Supplemental Table 1

Multivariate Analysis Multivariate model showing SNPs (ranked by p-value) associated with time to CGD, stratified by transplant center. Model also adjusted for confounders such as donor age and recipient characteristics such as African-American race, smoking status, recipient-donor CMV status, and age. Analysis conducted using a Cox proportional hazards model.

SNP	Gene	HR	95% Lower CI	95% Upper CI	P Value	Minor allele in AA	MAF in AA	Minor allele in non-AA	MAF in non-AA
rs7886938	FMO6	1.60	1.26	2.04	1.47E-04	A	0.19	A	0.16
rs7889839	FMO6	1.60	1.25	2.04	1.58E-04	G	0.19	G	0.16
rs2272797	FMO6	1.57	1.23	2.01	3.15E-04	A	0.17	A	0.16
rs909530	FMO3	1.50	1.20	1.87	3.52E-04	T	0.48	T	0.25
rs3769148	ZAK	0.68	0.54	0.85	5.61E-04	A	0.11	A	0.47
rs2369679	AK7	1.58	1.20	2.08	1.07E-03	C	0.03	C	0.17
rs2239360	FANCA	1.42	1.15	1.76	1.22E-03	C	0.35	T	0.34
rs10916	CYP1B1	1.45	1.16	1.83	1.38E-03	G	0.30	G	0.21
rs2242480	CYP3A4	1.59	1.19	2.13	1.59E-03	C	0.29	T	0.11
rs916864	PON3	0.62	0.46	0.84	1.78E-03	T	0.09	T	0.22
rs609636	CYP4F12	0.37	0.20	0.69	1.85E-03	T	0.07	T	0.06
rs609290	CYP4F12	0.37	0.20	0.69	1.89E-03	T	0.07	T	0.06
rs1639	PON2	0.63	0.47	0.85	2.13E-03	G	0.10	G	0.23
rs7190823	FANCA	1.39	1.12	1.72	2.59E-03	T	0.32	C	0.42
rs12448860	FANCA	1.37	1.11	1.69	3.17E-03	T	0.37	A	0.42
rs2300703	SRD5A2	1.37	1.11	1.69	3.91E-03	C	0.39	T	0.43
rs6500452	FANCA	1.37	1.11	1.70	3.98E-03	C	0.48	C	0.33
rs2410558	NAT2	1.36	1.10	1.68	5.11E-03	T	0.40	T	0.30
rs1800287	FANCA	1.35	1.09	1.67	5.20E-03	G	0.28	C	0.42
rs12470143	SRD5A2	0.73	0.59	0.91	5.31E-03	T	0.31	T	0.47
rs6196	NR3C1	0.64	0.47	0.88	6.07E-03	G	0.17	G	0.15
rs2266780	FMO3	1.44	1.11	1.87	6.19E-03	G	0.04	G	0.18
rs1799930	NAT2	0.71	0.55	0.91	6.24E-03	A	0.32	A	0.29
rs2794520	CRP	0.73	0.58	0.92	7.06E-03	T	0.23	T	0.34
rs4148733	ABCB1	1.46	1.10	1.92	8.00E-03	C	0.19	C	0.16
rs3740526	MMS19	1.33	1.08	1.64	8.28E-03	A	0.20	A	0.40
rs903881	ABCC1	1.40	1.09	1.81	8.43E-03	T	0.22	T	0.19
rs5745325	MSH4	0.72	0.56	0.92	8.53E-03	A	0.33	A	0.27
rs12954	FMO1	1.44	1.10	1.90	8.92E-03	A	0.10	A	0.15
rs2072374	NCAPD2	0.69	0.52	0.91	9.36E-03	T	0.05	T	0.27
rs585890	SRD5A2	0.75	0.61	0.93	9.94E-03	T	0.43	T	0.47
rs5759197	TSPO	1.31	1.07	1.62	1.05E-02	T	0.22	C	0.35
rs3772173	SKIL	1.35	1.07	1.70	1.07E-02	T	0.49	C	0.21
rs1061646	FANCA	1.32	1.07	1.63	1.08E-02	C	0.45	T	0.33
rs1205	CRP	0.74	0.59	0.94	1.16E-02	T	0.20	T	0.34
rs2229032	ATR	0.65	0.47	0.91	1.21E-02	A	0.09	A	0.16
rs4986790	TLR4	0.38	0.18	0.81	1.24E-02	G	0.05	G	0.05
rs17780143	MAP4K5	1.68	1.12	2.52	1.28E-02	A	0.03	A	0.05
rs1130499	PTPRN2	1.31	1.06	1.63	1.34E-02	A	0.46	A	0.33
rs2299267	PON2	0.67	0.49	0.92	1.43E-02	G	0.12	G	0.18

rs4253211	ERCC6	0.56	0.35	0.89	1.48E-02	C	0.02	C	0.10
rs11515	C9orf53	1.44	1.07	1.94	1.54E-02	G	0.20	G	0.12
rs13115754	PPP3CA	1.32	1.05	1.65	1.63E-02	C	0.25	G	0.31
rs11030918	RRM1	0.76	0.61	0.95	1.63E-02	C	0.21	C	0.34
rs2070150	ATF6	1.48	1.07	2.04	1.70E-02	C	0.06	C	0.10
rs3761936	AP4B1	1.37	1.06	1.77	1.70E-02	C	0.06	C	0.21
rs872723	SHH	1.39	1.06	1.82	1.71E-02	T	0.13	T	0.17
rs12659	SLC19A1	0.77	0.62	0.95	1.72E-02	T	0.47	T	0.41
rs419029	TNFRSF17	2.01	1.13	3.58	1.73E-02	A	0.09	A	0.00
rs1005658	TSPO	1.30	1.05	1.60	1.75E-02	A	0.35	A	0.30
rs873301	SUMO3	0.65	0.46	0.93	1.81E-02	T	0.04	T	0.16
rs2602381	UGT1A10	1.31	1.05	1.65	1.82E-02	C	0.48	T	0.47
rs11765552	LMTK2	0.76	0.61	0.96	1.85E-02	A	0.12	A	0.49
rs2241279	FGF6	0.77	0.61	0.96	1.87E-02	T	0.46	C	0.39
rs6413420	CYP2E1	0.43	0.21	0.87	1.89E-02	T	0.01	T	0.06
rs4952220	SRD5A2	1.28	1.04	1.58	1.91E-02	A	0.41	C	0.44
rs1564483	BCL2	0.73	0.56	0.95	1.93E-02	A	0.09	A	0.26
rs1405655	NR1H2	1.29	1.04	1.59	1.94E-02	C	0.45	C	0.33
rs1881421	ALK	1.28	1.04	1.57	1.94E-02	C	0.42	G	0.41
rs17112809	MMS19	1.90	1.11	3.27	1.96E-02	T	0.12	T	0.01
rs1799794	XRCC3	1.32	1.04	1.67	2.05E-02	G	0.24	G	0.20
rs212082	ABCC1	0.70	0.51	0.95	2.11E-02	C	0.11	C	0.19
rs2281677	SLC7A7	1.28	1.04	1.59	2.20E-02	C	0.48	T	0.43
rs246241	ABCC1	1.39	1.05	1.84	2.33E-02	T	0.23	T	0.12
rs1076153	DBH	1.32	1.04	1.68	2.35E-02	T	0.16	T	0.21
rs7708626	RAD50	2.13	1.10	4.12	2.42E-02	A	0.17	A	0.00
rs3803258	SLC10A2	0.71	0.52	0.96	2.42E-02	C	0.07	C	0.20
rs3794318	AICDA	1.42	1.05	1.93	2.44E-02	C	0.37	C	0.08
rs1143634	IL1B	0.73	0.55	0.96	2.56E-02	T	0.13	T	0.23
rs12022378	AP4B1	1.34	1.04	1.74	2.57E-02	T	0.06	T	0.21
rs1669703	ADRB3	0.78	0.63	0.97	2.58E-02	T	0.41	T	0.50
rs1071676	IL1B	0.73	0.55	0.96	2.61E-02	C	0.13	C	0.23
rs504348	ABCC1	1.33	1.03	1.71	2.62E-02	C	0.39	G	0.16
rs17561	IL1A	0.76	0.60	0.97	2.67E-02	T	0.18	T	0.29
rs373572	RAD18	1.29	1.03	1.61	2.68E-02	G	0.34	G	0.29
rs1256061	ESR2	0.79	0.64	0.97	2.75E-02	A	0.32	A	0.46
rs10479008	RAD50	2.09	1.08	4.03	2.76E-02	A	0.18	A	0.00
rs6998760	PSKH2	1.28	1.03	1.59	2.76E-02	A	0.12	A	0.36
rs680695	MRE11A	1.29	1.03	1.61	2.78E-02	G	0.19	G	0.33
rs1800566	NQO1	1.32	1.03	1.68	2.82E-02	T	0.21	T	0.20
rs1800286	FANCA	0.77	0.61	0.97	2.86E-02	A	0.10	A	0.38
rs16836266	NEK11	1.43	1.04	1.96	2.87E-02	C	0.29	C	0.07
rs1625895	TP53	0.69	0.49	0.96	2.90E-02	A	0.27	A	0.12
rs1126672	ADH4	0.76	0.59	0.97	2.94E-02	T	0.10	T	0.27
rs117854	ABCC1	1.29	1.03	1.62	2.96E-02	G	0.40	C	0.29
rs2070507	PPM1F	1.55	1.04	2.29	2.96E-02	C	0.01	C	0.05
rs11547160	TCF7L1	1.52	1.04	2.23	3.00E-02	T	0.01	T	0.06
rs1047768	ERCC5	1.25	1.02	1.52	3.02E-02	T	0.32	T	0.41
rs708155	CD81	1.32	1.03	1.69	3.12E-02	A	0.19	A	0.19
rs2384937	ABCC1	1.37	1.03	1.84	3.27E-02	C	0.16	C	0.11

rs2365778	SRD5A2	0.79	0.64	0.98	3.33E-02	C	0.45	C	0.49
rs662799	APOA5	1.41	1.03	1.94	3.38E-02	G	0.13	G	0.07
rs2235047	ABCB1	1.67	1.04	2.68	3.38E-02	G	0.16	G	0.03
rs2271010	ATF6	1.37	1.02	1.83	3.39E-02	C	0.17	C	0.12
rs3093106	CYP4F2	1.31	1.02	1.68	3.40E-02	G	0.32	G	0.18
rs1139488	ALAD	1.26	1.02	1.56	3.41E-02	C	0.31	C	0.38
rs8016621	SALL2	1.75	1.04	2.94	3.44E-02	A	0.18	A	0.01
rs17710008	MYCT1	1.35	1.02	1.79	3.49E-02	A	0.04	A	0.16
rs4986791	TLR4	0.44	0.20	0.95	3.56E-02	T	0.01	T	0.05
rs11673726	UGT1A10	1.28	1.02	1.62	3.58E-02	T	0.36	T	0.35
rs1800668	GPX1	0.77	0.60	0.98	3.71E-02	T	0.25	T	0.28
rs1143623	IL1B	1.28	1.01	1.62	3.81E-02	C	0.12	C	0.30
rs212079	ABCC1	1.57	1.02	2.40	3.89E-02	A	0.03	A	0.05
rs3748022	IKBKE	0.75	0.57	0.99	3.95E-02	T	0.07	T	0.23
rs483536	NFKBIE	0.79	0.63	0.99	3.96E-02	T	0.28	T	0.35
rs1051296	SLC19A1	0.79	0.62	0.99	3.98E-02	G	0.48	G	0.42
rs2070677	CYP2E1	0.70	0.50	0.98	3.98E-02	A	0.38	T	0.12
rs2069718	IFNG	1.24	1.01	1.52	4.02E-02	C	0.41	T	0.42
rs2241280	FGF6	0.79	0.63	0.99	4.05E-02	T	0.50	C	0.39
rs3766730	TNFRSF1B	0.72	0.52	0.99	4.07E-02	T	0.04	T	0.17
rs10263741	ABCB1	2.05	1.03	4.08	4.07E-02	T	0.09	T	0.00
rs6731242	UGT1A10	0.74	0.55	0.99	4.09E-02	G	0.23	G	0.17
rs2152092	MMS19	1.24	1.01	1.52	4.10E-02	T	0.42	C	0.44
rs2242046	SLC28A1	0.80	0.64	0.99	4.13E-02	T	0.09	T	0.48
rs2043449	CYP20A1	1.51	1.02	2.23	4.15E-02	G	0.24	G	0.04
rs1851426	CYP3A4	1.49	1.02	2.17	4.16E-02	C	0.33	T	0.04
rs754	LOC729296	1.37	1.01	1.84	4.24E-02	G	0.48	G	0.09
rs2909430	TP53	0.70	0.49	0.99	4.25E-02	G	0.25	G	0.12
UGT2B7_1d	UGT2B7	0.72	0.52	0.99	4.26E-02	G	0.09	G	0.19
rs2272037	IGF1R	0.79	0.64	0.99	4.29E-02	G	0.27	A	0.41
rs410509	EDEM1	1.60	1.01	2.54	4.31E-02	C	0.12	C	0.03
rs1555025	ID3	1.26	1.01	1.58	4.31E-02	T	0.35	T	0.46
rs1530259	PPP3CA	1.26	1.01	1.58	4.35E-02	C	0.22	G	0.33
rs2227564	C10orf55	0.76	0.58	0.99	4.44E-02	T	0.06	T	0.26
rs4646285	SLC10A1	0.61	0.38	0.99	4.44E-02	A	0.02	A	0.09
rs1801394	FASTKD3	0.80	0.64	0.99	4.49E-02	G	0.30	A	0.46
rs2007231	CSDE1	0.78	0.61	0.99	4.50E-02	C	0.09	C	0.35
rs2266782	FMO3	1.23	1.00	1.50	4.51E-02	A	0.44	A	0.41
rs2235048	ABCB1	0.80	0.65	1.00	4.53E-02	C	0.23	T	0.47
rs17683288	ARHGEF10	0.59	0.35	0.99	4.56E-02	G	0.01	G	0.07
rs1051298	SLC19A1	0.80	0.64	1.00	4.59E-02	C	0.48	T	0.43
rs182482	ABCC1	1.26	1.00	1.58	4.66E-02	A	0.49	G	0.28
rs3856806	PPARG	1.37	1.00	1.86	4.67E-02	T	0.07	T	0.14
rs129116	ABCC1	1.26	1.00	1.58	4.68E-02	C	0.50	C	0.27
rs13712	MLH3	0.80	0.64	1.00	4.72E-02	G	0.44	A	0.46
rs1045642	ABCB1	0.80	0.64	1.00	4.76E-02	T	0.22	C	0.47
rs1800469	B9D2	1.26	1.00	1.58	4.78E-02	T	0.30	T	0.33
rs2301157	SLC10A2	1.25	1.00	1.56	4.78E-02	C	0.30	T	0.45
rs836802	MSH3	0.76	0.58	1.00	4.84E-02	G	0.28	G	0.24
rs1171276	LEPR	1.29	1.00	1.66	4.85E-02	G	0.42	G	0.17

rs3770582	ABCB11	1.23	1.00	1.52	4.87E-02	G	0.28	A	0.42
rs1736565	FMO6	0.80	0.65	1.00	4.91E-02	C	0.18	C	0.45
rs2259458	AKR1B1	0.78	0.61	1.00	4.92E-02	T	0.29	T	0.28
rs1805389	LIG4	1.52	1.00	2.31	5.12E-02	T	0.00	T	0.06
rs2020903	CASP9	1.23	1.00	1.53	5.18E-02	C	0.29	C	0.48
rs11989	Magmas	1.46	1.00	2.13	5.23E-02	T	0.15	T	0.06
rs2294038	ARHGEF10	0.71	0.51	1.00	5.23E-02	C	0.11	C	0.14
rs914358	AKAP2	1.23	1.00	1.51	5.26E-02	A	0.48	G	0.47
rs4646421	CYP1A1	1.31	1.00	1.71	5.27E-02	T	0.37	T	0.13
rs2230635	CHAF1A	1.87	0.99	3.54	5.28E-02	G	0.07	G	0.00
rs3761142	GSS	0.80	0.63	1.00	5.28E-02	A	0.32	A	0.28
rs915909	CYP2E1	0.14	0.02	1.03	5.32E-02	T	0.10	T	0.00
rs431240	SLC36A2	0.81	0.65	1.00	5.51E-02	G	0.40	G	0.44
rs4646032	CASP9	1.23	1.00	1.52	5.51E-02	C	0.29	C	0.48
rs13321	TNC	1.25	0.99	1.56	5.54E-02	G	0.29	G	0.28
rs3790433	LEPR	1.24	0.99	1.56	5.60E-02	G	0.27	A	0.27
rs1364283	HSD17B2	1.23	0.99	1.53	5.64E-02	A	0.24	C	0.50
rs8044995	NFATC3	0.77	0.58	1.01	5.85E-02	A	0.31	A	0.17
rs1126670	ADH4	0.79	0.62	1.01	5.85E-02	G	0.17	G	0.29
rs1881420	ALK	1.24	0.99	1.54	5.88E-02	G	0.23	G	0.30
rs2740574	CYP3A4	1.45	0.99	2.12	5.88E-02	A	0.38	G	0.04
rs328	LPL	0.69	0.47	1.01	5.89E-02	G	0.10	G	0.10
rs9808232	ROCK2	1.24	0.99	1.54	5.93E-02	T	0.28	G	0.46
rs9332093	CYP2C9	0.59	0.35	1.02	5.95E-02	G	0.03	G	0.06
rs212086	ABCC1	0.75	0.55	1.01	5.97E-02	A	0.11	A	0.18
rs1348161	PPP3CA	1.24	0.99	1.55	5.97E-02	G	0.27	A	0.33
rs743534	CYP2E1	0.73	0.52	1.01	6.01E-02	T	0.38	G	0.12
rs6427630	ATF6	1.34	0.99	1.83	6.10E-02	G	0.14	G	0.11
rs12806698	RRM1	0.78	0.60	1.01	6.13E-02	A	0.06	A	0.28
rs2069807	IL5	1.80	0.97	3.32	6.13E-02	T	0.17	T	0.00
rs2389603	ABCB11	1.47	0.98	2.21	6.15E-02	T	0.21	T	0.04
rs1799811	GSTP1	0.64	0.40	1.02	6.18E-02	T	0.03	T	0.08
rs4646034	CASP9	1.22	0.99	1.51	6.20E-02	A	0.29	A	0.48
rs1052576	CASP9	1.23	0.99	1.52	6.22E-02	A	0.29	A	0.48
rs207440	XDH	1.48	0.98	2.24	6.24E-02	A	0.07	A	0.05
rs1056836	CYP1B1	1.23	0.99	1.54	6.24E-02	C	0.19	G	0.41
rs500760	PGR	0.79	0.61	1.01	6.34E-02	G	0.38	G	0.23
rs521102	CHEK1	1.23	0.99	1.53	6.37E-02	T	0.30	C	0.50
rs2302387	ABCB4	1.30	0.99	1.70	6.40E-02	A	0.43	A	0.13
rs1041983	NAT2	0.81	0.64	1.01	6.49E-02	T	0.49	T	0.32
rs2515641	CYP2E1	0.73	0.52	1.02	6.49E-02	C	0.38	T	0.13
rs6945984	CYP3A4	1.31	0.98	1.74	6.57E-02	T	0.34	C	0.12
rs163077	FAM82A	1.25	0.99	1.58	6.59E-02	A	0.06	A	0.28
rs2257212	SLC15A2	0.82	0.66	1.01	6.66E-02	A	0.48	A	0.43
rs1126671	ADH4	0.80	0.63	1.02	6.68E-02	A	0.17	A	0.29
rs6971	TSPO	0.79	0.61	1.02	6.71E-02	T	0.22	T	0.29
rs312016	LRP5	1.23	0.99	1.53	6.74E-02	A	0.17	A	0.30
rs12500797	PTPN13	1.37	0.98	1.91	6.78E-02	A	0.04	A	0.09
rs2020895	CASP9	1.22	0.99	1.51	6.79E-02	T	0.26	T	0.47
rs3822430	SRD5A1	0.82	0.66	1.01	6.81E-02	C	0.37	C	0.36

rs7172	PSMB4	1.24	0.98	1.55	6.93E-02	A	0.37	G	0.23
rs215101	ABCC1	1.28	0.98	1.66	6.93E-02	C	0.21	C	0.14
rs2227929	ATR	1.23	0.98	1.53	6.97E-02	C	0.19	C	0.38
rs1057910	CYP2C9	0.61	0.35	1.04	6.99E-02	C	0.02	C	0.06
rs1057911	CYP2C9	0.61	0.35	1.04	6.99E-02	T	0.02	T	0.06
rs7533315	MTHFR	1.21	0.98	1.49	7.03E-02	T	0.31	T	0.26
rs7668282	UGT2B7	1.72	0.96	3.10	7.06E-02	C	0.05	C	0.01
rs2240871	NCAPD2	1.29	0.98	1.69	7.16E-02	G	0.05	G	0.19
rs1799722	BDKRB2	0.80	0.63	1.02	7.20E-02	T	0.30	T	0.43
rs165815	ARVCF	1.25	0.98	1.58	7.26E-02	C	0.47	C	0.18
rs1802904	ATR	1.31	0.98	1.77	7.28E-02	G	0.04	G	0.15
rs1983346	NDC80	0.78	0.60	1.02	7.36E-02	C	0.17	C	0.23
rs2230129	TAF1C	0.81	0.65	1.02	7.36E-02	A	0.21	A	0.40
rs16846208	ATF6	1.32	0.97	1.80	7.39E-02	T	0.14	T	0.10
rs17779352	AHR	0.64	0.40	1.04	7.41E-02	C	0.02	C	0.09
rs3113199	HNMT	0.45	0.19	1.08	7.42E-02	T	0.21	T	0.00
rs2271012	ATF6	1.32	0.97	1.80	7.43E-02	T	0.14	T	0.10
rs660339	UCP2	1.21	0.98	1.50	7.52E-02	T	0.43	T	0.42
rs1042858	RRM1	1.34	0.97	1.85	7.56E-02	G	0.14	G	0.08
rs1029702	NPC2	1.24	0.98	1.58	7.56E-02	A	0.37	A	0.18
rs3735481	PPIA	1.23	0.98	1.56	7.62E-02	C	0.40	A	0.21
rs5745549	MSH4	1.40	0.97	2.03	7.64E-02	A	0.12	A	0.04
rs7867504	SLC28A3	1.22	0.98	1.52	7.65E-02	T	0.28	C	0.31
rs169985	ABCC1	1.24	0.98	1.57	7.72E-02	A	0.15	G	0.32
rs582054	IL12A	0.82	0.66	1.02	7.74E-02	A	0.28	A	0.46
rs7751481	PPARD	0.81	0.64	1.02	7.79E-02	G	0.36	A	0.24
rs630303	MUS81	1.22	0.98	1.52	7.80E-02	A	0.26	G	0.35
rs3842787	PTGS1	0.66	0.41	1.05	7.81E-02	T	0.13	T	0.07
rs274548	SLC22A5	1.25	0.98	1.60	7.83E-02	A	0.50	A	0.15
rs9332098	CYP2C9	0.61	0.36	1.06	7.84E-02	A	0.02	A	0.06
rs7847	CHST11	1.22	0.98	1.53	7.87E-02	C	0.18	C	0.32
rs1967120	ABCC1	1.21	0.98	1.50	7.88E-02	C	0.39	C	0.32
rs8645	SUMO3	0.77	0.57	1.03	7.92E-02	C	0.24	C	0.17
rs1456432	CYP1A1	1.25	0.97	1.61	7.96E-02	A	0.48	G	0.17
rs1143671	SLC15A2	0.83	0.67	1.02	8.07E-02	T	0.48	T	0.43
rs6133	SELP	1.31	0.97	1.76	8.07E-02	G	0.47	T	0.11
rs1143672	SLC15A2	0.83	0.67	1.02	8.09E-02	A	0.48	A	0.43
rs1140409	DDX5	0.62	0.36	1.06	8.10E-02	G	0.01	G	0.06
rs5368	SELE	1.32	0.96	1.82	8.21E-02	T	0.07	T	0.12
rs582537	IL12A	0.82	0.66	1.03	8.24E-02	A	0.28	A	0.46
rs2227314	IL12A	0.82	0.66	1.03	8.27E-02	G	0.31	G	0.46
rs2404955	CYP3A4	1.29	0.97	1.73	8.27E-02	G	0.34	A	0.13
rs10929302	UGT1A10	1.23	0.97	1.56	8.33E-02	A	0.31	A	0.30
rs2229086		1.41	0.95	2.09	8.39E-02	G	0.02	G	0.06
rs3856748	CTNNB1	1.94	0.92	4.11	8.39E-02	T	0.08	T	0.00
rs7201683	WWOX	0.49	0.21	1.10	8.42E-02	G	0.10	G	0.02
rs2853563	VDR	1.44	0.95	2.17	8.48E-02	A	0.20	A	0.03
rs2227931	ATR	1.21	0.97	1.52	8.48E-02	C	0.19	C	0.38
rs2241868	HMGCS2	1.37	0.96	1.96	8.54E-02	C	0.07	C	0.08
rs299290	HMMR	0.80	0.62	1.03	8.54E-02	C	0.31	C	0.28

rs2293616	SLC15A2	0.83	0.67	1.03	8.58E-02	T	0.48	T	0.43
rs6474491	STAR	0.80	0.62	1.03	8.62E-02	C	0.24	C	0.25
rs3136682	CCL1	1.61	0.93	2.77	8.67E-02	T	0.07	T	0.03
rs540199	ANKRD49	1.21	0.97	1.51	8.82E-02	G	0.22	G	0.35
rs2307340	MCM5	0.68	0.44	1.06	8.84E-02	G	0.02	G	0.08
rs2839686	CXCL12	0.82	0.65	1.03	8.92E-02	T	0.26	T	0.30
rs1052555	ERCC2	0.82	0.65	1.03	8.93E-02	T	0.08	T	0.32
rs3093105	CYP4F2	1.25	0.97	1.61	8.94E-02	G	0.24	G	0.18
rs1758566		0.71	0.47	1.06	9.02E-02	C	0.19	C	0.09
rs2237580	PON1	0.70	0.47	1.06	9.02E-02	G	0.09	G	0.11
rs2235074	ABCB1	0.57	0.30	1.09	9.06E-02	T	0.11	T	0.04
rs10517	NQO1	0.74	0.53	1.05	9.11E-02	T	0.16	T	0.13
rs1052133	CAMK1	1.24	0.97	1.58	9.15E-02	G	0.15	G	0.25
rs1800587	IL1A	0.82	0.65	1.03	9.15E-02	T	0.35	T	0.29
rs673548	APOB	0.80	0.62	1.04	9.21E-02	A	0.19	A	0.25
rs2299255	PON1	1.27	0.96	1.69	9.29E-02	C	0.13	C	0.14
rs16944	IL1B	1.20	0.97	1.49	9.29E-02	G	0.45	A	0.35
rs4994	ADRB3	1.35	0.95	1.91	9.37E-02	C	0.12	C	0.09
rs5491	ICAM1	1.58	0.93	2.68	9.38E-02	T	0.19	T	0.01
rs6041750	FKBP1A	0.83	0.67	1.03	9.42E-02	C	0.50	C	0.37
rs954923	DPYD	1.75	0.91	3.36	9.48E-02	T	0.09	T	0.00
rs3764006	SLCO1B3	1.28	0.96	1.72	9.54E-02	T	0.33	C	0.11
rs2234962	BAG3	1.26	0.96	1.66	9.56E-02	C	0.03	C	0.19
rs4947324	TNF	1.31	0.95	1.79	9.57E-02	T	0.15	T	0.09
rs1805327	RAD1	1.39	0.94	2.05	9.64E-02	G	0.01	G	0.08
rs430397	HSPA5	1.34	0.95	1.90	9.73E-02	A	0.17	A	0.08
rs4149057	SLCO1B1	1.20	0.97	1.48	9.77E-02	C	0.21	T	0.39
rs5742714	IGF1	0.73	0.50	1.06	9.78E-02	C	0.08	C	0.10
rs3093662	TNF	1.39	0.94	2.05	9.78E-02	G	0.10	G	0.06
rs1256063	ESR2	1.34	0.95	1.89	9.92E-02	T	0.01	T	0.07
rs7195066	FANCA	1.19	0.97	1.48	9.94E-02	C	0.35	T	0.34
rs1805059	SLC7A7	1.20	0.97	1.49	9.96E-02	A	0.48	G	0.40
rs5303	CYP11B1	0.83	0.66	1.04	9.97E-02	T	0.22	T	0.42
rs1143627	IL1B	1.20	0.97	1.48	9.98E-02	T	0.41	C	0.35
rs13817	MUS81	1.21	0.96	1.51	1.01E-01	A	0.27	G	0.36
rs557148	MRE11A	1.19	0.97	1.47	1.01E-01	T	0.34	C	0.44
rs241424	TAP2	1.18	0.97	1.45	1.01E-01	C	0.40	T	0.48
rs588701	MRE11A	1.20	0.96	1.50	1.01E-01	A	0.22	A	0.35
rs1470414	PASK	0.82	0.64	1.04	1.02E-01	A	0.12	A	0.34
rs3218097	CCND3	0.80	0.61	1.05	1.02E-01	T	0.10	T	0.24
rs3813865	CYP2E1	1.45	0.93	2.26	1.02E-01	C	0.14	C	0.03
rs10979601	IKBKAP	1.22	0.96	1.56	1.03E-01	T	0.43	T	0.22
rs4426527	AGXT	0.77	0.56	1.06	1.05E-01	G	0.04	G	0.19
rs17037102	DKK2	1.31	0.95	1.80	1.05E-01	A	0.03	A	0.11
rs2306862	LRP5	1.26	0.95	1.67	1.05E-01	T	0.05	T	0.16
rs1530031	CHST10	0.84	0.69	1.04	1.06E-01	A	0.37	G	0.48
rs8179183	LEPR	1.24	0.96	1.60	1.07E-01	C	0.19	C	0.17
rs11188254	PDLIM1	0.83	0.66	1.04	1.07E-01	A	0.48	A	0.32
rs13652	FN1	1.29	0.95	1.75	1.08E-01	G	0.18	G	0.12
rs4128473	DPYD	1.26	0.95	1.68	1.09E-01	C	0.45	C	0.13

rs7877	FMO1	1.21	0.96	1.54	1.09E-01	G	0.29	A	0.27
rs712704	PAX4	1.22	0.96	1.56	1.09E-01	C	0.07	C	0.23
rs546382	IGHMBP2	1.21	0.96	1.54	1.10E-01	T	0.12	T	0.29
rs2069443	CDK5	0.83	0.65	1.04	1.10E-01	C	0.43	C	0.29
rs10733103	HSD3B1	1.20	0.96	1.50	1.10E-01	G	0.36	G	0.33
rs1887994	ESR2	0.70	0.45	1.08	1.10E-01	T	0.05	T	0.09
rs523349	SRD5A2	1.20	0.96	1.51	1.11E-01	G	0.25	G	0.30
rs2056822	CYP4F8	0.81	0.62	1.05	1.11E-01	A	0.26	A	0.26
rs1448905	ADAM23	0.84	0.68	1.04	1.11E-01	C	0.38	C	0.41
rs8192879	CYP7A1	1.19	0.96	1.46	1.11E-01	A	0.23	A	0.41
rs744389	PRX	0.77	0.56	1.06	1.12E-01	T	0.02	T	0.18
rs1135961	PSMA7	0.76	0.55	1.07	1.12E-01	T	0.11	T	0.14
rs875120	TTR	0.61	0.33	1.12	1.12E-01	T	0.08	T	0.04
rs10493753	SPATA1	0.67	0.41	1.10	1.12E-01	G	0.27	G	0.03
rs1042718	ADRB2	1.23	0.95	1.58	1.13E-01	A	0.29	A	0.18
rs10176426	UGT1A10	0.71	0.47	1.08	1.13E-01	T	0.03	T	0.10
rs450808	ABCG1	0.82	0.65	1.05	1.13E-01	A	0.34	A	0.25
rs2275554	AK7	0.81	0.62	1.05	1.13E-01	A	0.21	A	0.25
rs2857713	LTA	1.21	0.96	1.53	1.13E-01	G	0.32	G	0.26
rs5299	CYP11B1	0.83	0.67	1.04	1.14E-01	A	0.36	A	0.42
rs2305367	SLC28A1	1.19	0.96	1.47	1.15E-01	T	0.39	T	0.39
rs6068816	CYP24A1	0.74	0.51	1.08	1.15E-01	T	0.04	T	0.13
rs6945306	STK31	0.83	0.65	1.05	1.16E-01	C	0.18	C	0.32
rs3097	CYP11B2	0.81	0.61	1.05	1.16E-01	A	0.05	A	0.26
rs1464645	BCL6	1.24	0.95	1.62	1.16E-01	T	0.34	T	0.15
rs2230806	ABCA1	0.82	0.65	1.05	1.16E-01	G	0.39	A	0.27
rs6874005	NSUN2	0.84	0.68	1.04	1.17E-01	T	0.31	T	0.36
rs816060	TNFRSF1B	0.84	0.67	1.05	1.18E-01	C	0.12	C	0.42
rs310831	E2F7	0.71	0.46	1.09	1.19E-01	T	0.02	T	0.11
rs2606241	C18orf56	1.19	0.96	1.49	1.19E-01	T	0.47	T	0.28
rs2310235	IL1RL2	0.83	0.65	1.05	1.19E-01	T	0.10	T	0.34
rs11568943	EGF	1.31	0.93	1.83	1.19E-01	A	0.19	A	0.08
rs2243251	IL4	0.47	0.18	1.22	1.20E-01	G	0.17	G	0.00
rs1709182	ESR1	0.83	0.65	1.05	1.20E-01	C	0.11	C	0.36
rs10515783	UBLCP1	0.83	0.66	1.05	1.20E-01	T	0.17	T	0.31
rs7802773	ABCB1	1.19	0.96	1.47	1.20E-01	A	0.49	A	0.49
rs6019	F5	1.34	0.93	1.94	1.21E-01	C	0.32	C	0.05
rs2687116	CYP3A4	1.34	0.92	1.96	1.21E-01	T	0.40	G	0.04
rs2214102	ABCB1	0.71	0.46	1.10	1.22E-01	A	0.02	A	0.09
rs2239185	VDR	1.18	0.96	1.46	1.22E-01	C	0.44	C	0.47
rs757158	PON1	0.84	0.67	1.05	1.23E-01	C	0.17	T	0.45
rs207932	XRCC5	1.18	0.96	1.45	1.23E-01	T	0.32	T	0.44
rs504122	SPRY2	1.19	0.95	1.49	1.24E-01	T	0.09	T	0.37
rs1048943	CYP1A1	1.49	0.90	2.46	1.24E-01	G	0.01	G	0.06
rs5743557	TLR1	0.79	0.59	1.07	1.24E-01	T	0.03	T	0.20
rs2237585	PON2	0.84	0.68	1.05	1.25E-01	T	0.49	C	0.47
rs2687105	CYP3A4	1.33	0.92	1.91	1.25E-01	A	0.38	T	0.05
rs11706052	IMPDH2	0.72	0.47	1.10	1.27E-01	G	0.01	G	0.10
rs1760215	DPYD	1.33	0.92	1.92	1.27E-01	G	0.01	G	0.10
rs3803390	SLC28A1	1.40	0.91	2.16	1.28E-01	A	0.02	A	0.06

rs11247367	IGF1R	1.32	0.92	1.90	1.28E-01	A	0.11	A	0.07
rs12441817	CYP1A1	1.26	0.94	1.70	1.28E-01	C	0.21	C	0.11
rs679899	APOB	0.84	0.67	1.05	1.28E-01	A	0.18	A	0.49
rs9862	SYN3	0.85	0.68	1.05	1.28E-01	T	0.14	T	0.50
rs2515644	CYP2E1	0.81	0.62	1.06	1.29E-01	C	0.30	A	0.22
rs9640663	PTPN12	1.18	0.95	1.45	1.29E-01	G	0.16	G	0.39
rs9282574	ABCG8	0.57	0.28	1.18	1.29E-01	A	0.06	A	0.03
rs1361600	F3	1.18	0.95	1.46	1.30E-01	A	0.37	G	0.45
rs1042713	ADRB2	0.84	0.67	1.05	1.31E-01	A	0.50	A	0.37
rs4951629	ATF3	1.33	0.92	1.92	1.31E-01	C	0.17	C	0.07
rs2069442	CDK5	0.84	0.67	1.05	1.31E-01	G	0.42	G	0.28
rs2295475	XDH	0.82	0.64	1.06	1.31E-01	A	0.06	A	0.31
rs6673324	LEPR	1.19	0.95	1.48	1.32E-01	A	0.47	G	0.47
rs2236654	IGHMBP2	0.81	0.61	1.07	1.32E-01	A	0.17	A	0.23
rs2463437	CHST11	1.18	0.95	1.46	1.32E-01	C	0.36	C	0.34
rs2071048	HNMT	0.85	0.68	1.05	1.33E-01	C	0.41	C	0.41
rs710411	NOTCH1	0.82	0.64	1.06	1.33E-01	A	0.46	G	0.39
rs2279574	DUSP6	0.84	0.68	1.05	1.33E-01	A	0.29	C	0.47
rs2839685	CXCL12	1.23	0.94	1.61	1.34E-01	T	0.26	T	0.14
rs2145853	ABCC2	1.19	0.95	1.50	1.35E-01	A	0.40	A	0.41
rs2020870	FMO2	0.72	0.46	1.11	1.35E-01	G	0.09	G	0.07
rs3093153	CYP4F2	0.68	0.42	1.12	1.35E-01	T	0.03	T	0.06
rs3212860	CCND1	1.73	0.84	3.56	1.35E-01	T	0.13	T	0.00
rs894469	FMO5	0.73	0.48	1.10	1.35E-01	G	0.14	G	0.07
rs1952467	CYP2E1	0.82	0.62	1.07	1.36E-01	G	0.30	T	0.22
rs16941	BRCA1	1.18	0.95	1.47	1.36E-01	G	0.18	G	0.33
rs1855363	DPYD	1.50	0.88	2.55	1.36E-01	A	0.14	A	0.01
rs5997917	LIMK2	1.23	0.94	1.62	1.37E-01	A	0.44	A	0.12
rs2237051	EGF	1.18	0.95	1.46	1.37E-01	G	0.22	A	0.41
rs569143	MRE11A	1.17	0.95	1.44	1.38E-01	C	0.49	G	0.44
rs1048691	MARCH9	0.80	0.60	1.07	1.38E-01	T	0.36	T	0.23
rs2069705	IFNG	1.17	0.95	1.44	1.38E-01	C	0.44	C	0.36
rs578430	MUSK	1.41	0.89	2.23	1.38E-01	T	0.23	T	0.02
rs2738258	CYP3A4	1.47	0.88	2.43	1.38E-01	A	0.32	A	0.00
rs3821207	IL1RL2	0.84	0.66	1.06	1.39E-01	G	0.16	G	0.34
rs1558093	SMAD5	0.84	0.67	1.06	1.39E-01	T	0.45	C	0.28
rs2231926	FLJ10213	0.85	0.69	1.05	1.39E-01	A	0.35	A	0.49
rs7190307	NFATC3	1.18	0.95	1.46	1.40E-01	G	0.12	A	0.46
rs7563233	ABCB11	1.38	0.90	2.13	1.40E-01	C	0.34	C	0.02
rs25680	CD27	1.22	0.94	1.59	1.41E-01	A	0.15	A	0.22
rs1892534	LEPR	1.17	0.95	1.45	1.42E-01	A	0.47	A	0.41
rs10895068	PGR	1.41	0.89	2.23	1.43E-01	A	0.01	A	0.05
rs880324	NFATC2	1.20	0.94	1.54	1.43E-01	A	0.26	A	0.22
rs1800206	PPARA	0.67	0.39	1.15	1.43E-01	0	0.00	G	0.06
rs10521092	IKBKAP	1.54	0.86	2.76	1.43E-01	T	0.22	0	0.00
rs4648058	NFKB1	1.18	0.95	1.47	1.43E-01	C	0.24	C	0.31
rs3828034	LEPR	1.23	0.93	1.61	1.44E-01	C	0.03	C	0.17
rs2147668	RFC3	1.23	0.93	1.61	1.44E-01	T	0.50	G	0.10
rs2074351	PON1	0.84	0.66	1.06	1.44E-01	A	0.20	A	0.32
rs2335052	GATA2	0.80	0.60	1.08	1.44E-01	A	0.23	A	0.17

rs799917	BRCA1	1.18	0.94	1.48	1.45E-01	C	0.18	T	0.35
rs1048804	NRP1	0.84	0.66	1.06	1.46E-01	T	0.49	C	0.25
rs1009373	CD40	1.21	0.94	1.55	1.46E-01	T	0.07	T	0.25
rs2239184	VDR	1.17	0.95	1.45	1.47E-01	C	0.37	C	0.46
rs169097	CXCL12	1.68	0.83	3.39	1.47E-01	A	0.14	A	0.00
rs3770602	ABCB11	0.83	0.64	1.07	1.48E-01	A	0.13	A	0.30
rs11045819	SLCO1B1	0.79	0.57	1.09	1.48E-01	A	0.08	A	0.15
rs973013	HNMT	0.83	0.64	1.07	1.48E-01	T	0.37	T	0.20
rs5490	ICAM1	1.46	0.87	2.43	1.48E-01	C	0.20	C	0.00
rs6752026	APOB	1.51	0.86	2.65	1.48E-01	A	0.15	A	0.00
rs8192678	PPARGC1A	1.19	0.94	1.49	1.48E-01	A	0.09	A	0.34
rs2014800	ABCC1	1.17	0.95	1.44	1.48E-01	T	0.39	C	0.42
rs10759326	IKBKAP	1.20	0.94	1.53	1.48E-01	G	0.45	G	0.22
rs10146482	NEK9	1.17	0.94	1.46	1.49E-01	T	0.34	T	0.49
rs1284605	MBD6	0.81	0.61	1.08	1.49E-01	T	0.23	T	0.16
rs8551	DPAGT1	0.85	0.69	1.06	1.49E-01	T	0.28	T	0.43
rs3779620	PBK	1.25	0.92	1.70	1.49E-01	G	0.27	G	0.11
rs5275	PTGS2	0.85	0.68	1.06	1.50E-01	T	0.38	C	0.36
rs1202283	ABCB4	0.85	0.67	1.06	1.50E-01	A	0.11	G	0.44
rs2076167	PPARD	0.84	0.66	1.07	1.50E-01	A	0.43	G	0.23
rs1132054	SULT2B1	1.17	0.94	1.45	1.50E-01	T	0.24	C	0.44
rs622082	IGHMBP2	1.19	0.94	1.51	1.51E-01	G	0.12	G	0.29
rs2069763	IL2	1.17	0.94	1.45	1.51E-01	T	0.14	T	0.36
rs1799966	BRCA1	1.17	0.94	1.46	1.52E-01	G	0.23	G	0.33
rs6463247	PPIA	1.19	0.94	1.51	1.52E-01	T	0.33	C	0.22
rs1677649	MSH3	0.83	0.65	1.07	1.53E-01	A	0.36	A	0.26
rs643788	DPAGT1	0.85	0.69	1.06	1.54E-01	C	0.28	C	0.43
rs1861494	IFNG	1.18	0.94	1.49	1.54E-01	C	0.16	C	0.29
rs3100725	HNMT	0.83	0.64	1.07	1.54E-01	T	0.26	T	0.20
rs2303400	XRCC5	1.17	0.94	1.44	1.54E-01	C	0.27	C	0.43
rs2228233	NFATC4	1.18	0.94	1.48	1.54E-01	T	0.37	T	0.29
rs2090949	CYP3A7	1.24	0.92	1.66	1.54E-01	A	0.49	G	0.10
rs6802898	PPARG	1.22	0.93	1.59	1.54E-01	C	0.39	T	0.13
rs776746	CYP3A5	1.26	0.92	1.73	1.55E-01	G	0.35	A	0.08
rs903247	CHST11	1.17	0.94	1.44	1.56E-01	C	0.44	C	0.36
rs1378321	HNMT	0.83	0.63	1.08	1.56E-01	C	0.20	C	0.20
rs1357319	CYP3A7	1.24	0.92	1.66	1.57E-01	C	0.49	A	0.10
rs4525938	DCK	0.76	0.52	1.11	1.57E-01	T	0.48	T	0.04
rs2857009	TNXB	1.18	0.94	1.49	1.57E-01	G	0.06	G	0.32
rs1405938	CASP3	1.22	0.93	1.61	1.57E-01	A	0.07	A	0.18
rs3917724	SELP	1.90	0.78	4.63	1.59E-01	T	0.06	T	0.00
rs2222411	CYP3A7	1.23	0.92	1.66	1.59E-01	C	0.49	G	0.10
rs2687142	CYP3A7	1.23	0.92	1.66	1.59E-01	C	0.49	T	0.10
rs2687145	CYP3A7	1.23	0.92	1.66	1.59E-01	C	0.49	T	0.10
rs11669576	LDLR	0.71	0.44	1.15	1.59E-01	A	0.21	A	0.04
rs17064	ABCB1	1.30	0.90	1.87	1.59E-01	T	0.16	T	0.06
rs2037499	CYP3A7	1.23	0.92	1.65	1.59E-01	G	0.49	C	0.10
rs2037497	CYP3A7	1.23	0.92	1.66	1.59E-01	T	0.49	C	0.10
rs524	PPP1R15A	0.84	0.66	1.07	1.59E-01	G	0.47	A	0.25
rs2687140	CYP3A7	1.23	0.92	1.65	1.59E-01	G	0.49	A	0.11

rs730566	ATRIP	0.84	0.66	1.07	1.60E-01	T	0.10	T	0.30
rs2687143	CYP3A7	1.23	0.92	1.65	1.60E-01	A	0.49	G	0.10
rs1799793	ERCC2	0.85	0.68	1.07	1.60E-01	A	0.08	A	0.35
rs2618346	DUSP1	0.75	0.50	1.12	1.61E-01	T	0.04	T	0.10
rs8058690	NFATC3	0.81	0.61	1.09	1.62E-01	G	0.26	G	0.15
rs2278294	IMPDH1	1.17	0.94	1.47	1.62E-01	A	0.39	A	0.36
rs1327474	IFNGR1	0.85	0.67	1.07	1.62E-01	G	0.12	G	0.42
rs164938	TATDN2	1.16	0.94	1.43	1.62E-01	G	0.40	T	0.42
rs212091	ABCC1	0.80	0.58	1.09	1.63E-01	G	0.11	G	0.16
rs8030950	IGF1R	1.17	0.94	1.47	1.63E-01	A	0.38	A	0.29
rs1076150	DBH	0.87	0.71	1.06	1.63E-01	G	0.49	G	0.48
rs715147	NFATC2	0.86	0.69	1.07	1.63E-01	A	0.23	G	0.50
rs9932251	NFATC3	0.81	0.61	1.09	1.64E-01	A	0.26	A	0.15
rs1544094	LOC100130458	1.23	0.92	1.65	1.64E-01	G	0.42	C	0.11
rs2066471	MTHFR	1.20	0.93	1.55	1.64E-01	A	0.02	A	0.18
rs7759	DPAGT1	0.85	0.68	1.07	1.64E-01	G	0.15	G	0.37
rs3743135	PAK6	0.76	0.52	1.12	1.64E-01	G	0.29	G	0.07
rs2070151	ATF6	1.25	0.91	1.72	1.64E-01	T	0.15	T	0.10
rs3731722	AOX1	0.72	0.45	1.14	1.64E-01	C	0.05	C	0.08
rs1060584	FLJ10213	0.86	0.70	1.06	1.65E-01	C	0.35	C	0.49
rs1549758	NOS3	1.19	0.93	1.52	1.66E-01	T	0.12	T	0.30
rs8191448	GSTP1	0.44	0.13	1.41	1.66E-01	T	0.12	T	0.00
rs1805388	LIG4	1.20	0.93	1.56	1.66E-01	T	0.10	T	0.17
rs639838	PGR	1.17	0.94	1.46	1.66E-01	C	0.49	C	0.30
rs1805016	IL4R	0.73	0.47	1.14	1.67E-01	G	0.26	G	0.05
rs520354	APOB	0.85	0.68	1.07	1.68E-01	G	0.19	G	0.49
rs11959820	PPARGC1B	0.70	0.42	1.16	1.68E-01	A	0.19	A	0.03
rs3775289	DCK	0.74	0.49	1.13	1.69E-01	G	0.48	A	0.04
rs3100702	HNMT	0.86	0.69	1.07	1.69E-01	T	0.32	T	0.41
rs2261144	CYP2A7	1.16	0.94	1.44	1.70E-01	G	0.19	G	0.32
rs3136516	F2	1.17	0.94	1.45	1.71E-01	A	0.09	G	0.47
rs7386926	CYP11B1	0.86	0.69	1.07	1.72E-01	A	0.36	A	0.42
rs7698628	SPARCL1	1.17	0.93	1.47	1.73E-01	G	0.21	T	0.38
rs2235000	ATM	1.79	0.77	4.15	1.73E-01	A	0.07	0	0.00
rs11421	FCER1G	1.21	0.92	1.60	1.74E-01	C	0.10	C	0.16
rs1800682	FAS	1.16	0.94	1.43	1.74E-01	T	0.30	C	0.45
rs2740560	CYP3A7	1.22	0.92	1.63	1.74E-01	T	0.49	A	0.11
rs6898097	RAD50	1.41	0.86	2.31	1.74E-01	G	0.42	G	0.01
rs568408	IL12A	1.21	0.92	1.60	1.74E-01	A	0.20	A	0.13
rs4766003	C12orf32	1.17	0.93	1.46	1.74E-01	G	0.39	A	0.37
rs3204145	IKBKAP	0.83	0.63	1.09	1.74E-01	A	0.31	A	0.18
rs3740066	ABCC2	1.16	0.93	1.45	1.74E-01	A	0.24	A	0.37
rs6744284	UGT1A10	1.17	0.93	1.48	1.75E-01	C	0.45	T	0.29
rs1611755	SPRR1A	0.86	0.69	1.07	1.76E-01	T	0.36	T	0.45
rs16940	BRCA1	1.17	0.93	1.45	1.76E-01	C	0.18	C	0.33
rs2304975	PSMB6	0.73	0.46	1.15	1.76E-01	T	0.02	T	0.09
rs2756105	ABCC2	1.17	0.93	1.47	1.76E-01	T	0.24	T	0.42
rs2968557	ADCK2	0.81	0.59	1.10	1.76E-01	A	0.40	G	0.12
rs2230593	MST1R	0.69	0.41	1.18	1.77E-01	A	0.01	A	0.08
rs2857605	NFKBIL1	0.82	0.61	1.10	1.78E-01	G	0.07	G	0.19

rs1060915	BRCA1	1.16	0.93	1.45	1.78E-01	C	0.18	C	0.33
rs1049544	SPARCL1	1.17	0.93	1.47	1.79E-01	C	0.20	G	0.38
rs1879612	IGF1R	1.15	0.94	1.42	1.80E-01	T	0.46	C	0.40
rs3743260	IGF1R	1.47	0.84	2.57	1.81E-01	A	0.06	A	0.03
rs1043720	ADRB3	0.85	0.67	1.08	1.81E-01	A	0.12	A	0.31
rs2058996	ABCB11	0.85	0.68	1.08	1.81E-01	A	0.26	A	0.44
rs915057	SYNE2	1.16	0.93	1.45	1.82E-01	T	0.12	T	0.43
rs2020898	CASP9	1.16	0.93	1.44	1.82E-01	T	0.12	T	0.45
rs3213469	ATF6B	1.18	0.92	1.51	1.82E-01	G	0.05	G	0.28
rs1134095	CYP11B1	0.86	0.69	1.07	1.82E-01	C	0.36	C	0.42
rs1536826	CYP2E1	0.83	0.63	1.09	1.83E-01	C	0.22	A	0.20
rs4073	IL8	1.16	0.93	1.44	1.83E-01	T	0.22	A	0.48
rs3748338	RNASE4	0.78	0.53	1.13	1.83E-01	T	0.05	T	0.16
rs2062541	ABCC1	1.16	0.93	1.46	1.84E-01	T	0.49	C	0.41
rs717620	ABCC2	1.20	0.92	1.57	1.84E-01	A	0.03	A	0.19
rs275704	Intergenic	0.84	0.64	1.09	1.84E-01	C	0.23	G	0.22
rs5918	ITGB3	0.79	0.56	1.12	1.84E-01	C	0.09	C	0.13
rs2706357	RAD50	1.40	0.85	2.29	1.85E-01	C	0.43	C	0.01
rs3021094	IL10	0.76	0.50	1.14	1.86E-01	C	0.02	C	0.10
rs11537643	VWF	0.62	0.31	1.26	1.86E-01	A	0.18	A	0.00
rs937369	ABCC1	1.15	0.93	1.43	1.86E-01	G	0.38	A	0.42
rs10895065	PGR	0.85	0.67	1.08	1.87E-01	A	0.36	A	0.32
rs4886605	CYP1A1	1.18	0.92	1.52	1.87E-01	C	0.47	T	0.18
rs1926201	FAS	0.87	0.70	1.07	1.87E-01	C	0.25	G	0.45
rs2295155	CARD10	0.75	0.50	1.15	1.88E-01	A	0.02	A	0.11
rs1572983	BAAT	0.85	0.67	1.08	1.88E-01	C	0.48	C	0.32
rs875119	TTR	0.68	0.39	1.21	1.89E-01	G	0.08	G	0.04
rs1464890	ZC3HC1	0.86	0.69	1.07	1.89E-01	C	0.18	T	0.41
rs10018297	Intergenic	1.83	0.74	4.50	1.89E-01	G	0.08	G	0.00
rs268673	PRX	0.86	0.70	1.07	1.89E-01	G	0.31	G	0.41
rs2308327	LOC100129103	0.77	0.52	1.14	1.90E-01	G	0.01	G	0.12
rs4348159	UGT2B7	0.77	0.52	1.14	1.91E-01	T	0.28	T	0.09
rs3808553	FZD6	1.15	0.93	1.43	1.91E-01	G	0.29	G	0.48
rs1913262	MGST1	0.86	0.68	1.08	1.92E-01	A	0.35	A	0.29
rs11574528	MCAT	0.84	0.65	1.09	1.92E-01	T	0.38	T	0.19
rs1801265	DPYD	0.85	0.66	1.09	1.92E-01	C	0.38	C	0.23
rs1399290	DPYD	1.38	0.85	2.25	1.93E-01	G	0.22	G	0.01
rs914937	DPYD	1.38	0.85	2.24	1.93E-01	A	0.22	A	0.01
rs4418320	CYP11B1	1.15	0.93	1.42	1.94E-01	A	0.38	A	0.50
rs348475	ALDH1A1	0.87	0.70	1.07	1.94E-01	G	0.31	G	0.48
rs4918907	PDLIM1	0.86	0.69	1.08	1.94E-01	A	0.49	A	0.32
rs6027	F5	1.31	0.87	1.98	1.95E-01	G	0.02	G	0.06
rs1514347	ESR1	0.84	0.64	1.09	1.95E-01	A	0.12	A	0.25
rs11879620	VRK3	1.46	0.82	2.58	1.95E-01	C	0.17	C	0.00
rs2286940	MLH1	0.86	0.69	1.08	1.95E-01	T	0.20	T	0.43
rs2074900	CYP4F2	0.84	0.65	1.09	1.95E-01	A	0.19	A	0.27
rs1126667	ALOX12	1.15	0.93	1.43	1.96E-01	A	0.34	A	0.42
rs1800686	CD40	1.18	0.92	1.53	1.96E-01	A	0.07	A	0.25
rs1799998	CYP11B2	1.16	0.93	1.44	1.97E-01	C	0.20	C	0.44
rs628816	DPYD	0.59	0.26	1.32	1.97E-01	A	0.12	A	0.01

rs1799949	BRCA1	1.16	0.93	1.44	1.97E-01	T	0.22	T	0.30
rs5742671	IGF1	0.81	0.59	1.11	1.98E-01	T	0.04	T	0.16
rs6220	IGF1	0.85	0.67	1.09	1.98E-01	G	0.40	G	0.28
rs3814058	NR1I2	0.83	0.63	1.10	1.98E-01	C	0.44	C	0.20
rs1801196	WRN	0.85	0.67	1.09	1.99E-01	T	0.25	T	0.30
rs6666652	ABCA4	1.27	0.88	1.83	1.99E-01	A	0.48	A	0.04
rs7761731	CYP39A1	1.16	0.92	1.45	1.99E-01	A	0.32	T	0.27
rs2069849	IL6	1.39	0.84	2.28	2.00E-01	T	0.15	T	0.02
rs1053046	PPARD	0.78	0.54	1.14	2.01E-01	A	0.47	A	0.05
rs6416668	ABCC6	0.51	0.18	1.44	2.01E-01	T	0.09	T	0.00
rs874305	IGF1R	0.87	0.69	1.08	2.01E-01	A	0.45	A	0.40
rs5301	CYP11B1	1.15	0.93	1.42	2.01E-01	G	0.37	G	0.50
rs1148555	MBD6	0.83	0.62	1.11	2.02E-01	G	0.18	G	0.16
rs1538660	IKBKAP	0.84	0.64	1.10	2.02E-01	T	0.30	T	0.18
rs1049434	SLC16A1	0.87	0.69	1.08	2.02E-01	T	0.16	T	0.43
rs7169	SLC16A1	0.87	0.69	1.08	2.02E-01	C	0.16	C	0.43
rs3918022	CCNK	1.14	0.93	1.41	2.02E-01	G	0.35	G	0.43
rs1913263	MGST1	0.86	0.68	1.09	2.02E-01	G	0.35	G	0.29
rs4148949	CHST3	0.87	0.70	1.08	2.02E-01	T	0.16	T	0.42
rs2237586	PON2	1.17	0.92	1.50	2.03E-01	T	0.19	T	0.23
rs3258	FDFT1	1.15	0.93	1.44	2.03E-01	C	0.35	C	0.38
rs2234693	ESR1	0.87	0.70	1.08	2.03E-01	T	0.45	C	0.46
rs3811740	PLK4	0.86	0.68	1.09	2.04E-01	A	0.18	A	0.32
rs2266691	CCNH	1.82	0.72	4.59	2.04E-01	G	0.06	0	0.00
rs3791981	APOB	1.22	0.90	1.64	2.05E-01	G	0.42	G	0.10
rs2582790	HMGCS2	0.86	0.68	1.09	2.05E-01	T	0.37	T	0.30
rs4437575	ABCB1	1.15	0.92	1.44	2.06E-01	G	0.38	G	0.43
rs2066494	RAD9A	1.49	0.80	2.76	2.06E-01	C	0.06	C	0.02
rs13035	PYROXD1	1.15	0.93	1.42	2.06E-01	C	0.17	C	0.44
rs3100701	HNMT	0.87	0.70	1.08	2.07E-01	T	0.30	T	0.41
rs917394	NPC2	0.87	0.70	1.08	2.07E-01	T	0.29	T	0.39
rs4619	IGFBP1	1.15	0.93	1.42	2.08E-01	G	0.46	G	0.37
rs17012739	PLK4	0.86	0.68	1.09	2.08E-01	G	0.18	G	0.32
rs9808753	IFNGR2	1.19	0.91	1.57	2.08E-01	G	0.18	G	0.14
rs6911817	PPARD	0.71	0.42	1.21	2.08E-01	T	0.27	T	0.02
rs730821	SIRT1	1.17	0.92	1.50	2.08E-01	G	0.26	G	0.23
rs12680	LOC100129773	1.27	0.87	1.86	2.09E-01	C	0.28	C	0.08
rs246234	ABCC1	1.16	0.92	1.47	2.09E-01	G	0.48	C	0.32
rs216321	VWF	1.25	0.88	1.75	2.09E-01	T	0.03	T	0.09
rs439132	LIG1	1.41	0.83	2.39	2.09E-01	G	0.22	G	0.01
rs757081	NUCB2	1.17	0.92	1.48	2.11E-01	C	0.10	C	0.33
rs1799950	BRCA1	0.73	0.45	1.19	2.11E-01	G	0.01	G	0.07
rs1548216	IL6	1.31	0.86	1.99	2.12E-01	C	0.20	C	0.02
rs12713450	APOB	1.74	0.73	4.13	2.12E-01	T	0.09	T	0.00
rs3842	ABCB1	1.20	0.90	1.61	2.13E-01	G	0.19	G	0.13
rs7843746	C8orf68	0.86	0.68	1.09	2.13E-01	T	0.50	C	0.24
rs827423	ESR1	1.15	0.92	1.42	2.14E-01	T	0.38	C	0.49
rs2301159	SLC10A2	1.16	0.92	1.45	2.14E-01	T	0.33	T	0.25
rs3212254	ADCY4	1.27	0.87	1.84	2.14E-01	A	0.19	A	0.05
rs5742667	IGF1	0.86	0.67	1.09	2.14E-01	T	0.36	T	0.26

rs2231924	FLJ10213	0.87	0.71	1.08	2.14E-01	T	0.36	T	0.48
rs296365	SULT2A1	0.86	0.68	1.09	2.15E-01	C	0.50	G	0.27
rs3803036	PTPRR	0.85	0.65	1.10	2.15E-01	G	0.40	A	0.20
rs2291462	IL17RD	0.84	0.64	1.11	2.15E-01	T	0.35	T	0.14
rs2302524	PLAUR	0.83	0.62	1.12	2.15E-01	C	0.22	C	0.17
rs2288550	IMPDH1	0.83	0.61	1.12	2.16E-01	C	0.08	C	0.18
rs2276299	SLC22A8	1.19	0.90	1.56	2.16E-01	T	0.07	T	0.19
rs4647688	CASP3	1.20	0.90	1.59	2.16E-01	A	0.03	A	0.18
rs3218171	E2F2	0.87	0.69	1.09	2.17E-01	T	0.08	G	0.50
rs1544410	VDR	0.87	0.70	1.08	2.17E-01	A	0.26	A	0.39
rs2706364	RAD50	1.36	0.83	2.23	2.17E-01	A	0.43	A	0.01
rs3741378	SIPA1	0.82	0.60	1.13	2.17E-01	A	0.28	A	0.13
rs308394	FGF2	1.43	0.81	2.51	2.18E-01	C	0.12	C	0.01
rs2278293	IMPDH1	1.15	0.92	1.42	2.18E-01	A	0.48	A	0.46
rs7441750	UGT2B7	1.15	0.92	1.42	2.18E-01	G	0.26	A	0.48
rs1573496	ADH7	0.78	0.52	1.16	2.19E-01	G	0.02	G	0.09
rs3742106	ABCC4	0.87	0.70	1.08	2.19E-01	C	0.36	C	0.39
rs16754	WT1	1.18	0.90	1.55	2.19E-01	G	0.16	G	0.15
rs1134921	GAK	0.81	0.59	1.13	2.19E-01	A	0.01	A	0.14
rs1962	THBD	1.16	0.91	1.49	2.20E-01	C	0.36	C	0.24
rs1048201	FGF2	0.83	0.62	1.12	2.20E-01	T	0.07	T	0.18
rs2239330	ABCC1	1.17	0.91	1.50	2.21E-01	T	0.12	T	0.29
rs1951765	FKBP1A	1.16	0.92	1.46	2.21E-01	A	0.16	A	0.25
rs854570	PON1	1.15	0.92	1.43	2.22E-01	A	0.28	C	0.38
rs2839668	MYO3A	0.77	0.50	1.17	2.22E-01	G	0.08	G	0.09
rs1751034	ABCC4	1.18	0.90	1.54	2.22E-01	C	0.30	C	0.20
rs217434	NPC1L1	0.84	0.64	1.11	2.23E-01	G	0.16	G	0.20
rs7009367	C8orf68	0.85	0.66	1.10	2.23E-01	G	0.45	G	0.18
rs2375005	PON2	0.87	0.71	1.09	2.23E-01	T	0.42	A	0.48
rs1364726	XRCC5	1.21	0.89	1.66	2.24E-01	T	0.18	T	0.13
rs853778	ABCB11	0.88	0.71	1.08	2.24E-01	G	0.49	A	0.44
rs11582663	FCRL4	0.81	0.58	1.14	2.25E-01	T	0.04	T	0.14
rs2479383	PSMB4	1.18	0.90	1.55	2.25E-01	C	0.08	C	0.18
rs1587241	PPP3CA	0.86	0.68	1.10	2.26E-01	C	0.48	G	0.28
rs7987433	SLC10A2	1.20	0.89	1.61	2.26E-01	C	0.19	C	0.14
rs398700	RUNDC2A	1.18	0.90	1.55	2.26E-01	G	0.43	G	0.17
rs484066	ABCB11	0.88	0.71	1.09	2.26E-01	A	0.45	T	0.36
rs496190	MRE11A	1.14	0.92	1.40	2.26E-01	T	0.34	C	0.46
rs43037	PON2	1.14	0.92	1.43	2.27E-01	C	0.20	C	0.38
rs1413228	DPYD	1.21	0.89	1.65	2.27E-01	G	0.27	G	0.09
rs2020917	COMT	0.85	0.66	1.10	2.27E-01	T	0.11	T	0.27
rs1050900	HNMT	0.85	0.65	1.11	2.27E-01	A	0.16	A	0.20
rs2243248	IL4	0.78	0.52	1.17	2.28E-01	G	0.16	G	0.08
rs2235041	ABCB1	1.71	0.71	4.10	2.28E-01	T	0.07	T	0.00
rs35597	ABCC1	0.88	0.71	1.09	2.28E-01	A	0.30	A	0.47
rs228851	NFATC2	0.87	0.70	1.09	2.29E-01	T	0.11	T	0.48
rs1540339	VDR	1.13	0.92	1.39	2.29E-01	A	0.24	A	0.37
rs434455	RUNDC2A	1.17	0.90	1.52	2.29E-01	T	0.43	T	0.16
rs3181366	TNFSF8	0.88	0.71	1.09	2.30E-01	T	0.26	T	0.43
rs676210	APOB	0.85	0.65	1.11	2.30E-01	A	0.14	A	0.25

rs2075685	TMEM167	0.88	0.71	1.09	2.30E-01	G	0.43	T	0.45
rs1496496	IGFBP3	1.14	0.92	1.43	2.30E-01	G	0.44	G	0.37
rs7515157	FMO2	0.87	0.69	1.09	2.30E-01	T	0.49	T	0.29
rs398734	CD44	1.15	0.91	1.46	2.30E-01	A	0.47	A	0.27
rs1050891	HNMT	0.85	0.65	1.11	2.30E-01	C	0.16	C	0.20
rs268687	SERTAD1	1.15	0.92	1.44	2.31E-01	A	0.14	A	0.47
rs3739942	KIAA1984	1.15	0.92	1.44	2.32E-01	G	0.24	G	0.27
rs4987131	CYBA	0.43	0.11	1.73	2.33E-01	C	0.11	C	0.00
rs10034373	WHSC1	0.50	0.16	1.57	2.33E-01	T	0.12	0	0.00
rs10018198	Intergenic	1.17	0.90	1.52	2.34E-01	C	0.08	C	0.23
rs11572081	CYP2C8	1.53	0.76	3.08	2.34E-01	A	0.17	A	0.00
rs1199039	TIE1	1.14	0.92	1.42	2.34E-01	C	0.18	C	0.39
rs28900388	UGT1A10	0.41	0.09	1.79	2.34E-01	C	0.07	C	0.00
rs16938893	GDAP1	1.15	0.91	1.45	2.34E-01	G	0.11	G	0.34
rs1870377	KDR	1.17	0.90	1.51	2.35E-01	A	0.12	A	0.25
rs773902	F2RL3	0.85	0.64	1.11	2.35E-01	G	0.46	A	0.18
rs10248420	ABCB1	1.18	0.90	1.55	2.35E-01	G	0.47	G	0.16
rs6714486	UGT1A10	1.25	0.86	1.82	2.35E-01	A	0.17	A	0.06
rs3024496	IL10	0.88	0.71	1.09	2.35E-01	C	0.43	C	0.45
rs2071421	ARSA	1.20	0.89	1.62	2.35E-01	G	0.24	G	0.14
rs543304	BRCA2	1.18	0.90	1.54	2.35E-01	C	0.17	C	0.18
rs3739922	SETX	1.29	0.85	1.96	2.35E-01	G	0.07	G	0.05
rs1417938	CRP	1.15	0.91	1.44	2.36E-01	A	0.12	A	0.30
rs7602171	ABCB11	0.86	0.66	1.11	2.36E-01	A	0.12	A	0.29
rs769218	CAT	0.85	0.64	1.12	2.37E-01	A	0.15	A	0.22
rs207921	XRCC5	1.14	0.92	1.40	2.37E-01	G	0.25	G	0.44
rs2069810	IL5	0.70	0.38	1.27	2.38E-01	G	0.29	G	0.01
rs1799977	MLH1	0.86	0.67	1.10	2.38E-01	G	0.05	G	0.30
rs3212859	CCND1	1.30	0.84	1.99	2.39E-01	T	0.21	T	0.03
rs6018	F5	1.29	0.85	1.96	2.39E-01	G	0.02	G	0.06
rs1913474	ESR1	0.85	0.65	1.11	2.39E-01	T	0.12	T	0.25
rs12456560	NDC80	1.20	0.88	1.64	2.40E-01	T	0.06	T	0.14
rs10028494	UGT2B7	1.24	0.87	1.76	2.40E-01	C	0.07	C	0.16
rs6773295	NR1I2	0.61	0.27	1.39	2.41E-01	G	0.14	G	0.02
rs2300697	SRD5A2	1.14	0.92	1.41	2.41E-01	C	0.29	C	0.42
rs10017297	Intergenic	1.34	0.82	2.18	2.41E-01	T	0.25	T	0.01
rs5743611	TLR1	1.26	0.86	1.86	2.42E-01	C	0.01	C	0.10
rs3757280	HSP90AB1	0.78	0.52	1.18	2.42E-01	C	0.02	C	0.09
rs2267237	LARGE	0.82	0.58	1.15	2.42E-01	C	0.25	C	0.11
rs3093057	CSF1	1.15	0.91	1.46	2.42E-01	T	0.12	T	0.37
rs1322055	TNFSF8	0.82	0.58	1.15	2.43E-01	C	0.06	C	0.13
rs472344	ANKRD49	1.13	0.92	1.39	2.44E-01	A	0.38	T	0.46
rs4150474	ERCC3	0.87	0.69	1.10	2.44E-01	G	0.29	G	0.29
rs10410075	VRK3	1.41	0.79	2.51	2.44E-01	A	0.17	A	0.00
rs9944225	CYP19A1	0.77	0.50	1.19	2.44E-01	A	0.08	A	0.08
rs7801671	CYP3A4	1.45	0.77	2.73	2.44E-01	A	0.21	A	0.00
rs186556	SLC29A1	1.67	0.70	3.97	2.44E-01	T	0.07	T	0.00
rs173537	HERPUD1	1.14	0.91	1.42	2.44E-01	T	0.36	C	0.27
rs1130864	CRP	1.14	0.91	1.42	2.45E-01	T	0.20	T	0.30
rs688755	CYP4F12	0.87	0.68	1.10	2.45E-01	C	0.37	C	0.27

rs4251545	IRAK4	0.82	0.58	1.15	2.47E-01	A	0.30	A	0.10
rs1677715	PDSS1	1.15	0.91	1.44	2.47E-01	G	0.49	A	0.30
rs4722266	STK31	1.18	0.89	1.56	2.47E-01	A	0.19	A	0.15
rs894817	IGF2R	0.87	0.69	1.10	2.48E-01	A	0.27	A	0.35
rs4792147	ALOX15B	0.88	0.71	1.09	2.49E-01	A	0.17	G	0.50
rs1334811	TEK	1.32	0.82	2.11	2.49E-01	A	0.14	A	0.04
rs12072582	FMO3	0.43	0.10	1.80	2.49E-01	C	0.07	C	0.00
rs3322	LOC100129773	0.76	0.48	1.21	2.49E-01	A	0.01	A	0.08
rs3093056	CSF1	1.15	0.91	1.45	2.50E-01	A	0.18	A	0.37
rs762551	CYP1A2	0.87	0.69	1.10	2.50E-01	C	0.42	C	0.29
rs2741872	CYP3A7	1.20	0.88	1.62	2.51E-01	A	0.46	A	0.09
rs1042034	APOB	0.86	0.66	1.12	2.51E-01	G	0.14	G	0.25
rs3138045	NFKBIA	0.86	0.66	1.11	2.51E-01	G	0.26	G	0.21
rs13141136	HELQ	1.13	0.91	1.41	2.51E-01	G	0.11	G	0.44
rs454078	IL1RN	1.16	0.90	1.48	2.52E-01	T	0.07	T	0.29
rs1270146	MRE11A	1.13	0.92	1.38	2.52E-01	T	0.37	C	0.46
rs3847262	TPD52L3	0.77	0.49	1.21	2.53E-01	T	0.17	T	0.05
rs839763	CDC20	1.13	0.91	1.40	2.53E-01	G	0.28	G	0.38
rs6577	GSTA2	1.22	0.87	1.71	2.53E-01	A	0.39	C	0.06
rs2070673	CYP2E1	0.85	0.64	1.13	2.53E-01	T	0.36	A	0.18
rs1514346	IRF4	1.18	0.89	1.57	2.53E-01	A	0.40	A	0.14
rs5082	APOA2	0.88	0.72	1.09	2.54E-01	C	0.23	C	0.38
rs1003483	IGF2	0.88	0.71	1.10	2.54E-01	G	0.19	G	0.50
rs4646227	SLC15A1	0.72	0.42	1.26	2.55E-01	C	0.11	C	0.02
rs978458	IGF1	0.87	0.68	1.11	2.55E-01	A	0.37	A	0.26
rs2290272	SLC28A1	1.13	0.91	1.40	2.55E-01	T	0.25	T	0.38
rs2072330	ALDH3A1	1.13	0.91	1.40	2.55E-01	A	0.12	A	0.39
rs2241342	ABCB11	0.88	0.70	1.10	2.55E-01	A	0.38	A	0.36
rs207927	XRCC5	1.13	0.92	1.40	2.56E-01	G	0.25	G	0.44
rs3731258	CDK6	1.37	0.80	2.36	2.56E-01	T	0.14	T	0.01
rs667515	CCND1	0.87	0.69	1.10	2.57E-01	C	0.36	C	0.37
rs871514	UGT1A10	1.14	0.91	1.41	2.57E-01	A	0.27	G	0.44
rs2686184	FDFT1	0.88	0.70	1.10	2.57E-01	A	0.46	A	0.40
rs2053098	SLCO1B3	1.16	0.90	1.50	2.57E-01	G	0.42	A	0.14
rs6768093	ATR	0.88	0.71	1.10	2.58E-01	A	0.16	A	0.44
rs32950	MSH3	1.13	0.91	1.41	2.59E-01	A	0.50	G	0.44
rs6756629	ABCG5	1.25	0.85	1.82	2.59E-01	A	0.06	A	0.06
rs138056	SULT4A1	1.16	0.90	1.49	2.59E-01	A	0.31	A	0.20
rs1060250	SLC7A5	1.66	0.69	4.00	2.60E-01	G	0.06	0	0.00
rs1934963	CYP2C9	0.85	0.64	1.13	2.60E-01	C	0.21	C	0.17
rs4148946	CHST3	0.88	0.71	1.10	2.60E-01	C	0.21	C	0.42
rs3743261	IGF1R	1.38	0.79	2.40	2.60E-01	T	0.07	T	0.03
rs2229362	BCL6	1.17	0.89	1.54	2.61E-01	A	0.37	A	0.15
rs1051266	SLC19A1	0.88	0.70	1.10	2.61E-01	G	0.37	A	0.43
rs1934951	CYP2C8	1.16	0.90	1.50	2.62E-01	A	0.34	A	0.17
rs2808630	CRP	1.14	0.91	1.44	2.62E-01	C	0.18	C	0.28
rs1137115	CYP2A6	1.14	0.91	1.44	2.62E-01	A	0.21	A	0.26
rs10896380	IGHMBP2	0.85	0.64	1.13	2.63E-01	G	0.10	G	0.23
rs6028	F5	1.15	0.90	1.45	2.63E-01	C	0.05	C	0.30
rs1054875	POLG	0.88	0.70	1.10	2.63E-01	A	0.41	T	0.40

rs947894	GSTP1	1.13	0.91	1.41	2.64E-01	G	0.44	G	0.35
rs2070672	CYP2E1	1.30	0.82	2.05	2.64E-01	G	0.14	G	0.03
rs4072037	MUC1	0.89	0.72	1.10	2.65E-01	G	0.36	G	0.43
rs207928	XRCC5	1.13	0.91	1.39	2.65E-01	A	0.25	A	0.44
rs212090	ABCC1	1.14	0.90	1.44	2.65E-01	A	0.20	A	0.44
rs163078	FAM82A	1.13	0.91	1.40	2.66E-01	T	0.30	T	0.38
rs3087455	CASP3	1.13	0.91	1.42	2.66E-01	C	0.22	C	0.37
rs2508784	MRE11A	1.12	0.91	1.38	2.66E-01	A	0.36	G	0.46
rs2687081	CYP3A7	1.19	0.88	1.60	2.66E-01	T	0.45	C	0.10
rs7778377	STARD3NL	0.86	0.65	1.13	2.66E-01	T	0.10	T	0.19
rs2071426	CYP2C8	0.87	0.68	1.11	2.66E-01	G	0.24	G	0.28
rs2275801	ZMYND8	0.81	0.56	1.18	2.67E-01	A	0.45	G	0.07
rs7895372	ITGA8	1.42	0.76	2.64	2.67E-01	G	0.10	G	0.00
rs6410	CYP11B1	0.88	0.70	1.10	2.68E-01	G	0.41	A	0.46
rs3917974	CSF3R	0.45	0.11	1.86	2.68E-01	G	0.07	G	0.00
rs759845	ADAM23	1.13	0.91	1.42	2.68E-01	C	0.33	C	0.40
rs4647001	JUN	0.88	0.71	1.10	2.68E-01	C	0.35	G	0.35
rs2069843	IL6	1.35	0.79	2.29	2.69E-01	A	0.12	A	0.02
rs1770810	SLC2A1	0.85	0.63	1.14	2.70E-01	T	0.16	T	0.19
rs13166360	ADCY2	0.85	0.63	1.14	2.71E-01	T	0.08	T	0.20
rs5898	F2	0.78	0.51	1.21	2.71E-01	A	0.04	A	0.08
rs2304821	PTPRB	0.80	0.53	1.19	2.72E-01	A	0.10	A	0.10
rs497763	ANKRD49	1.13	0.91	1.39	2.72E-01	A	0.37	A	0.45
rs5744934	POLE	1.18	0.88	1.59	2.72E-01	G	0.15	G	0.11
rs2075724	CSF2RB	1.13	0.91	1.40	2.72E-01	T	0.14	G	0.44
rs241440	TAP2	0.87	0.68	1.12	2.72E-01	A	0.13	A	0.23
rs7805658	SHFM1	0.88	0.70	1.10	2.73E-01	A	0.12	A	0.44
rs3733890	BHMT	0.88	0.69	1.11	2.73E-01	A	0.23	A	0.32
rs3743258	IGF1R	1.14	0.90	1.44	2.73E-01	A	0.32	A	0.31
rs35605	ABCC1	1.17	0.88	1.55	2.73E-01	T	0.07	T	0.19
rs3755160	ABCB11	1.13	0.91	1.41	2.74E-01	T	0.17	T	0.38
rs934197	APOB	1.14	0.90	1.43	2.74E-01	A	0.16	A	0.32
rs557462	ABCB11	0.88	0.69	1.11	2.74E-01	G	0.05	G	0.31
rs2687079	CYP3A7	1.18	0.88	1.60	2.75E-01	T	0.45	A	0.10
rs2687084	CYP3A7	1.18	0.88	1.60	2.75E-01	T	0.45	G	0.10
rs2299264	PON2	1.15	0.90	1.46	2.75E-01	T	0.23	T	0.24
rs3829963	LOC100131484	1.17	0.88	1.55	2.75E-01	A	0.31	A	0.15
rs329003	PPP4R1	0.81	0.55	1.19	2.75E-01	G	0.00	G	0.11
rs2687078	CYP3A7	1.18	0.87	1.60	2.76E-01	A	0.45	G	0.10
rs5370	EDN1	1.15	0.89	1.48	2.76E-01	T	0.21	T	0.23
rs1851425	CYP3A7	1.18	0.87	1.60	2.77E-01	T	0.45	C	0.10
rs1346044	WRN	1.14	0.90	1.46	2.77E-01	C	0.14	C	0.26
rs2297404	ABCA1	0.76	0.46	1.25	2.77E-01	C	0.05	C	0.08
rs2740565	CYP3A7	1.18	0.87	1.60	2.78E-01	T	0.45	A	0.10
rs1024611	CCL2	1.13	0.91	1.41	2.78E-01	C	0.19	C	0.30
rs2479717	CCND3	0.87	0.67	1.12	2.78E-01	T	0.03	T	0.27
rs3138047	NFKBIA	0.87	0.67	1.12	2.79E-01	T	0.26	T	0.21
rs17151919	LEP	0.51	0.15	1.74	2.79E-01	A	0.07	A	0.00
rs2296241	CYP24A1	1.12	0.91	1.38	2.79E-01	G	0.47	G	0.48
rs755622	MIF	1.15	0.90	1.46	2.79E-01	G	0.41	G	0.19

rs3113224	HNMT	0.87	0.68	1.12	2.80E-01	A	0.49	A	0.20
rs730722	CHST3	1.21	0.86	1.70	2.80E-01	G	0.29	G	0.05
rs2234700	EPHX1	0.45	0.11	1.92	2.80E-01	C	0.07	C	0.00
rs2299266	PON2	1.14	0.90	1.46	2.80E-01	G	0.23	G	0.24
rs4839469	VANGL1	1.17	0.88	1.56	2.81E-01	A	0.07	A	0.14
rs776742	CYP3A7	1.18	0.87	1.60	2.81E-01	G	0.45	A	0.10
rs3783408	MAP4K5	0.87	0.67	1.13	2.81E-01	A	0.08	A	0.26
rs8192707	PLCG1	1.17	0.88	1.56	2.82E-01	G	0.11	G	0.14
rs820196	LOC100132011	0.86	0.64	1.14	2.82E-01	C	0.25	C	0.22
rs28948385	UGT1A8	0.68	0.33	1.38	2.83E-01	G	0.15	G	0.03
rs2267665	PPARD	0.85	0.64	1.14	2.83E-01	A	0.11	A	0.17
rs628959	DPYD	0.87	0.68	1.12	2.84E-01	G	0.11	G	0.27
rs854544	PPP1R9A	0.88	0.70	1.11	2.84E-01	C	0.24	T	0.35
rs1367117	APOB	1.13	0.90	1.43	2.84E-01	A	0.15	A	0.32
rs1492078	AGTR1	0.88	0.70	1.11	2.84E-01	G	0.15	A	0.36
rs1609519	DPYD	0.87	0.68	1.12	2.84E-01	G	0.07	G	0.27
rs2068604	PON2	1.14	0.89	1.46	2.84E-01	T	0.25	T	0.24
rs4554144	UGT2B7	1.13	0.91	1.40	2.85E-01	C	0.24	T	0.49
rs2255235	B2M	1.18	0.87	1.60	2.85E-01	T	0.36	T	0.12
rs1805331	RAD23B	1.25	0.83	1.87	2.85E-01	A	0.05	A	0.07
rs10499926	SHFM1	0.88	0.71	1.11	2.86E-01	C	0.12	C	0.44
rs348472	ALDH1A1	0.81	0.55	1.20	2.86E-01	A	0.36	A	0.04
rs6661174	FMO2	0.61	0.24	1.52	2.87E-01	C	0.15	C	0.00
rs6671692	FMO2	0.61	0.24	1.53	2.88E-01	A	0.15	A	0.00
rs35604	ABCC1	1.16	0.88	1.54	2.88E-01	G	0.07	G	0.19
rs1800896	IL10	0.89	0.71	1.11	2.88E-01	G	0.36	G	0.45
rs7536646	FMO2	0.61	0.24	1.53	2.89E-01	A	0.15	A	0.00
rs6941583	POLH	0.79	0.51	1.22	2.89E-01	T	0.30	T	0.03
rs731236	VDR	0.89	0.71	1.11	2.89E-01	C	0.27	C	0.38
rs737865	COMT	0.88	0.69	1.12	2.89E-01	C	0.15	C	0.28
rs1128503	ABCB1	0.88	0.71	1.11	2.90E-01	T	0.20	T	0.43
rs2287498	TP53	1.19	0.86	1.65	2.90E-01	A	0.25	A	0.09
rs3783613	VCAM1	0.53	0.16	1.72	2.90E-01	C	0.10	C	0.00
rs1029871	NEK4	1.13	0.90	1.41	2.91E-01	G	0.16	G	0.42
rs2300095	FRAP1	1.13	0.90	1.43	2.92E-01	C	0.45	T	0.27
rs474320	PGR	0.84	0.60	1.16	2.92E-01	A	0.03	A	0.15
rs963065	PPP3CA	0.89	0.71	1.11	2.93E-01	G	0.16	A	0.44
rs5277	PTGS2	0.85	0.63	1.15	2.93E-01	C	0.02	C	0.14
rs2239393	COMT	0.89	0.71	1.11	2.93E-01	G	0.42	G	0.36
rs1799929	NAT2	0.89	0.72	1.10	2.93E-01	T	0.21	T	0.42
rs2480452	PPP2R4	0.78	0.50	1.24	2.93E-01	A	0.01	A	0.07
rs2216504	ABCB11	1.27	0.81	1.99	2.94E-01	A	0.12	A	0.04
rs1801282	PPARG	1.19	0.86	1.65	2.95E-01	G	0.02	G	0.12
rs1800925	IL13	1.14	0.89	1.45	2.96E-01	T	0.40	T	0.20
rs8940	CAV2	0.86	0.65	1.14	2.96E-01	G	0.21	G	0.16
rs288326	FRZB	0.81	0.55	1.20	2.96E-01	A	0.03	A	0.11
rs2142694	CYP2D6	1.12	0.90	1.40	2.96E-01	A	0.37	A	0.48
rs2165627	PTPRB	0.84	0.61	1.16	2.97E-01	G	0.13	G	0.14
rs2296239	CYP24A1	1.13	0.90	1.43	2.97E-01	T	0.47	T	0.23
rs993891	HNMT	0.87	0.68	1.13	2.97E-01	C	0.38	A	0.20

rs3795498	STK40	1.15	0.88	1.49	2.98E-01	A	0.19	A	0.23
rs2762934	CYP24A1	1.15	0.88	1.51	2.98E-01	A	0.15	A	0.17
rs811925	PRDM1	1.16	0.88	1.53	2.98E-01	C	0.16	C	0.16
rs7586110	UGT1A10	1.12	0.90	1.40	2.99E-01	G	0.23	G	0.37
rs1409986	PTGER3	0.76	0.46	1.27	2.99E-01	T	0.02	T	0.07
rs1800629	TNF	0.85	0.63	1.15	2.99E-01	A	0.10	A	0.18
rs7311358	SLCO1B3	1.15	0.88	1.49	3.00E-01	A	0.42	G	0.14
rs828063	DPYD	0.86	0.65	1.14	3.00E-01	A	0.18	A	0.17
rs472614	ABCB11	0.90	0.73	1.10	3.01E-01	A	0.42	A	0.45
rs3817405	PLXDC2	0.89	0.72	1.11	3.01E-01	C	0.34	C	0.37
rs2238335	BLM	1.27	0.81	1.99	3.01E-01	C	0.18	C	0.02
rs737693	MMP12	0.83	0.59	1.18	3.02E-01	T	0.02	T	0.14
rs875740	ABCC1	1.12	0.90	1.39	3.03E-01	G	0.45	G	0.36
rs11547883	VRK3	1.36	0.75	2.46	3.04E-01	G	0.17	G	0.00
rs512535	APOB	0.89	0.71	1.11	3.04E-01	G	0.23	A	0.46
rs2286232	PON2	1.14	0.89	1.45	3.05E-01	T	0.24	T	0.24
rs2299263	PON2	1.14	0.89	1.45	3.05E-01	T	0.24	T	0.24
rs4987164	DMC1	1.31	0.78	2.19	3.05E-01	C	0.12	C	0.02
rs9666607	CD44	0.88	0.69	1.12	3.06E-01	A	0.14	A	0.30
rs697221	DDIT3	0.87	0.66	1.14	3.06E-01	A	0.23	A	0.16
rs10836230	CAT	0.88	0.69	1.12	3.07E-01	T	0.17	T	0.35
rs994174	NRG3	0.89	0.71	1.11	3.08E-01	A	0.27	G	0.32
rs2069783	IL3	1.41	0.73	2.74	3.08E-01	C	0.18	C	0.00
rs854555	PON1	0.89	0.72	1.11	3.08E-01	C	0.34	A	0.38
rs3786187	NFATC1	0.90	0.73	1.11	3.08E-01	G	0.46	C	0.42
rs8187799	ABCB4	0.83	0.58	1.19	3.09E-01	G	0.33	G	0.08
rs1709082	CYP2A13	1.18	0.86	1.62	3.09E-01	G	0.37	G	0.10
rs1020678	HNMT	0.90	0.73	1.10	3.10E-01	G	0.44	G	0.39
rs11572073	CYP2C8	1.53	0.67	3.50	3.10E-01	T	0.12	T	0.00
rs2234997	ATM	0.66	0.30	1.46	3.10E-01	A	0.19	A	0.00
rs2238783	ARVCF	1.12	0.90	1.38	3.10E-01	C	0.45	G	0.36
rs1780196	PDSS1	1.16	0.87	1.55	3.10E-01	A	0.10	A	0.15
rs3778893	STARD3NL	0.87	0.67	1.13	3.10E-01	A	0.22	A	0.22
rs1023244	DPYD	1.22	0.83	1.81	3.10E-01	G	0.02	G	0.07
rs5742980	PMS1	0.35	0.05	2.63	3.10E-01	C	0.07	0	0.00
rs4987310	SELL	1.15	0.88	1.50	3.10E-01	T	0.26	T	0.16
rs2011404	UGT1A10	1.17	0.86	1.58	3.10E-01	T	0.05	T	0.14
rs593421	CYP4F12	0.88	0.69	1.13	3.11E-01	C	0.35	C	0.27
rs1296028	FDFT1	0.87	0.67	1.13	3.11E-01	G	0.12	G	0.26
rs3087461	WT1	0.81	0.54	1.22	3.11E-01	T	0.10	T	0.09
rs3218273	IL2RB	1.66	0.62	4.42	3.12E-01	T	0.07	0	0.00
rs608343	LRP5	1.12	0.90	1.38	3.12E-01	A	0.40	G	0.32
rs499009	DPYD	0.88	0.69	1.13	3.13E-01	A	0.08	A	0.27
rs3118529	RXRA	0.86	0.64	1.15	3.13E-01	T	0.21	C	0.32
rs3088142	DUSP13	1.12	0.90	1.38	3.13E-01	C	0.29	T	0.44
rs4766002	C12orf32	1.12	0.90	1.40	3.14E-01	G	0.30	T	0.38
rs10429965	NEK2	1.15	0.87	1.52	3.14E-01	C	0.13	C	0.14
rs2305948	KDR	1.18	0.86	1.62	3.15E-01	T	0.28	T	0.10
rs5742666	IGF1	0.88	0.68	1.13	3.15E-01	G	0.23	G	0.23
rs8191754	IGF2R	0.85	0.61	1.17	3.15E-01	G	0.15	G	0.14

rs1059293	IFNGR2	0.90	0.73	1.11	3.15E-01	C	0.24	T	0.49
rs4656994	NDUFS2	1.14	0.89	1.46	3.15E-01	A	0.19	A	0.22
rs3776432	NSUN2	1.12	0.90	1.38	3.16E-01	A	0.28	A	0.33
rs1800169	CNTF	0.84	0.59	1.19	3.17E-01	A	0.05	A	0.14
rs207943	XRCC5	0.90	0.73	1.11	3.17E-01	C	0.49	G	0.45
rs3793524	PTPN3	1.12	0.90	1.39	3.17E-01	C	0.48	C	0.36
rs540742	GIPC2	1.13	0.89	1.45	3.18E-01	C	0.21	C	0.23
rs9894946	TP53	0.85	0.61	1.17	3.18E-01	A	0.03	A	0.17
rs1131532	TNFSF10	0.89	0.70	1.12	3.19E-01	T	0.24	T	0.37
rs1455158	HNMT	0.88	0.68	1.13	3.19E-01	G	0.49	A	0.20
rs3829888	ABCB11	1.27	0.80	2.01	3.19E-01	C	0.13	C	0.04
rs6271	DBH	1.24	0.81	1.91	3.20E-01	T	0.03	T	0.06
rs4926	SERPING1	1.14	0.88	1.46	3.20E-01	A	0.11	A	0.26
rs144848	BRCA2	1.12	0.89	1.42	3.20E-01	G	0.12	G	0.28
rs1129923	DUSP23	0.80	0.52	1.24	3.20E-01	A	0.02	A	0.09
rs2472299	CYP1A1	0.89	0.71	1.12	3.20E-01	A	0.40	A	0.29
rs348459	ALDH1A1	0.78	0.48	1.27	3.20E-01	G	0.18	G	0.04
rs1801279	NAT2	1.62	0.63	4.16	3.20E-01	A	0.06	A	0.00
rs3886641	GARS	0.50	0.13	1.97	3.20E-01	A	0.05	A	0.00
rs2380165	BLM	0.89	0.71	1.12	3.22E-01	A	0.43	G	0.29
rs207878	XRCC5	0.90	0.73	1.11	3.23E-01	G	0.13	G	0.48
rs2270423	GSTZ1	0.89	0.71	1.12	3.23E-01	A	0.28	A	0.30
rs1799782	XRCC1	0.81	0.54	1.23	3.24E-01	T	0.07	T	0.09
rs10018625	TLR3	0.88	0.69	1.13	3.24E-01	T	0.38	T	0.23
rs2306168	SLCO2B1	1.27	0.79	2.04	3.24E-01	T	0.29	T	0.03
rs7665103	HELQ	1.11	0.90	1.38	3.25E-01	G	0.45	G	0.44
rs4149117	SLCO1B3	1.14	0.88	1.48	3.26E-01	G	0.42	T	0.14
rs26312	GHRL	0.85	0.62	1.18	3.27E-01	A	0.23	A	0.13
rs3731680	SULT1C2	0.77	0.45	1.30	3.27E-01	C	0.02	C	0.07
rs2227552	C10orf55	0.88	0.69	1.13	3.27E-01	C	0.21	C	0.30
rs1537514	C1orf167	0.83	0.58	1.20	3.27E-01	G	0.09	G	0.11
rs971074	ADH7	0.85	0.60	1.18	3.28E-01	A	0.16	A	0.11
rs1801132	ESR1	0.88	0.67	1.14	3.28E-01	G	0.10	G	0.24
rs8832	IL4R	0.90	0.72	1.11	3.29E-01	G	0.25	A	0.46
rs1129055	CD86	1.13	0.89	1.44	3.29E-01	A	0.21	A	0.26
rs10017301	ZNF827	0.81	0.52	1.24	3.30E-01	T	0.29	T	0.04
rs1929860	CDC42BPA	1.12	0.89	1.41	3.30E-01	A	0.25	A	0.34
rs2251660	RDM1	0.87	0.65	1.15	3.30E-01	G	0.40	G	0.14
rs7512785	FMO2	0.89	0.71	1.12	3.30E-01	T	0.34	T	0.29
rs6330	NGF	0.89	0.71	1.12	3.30E-01	T	0.18	T	0.44
rs8187706	ABCC2	0.57	0.19	1.76	3.31E-01	A	0.12	0	0.00
rs1455162	HNMT	0.88	0.69	1.14	3.31E-01	C	0.49	C	0.20
rs2274756	LOC100128028	0.86	0.64	1.16	3.31E-01	A	0.17	A	0.16
rs448012	FLT4	0.89	0.71	1.12	3.31E-01	G	0.48	G	0.37
rs1014666	MRE11A	1.11	0.90	1.36	3.31E-01	C	0.50	C	0.46
rs6457813	PPARD	0.79	0.48	1.28	3.31E-01	T	0.21	T	0.03
rs423904	IL1RN	1.13	0.88	1.44	3.32E-01	T	0.08	T	0.30
rs508078	GSTA4	1.20	0.83	1.75	3.32E-01	A	0.07	A	0.09
rs405509	APOE	1.11	0.90	1.38	3.32E-01	A	0.27	A	0.48
rs2229532	ACP5	1.46	0.68	3.15	3.33E-01	A	0.11	A	0.00

rs12360	CYP3A7	1.16	0.86	1.58	3.33E-01	T	0.45	C	0.10
rs1133818	MYCBPAP	0.88	0.69	1.13	3.33E-01	C	0.16	C	0.28
rs1509618	LOC728442	0.89	0.71	1.12	3.34E-01	T	0.34	C	0.39
rs16845759	TNFSF10	1.57	0.63	3.94	3.34E-01	T	0.07	T	0.00
rs915927	XRCC1	1.11	0.90	1.36	3.35E-01	G	0.42	G	0.43
rs1358312	PPP3CA	0.87	0.65	1.16	3.35E-01	A	0.18	A	0.18
rs20541	IL13	1.13	0.88	1.44	3.36E-01	T	0.17	T	0.21
rs1566734	PTPRJ	0.85	0.62	1.18	3.36E-01	G	0.13	G	0.15
rs12233949	GHR	0.89	0.69	1.13	3.37E-01	C	0.05	C	0.29
rs1800468	B9D2	0.81	0.53	1.25	3.37E-01	A	0.04	A	0.08
rs4646312	COMT	0.89	0.71	1.12	3.37E-01	C	0.17	C	0.36
rs6095558	PTGIS	0.88	0.68	1.14	3.38E-01	T	0.13	T	0.25
rs3024944	STAT6	1.52	0.65	3.56	3.38E-01	C	0.08	C	0.00
rs1800788	FGB	0.87	0.67	1.15	3.38E-01	T	0.10	T	0.21
rs529126	MRE11A	1.12	0.89	1.40	3.39E-01	A	0.30	A	0.27
rs853785	ABCB11	0.90	0.73	1.11	3.39E-01	A	0.37	G	0.44
rs875444	RXRA	1.12	0.89	1.39	3.39E-01	A	0.15	G	0.39
rs2109505	ABCB4	1.14	0.87	1.49	3.39E-01	A	0.33	A	0.17
rs3092906	ATM	0.68	0.31	1.50	3.39E-01	G	0.18	G	0.00
rs2124459	CBS	1.11	0.90	1.38	3.40E-01	C	0.40	C	0.39
rs2227956	HSPA1L	0.86	0.62	1.18	3.40E-01	C	0.02	C	0.16
rs9482	ATF6	1.12	0.89	1.40	3.41E-01	G	0.49	A	0.28
rs1344642	STK36	0.90	0.73	1.11	3.41E-01	G	0.37	A	0.42
rs7689099	NEIL3	1.16	0.85	1.59	3.41E-01	G	0.08	G	0.11
rs6759892	UGT1A10	1.11	0.90	1.38	3.42E-01	G	0.35	G	0.40
rs2687117	CYP3A4	0.74	0.40	1.37	3.42E-01	T	0.32	T	0.00
rs689462	PTGS2	0.80	0.50	1.27	3.43E-01	C	0.25	C	0.03
rs2295298	NFATC4	1.11	0.89	1.38	3.44E-01	G	0.15	A	0.42
rs1052536	LIG3	1.11	0.89	1.38	3.44E-01	T	0.18	T	0.45
rs2193587	DGKG	1.13	0.88	1.46	3.44E-01	G	0.09	G	0.23
rs1380657	MYCBPAP	0.89	0.69	1.14	3.44E-01	G	0.16	G	0.28
rs11818239	BMPR1A	1.47	0.66	3.25	3.44E-01	A	0.12	A	0.00
rs827500	DPYD	0.89	0.69	1.14	3.44E-01	T	0.08	T	0.27
rs10211	CYP3A7	1.16	0.85	1.57	3.44E-01	A	0.45	G	0.10
rs1136410	PARP1	1.14	0.87	1.51	3.44E-01	C	0.06	C	0.19
rs4646487	CYP4B1	0.86	0.62	1.18	3.45E-01	T	0.19	T	0.13
rs9576175	CSNK1A1L	0.90	0.73	1.12	3.45E-01	G	0.47	T	0.49
rs419833	GSTA4	0.90	0.73	1.12	3.46E-01	C	0.42	G	0.49
rs212087	ABCC1	1.12	0.89	1.41	3.47E-01	T	0.20	T	0.43
rs7136446	IGF1	1.11	0.89	1.38	3.47E-01	C	0.26	C	0.38
rs2489581	PDSS1	1.11	0.89	1.38	3.47E-01	C	0.34	G	0.40
rs6102	SERPINB2	1.13	0.87	1.46	3.48E-01	G	0.21	G	0.21
rs1059751	ABCC4	0.90	0.73	1.12	3.48E-01	C	0.30	C	0.46
rs3828942	LEP	0.90	0.72	1.12	3.49E-01	A	0.19	A	0.45
rs1062372	JTV1	0.88	0.68	1.15	3.49E-01	A	0.32	A	0.22
rs12922317	RUNDC2A	1.11	0.89	1.37	3.49E-01	G	0.30	G	0.35
rs28365094	CYP3A5	1.19	0.82	1.72	3.49E-01	G	0.01	G	0.11
rs1891073	CYP2C8	0.90	0.72	1.12	3.50E-01	C	0.22	C	0.38
rs1934953	CYP2C8	0.90	0.72	1.12	3.50E-01	G	0.21	G	0.38
rs2273697	ABCC2	0.88	0.67	1.15	3.50E-01	A	0.19	A	0.19

rs2470146	CYP19A1	1.21	0.81	1.79	3.51E-01	C	0.01	C	0.07
rs281432	ICAM1	1.10	0.90	1.35	3.51E-01	C	0.34	G	0.47
rs4648133	NFKB1	1.12	0.88	1.43	3.51E-01	C	0.12	C	0.29
rs3740469	SLK	1.13	0.87	1.46	3.52E-01	A	0.10	A	0.23
rs2228065	ALOX5	0.58	0.18	1.83	3.52E-01	A	0.07	A	0.00
rs10018239	PPARGC1A	1.10	0.90	1.36	3.56E-01	A	0.49	G	0.36
rs4713858	PPARD	0.87	0.64	1.17	3.56E-01	A	0.11	A	0.16
rs909253	LTA	0.90	0.72	1.13	3.57E-01	C	0.42	C	0.38
rs2108622	CYP4F2	1.11	0.88	1.40	3.57E-01	T	0.13	T	0.30
rs40947	THAP5	0.89	0.70	1.14	3.57E-01	A	0.29	A	0.30
rs4455491	UGT2B7	1.10	0.89	1.37	3.59E-01	A	0.26	G	0.50
rs3100699	HNMT	0.70	0.33	1.49	3.60E-01	C	0.21	C	0.00
rs11569017	EGF	1.23	0.79	1.93	3.60E-01	T	0.01	T	0.06
rs2972388	CDK7	1.10	0.89	1.36	3.60E-01	G	0.27	G	0.46
rs3743259	IGF1R	1.11	0.89	1.38	3.60E-01	G	0.37	G	0.32
rs502570	ABCB11	0.90	0.71	1.13	3.61E-01	T	0.10	T	0.32
rs7662029	UGT2B7	1.10	0.89	1.36	3.61E-01	A	0.26	G	0.49
rs359974	IHH	1.15	0.85	1.55	3.61E-01	C	0.05	C	0.21
rs17829584	PPP3CA	0.85	0.60	1.21	3.61E-01	C	0.12	C	0.13
rs2307492	FMO2	0.86	0.62	1.19	3.61E-01	C	0.16	C	0.10
rs1799999	PPP1R3A	1.14	0.86	1.50	3.62E-01	T	0.21	T	0.13
rs2282079	LOC100130458	0.80	0.49	1.30	3.62E-01	A	0.10	A	0.05
rs1049007	BMP2	1.11	0.89	1.38	3.62E-01	A	0.13	A	0.38
rs1873196	TLR1	0.72	0.36	1.45	3.62E-01	T	0.13	T	0.01
rs2606345	CYP1A1	1.11	0.89	1.38	3.62E-01	A	0.14	C	0.37
rs11155472	SIM1	0.91	0.74	1.12	3.62E-01	T	0.38	A	0.49
rs537183	ABCB11	0.90	0.71	1.13	3.63E-01	G	0.10	G	0.31
rs1805034	TNFRSF11A	0.90	0.73	1.12	3.63E-01	C	0.37	C	0.46
rs4987875	ATM	0.57	0.17	1.93	3.64E-01	T	0.08	0	0.00
rs4148551	ABCC4	0.91	0.73	1.12	3.65E-01	A	0.45	G	0.40
rs2073618	TNFRSF11B	0.90	0.72	1.13	3.65E-01	C	0.12	G	0.47
rs1736557	FMO3	0.82	0.53	1.26	3.65E-01	A	0.05	A	0.08
rs2229653	SPN	0.61	0.21	1.79	3.66E-01	T	0.08	0	0.00
rs2230399	ICAM3	0.84	0.57	1.23	3.67E-01	C	0.19	C	0.08
rs2598483	STAT6	0.84	0.58	1.22	3.67E-01	T	0.03	T	0.11
rs4073054	NR1I3	0.91	0.74	1.12	3.67E-01	G	0.23	G	0.37
rs7709790	GHR	1.12	0.87	1.44	3.68E-01	G	0.40	G	0.19
rs884716	SHFM1	1.11	0.89	1.39	3.68E-01	A	0.29	A	0.27
rs2243267	IL4	1.13	0.87	1.47	3.69E-01	C	0.37	C	0.21
rs1494961	HELQ	0.91	0.73	1.12	3.69E-01	C	0.23	C	0.48
rs1611764	SPRR1A	0.90	0.73	1.13	3.69E-01	G	0.37	G	0.46
rs1884725	XDH	1.12	0.87	1.45	3.70E-01	A	0.23	A	0.23
rs1064796	CYP4F11	0.90	0.72	1.13	3.70E-01	C	0.24	C	0.26
rs3774968	NFKB1	0.90	0.72	1.13	3.70E-01	A	0.20	A	0.44
rs3826573	CTDP1	1.11	0.88	1.40	3.70E-01	T	0.33	T	0.41
rs910416	ESR1	0.91	0.74	1.12	3.71E-01	C	0.44	T	0.49
rs10079641	MSH3	0.82	0.53	1.27	3.71E-01	G	0.07	G	0.08
rs4135113	TDG	1.26	0.76	2.11	3.71E-01	A	0.18	A	0.03
rs1800947	CRP	0.79	0.47	1.33	3.71E-01	C	0.02	C	0.06
rs228589	ATM	1.10	0.89	1.37	3.72E-01	A	0.43	T	0.44

rs156641	LIG1	0.90	0.72	1.13	3.72E-01	A	0.17	A	0.36
rs3770596	ABCB11	0.91	0.73	1.13	3.72E-01	A	0.35	A	0.46
rs1135148	BNIP2	1.11	0.89	1.38	3.73E-01	C	0.14	C	0.37
rs2072446	NGFR	0.79	0.47	1.33	3.73E-01	T	0.01	T	0.05
rs526645	DPYD	0.89	0.70	1.14	3.74E-01	C	0.08	C	0.27
rs1045105	CATSPER4	0.86	0.62	1.20	3.74E-01	A	0.09	A	0.12
rs4752904	PTPRJ	1.10	0.89	1.37	3.74E-01	C	0.14	G	0.44
rs1931072	DPYD	0.90	0.72	1.13	3.74E-01	A	0.38	A	0.28
rs2465811	PTPRB	0.90	0.72	1.13	3.74E-01	C	0.40	C	0.29
rs2227551	PLAU	0.90	0.71	1.14	3.74E-01	G	0.45	G	0.29
rs2037483	HUS1	0.91	0.73	1.12	3.75E-01	A	0.33	G	0.47
rs7438135	UGT2B7	1.10	0.89	1.36	3.75E-01	G	0.26	A	0.49
rs7668258	UGT2B7	1.10	0.89	1.36	3.75E-01	T	0.26	C	0.49
rs1137101	LEPR	0.91	0.74	1.12	3.75E-01	A	0.42	G	0.46
rs1052637	DDX18	0.90	0.72	1.13	3.75E-01	G	0.39	C	0.35
rs6104	SERPINB2	1.12	0.87	1.43	3.75E-01	G	0.33	G	0.24
rs4252749	CCNI	1.35	0.69	2.64	3.76E-01	C	0.14	C	0.00
rs987539	PON2	1.10	0.89	1.37	3.76E-01	C	0.34	T	0.48
rs2280712	PARP1	0.87	0.64	1.18	3.77E-01	A	0.05	A	0.18
rs7164902	SLC12A6	0.89	0.70	1.15	3.77E-01	A	0.23	A	0.26
rs6919734	PPARD	0.76	0.42	1.40	3.78E-01	A	0.11	A	0.02
rs1051775	GSTA1	0.90	0.72	1.13	3.78E-01	G	0.12	G	0.40
rs3738880	GLI2	0.89	0.69	1.15	3.78E-01	A	0.41	C	0.28
rs2277624	ABCC3	1.12	0.87	1.43	3.78E-01	A	0.37	A	0.22
rs20432	PTGS2	0.89	0.68	1.16	3.79E-01	T	0.43	G	0.16
rs770087	DUSP6	1.12	0.87	1.44	3.79E-01	G	0.42	G	0.19
rs1419745	CYP3A5	1.20	0.80	1.80	3.79E-01	G	0.40	G	0.04
rs3212723	JAK3	1.44	0.64	3.27	3.80E-01	A	0.09	A	0.00
rs2227306	IL8	0.91	0.73	1.13	3.80E-01	T	0.17	T	0.43
rs1130371	CCL3	0.89	0.68	1.16	3.80E-01	T	0.12	T	0.24
rs967935	ABCC3	1.19	0.80	1.77	3.80E-01	T	0.17	T	0.06
rs2227307	IL8	0.91	0.73	1.12	3.80E-01	T	0.47	G	0.47
rs2522397	RAD50	1.24	0.77	1.99	3.81E-01	T	0.46	T	0.01
rs4648276	PTGS2	0.87	0.63	1.19	3.81E-01	C	0.15	C	0.13
rs4364	ACE	0.68	0.29	1.61	3.81E-01	A	0.11	A	0.00
rs7483	GSTM3	1.11	0.88	1.41	3.81E-01	A	0.10	A	0.31
rs1801275	IL4R	0.90	0.70	1.15	3.81E-01	A	0.35	G	0.23
rs289747	NLRC5	0.91	0.73	1.13	3.82E-01	A	0.39	A	0.40
rs2243289	IL4	1.12	0.87	1.45	3.82E-01	G	0.24	G	0.18
rs3770601	ABCB11	1.17	0.82	1.66	3.82E-01	T	0.07	T	0.09
rs132806	NHP2L1	0.90	0.71	1.14	3.82E-01	T	0.08	T	0.35
rs1010844	CART	0.88	0.67	1.17	3.82E-01	C	0.47	C	0.15
rs299295	HMMR	0.89	0.69	1.15	3.83E-01	T	0.28	T	0.24
rs2853559	VDR	0.90	0.71	1.14	3.83E-01	T	0.20	T	0.38
rs4128474	DPYD	1.18	0.82	1.69	3.83E-01	C	0.04	C	0.11
rs2275586	MMS19	0.76	0.41	1.40	3.83E-01	G	0.14	G	0.02
rs7732671	PPARGC1B	1.15	0.84	1.58	3.84E-01	C	0.17	C	0.09
rs2440	XRCC5	1.10	0.89	1.35	3.84E-01	T	0.27	T	0.41
rs3735586	PON2	1.11	0.87	1.42	3.84E-01	A	0.27	A	0.24
rs861529	XRCC3	1.20	0.80	1.80	3.85E-01	A	0.18	A	0.05

rs3730931	LIG1	1.13	0.85	1.51	3.85E-01	G	0.27	G	0.12
rs592792	GSTM2	1.14	0.85	1.54	3.86E-01	A	0.19	A	0.13
rs4986826	AHR	0.53	0.13	2.23	3.86E-01	A	0.05	A	0.00
rs2276235	ABCG1	0.91	0.73	1.13	3.86E-01	A	0.35	A	0.41
rs10017295	BST1	0.90	0.72	1.14	3.86E-01	C	0.22	C	0.29
rs500079	PPP1R15A	0.89	0.68	1.16	3.87E-01	T	0.45	C	0.26
rs599554	CTDP1	1.13	0.86	1.47	3.87E-01	A	0.27	A	0.16
rs7796976	AHR	1.12	0.87	1.45	3.87E-01	A	0.10	A	0.23
rs3742424	PPP2R5C	1.16	0.83	1.60	3.88E-01	C	0.28	C	0.08
rs1614984	TP53	0.91	0.73	1.13	3.88E-01	T	0.44	T	0.44
rs2275622	CYP2C8	0.91	0.72	1.13	3.88E-01	T	0.20	T	0.38
rs10264715	NPC1L1	0.89	0.68	1.16	3.89E-01	A	0.05	A	0.22
rs13815	MCAT	0.91	0.73	1.13	3.89E-01	G	0.25	C	0.33
rs2246176	RAD50	1.11	0.87	1.41	3.89E-01	T	0.37	C	0.21
rs6519270	NHP2L1	1.11	0.88	1.40	3.90E-01	G	0.35	A	0.22
rs11670988	HIPK4	1.18	0.81	1.70	3.90E-01	T	0.02	T	0.09
rs3730017	NOS2	0.80	0.49	1.32	3.90E-01	T	0.21	T	0.03
rs4660	SPP1	1.49	0.60	3.72	3.90E-01	A	0.06	A	0.00
rs3736599	SULT1E1	1.15	0.84	1.57	3.91E-01	A	0.16	A	0.11
rs2960306	GRK4	0.91	0.73	1.13	3.91E-01	G	0.49	T	0.35
rs17110453	CYP2C8	1.15	0.84	1.56	3.91E-01	C	0.03	C	0.14
rs1185193	SETX	1.12	0.87	1.44	3.93E-01	A	0.40	A	0.17
rs2072352	BLM	0.91	0.72	1.14	3.94E-01	C	0.39	T	0.28
rs4833095	TLR1	0.90	0.71	1.14	3.94E-01	T	0.22	C	0.27
rs17655	ERCC5	1.10	0.88	1.38	3.94E-01	G	0.44	G	0.22
rs1891072	CYP2C8	0.91	0.73	1.13	3.94E-01	C	0.20	C	0.38
rs6428830	HSD3B1	1.12	0.87	1.44	3.94E-01	A	0.08	A	0.28
rs700241	DAB2	1.26	0.74	2.14	3.95E-01	A	0.14	A	0.02
rs4252228	TAF9	1.10	0.88	1.37	3.95E-01	T	0.13	T	0.45
rs3770603	ABCB11	1.16	0.83	1.62	3.95E-01	T	0.16	T	0.09
rs11940316	UGT2B7	1.10	0.89	1.35	3.95E-01	T	0.26	C	0.49
rs13112358	NEIL3	0.90	0.71	1.15	3.95E-01	C	0.32	C	0.25
rs2072052	CDK4	1.11	0.88	1.40	3.95E-01	C	0.06	C	0.32
rs1611753	SPRR1A	0.91	0.73	1.13	3.96E-01	C	0.45	C	0.46
rs1471001	HNMT	0.68	0.28	1.66	3.96E-01	G	0.15	G	0.00
rs7577677	UGT1A10	1.10	0.88	1.38	3.97E-01	A	0.23	A	0.37
rs6084	LIPC	0.91	0.74	1.13	3.97E-01	G	0.27	G	0.48
rs994502	MYO3A	1.11	0.87	1.42	3.97E-01	T	0.40	C	0.20
rs1471000	HNMT	0.68	0.28	1.66	3.97E-01	C	0.15	C	0.00
rs3218536	XRCC2	1.18	0.80	1.74	3.98E-01	A	0.02	A	0.08
rs2685803	ABCB11	0.91	0.74	1.13	3.98E-01	G	0.31	A	0.44
rs6457816	PPARD	0.86	0.61	1.22	3.99E-01	T	0.40	C	0.07
rs1043615	DNAJB9	0.91	0.73	1.14	3.99E-01	A	0.30	A	0.49
rs10018786	POLN	0.88	0.65	1.18	4.00E-01	T	0.41	G	0.13
rs7853758	SLC28A3	1.12	0.86	1.48	4.00E-01	A	0.30	A	0.15
rs730365	PON2	0.88	0.66	1.18	4.00E-01	T	0.26	T	0.14
rs3797896	MSH3	1.16	0.82	1.63	4.00E-01	G	0.10	G	0.09
rs853783	ABCB11	0.91	0.74	1.13	4.00E-01	G	0.43	T	0.44
rs1049631	IL4R	0.91	0.74	1.13	4.01E-01	A	0.25	G	0.47
rs10276036	ABCB1	0.91	0.73	1.13	4.01E-01	C	0.27	C	0.43

rs11569046	EGF	0.64	0.23	1.81	4.02E-01	C	0.11	0	0.00
rs488133	ESR1	1.10	0.88	1.39	4.02E-01	T	0.07	T	0.30
rs1673026	POLD1	1.16	0.82	1.65	4.02E-01	T	0.25	T	0.07
rs607887	LRP5	1.10	0.88	1.36	4.02E-01	C	0.48	T	0.32
rs1044250	ANGPTL4	0.90	0.71	1.15	4.03E-01	T	0.24	T	0.30
rs3828193	CHST10	1.10	0.88	1.36	4.03E-01	A	0.13	A	0.48
rs2288378	IGF1	0.90	0.69	1.16	4.03E-01	A	0.22	A	0.23
rs3743372	C15orf42	1.11	0.87	1.40	4.04E-01	A	0.10	A	0.34
rs2185571	CYP2C8	0.90	0.70	1.16	4.04E-01	T	0.13	T	0.28
rs1059262	ALKBH2	1.12	0.86	1.46	4.05E-01	G	0.24	G	0.17
rs1800822	FMO3	1.19	0.79	1.77	4.05E-01	T	0.10	T	0.06
rs12254557	MBL2	1.31	0.70	2.45	4.05E-01	C	0.11	C	0.00
rs4646453	CYP3A5	1.26	0.73	2.16	4.05E-01	T	0.07	T	0.03
rs4757707	PTPN5	0.90	0.70	1.15	4.06E-01	C	0.08	C	0.39
rs1520664	DPYD	0.91	0.73	1.14	4.06E-01	T	0.44	T	0.37
rs348485	ALDH1A1	1.11	0.87	1.42	4.06E-01	C	0.22	C	0.21
rs2089891	PPP1R15B	0.84	0.56	1.26	4.06E-01	G	0.05	G	0.09
rs1042821	MSH6	1.12	0.86	1.46	4.07E-01	T	0.23	T	0.18
rs3798134	RAD50	1.11	0.87	1.41	4.07E-01	T	0.39	T	0.21
rs4150526	GTF2H1	1.10	0.88	1.38	4.08E-01	G	0.23	G	0.30
rs2241529	DKK1	1.10	0.88	1.36	4.09E-01	A	0.29	A	0.47
rs1570070	IGF2R	0.91	0.72	1.14	4.09E-01	G	0.25	G	0.37
rs12721613	NR1I2	0.66	0.25	1.76	4.09E-01	T	0.10	T	0.00
rs10018622	KLHL5	1.10	0.88	1.36	4.09E-01	A	0.37	G	0.41
rs2241339	ABCB11	1.15	0.83	1.60	4.09E-01	T	0.32	T	0.07
rs16931996	DUSP13	0.71	0.31	1.62	4.09E-01	C	0.11	C	0.00
rs1044141	STK17A	0.89	0.67	1.18	4.09E-01	A	0.07	A	0.22
rs1051640	ABCC3	1.14	0.84	1.54	4.10E-01	G	0.09	G	0.16
rs541731	SPRY2	1.09	0.89	1.35	4.10E-01	A	0.47	A	0.39
rs1803250	CTSB	1.14	0.83	1.57	4.10E-01	G	0.07	G	0.12
rs2966245	HSD17B2	1.09	0.89	1.34	4.12E-01	C	0.34	C	0.42
rs6892398	RAD50	0.64	0.22	1.86	4.12E-01	C	0.09	0	0.00
rs2074570	IL4R	0.83	0.53	1.30	4.12E-01	G	0.14	G	0.05
rs757343	VDR	0.88	0.64	1.20	4.12E-01	A	0.07	A	0.15
rs3092856	ATM	1.41	0.62	3.20	4.13E-01	T	0.08	T	0.00
rs740603	COMT	0.91	0.74	1.13	4.13E-01	G	0.46	G	0.49
rs911605	TNFSF8	0.90	0.71	1.15	4.14E-01	G	0.10	G	0.29
rs2066470	MTHFR	0.86	0.61	1.23	4.14E-01	T	0.10	T	0.10
rs1002153	PARP1	0.90	0.69	1.16	4.14E-01	C	0.38	C	0.18
rs3851294	RIPK5	0.84	0.54	1.29	4.14E-01	A	0.02	A	0.09
rs715948	LRP1	1.09	0.88	1.36	4.14E-01	A	0.20	A	0.32
rs1056663	HUS1	0.91	0.74	1.13	4.14E-01	A	0.33	G	0.47
rs3729512	LIG1	1.13	0.84	1.52	4.14E-01	A	0.28	A	0.12
rs656583	LRP5	0.78	0.44	1.41	4.14E-01	C	0.26	C	0.00
rs2235033	ABCB1	1.09	0.88	1.35	4.15E-01	C	0.47	C	0.50
rs2270422	GSTZ1	0.91	0.72	1.15	4.15E-01	C	0.11	C	0.41
rs1051685	XRCC5	1.14	0.84	1.55	4.16E-01	G	0.30	G	0.12
rs9658655	CHGA	1.15	0.82	1.59	4.17E-01	C	0.21	C	0.08
rs4337089	SLCO1A2	0.86	0.60	1.23	4.17E-01	T	0.02	T	0.12
rs1130643	SPARCL1	1.13	0.84	1.51	4.17E-01	G	0.44	G	0.12

rs4148553	ABCC4	0.92	0.74	1.13	4.18E-01	A	0.30	A	0.46
rs1520663	DPYD	0.91	0.73	1.14	4.18E-01	T	0.43	T	0.37
rs10046	CYP19A1	1.09	0.88	1.36	4.19E-01	T	0.24	C	0.48
rs1805329	RAD23B	0.89	0.67	1.18	4.19E-01	T	0.02	T	0.22
rs4337789	UGT2B7	1.09	0.88	1.35	4.19E-01	A	0.20	T	0.49
rs133417	MCM5	0.83	0.54	1.30	4.19E-01	C	0.19	C	0.05
rs3211892	CD36	1.22	0.75	1.99	4.19E-01	A	0.22	A	0.02
rs11407	LOC390940	1.12	0.85	1.49	4.19E-01	A	0.15	A	0.18
rs207908	XRCC5	0.92	0.74	1.13	4.20E-01	T	0.49	T	0.48
rs4364327	UGT2B7	1.09	0.88	1.35	4.21E-01	C	0.20	T	0.49
rs367836	GSTA4	1.09	0.88	1.35	4.21E-01	C	0.47	C	0.42
rs799923	BRCA1	0.89	0.67	1.18	4.21E-01	A	0.03	A	0.21
rs162555	CYP1B1	0.89	0.68	1.18	4.21E-01	G	0.19	G	0.19
rs6413436	RAD52	1.10	0.88	1.37	4.21E-01	C	0.29	C	0.41
rs2368564	REN	0.91	0.72	1.15	4.22E-01	C	0.31	T	0.26
rs7081	SLC5A6	0.86	0.60	1.24	4.22E-01	A	0.50	G	0.06
rs241448	TAP2	0.90	0.71	1.16	4.22E-01	C	0.20	C	0.23
rs1467558	CD44	0.89	0.66	1.19	4.22E-01	A	0.04	A	0.17
rs13706	CDC6	0.88	0.65	1.20	4.22E-01	A	0.42	A	0.12
rs1058932	CYP2C8	1.11	0.86	1.44	4.22E-01	T	0.35	T	0.18
rs2522406	RAD50	0.78	0.42	1.44	4.22E-01	T	0.26	T	0.01
rs2306508	FNDC8	1.09	0.88	1.35	4.22E-01	A	0.14	A	0.45
rs2303317	ALDH1A1	0.92	0.75	1.13	4.24E-01	T	0.22	T	0.50
rs2671272	EPHX1	0.90	0.70	1.16	4.24E-01	C	0.45	T	0.21
rs2049110	DPYD	0.65	0.23	1.87	4.24E-01	A	0.10	0	0.00
rs610308	PPP1R15A	0.91	0.72	1.15	4.25E-01	T	0.25	C	0.31
rs16879427	PSKH2	0.79	0.44	1.41	4.25E-01	C	0.31	C	0.00
rs2292305	THBS1	0.89	0.66	1.19	4.26E-01	C	0.44	C	0.13
rs3798343	PPARD	0.83	0.52	1.32	4.27E-01	G	0.17	G	0.03
rs35596	ABCC1	0.91	0.71	1.15	4.27E-01	T	0.38	C	0.23
rs12338	CTSB	1.10	0.87	1.38	4.27E-01	G	0.34	G	0.37
rs2228527	ERCC6	0.90	0.69	1.17	4.28E-01	G	0.14	G	0.22
rs1545981	IL17RD	0.88	0.65	1.20	4.28E-01	T	0.22	T	0.11
rs3774932	NFKB1	0.91	0.73	1.14	4.29E-01	A	0.27	A	0.45
rs610529	ALDH1A1	1.09	0.89	1.33	4.29E-01	C	0.46	C	0.46
rs2267668	PPARD	0.89	0.67	1.18	4.30E-01	G	0.12	G	0.17
rs2227932	ATR	0.86	0.59	1.26	4.30E-01	C	0.01	C	0.10
rs7102464	SBF2	0.84	0.55	1.29	4.31E-01	T	0.02	T	0.09
rs853790	ABCB11	0.92	0.74	1.14	4.31E-01	A	0.34	T	0.45
rs2973015	GHR	0.92	0.74	1.14	4.31E-01	G	0.41	G	0.46
rs1760944	APEX1	1.09	0.88	1.34	4.31E-01	A	0.34	A	0.40
rs2892806	ABCB11	1.19	0.78	1.81	4.31E-01	T	0.06	T	0.05
rs20551	EP300	1.10	0.87	1.39	4.31E-01	G	0.07	G	0.28
rs696217	GHRL	0.84	0.55	1.30	4.32E-01	T	0.01	T	0.08
rs7588635	MERTK	1.28	0.69	2.40	4.32E-01	A	0.15	A	0.00
rs2032582_A	ABCB1	0.91	0.73	1.15	4.32E-01	T	0.07	T	0.45
rs8178318	LPO	0.56	0.13	2.37	4.32E-01	T	0.06	T	0.00
rs16975748	LIPE	1.41	0.60	3.35	4.33E-01	T	0.10	T	0.00
rs207905	XRCC5	0.88	0.63	1.22	4.33E-01	G	0.19	G	0.13
rs6103	SERPINB2	1.10	0.86	1.41	4.34E-01	G	0.34	G	0.24

rs1052763	DGCR14	0.90	0.70	1.16	4.34E-01	T	0.37	T	0.19
rs2193831	ABCB11	0.92	0.74	1.14	4.34E-01	G	0.43	G	0.38
rs17572019	PPARGC1B	1.15	0.81	1.63	4.34E-01	A	0.02	A	0.09
rs4148951	CHST3	1.30	0.67	2.51	4.35E-01	A	0.16	A	0.01
rs2854455	EPHX1	0.90	0.70	1.16	4.35E-01	T	0.45	C	0.21
rs4588522	UGT2B7	1.09	0.88	1.35	4.35E-01	C	0.21	G	0.49
rs2305799	ACP5	0.87	0.61	1.24	4.35E-01	T	0.04	T	0.11
rs2228088	TNF	0.63	0.20	2.02	4.36E-01	T	0.05	T	0.01
rs2229531	ACP5	0.86	0.60	1.25	4.37E-01	A	0.03	A	0.11
rs1126580	IL8RB	0.91	0.72	1.15	4.37E-01	A	0.43	A	0.41
rs1130496	PTPRN2	0.92	0.73	1.14	4.38E-01	A	0.18	A	0.44
rs1822825	PPARG	1.09	0.88	1.35	4.38E-01	C	0.20	C	0.46
rs669674	GSTA4	1.14	0.82	1.59	4.38E-01	T	0.05	T	0.10
rs4536	CYP11B2	1.18	0.77	1.80	4.38E-01	A	0.25	A	0.03
rs348457	ALDH1A1	1.08	0.88	1.33	4.38E-01	G	0.46	G	0.46
rs696221	SEC13	0.92	0.74	1.14	4.39E-01	C	0.22	C	0.45
rs3177429	GSTZ1	0.85	0.57	1.28	4.39E-01	A	0.03	A	0.09
rs246218	ABCC1	0.89	0.67	1.19	4.40E-01	T	0.16	T	0.14
rs1799941	SHBG	0.90	0.69	1.17	4.40E-01	A	0.08	A	0.26
rs8187915	ALDH1A1	0.92	0.75	1.14	4.40E-01	T	0.21	T	0.49
rs3024491	IL10	0.92	0.73	1.15	4.41E-01	T	0.32	T	0.44
rs2078486	TP53	1.13	0.83	1.53	4.41E-01	A	0.29	A	0.09
rs3813627	APOA2	1.09	0.87	1.37	4.41E-01	T	0.12	T	0.35
rs3760413	EME1	0.89	0.65	1.21	4.41E-01	T	0.02	T	0.15
rs2412504	PAK6	0.86	0.60	1.25	4.41E-01	G	0.27	G	0.08
rs7797834	CYP51A1	1.09	0.88	1.35	4.42E-01	G	0.45	G	0.38
rs1800890	IL10	0.91	0.73	1.15	4.42E-01	A	0.28	A	0.37
rs1537015	TNC	1.09	0.88	1.35	4.42E-01	T	0.46	C	0.35
rs169547	BRCA2	0.63	0.19	2.05	4.42E-01	A	0.07	A	0.00
rs3025039	VEGFA	1.12	0.84	1.51	4.42E-01	T	0.11	T	0.15
rs7441774	UGT2B7	1.10	0.87	1.38	4.43E-01	G	0.22	G	0.46
rs7643645	NR1I2	1.09	0.87	1.36	4.43E-01	G	0.12	G	0.39
rs1946235	GPX3	0.88	0.64	1.21	4.43E-01	C	0.20	C	0.15
rs3897933	DPYD	0.91	0.72	1.15	4.43E-01	A	0.27	A	0.28
rs7921	CD79B	1.09	0.87	1.38	4.43E-01	T	0.28	T	0.25
rs3136430	F2	0.65	0.22	1.95	4.43E-01	T	0.07	T	0.00
rs6041884	FKBP1A	1.09	0.87	1.36	4.43E-01	G	0.28	G	0.29
rs805657	SLK	0.90	0.68	1.18	4.44E-01	A	0.33	A	0.17
rs1801280	NAT2	0.92	0.75	1.14	4.45E-01	C	0.26	C	0.43
rs2305706	CYP19A1	1.11	0.85	1.44	4.45E-01	A	0.47	G	0.19
rs6098	SERPINB2	1.10	0.86	1.41	4.45E-01	G	0.34	G	0.24
rs6868365	RAD50	0.56	0.13	2.48	4.46E-01	T	0.06	0	0.00
rs998074	IGF2R	0.92	0.74	1.14	4.46E-01	A	0.38	G	0.49
rs9503893	PRPF4B	0.91	0.72	1.15	4.47E-01	A	0.27	A	0.32
rs7089422	CYP17A1	0.90	0.67	1.19	4.48E-01	T	0.10	T	0.16
rs8191613	NEIL2	1.27	0.68	2.36	4.48E-01	A	0.06	A	0.02
rs2241230	SCARF2	1.16	0.79	1.69	4.49E-01	T	0.12	T	0.10
rs2331390	IGFBP1	0.92	0.74	1.14	4.49E-01	A	0.42	A	0.48
rs3730849	LIG1	0.92	0.73	1.15	4.49E-01	T	0.16	T	0.37
rs5030737	MBL2	0.84	0.54	1.31	4.49E-01	T	0.02	T	0.08

rs35620	ABCC1	1.12	0.84	1.49	4.50E-01	G	0.09	G	0.18
rs1798745	DPYD	0.71	0.29	1.73	4.50E-01	T	0.14	T	0.00
rs3783615	VCAM1	0.46	0.06	3.42	4.50E-01	T	0.05	T	0.00
rs182623	GSTA4	1.09	0.87	1.36	4.50E-01	A	0.42	A	0.27
rs853772	ABCB11	1.09	0.88	1.34	4.51E-01	A	0.30	C	0.46
rs1527463	CD36	0.75	0.35	1.60	4.51E-01	G	0.06	G	0.02
rs16839100	FCRL2	1.44	0.55	3.76	4.52E-01	T	0.05	T	0.00
rs35683	GHRL	0.92	0.75	1.14	4.52E-01	A	0.35	A	0.45
rs983101	DPYD	1.51	0.52	4.40	4.52E-01	C	0.05	0	0.00
rs769224	COMT	1.20	0.74	1.94	4.53E-01	A	0.11	A	0.04
rs7006788	C8orf42	0.92	0.73	1.15	4.53E-01	T	0.19	T	0.37
rs1063743	TACC3	0.91	0.72	1.16	4.53E-01	A	0.15	A	0.26
rs348445	ALDH1A1	1.19	0.75	1.89	4.53E-01	T	0.13	T	0.03
rs139884	SOX10	1.09	0.87	1.36	4.54E-01	A	0.19	A	0.36
rs3448	GPX1	0.91	0.71	1.17	4.54E-01	T	0.28	T	0.25
rs2010963	VEGFA	0.92	0.74	1.14	4.54E-01	C	0.31	C	0.31
rs1801131	MTHFR	1.09	0.87	1.37	4.54E-01	C	0.10	C	0.33
rs3212961	ERCC1	1.11	0.84	1.47	4.55E-01	A	0.25	A	0.14
rs2287623	ABCB11	0.92	0.74	1.14	4.55E-01	C	0.43	C	0.38
rs2161811	ALDH1A1	0.92	0.75	1.14	4.56E-01	G	0.23	G	0.49
rs5993875	TXNRD2	1.08	0.88	1.33	4.56E-01	A	0.29	A	0.43
rs1805405	PARP1	0.91	0.70	1.18	4.57E-01	A	0.37	A	0.18
rs1799955	BRCA2	1.10	0.85	1.43	4.57E-01	G	0.27	G	0.22
rs17064676	NEIL3	1.33	0.63	2.81	4.57E-01	G	0.09	G	0.00
rs4148947	CHST3	1.08	0.88	1.33	4.58E-01	C	0.29	C	0.46
rs2292245	PTPRG	0.89	0.66	1.21	4.58E-01	A	0.13	A	0.16
rs921519	ERICH1	0.90	0.68	1.19	4.58E-01	C	0.14	C	0.21
rs1200314	CYP2C9	0.83	0.50	1.37	4.58E-01	C	0.10	C	0.04
rs2292334	SLC22A3	0.92	0.74	1.15	4.59E-01	T	0.15	T	0.40
rs3217805	CCND2	0.92	0.73	1.15	4.59E-01	G	0.17	G	0.39
rs3816540	RPS6KA1	0.90	0.67	1.19	4.59E-01	C	0.05	C	0.21
rs7731453	HMMR	0.88	0.64	1.23	4.59E-01	A	0.03	A	0.12
rs4531	DBH	0.86	0.58	1.28	4.60E-01	T	0.09	T	0.08
rs7290221	COMT	0.93	0.76	1.14	4.60E-01	C	0.47	G	0.48
rs865242	DPYD	0.91	0.72	1.16	4.61E-01	G	0.15	G	0.28
rs598599	MRE11A	1.09	0.86	1.38	4.61E-01	A	0.17	A	0.29
rs1799801	ERCC4	1.09	0.87	1.37	4.61E-01	C	0.19	C	0.28
rs426169	GSTA4	0.92	0.75	1.14	4.61E-01	T	0.40	C	0.49
rs8053	PSMA4	1.08	0.87	1.35	4.63E-01	T	0.19	T	0.42
rs2242665	SLC44A4	1.08	0.87	1.35	4.64E-01	G	0.35	G	0.47
rs2546893	IL12B	0.92	0.74	1.14	4.64E-01	A	0.29	A	0.49
rs894157	C15orf42	1.14	0.80	1.63	4.64E-01	C	0.02	C	0.10
rs2790	TYMS	0.91	0.70	1.18	4.64E-01	G	0.29	G	0.21
rs1137282	KRAS	1.09	0.86	1.39	4.64E-01	C	0.17	C	0.21
rs17473423	KRAS	1.09	0.86	1.39	4.64E-01	G	0.17	G	0.21
rs2256327	FAM82A	0.91	0.69	1.18	4.65E-01	G	0.25	G	0.20
rs6180	GHR	0.92	0.74	1.15	4.65E-01	C	0.44	C	0.45
rs2855262	SOD3	0.92	0.73	1.15	4.66E-01	C	0.18	T	0.36
rs6046	F7	0.88	0.64	1.23	4.66E-01	T	0.15	T	0.10
rs864373	ABCB11	0.92	0.75	1.14	4.66E-01	C	0.44	T	0.45

rs2008691	CYP19A1	1.10	0.85	1.42	4.66E-01	G	0.41	G	0.17
rs4220	FGB	1.11	0.84	1.45	4.66E-01	A	0.08	A	0.18
rs2048074	NEIL3	0.91	0.72	1.17	4.67E-01	A	0.32	A	0.25
rs2229712	RPS6KA1	0.90	0.68	1.20	4.67E-01	C	0.05	C	0.21
rs3212219	IL12B	1.09	0.86	1.39	4.67E-01	T	0.32	T	0.24
rs3138052	NFKBIA	0.92	0.72	1.16	4.67E-01	G	0.28	G	0.27
rs1295686	IL13	1.09	0.86	1.39	4.68E-01	G	0.33	A	0.22
rs3740955	RAG1	1.09	0.87	1.36	4.69E-01	A	0.26	G	0.35
rs2020873	MLH1	0.65	0.21	2.07	4.69E-01	T	0.09	0	0.00
rs2854184	GH1	0.92	0.74	1.15	4.69E-01	T	0.18	T	0.41
rs1048013	CYP20A1	0.93	0.76	1.14	4.69E-01	T	0.24	C	0.45
rs348476	ALDH1A1	1.27	0.66	2.46	4.69E-01	C	0.08	C	0.00
rs2363642	GSTZ1	0.92	0.73	1.16	4.71E-01	T	0.30	T	0.29
rs43038	PON2	0.90	0.67	1.21	4.72E-01	G	0.28	G	0.14
rs2267669	PPARD	0.90	0.67	1.20	4.72E-01	G	0.12	G	0.17
rs6063528	PTPN1	1.08	0.87	1.34	4.72E-01	A	0.32	A	0.38
rs3764340	WWOX	0.85	0.54	1.33	4.73E-01	G	0.10	G	0.06
rs17110944	PDGFRB	1.25	0.68	2.28	4.73E-01	A	0.22	A	0.00
rs1805403	PARP1	0.91	0.70	1.18	4.73E-01	A	0.06	A	0.23
rs2260655	DAK	1.18	0.75	1.88	4.74E-01	G	0.50	G	0.01
rs316132	GSTA4	1.08	0.87	1.33	4.74E-01	G	0.49	G	0.42
rs3785457	PCGF2	0.90	0.66	1.21	4.74E-01	A	0.12	A	0.16
rs13418420	UGT1A10	0.91	0.71	1.17	4.74E-01	C	0.19	C	0.26
rs3218005	CDKN2B	1.13	0.81	1.58	4.75E-01	G	0.27	G	0.10
rs1319869	IGF1R	1.10	0.84	1.45	4.76E-01	A	0.38	C	0.11
rs4713853	PPARD	0.90	0.66	1.21	4.76E-01	T	0.33	C	0.10
rs998075	IGF2R	0.93	0.75	1.14	4.76E-01	T	0.37	C	0.49
rs2274405	ABCC4	0.92	0.74	1.15	4.77E-01	T	0.32	T	0.35
rs8187737	SLC28A1	1.36	0.58	3.17	4.77E-01	T	0.07	T	0.00
rs1885472	SIRT1	1.08	0.87	1.33	4.78E-01	G	0.35	G	0.36
rs8058696	ABCC6	0.92	0.74	1.15	4.78E-01	C	0.35	G	0.50
rs25648	VEGFA	1.10	0.84	1.45	4.78E-01	T	0.06	T	0.17
rs10018064	Intergenic	0.92	0.74	1.15	4.79E-01	C	0.35	C	0.41
rs2228526	ERCC6	0.91	0.70	1.18	4.80E-01	G	0.12	G	0.22
rs2069835	IL6	0.85	0.55	1.33	4.80E-01	C	0.10	C	0.06
rs7208693	MPO	0.87	0.59	1.29	4.81E-01	A	0.16	A	0.07
rs8679	PARP1	0.91	0.70	1.18	4.82E-01	C	0.06	C	0.23
rs7242	SERPINE1	0.92	0.74	1.15	4.83E-01	T	0.49	G	0.42
rs6761641	PASK	0.91	0.69	1.19	4.83E-01	A	0.49	C	0.13
rs5496	ICAM1	0.66	0.21	2.11	4.83E-01	A	0.09	A	0.00
rs651852	BHMT	1.08	0.87	1.33	4.84E-01	A	0.22	A	0.49
rs1057056	CHST10	1.17	0.75	1.81	4.84E-01	A	0.35	A	0.02
rs9328764	POLN	0.90	0.67	1.21	4.84E-01	G	0.44	A	0.13
rs2238475	ABCC1	1.20	0.72	1.99	4.84E-01	C	0.03	C	0.05
rs2075800	HSPA1L	1.09	0.86	1.37	4.85E-01	A	0.08	A	0.32
rs1050152	SLC22A4	0.92	0.72	1.17	4.85E-01	T	0.05	T	0.37
rs2229113	IL10RA	1.08	0.86	1.36	4.85E-01	A	0.21	A	0.31
rs2725362	WRN	0.93	0.75	1.15	4.85E-01	G	0.50	T	0.44
rs2234721	ABCG1	0.92	0.73	1.16	4.86E-01	T	0.24	T	0.35
rs2157930	ABCB1	0.90	0.66	1.22	4.87E-01	T	0.14	T	0.22

rs610899	MRE11A	1.08	0.87	1.33	4.87E-01	G	0.37	G	0.43
rs17563	BMP4	0.93	0.76	1.14	4.87E-01	C	0.23	T	0.45
rs6817280	HELQ	1.23	0.68	2.22	4.88E-01	A	0.29	A	0.00
rs1138357	BCL2A1	1.08	0.86	1.36	4.88E-01	A	0.28	A	0.29
rs6413419	CYP2E1	1.21	0.71	2.06	4.88E-01	A	0.18	A	0.02
rs2681417	CD86	0.88	0.60	1.28	4.88E-01	G	0.34	G	0.07
rs2242048	SLC28A1	1.12	0.81	1.57	4.89E-01	T	0.04	T	0.12
rs187238	IL18	1.08	0.86	1.36	4.90E-01	G	0.23	G	0.27
rs11003127	MBL2	1.08	0.86	1.36	4.90E-01	G	0.45	C	0.22
rs207906	XRCC5	0.89	0.63	1.25	4.90E-01	A	0.10	A	0.13
rs3759207	MGST1	0.92	0.73	1.16	4.90E-01	G	0.26	G	0.31
rs1800392	WRN	0.93	0.75	1.15	4.91E-01	T	0.40	T	0.45
rs2972393	GHR	1.08	0.87	1.35	4.91E-01	G	0.49	A	0.41
rs769217	CAT	0.91	0.70	1.19	4.92E-01	T	0.16	T	0.23
rs4148217	ABCG8	1.09	0.85	1.41	4.92E-01	A	0.29	A	0.20
rs2282140	IGF2R	0.89	0.63	1.25	4.92E-01	T	0.15	T	0.13
rs7071882	MBL2	1.08	0.86	1.36	4.93E-01	G	0.46	T	0.21
rs3749442	ABCC5	0.91	0.69	1.20	4.93E-01	T	0.18	T	0.20
rs1805335	RAD23B	1.08	0.87	1.32	4.93E-01	A	0.42	A	0.45
rs1946518	IL18	1.08	0.87	1.34	4.93E-01	T	0.35	T	0.41
rs7514102	PROK1	1.08	0.87	1.34	4.94E-01	A	0.41	A	0.42
rs1341162	CYP2C8	1.09	0.85	1.40	4.94E-01	A	0.44	A	0.20
rs316133	GSTA4	1.08	0.87	1.33	4.94E-01	C	0.49	C	0.42
rs673197	GSTA4	1.08	0.87	1.33	4.94E-01	A	0.49	A	0.42
rs8018462	SLC7A7	1.08	0.87	1.34	4.94E-01	G	0.47	A	0.45
rs1555026	ID3	1.15	0.77	1.72	4.94E-01	C	0.16	C	0.06
rs17006794	HELQ	0.71	0.27	1.88	4.95E-01	T	0.11	0	0.00
rs6935443	ESR1	1.09	0.85	1.39	4.96E-01	A	0.42	G	0.22
rs874401	LOC729734	0.91	0.71	1.18	4.96E-01	T	0.25	T	0.20
rs5970	F11	1.11	0.82	1.50	4.96E-01	C	0.19	C	0.15
rs664677	ATM	1.08	0.87	1.33	4.97E-01	C	0.23	C	0.43
rs730720	CHST3	1.07	0.87	1.32	4.99E-01	A	0.44	A	0.47
rs2072351	BLM	0.93	0.74	1.16	4.99E-01	A	0.48	T	0.28
rs4764883	IGF1	0.92	0.73	1.16	4.99E-01	T	0.46	C	0.29
rs9282718	IGF1R	1.14	0.78	1.67	4.99E-01	G	0.07	G	0.06
rs16480	NPY	0.92	0.72	1.17	4.99E-01	C	0.38	C	0.21
rs2277461	PSMA6	1.14	0.78	1.65	5.00E-01	C	0.34	C	0.05
rs2288087	ALDH1A1	0.93	0.75	1.15	5.00E-01	T	0.22	T	0.50
rs7103126	MYEOV	0.92	0.71	1.18	5.00E-01	T	0.26	C	0.21
rs689470	PTGS2	0.87	0.58	1.31	5.00E-01	T	0.42	T	0.03
rs3181218	IL12B	1.09	0.86	1.38	5.01E-01	A	0.32	A	0.24
rs9352	CHAF1A	0.93	0.75	1.15	5.01E-01	T	0.49	C	0.43
rs2938395	PPARG	0.92	0.73	1.16	5.01E-01	C	0.20	C	0.37
rs10249476	LEP	1.08	0.87	1.34	5.01E-01	T	0.31	T	0.38
rs8192341	BMP1	0.91	0.70	1.19	5.01E-01	A	0.06	A	0.25
rs10794486	IGF1R	1.08	0.86	1.35	5.01E-01	A	0.38	G	0.31
rs6031	F5	1.35	0.56	3.22	5.02E-01	T	0.07	T	0.00
rs1491961	CCR1	1.09	0.85	1.39	5.02E-01	T	0.07	T	0.25
rs2287622	ABCB11	0.93	0.75	1.15	5.02E-01	T	0.43	T	0.38
rs1236913	PTGS1	0.85	0.53	1.37	5.02E-01	T	0.01	T	0.07

rs1966265	FGFR4	0.91	0.70	1.19	5.02E-01	A	0.06	A	0.23
rs1800591	MTTP	0.93	0.74	1.16	5.02E-01	T	0.31	T	0.26
rs1520658	DPYD	0.90	0.67	1.22	5.03E-01	G	0.04	G	0.15
rs2228570	VDR	1.08	0.87	1.33	5.03E-01	T	0.27	T	0.42
rs7744392	PPARD	0.87	0.57	1.31	5.04E-01	G	0.26	G	0.05
rs405729	GSTA4	1.07	0.87	1.32	5.04E-01	G	0.49	A	0.48
rs3218651	POLQ	1.09	0.84	1.42	5.04E-01	G	0.12	G	0.19
rs2397118	GSTA5	0.85	0.52	1.37	5.04E-01	C	0.16	C	0.04
rs2076655	FRAP1	0.92	0.72	1.17	5.04E-01	A	0.22	G	0.29
rs713865	CACNA1I	1.07	0.87	1.32	5.05E-01	T	0.17	T	0.46
rs2012199	FCRL5	0.90	0.66	1.22	5.05E-01	C	0.23	C	0.13
rs2137680	IGF1R	1.08	0.86	1.36	5.06E-01	C	0.37	T	0.30
rs434473	ALOX12	1.08	0.86	1.35	5.07E-01	G	0.23	G	0.42
rs15922	TAF11	1.18	0.73	1.91	5.07E-01	G	0.01	G	0.06
rs397589	CBS	1.07	0.87	1.33	5.07E-01	G	0.44	T	0.49
rs7214723	CAMKK1	1.07	0.87	1.32	5.07E-01	C	0.14	C	0.46
rs734351	IGF2	1.07	0.87	1.32	5.07E-01	C	0.27	C	0.41
rs7011	CINP	0.92	0.72	1.18	5.08E-01	T	0.11	T	0.27
rs6162	CYP17A1	1.07	0.87	1.33	5.08E-01	A	0.38	A	0.44
rs2074113	AHR	1.12	0.80	1.56	5.11E-01	A	0.16	A	0.10
rs632478	MMP3	0.93	0.75	1.15	5.11E-01	A	0.41	C	0.50
rs1634499	CCL3	0.92	0.71	1.19	5.11E-01	G	0.18	G	0.24
rs2303428	MSH2	0.89	0.63	1.26	5.11E-01	C	0.03	C	0.12
rs2297518	NOS2	1.10	0.83	1.45	5.12E-01	A	0.08	A	0.19
rs10018288	Intergenic	1.09	0.85	1.40	5.12E-01	G	0.47	G	0.20
rs2066827	CDKN1B	1.09	0.84	1.43	5.12E-01	T	0.29	G	0.23
rs462779	REV3L	1.08	0.86	1.36	5.13E-01	T	0.45	C	0.23
rs1061494	TNC	0.93	0.75	1.15	5.14E-01	T	0.45	C	0.45
rs487848	POLQ	1.15	0.75	1.76	5.14E-01	A	0.17	A	0.06
rs3181077	CCR1	1.09	0.85	1.39	5.15E-01	G	0.07	G	0.25
rs2230748	CD97	0.91	0.68	1.21	5.15E-01	A	0.09	A	0.15
rs6668589	PHGDH	0.93	0.73	1.17	5.16E-01	C	0.34	C	0.29
rs667565	DPYD	1.07	0.87	1.31	5.16E-01	G	0.42	G	0.39
rs279941	SLC10A2	1.11	0.81	1.52	5.17E-01	T	0.09	T	0.13
rs3746101	MKNK2	0.86	0.55	1.35	5.18E-01	T	0.01	T	0.09
rs2802269	CDC42BPA	0.88	0.61	1.29	5.18E-01	G	0.09	G	0.09
rs3020314	ESR1	0.93	0.75	1.15	5.18E-01	T	0.33	C	0.36
rs776741	CYP3A5	1.14	0.76	1.72	5.19E-01	C	0.39	C	0.04
rs2250889	MMP9	1.13	0.77	1.66	5.20E-01	G	0.17	G	0.07
rs1805313	ALAD	1.07	0.87	1.33	5.20E-01	C	0.49	C	0.36
rs2241228	GPRC5A	0.93	0.74	1.16	5.21E-01	G	0.43	A	0.43
rs941798	PTPN1	1.07	0.87	1.33	5.21E-01	G	0.29	G	0.45
rs2028373	AICDA	1.08	0.86	1.34	5.21E-01	A	0.33	G	0.37
rs3821107	XRCC5	1.08	0.85	1.38	5.21E-01	G	0.41	G	0.24
rs1805408	PARP1	0.92	0.71	1.19	5.22E-01	G	0.39	G	0.19
rs4760	PLAUR	1.11	0.80	1.54	5.22E-01	C	0.02	C	0.14
rs4341514	IGF2	1.07	0.87	1.32	5.22E-01	C	0.29	T	0.36
rs316003	SLC22A2	0.92	0.72	1.18	5.22E-01	T	0.46	C	0.23
rs7304504	LRP1	0.84	0.50	1.43	5.23E-01	A	0.23	A	0.01
rs8177877	GCSH	0.78	0.36	1.69	5.23E-01	G	0.13	G	0.00

rs1049216	CASP3	1.07	0.87	1.32	5.23E-01	C	0.23	C	0.31
rs725349	HGF	1.08	0.85	1.38	5.23E-01	T	0.46	T	0.19
rs722921	ALDH1A1	0.93	0.75	1.15	5.23E-01	A	0.17	A	0.49
rs2272225	SHFM1	1.14	0.76	1.71	5.23E-01	A	0.10	A	0.06
rs3770	ABCC4	0.93	0.75	1.15	5.25E-01	A	0.46	A	0.40
rs664143	ATM	1.07	0.87	1.32	5.25E-01	T	0.34	T	0.43
rs3741883	NUAK1	1.09	0.83	1.44	5.26E-01	C	0.08	C	0.22
rs2269112	BRPF1	1.10	0.82	1.46	5.26E-01	T	0.04	T	0.18
rs6041759	FKBP1A	0.89	0.63	1.27	5.26E-01	C	0.24	C	0.09
rs6742078	UGT1A1	1.08	0.85	1.36	5.27E-01	T	0.39	T	0.32
rs1801278	IRS1	1.15	0.75	1.76	5.27E-01	A	0.05	A	0.06
rs9282626	CAT	1.16	0.74	1.82	5.27E-01	C	0.07	C	0.04
rs1870049	CYP19A1	0.91	0.67	1.23	5.27E-01	C	0.40	C	0.12
rs1801105		0.89	0.61	1.29	5.27E-01	T	0.01	T	0.11
rs9282616	BLM	0.86	0.55	1.36	5.28E-01	G	0.20	G	0.03
rs2237060	RAD50	0.93	0.73	1.17	5.28E-01	C	0.07	C	0.40
rs2228529	ERCC6	0.92	0.70	1.20	5.28E-01	G	0.11	G	0.21
rs2243290	IL4	1.09	0.84	1.40	5.28E-01	A	0.32	A	0.18
rs419129	GSTA4	1.07	0.87	1.32	5.29E-01	G	0.46	T	0.48
rs1041981	LTA	0.93	0.74	1.17	5.29E-01	A	0.42	A	0.37
rs552976	ABCB11	0.93	0.75	1.16	5.30E-01	T	0.40	T	0.32
rs4149056	SLCO1B1	1.10	0.82	1.47	5.31E-01	C	0.04	C	0.15
rs4148221	ABCG8	1.09	0.83	1.44	5.31E-01	T	0.20	T	0.16
rs13027171	MERTK	0.92	0.72	1.19	5.31E-01	A	0.07	A	0.29
rs2165810	MBL2	1.08	0.85	1.35	5.32E-01	T	0.45	A	0.21
rs694564	ALDH1A1	1.15	0.74	1.81	5.33E-01	A	0.14	A	0.03
rs3176878	VCAM1	0.91	0.67	1.23	5.33E-01	T	0.16	T	0.16
rs234706	CBS	0.92	0.70	1.20	5.33E-01	A	0.22	A	0.34
rs923796	NAT2	0.94	0.76	1.16	5.34E-01	G	0.21	G	0.40
rs2242664	SLC44A4	1.07	0.86	1.33	5.34E-01	G	0.35	G	0.46
rs2069391	CDK2	1.12	0.78	1.63	5.34E-01	T	0.11	T	0.07
rs8190315	BID	1.21	0.66	2.22	5.34E-01	G	0.06	G	0.02
rs2305801	CYP4F11	0.92	0.72	1.19	5.34E-01	A	0.40	A	0.19
rs2515363	CNTF	0.93	0.75	1.16	5.34E-01	G	0.36	C	0.41
rs2137975	DPYD	0.93	0.74	1.17	5.35E-01	C	0.36	C	0.31
rs854556	PON1	1.08	0.85	1.37	5.35E-01	T	0.20	T	0.32
rs4820889	TCN2	0.83	0.46	1.51	5.36E-01	A	0.10	A	0.03
rs11848612	ADSSL1	0.93	0.75	1.16	5.36E-01	C	0.46	G	0.45
rs527221	DMPK	1.11	0.80	1.55	5.36E-01	C	0.07	C	0.12
rs1043424	PINK1	0.93	0.73	1.18	5.36E-01	C	0.31	C	0.27
rs3748433	CEP250	0.89	0.61	1.29	5.36E-01	T	0.18	T	0.08
rs6030	F5	1.07	0.86	1.35	5.37E-01	G	0.18	G	0.33
rs3177980	SELL	0.92	0.72	1.19	5.37E-01	C	0.14	C	0.24
rs7746988	PPARD	0.86	0.53	1.39	5.38E-01	C	0.31	C	0.02
rs1801516	ATM	0.91	0.66	1.24	5.38E-01	A	0.03	A	0.13
rs4918758	CYP2C9	0.93	0.74	1.17	5.39E-01	C	0.33	C	0.34
rs1946519	IL18	1.07	0.86	1.33	5.40E-01	A	0.35	A	0.41
rs6056	FGB	1.09	0.83	1.43	5.40E-01	T	0.08	T	0.18
rs2303929	SLC4A2	0.93	0.73	1.18	5.40E-01	A	0.13	A	0.25
rs742350	FMO1	0.91	0.68	1.22	5.41E-01	A	0.47	A	0.12

rs7803574	SHFM1	1.14	0.76	1.70	5.41E-01	T	0.10	T	0.06
rs549908	IL18	1.07	0.86	1.34	5.41E-01	G	0.20	G	0.31
rs3738136	PINK1	0.85	0.52	1.42	5.41E-01	A	0.03	A	0.07
rs2287620	ABCB11	0.93	0.75	1.16	5.41E-01	A	0.26	A	0.43
rs13436	LIG1	0.93	0.74	1.17	5.41E-01	G	0.47	C	0.42
rs3813867	CYP2E1	0.85	0.51	1.42	5.41E-01	C	0.07	C	0.04
rs664982	ATM	1.07	0.87	1.31	5.42E-01	A	0.41	G	0.44
rs2640	EIF2AK1	0.87	0.55	1.37	5.42E-01	C	0.02	C	0.07
rs801720	CERK	0.93	0.75	1.16	5.43E-01	G	0.31	T	0.40
rs3736265	PPARGC1A	0.86	0.54	1.38	5.44E-01	A	0.07	A	0.06
rs2072671	CDA	0.93	0.74	1.18	5.44E-01	C	0.08	C	0.33
rs2214827	HGF	1.08	0.84	1.39	5.44E-01	G	0.06	G	0.22
rs3752988	CYP2C8	1.07	0.86	1.34	5.44E-01	C	0.46	C	0.30
rs5320	DBH	0.88	0.57	1.35	5.44E-01	A	0.17	A	0.06
rs1049897	MGP	1.07	0.86	1.32	5.45E-01	T	0.37	T	0.37
rs667126	LRP5	1.07	0.85	1.35	5.45E-01	T	0.48	C	0.25
rs1760212	DPYD	0.93	0.75	1.17	5.45E-01	T	0.43	T	0.38
rs1514497	DPYD	1.07	0.85	1.35	5.45E-01	T	0.45	T	0.27
rs2509915	CNTF	0.93	0.75	1.17	5.45E-01	A	0.35	G	0.41
rs1805407	PARP1	0.92	0.71	1.20	5.46E-01	G	0.39	G	0.19
rs17773251	CSNK1A1L	1.11	0.79	1.57	5.46E-01	G	0.07	G	0.09
rs673	TNF	0.65	0.16	2.66	5.46E-01	A	0.06	A	0.00
rs3212218	IL12B	0.92	0.69	1.22	5.47E-01	T	0.31	T	0.24
rs6902123	PPARD	0.90	0.63	1.28	5.47E-01	T	0.37	C	0.07
rs2979895	POLB	0.90	0.65	1.25	5.48E-01	T	0.36	C	0.08
rs1014136	STARD3NL	1.08	0.84	1.37	5.48E-01	C	0.21	C	0.24
rs2269429	TNXB	0.89	0.61	1.30	5.49E-01	A	0.18	A	0.08
rs4251710	TAF15	1.11	0.78	1.59	5.49E-01	C	0.33	C	0.07
rs11571117	REN	0.65	0.15	2.70	5.49E-01	A	0.06	0	0.00
rs447804	BLM	0.93	0.73	1.18	5.50E-01	C	0.40	C	0.33
rs858521	SAT2	1.07	0.86	1.34	5.50E-01	G	0.12	G	0.37
rs1567868	IL8RA	0.89	0.61	1.30	5.50E-01	C	0.23	C	0.06
rs2299257	PON1	0.94	0.76	1.16	5.50E-01	A	0.43	C	0.44
rs4765181	SCARB1	1.07	0.85	1.35	5.51E-01	A	0.27	A	0.38
rs3181078	CCR1	0.88	0.57	1.36	5.51E-01	G	0.02	G	0.08
rs2288648	FASTK	0.75	0.30	1.91	5.52E-01	A	0.06	A	0.01
rs663530	MRE11A	1.08	0.85	1.37	5.52E-01	T	0.16	T	0.27
rs581002	MRE11A	1.07	0.85	1.36	5.52E-01	T	0.17	T	0.26
rs4443426	MGC42105	0.94	0.76	1.16	5.53E-01	C	0.43	C	0.48
rs3850997	TNFRSF17	1.08	0.84	1.37	5.54E-01	T	0.11	T	0.34
rs2292954	SPG7	0.91	0.67	1.24	5.54E-01	C	0.06	C	0.18
rs617219	BHMT	1.07	0.86	1.33	5.54E-01	C	0.30	C	0.36
rs348458	ALDH1A1	1.06	0.87	1.30	5.55E-01	A	0.47	A	0.47
rs3091336	IL3	1.16	0.71	1.91	5.56E-01	A	0.31	A	0.01
rs8187758	SLC28A1	1.08	0.84	1.38	5.56E-01	A	0.19	A	0.24
rs230547	NFKB1	0.90	0.62	1.29	5.56E-01	T	0.15	T	0.09
rs299284	HMMR	0.90	0.65	1.27	5.57E-01	T	0.11	T	0.12
rs1866928	C15orf42	1.07	0.85	1.35	5.57E-01	A	0.41	A	0.35
rs2270628	IGFBP3	1.08	0.84	1.38	5.57E-01	T	0.38	T	0.20
rs6092	SERPINE1	0.89	0.60	1.31	5.57E-01	A	0.02	A	0.10

rs2899472	CYP19A1	0.92	0.71	1.21	5.58E-01	A	0.05	A	0.24
rs741817	CYP8B1	1.26	0.58	2.71	5.58E-01	T	0.07	T	0.00
rs10775648	HUNK	0.92	0.70	1.21	5.59E-01	T	0.08	T	0.23
rs2813545	ESR1	1.07	0.85	1.36	5.59E-01	C	0.27	C	0.22
rs348449	ALDH1A1	1.14	0.74	1.76	5.60E-01	C	0.13	C	0.03
rs1052248	LST1	1.07	0.85	1.36	5.60E-01	A	0.23	A	0.25
rs3547	XRCC1	1.07	0.86	1.32	5.60E-01	T	0.34	T	0.42
rs5743553	TLR1	0.84	0.47	1.51	5.61E-01	A	0.16	A	0.01
rs28899170	UGT1A10	1.07	0.85	1.35	5.61E-01	A	0.27	A	0.28
rs2243268	IL4	1.08	0.83	1.40	5.62E-01	C	0.24	C	0.18
rs7393105	ABCC2	1.07	0.86	1.33	5.63E-01	C	0.42	C	0.43
rs2066853	AHR	1.09	0.81	1.48	5.63E-01	A	0.43	A	0.11
rs2297345	PAK7	1.07	0.85	1.34	5.63E-01	C	0.18	T	0.30
rs743616	ARSA	0.94	0.77	1.15	5.63E-01	C	0.44	G	0.47
rs6005	F5	0.72	0.24	2.16	5.63E-01	G	0.08	0	0.00
rs2279103	CTDP1	1.08	0.83	1.42	5.63E-01	T	0.05	T	0.17
rs207910	XRCC5	1.09	0.81	1.47	5.63E-01	G	0.22	G	0.13
rs196912	ERN1	1.07	0.85	1.36	5.64E-01	C	0.34	T	0.23
rs1800457	CYB5R3	1.19	0.65	2.19	5.66E-01	G	0.27	G	0.00
rs1126579	IL8RB	1.07	0.85	1.33	5.66E-01	T	0.18	T	0.46
rs2302465	BST1	0.91	0.64	1.27	5.67E-01	T	0.01	T	0.12
rs4148211	ABCG8	0.94	0.74	1.18	5.67E-01	G	0.19	G	0.40
rs11466155	NGFR	1.07	0.85	1.34	5.67E-01	T	0.08	T	0.33
rs1260326	GCKR	1.07	0.85	1.36	5.67E-01	T	0.16	T	0.38
rs1202170	ABCB1	1.07	0.86	1.32	5.68E-01	G	0.48	G	0.49
rs491347	LRP5	1.07	0.85	1.34	5.68E-01	T	0.46	C	0.25
rs2302538	UGT1A1	1.09	0.81	1.45	5.69E-01	G	0.33	G	0.13
rs1294689	FKBP1A	1.07	0.85	1.35	5.69E-01	C	0.18	C	0.31
rs8187755	SLC28A1	1.26	0.57	2.78	5.71E-01	T	0.08	T	0.00
rs10018199	SPOCK3	1.07	0.85	1.35	5.71E-01	G	0.33	G	0.25
rs8192719	CYP2B6	1.07	0.84	1.36	5.71E-01	T	0.39	T	0.27
rs907806	IGF1R	1.09	0.81	1.47	5.72E-01	G	0.25	G	0.13
rs2269829	PON1	1.07	0.85	1.33	5.72E-01	A	0.47	G	0.32
rs11804091	LEPR	1.09	0.81	1.46	5.73E-01	G	0.16	G	0.15
rs1051137	GSTM4	0.93	0.73	1.19	5.73E-01	T	0.16	T	0.35
rs1801058	GRK4	0.94	0.75	1.17	5.73E-01	T	0.16	T	0.42
rs162549	CYP1B1	0.92	0.70	1.21	5.73E-01	T	0.19	T	0.20
rs9935059	EEF2K	1.10	0.80	1.51	5.73E-01	G	0.29	G	0.09
rs3116496	CD28	0.92	0.68	1.24	5.74E-01	C	0.06	C	0.18
rs274558	SLC22A5	0.94	0.74	1.18	5.74E-01	C	0.39	C	0.43
rs4681	FGB	1.08	0.82	1.44	5.74E-01	T	0.03	T	0.17
rs6886047	GHR	0.94	0.74	1.18	5.75E-01	T	0.45	T	0.25
rs3748415	APCDD1	0.91	0.64	1.28	5.76E-01	T	0.01	T	0.12
rs2230590	MST1R	0.94	0.75	1.18	5.76E-01	A	0.33	G	0.49
rs3793345	IGFBP3	0.92	0.70	1.22	5.76E-01	C	0.20	C	0.19
rs1709409	DPYD	1.07	0.84	1.38	5.77E-01	G	0.22	G	0.23
rs1866389	LOC100129870	1.08	0.83	1.40	5.77E-01	G	0.09	G	0.22
rs3749228	CHRD	1.12	0.75	1.68	5.77E-01	G	0.12	G	0.06
rs2039449	DPYD	1.07	0.85	1.35	5.78E-01	C	0.45	C	0.26
rs6508	WIT1	1.10	0.79	1.52	5.79E-01	A	0.36	A	0.07

rs2071520	TNC	1.07	0.85	1.34	5.79E-01	C	0.26	C	0.33
rs1801133	MTHFR	0.94	0.74	1.19	5.79E-01	T	0.12	T	0.32
rs7218866	PSMB6	0.84	0.46	1.55	5.79E-01	T	0.05	T	0.03
rs3218222	CDKN2D	1.07	0.84	1.36	5.80E-01	A	0.25	A	0.27
rs2236379	PRKCQ	1.07	0.84	1.37	5.80E-01	T	0.34	T	0.25
rs376618	FGFR4	1.07	0.84	1.36	5.80E-01	G	0.34	G	0.23
rs1805061	SLC7A7	1.08	0.83	1.41	5.80E-01	C	0.22	C	0.15
rs17006837	HELQ	1.17	0.67	2.04	5.80E-01	G	0.48	G	0.00
rs496550	ABCB11	0.94	0.76	1.16	5.81E-01	G	0.30	A	0.45
rs1060896	SLC28A2	1.06	0.85	1.32	5.81E-01	A	0.17	C	0.38
rs2706338	RAD50	1.08	0.83	1.40	5.81E-01	T	0.05	T	0.20
rs7736656	UBLCP1	1.08	0.82	1.42	5.82E-01	A	0.18	A	0.18
rs4983543	ADSSL1	0.94	0.76	1.17	5.83E-01	T	0.12	C	0.47
rs2235937	PTPRU	0.94	0.74	1.18	5.83E-01	G	0.20	G	0.26
rs3756772	FRK	1.06	0.86	1.32	5.83E-01	A	0.23	A	0.44
rs769412	MDM2	1.13	0.73	1.75	5.84E-01	G	0.12	G	0.05
rs26279	MSH3	0.94	0.75	1.18	5.84E-01	G	0.33	G	0.29
rs2522390	RAD50	0.76	0.29	2.02	5.86E-01	C	0.10	0	0.00
rs16913653	IKBKAP	1.22	0.60	2.50	5.86E-01	T	0.12	0	0.00
rs2706375	RAD50	0.76	0.29	2.02	5.86E-01	C	0.10	0	0.00
rs2260863	EPHX1	1.06	0.85	1.33	5.87E-01	G	0.43	G	0.27
rs10261833	SHFM1	1.08	0.82	1.42	5.87E-01	C	0.16	C	0.18
rs3942589	SHFM1	0.90	0.61	1.33	5.88E-01	G	0.14	G	0.07
rs1805411	PARP1	1.08	0.82	1.42	5.89E-01	A	0.11	A	0.19
rs2228059	IL15RA	1.06	0.86	1.30	5.89E-01	A	0.32	C	0.49
rs3745202	PRX	0.92	0.67	1.26	5.90E-01	C	0.02	C	0.18
rs8252	GADD45G	0.88	0.54	1.42	5.90E-01	A	0.10	A	0.03
rs3811635	MERTK	1.06	0.86	1.31	5.90E-01	A	0.36	A	0.40
rs4148950	CHST3	1.06	0.86	1.30	5.90E-01	A	0.29	A	0.46
rs3793771	WNT8B	1.07	0.83	1.38	5.90E-01	G	0.21	G	0.22
rs4938016	ANKK1	1.06	0.85	1.32	5.91E-01	C	0.47	G	0.34
rs188096	SLC10A2	1.09	0.79	1.50	5.91E-01	A	0.08	A	0.13
rs664393	FLT1	1.10	0.78	1.53	5.91E-01	A	0.05	A	0.12
rs11574138	VDR	0.73	0.23	2.32	5.91E-01	G	0.09	G	0.00
rs5888	SCARB1	0.94	0.76	1.17	5.92E-01	T	0.21	T	0.46
rs2020863	FMO2	1.09	0.79	1.52	5.93E-01	G	0.06	G	0.10
rs2296869	SETX	1.07	0.84	1.37	5.93E-01	A	0.36	G	0.18
rs5896	F2	1.09	0.80	1.48	5.94E-01	T	0.04	T	0.16
rs4645878	BAX	1.09	0.79	1.52	5.94E-01	A	0.10	A	0.11
rs2522393	RAD50	0.85	0.46	1.55	5.94E-01	T	0.25	T	0.01
rs2706369	RAD50	0.85	0.46	1.55	5.94E-01	T	0.25	T	0.01
rs4529	TBXAS1	1.24	0.56	2.71	5.94E-01	G	0.10	G	0.00
rs2297881	KIF1B	1.16	0.67	2.01	5.94E-01	C	0.06	C	0.03
rs1549760	CDK5	0.94	0.74	1.19	5.94E-01	T	0.29	T	0.25
rs2295275	TRERF1	0.88	0.55	1.40	5.95E-01	A	0.01	A	0.07
rs16975750	LIPE	1.19	0.63	2.27	5.95E-01	G	0.21	G	0.00
rs2040968	HGF	1.07	0.84	1.35	5.95E-01	C	0.34	C	0.22
rs1148459	TNFRSF1B	1.06	0.86	1.30	5.95E-01	C	0.41	A	0.47
rs943584	PLEKHG5	1.11	0.76	1.61	5.96E-01	T	0.22	T	0.08
rs1189466	ABCC4	0.89	0.57	1.38	5.96E-01	A	0.12	A	0.06

rs2228001	XPC	1.06	0.85	1.32	5.96E-01	C	0.26	C	0.39
rs35595	ABCC1	1.07	0.83	1.40	5.96E-01	A	0.46	A	0.14
rs1063169	FOS	0.91	0.65	1.29	5.96E-01	T	0.04	T	0.16
rs2228262	THBS1	1.09	0.79	1.52	5.97E-01	G	0.02	G	0.11
rs6874941	CART	0.93	0.71	1.22	5.97E-01	C	0.45	C	0.15
rs2287395	GSTZ1	0.94	0.75	1.18	5.97E-01	G	0.28	G	0.30
rs40228	TPK1	1.08	0.82	1.41	5.97E-01	T	0.38	T	0.17
rs323870	PARP3	1.19	0.62	2.30	5.97E-01	G	0.14	G	0.00
rs3024680	IL4R	0.86	0.50	1.49	5.97E-01	C	0.24	C	0.01
rs6003	F13B	1.08	0.80	1.46	5.97E-01	A	0.42	G	0.09
rs10018618	C1QTNF7	1.18	0.64	2.17	5.97E-01	C	0.26	C	0.00
rs1822017	DCBLD2	1.08	0.81	1.45	5.98E-01	T	0.19	T	0.15
rs7663494	DCTD	1.06	0.85	1.32	5.99E-01	A	0.49	G	0.29
rs1060253	SLC7A5	0.94	0.75	1.18	5.99E-01	G	0.13	G	0.28
rs1341160	CYP2C8	1.09	0.79	1.50	5.99E-01	A	0.04	A	0.13
rs1532268	MTRR	1.06	0.85	1.32	5.99E-01	A	0.29	A	0.35
rs2230365	NFKBIL1	0.92	0.68	1.25	6.00E-01	T	0.07	T	0.15
rs514658	TATDN2	1.06	0.84	1.34	6.00E-01	T	0.36	T	0.24
rs560096	IGHMBP2	0.93	0.71	1.22	6.01E-01	T	0.36	T	0.17
rs1801701	APOB	1.11	0.75	1.64	6.01E-01	A	0.03	A	0.09
rs17680881	TACC3	0.94	0.73	1.20	6.01E-01	A	0.15	A	0.26
rs17162549	MAP3K6	1.13	0.72	1.78	6.01E-01	G	0.23	G	0.03
rs316019	SLC22A2	0.91	0.64	1.30	6.01E-01	T	0.16	T	0.11
rs10264952	STK31	1.08	0.80	1.46	6.01E-01	A	0.10	A	0.17
rs7120118	NR1H3	1.06	0.85	1.33	6.02E-01	C	0.42	C	0.31
rs8034835	CYP19A1	1.06	0.85	1.32	6.02E-01	G	0.23	A	0.48
rs731027	CHST3	1.06	0.86	1.30	6.03E-01	C	0.43	C	0.47
rs1800738	TPP1	0.94	0.76	1.17	6.03E-01	A	0.25	T	0.41
rs2274406	ABCC4	0.94	0.76	1.17	6.04E-01	C	0.38	T	0.35
rs4809957	CYP24A1	1.07	0.83	1.36	6.04E-01	G	0.42	G	0.23
rs2270132	BLM	0.94	0.76	1.18	6.04E-01	G	0.13	G	0.44
rs2032349	ADH4	1.15	0.67	1.97	6.04E-01	T	0.07	T	0.03
rs1469167	ALDH1A1	1.10	0.76	1.60	6.04E-01	G	0.27	G	0.05
rs9606756	TCN2	1.08	0.81	1.45	6.06E-01	G	0.16	G	0.12
rs4724445	IGFBP1	1.08	0.81	1.44	6.06E-01	A	0.09	A	0.18
rs1938484	LEPR	1.07	0.83	1.39	6.06E-01	A	0.17	A	0.21
rs10743597	A2M	0.95	0.76	1.17	6.06E-01	G	0.34	G	0.33
rs689453	NQO1	0.90	0.60	1.35	6.07E-01	A	0.04	A	0.08
rs35766	IGF1	0.93	0.71	1.22	6.07E-01	A	0.45	G	0.18
rs4149965	EXO1	1.07	0.83	1.38	6.07E-01	A	0.05	A	0.23
rs529948	NFKBIE	1.09	0.79	1.49	6.08E-01	A	0.03	A	0.14
rs952005	SHFM1	0.90	0.62	1.33	6.08E-01	T	0.14	T	0.07
rs373496	TNFRSF17	0.83	0.40	1.71	6.08E-01	T	0.08	T	0.01
rs11401	CCDC101	0.93	0.69	1.24	6.09E-01	C	0.17	C	0.18
rs1181795	PPARG	0.90	0.59	1.36	6.09E-01	T	0.02	T	0.08
rs35594	ABCC1	0.94	0.75	1.19	6.10E-01	G	0.33	A	0.28
rs8187694		1.12	0.72	1.76	6.10E-01	A	0.05	A	0.05
rs10409482	VRK3	1.18	0.63	2.21	6.11E-01	T	0.16	T	0.00
rs6644	ADSSL1	0.95	0.76	1.17	6.11E-01	T	0.12	C	0.47
rs1249958	PPP1R1A	1.33	0.44	4.06	6.11E-01	T	0.07	T	0.00

rs216867	VWF	1.08	0.79	1.48	6.12E-01	A	0.26	A	0.12
rs2307145	IL12RB2	0.88	0.52	1.46	6.12E-01	C	0.08	C	0.04
rs5987	F13A1	0.87	0.51	1.48	6.12E-01	A	0.03	A	0.05
rs714629	AICDA	0.95	0.77	1.17	6.12E-01	G	0.39	C	0.48
rs3774936	NFKB1	1.06	0.84	1.35	6.13E-01	T	0.07	T	0.33
rs7903344	CHUK	1.06	0.85	1.31	6.13E-01	C	0.25	C	0.50
rs3923647	TLR1	0.86	0.48	1.55	6.14E-01	T	0.08	T	0.03
rs4674258	IL8RB	0.95	0.77	1.17	6.14E-01	C	0.46	T	0.47
rs165974	ABCC1	0.92	0.68	1.26	6.15E-01	T	0.09	T	0.16
rs887241	ALDH3A1	0.94	0.75	1.18	6.15E-01	T	0.34	T	0.33
rs2107538	CCL5	0.93	0.72	1.22	6.16E-01	T	0.38	T	0.19
rs5993883	COMT	0.95	0.77	1.17	6.17E-01	G	0.42	G	0.50
rs1805404	PARP1	1.07	0.81	1.42	6.17E-01	T	0.12	T	0.18
rs4371387	APOB	0.93	0.71	1.22	6.18E-01	A	0.13	A	0.19
rs17197552	PPP2R3A	0.94	0.75	1.19	6.18E-01	G	0.19	G	0.28
rs1341164	CYP2C8	0.94	0.74	1.20	6.18E-01	C	0.29	C	0.28
rs2249317	SIRPD	1.07	0.82	1.41	6.19E-01	T	0.10	T	0.17
rs5742659	IGF1	0.78	0.30	2.07	6.19E-01	C	0.12	C	0.00
rs1061472	ATP7B	1.05	0.86	1.29	6.19E-01	A	0.49	A	0.43
rs2641806	CHST5	1.06	0.85	1.32	6.20E-01	T	0.29	C	0.34
rs1801200	ERBB2	0.94	0.72	1.21	6.20E-01	G	0.06	G	0.25
rs25487	XRCC1	1.06	0.84	1.34	6.20E-01	A	0.17	A	0.33
rs2272611	ARHGEF10	0.93	0.69	1.24	6.20E-01	A	0.09	A	0.15
rs543573	SETX	1.06	0.83	1.36	6.20E-01	C	0.36	T	0.18
rs11875	MGST1	0.90	0.59	1.38	6.21E-01	A	0.03	A	0.08
rs1805415	PARP1	1.07	0.81	1.41	6.21E-01	A	0.12	A	0.19
rs1270764	TSSK4	0.81	0.36	1.84	6.21E-01	C	0.14	C	0.00
rs1799964	LTA	1.07	0.83	1.37	6.21E-01	C	0.18	C	0.22
rs1800610	TNF	1.10	0.75	1.60	6.22E-01	T	0.05	T	0.09
rs3218649	POLQ	0.95	0.77	1.17	6.22E-01	C	0.42	C	0.35
rs1390358	NAT2	0.95	0.77	1.17	6.22E-01	C	0.21	C	0.40
rs4292454	GHR	1.06	0.85	1.31	6.22E-01	T	0.32	C	0.39
rs2278815	LEP	0.95	0.76	1.18	6.22E-01	A	0.13	G	0.45
rs1537234	GSTM3	1.06	0.85	1.31	6.23E-01	T	0.21	T	0.43
rs1042031	APOB	0.93	0.71	1.22	6.23E-01	A	0.20	A	0.17
rs6901410	PPARD	0.92	0.65	1.30	6.24E-01	T	0.37	C	0.07
rs4919682	CYP17A1	1.06	0.84	1.33	6.24E-01	T	0.14	T	0.29
rs235768	BMP2	1.06	0.84	1.33	6.24E-01	A	0.05	A	0.38
rs10228128	SHFM1	1.19	0.59	2.39	6.25E-01	C	0.08	C	0.00
rs1061047	GPRC5A	1.06	0.83	1.36	6.25E-01	C	0.28	C	0.23
rs2256871	CYP2C9	0.79	0.30	2.07	6.26E-01	C	0.08	0	0.00
rs1056522	CHST13	1.06	0.85	1.31	6.26E-01	T	0.46	T	0.31
rs2280789	CCL5	0.93	0.69	1.25	6.27E-01	C	0.18	C	0.14
rs593818	CYP4F12	1.06	0.85	1.31	6.27E-01	A	0.42	A	0.45
rs2280509	FZD7	1.07	0.81	1.43	6.27E-01	T	0.05	T	0.18
rs1395119	SIM1	0.95	0.76	1.18	6.27E-01	T	0.24	T	0.36
rs9529	CCND3	0.94	0.73	1.21	6.27E-01	A	0.03	A	0.28
rs1169288	HNF1A	0.94	0.72	1.22	6.27E-01	G	0.13	G	0.32
rs5939	PTAFR	0.75	0.24	2.39	6.28E-01	G	0.07	G	0.00
rs7775	FRZB	0.92	0.64	1.31	6.28E-01	G	0.31	G	0.07

rs8187692	ABCC2	0.77	0.27	2.22	6.28E-01	T	0.07	T	0.00
rs3828855	BYSL	1.09	0.78	1.52	6.29E-01	A	0.10	A	0.10
rs2167270	LEP	1.05	0.85	1.30	6.29E-01	A	0.43	A	0.38
rs1799986	LRP1	0.92	0.66	1.28	6.29E-01	T	0.06	T	0.13
rs3731151	XPC	0.94	0.74	1.20	6.29E-01	A	0.29	A	0.26
rs2283512	ABCC1	1.06	0.85	1.32	6.29E-01	G	0.38	T	0.32
rs8032477	IGF1R	0.95	0.76	1.18	6.29E-01	T	0.32	C	0.41
rs2235040	ABCB1	1.09	0.77	1.52	6.30E-01	A	0.13	A	0.11
rs2778979	PLXDC2	0.93	0.68	1.27	6.31E-01	T	0.07	T	0.13
rs1047643	FDFT1	1.07	0.81	1.40	6.31E-01	C	0.35	C	0.14
rs3738099	ALPL	0.93	0.68	1.27	6.31E-01	G	0.27	G	0.12
rs3088440	C9orf53	1.08	0.78	1.51	6.31E-01	A	0.16	A	0.11
rs2285460	BLM	0.94	0.72	1.22	6.31E-01	T	0.25	T	0.19
rs989902	PTPN13	1.06	0.84	1.32	6.31E-01	A	0.20	C	0.39
rs2273642	NFATC2	1.06	0.84	1.34	6.31E-01	A	0.20	A	0.29
rs2522391	RAD50	0.86	0.47	1.58	6.32E-01	A	0.24	A	0.01
rs2233406	NFKBIA	0.94	0.75	1.19	6.32E-01	T	0.27	T	0.27
rs619824	CYP17A1	1.05	0.85	1.30	6.32E-01	G	0.34	T	0.46
rs5988	F13A1	0.93	0.70	1.24	6.34E-01	C	0.18	C	0.16
rs2231142	ABCG2	0.91	0.63	1.32	6.34E-01	A	0.03	A	0.12
rs279942	SLC10A2	1.06	0.83	1.35	6.36E-01	G	0.28	G	0.22
rs2228226	ARHGAP9	1.05	0.85	1.32	6.36E-01	G	0.25	G	0.34
rs3759259	STYK1	1.05	0.85	1.30	6.36E-01	G	0.35	A	0.35
rs2066530	FMO3	0.72	0.19	2.79	6.37E-01	C	0.06	C	0.00
rs838827	IKBKAP	0.91	0.61	1.36	6.37E-01	T	0.11	T	0.07
rs4577050	SLC12A6	0.95	0.75	1.19	6.37E-01	A	0.38	G	0.34
rs35599	ABCC1	1.08	0.79	1.48	6.37E-01	C	0.09	C	0.12
rs3732378	CX3CR1	0.93	0.69	1.25	6.37E-01	A	0.04	A	0.18
rs1374993	C8orf42	1.06	0.84	1.33	6.37E-01	G	0.30	G	0.34
rs5882	CETP	1.05	0.85	1.30	6.38E-01	A	0.42	G	0.33
rs1514499	DPYD	1.19	0.57	2.51	6.39E-01	C	0.07	C	0.01
rs1126526	ATF3	0.94	0.72	1.23	6.39E-01	T	0.12	T	0.19
rs1884614	HNF4a	0.94	0.72	1.22	6.39E-01	T	0.13	T	0.21
rs907807	IGF1R	1.07	0.81	1.42	6.39E-01	G	0.33	G	0.13
rs3750898	DCLRE1A	0.94	0.74	1.21	6.39E-01	C	0.38	G	0.23
rs1801018	BCL2	0.95	0.75	1.20	6.40E-01	G	0.10	G	0.42
rs1201689	MAPKBP1	0.94	0.74	1.20	6.40E-01	G	0.36	G	0.37
rs12636461	PPARG	0.95	0.75	1.19	6.40E-01	G	0.27	G	0.29
rs2972164	PPARG	1.06	0.84	1.33	6.40E-01	C	0.23	T	0.44
rs12450550	EME1	1.06	0.83	1.35	6.40E-01	C	0.11	C	0.28
rs241447	TAP2	0.94	0.73	1.21	6.40E-01	G	0.16	G	0.24
rs246217	ABCC1	0.93	0.70	1.25	6.41E-01	A	0.16	A	0.14
rs4148416	ABCC3	1.10	0.73	1.66	6.41E-01	T	0.19	T	0.06
rs10018284	Intergenic	1.05	0.85	1.31	6.41E-01	C	0.34	C	0.34
rs1042157	SULT1A1	1.05	0.85	1.31	6.42E-01	T	0.23	T	0.42
rs709816	NBN	0.95	0.77	1.17	6.42E-01	A	0.24	G	0.38
rs3739927	SETX	0.88	0.52	1.50	6.42E-01	G	0.13	G	0.04
rs3813572	PSMA4	1.05	0.85	1.31	6.43E-01	G	0.15	G	0.41
rs2980374	CYP3A7	0.85	0.44	1.67	6.43E-01	T	0.21	T	0.00
rs6720173	ABCG5	1.06	0.82	1.38	6.43E-01	C	0.29	C	0.17

rs7871785	PSMB7	0.95	0.76	1.18	6.44E-01	A	0.45	G	0.42
rs7181886	CYP19A1	1.09	0.77	1.54	6.44E-01	G	0.33	G	0.06
rs6544718	ABCG8	1.06	0.82	1.38	6.44E-01	T	0.04	T	0.22
rs1800875	CMA1	0.95	0.77	1.17	6.45E-01	A	0.29	A	0.50
rs1801198	TCN2	0.95	0.76	1.18	6.45E-01	G	0.26	G	0.43
rs833061	VEGFA	1.05	0.85	1.29	6.45E-01	C	0.34	C	0.49
rs8191842	IGF2R	0.75	0.22	2.52	6.46E-01	T	0.05	T	0.00
rs77905	DBH	0.95	0.77	1.17	6.47E-01	T	0.44	T	0.47
rs160632	RIOK2	0.95	0.77	1.17	6.47E-01	G	0.48	G	0.41
rs3093664	TNF	1.09	0.75	1.58	6.48E-01	G	0.10	G	0.07
rs25882	CSF2	0.94	0.73	1.22	6.48E-01	C	0.31	C	0.21
rs2953993	POLB	0.93	0.67	1.28	6.49E-01	G	0.36	A	0.08
rs2228468	CCBP2	0.95	0.76	1.19	6.50E-01	C	0.25	C	0.38
rs10264272	CYP3A5	0.80	0.30	2.13	6.50E-01	T	0.09	T	0.00
rs10898	LOC100129773	0.95	0.74	1.21	6.52E-01	C	0.37	C	0.26
rs4148380	ABCC1	0.89	0.55	1.46	6.52E-01	A	0.03	A	0.06
rs2687080	CYP3A7	0.82	0.35	1.92	6.52E-01	C	0.11	C	0.00
rs11549465	HIF1A	1.09	0.74	1.60	6.52E-01	T	0.03	T	0.10
rs2452600	PDLIM5	0.95	0.74	1.21	6.52E-01	T	0.15	T	0.31
rs2041049	DBF4	1.13	0.66	1.96	6.53E-01	C	0.08	C	0.03
rs290861	DPYD	1.07	0.81	1.40	6.53E-01	G	0.25	G	0.17
rs1505	CYP2C9	0.95	0.76	1.19	6.53E-01	C	0.33	C	0.34
rs776740	CYP3A7	0.82	0.35	1.92	6.53E-01	A	0.11	A	0.00
rs5361	SELE	1.09	0.75	1.57	6.53E-01	C	0.04	C	0.09
rs7904678	ABCC2	1.11	0.71	1.74	6.53E-01	T	0.06	T	0.05
rs5743612	TLR1	1.23	0.50	3.00	6.53E-01	T	0.08	T	0.00
rs158634	DPYD	1.06	0.81	1.39	6.54E-01	G	0.26	G	0.17
rs440454	RDBP	1.05	0.84	1.33	6.54E-01	T	0.09	T	0.30
rs700518	CYP19A1	1.05	0.85	1.31	6.54E-01	G	0.20	A	0.50
rs2275565	MTR	1.06	0.82	1.36	6.54E-01	A	0.45	A	0.22
rs2162679	IGF1	1.06	0.81	1.39	6.54E-01	G	0.44	G	0.17
rs3100697	HNMT	0.84	0.40	1.78	6.54E-01	C	0.18	C	0.00
rs699517	ENOSF1	0.95	0.76	1.18	6.55E-01	C	0.42	T	0.32
rs1056932	BCL6	1.05	0.85	1.30	6.55E-01	T	0.17	C	0.32
rs1329568	LOC100130458	0.86	0.45	1.64	6.56E-01	A	0.16	A	0.01
rs3824134	ARHGEF10	0.95	0.74	1.21	6.56E-01	C	0.27	C	0.23
rs1962589	IGF1R	1.07	0.81	1.41	6.56E-01	C	0.45	C	0.13
rs3824120	MYC	1.07	0.78	1.47	6.57E-01	A	0.05	A	0.14
rs2363641	POMT2	0.95	0.76	1.19	6.57E-01	G	0.34	G	0.32
rs1800791	FGB	0.94	0.70	1.25	6.57E-01	A	0.09	A	0.18
rs3131637	TNF	0.95	0.76	1.19	6.58E-01	T	0.31	T	0.36
rs2575875	ABCA1	1.05	0.85	1.30	6.58E-01	G	0.32	A	0.39
rs2470144	CYP19A1	1.05	0.84	1.31	6.58E-01	A	0.10	G	0.48
rs680055	CYP3A43	0.92	0.62	1.36	6.58E-01	C	0.32	C	0.05
rs3020411	ESR1	1.05	0.84	1.31	6.59E-01	A	0.40	G	0.33
rs189037	ATM	1.05	0.85	1.29	6.59E-01	A	0.27	G	0.44
rs2057768	IL4R	0.95	0.75	1.20	6.60E-01	A	0.27	A	0.30
rs2301870	LPO	1.07	0.79	1.44	6.60E-01	T	0.24	T	0.13
rs752760	CYP19A1	1.05	0.84	1.30	6.60E-01	C	0.12	T	0.44
rs11862958	TNFRSF17	0.95	0.76	1.19	6.61E-01	T	0.13	T	0.35

rs2107356	IL4R	1.05	0.85	1.30	6.61E-01	A	0.22	A	0.40
rs877518	ID3	1.09	0.75	1.58	6.62E-01	A	0.24	A	0.07
rs567754	BHMT	1.05	0.83	1.33	6.62E-01	T	0.07	T	0.34
rs6637	GSTZ1	0.95	0.75	1.20	6.62E-01	G	0.14	G	0.40
rs2860840	CYP2C18	0.95	0.75	1.20	6.63E-01	T	0.08	T	0.35
rs1800331	FANCA	1.10	0.73	1.65	6.63E-01	T	0.03	T	0.08
rs230521	NFKB1	1.05	0.84	1.31	6.64E-01	G	0.42	G	0.40
rs4803418	CYP2B6	0.95	0.75	1.21	6.64E-01	G	0.10	G	0.33
rs915907	CYP2E1	1.06	0.81	1.39	6.64E-01	A	0.16	A	0.17
rs2275566	MTR	0.95	0.76	1.19	6.65E-01	C	0.10	C	0.33
rs2228224	GLI1	1.05	0.84	1.31	6.65E-01	A	0.23	G	0.41
rs2279238	NR1H3	1.06	0.82	1.37	6.66E-01	A	0.35	A	0.18
rs10475	ATF3	1.06	0.82	1.37	6.67E-01	T	0.23	T	0.23
rs1065780	IGFBP1	1.05	0.85	1.30	6.67E-01	A	0.43	A	0.40
rs3176879	VCAM1	0.90	0.57	1.44	6.68E-01	G	0.29	G	0.03
rs442332	RUNDC2A	1.08	0.76	1.54	6.68E-01	C	0.26	C	0.07
rs2275008	OSGEP	0.95	0.76	1.19	6.68E-01	G	0.34	G	0.30
rs228832	NFATC2	1.05	0.84	1.32	6.68E-01	C	0.40	T	0.26
rs11632547	CYP1A1	1.11	0.68	1.82	6.68E-01	A	0.10	A	0.04
rs8190955	GSR	1.17	0.56	2.44	6.69E-01	T	0.08	T	0.00
rs2236579	ITGA8	1.06	0.80	1.42	6.70E-01	C	0.06	C	0.17
rs11229545	ZFP91	1.06	0.82	1.36	6.70E-01	G	0.15	G	0.24
rs698708	KDSR	1.05	0.84	1.32	6.70E-01	G	0.40	G	0.27
rs2228083	ALAD	1.08	0.75	1.55	6.70E-01	T	0.11	T	0.09
rs2286007	WNK1	1.10	0.72	1.66	6.70E-01	T	0.01	T	0.06
rs3217773	CCNA2	0.95	0.75	1.20	6.71E-01	C	0.16	C	0.32
rs939336	ABCC5	0.96	0.77	1.18	6.71E-01	A	0.25	A	0.42
rs729940	CHGA	1.07	0.79	1.44	6.72E-01	T	0.05	T	0.18
rs1413227	DPYD	1.05	0.84	1.32	6.72E-01	A	0.09	A	0.33
rs2242578	GLI1	1.05	0.85	1.30	6.73E-01	C	0.48	G	0.35
rs2111699	GSTZ1	0.95	0.76	1.19	6.73E-01	G	0.28	G	0.31
rs1132776	ABCC5	0.96	0.78	1.18	6.73E-01	T	0.26	T	0.43
rs551754	ABCB11	1.05	0.85	1.29	6.74E-01	A	0.26	G	0.45
rs2927922	PDSS1	0.95	0.76	1.20	6.74E-01	T	0.27	T	0.38
rs878201	Intergenic	1.05	0.83	1.32	6.74E-01	A	0.45	A	0.28
rs246214	ABCC1	0.94	0.69	1.27	6.74E-01	T	0.09	T	0.15
rs6540964	FRAP1	0.95	0.74	1.22	6.75E-01	T	0.18	C	0.26
rs11632814	CYP1A2	1.11	0.69	1.79	6.75E-01	A	0.11	A	0.04
rs2069522	CYP1A2	1.11	0.69	1.79	6.75E-01	C	0.11	C	0.04
rs9282787	MTRR	0.94	0.71	1.25	6.76E-01	C	0.11	C	0.20
rs4883263	CD163	1.08	0.75	1.57	6.76E-01	T	0.39	T	0.04
rs17342647	CYP3A43	1.08	0.76	1.53	6.76E-01	T	0.03	T	0.10
rs828052	DPYD	0.96	0.77	1.18	6.76E-01	T	0.16	T	0.45
rs1034809	PON2	1.05	0.84	1.31	6.76E-01	A	0.22	A	0.27
rs1065341	CCL5	0.91	0.57	1.44	6.76E-01	G	0.22	G	0.04
rs2069812	IL5	0.95	0.76	1.20	6.77E-01	C	0.18	T	0.30
rs1800590	LPL	1.09	0.72	1.65	6.78E-01	G	0.38	G	0.02
rs4150416	ERCC3	0.95	0.76	1.20	6.78E-01	G	0.43	G	0.33
rs2291075	SLCO1B1	0.96	0.77	1.18	6.78E-01	C	0.44	T	0.39
rs9954562	NFATC1	0.96	0.77	1.18	6.78E-01	T	0.38	T	0.38

rs10846748	SCARB1	1.05	0.84	1.30	6.78E-01	T	0.45	T	0.35
rs459552	APC	0.94	0.72	1.24	6.79E-01	A	0.05	A	0.23
rs1801157	CXCL12	1.06	0.80	1.41	6.80E-01	A	0.06	A	0.19
rs1047840	EXO1	1.05	0.84	1.29	6.81E-01	A	0.48	A	0.37
rs1045020	SLC22A5	1.07	0.77	1.49	6.81E-01	T	0.03	T	0.14
rs1413233	DPYD	0.78	0.23	2.59	6.81E-01	C	0.07	C	0.00
rs2856585	ABCC6	0.90	0.53	1.52	6.82E-01	A	0.11	A	0.07
rs8187710	ABCC2	0.91	0.59	1.42	6.83E-01	A	0.17	A	0.05
rs497692	ABCB11	0.96	0.78	1.18	6.83E-01	G	0.27	A	0.45
rs2071336	TNFRSF17	0.89	0.51	1.55	6.83E-01	T	0.08	T	0.03
rs753381	PLCG1	0.95	0.76	1.20	6.83E-01	A	0.07	A	0.44
rs3172469	BCL6	1.05	0.83	1.32	6.83E-01	C	0.42	C	0.26
rs478333	ABCB11	0.96	0.78	1.18	6.84E-01	T	0.26	C	0.45
rs930508	MBL2	1.06	0.81	1.37	6.84E-01	G	0.35	G	0.19
rs215073	ABCC1	0.92	0.60	1.40	6.84E-01	A	0.07	A	0.07
rs3218634	POLQ	1.09	0.72	1.64	6.85E-01	G	0.18	G	0.06
rs17273563	BLM	1.06	0.81	1.39	6.85E-01	A	0.14	A	0.18
rs12114000	CYP3A4	1.14	0.60	2.19	6.85E-01	A	0.18	A	0.00
rs10509681	CYP2C8	1.08	0.74	1.57	6.85E-01	C	0.02	C	0.10
rs2464196	HNF1A	1.05	0.83	1.33	6.86E-01	T	0.14	T	0.30
rs693	APOB	1.05	0.84	1.30	6.86E-01	T	0.24	T	0.48
rs7604639	MERTK	1.04	0.85	1.29	6.88E-01	G	0.36	G	0.39
rs3093930	PARP2	1.05	0.83	1.32	6.88E-01	C	0.33	T	0.33
rs2227973	RAG1	1.07	0.78	1.46	6.89E-01	G	0.13	G	0.11
rs6888011	ADRB2	0.95	0.76	1.20	6.89E-01	C	0.39	C	0.34
rs2286233	PON2	0.94	0.69	1.27	6.89E-01	T	0.25	T	0.13
rs3093816	CCNH	1.05	0.84	1.30	6.91E-01	C	0.25	C	0.41
rs3750050	PTPN12	1.05	0.82	1.36	6.91E-01	G	0.24	G	0.19
rs2074086	ABCC1	1.05	0.84	1.31	6.91E-01	T	0.34	C	0.32
rs12373018	TRAP1	1.06	0.80	1.41	6.92E-01	C	0.03	C	0.17
rs930507	MBL2	1.05	0.81	1.37	6.92E-01	G	0.34	G	0.17
rs932477	ESR1	0.94	0.67	1.30	6.92E-01	A	0.19	A	0.11
rs4526098	RAD50	0.88	0.47	1.65	6.94E-01	G	0.25	G	0.01
rs9403723	SIM1	0.96	0.77	1.19	6.95E-01	G	0.24	G	0.36
rs4646491	CYP4B1	1.06	0.78	1.45	6.96E-01	T	0.06	T	0.15
rs905594	ATF6	0.96	0.77	1.19	6.96E-01	C	0.14	T	0.38
rs40401	IL3	1.05	0.83	1.32	6.97E-01	C	0.45	T	0.24
rs3778082	ESR1	0.94	0.70	1.26	6.97E-01	A	0.43	A	0.12
rs2070682	SERPINE1	0.96	0.77	1.19	6.98E-01	C	0.49	C	0.42
rs2069824	IL6	0.93	0.63	1.36	6.98E-01	C	0.12	C	0.08
rs1802059	MTRR	1.04	0.84	1.30	6.98E-01	A	0.28	A	0.36
rs1760210	DPYD	0.95	0.73	1.24	6.98E-01	C	0.19	C	0.18
rs2243270	IL4	1.05	0.82	1.34	7.00E-01	A	0.34	G	0.19
rs3136748	POLB	1.08	0.73	1.59	7.00E-01	T	0.29	T	0.04
rs246230	ABCC1	1.05	0.80	1.38	7.00E-01	T	0.34	T	0.14
rs610611	MRE11A	0.95	0.75	1.21	7.01E-01	A	0.26	A	0.31
rs480562	ABCB11	0.96	0.78	1.19	7.01E-01	T	0.44	A	0.44
rs11539762	MYEOV	0.93	0.66	1.32	7.02E-01	A	0.11	A	0.11
rs4149180	SLC22A8	1.09	0.71	1.66	7.02E-01	G	0.46	A	0.03
rs2291439	RAD54B	0.96	0.77	1.19	7.02E-01	G	0.36	G	0.37

rs11700112	PAK7	1.07	0.77	1.48	7.02E-01	G	0.07	G	0.11
rs3788409	XBP1	1.04	0.84	1.29	7.03E-01	T	0.47	G	0.32
rs4646315	COMT	1.06	0.80	1.40	7.03E-01	C	0.12	C	0.18
rs16963927	CCL5	0.91	0.57	1.46	7.03E-01	G	0.21	G	0.04
rs35592	ABCC1	0.96	0.76	1.21	7.04E-01	T	0.49	C	0.23
rs3824874	MTMR2	1.05	0.83	1.33	7.05E-01	G	0.13	G	0.37
rs882709	SETX	1.06	0.77	1.46	7.05E-01	G	0.23	G	0.08
rs215067	ABCC1	1.09	0.70	1.68	7.06E-01	G	0.02	G	0.06
rs2687074	CYP3A7	0.88	0.45	1.71	7.06E-01	C	0.21	C	0.00
rs230533	NFKB1	1.05	0.83	1.32	7.06E-01	T	0.20	T	0.33
rs2066534	FMO3	0.96	0.77	1.20	7.07E-01	G	0.22	G	0.23
rs2020924	PLAT	0.93	0.66	1.33	7.07E-01	C	0.02	C	0.13
rs8353	KLHL22	0.95	0.73	1.24	7.08E-01	T	0.04	T	0.23
rs10515114	CARTPT	1.06	0.78	1.45	7.08E-01	C	0.22	C	0.10
rs2267130	CHEK2	0.96	0.78	1.19	7.09E-01	C	0.09	C	0.46
rs3176260	FGF17	1.07	0.76	1.51	7.09E-01	T	0.03	T	0.12
rs2241766	ADIPOQ	0.94	0.66	1.33	7.09E-01	G	0.04	G	0.12
rs2151846	ABCA4	0.96	0.78	1.19	7.10E-01	C	0.40	C	0.40
rs16880254	TPMT	1.09	0.68	1.75	7.10E-01	G	0.07	G	0.05
rs2097461	XBP1	1.04	0.84	1.28	7.10E-01	T	0.48	C	0.32
rs351855	FGFR4	0.95	0.75	1.22	7.10E-01	T	0.12	T	0.34
rs1062033	CYP19A1	1.04	0.84	1.30	7.10E-01	C	0.14	C	0.46
rs1051740	EPHX1	1.04	0.83	1.32	7.10E-01	C	0.18	C	0.33
rs1800451	MBL2	1.08	0.72	1.62	7.11E-01	A	0.27	A	0.02
rs1861887	GSTZ1	1.05	0.81	1.37	7.11E-01	T	0.13	T	0.19
rs1424482	ALDH1A1	0.96	0.77	1.20	7.11E-01	T	0.33	C	0.35
rs2953983	POLB	0.94	0.68	1.30	7.12E-01	T	0.36	C	0.08
rs2271922	MEIS2	0.92	0.59	1.43	7.12E-01	C	0.30	C	0.03
rs169758	TPTE	1.09	0.70	1.69	7.12E-01	A	0.26	A	0.05
rs1805386	LIG4	1.05	0.80	1.40	7.12E-01	C	0.09	C	0.18
rs854548	PPP1R9A	1.04	0.83	1.32	7.12E-01	A	0.34	A	0.27
rs2375744	HNMT	1.05	0.80	1.38	7.12E-01	A	0.05	A	0.19
rs747659	PARP1	0.95	0.72	1.25	7.14E-01	T	0.36	T	0.18
rs3218619	FAS	1.16	0.53	2.55	7.14E-01	A	0.11	0	0.00
rs2020865	FMO2	1.07	0.74	1.54	7.14E-01	G	0.27	G	0.05
rs6763816	TNFSF10	0.80	0.23	2.70	7.15E-01	T	0.05	0	0.00
rs1061622	TNFRSF1B	1.04	0.83	1.32	7.15E-01	G	0.21	G	0.24
rs10857971	PPM1J	0.83	0.32	2.20	7.16E-01	C	0.09	C	0.00
rs518276	MRE11A	1.04	0.85	1.28	7.17E-01	A	0.46	A	0.40
rs611251	PPP1R15A	0.95	0.71	1.27	7.17E-01	G	0.45	G	0.13
rs8305	POLI	0.95	0.74	1.23	7.17E-01	G	0.06	G	0.29
rs5030125	WT1	1.15	0.53	2.49	7.18E-01	A	0.09	A	0.00
rs503931	ABCB11	0.96	0.78	1.19	7.18E-01	G	0.26	T	0.45
rs532411	POLQ	1.08	0.72	1.63	7.18E-01	T	0.18	T	0.06
rs11995670	ADRB3	1.04	0.83	1.31	7.19E-01	G	0.18	G	0.35
rs35587	ABCC1	0.96	0.76	1.21	7.19E-01	T	0.38	C	0.30
rs1052369	ANKRD29	1.04	0.84	1.28	7.20E-01	T	0.15	A	0.41
rs828057	DPYD	0.95	0.73	1.24	7.21E-01	T	0.19	T	0.18
rs1271079	MRE11A	1.04	0.82	1.32	7.21E-01	G	0.17	G	0.28
rs1867351	SLC22A1	1.05	0.82	1.33	7.21E-01	G	0.31	G	0.22

rs3766871	RYR2	1.09	0.69	1.71	7.22E-01	A	0.15	A	0.03
rs1615035	ANKRD29	0.96	0.78	1.18	7.22E-01	A	0.49	G	0.32
rs1805087	MTR	0.95	0.73	1.25	7.22E-01	G	0.22	G	0.20
rs2470893	CYP1A1	1.05	0.82	1.33	7.22E-01	A	0.06	A	0.30
rs2297595	DPYD	1.07	0.74	1.53	7.23E-01	C	0.03	C	0.08
rs1051303	LTBP4	1.04	0.84	1.29	7.24E-01	A	0.46	G	0.42
rs1801020	F12	0.96	0.76	1.21	7.24E-01	T	0.44	T	0.28
rs2227999	XPC	0.92	0.59	1.45	7.24E-01	A	0.02	A	0.06
rs1149901	FLJ45983	0.96	0.75	1.22	7.24E-01	T	0.11	T	0.25
rs4986993	NAT1	0.96	0.75	1.22	7.24E-01	G	0.49	T	0.25
rs1137100	LEPR	1.04	0.82	1.32	7.25E-01	G	0.14	G	0.29
UGT2B7_1c	UGT2B7	1.06	0.77	1.46	7.25E-01	G	0.16	G	0.12
rs1800790	FGB	1.05	0.80	1.38	7.26E-01	A	0.04	A	0.20
rs25406	PCNA	0.96	0.78	1.19	7.27E-01	T	0.42	T	0.40
rs638456	DPYD	1.04	0.84	1.28	7.27E-01	C	0.42	C	0.38
rs10082466	MBL2	0.96	0.76	1.21	7.28E-01	G	0.43	G	0.24
rs2955617	SHBG	0.96	0.77	1.20	7.28E-01	T	0.27	G	0.34
rs7175052	IGF1R	1.04	0.82	1.34	7.28E-01	A	0.29	A	0.21
rs2120132	MBL2	0.96	0.76	1.21	7.28E-01	C	0.43	C	0.24
rs1219663	ACBD3	0.96	0.75	1.22	7.28E-01	C	0.25	C	0.22
rs3181217	IL12B	1.04	0.82	1.32	7.29E-01	A	0.31	A	0.23
rs1503185	PTPRJ	0.95	0.70	1.28	7.30E-01	T	0.28	T	0.15
rs6512087	CIB3	0.96	0.74	1.23	7.30E-01	C	0.27	C	0.19
rs1138358	BCL2A1	1.04	0.83	1.29	7.30E-01	T	0.42	G	0.29
rs13181	ERCC2	0.96	0.77	1.20	7.31E-01	G	0.22	G	0.36
rs11572076	CYP2C8	0.86	0.37	2.01	7.31E-01	A	0.15	A	0.00
rs1800391	WRN	1.08	0.70	1.65	7.31E-01	A	0.01	A	0.08
rs3743591	TNFRSF17	1.07	0.72	1.60	7.31E-01	G	0.24	G	0.05
rs31473	CSF2	1.04	0.82	1.32	7.32E-01	A	0.43	T	0.24
rs2017662	TNFRSF17	1.07	0.72	1.60	7.32E-01	T	0.24	T	0.05
rs2706377	RAD50	0.90	0.49	1.66	7.33E-01	G	0.24	G	0.01
rs1920313	SLC15A2	0.82	0.26	2.59	7.33E-01	A	0.07	0	0.00
rs275652	AGTR1	0.95	0.73	1.25	7.33E-01	C	0.27	C	0.17
rs246228	ABCC1	0.96	0.76	1.21	7.33E-01	A	0.38	C	0.30
rs2239995	ABCC1	1.05	0.79	1.39	7.33E-01	A	0.10	A	0.19
rs848291	FANCL	0.96	0.76	1.21	7.33E-01	T	0.12	T	0.38
rs1800787	FGB	1.05	0.80	1.37	7.34E-01	T	0.10	T	0.20
rs1760209	DPYD	0.96	0.74	1.24	7.34E-01	T	0.19	T	0.18
rs5974	F11	1.05	0.79	1.39	7.35E-01	G	0.21	G	0.15
rs1496499	IGFBP3	0.96	0.78	1.19	7.35E-01	T	0.35	G	0.48
rs949037	BCL2	0.96	0.77	1.20	7.35E-01	T	0.49	T	0.42
rs8058694	ABCC6	0.96	0.78	1.20	7.35E-01	T	0.36	G	0.50
rs1396080	CCNA2	0.96	0.78	1.20	7.35E-01	A	0.38	C	0.34
rs2303078	HMMR	0.91	0.54	1.54	7.36E-01	0	0.00	A	0.06
rs2032583	ABCB1	1.06	0.77	1.44	7.36E-01	C	0.15	C	0.11
rs2066870	FGG	1.14	0.54	2.37	7.36E-01	C	0.08	C	0.00
rs10735510	ATF3	1.04	0.84	1.28	7.36E-01	C	0.25	C	0.47
rs1801426	BRCA2	1.13	0.56	2.25	7.36E-01	G	0.11	G	0.00
rs10501815	MRE11A	0.94	0.63	1.38	7.36E-01	A	0.05	A	0.10
rs2020955	ERCC4	0.88	0.41	1.89	7.36E-01	C	0.16	C	0.00

rs1050909	FBXO25	0.96	0.77	1.21	7.37E-01	G	0.41	T	0.27
rs1183768	SETX	1.04	0.81	1.34	7.37E-01	T	0.37	C	0.19
rs12418	CHST3	1.04	0.84	1.28	7.38E-01	A	0.28	A	0.46
rs2522395	RAD50	0.90	0.49	1.66	7.39E-01	G	0.24	G	0.01
rs248805	SRD5A1	1.04	0.84	1.27	7.39E-01	A	0.31	A	0.49
rs12828016	WNK1	1.04	0.83	1.30	7.40E-01	T	0.47	T	0.37
rs135539	PPARA	1.04	0.84	1.28	7.41E-01	T	0.35	G	0.43
rs1060463	CYP4F11	1.03	0.85	1.27	7.41E-01	A	0.48	G	0.43
rs1208	NAT2	0.97	0.78	1.19	7.41E-01	G	0.34	G	0.41
rs2033178	IGF1	0.93	0.59	1.47	7.42E-01	T	0.03	T	0.07
rs6463524	PMS2	0.96	0.75	1.23	7.43E-01	G	0.16	G	0.19
rs2269352	UGT1A8	0.95	0.68	1.32	7.43E-01	C	0.13	C	0.21
rs592943	MRE11A	0.96	0.76	1.22	7.44E-01	T	0.25	T	0.31
rs1805129	CHEK2	0.92	0.54	1.55	7.45E-01	G	0.08	G	0.03
rs9997	KLHL22	1.04	0.83	1.30	7.45E-01	C	0.49	C	0.32
rs2020902	CASP9	0.95	0.69	1.30	7.46E-01	C	0.09	C	0.14
rs17882248	IL5RA	0.96	0.77	1.20	7.46E-01	G	0.38	G	0.35
rs2274419	MUSK	1.05	0.78	1.41	7.47E-01	T	0.05	T	0.14
rs1413239	DPYD	0.96	0.77	1.20	7.47E-01	C	0.47	T	0.32
rs2320165	CART	0.96	0.78	1.20	7.47E-01	C	0.18	C	0.48
rs2426157	PTPN1	0.96	0.76	1.21	7.48E-01	G	0.18	G	0.29
rs3730477	POLL	1.05	0.79	1.38	7.48E-01	T	0.06	T	0.19
rs735943	EXO1	1.03	0.84	1.27	7.48E-01	T	0.38	T	0.42
rs2066479	HSD17B3	1.07	0.70	1.64	7.48E-01	A	0.08	A	0.06
rs4342522	SHFM1	1.04	0.82	1.33	7.49E-01	G	0.46	A	0.25
rs1008563	IL8RA	0.97	0.78	1.20	7.49E-01	T	0.47	T	0.42
rs880303	GJA9	0.97	0.78	1.20	7.50E-01	T	0.20	T	0.41
rs2288831	IL12B	1.04	0.82	1.31	7.50E-01	C	0.31	C	0.23
rs2297809	CYP4B1	1.05	0.78	1.42	7.50E-01	A	0.14	A	0.15
rs3808600	ZHX2	1.04	0.81	1.34	7.51E-01	T	0.07	T	0.33
rs389480	BLM	0.97	0.78	1.19	7.52E-01	T	0.47	T	0.47
rs2234900	IL4R	0.96	0.73	1.26	7.53E-01	T	0.46	C	0.14
rs12717	PSMB1	1.03	0.84	1.28	7.53E-01	G	0.32	G	0.42
rs7804387	MAD1L1	1.06	0.72	1.56	7.54E-01	A	0.31	A	0.07
rs246240	ABCC1	0.95	0.70	1.29	7.54E-01	G	0.10	G	0.15
rs552926	DPYD	1.03	0.84	1.27	7.54E-01	G	0.43	G	0.38
rs3765070	CYP4F11	1.03	0.84	1.26	7.55E-01	C	0.48	T	0.43
rs2434470	ALKBH3	0.96	0.74	1.25	7.55E-01	G	0.08	G	0.25
rs17021877	IKBKE	0.88	0.38	2.02	7.55E-01	A	0.06	A	0.01
rs2847609	TYMS	0.96	0.77	1.21	7.55E-01	A	0.42	G	0.32
rs338599	CYP2S1	0.93	0.61	1.44	7.56E-01	C	0.14	C	0.05
rs11569913	TNFRSF8	1.07	0.68	1.69	7.56E-01	G	0.18	G	0.04
rs13330634	TNFRSF17	1.07	0.69	1.67	7.56E-01	A	0.04	A	0.07
rs215059	ABCC1	1.05	0.78	1.41	7.56E-01	T	0.13	T	0.13
rs10520114	RAD50	1.04	0.80	1.36	7.56E-01	C	0.10	C	0.20
rs2070180	HCLS1	1.04	0.82	1.32	7.57E-01	A	0.15	A	0.26
rs533984	MRE11A	1.03	0.84	1.27	7.57E-01	G	0.37	A	0.40
rs2074085	ABCC1	0.95	0.70	1.30	7.58E-01	G	0.24	G	0.11
rs1046515	ADCK2	1.06	0.74	1.51	7.58E-01	T	0.15	T	0.09
rs1063857	VWF	0.97	0.78	1.20	7.59E-01	T	0.40	C	0.34

rs506008	GSTM4	1.05	0.78	1.40	7.59E-01	A	0.34	A	0.14
rs17129772	IL12RB2	1.17	0.44	3.10	7.59E-01	G	0.08	0	0.00
rs4646091	CASP9	0.96	0.74	1.24	7.60E-01	G	0.40	G	0.21
rs157580	TOMM40	1.04	0.82	1.30	7.60E-01	G	0.14	G	0.38
rs914959	DPYD	0.97	0.78	1.20	7.60E-01	A	0.08	A	0.37
rs1800935	MSH6	1.04	0.81	1.32	7.63E-01	C	0.15	C	0.29
rs4680	COMT	1.04	0.83	1.29	7.63E-01	A	0.24	A	0.50
rs2070959	UGT1A10	0.96	0.76	1.22	7.63E-01	G	0.20	G	0.31
rs1131620	LTBP4	1.03	0.84	1.27	7.63E-01	A	0.46	G	0.43
rs8187858	ABCC1	0.94	0.64	1.39	7.64E-01	T	0.03	T	0.09
rs2274407	ABCC4	0.94	0.64	1.38	7.64E-01	A	0.17	A	0.08
rs10018260	Intergenic	0.96	0.73	1.26	7.65E-01	T	0.15	T	0.22
rs1056503	XRCC4	1.04	0.80	1.35	7.65E-01	G	0.43	G	0.16
rs1805377	XRCC4	1.04	0.80	1.35	7.65E-01	A	0.43	A	0.16
rs849526	NRP2	1.03	0.83	1.28	7.65E-01	G	0.18	A	0.47
rs3733549	BMP3	1.05	0.74	1.50	7.65E-01	A	0.09	A	0.07
rs541463	PGR	0.95	0.70	1.31	7.66E-01	A	0.04	A	0.16
rs683369	SLC22A1	0.96	0.74	1.25	7.66E-01	G	0.04	G	0.23
rs2974938	PPP1R3A	0.89	0.40	1.95	7.66E-01	T	0.11	T	0.00
rs903880	ABCC1	1.04	0.81	1.33	7.67E-01	C	0.24	A	0.21
rs603965	CCND1	1.03	0.84	1.27	7.67E-01	A	0.24	A	0.49
rs9436299	LEPR	1.04	0.82	1.30	7.67E-01	C	0.14	C	0.34
rs17012064	PTPN13	0.84	0.25	2.74	7.68E-01	C	0.06	C	0.00
rs348463	ALDH1A1	1.04	0.81	1.32	7.69E-01	C	0.31	C	0.28
rs246220	ABCC1	0.96	0.73	1.27	7.69E-01	G	0.33	G	0.14
rs2307424	NR1I3	1.04	0.82	1.30	7.69E-01	T	0.13	T	0.34
rs1801243	ATP7B	0.97	0.78	1.20	7.70E-01	G	0.22	G	0.50
rs7739752	PPARD	0.95	0.68	1.33	7.71E-01	C	0.39	T	0.07
rs2227538	IL8	0.90	0.45	1.79	7.71E-01	T	0.22	T	0.00
rs679620	MMP3	0.97	0.78	1.20	7.72E-01	A	0.40	G	0.49
rs1801406	BRCA2	1.04	0.82	1.31	7.72E-01	G	0.29	G	0.29
rs2472304	CYP1A2	1.03	0.82	1.30	7.72E-01	A	0.13	G	0.41
rs3204141	ZHX2	1.04	0.81	1.33	7.73E-01	A	0.07	A	0.33
rs3918226	NOS3	1.06	0.72	1.55	7.73E-01	T	0.01	T	0.08
rs3733182	STK32B	0.96	0.71	1.28	7.73E-01	C	0.18	C	0.15
rs1042194	CYP2C18	0.96	0.70	1.30	7.74E-01	T	0.18	T	0.14
rs1144945	MDM2	0.90	0.44	1.84	7.74E-01	T	0.05	T	0.01
rs798757	TACC3	0.96	0.72	1.27	7.74E-01	G	0.22	G	0.17
rs4150514	ERCC3	0.96	0.74	1.25	7.74E-01	G	0.12	G	0.21
rs1805355	MSH3	1.05	0.75	1.46	7.76E-01	A	0.18	A	0.09
rs735320	CYP8B1	1.04	0.80	1.36	7.76E-01	A	0.16	A	0.16
rs2074087	ABCC1	1.04	0.78	1.39	7.76E-01	C	0.14	C	0.17
rs1046428	GSTZ1	1.04	0.79	1.37	7.76E-01	T	0.10	T	0.19
rs5297	CYP11B1	1.05	0.74	1.50	7.77E-01	C	0.27	C	0.08
rs1017186	GSTZ1	1.04	0.79	1.37	7.77E-01	G	0.10	G	0.20
rs7496	GSTA4	1.04	0.81	1.33	7.78E-01	A	0.25	A	0.14
rs751019	PTK2B	1.03	0.83	1.28	7.78E-01	C	0.31	C	0.44
rs9286998	ACBD3	0.97	0.79	1.20	7.79E-01	C	0.49	C	0.44
rs1934954	CYP2C9	0.93	0.58	1.50	7.80E-01	G	0.01	G	0.07
rs215106	ABCC1	1.05	0.77	1.43	7.80E-01	G	0.07	G	0.12

rs2069832	IL6	1.03	0.83	1.28	7.80E-01	A	0.08	A	0.37
rs3136027	LIG3	1.06	0.69	1.65	7.80E-01	T	0.00	T	0.07
rs2144908	HNF4A	0.96	0.74	1.25	7.80E-01	A	0.12	A	0.21
rs6136	SELP	1.05	0.73	1.51	7.80E-01	C	0.00	C	0.10
rs17567	EPS15	1.04	0.81	1.32	7.80E-01	C	0.50	C	0.22
rs4775936	CYP19A1	1.03	0.83	1.28	7.80E-01	T	0.15	T	0.47
rs2306134	PPP4R1	1.04	0.79	1.37	7.80E-01	T	0.18	T	0.18
rs1399291	DPYD	0.97	0.79	1.20	7.82E-01	T	0.28	C	0.49
rs1341163	CYP2C8	0.97	0.78	1.20	7.83E-01	A	0.25	A	0.42
rs1934985	CYP2C8	0.97	0.78	1.20	7.83E-01	G	0.25	G	0.42
rs2275620	CYP2C8	0.97	0.78	1.20	7.83E-01	T	0.25	T	0.42
rs6021275	NFATC2	0.97	0.78	1.20	7.85E-01	G	0.40	G	0.42
rs2239359	FANCA	1.03	0.84	1.27	7.85E-01	C	0.29	T	0.42
rs2066457	PMS1	1.18	0.36	3.92	7.86E-01	C	0.05	C	0.00
rs3789452	ABCA4	1.03	0.82	1.30	7.86E-01	A	0.07	A	0.33
rs215050	ABCC1	1.04	0.79	1.36	7.86E-01	A	0.08	A	0.16
rs2227930	ATR	0.97	0.78	1.20	7.87E-01	T	0.23	T	0.44
rs12714192	APOB	1.12	0.49	2.55	7.87E-01	A	0.10	A	0.00
rs8064946	TP53	1.04	0.77	1.40	7.87E-01	G	0.27	C	0.13
rs3766934	EPHX1	1.05	0.73	1.52	7.88E-01	T	0.05	T	0.10
rs4148301	UGT2A1	0.95	0.65	1.38	7.88E-01	A	0.06	A	0.09
rs3219484	MUTYH	1.06	0.68	1.65	7.88E-01	A	0.01	A	0.06
rs1629816	SEC13L1	0.97	0.79	1.20	7.89E-01	A	0.44	A	0.42
rs1057335	SERPINF2	1.04	0.80	1.35	7.89E-01	A	0.23	A	0.20
rs17037390	MTHFR	1.04	0.79	1.36	7.90E-01	A	0.22	A	0.16
rs2256974	LST1	0.96	0.74	1.26	7.90E-01	T	0.33	T	0.21
rs7578587	ABCB11	1.10	0.54	2.25	7.90E-01	C	0.16	0	0.00
rs12009	HSPA5	0.97	0.79	1.19	7.90E-01	T	0.48	C	0.46
rs1800796	IL6	1.05	0.73	1.51	7.90E-01	C	0.11	C	0.09
rs6457815	PPARD	1.05	0.73	1.51	7.90E-01	C	0.42	C	0.04
rs4129472	GHR	1.04	0.78	1.40	7.91E-01	G	0.04	G	0.19
rs1043641	ACBD3	0.96	0.72	1.28	7.91E-01	A	0.07	A	0.16
rs2227914	DMC1	0.89	0.39	2.07	7.92E-01	G	0.14	G	0.00
rs16147	NPY	1.03	0.83	1.28	7.92E-01	G	0.38	A	0.49
rs925585	IGF1R	1.04	0.78	1.38	7.92E-01	C	0.16	C	0.15
rs1063311	MAPK1	0.97	0.77	1.22	7.92E-01	A	0.36	A	0.40
rs4725387	FASTK	0.95	0.63	1.41	7.92E-01	G	0.03	G	0.10
rs1042714	ADRB2	1.03	0.83	1.28	7.93E-01	G	0.22	G	0.41
rs10824792	MBL2	0.97	0.79	1.20	7.93E-01	T	0.20	C	0.41
rs5769	TBXAS1	0.88	0.34	2.28	7.94E-01	G	0.05	0	0.00
rs4148944	CHST3	1.05	0.75	1.46	7.95E-01	A	0.31	A	0.10
rs10380	MTRR	1.05	0.74	1.48	7.95E-01	T	0.29	T	0.09
rs4917636	CYP2C9	1.05	0.74	1.48	7.95E-01	G	0.02	G	0.12
rs6962039	SLC13A1	1.03	0.81	1.31	7.95E-01	A	0.33	A	0.27
rs2277448	ALG11	0.97	0.78	1.21	7.95E-01	T	0.33	G	0.31
rs743572	CYP17A1	1.03	0.83	1.27	7.96E-01	G	0.38	G	0.42
rs1729409	APOA5	1.03	0.83	1.28	7.97E-01	C	0.18	T	0.47
rs9890721	MYCBPAP	1.03	0.82	1.29	7.97E-01	T	0.20	C	0.48
rs1934962	CYP2C9	0.91	0.43	1.92	7.98E-01	T	0.15	T	0.00
rs5960	F10	0.96	0.73	1.27	7.98E-01	C	0.49	C	0.16

rs2976436	NEFL	1.03	0.83	1.28	7.99E-01	C	0.29	T	0.35
rs16118	NPY	1.03	0.83	1.27	7.99E-01	C	0.44	C	0.40
rs652438	MMP12	0.94	0.59	1.50	7.99E-01	G	0.18	G	0.04
rs982424	MTTP	1.05	0.73	1.51	8.00E-01	C	0.25	C	0.07
rs11770116	IMPDH1	1.03	0.82	1.29	8.00E-01	T	0.31	T	0.31
rs2392221	VCAM1	0.96	0.71	1.31	8.01E-01	T	0.06	T	0.16
rs348481	ALDH1A1	1.03	0.81	1.32	8.01E-01	C	0.31	C	0.22
rs186997	ALDH1A1	0.94	0.61	1.47	8.01E-01	G	0.25	G	0.03
rs3136820	APEX1	0.97	0.79	1.20	8.02E-01	G	0.37	G	0.48
rs12713675	APOB	0.90	0.39	2.06	8.02E-01	A	0.09	A	0.00
rs315952	IL1RN	1.03	0.81	1.31	8.02E-01	C	0.43	C	0.28
rs2665802	GH1	0.97	0.78	1.21	8.02E-01	T	0.14	T	0.41
rs2472680	NR1I2	1.07	0.65	1.75	8.02E-01	T	0.22	T	0.05
rs6131	SELP	0.97	0.75	1.25	8.03E-01	A	0.34	A	0.18
rs743535	CYP2E1	1.04	0.76	1.42	8.03E-01	T	0.17	T	0.10
rs10017302	UGT8	0.93	0.55	1.59	8.03E-01	G	0.18	G	0.02
rs2421047	IL12B	1.03	0.82	1.30	8.03E-01	A	0.31	A	0.23
rs20579	LIG1	0.96	0.72	1.30	8.03E-01	T	0.29	T	0.13
rs2267131	XBP1	1.04	0.74	1.47	8.04E-01	C	0.04	C	0.13
rs1757095	TNC	0.94	0.60	1.50	8.04E-01	T	0.11	T	0.06
rs1061302	NBN	0.97	0.78	1.21	8.05E-01	G	0.22	G	0.33
rs2104772	TNC	1.03	0.84	1.26	8.05E-01	A	0.44	T	0.44
rs2536512	SOD3	1.03	0.83	1.28	8.05E-01	A	0.21	G	0.38
rs2227928	ATR	0.97	0.79	1.21	8.05E-01	T	0.23	T	0.44
rs1272744	MRE11A	0.97	0.79	1.20	8.05E-01	C	0.47	C	0.39
rs1501299	ADIPOQ	1.03	0.81	1.30	8.06E-01	A	0.36	A	0.27
rs4459610	ACE	1.03	0.83	1.28	8.07E-01	A	0.41	A	0.46
rs6334	NTRK1	0.96	0.72	1.29	8.08E-01	A	0.14	A	0.21
rs3734354	SIM1	1.04	0.76	1.42	8.08E-01	A	0.03	A	0.14
rs2228309	FASN	0.97	0.78	1.22	8.08E-01	C	0.49	T	0.45
rs4253199	ERCC6	1.16	0.35	3.90	8.09E-01	T	0.06	0	0.00
rs35621	ABCC1	1.04	0.76	1.42	8.10E-01	T	0.12	T	0.11
rs1005230	VEGFA	1.03	0.83	1.27	8.10E-01	T	0.19	T	0.49
rs16859180	STK36	1.06	0.64	1.76	8.10E-01	T	0.02	T	0.06
rs1330286	ALDH1A1	1.03	0.82	1.29	8.10E-01	C	0.44	G	0.34
rs1788817	C18orf8	0.97	0.79	1.20	8.10E-01	G	0.50	G	0.49
rs11226	RAD52	0.97	0.78	1.21	8.10E-01	T	0.40	T	0.47
rs2518144	AICDA	0.97	0.79	1.20	8.11E-01	G	0.26	A	0.47
rs699947	VEGFA	1.03	0.83	1.26	8.11E-01	A	0.19	A	0.49
rs361525	TNF	1.06	0.67	1.65	8.11E-01	A	0.05	A	0.05
rs2071214	BIRC5	0.93	0.53	1.64	8.12E-01	G	0.01	G	0.05
rs4543	CYP11B2	1.04	0.73	1.49	8.12E-01	A	0.21	A	0.08
rs12720855	APOB	0.90	0.39	2.08	8.12E-01	C	0.09	C	0.00
rs3826705	POU2F2	0.96	0.67	1.36	8.13E-01	C	0.05	C	0.12
rs13332630	TNFRSF17	1.06	0.67	1.66	8.13E-01	C	0.04	C	0.07
rs701106	SCARB1	1.03	0.78	1.36	8.13E-01	A	0.25	A	0.17
rs6873545	GHR	0.97	0.77	1.22	8.14E-01	C	0.45	C	0.26
rs2000813	LIPG	0.97	0.76	1.24	8.14E-01	T	0.12	T	0.30
rs2687127	CYP3A7	1.09	0.51	2.33	8.14E-01	C	0.08	C	0.00
rs5186	AGTR1	0.97	0.76	1.24	8.14E-01	C	0.06	C	0.29

rs230532	NFKB1	1.03	0.81	1.30	8.15E-01	A	0.15	A	0.33
rs10516782	PTPN13	0.97	0.73	1.29	8.15E-01	G	0.03	G	0.17
rs1990277	ARVCF	0.97	0.77	1.23	8.16E-01	A	0.24	A	0.40
rs584589	NGFR	0.96	0.71	1.31	8.16E-01	G	0.14	G	0.14
rs121	OSBPL3	1.03	0.83	1.27	8.17E-01	A	0.26	G	0.48
rs246221	ABCC1	0.97	0.78	1.22	8.17E-01	T	0.39	C	0.30
rs11688	JUN	1.05	0.68	1.62	8.19E-01	A	0.19	A	0.05
rs3744644	SCARF1	1.06	0.63	1.81	8.19E-01	G	0.25	G	0.01
rs13926	TRAP1	1.03	0.82	1.28	8.19E-01	G	0.19	G	0.43
rs608452	MRE11A	1.11	0.46	2.65	8.19E-01	T	0.11	T	0.00
rs680	IGF2	1.03	0.81	1.30	8.20E-01	A	0.08	A	0.28
rs1105880	UGT1A10	1.03	0.82	1.28	8.20E-01	C	0.34	C	0.35
rs9332485	F5	1.14	0.37	3.54	8.20E-01	A	0.05	0	0.00
rs2332673	BCL2	0.95	0.61	1.47	8.20E-01	C	0.22	C	0.04
rs1801244	ATP7B	0.97	0.78	1.22	8.21E-01	C	0.27	C	0.48
rs31480	IL3	0.97	0.75	1.25	8.22E-01	T	0.15	T	0.23
rs2069833	IL6	1.03	0.82	1.28	8.23E-01	C	0.08	C	0.37
rs1799809	PROC	1.03	0.81	1.30	8.23E-01	A	0.33	G	0.41
rs2076169	PPARD	0.96	0.67	1.38	8.24E-01	C	0.02	C	0.10
rs2741045	UGT1A10	1.03	0.80	1.32	8.24E-01	T	0.08	T	0.28
rs2741046	UGT1A10	1.03	0.80	1.32	8.24E-01	C	0.08	C	0.28
rs216902	VWF	0.98	0.79	1.20	8.24E-01	A	0.33	A	0.40
rs1063742	TACC3	0.97	0.76	1.24	8.24E-01	T	0.15	T	0.26
rs230496	NFKB1	1.03	0.82	1.28	8.24E-01	G	0.41	G	0.40
rs10977171	PTPRD	0.94	0.57	1.57	8.25E-01	C	0.02	C	0.06
rs10407115	PPAP2C	1.02	0.83	1.26	8.26E-01	A	0.43	A	0.43
rs2232642	LIG4	1.09	0.52	2.28	8.26E-01	A	0.14	A	0.00
rs1566439	NLRC5	1.02	0.82	1.28	8.26E-01	G	0.25	G	0.40
rs2306283	SLCO1B1	1.02	0.82	1.28	8.26E-01	T	0.25	C	0.41
rs13428823	EFR3B	1.02	0.83	1.26	8.26E-01	G	0.49	G	0.38
rs2297322	SLC15A1	1.03	0.78	1.36	8.27E-01	T	0.30	T	0.14
rs3795837	ATF3	1.04	0.76	1.41	8.27E-01	C	0.19	C	0.12
rs828059	DPYD	0.97	0.75	1.26	8.27E-01	G	0.19	G	0.18
rs4244285	CYP2C19	0.97	0.71	1.31	8.28E-01	A	0.16	A	0.14
rs10018287	MGC48628	1.02	0.82	1.28	8.29E-01	T	0.43	T	0.32
rs1557044	CYP2C9	0.97	0.73	1.29	8.29E-01	C	0.16	C	0.18
rs2976437	NEFL	1.02	0.82	1.28	8.29E-01	A	0.29	G	0.35
rs9840993	MYLK	0.95	0.58	1.56	8.30E-01	G	0.33	G	0.01
rs1004588	DGKG	1.02	0.83	1.26	8.30E-01	G	0.43	C	0.47
rs348479	ALDH1A1	1.03	0.80	1.31	8.30E-01	G	0.32	G	0.21
rs4646316	COMT	0.97	0.75	1.26	8.31E-01	T	0.21	T	0.23
rs6003071	MCAT	0.98	0.79	1.21	8.33E-01	T	0.49	T	0.43
rs231775	CTLA4	0.98	0.79	1.21	8.33E-01	G	0.42	G	0.41
rs3763497	IGFBP1	1.03	0.81	1.29	8.33E-01	T	0.21	T	0.34
rs3732379	CX3CR1	0.97	0.76	1.25	8.33E-01	T	0.14	T	0.27
rs408820	GSTA4	0.95	0.60	1.51	8.34E-01	G	0.04	G	0.06
rs6941	XRCC5	0.96	0.69	1.35	8.35E-01	A	0.13	A	0.11
rs1051677	XRCC5	0.96	0.69	1.36	8.35E-01	C	0.13	C	0.11
rs2270565	UCP1	1.05	0.69	1.59	8.36E-01	A	0.01	A	0.08
rs2153629	CYP2C9	1.04	0.73	1.49	8.36E-01	G	0.02	G	0.11

rs2277119	CYP39A1	0.97	0.76	1.25	8.37E-01	A	0.27	A	0.23
rs7957203	SLCO1A2	0.98	0.78	1.22	8.37E-01	T	0.30	T	0.31
rs2243250	IL4	1.03	0.80	1.31	8.37E-01	C	0.34	T	0.19
rs215048	ABCC1	1.03	0.76	1.40	8.37E-01	A	0.06	A	0.15
rs2707466	WNT16	1.02	0.82	1.28	8.38E-01	G	0.18	A	0.44
rs4988515	IGFBP1	0.96	0.63	1.46	8.38E-01	T	0.19	T	0.05
rs3112831	ABCA4	1.02	0.82	1.28	8.39E-01	G	0.23	G	0.31
rs5982	F13A1	0.97	0.75	1.27	8.39E-01	T	0.13	T	0.21
rs9332100	CYP2C9	1.04	0.73	1.48	8.39E-01	T	0.02	T	0.11
rs6032	F5	0.97	0.76	1.26	8.39E-01	G	0.18	G	0.28
rs4774584	CYP19A1	1.02	0.83	1.26	8.39E-01	A	0.44	A	0.45
rs1395	SLC5A6	0.98	0.78	1.23	8.40E-01	A	0.26	G	0.31
rs2239815	XBP1	0.98	0.79	1.22	8.40E-01	T	0.31	C	0.32
rs8192284	IL6R	1.02	0.81	1.29	8.40E-01	C	0.14	C	0.40
rs348462	ALDH1A1	1.02	0.81	1.30	8.41E-01	G	0.46	C	0.30
rs12917	MGMT	1.03	0.76	1.40	8.41E-01	T	0.16	T	0.15
rs2140516	SLC13A1	1.02	0.82	1.28	8.41E-01	C	0.28	C	0.32
rs557806	PPP1R15A	0.97	0.72	1.31	8.42E-01	C	0.36	G	0.12
rs1888202	ALDH1A1	0.98	0.79	1.22	8.42E-01	G	0.19	G	0.50
rs10473282	GHR	0.98	0.78	1.23	8.42E-01	A	0.18	A	0.36
rs2279344	CYP2B6	1.02	0.81	1.30	8.43E-01	G	0.15	G	0.34
rs11572103	CYP2C8	0.93	0.44	1.97	8.43E-01	T	0.16	T	0.00
rs2252784	PTPRB	0.98	0.79	1.22	8.43E-01	G	0.31	A	0.42
rs3125001	NOTCH1	1.03	0.78	1.35	8.44E-01	C	0.33	T	0.39
rs16945474	PHKB	1.04	0.68	1.61	8.44E-01	G	0.11	G	0.04
rs3212227	IL12B	1.02	0.81	1.30	8.45E-01	C	0.32	C	0.23
rs2544794	SULT2B1	0.97	0.74	1.28	8.45E-01	A	0.24	A	0.16
rs215072	ABCC1	0.96	0.62	1.48	8.45E-01	T	0.07	T	0.06
rs4252596	ERBB2	1.03	0.74	1.44	8.46E-01	A	0.03	A	0.14
rs2039447	DPYD	0.98	0.78	1.22	8.46E-01	T	0.47	C	0.32
rs2706358	RAD50	0.94	0.51	1.75	8.46E-01	A	0.24	A	0.01
rs6163	CYP17A1	1.02	0.83	1.26	8.46E-01	A	0.38	A	0.42
rs1805794	NBN	0.98	0.79	1.22	8.47E-01	G	0.22	G	0.33
rs2732497	PPP3CA	0.98	0.79	1.22	8.47E-01	T	0.34	T	0.49
rs2276583	ERCC3	1.02	0.82	1.27	8.48E-01	A	0.23	A	0.39
rs1041163	VCAM1	0.97	0.74	1.28	8.48E-01	C	0.18	C	0.17
rs2281891	CYP2C18	0.97	0.72	1.32	8.49E-01	A	0.16	A	0.14
rs4986894	CYP2C19	0.97	0.72	1.32	8.49E-01	C	0.16	C	0.14
rs3791878	GAD1	0.98	0.77	1.24	8.49E-01	A	0.06	A	0.29
rs2069762	IL2	1.02	0.80	1.30	8.50E-01	G	0.12	G	0.30
rs16834521	MTR	1.02	0.82	1.28	8.50E-01	G	0.22	G	0.43
rs5276	PTGS2	0.94	0.48	1.82	8.51E-01	A	0.14	A	0.00
rs5498	ICAM1	1.02	0.81	1.29	8.52E-01	G	0.22	G	0.42
rs1805097	IRS2	0.98	0.77	1.25	8.52E-01	A	0.13	A	0.33
rs5744751	POLE	1.03	0.73	1.46	8.53E-01	T	0.02	T	0.11
rs2230592	MST1R	1.09	0.44	2.72	8.54E-01	G	0.08	G	0.00
rs973874	NAT2	1.08	0.46	2.53	8.54E-01	T	0.06	T	0.01
rs6427384	FCRL5	0.97	0.74	1.29	8.54E-01	T	0.41	C	0.14
rs12221497	NR1H3	1.03	0.74	1.44	8.55E-01	A	0.02	A	0.13
rs4633	COMT	1.02	0.83	1.26	8.55E-01	T	0.29	C	0.48

rs6717546	UGT1A1	1.02	0.81	1.28	8.55E-01	A	0.45	A	0.36
rs1138294	MAP3K6	0.98	0.78	1.23	8.55E-01	T	0.14	T	0.36
rs1407309	TNFSF8	1.02	0.82	1.26	8.56E-01	G	0.24	A	0.47
rs3176875	VCAM1	1.05	0.60	1.85	8.56E-01	A	0.13	A	0.03
rs2228638	NRP1	1.03	0.73	1.46	8.56E-01	A	0.03	A	0.11
rs1838066	MBL2	0.98	0.79	1.22	8.57E-01	G	0.13	G	0.38
rs2352984	MON1A	0.98	0.79	1.22	8.57E-01	C	0.39	C	0.42
rs2305030	LTK	1.03	0.74	1.43	8.58E-01	T	0.12	T	0.13
rs11615	ERCC1	0.98	0.79	1.22	8.58E-01	T	0.13	C	0.41
rs10017306	SLC39A8	0.98	0.79	1.22	8.58E-01	T	0.39	T	0.40
rs2274750	TNC	1.05	0.62	1.76	8.59E-01	A	0.08	A	0.03
rs5005	ADM	1.08	0.44	2.65	8.59E-01	G	0.06	G	0.00
rs2582783	HMGCS2	1.02	0.80	1.30	8.59E-01	A	0.38	A	0.25
rs458017	REV3L	0.96	0.64	1.45	8.60E-01	C	0.06	C	0.06
rs5742909	CTLA4	0.97	0.66	1.42	8.60E-01	T	0.02	T	0.10
rs2758346	SOD2	0.98	0.79	1.21	8.60E-01	T	0.40	C	0.49
rs428073	LOC100130562	0.98	0.78	1.23	8.61E-01	C	0.25	C	0.34
rs2082382	ADRB2	0.98	0.78	1.23	8.61E-01	G	0.09	G	0.41
rs3797897	MSH3	1.03	0.73	1.45	8.61E-01	G	0.03	G	0.10
rs2180314	GSTA2	0.98	0.79	1.22	8.63E-01	G	0.30	C	0.38
rs3774306	BCL6	1.02	0.82	1.26	8.63E-01	A	0.14	G	0.36
rs2023410	ADRB3	0.98	0.77	1.24	8.64E-01	A	0.33	G	0.21
rs1061040	SLC7A7	0.97	0.71	1.33	8.65E-01	A	0.47	A	0.10
rs3818644	DNAJA1	1.02	0.81	1.28	8.65E-01	T	0.19	T	0.36
rs1863703	STK36	1.03	0.72	1.48	8.65E-01	G	0.27	G	0.06
rs699473	SOD3	1.02	0.82	1.26	8.65E-01	T	0.33	C	0.36
rs16876805	PSKH2	0.94	0.49	1.82	8.66E-01	C	0.15	C	0.01
rs7823144	LSM1	1.03	0.74	1.43	8.66E-01	A	0.29	A	0.08
rs2020869	FMO2	1.02	0.77	1.36	8.66E-01	G	0.17	G	0.14
rs1140616	FASN	0.98	0.78	1.23	8.67E-01	T	0.21	C	0.49
rs1059393	ENOSF1	0.97	0.71	1.33	8.67E-01	C	0.14	C	0.14
rs2016347	IGF1R	0.98	0.80	1.21	8.68E-01	A	0.37	C	0.47
rs602990	VAV2	1.02	0.81	1.28	8.68E-01	T	0.21	T	0.48
rs2695232	SOD3	0.98	0.79	1.22	8.68E-01	T	0.17	C	0.36
rs1157745	PON1	1.02	0.82	1.27	8.69E-01	G	0.33	T	0.34
rs20581	LIG1	1.02	0.82	1.26	8.69E-01	T	0.16	T	0.46
rs1048977	CDA	1.02	0.82	1.27	8.69E-01	T	0.40	T	0.31
rs3738000	NEK11	1.02	0.82	1.27	8.70E-01	T	0.29	A	0.31
rs215060	ABCC1	0.97	0.71	1.34	8.71E-01	G	0.06	G	0.13
rs165599	COMT	0.98	0.78	1.23	8.71E-01	A	0.31	G	0.34
rs7517376	FMO1	0.98	0.73	1.30	8.71E-01	A	0.46	G	0.13
rs2286194	HGF	0.98	0.74	1.29	8.71E-01	A	0.18	A	0.20
rs1368408	SCGB3A2	1.02	0.77	1.35	8.71E-01	A	0.34	A	0.14
rs3176123	THBD	0.98	0.73	1.31	8.71E-01	C	0.05	C	0.19
rs2159499	STARD3NL	1.02	0.82	1.26	8.72E-01	G	0.35	G	0.47
rs363717	ABCA1	1.02	0.78	1.35	8.72E-01	G	0.08	G	0.18
rs11549147	FDFT1	0.97	0.63	1.48	8.73E-01	G	0.02	G	0.08
rs1856908	CYP2C9	1.02	0.82	1.27	8.73E-01	T	0.23	T	0.41
rs3914142	ACBD3	0.98	0.80	1.21	8.73E-01	G	0.49	C	0.45
rs2020911	MSH6	0.98	0.78	1.23	8.74E-01	T	0.13	T	0.40

rs6489738	GNB3	0.98	0.78	1.24	8.75E-01	C	0.25	T	0.33
rs3177427	GSTZ1	0.98	0.79	1.22	8.75E-01	A	0.27	A	0.32
rs2237582	PON1	1.02	0.82	1.27	8.76E-01	A	0.30	G	0.34
rs2234719	ABCG1	0.98	0.77	1.25	8.77E-01	T	0.29	T	0.27
rs135549	PPARA	1.02	0.82	1.27	8.77E-01	A	0.37	G	0.39
rs2020860	FMO2	1.03	0.71	1.50	8.77E-01	C	0.24	C	0.05
rs20580	LIG1	1.02	0.83	1.24	8.79E-01	C	0.42	A	0.49
rs2684773	IGF1R	1.02	0.77	1.35	8.81E-01	G	0.41	G	0.13
rs215095	ABCC1	1.02	0.75	1.41	8.82E-01	C	0.05	C	0.13
rs3741367	CD248	1.02	0.82	1.26	8.83E-01	C	0.22	C	0.44
rs1800797	IL6	0.98	0.79	1.23	8.83E-01	A	0.08	A	0.36
rs11574	ID3	1.02	0.79	1.31	8.85E-01	A	0.03	A	0.24
rs4698803	EGF	1.02	0.77	1.35	8.85E-01	A	0.04	A	0.21
rs1652342	C18orf8	1.02	0.80	1.30	8.85E-01	G	0.10	G	0.35
rs12680113	ZNF596	0.98	0.79	1.23	8.86E-01	T	0.24	T	0.36
rs13392272	APOB	0.98	0.79	1.23	8.86E-01	T	0.23	T	0.46
rs2072360	FOXM1	1.02	0.78	1.33	8.86E-01	G	0.36	G	0.20
rs1051130	CCND3	1.02	0.82	1.25	8.87E-01	T	0.15	T	0.47
rs1413229	DPYD	0.98	0.79	1.23	8.87E-01	A	0.10	A	0.36
rs5343	EDNRA	0.98	0.78	1.24	8.87E-01	T	0.15	T	0.34
rs2072501	ZNF71	0.98	0.72	1.33	8.88E-01	A	0.25	A	0.18
rs3887412	ABCC1	0.98	0.77	1.26	8.88E-01	T	0.49	T	0.17
rs2288548	IMPDH1	0.98	0.77	1.25	8.89E-01	A	0.30	A	0.22
rs11003125	MBL2	0.98	0.79	1.23	8.89E-01	C	0.13	C	0.38
rs2238476	ABCC1	0.97	0.64	1.48	8.89E-01	T	0.03	T	0.06
rs2069830	IL6	1.06	0.45	2.51	8.90E-01	T	0.09	T	0.00
rs7096206	MBL2	1.02	0.78	1.33	8.90E-01	G	0.13	G	0.22
rs2410478	NAT1	0.92	0.30	2.87	8.91E-01	C	0.05	C	0.00
rs6671288	NR1I3	0.98	0.73	1.31	8.91E-01	G	0.19	G	0.16
rs9896405	EME1	0.95	0.46	1.97	8.91E-01	G	0.13	G	0.00
rs6597801	LHPP	1.02	0.72	1.46	8.91E-01	A	0.02	A	0.12
rs9282564	ABCB1	1.03	0.72	1.46	8.91E-01	G	0.02	G	0.11
rs769214	CAT	0.99	0.79	1.22	8.91E-01	G	0.39	G	0.35
rs584531	MRE11A	0.98	0.79	1.23	8.92E-01	G	0.41	G	0.31
rs6664	CHST2	0.98	0.78	1.24	8.92E-01	C	0.37	T	0.33
rs2072651	TPP1	0.98	0.75	1.29	8.92E-01	T	0.20	T	0.17
rs1980499	LOC728383	1.02	0.82	1.26	8.93E-01	C	0.14	C	0.50
rs759853	AKR1B1	1.01	0.82	1.26	8.93E-01	A	0.22	A	0.42
rs1799799	ERCC4	1.02	0.81	1.27	8.93E-01	C	0.47	C	0.34
rs2269800	ABCC1	0.98	0.72	1.33	8.93E-01	G	0.24	G	0.11
rs1152888	IRAK3	1.02	0.73	1.44	8.94E-01	G	0.50	A	0.07
rs1381057	POLQ	0.98	0.79	1.23	8.94E-01	T	0.33	T	0.31
rs1800849	UCP3	0.98	0.76	1.27	8.94E-01	T	0.10	T	0.24
rs7185307	TNFRSF17	1.02	0.80	1.30	8.94E-01	T	0.25	C	0.24
rs596104	PHGDH	0.99	0.80	1.22	8.95E-01	A	0.34	A	0.44
rs2071724	TTLL12	0.99	0.80	1.22	8.96E-01	A	0.45	A	0.41
rs1051992	PRKCDBP	0.99	0.80	1.21	8.97E-01	C	0.38	T	0.46
rs585800	BHMT	1.02	0.79	1.31	8.98E-01	T	0.04	T	0.27
rs1432793	SH3TC2	1.01	0.83	1.24	8.98E-01	T	0.42	C	0.46
rs2071746	HMOX1	0.99	0.79	1.22	8.98E-01	A	0.33	T	0.41

rs1805075	IGF2R	0.97	0.61	1.55	8.99E-01	G	0.01	G	0.07
rs1970142	DPYD	1.02	0.80	1.29	9.00E-01	T	0.08	T	0.33
rs6808205	PLS1	1.01	0.82	1.25	9.00E-01	A	0.35	A	0.38
rs7658300	TXK	1.02	0.79	1.30	9.00E-01	T	0.11	T	0.36
rs17685	POR	1.02	0.79	1.30	9.02E-01	T	0.21	T	0.26
rs1802061	GSTA4	1.03	0.65	1.64	9.03E-01	A	0.01	A	0.06
rs3218012	CDKN2A	0.99	0.79	1.23	9.03E-01	T	0.34	T	0.46
rs2270165	STARD3NL	0.98	0.74	1.31	9.03E-01	A	0.09	A	0.16
rs1801274	FCGR2A	0.99	0.80	1.22	9.03E-01	T	0.41	C	0.47
rs885622	DPYD	1.01	0.81	1.27	9.04E-01	A	0.08	A	0.35
rs1801376	BUB1B	0.99	0.78	1.25	9.04E-01	G	0.19	G	0.30
rs9282682	FANCA	1.02	0.71	1.46	9.04E-01	C	0.15	C	0.09
rs4149963	EXO1	1.02	0.71	1.47	9.04E-01	T	0.02	T	0.10
rs619487	PGR	0.99	0.77	1.26	9.06E-01	G	0.07	G	0.32
rs2070744	NOS3	0.99	0.78	1.25	9.07E-01	C	0.16	C	0.34
rs183484	RRM1	1.01	0.82	1.25	9.07E-01	T	0.13	G	0.48
rs762623	CDKN1A	0.98	0.71	1.35	9.07E-01	A	0.08	A	0.14
rs1799725	SOD2	0.99	0.80	1.22	9.08E-01	C	0.40	T	0.49
rs17274095	BLM	0.98	0.74	1.30	9.08E-01	A	0.09	A	0.19
rs1051741	EPHX1	0.98	0.70	1.38	9.08E-01	T	0.11	T	0.10
rs2070904	CYP2D6	1.01	0.82	1.24	9.08E-01	G	0.36	G	0.46
rs747657	PARP1	0.99	0.80	1.22	9.08E-01	C	0.46	G	0.38
rs1178027	PTPRA	1.02	0.76	1.36	9.08E-01	C	0.45	T	0.10
rs2368184	ABI1	1.01	0.81	1.27	9.08E-01	T	0.21	G	0.45
rs2664538	MMP9	0.99	0.80	1.22	9.09E-01	G	0.34	G	0.37
rs11574790	IL12B	0.98	0.70	1.38	9.09E-01	T	0.18	T	0.10
rs7312411	VWF	1.01	0.81	1.27	9.10E-01	A	0.39	G	0.35
rs35629	ABCC1	0.98	0.72	1.33	9.10E-01	T	0.46	T	0.12
rs3747258	CERK	1.02	0.69	1.52	9.11E-01	A	0.35	A	0.04
rs3136228	MSH6	0.99	0.79	1.24	9.12E-01	G	0.22	G	0.35
rs2185379	PRDM1	0.97	0.55	1.69	9.12E-01	A	0.08	A	0.03
rs1801320	LOC729029	1.02	0.74	1.41	9.13E-01	C	0.24	C	0.09
rs9885672	FIG4	0.98	0.75	1.29	9.13E-01	T	0.30	C	0.17
rs2069837	IL6	0.98	0.65	1.46	9.14E-01	G	0.10	G	0.07
rs2217332	HERPUD1	1.02	0.76	1.36	9.14E-01	T	0.11	T	0.15
rs1703874	FLJ00290	0.99	0.78	1.25	9.14E-01	A	0.14	A	0.27
rs1801702	APOB	0.97	0.57	1.66	9.15E-01	C	0.09	C	0.03
rs2645444	FDFT1	0.99	0.75	1.29	9.15E-01	G	0.23	G	0.17
rs3784932	CHST5	0.99	0.75	1.29	9.16E-01	C	0.12	C	0.20
rs963981	KIAA1804	0.99	0.76	1.27	9.17E-01	C	0.18	C	0.20
rs891507	CDK5	0.98	0.73	1.33	9.18E-01	T	0.09	T	0.15
rs2272615	POLB	0.99	0.74	1.31	9.18E-01	A	0.36	G	0.12
rs163081	FAM82A	0.99	0.76	1.29	9.19E-01	T	0.24	T	0.22
rs9462088	FANCE	1.02	0.72	1.45	9.20E-01	A	0.37	A	0.06
rs913118	MGMT	1.01	0.82	1.25	9.20E-01	C	0.49	T	0.43
rs4980999	CAMKK2	1.01	0.77	1.33	9.21E-01	A	0.26	A	0.14
rs2844482	LTA	0.98	0.72	1.35	9.21E-01	A	0.10	A	0.13
rs943975	CYP2E1	1.02	0.74	1.40	9.21E-01	C	0.46	C	0.09
rs1019731	IGF1	0.98	0.71	1.37	9.22E-01	T	0.02	T	0.13
rs1063045	NBN	0.99	0.80	1.22	9.22E-01	T	0.30	T	0.33

rs3795374	KIAA1804	0.99	0.77	1.27	9.23E-01	A	0.18	A	0.20
rs1801249	ATP7B	0.99	0.80	1.22	9.23E-01	T	0.44	T	0.41
rs16900023	C6orf26	1.03	0.52	2.06	9.23E-01	T	0.10	T	0.02
rs7909236	CYP2C8	0.99	0.76	1.28	9.23E-01	T	0.07	T	0.24
rs2048426	PARP1	1.01	0.82	1.25	9.23E-01	C	0.40	T	0.38
rs662	PON1	1.01	0.81	1.26	9.24E-01	A	0.33	G	0.34
rs3213195	BLM	1.01	0.78	1.32	9.24E-01	G	0.13	G	0.19
rs6737156	DGUOK	0.98	0.61	1.57	9.24E-01	C	0.16	C	0.04
rs1934961	CYP2C9	0.97	0.47	2.00	9.24E-01	A	0.16	A	0.00
rs601391	MRE11A	0.99	0.79	1.24	9.24E-01	T	0.41	T	0.31
rs17612126	IGHMBP2	1.01	0.79	1.29	9.24E-01	A	0.09	A	0.30
rs2253635	CYP2C9	1.01	0.81	1.26	9.25E-01	G	0.23	G	0.42
rs1800378	VWF	1.01	0.81	1.27	9.25E-01	G	0.21	A	0.35
rs3806798	IL15	0.98	0.69	1.40	9.25E-01	T	0.03	T	0.12
rs17057718	IL17RD	1.01	0.75	1.37	9.26E-01	T	0.04	T	0.18
rs948516	PGR	0.99	0.77	1.27	9.27E-01	G	0.10	G	0.30
rs183374	NFATC1	0.99	0.80	1.22	9.27E-01	A	0.33	A	0.45
rs3219489	MUTYH	1.01	0.80	1.28	9.27E-01	C	0.29	C	0.24
rs2544773	RIOK2	1.01	0.81	1.26	9.28E-01	C	0.12	C	0.41
rs11550540	TP53RK	1.02	0.69	1.51	9.28E-01	G	0.01	G	0.09
rs2238136	VDR	0.99	0.77	1.27	9.28E-01	A	0.10	A	0.25
rs628031	SLC22A1	1.01	0.82	1.25	9.28E-01	A	0.27	A	0.39
rs800667	CYP3A43	1.01	0.73	1.41	9.29E-01	G	0.45	G	0.08
rs3014626	PPP1R15B	1.05	0.39	2.79	9.29E-01	T	0.07	0	0.00
rs487989	POLA2	0.99	0.74	1.32	9.30E-01	A	0.19	A	0.14
rs1800802	MGP	1.01	0.78	1.31	9.30E-01	C	0.04	C	0.20
rs3795375	KIAA1804	1.01	0.78	1.31	9.31E-01	T	0.13	T	0.20
rs2276078	HSPA8	1.04	0.43	2.51	9.32E-01	G	0.06	G	0.01
rs12720356	TYK2	0.98	0.67	1.45	9.33E-01	G	0.01	G	0.09
rs1776148	EXO1	1.01	0.81	1.25	9.33E-01	A	0.33	A	0.35
rs1805011	IL4R	0.99	0.74	1.31	9.34E-01	A	0.48	C	0.13
rs9350	EXO1	1.01	0.77	1.32	9.34E-01	T	0.14	T	0.19
rs1024323	GRK4	0.99	0.80	1.23	9.34E-01	G	0.42	A	0.39
rs2725349	WRN	1.01	0.81	1.26	9.35E-01	C	0.49	C	0.30
rs1565684	NAT2	1.01	0.82	1.24	9.36E-01	C	0.29	T	0.47
rs7525957	FRAP1	1.01	0.79	1.29	9.37E-01	T	0.35	C	0.25
rs1803965	MGMT	1.01	0.73	1.40	9.37E-01	T	0.19	T	0.13
rs1469149	CSF2	0.99	0.79	1.24	9.38E-01	A	0.49	C	0.34
rs3771342	UGT1A1	1.01	0.75	1.36	9.39E-01	A	0.15	A	0.15
rs732774	ATP7B	0.99	0.81	1.22	9.39E-01	G	0.46	G	0.41
rs3817074	BAX	1.01	0.73	1.41	9.40E-01	T	0.10	T	0.11
rs4987876	ATM	1.01	0.70	1.47	9.40E-01	T	0.06	T	0.10
rs15524	CYP3A5	0.99	0.71	1.37	9.41E-01	T	0.45	C	0.09
rs2301241	TXN	0.99	0.80	1.23	9.41E-01	C	0.42	C	0.39
rs9282715	IGF1R	1.01	0.70	1.47	9.42E-01	C	0.28	C	0.08
rs1800795	IL6	0.99	0.80	1.23	9.42E-01	C	0.08	C	0.38
rs2292566	EPHX1	1.01	0.75	1.36	9.43E-01	A	0.11	A	0.15
rs930509	MBL2	0.99	0.74	1.32	9.43E-01	C	0.11	C	0.18
rs4525	F5	0.99	0.77	1.27	9.43E-01	G	0.15	G	0.26
rs9306354	XRCC6	0.98	0.54	1.77	9.43E-01	T	0.24	T	0.00

rs4655537	LEPR	1.01	0.81	1.25	9.44E-01	A	0.37	A	0.36
rs1678339	ABCC4	0.99	0.65	1.49	9.44E-01	T	0.17	T	0.06
rs1800872	IL10	0.99	0.78	1.26	9.44E-01	A	0.38	A	0.26
rs4149272	ABCA1	0.99	0.80	1.24	9.45E-01	G	0.25	A	0.38
rs4762	AGT	0.99	0.70	1.39	9.45E-01	T	0.06	T	0.13
rs1058172	CYP2D6	1.01	0.73	1.41	9.45E-01	A	0.03	A	0.15
rs4665766	EFR3B	1.01	0.79	1.28	9.46E-01	T	0.39	T	0.24
rs854569	PON1	1.01	0.80	1.27	9.47E-01	G	0.32	T	0.24
rs2234898	IL4R	0.99	0.75	1.31	9.47E-01	G	0.48	T	0.13
rs16932374	VWF	1.02	0.52	2.02	9.48E-01	T	0.16	T	0.00
rs4524	F5	0.99	0.78	1.27	9.49E-01	G	0.16	G	0.27
rs17841292	EEF2K	0.99	0.66	1.47	9.49E-01	G	0.03	G	0.09
rs2580874	AICDA	0.99	0.81	1.22	9.49E-01	G	0.30	A	0.47
rs3087243	CTLA4	1.01	0.80	1.26	9.50E-01	A	0.21	A	0.41
rs3136664	CCR1	0.97	0.40	2.37	9.50E-01	A	0.08	A	0.00
rs2243828	MPO	1.01	0.79	1.29	9.51E-01	G	0.38	G	0.22
rs2585	IGF2	1.01	0.80	1.27	9.51E-01	T	0.10	T	0.29
rs2608555	GAN	1.01	0.79	1.29	9.52E-01	T	0.18	T	0.25
rs2303425	MSH2	1.01	0.72	1.41	9.52E-01	C	0.02	C	0.13
rs888580	ADRB3	1.01	0.81	1.25	9.53E-01	A	0.24	A	0.37
rs3212948	ERCC1	0.99	0.80	1.24	9.53E-01	C	0.13	G	0.38
rs1063856	VWF	0.99	0.80	1.23	9.53E-01	A	0.40	G	0.34
rs12347	MTRR	1.01	0.73	1.40	9.53E-01	T	0.32	T	0.11
rs3826007	BCL2A1	1.01	0.79	1.28	9.54E-01	A	0.09	A	0.27
rs305968	CYP2F1	0.99	0.79	1.24	9.55E-01	G	0.41	A	0.31
rs2850992	PPP3CA	1.01	0.79	1.29	9.55E-01	C	0.05	C	0.31
rs3136717	POLB	0.99	0.74	1.32	9.56E-01	T	0.34	C	0.12
rs1063147	BLM	0.99	0.75	1.31	9.56E-01	T	0.08	T	0.19
rs2659543	PPP3CA	0.99	0.64	1.52	9.56E-01	G	0.37	G	0.06
rs3850751	NAT1	0.99	0.80	1.24	9.57E-01	C	0.18	C	0.43
rs168351	ALDH1A1	1.01	0.75	1.35	9.58E-01	G	0.02	G	0.16
rs513349	BAK1	1.01	0.82	1.24	9.58E-01	A	0.33	G	0.42
rs152029	ABCC1	0.99	0.75	1.32	9.59E-01	T	0.49	G	0.12
rs1051061	VRK2	1.01	0.80	1.26	9.59E-01	G	0.08	G	0.36
rs4925	GSTO1	1.01	0.79	1.28	9.59E-01	A	0.12	A	0.29
rs2274578	BYSL	1.01	0.81	1.24	9.59E-01	G	0.36	C	0.50
rs8659	MTRR	0.99	0.78	1.26	9.60E-01	T	0.45	T	0.35
rs2274760	GSTA4	0.99	0.71	1.38	9.62E-01	C	0.02	C	0.11
rs1035130	IL18R1	1.01	0.79	1.27	9.62E-01	A	0.17	A	0.27
rs2908004	WNT16	1.01	0.81	1.25	9.63E-01	C	0.17	T	0.44
rs2069456	CDK5	0.99	0.79	1.25	9.64E-01	C	0.26	C	0.25
rs10017300	Intergenic	0.99	0.79	1.26	9.64E-01	C	0.19	C	0.31
rs17057901	PBK	1.02	0.37	2.87	9.64E-01	G	0.07	G	0.00
rs1040090	DPYD	1.01	0.75	1.34	9.65E-01	A	0.10	A	0.16
rs1263167	APOA5	1.01	0.75	1.35	9.65E-01	G	0.06	G	0.19
rs3093873	LOC100132444	1.01	0.72	1.41	9.66E-01	C	0.38	T	0.05
rs13339152	RUNDC2A	0.99	0.70	1.41	9.66E-01	C	0.28	C	0.07
rs3802762	CHST1	0.99	0.76	1.30	9.66E-01	C	0.45	T	0.16
rs3749229	CHRD	1.01	0.72	1.42	9.66E-01	A	0.16	A	0.12
rs16944831	BLM	0.99	0.67	1.46	9.67E-01	T	0.32	T	0.04

rs7926138	MRE11A	1.01	0.60	1.71	9.67E-01	A	0.26	A	0.01
rs1800871	IL10	1.01	0.79	1.28	9.67E-01	T	0.38	T	0.26
rs1126643	ITGA2	1.00	0.81	1.24	9.67E-01	T	0.29	T	0.40
rs26784	MSH3	1.00	0.79	1.25	9.69E-01	C	0.23	C	0.40
rs1333728	DPYD	0.99	0.68	1.46	9.70E-01	T	0.02	T	0.09
rs1805414	PARP1	1.00	0.81	1.23	9.70E-01	T	0.46	C	0.38
rs1800471	TGFB1	1.01	0.66	1.55	9.70E-01	C	0.06	C	0.07
rs554715	MRE11A	1.00	0.80	1.25	9.71E-01	C	0.40	C	0.31
rs2470890	CYP1A2	1.00	0.80	1.25	9.71E-01	T	0.12	C	0.41
rs17420378	STK4	1.00	0.79	1.28	9.72E-01	A	0.14	A	0.29
rs3747806	ABCB4	1.01	0.64	1.58	9.72E-01	C	0.20	C	0.04
rs928169	ATP7B	1.00	0.82	1.23	9.72E-01	C	0.49	C	0.41
rs17098707	GRK5	0.99	0.58	1.68	9.72E-01	T	0.27	T	0.01
rs2046136	BCL2	1.00	0.79	1.27	9.72E-01	C	0.20	C	0.29
rs5936	PROC	1.00	0.80	1.26	9.72E-01	G	0.25	G	0.29
rs1062633	MST1R	1.00	0.80	1.24	9.73E-01	A	0.32	G	0.49
rs868891	MON1A	1.00	0.80	1.24	9.73E-01	C	0.26	C	0.41
rs2239704	LTA	1.00	0.81	1.25	9.73E-01	T	0.31	T	0.37
rs3776969	MSH3	0.99	0.71	1.39	9.73E-01	A	0.18	A	0.09
rs10018280	PDE5A	1.00	0.80	1.25	9.75E-01	G	0.34	G	0.30
rs8827	SPRED2	1.00	0.78	1.28	9.75E-01	C	0.15	C	0.28
rs1635498	EXO1	0.99	0.59	1.67	9.77E-01	G	0.09	G	0.03
rs6949295	IMPDH1	1.00	0.78	1.28	9.78E-01	C	0.30	C	0.23
rs919766	IL12B	1.00	0.71	1.39	9.78E-01	C	0.20	C	0.10
rs4905475	BDKRB1	1.01	0.69	1.46	9.79E-01	C	0.02	C	0.10
rs11595876	MBL2	0.99	0.63	1.58	9.79E-01	C	0.01	C	0.06
rs2274736	PTPN21	1.00	0.80	1.25	9.79E-01	C	0.47	C	0.34
rs3743527	ABCC1	1.00	0.76	1.32	9.79E-01	T	0.15	T	0.21
rs3217772	CCNA2	1.00	0.80	1.25	9.80E-01	C	0.10	C	0.40
rs2070874	IL4	1.00	0.78	1.30	9.80E-01	T	0.40	T	0.18
rs1124	BMP1	1.00	0.77	1.31	9.80E-01	A	0.14	A	0.32
rs2298037	CYP2C9	1.00	0.74	1.36	9.80E-01	T	0.05	T	0.17
rs2227631	SERPINE1	1.00	0.80	1.25	9.80E-01	A	0.28	G	0.43
rs3762412	DPYD	1.00	0.80	1.25	9.81E-01	T	0.08	T	0.36
rs5182	AGTR1	1.00	0.81	1.24	9.81E-01	T	0.19	T	0.48
rs6482573	PDSS1	1.00	0.81	1.25	9.82E-01	G	0.30	A	0.37
rs886205	ALDH2	1.00	0.77	1.31	9.82E-01	T	0.40	C	0.21
rs769243	CCNA2	0.99	0.63	1.57	9.82E-01	A	0.40	A	0.02
rs436525	ADAMTS1	1.00	0.81	1.23	9.82E-01	G	0.36	G	0.33
rs3130618	BAT4	1.00	0.78	1.29	9.83E-01	A	0.22	A	0.22
rs2229765	IGF1R	1.00	0.81	1.24	9.83E-01	A	0.26	A	0.42
rs1536474	RXRA	1.00	0.77	1.30	9.84E-01	G	0.31	T	0.25
rs16905649	PTPRJ	1.01	0.41	2.46	9.85E-01	A	0.09	A	0.00
rs2230517	MERTK	1.00	0.61	1.62	9.85E-01	A	0.19	A	0.03
rs954619	CCND1	1.01	0.55	1.83	9.86E-01	T	0.13	T	0.01
rs1799969	ICAM1	1.00	0.72	1.39	9.86E-01	A	0.03	A	0.12
rs1760217	DPYD	1.00	0.78	1.29	9.87E-01	C	0.17	C	0.23
rs2401751	PTPN21	1.00	0.80	1.25	9.87E-01	T	0.35	T	0.34
rs1805312	ALAD	1.00	0.67	1.51	9.88E-01	C	0.02	C	0.09
rs827528	FZD6	1.00	0.78	1.29	9.88E-01	G	0.19	G	0.23

rs1760216	DPYD	1.00	0.76	1.31	9.88E-01	A	0.10	A	0.20
rs2011713	PCGF2	1.00	0.65	1.53	9.88E-01	A	0.02	A	0.08
rs956868	WNK1	1.00	0.75	1.34	9.89E-01	A	0.17	A	0.16
rs246	OPCML	1.00	0.78	1.27	9.89E-01	A	0.21	A	0.22
rs1051332	ATP7B	1.00	0.80	1.24	9.90E-01	A	0.15	A	0.46
rs3135506	APOA5	1.00	0.64	1.56	9.91E-01	C	0.06	C	0.07
rs476632	HSP90AB1	1.00	0.80	1.25	9.91E-01	A	0.17	A	0.34
rs3917991	CSF3R	1.00	0.55	1.82	9.92E-01	C	0.16	C	0.01
rs9282612	BLM	1.00	0.76	1.32	9.92E-01	G	0.09	G	0.19
rs3219090	PARP1	1.00	0.81	1.23	9.92E-01	G	0.45	A	0.37
rs9333269	ITGA8	1.00	0.68	1.48	9.92E-01	C	0.01	C	0.09
rs11632706	CYP1A2	1.00	0.60	1.65	9.93E-01	T	0.10	T	0.04
rs1042579	THBD	1.00	0.75	1.34	9.93E-01	T	0.04	T	0.19
rs2069526	CYP1A2	1.00	0.60	1.65	9.93E-01	G	0.10	G	0.04
rs2056048	DPYD	1.00	0.81	1.23	9.94E-01	C	0.33	A	0.49
rs1165678	HSP90B1	1.00	0.81	1.23	9.94E-01	G	0.26	G	0.38
rs3136794	POLB	1.00	0.75	1.33	9.94E-01	A	0.37	G	0.12
rs505770	MMP12	1.00	0.65	1.54	9.95E-01	A	0.27	A	0.04
rs9332	MTRR	1.00	0.72	1.38	9.95E-01	T	0.32	T	0.11
rs1042482	DPYD	1.00	0.68	1.46	9.95E-01	A	0.03	A	0.09
rs1530662	FBXO25	1.00	0.81	1.24	9.95E-01	T	0.20	C	0.44
rs1042580	THBD	1.00	0.80	1.25	9.95E-01	G	0.22	G	0.38
rs993568	DPYD	1.00	0.81	1.23	9.95E-01	G	0.33	A	0.49
rs1641536	SHBG	1.00	0.76	1.31	9.96E-01	G	0.48	A	0.14
rs228843	NFATC2	1.00	0.80	1.24	9.96E-01	G	0.26	A	0.42
rs2760501	JUN	1.00	0.72	1.38	9.96E-01	T	0.28	G	0.09
rs867186	PROCR	1.00	0.70	1.43	9.96E-01	G	0.09	G	0.11
rs162036	MTRR	1.00	0.72	1.38	9.96E-01	G	0.32	G	0.11
rs3204953	LOC100128477	1.00	0.71	1.42	9.96E-01	A	0.02	A	0.13
rs3802265	ZHX2	1.00	0.80	1.25	9.98E-01	C	0.45	C	0.37
rs4303	ACE	1.00	0.35	2.84	9.98E-01	T	0.09	T	0.00
rs1799800	ERCC4	1.00	0.79	1.27	9.98E-01	A	0.19	A	0.26
rs2602376	UGT1A10	1.00	0.77	1.29	9.99E-01	T	0.07	T	0.28
rs3759217	CDKN1B	1.00	0.72	1.40	1.00E+00	T	0.06	T	0.12