	41795056	41795056	C	-	frameshift	ITPKA	NO	85%
chr15	nucleotide_insertion	65627742	65627742	C	-	frameshift	IGDCC3	YES	23%

chr16	nucleotide_insertion	68331210	68331210	A	-	frameshift	SLC7A6	NO	99%
chr16	nucleotide_deletion	81399024	81399024	-	C	frameshift	GAN	YES	80%
chr16	nucleotide_insertion	88495412	88495412	C	-	frameshift	ZNF469	YES	13%
chr17	nucleotide_insertion	29548924	29548924	C	-	frameshift	NF1	YES	20%
chr17	nucleotide_insertion	39684407	39684407	A	-	frameshift	KRT19	YES	8%
chr17	nucleotide_deletion	39684411	39684411	-	G	frameshift	KRT19	YES	7%
chr17	nucleotide_deletion	73999342	73999343	-	CT	frameshift	C17orf106	NO	71%
chr19	nucleotide_insertion	20728108	20728108	T	-	frameshift	ZNF737	NO	56%
chr2	nucleotide_insertion	24207579	24207579	C	-	frameshift	UBXN2A	YES	59%
chr2	nucleotide_insertion	27717525	27717525	G	-	frameshift	FNDC4	NO	3%
chr2	nucleotide_insertion	162891786	162891786	A	-	frameshift	DPP4	YES	29%
chr2	nucleotide_deletion	191381083	191381083	-	C	frameshift	TMEM194B	YES	51%
chr3	nucleotide_deletion	32576045	32576046	-	TA	frameshift	DYNC1LI1	YES	59%
chr3	nucleotide_insertion	48207343	48207343	T	-	frameshift	CDC25A	YES	68%
chr3	nucleotide_insertion	52454441	52454441	T	-	frameshift	PHF7	YES	35%
chr3	nucleotide_deletion	97887850	97887850	-	T	frameshift	OR5H15	N/A	33%
chr4	nucleotide_insertion	15688772	15688772	A	-	frameshift	FAM200B	N/A	9%
chr4	nucleotide_deletion	17812767	17812767	-	A	frameshift	NCAPG	YES	2%
chr4	nucleotide_insertion	55987332	55987332	G	-	frameshift	KDR	YES	2%
chr4	nucleotide_insertion	128819613	128819613	A	-	frameshift	PLK4	NO	97%
chr4	nucleotide_insertion	128842780	128842780	G	-	frameshift	MFSD8	NO	80%
chr7	nucleotide_insertion	15405146	15405146	A	-	frameshift	AGMO	NO	94%
chr7	nucleotide_deletion	70255592	70255593	-	CC	frameshift	AUTS2	NO	90%
chr8	nucleotide_insertion	89054014	89054014	A	-	frameshift	MMP16	NO	82%
chr9	nucleotide_deletion	5231638	5231639	-	TT	frameshift	INSL4	NO	27%
chr9	nucleotide_insertion	131287687	131287687	G	-	frameshift	GLE1	YES	53%
chr9	nucleotide_insertion	114521435	114521435	A	-	splice donor	C9orf84		
chr6	nucleotide_insertion	42611951	42611951	A	-	splice acceptor	UBR2		

^a nonsense-mediated decay