Supplemental Table 2

SNPs associated with severity of ct-scores (chronic tubular atrophy) using an adjusted multinomial logistic regression with 3 outcome groups, ct score ≥2 (n=52), ct-score ≤1 (n=195) and no biopsy group (n=687). SNPs are ranked by p-values for the ct≥2 versus ct≤ 1 groups. The model was adjusted for SPK versus kidney alone, donor age, recipient age, recipient African American race, and baseline creatinine at 3 months post-transplant, smoking status and steroid withdrawal status at 14 days post-transplant.

SNP	Gene	Allele	Freq	ct≤1 vs no biopsy OR	ct≤1 vs no biopsy 95% C.I.	ct≤1 vs no biopsy Pvalue	ct≥2 vs no biopsy OR	ct≥2 vs no biopsy 95% C.I.	ct≥2 vs no biopsy Pvalue	ct≥2 vs ct≤1 OR	ct≥2 vs ct≤1 95% C.I.	ct≥2 vs ct≤1 Pvalue	Overall Pvalue
rs8179183	LEPR	C	0.172	0.927	[0.669,1.284]	0.649	2.474	[1.501,4.076]	<0.001	2.668	[1.538,4.627]	<0.001	0.001
rs3828034	LEPR	C	0.146	0.894	[0.634,1.261]	0.524	2.447	[1.452,4.124]	0.001	2.736	[1.537,4.873]	0.001	0.002
rs593421	CYP4F12	C	0.287	1.450	[1.112,1.891]	0.006	0.550	[0.317,0.955]	0.034	0.379	[0.211,0.68]	0.001	0.001
rs491347	LRP5	C	0.299	0.884	[0.674,1.158]	0.370	1.940	[1.245,3.022]	0.003	2.195	[1.35,3.57]	0.002	0.006
rs2853559	VDR	T	0.350	1.115	[0.861,1.444]	0.411	0.454	[0.267,0.774]	0.004	0.408	[0.232,0.717]	0.002	0.008
rs2238136	VDR	A	0.221	0.850	[0.636,1.136]	0.273	1.873	[1.192,2.944]	0.007	2.203	[1.337,3.63]	0.002	0.008
rs667126	LRP5	C	0.293	0.898	[0.685,1.178]	0.437	1.947	[1.244,3.049]	0.004	2.168	[1.328,3.539]	0.002	0.007
rs875444	RXRA	G	0.475	1.180	[0.914,1.523]	0.204	0.519	[0.317,0.851]	0.009	0.440	[0.26,0.746]	0.002	0.009
rs2306862	LRP5	T	0.139	0.974	[0.687,1.379]	0.880	2.380	[1.42,3.989]	0.001	2.444	[1.376,4.344]	0.002	0.004
rs7533315	MTHFR	T	0.267	1.133	[0.88,1.457]	0.332	2.297	[1.508,3.499]	<0.001	2.028	[1.286,3.197]	0.002	0.001
rs688755	CYP4F12	C	0.289	1.394	[1.079,1.801]	0.011	0.577	[0.337,0.989]	0.045	0.414	[0.235,0.73]	0.002	0.003
rs2237580	PON1	G	0.104	0.415	[0.255,0.676]	0.000	1.297	[0.696,2.416]	0.413	3.122	[1.486,6.561]	0.003	0.001
rs2955617	SHBG	G	0.407	1.151	[0.902,1.469]	0.259	0.519	[0.317,0.849]	0.009	0.451	[0.267,0.759]	0.003	0.011
rs915057	SYNE2	T	0.380	0.866	[0.674,1.111]	0.257	1.797	[1.152,2.804]	0.010	2.077	[1.284,3.357]	0.003	0.012
rs2066471	MTHFR	A	0.155	1.042	[0.767,1.415]	0.792	2.293	[1.427,3.685]	0.001	2.201	[1.309,3.699]	0.003	0.003
rs6637	GSTZ1	G	0.358	0.825	[0.64,1.064]	0.139	1.719	[1.097,2.692]	0.018	2.082	[1.28,3.386]	0.003	0.012
rs4752904	PTPRJ	C	0.484	0.863	[0.681,1.095]	0.227	1.805	[1.141,2.855]	0.012	2.090	[1.281,3.411]	0.003	0.013
rs2249317	SIRPD	T	0.157	0.852	[0.613,1.184]	0.341	1.931	[1.184,3.148]	0.008	2.266	[1.313,3.912]	0.003	0.012
rs2243828	MPO	G	0.245	0.820	[0.615,1.092]	0.174	1.677	[1.073,2.623]	0.023	2.046	[1.246,3.36]	0.005	0.018
rs2071746	HMOX1	T	0.455	0.955	[0.747,1.221]	0.715	1.913	[1.218,3.005]	0.005	2.002	[1.235,3.246]	0.005	0.014
rs1042713	ADRB2	A	0.394	0.972	[0.762,1.238]	0.817	0.458	[0.279,0.752]	0.002	0.471	[0.279,0.796]	0.005	0.008
rs2070744	NOS3	C	0.310	0.874	[0.673,1.135]	0.314	1.759	[1.12,2.761]	0.014	2.011	[1.233,3.282]	0.005	0.020
rs1801157	CXCL12	A	0.164	0.752	[0.536,1.055]	0.099	1.704	[1.012,2.87]	0.045	2.265	[1.265,4.056]	0.006	0.021
rs4455491	UGT2B7	A	0.460	0.879	[0.69,1.119]	0.293	1.693	[1.097,2.614]	0.017	1.927	[1.206,3.079]	0.006	0.023
rs7438135	UGT2B7	G	0.463	0.879	[0.691,1.118]	0.293	1.672	[1.084,2.578]	0.020	1.902	[1.192,3.034]	0.007	0.026
rs7668258	UGT2B7	T	0.463	0.879	[0.691,1.118]	0.293	1.672	[1.084,2.578]	0.020	1.902	[1.192,3.034]	0.007	0.026
rs4554144	UGT2B7	C	0.462	0.887	[0.69,1.14]	0.348	1.708	[1.1,2.651]	0.017	1.926	[1.195,3.105]	0.007	0.026
rs7662029	UGT2B7	A	0.463	0.882	[0.693,1.121]	0.304	1.674	[1.086,2.582]	0.020	1.899	[1.19,3.031]	0.007	0.027
rs2271922	MEIS2	C	0.081	1.359	[0.867,2.129]	0.181	0.079	[0.01,0.618]	0.016	0.058	[0.007,0.468]	0.007	0.019
rs4364327	UGT2B7	C	0.453	0.850	[0.667,1.083]	0.188	1.600	[1.038,2.467]	0.033	1.883	[1.179,3.006]	0.008	0.029
rs487989	POLA2	A	0.153	0.990	[0.71,1.38]	0.954	1.997	[1.259,3.168]	0.003	2.017	[1.2,3.39]	0.008	0.011

rs4588522	UGT2B7	C	0.455	0.844	[0.663,1.075]	0.169	1.582	[1.029,2.433]	0.037	1.875	[1.177,2.987]	0.008	0.028
rs4337789	UGT2B7	A	0.454	0.854	[0.67,1.089]	0.204	1.601	[1.039,2.466]	0.033	1.873	[1.173,2.991]	0.009	0.031
rs582054	IL12A	A	0.429	1.048	[0.826,1.329]	0.701	0.534	[0.332,0.86]	0.010	0.510	[0.308,0.845]	0.009	0.028
rs630303	MUS81	G	0.419	1.433	[1.123,1.829]	0.004	0.746	[0.472,1.18]	0.211	0.521	[0.319,0.85]	0.009	0.004
rs458017	REV3L	C	0.061	0.867	[0.514,1.462]	0.592	2.443	[1.245,4.794]	0.009	2.818	[1.288,6.168]	0.010	0.021
rs2227314	IL12A	G	0.433	1.029	[0.812,1.306]	0.811	0.533	[0.333,0.852]	0.009	0.517	[0.314,0.852]	0.010	0.027
rs4150474	ERCC3	G	0.286	0.733	[0.557,0.964]	0.026	1.400	[0.898,2.183]	0.137	1.911	[1.17,3.121]	0.010	0.017
rs11940316	UGT2B7	T	0.463	0.879	[0.692,1.118]	0.294	1.628	[1.053,2.517]	0.028	1.851	[1.157,2.961]	0.010	0.037
rs582537	IL12A	A	0.429	1.046	[0.825,1.326]	0.712	0.544	[0.34,0.87]	0.011	0.520	[0.315,0.856]	0.010	0.031
rs10735510	ATF3	C	0.434	0.913	[0.721,1.156]	0.450	1.664	[1.084,2.557]	0.020	1.823	[1.15,2.888]	0.011	0.037
rs7441750	UGT2B7	G	0.472	0.938	[0.733,1.2]	0.610	1.742	[1.12,2.711]	0.014	1.858	[1.152,2.995]	0.011	0.034
rs3802762	CHST1	T	0.231	1.303	[0.976,1.741]	0.073	0.589	[0.331,1.049]	0.073	0.452	[0.245,0.835]	0.011	0.026
rs1256061	ESR2	A	0.435	0.991	[0.785,1.252]	0.943	0.532	[0.336,0.842]	0.007	0.536	[0.329,0.874]	0.012	0.025
rs607887	LRP5	T	0.351	0.812	[0.633,1.042]	0.102	1.466	[0.956,2.247]	0.079	1.804	[1.134,2.871]	0.013	0.036
rs3177429	GSTZ1	A	0.075	0.672	[0.411,1.1]	0.114	1.831	[0.924,3.625]	0.083	2.722	[1.237,5.99]	0.013	0.042
rs8030950	IGF1R	A	0.310	1.014	[0.789,1.302]	0.916	1.814	[1.188,2.772]	0.006	1.790	[1.131,2.834]	0.013	0.021
rs2602376	UGT1A10	T	0.244	0.851	[0.631,1.147]	0.289	1.680	[1.028,2.745]	0.038	1.974	[1.152,3.383]	0.013	0.047
rs2274406	ABCC4	T	0.399	0.844	[0.655,1.088]	0.191	1.539	[0.991,2.391]	0.055	1.823	[1.13,2.94]	0.014	0.046
rs2097461	XBP1	C	0.354	0.837	[0.652,1.073]	0.160	1.483	[0.975,2.254]	0.065	1.772	[1.122,2.797]	0.014	0.045
rs2056822	CYP4F8	A	0.263	0.941	[0.718,1.233]	0.657	1.742	[1.102,2.755]	0.018	1.853	[1.126,3.047]	0.015	0.044
rs1800468	B9D2	A	0.076	1.020	[0.651,1.6]	0.931	2.451	[1.307,4.596]	0.005	2.403	[1.184,4.876]	0.015	0.019
rs6030	F5	G	0.301	0.848	[0.651,1.105]	0.223	1.558	[0.991,2.448]	0.055	1.837	[1.124,3.002]	0.015	0.051
rs1799793	ERCC2	A	0.301	0.845	[0.656,1.09]	0.195	1.522	[0.982,2.357]	0.060	1.800	[1.12,2.892]	0.015	0.050
rs2368184	ABI1	T	0.492	0.766	[0.595,0.986]	0.039	1.411	[0.888,2.241]	0.145	1.841	[1.12,3.027]	0.016	0.026
rs3788409	XBP1	G	0.354	0.839	[0.652,1.078]	0.170	1.475	[0.966,2.251]	0.072	1.758	[1.109,2.788]	0.016	0.052
rs11421	FCER1G	C	0.148	0.923	[0.659,1.294]	0.644	1.873	[1.112,3.154]	0.018	2.028	[1.138,3.613]	0.016	0.044
rs3776432	NSUN2	A	0.323	1.010	[0.787,1.297]	0.935	1.756	[1.15,2.681]	0.009	1.738	[1.099,2.747]	0.018	0.032
rs1802061	GSTA4	A	0.048	0.507	[0.26,0.987]	0.046	1.612	[0.739,3.514]	0.230	3.179	[1.217,8.302]	0.018	0.047
rs608343	LRP5	G	0.365	0.832	[0.648,1.068]	0.149	1.460	[0.95,2.244]	0.084	1.756	[1.1,2.802]	0.018	0.054
rs1256063	ESR2	T	0.061	0.991	[0.612,1.605]	0.970	2.410	[1.235,4.702]	0.010	2.432	[1.159,5.101]	0.019	0.031
rs6874005	NSUN2	T	0.351	1.126	[0.887,1.429]	0.329	0.607	[0.372,0.989]	0.045	0.539	[0.321,0.904]	0.019	0.063
rs1049216	CASP3	C	0.292	0.881	[0.685,1.132]	0.322	1.519	[1,2.306]	0.050	1.724	[1.092,2.722]	0.019	0.065
rs628959	DPYD	G	0.246	1.081	[0.83,1.408]	0.565	0.515	[0.284,0.935]	0.029	0.477	[0.256,0.888]	0.020	0.065
rs5993883	COMT	G	0.482	1.049	[0.831,1.324]	0.690	1.817	[1.18,2.798]	0.007	1.733	[1.092,2.75]	0.020	0.025
rs4459610	ACE	A	0.448	0.741	[0.582,0.944]	0.015	1.289	[0.837,1.985]	0.250	1.739	[1.09,2.773]	0.020	0.018
rs2228468	CCBP2	C	0.357	1.120	[0.874,1.435]	0.370	0.597	[0.361,0.987]	0.044	0.533	[0.313,0.907]	0.020	0.068
rs994174	NRG3	G	0.387	0.977	[0.756,1.262]	0.858	0.519	[0.314,0.858]	0.011	0.531	[0.311,0.907]	0.021	0.038
rs40228	TPK1	T	0.205	1.196	[0.89,1.608]	0.235	0.557	[0.302,1.029]	0.062	0.466	[0.244,0.89]	0.021	0.063
rs505770	MMP12	A	0.081	1.264	[0.797,2.005]	0.320	0.283	[0.083,0.965]	0.044	0.224	[0.063,0.796]	0.021	0.064
rs1801131	MTHFR	C	0.287	0.915	[0.701,1.193]	0.512	1.638	[1.037,2.587]	0.034	1.790	[1.091,2.939]	0.021	0.067
rs2270422	GSTZ1	C	0.356	0.852	[0.661,1.099]	0.217	1.506	[0.959,2.365]	0.076	1.767	[1.085,2.878]	0.022	0.068

rs2180314	GSTA2	C	0.441	1.001	[0.787,1.273]	0.993	0.566	[0.358,0.895]	0.015	0.565	[0.346,0.922]	0.022	0.049
rs1800935	MSH6	C	0.268	1.066	[0.822,1.384]	0.629	0.537	[0.306,0.941]	0.030	0.503	[0.279,0.908]	0.023	0.071
rs10249476	LEP	T	0.368	0.881	[0.689,1.127]	0.314	1.521	[0.983,2.355]	0.060	1.726	[1.077,2.767]	0.023	0.076
rs6095558	PTGIS	T	0.226	1.079	[0.827,1.406]	0.576	0.525	[0.289,0.955]	0.035	0.487	[0.261,0.909]	0.024	0.077
rs5299	CYP11B1	A	0.409	0.809	[0.634,1.033]	0.089	1.397	[0.9,2.17]	0.136	1.727	[1.074,2.776]	0.024	0.053
rs2813545	ESR1	C	0.226	0.934	[0.701,1.246]	0.643	1.675	[1.053,2.666]	0.029	1.793	[1.08,2.979]	0.024	0.067
rs628031	SLC22A1	A	0.366	0.788	[0.618,1.006]	0.056	1.347	[0.875,2.073]	0.176	1.708	[1.071,2.725]	0.025	0.044
rs6482573	PDSS1	A	0.428	1.295	[1.013,1.656]	0.039	0.741	[0.469,1.171]	0.199	0.572	[0.351,0.933]	0.025	0.034
rs2167270	LEP	A	0.388	0.877	[0.688,1.118]	0.290	1.492	[0.969,2.297]	0.069	1.701	[1.068,2.71]	0.025	0.081
rs8192678	PPARGC1A	A	0.294	0.928	[0.708,1.216]	0.590	1.668	[1.033,2.692]	0.036	1.797	[1.074,3.007]	0.026	0.078
rs4348159	UGT2B7	T	0.118	1.372	[0.93,2.025]	0.111	0.469	[0.189,1.164]	0.103	0.341	[0.133,0.879]	0.026	0.052
rs861529	XRCC3	A	0.076	1.458	[0.937,2.267]	0.094	0.352	[0.104,1.184]	0.092	0.241	[0.069,0.843]	0.026	0.044
rs13817	MUS81	G	0.426	1.465	[1.136,1.889]	0.003	0.835	[0.526,1.325]	0.444	0.570	[0.347,0.937]	0.027	0.007
rs16754	WT1	G	0.149	1.561	[1.164,2.093]	0.003	0.703	[0.356,1.39]	0.311	0.451	[0.222,0.913]	0.027	0.004
rs827500	DPYD	T	0.240	1.081	[0.829,1.411]	0.565	0.535	[0.295,0.973]	0.040	0.495	[0.265,0.924]	0.027	0.087
rs348449	ALDH1A1	C	0.050	0.662	[0.357,1.229]	0.191	1.791	[0.865,3.711]	0.117	2.706	[1.117,6.556]	0.027	0.088
rs499009	DPYD	A	0.240	1.075	[0.824,1.403]	0.596	0.533	[0.293,0.968]	0.039	0.496	[0.266,0.925]	0.027	0.087
rs348445	ALDH1A1	T	0.051	0.640	[0.338,1.209]	0.169	1.820	[0.835,3.968]	0.132	2.845	[1.122,7.213]	0.028	0.087
rs3789452	ABCA4	A	0.282	0.974	[0.746,1.273]	0.848	1.712	[1.077,2.721]	0.023	1.757	[1.064,2.903]	0.028	0.066
rs4646285	SLC10A1	A	0.077	1.035	[0.677,1.582]	0.875	0.106	[0.014,0.79]	0.029	0.102	[0.013,0.781]	0.028	0.088
rs909253	LTA	C	0.384	1.150	[0.903,1.465]	0.256	0.658	[0.41,1.053]	0.081	0.572	[0.346,0.944]	0.029	0.085
rs8053	PSMA4	T	0.377	0.880	[0.69,1.123]	0.305	1.493	[0.962,2.316]	0.074	1.696	[1.056,2.724]	0.029	0.091
rs4648058	NFKB1	C	0.297	1.206	[0.942,1.543]	0.137	0.663	[0.398,1.102]	0.113	0.550	[0.321,0.941]	0.029	0.068
rs967935	ABCC3	T	0.080	1.442	[0.941,2.208]	0.093	0.367	[0.111,1.217]	0.101	0.255	[0.074,0.872]	0.029	0.046
rs2276583	ERCC3	A	0.366	1.240	[0.976,1.577]	0.079	0.706	[0.438,1.14]	0.154	0.570	[0.343,0.946]	0.030	0.054
rs4656994	NDUFS2	A	0.218	0.833	[0.62,1.119]	0.224	1.476	[0.925,2.357]	0.103	1.772	[1.056,2.974]	0.030	0.092
rs712704	PAX4	C	0.205	1.204	[0.902,1.606]	0.208	2.110	[1.319,3.377]	0.002	1.754	[1.054,2.917]	0.031	0.006
rs526645	DPYD	C	0.239	1.062	[0.814,1.386]	0.657	0.536	[0.295,0.973]	0.040	0.505	[0.271,0.941]	0.031	0.096
rs7386926	CYP11B1	A	0.414	0.815	[0.641,1.036]	0.095	1.351	[0.882,2.07]	0.166	1.658	[1.046,2.629]	0.031	0.067
rs1134095	CYP11B1	C	0.414	0.819	[0.644,1.041]	0.103	1.358	[0.886,2.08]	0.160	1.658	[1.045,2.629]	0.032	0.070
rs2687117	CYP3A4	T	0.057	1.086	[0.567,2.08]	0.804	0.180	[0.038,0.86]	0.032	0.166	[0.032,0.855]	0.032	0.090
rs737865	COMT	C	0.253	0.865	[0.659,1.135]	0.294	1.501	[0.943,2.389]	0.087	1.737	[1.049,2.876]	0.032	0.099
rs4648133	NFKB1	C	0.260	1.257	[0.967,1.635]	0.088	0.664	[0.381,1.158]	0.149	0.528	[0.294,0.948]	0.032	0.058
rs6664	CHST2	T	0.384	1.021	[0.793,1.314]	0.874	0.580	[0.356,0.945]	0.029	0.568	[0.337,0.956]	0.033	0.083
rs207932	XRCC5	T	0.418	0.813	[0.639,1.034]	0.092	1.335	[0.876,2.035]	0.178	1.643	[1.04,2.594]	0.033	0.069
rs13115754	PPP3CA	G	0.388	1.228	[0.962,1.568]	0.099	0.708	[0.439,1.142]	0.157	0.577	[0.347,0.958]	0.033	0.066
rs4536	CYP11B2	A	0.069	1.197	[0.741,1.936]	0.462	0.291	[0.083,1.025]	0.055	0.243	[0.066,0.897]	0.034	0.104
rs1892534	LEPR	A	0.417	0.999	[0.788,1.267]	0.992	1.646	[1.071,2.529]	0.023	1.648	[1.038,2.616]	0.034	0.072
rs3093930	PARP2	T	0.391	1.193	[0.926,1.537]	0.173	0.687	[0.426,1.107]	0.123	0.576	[0.346,0.96]	0.034	0.088
rs801720	CERK	T	0.453	0.962	[0.753,1.229]	0.757	1.607	[1.03,2.506]	0.037	1.670	[1.036,2.691]	0.035	0.094
rs4148416	ABCC3	T	0.082	1.307	[0.85,2.01]	0.223	0.349	[0.105,1.159]	0.086	0.267	[0.078,0.918]	0.036	0.086

rs7698628	SPARCL1	T	0.449	1.066	[0.831,1.368]	0.614	1.800	[1.138,2.846]	0.012	1.688	[1.034,2.757]	0.036	0.042
rs2275566	MTR	C	0.292	1.217	[0.947,1.563]	0.125	0.689	[0.416,1.141]	0.148	0.566	[0.332,0.965]	0.037	0.077
rs1801196	WRN	T	0.292	0.818	[0.627,1.067]	0.139	1.372	[0.877,2.147]	0.166	1.677	[1.03,2.732]	0.038	0.092
rs2741045	UGT1A10	T	0.248	0.912	[0.688,1.209]	0.522	1.587	[0.98,2.572]	0.061	1.740	[1.031,2.937]	0.038	0.113
rs2741046	UGT1A10	C	0.248	0.912	[0.688,1.209]	0.522	1.587	[0.98,2.572]	0.061	1.740	[1.031,2.937]	0.038	0.113
rs338599	CYP2S1	C	0.065	0.690	[0.41,1.162]	0.163	1.570	[0.812,3.036]	0.180	2.274	[1.046,4.944]	0.038	0.111
rs121	OSBPL3	A	0.473	1.195	[0.946,1.51]	0.136	0.733	[0.476,1.129]	0.159	0.613	[0.386,0.975]	0.039	0.088
rs7441774	UGT2B7	G	0.419	0.854	[0.654,1.115]	0.247	1.498	[0.912,2.458]	0.110	1.753	[1.029,2.988]	0.039	0.110
rs1049544	SPARCL1	G	0.450	1.072	[0.835,1.378]	0.584	1.797	[1.135,2.847]	0.012	1.676	[1.024,2.742]	0.040	0.043
rs3822430	SRD5A1	C	0.358	1.115	[0.885,1.405]	0.357	0.671	[0.425,1.061]	0.088	0.602	[0.37,0.979]	0.041	0.121
rs1368408	SCGB3A2	A	0.176	1.384	[1.027,1.864]	0.033	0.698	[0.372,1.309]	0.262	0.504	[0.261,0.976]	0.042	0.038
rs26784	MSH3	C	0.374	0.767	[0.596,0.987]	0.039	1.254	[0.81,1.942]	0.310	1.635	[1.017,2.628]	0.042	0.051
rs2618346	DUSP1	T	0.088	0.856	[0.559,1.311]	0.474	1.828	[0.946,3.536]	0.073	2.137	[1.026,4.449]	0.042	0.124
rs408820	GSTA4	G	0.054	0.561	[0.304,1.036]	0.065	1.455	[0.676,3.133]	0.338	2.593	[1.033,6.51]	0.042	0.089
rs10018198	Intergenic	C	0.207	0.842	[0.618,1.148]	0.278	1.507	[0.9,2.525]	0.119	1.789	[1.018,3.146]	0.043	0.126
rs7823144	LSM1	A	0.120	1.128	[0.781,1.631]	0.520	0.453	[0.194,1.056]	0.067	0.401	[0.165,0.973]	0.043	0.130
rs3806798	IL15	T	0.101	1.056	[0.716,1.556]	0.784	2.065	[1.141,3.738]	0.017	1.956	[1.019,3.755]	0.044	0.056
rs2741872	CYP3A7	A	0.150	1.394	[0.996,1.95]	0.053	0.677	[0.349,1.314]	0.249	0.486	[0.241,0.981]	0.044	0.056
rs811925	PRDM1	C	0.156	1.138	[0.83,1.56]	0.421	0.522	[0.252,1.082]	0.081	0.459	[0.214,0.981]	0.045	0.130
rs4674258	IL8RB	T	0.485	0.987	[0.785,1.24]	0.909	0.620	[0.405,0.949]	0.028	0.628	[0.398,0.99]	0.045	0.087
rs3766730	TNFRSF1B	T	0.148	0.605	[0.419,0.871]	0.007	1.161	[0.657,2.054]	0.607	1.921	[1.014,3.639]	0.045	0.018
rs1249958	PPP1R1A	T	0.013	0.705	[0.146,3.418]	0.665	5.646	[1.183,26.958]	0.030	8.005	[1.038,61.719]	0.046	0.070
rs17342647	CYP3A43	T	0.089	0.951	[0.624,1.45]	0.817	1.949	[1.025,3.706]	0.042	2.049	[1.011,4.15]	0.046	0.106
rs3020314	ESR1	C	0.414	1.244	[0.977,1.584]	0.077	0.761	[0.484,1.196]	0.236	0.611	[0.377,0.992]	0.046	0.075
rs3176879	VCAM1	G	0.077	1.398	[0.862,2.268]	0.175	0.453	[0.158,1.302]	0.142	0.324	[0.107,0.986]	0.047	0.106
rs3734354	SIM1	A	0.122	0.970	[0.673,1.399]	0.872	1.869	[1.031,3.388]	0.039	1.926	[1.007,3.684]	0.048	0.106
rs11959820	PPARGC1B	A	0.061	0.581	[0.329,1.028]	0.062	1.394	[0.665,2.92]	0.379	2.398	[1.009,5.701]	0.048	0.089
rs7208693	MPO	A	0.089	1.265	[0.854,1.872]	0.241	0.424	[0.149,1.208]	0.108	0.336	[0.114,0.991]	0.048	0.114
rs246230	ABCC1	T	0.179	1.049	[0.772,1.424]	0.761	1.779	[1.102,2.871]	0.018	1.696	[1.004,2.865]	0.048	0.062
rs816060	TNFRSF1B	C	0.367	0.775	[0.606,0.991]	0.042	1.248	[0.805,1.935]	0.321	1.610	[1.003,2.585]	0.048	0.057
rs3176875	VCAM1	A	0.045	1.669	[0.974,2.86]	0.062	0.345	[0.074,1.594]	0.173	0.206	[0.043,0.993]	0.049	0.052
rs1887994	ESR2	T	0.082	1.397	[0.93,2.1]	0.107	0.472	[0.165,1.353]	0.162	0.338	[0.114,0.999]	0.050	0.077
rs3821107	XRCC5	G	0.267	1.182	[0.903,1.548]	0.223	0.673	[0.396,1.145]	0.144	0.570	[0.324,1.001]	0.050	0.126
rs3746101	MKNK2	T	0.076	1.327	[0.854,2.061]	0.208	0.382	[0.113,1.291]	0.121	0.288	[0.082,1.005]	0.051	0.108
rs1327474	IFNGR1	G	0.364	0.754	[0.584,0.973]	0.030	1.221	[0.78,1.91]	0.382	1.619	[0.997,2.628]	0.051	0.047
rs2410558	NAT2	T	0.320	1.036	[0.803,1.336]	0.786	1.651	[1.068,2.552]	0.024	1.594	[0.996,2.549]	0.052	0.078
rs2695232	SOD3	C	0.445	1.117	[0.871,1.433]	0.384	0.674	[0.417,1.087]	0.106	0.603	[0.362,1.005]	0.052	0.150
rs2267665	PPARD	A	0.163	0.740	[0.525,1.044]	0.086	1.307	[0.785,2.178]	0.304	1.767	[0.992,3.145]	0.053	0.103
rs2239815	XBP1	C	0.382	0.805	[0.624,1.04]	0.097	1.290	[0.831,2.002]	0.257	1.601	[0.993,2.582]	0.053	0.098
rs1029702	NPC2	A	0.213	0.978	[0.727,1.315]	0.881	1.647	[1.015,2.674]	0.043	1.685	[0.992,2.861]	0.054	0.118
rs3087461	WT1	T	0.089	0.999	[0.664,1.502]	0.995	0.303	[0.094,0.98]	0.046	0.303	[0.09,1.019]	0.054	0.135

rs1128503	ABCB1	T	0.392	1.025	[0.802,1.312]	0.842	0.622	[0.385,1.004]	0.052	0.607	[0.365,1.008]	0.054	0.135
rs3774936	NFKB1	T	0.285	1.249	[0.962,1.621]	0.095	0.718	[0.421,1.224]	0.223	0.575	[0.327,1.009]	0.054	0.087
rs1052555	ERCC2	T	0.280	0.839	[0.646,1.09]	0.188	1.355	[0.864,2.126]	0.186	1.615	[0.992,2.63]	0.054	0.132
rs7926138	MRE11A	A	0.054	1.550	[0.874,2.748]	0.134	0.418	[0.118,1.483]	0.177	0.269	[0.071,1.026]	0.055	0.104
rs9808753	IFNGR2	G	0.150	1.160	[0.843,1.597]	0.361	1.969	[1.2,3.231]	0.007	1.697	[0.989,2.911]	0.055	0.025
rs12418	CHST3	A	0.433	0.941	[0.744,1.19]	0.611	1.468	[0.962,2.24]	0.075	1.561	[0.991,2.459]	0.055	0.153
rs35595	ABCC1	A	0.200	1.022	[0.755,1.384]	0.887	1.711	[1.057,2.767]	0.029	1.673	[0.989,2.832]	0.055	0.089
rs2279574	DUSP6	A	0.491	0.967	[0.756,1.237]	0.790	0.599	[0.379,0.946]	0.028	0.620	[0.38,1.011]	0.055	0.090
rs1609519	DPYD	G	0.238	1.062	[0.813,1.386]	0.660	0.587	[0.329,1.048]	0.071	0.553	[0.302,1.014]	0.056	0.157
rs3218536	XRCC2	A	0.066	1.868	[1.226,2.846]	0.004	0.578	[0.178,1.879]	0.362	0.310	[0.093,1.031]	0.056	0.007
rs3774932	NFKB1	A	0.422	0.837	[0.657,1.066]	0.149	1.308	[0.855,2.002]	0.215	1.564	[0.987,2.477]	0.057	0.124
rs2452600	PDLIM5	T	0.284	0.744	[0.564,0.981]	0.036	1.218	[0.763,1.943]	0.408	1.637	[0.984,2.725]	0.058	0.059
rs215067	ABCC1	G	0.054	1.093	[0.65,1.841]	0.737	2.363	[1.161,4.811]	0.018	2.161	[0.975,4.79]	0.058	0.060
rs4148947	CHST3	C	0.428	0.960	[0.757,1.218]	0.740	1.492	[0.978,2.276]	0.063	1.553	[0.985,2.448]	0.058	0.150
rs2267668	PPARD	G	0.163	0.765	[0.547,1.07]	0.118	1.328	[0.8,2.206]	0.273	1.737	[0.982,3.072]	0.058	0.124
rs4148944	CHST3	A	0.136	1.412	[0.991,2.014]	0.056	0.670	[0.323,1.39]	0.283	0.475	[0.22,1.026]	0.058	0.068
rs2020917	COMT	T	0.245	0.889	[0.669,1.182]	0.419	1.463	[0.914,2.342]	0.113	1.645	[0.983,2.752]	0.058	0.166
rs740603	COMT	G	0.481	0.956	[0.755,1.21]	0.709	1.505	[0.969,2.338]	0.069	1.574	[0.982,2.523]	0.059	0.158
rs769214	CAT	G	0.360	1.125	[0.884,1.43]	0.338	0.694	[0.432,1.116]	0.132	0.617	[0.372,1.023]	0.061	0.166
rs3739922	SETX	G	0.050	1.043	[0.61,1.783]	0.877	2.268	[1.087,4.731]	0.029	2.174	[0.963,4.907]	0.061	0.088
rs2151846	ABCA4	C	0.397	1.003	[0.786,1.281]	0.979	1.574	[1.015,2.442]	0.043	1.569	[0.978,2.518]	0.062	0.124
rs5301	CYP11B1	G	0.474	1.189	[0.942,1.501]	0.146	0.771	[0.504,1.178]	0.229	0.648	[0.411,1.023]	0.062	0.128
rs2968557	ADCK2	G	0.203	1.048	[0.753,1.458]	0.780	0.535	[0.275,1.04]	0.065	0.511	[0.252,1.035]	0.062	0.162
rs882709	SETX	G	0.105	0.840	[0.566,1.247]	0.387	1.529	[0.871,2.682]	0.139	1.820	[0.969,3.419]	0.063	0.176
rs1879612	IGF1R	C	0.428	1.100	[0.874,1.384]	0.417	1.680	[1.106,2.552]	0.015	1.528	[0.977,2.39]	0.063	0.046
rs9894946	TP53	A	0.141	1.029	[0.73,1.449]	0.871	0.461	[0.204,1.04]	0.062	0.448	[0.191,1.047]	0.064	0.164
rs1050152	SLC22A4	T	0.313	0.853	[0.657,1.108]	0.233	1.370	[0.86,2.183]	0.184	1.607	[0.973,2.655]	0.064	0.159
rs3818644	DNAJA1	T	0.328	0.917	[0.707,1.19]	0.516	1.454	[0.927,2.279]	0.103	1.585	[0.973,2.582]	0.064	0.179
rs2275801	ZMYND8	G	0.154	0.792	[0.537,1.168]	0.240	0.353	[0.157,0.793]	0.012	0.446	[0.189,1.051]	0.065	0.028
rs6018	F5	G	0.049	1.053	[0.623,1.781]	0.846	2.230	[1.1,4.52]	0.026	2.117	[0.954,4.696]	0.065	0.082
rs4713858	PPARD	A	0.147	0.763	[0.537,1.084]	0.131	1.337	[0.787,2.272]	0.283	1.753	[0.965,3.183]	0.065	0.141
rs2069763	IL2	T	0.325	1.359	[1.066,1.733]	0.013	0.854	[0.536,1.359]	0.505	0.628	[0.383,1.03]	0.065	0.028
rs1760215	DPYD	G	0.084	1.243	[0.824,1.875]	0.300	0.398	[0.122,1.295]	0.126	0.320	[0.095,1.076]	0.065	0.153
rs1399291	DPYD	T	0.472	0.823	[0.652,1.038]	0.100	1.260	[0.825,1.925]	0.284	1.532	[0.973,2.412]	0.066	0.110
rs3116496	CD28	C	0.155	0.841	[0.607,1.164]	0.295	0.389	[0.177,0.855]	0.019	0.463	[0.204,1.051]	0.066	0.046
rs1059262	ALKBH2	G	0.183	0.954	[0.707,1.288]	0.760	0.495	[0.254,0.964]	0.039	0.518	[0.257,1.044]	0.066	0.118
rs16941	BRCA1	G	0.302	0.849	[0.655,1.1]	0.215	1.335	[0.856,2.081]	0.202	1.573	[0.97,2.549]	0.066	0.161
rs3743259	IGF1R	G	0.328	0.932	[0.726,1.197]	0.584	1.446	[0.938,2.229]	0.095	1.551	[0.97,2.478]	0.067	0.182
rs2280509	FZD7	T	0.160	1.095	[0.8,1.498]	0.572	0.525	[0.247,1.116]	0.094	0.479	[0.218,1.052]	0.067	0.186
rs5182	AGTR1	T	0.432	0.900	[0.707,1.147]	0.395	1.397	[0.902,2.164]	0.134	1.552	[0.969,2.483]	0.067	0.185
rs5368	SELE	T	0.108	0.890	[0.601,1.319]	0.561	1.655	[0.908,3.017]	0.100	1.859	[0.957,3.612]	0.067	0.181

rs1061472	ATP7B	A	0.440	1.413	[1.114,1.791]	0.004	0.914	[0.592,1.412]	0.686	0.647	[0.406,1.031]	0.067	0.012
rs9954562	NFATC1	T	0.379	0.797	[0.625,1.017]	0.068	1.218	[0.801,1.851]	0.356	1.528	[0.97,2.406]	0.067	0.093
rs3136228	MSH6	G	0.329	0.987	[0.772,1.262]	0.917	0.604	[0.367,0.993]	0.047	0.612	[0.361,1.036]	0.068	0.137
rs1034809	PON2	A	0.260	1.219	[0.956,1.555]	0.111	0.753	[0.461,1.229]	0.256	0.617	[0.367,1.037]	0.068	0.112
rs2397118	GSTA5	C	0.061	1.381	[0.85,2.244]	0.193	0.425	[0.125,1.443]	0.170	0.308	[0.086,1.095]	0.069	0.137
rs5303	CYP11B1	T	0.388	0.799	[0.625,1.022]	0.074	1.239	[0.799,1.92]	0.338	1.550	[0.965,2.489]	0.070	0.098
rs593818	CYP4F12	A	0.447	0.794	[0.626,1.008]	0.058	1.219	[0.791,1.879]	0.369	1.535	[0.966,2.44]	0.070	0.084
rs652438	MMP12	G	0.064	1.008	[0.61,1.665]	0.975	0.255	[0.06,1.084]	0.064	0.253	[0.057,1.122]	0.071	0.177
rs2241342	ABCB11	A	0.367	0.915	[0.713,1.174]	0.486	1.407	[0.916,2.16]	0.119	1.537	[0.964,2.449]	0.071	0.195
rs6941583	POLH	T	0.080	0.590	[0.353,0.985]	0.044	0.147	[0.034,0.632]	0.010	0.249	[0.055,1.126]	0.071	0.007
rs3731722	AOX1	C	0.073	0.662	[0.403,1.089]	0.105	1.389	[0.692,2.79]	0.356	2.097	[0.938,4.689]	0.071	0.141
rs1132054	SULT2B1	C	0.494	1.005	[0.795,1.272]	0.964	1.537	[0.997,2.368]	0.051	1.528	[0.963,2.427]	0.072	0.146
rs2238475	ABCC1	C	0.049	1.592	[0.97,2.612]	0.066	0.248	[0.034,1.835]	0.172	0.156	[0.021,1.183]	0.072	0.060
rs3923647	TLR1	T	0.037	1.261	[0.691,2.301]	0.450	0.181	[0.023,1.447]	0.107	0.143	[0.017,1.192]	0.072	0.184
rs2297404	ABCA1	C	0.075	0.951	[0.615,1.471]	0.821	0.311	[0.095,1.018]	0.054	0.327	[0.096,1.111]	0.073	0.155
rs4148950	CHST3	A	0.432	0.961	[0.76,1.214]	0.739	1.451	[0.954,2.206]	0.082	1.510	[0.962,2.371]	0.073	0.186
rs4418320	CYP11B1	A	0.476	1.158	[0.916,1.463]	0.220	0.764	[0.5,1.167]	0.213	0.660	[0.418,1.04]	0.074	0.170
rs2839686	CXCL12	T	0.292	0.880	[0.683,1.135]	0.325	0.534	[0.319,0.896]	0.018	0.607	[0.351,1.05]	0.074	0.047
rs2056048	DPYD	C	0.481	0.837	[0.665,1.054]	0.130	1.259	[0.829,1.914]	0.280	1.505	[0.96,2.357]	0.074	0.136
rs1801018	BCL2	G	0.365	1.020	[0.787,1.321]	0.883	0.628	[0.381,1.037]	0.069	0.616	[0.362,1.05]	0.075	0.177
rs694564	ALDH1A1	A	0.053	0.690	[0.379,1.258]	0.226	1.561	[0.731,3.335]	0.250	2.263	[0.921,5.556]	0.075	0.197
rs7290221	COMT	G	0.486	0.980	[0.779,1.234]	0.866	1.495	[0.969,2.306]	0.069	1.525	[0.958,2.425]	0.075	0.177
rs2274405	ABCC4	T	0.343	0.811	[0.628,1.046]	0.107	1.248	[0.806,1.932]	0.320	1.539	[0.957,2.474]	0.075	0.128
rs1867351	SLC22A1	G	0.234	1.334	[1.029,1.728]	0.030	0.809	[0.48,1.366]	0.428	0.607	[0.349,1.054]	0.076	0.052
rs731027	CHST3	C	0.463	1.010	[0.8,1.275]	0.936	1.514	[0.997,2.299]	0.052	1.500	[0.957,2.349]	0.077	0.148
rs3181078	CCR1	G	0.069	0.803	[0.5,1.291]	0.366	1.673	[0.799,3.502]	0.172	2.082	[0.921,4.706]	0.078	0.210
rs928169	ATP7B	C	0.427	1.366	[1.078,1.731]	0.010	0.897	[0.58,1.388]	0.625	0.657	[0.411,1.048]	0.078	0.025
rs2602381	UGT1A10	T	0.479	1.302	[1.013,1.672]	0.039	0.856	[0.557,1.314]	0.476	0.657	[0.412,1.049]	0.078	0.073
rs207927	XRCC5	G	0.406	0.773	[0.605,0.986]	0.038	1.175	[0.763,1.808]	0.465	1.520	[0.953,2.424]	0.079	0.070
rs2335052	GATA2	A	0.185	0.984	[0.725,1.335]	0.917	0.526	[0.27,1.024]	0.059	0.534	[0.265,1.075]	0.079	0.166
rs3212948	ERCC1	G	0.464	0.957	[0.745,1.229]	0.728	1.469	[0.939,2.297]	0.092	1.535	[0.95,2.482]	0.080	0.203
rs13321	TNC	G	0.283	1.173	[0.906,1.519]	0.226	1.782	[1.153,2.755]	0.009	1.519	[0.95,2.429]	0.081	0.025
rs4986790	TLR4	G	0.049	0.882	[0.514,1.515]	0.650	0.137	[0.017,1.074]	0.058	0.155	[0.019,1.261]	0.081	0.158
rs3100701	HNMT	T	0.388	0.738	[0.576,0.947]	0.017	1.120	[0.726,1.726]	0.609	1.516	[0.948,2.424]	0.082	0.041
rs1041981	LTA	A	0.381	1.169	[0.914,1.495]	0.215	0.752	[0.472,1.2]	0.232	0.644	[0.392,1.058]	0.082	0.179
rs3118529	RXRA	C	0.388	0.980	[0.715,1.344]	0.901	0.548	[0.296,1.015]	0.056	0.559	[0.29,1.077]	0.082	0.160
rs2032582_A	ABCB1	T	0.384	0.958	[0.747,1.228]	0.735	0.607	[0.374,0.986]	0.044	0.634	[0.379,1.061]	0.083	0.131
rs9666607	CD44	A	0.271	0.715	[0.543,0.941]	0.017	1.117	[0.705,1.771]	0.637	1.564	[0.944,2.59]	0.083	0.042
rs5997917	LIMK2	A	0.179	1.174	[0.862,1.599]	0.310	0.659	[0.355,1.222]	0.185	0.561	[0.291,1.081]	0.084	0.205
rs6027	F5	G	0.050	1.098	[0.655,1.843]	0.722	2.209	[1.087,4.488]	0.028	2.011	[0.909,4.447]	0.084	0.091
rs602990	VAV2	T	0.436	1.015	[0.791,1.302]	0.909	1.561	[0.988,2.466]	0.056	1.538	[0.943,2.51]	0.085	0.160

rs3745202	PRX	C	0.156	1.133	[0.812,1.582]	0.462	0.557	[0.256,1.213]	0.141	0.492	[0.219,1.106]	0.086	0.223
rs2297345	PAK7	T	0.389	0.979	[0.757,1.266]	0.870	1.508	[0.953,2.387]	0.079	1.541	[0.941,2.524]	0.086	0.197
rs1641536	SHBG	A	0.208	1.168	[0.866,1.575]	0.310	0.666	[0.364,1.219]	0.187	0.570	[0.3,1.083]	0.086	0.209
rs7643645	NR1I2	G	0.339	0.930	[0.722,1.197]	0.573	1.409	[0.908,2.187]	0.126	1.516	[0.942,2.438]	0.086	0.228
rs207921	XRCC5	G	0.406	0.784	[0.615,1]	0.050	1.176	[0.766,1.807]	0.458	1.501	[0.943,2.388]	0.087	0.088
rs867186	PROCR	G	0.104	1.017	[0.685,1.508]	0.935	0.428	[0.165,1.108]	0.080	0.421	[0.156,1.133]	0.087	0.209
rs3813572	PSMA4	G	0.368	0.854	[0.667,1.092]	0.209	1.295	[0.831,2.017]	0.253	1.517	[0.941,2.445]	0.087	0.189
rs13330634	TNFRSF17	A	0.066	0.603	[0.34,1.069]	0.083	1.365	[0.603,3.093]	0.456	2.263	[0.886,5.778]	0.088	0.139
rs1059393	ENOSF1	C	0.138	0.980	[0.694,1.384]	0.908	0.485	[0.225,1.048]	0.066	0.495	[0.221,1.111]	0.088	0.183
rs800667	CYP3A43	G	0.141	1.192	[0.829,1.713]	0.343	0.616	[0.303,1.253]	0.181	0.517	[0.242,1.104]	0.088	0.220
rs7877	FMO1	A	0.346	1.068	[0.815,1.398]	0.634	1.648	[1.037,2.619]	0.034	1.544	[0.937,2.544]	0.088	0.105
rs2048074	NEIL3	A	0.266	1.030	[0.792,1.339]	0.827	0.633	[0.373,1.073]	0.090	0.614	[0.351,1.076]	0.089	0.216
rs3212961	ERCC1	A	0.160	1.197	[0.879,1.63]	0.254	0.661	[0.345,1.269]	0.214	0.553	[0.279,1.094]	0.089	0.194
rs2687105	CYP3A4	T	0.147	1.557	[1.036,2.339]	0.033	0.805	[0.402,1.612]	0.541	0.517	[0.242,1.106]	0.089	0.070
rs2287622	ABCB11	T	0.390	0.930	[0.728,1.187]	0.558	1.386	[0.906,2.121]	0.132	1.491	[0.941,2.364]	0.089	0.235
rs5993875	TXNRD2	A	0.409	1.082	[0.857,1.365]	0.509	0.713	[0.453,1.122]	0.144	0.659	[0.407,1.067]	0.090	0.238
rs3218222	CDKN2D	A	0.268	0.909	[0.684,1.207]	0.508	1.414	[0.886,2.259]	0.147	1.557	[0.933,2.598]	0.090	0.238
rs730720	CHST3	A	0.464	1.029	[0.817,1.294]	0.810	1.516	[0.996,2.307]	0.052	1.474	[0.94,2.31]	0.091	0.151
rs230532	NFKB1	A	0.302	1.202	[0.932,1.552]	0.157	0.760	[0.461,1.255]	0.284	0.632	[0.371,1.076]	0.091	0.165
rs4150416	ERCC3	G	0.345	0.886	[0.687,1.143]	0.351	1.331	[0.861,2.059]	0.199	1.502	[0.936,2.412]	0.092	0.233
UGT2B7_1d	UGT2B7	G	0.169	0.924	[0.673,1.27]	0.628	0.482	[0.233,0.993]	0.048	0.521	[0.244,1.113]	0.092	0.136
rs13181	ERCC2	G	0.331	0.910	[0.709,1.167]	0.458	1.360	[0.881,2.1]	0.165	1.495	[0.936,2.389]	0.093	0.242
rs13332630	TNFRSF17	C	0.065	0.626	[0.353,1.111]	0.109	1.398	[0.617,3.167]	0.421	2.232	[0.875,5.696]	0.093	0.166
rs2227999	XPC	A	0.053	1.006	[0.623,1.624]	0.982	0.180	[0.025,1.306]	0.090	0.179	[0.024,1.332]	0.093	0.235
rs3087455	CASP3	C	0.341	0.887	[0.689,1.143]	0.354	1.338	[0.86,2.084]	0.197	1.508	[0.934,2.437]	0.093	0.235
rs2706357	RAD50	C	0.080	1.490	[0.837,2.655]	0.175	0.594	[0.222,1.587]	0.299	0.398	[0.136,1.168]	0.093	0.190
rs6898097	RAD50	G	0.078	1.508	[0.843,2.698]	0.167	0.601	[0.226,1.6]	0.308	0.398	[0.136,1.168]	0.093	0.187
rs315952	IL1RN	C	0.304	1.113	[0.85,1.458]	0.436	1.690	[1.079,2.647]	0.022	1.518	[0.931,2.476]	0.094	0.065
rs6668589	PHGDH	C	0.298	1.138	[0.881,1.468]	0.322	0.728	[0.446,1.189]	0.205	0.640	[0.38,1.079]	0.094	0.227
rs2028373	AICDA	G	0.421	1.238	[0.969,1.58]	0.087	0.814	[0.514,1.289]	0.380	0.658	[0.403,1.075]	0.095	0.125
rs1045105	CATSPER4	A	0.119	0.757	[0.518,1.106]	0.150	1.317	[0.736,2.358]	0.354	1.740	[0.908,3.333]	0.095	0.186
rs2235937	PTPRU	G	0.251	0.999	[0.767,1.301]	0.994	0.614	[0.356,1.057]	0.078	0.614	[0.346,1.089]	0.096	0.207
rs2522406	RAD50	T	0.052	0.930	[0.488,1.773]	0.825	0.293	[0.082,1.044]	0.058	0.315	[0.081,1.225]	0.096	0.167
rs5745549	MSH4	A	0.055	0.802	[0.467,1.377]	0.424	1.609	[0.796,3.251]	0.185	2.005	[0.884,4.549]	0.096	0.249
rs2274750	TNC	A	0.040	1.784	[1.033,3.08]	0.038	0.313	[0.041,2.37]	0.261	0.176	[0.023,1.364]	0.096	0.049
rs3828193	CHST10	A	0.422	1.200	[0.944,1.526]	0.137	0.804	[0.516,1.251]	0.333	0.670	[0.417,1.075]	0.097	0.163
rs1803250	CTSB	G	0.110	1.378	[0.958,1.982]	0.084	2.311	[1.314,4.064]	0.004	1.678	[0.909,3.098]	0.098	0.007
rs168351	ALDH1A1	G	0.133	1.140	[0.813,1.601]	0.447	1.873	[1.088,3.225]	0.024	1.642	[0.912,2.957]	0.098	0.072
rs2706364	RAD50	A	0.081	1.444	[0.814,2.56]	0.209	0.584	[0.219,1.559]	0.283	0.405	[0.139,1.183]	0.098	0.210
rs1509618	LOC728442	C	0.441	1.016	[0.797,1.295]	0.898	0.676	[0.431,1.061]	0.089	0.666	[0.41,1.08]	0.099	0.221
rs296365	SULT2A1	G	0.310	1.017	[0.782,1.324]	0.899	0.651	[0.396,1.07]	0.091	0.640	[0.377,1.088]	0.099	0.224

rs2297518	NOS2	A	0.172	0.830	[0.602,1.146]	0.258	1.351	[0.795,2.297]	0.267	1.627	[0.911,2.906]	0.100	0.230
rs2240871	NCAPD2	G	0.166	1.183	[0.871,1.606]	0.283	0.659	[0.339,1.283]	0.220	0.557	[0.277,1.12]	0.101	0.220
rs10516782	PTPN13	G	0.149	0.910	[0.661,1.253]	0.564	1.453	[0.873,2.42]	0.151	1.597	[0.913,2.791]	0.101	0.257
rs5898	F2	A	0.073	0.438	[0.246,0.778]	0.005	0.955	[0.433,2.105]	0.908	2.182	[0.86,5.536]	0.101	0.019
rs3100702	HNMT	T	0.392	0.729	[0.57,0.934]	0.012	1.080	[0.701,1.665]	0.727	1.481	[0.926,2.368]	0.101	0.034
rs1051775	GSTA1	G	0.348	0.918	[0.714,1.18]	0.504	0.592	[0.361,0.97]	0.037	0.645	[0.382,1.089]	0.101	0.106
rs3765070	CYP4F11	T	0.445	1.083	[0.861,1.361]	0.497	0.739	[0.483,1.131]	0.164	0.683	[0.433,1.077]	0.101	0.260
rs7761731	CYP39A1	T	0.347	1.301	[1.008,1.68]	0.044	0.850	[0.529,1.368]	0.504	0.654	[0.393,1.086]	0.101	0.083
rs2230593	MST1R	A	0.069	0.991	[0.598,1.643]	0.973	0.286	[0.068,1.209]	0.089	0.288	[0.065,1.279]	0.102	0.234
rs667515	CCND1	C	0.372	0.820	[0.632,1.064]	0.136	1.229	[0.788,1.918]	0.363	1.498	[0.923,2.432]	0.102	0.176
rs1364283	HSD17B2	A	0.459	0.918	[0.723,1.166]	0.482	1.353	[0.877,2.088]	0.171	1.474	[0.926,2.348]	0.102	0.262
rs854570	PON1	C	0.438	0.988	[0.773,1.264]	0.925	1.459	[0.945,2.251]	0.088	1.476	[0.925,2.356]	0.102	0.220
rs12360	CYP3A7	C	0.179	1.267	[0.913,1.757]	0.156	0.723	[0.383,1.363]	0.316	0.570	[0.291,1.119]	0.102	0.177
rs9896405	EME1	G	0.025	1.547	[0.737,3.247]	0.249	0.259	[0.032,2.082]	0.204	0.167	[0.02,1.431]	0.103	0.197
rs10211	CYP3A7	G	0.179	1.266	[0.913,1.756]	0.158	0.723	[0.383,1.363]	0.316	0.571	[0.291,1.12]	0.103	0.179
rs2066470	MTHFR	T	0.103	0.904	[0.619,1.322]	0.604	0.381	[0.14,1.038]	0.059	0.421	[0.149,1.192]	0.103	0.159
rs5742659	IGF1	C	0.022	0.452	[0.144,1.423]	0.175	1.752	[0.468,6.559]	0.405	3.873	[0.756,19.825]	0.104	0.238
rs2522397	RAD50	T	0.085	1.247	[0.723,2.148]	0.428	0.539	[0.214,1.362]	0.191	0.433	[0.157,1.193]	0.105	0.268
rs3750898	DCLRE1A	G	0.294	0.907	[0.69,1.193]	0.486	1.367	[0.866,2.156]	0.179	1.506	[0.917,2.473]	0.106	0.270
rs3735586	PON2	A	0.245	1.181	[0.899,1.55]	0.232	0.744	[0.44,1.26]	0.271	0.630	[0.36,1.104]	0.106	0.219
rs2546893	IL12B	A	0.455	0.778	[0.612,0.988]	0.040	1.140	[0.74,1.756]	0.552	1.465	[0.922,2.33]	0.106	0.081
rs722921	ALDH1A1	A	0.437	0.988	[0.781,1.248]	0.917	0.669	[0.429,1.042]	0.076	0.677	[0.422,1.087]	0.107	0.204
rs9332098	CYP2C9	A	0.052	0.412	[0.209,0.812]	0.010	1.017	[0.402,2.574]	0.971	2.468	[0.823,7.401]	0.107	0.036
rs7843746	C8orf68	C	0.286	0.756	[0.579,0.988]	0.040	1.126	[0.724,1.751]	0.599	1.488	[0.917,2.414]	0.107	0.088
rs504122	SPRY2	T	0.317	1.002	[0.774,1.297]	0.986	1.502	[0.951,2.374]	0.081	1.499	[0.916,2.452]	0.107	0.213
rs5343	EDNRA	T	0.307	0.881	[0.684,1.135]	0.327	1.303	[0.838,2.025]	0.240	1.478	[0.918,2.38]	0.108	0.256
rs246228	ABCC1	C	0.351	0.896	[0.693,1.158]	0.401	1.325	[0.854,2.055]	0.210	1.479	[0.918,2.383]	0.108	0.269
rs9352	CHAF1A	C	0.444	0.938	[0.744,1.184]	0.592	0.641	[0.415,0.991]	0.046	0.683	[0.429,1.087]	0.108	0.131
rs156641	LIG1	A	0.331	0.868	[0.676,1.114]	0.267	1.275	[0.826,1.969]	0.273	1.469	[0.918,2.35]	0.108	0.242
rs1062372	JTV1	A	0.238	0.893	[0.676,1.18]	0.427	0.549	[0.313,0.961]	0.036	0.614	[0.339,1.114]	0.109	0.095
rs2509915	CNTF	G	0.453	1.009	[0.792,1.287]	0.940	0.675	[0.425,1.071]	0.095	0.669	[0.409,1.093]	0.109	0.237
rs1126580	IL8RB	A	0.418	0.911	[0.71,1.168]	0.462	0.596	[0.366,0.971]	0.038	0.654	[0.39,1.099]	0.109	0.104
rs3024680	IL4R	C	0.050	1.182	[0.685,2.041]	0.548	0.350	[0.084,1.468]	0.151	0.296	[0.067,1.313]	0.109	0.274
rs2687140	CYP3A7	A	0.177	1.319	[0.953,1.825]	0.095	0.776	[0.422,1.426]	0.414	0.588	[0.307,1.126]	0.109	0.141
rs2072052	CDK4	C	0.278	1.107	[0.859,1.428]	0.432	0.704	[0.416,1.192]	0.191	0.636	[0.365,1.107]	0.110	0.269
rs2960306	GRK4	T	0.376	0.859	[0.673,1.097]	0.224	1.252	[0.818,1.917]	0.300	1.457	[0.919,2.312]	0.110	0.230
rs10929302	UGT1A10	A	0.300	0.981	[0.748,1.286]	0.888	1.475	[0.928,2.342]	0.100	1.504	[0.912,2.479]	0.110	0.239
rs207928	XRCC5	A	0.406	0.774	[0.607,0.988]	0.039	1.128	[0.737,1.727]	0.579	1.457	[0.918,2.312]	0.110	0.084
rs3218651	POLQ	G	0.180	0.922	[0.681,1.248]	0.598	1.419	[0.874,2.304]	0.157	1.540	[0.907,2.613]	0.110	0.275
rs2286232	PON2	T	0.241	1.214	[0.924,1.595]	0.165	0.768	[0.452,1.302]	0.327	0.633	[0.361,1.11]	0.110	0.191
rs2299263	PON2	T	0.241	1.214	[0.924,1.595]	0.165	0.768	[0.452,1.302]	0.327	0.633	[0.361,1.11]	0.110	0.191

rs628816	DPYD	A	0.028	1.571	[0.738,3.345]	0.241	0.273	[0.034,2.206]	0.223	0.174	[0.02,1.49]	0.110	0.204
rs2185571	CYP2C8	T	0.252	0.764	[0.575,1.016]	0.065	1.178	[0.723,1.92]	0.510	1.542	[0.906,2.625]	0.111	0.120
rs4371387	APOB	A	0.181	0.885	[0.646,1.212]	0.445	1.424	[0.832,2.435]	0.197	1.609	[0.896,2.89]	0.111	0.279
rs1913474	ESR1	T	0.226	1.007	[0.758,1.338]	0.959	0.616	[0.348,1.093]	0.098	0.612	[0.334,1.12]	0.111	0.245
rs1801200	ERBB2	G	0.217	0.898	[0.682,1.182]	0.442	0.538	[0.296,0.981]	0.043	0.600	[0.32,1.126]	0.112	0.112
rs2238476	ABCC1	T	0.059	0.987	[0.606,1.608]	0.958	1.864	[0.92,3.778]	0.084	1.889	[0.863,4.136]	0.112	0.210
rs6032	F5	G	0.263	0.837	[0.625,1.12]	0.231	1.294	[0.79,2.12]	0.306	1.547	[0.904,2.647]	0.112	0.237
rs3774968	NFKB1	A	0.394	0.907	[0.713,1.154]	0.426	1.315	[0.859,2.012]	0.207	1.450	[0.916,2.294]	0.113	0.279
rs1130643	SPARCL1	G	0.178	0.775	[0.547,1.097]	0.151	1.275	[0.73,2.226]	0.393	1.645	[0.889,3.043]	0.113	0.203
rs3856806	PPARG	T	0.126	1.498	[1.064,2.108]	0.021	0.810	[0.39,1.68]	0.571	0.541	[0.252,1.158]	0.114	0.046
rs1677649	MSH3	A	0.276	0.936	[0.723,1.212]	0.616	0.597	[0.352,1.01]	0.055	0.637	[0.365,1.114]	0.114	0.152
rs5882	CETP	G	0.372	1.040	[0.816,1.327]	0.750	1.510	[0.982,2.32]	0.060	1.451	[0.915,2.302]	0.114	0.171
rs2032583	ABCB1	C	0.121	1.006	[0.696,1.456]	0.973	1.658	[0.946,2.904]	0.077	1.647	[0.886,3.061]	0.115	0.204
rs2299266	PON2	G	0.239	1.233	[0.938,1.62]	0.134	0.785	[0.463,1.331]	0.368	0.637	[0.363,1.116]	0.115	0.175
rs13112358	NEIL3	C	0.265	1.000	[0.771,1.298]	1.000	0.639	[0.378,1.081]	0.095	0.639	[0.366,1.116]	0.116	0.243
rs3918022	CCNK	G	0.419	1.071	[0.852,1.347]	0.557	1.531	[1.01,2.321]	0.045	1.430	[0.916,2.231]	0.116	0.128
rs2090949	CYP3A7	G	0.176	1.292	[0.934,1.787]	0.122	0.768	[0.419,1.41]	0.395	0.595	[0.311,1.137]	0.116	0.170
rs4698803	EGF	A	0.179	0.936	[0.688,1.274]	0.674	1.467	[0.875,2.46]	0.146	1.567	[0.894,2.747]	0.117	0.283
rs2470144	CYP19A1	A	0.444	1.108	[0.868,1.414]	0.409	0.749	[0.474,1.185]	0.217	0.676	[0.414,1.104]	0.118	0.284
rs6742078	UGT1A1	T	0.330	0.996	[0.766,1.295]	0.976	1.465	[0.938,2.29]	0.094	1.471	[0.907,2.388]	0.118	0.236
rs2740560	CYP3A7	A	0.179	1.252	[0.907,1.729]	0.172	0.748	[0.408,1.371]	0.348	0.597	[0.313,1.14]	0.118	0.206
rs2368564	REN	T	0.337	0.954	[0.736,1.237]	0.723	0.628	[0.384,1.026]	0.063	0.658	[0.39,1.112]	0.118	0.177
rs744389	PRX	T	0.154	0.896	[0.638,1.257]	0.525	0.474	[0.221,1.016]	0.055	0.529	[0.238,1.176]	0.118	0.145
rs246221	ABCC1	C	0.352	0.910	[0.705,1.176]	0.471	1.329	[0.857,2.061]	0.203	1.460	[0.907,2.35]	0.119	0.295
rs4524	F5	G	0.251	0.806	[0.606,1.072]	0.138	1.230	[0.754,2.005]	0.407	1.526	[0.897,2.596]	0.119	0.194
rs35587	ABCC1	C	0.352	0.900	[0.696,1.163]	0.421	1.314	[0.847,2.039]	0.223	1.460	[0.907,2.351]	0.119	0.292
rs4952220	SRD5A2	C	0.462	0.988	[0.78,1.253]	0.924	1.423	[0.929,2.181]	0.105	1.440	[0.91,2.279]	0.120	0.256
rs752760	CYP19A1	C	0.481	1.063	[0.83,1.36]	0.630	0.724	[0.462,1.136]	0.160	0.682	[0.42,1.105]	0.120	0.297
rs2037497	CYP3A7	C	0.175	1.292	[0.934,1.787]	0.121	0.774	[0.421,1.42]	0.407	0.599	[0.313,1.144]	0.121	0.173
rs1148459	TNFRSF1B	A	0.491	1.052	[0.836,1.323]	0.667	0.730	[0.475,1.123]	0.152	0.695	[0.438,1.101]	0.121	0.296
rs212082	ABCC1	C	0.174	1.047	[0.773,1.417]	0.769	0.619	[0.331,1.161]	0.135	0.592	[0.305,1.148]	0.121	0.291
rs10517	NQO1	T	0.135	0.972	[0.69,1.371]	0.874	0.527	[0.253,1.1]	0.088	0.542	[0.25,1.177]	0.122	0.233
rs4525	F5	G	0.244	0.809	[0.605,1.082]	0.153	1.233	[0.756,2.013]	0.401	1.524	[0.894,2.6]	0.122	0.208
rs2299264	PON2	T	0.238	1.207	[0.918,1.586]	0.177	0.775	[0.457,1.314]	0.344	0.642	[0.366,1.126]	0.122	0.211
rs2222411	CYP3A7	G	0.175	1.291	[0.933,1.784]	0.123	0.774	[0.421,1.421]	0.408	0.600	[0.314,1.146]	0.122	0.175
rs2687142	CYP3A7	T	0.175	1.291	[0.933,1.784]	0.123	0.774	[0.421,1.421]	0.408	0.600	[0.314,1.146]	0.122	0.175
rs2687145	CYP3A7	T	0.175	1.291	[0.933,1.784]	0.123	0.774	[0.421,1.421]	0.408	0.600	[0.314,1.146]	0.122	0.175
rs2037499	CYP3A7	C	0.175	1.289	[0.933,1.782]	0.124	0.773	[0.421,1.42]	0.407	0.600	[0.314,1.147]	0.122	0.177
rs2303317	ALDH1A1	T	0.450	0.949	[0.756,1.193]	0.655	0.662	[0.431,1.016]	0.059	0.697	[0.441,1.102]	0.122	0.165
rs2687143	CYP3A7	G	0.175	1.288	[0.932,1.781]	0.126	0.773	[0.421,1.419]	0.406	0.600	[0.314,1.147]	0.122	0.178
rs1357319	CYP3A7	A	0.175	1.289	[0.932,1.782]	0.125	0.773	[0.421,1.42]	0.407	0.600	[0.314,1.147]	0.122	0.177

rs680	IGF2	A	0.246	0.861	[0.655,1.132]	0.283	1.297	[0.801,2.101]	0.290	1.507	[0.896,2.535]	0.122	0.268
rs1798745	DPYD	T	0.025	1.799	[0.787,4.115]	0.164	0.320	[0.039,2.65]	0.291	0.178	[0.02,1.592]	0.123	0.185
rs1564483	BCL2	A	0.232	0.897	[0.679,1.187]	0.448	0.543	[0.296,0.995]	0.048	0.605	[0.319,1.145]	0.123	0.123
rs8187915	ALDH1A1	T	0.445	0.966	[0.767,1.217]	0.771	0.671	[0.435,1.036]	0.072	0.695	[0.437,1.104]	0.123	0.197
rs4526098	RAD50	G	0.049	1.024	[0.517,2.028]	0.946	0.327	[0.084,1.273]	0.107	0.320	[0.075,1.364]	0.123	0.265
rs3748433	CEP250	T	0.095	0.878	[0.57,1.353]	0.556	1.551	[0.814,2.955]	0.182	1.766	[0.856,3.64]	0.124	0.302
rs6752026	APOB	A	0.027	0.686	[0.275,1.713]	0.420	1.758	[0.675,4.58]	0.248	2.562	[0.773,8.496]	0.124	0.301
rs2301159	SLC10A2	T	0.261	1.122	[0.867,1.452]	0.382	0.737	[0.444,1.222]	0.236	0.657	[0.384,1.123]	0.125	0.290
rs2193831	ABCB11	G	0.389	0.928	[0.726,1.185]	0.548	1.332	[0.869,2.042]	0.188	1.436	[0.905,2.281]	0.125	0.308
rs2976436	NEFL	T	0.414	0.989	[0.772,1.266]	0.928	1.422	[0.925,2.186]	0.108	1.438	[0.904,2.288]	0.125	0.262
rs16834521	MTR	G	0.397	0.883	[0.688,1.133]	0.328	1.292	[0.822,2.029]	0.267	1.463	[0.9,2.378]	0.125	0.283
rs2522393	RAD50	T	0.049	1.000	[0.51,1.961]	0.999	0.329	[0.087,1.244]	0.101	0.329	[0.079,1.364]	0.125	0.257
rs2706369	RAD50	T	0.049	1.000	[0.51,1.961]	0.999	0.329	[0.087,1.244]	0.101	0.329	[0.079,1.364]	0.125	0.257
rs10018239	PPARGC1A	G	0.386	1.038	[0.819,1.316]	0.757	0.714	[0.455,1.119]	0.142	0.688	[0.426,1.11]	0.125	0.298
rs2522395	RAD50	G	0.047	1.117	[0.566,2.205]	0.751	0.368	[0.098,1.387]	0.140	0.329	[0.08,1.363]	0.125	0.298
rs2706377	RAD50	G	0.047	1.115	[0.565,2.203]	0.753	0.368	[0.098,1.386]	0.140	0.330	[0.08,1.364]	0.126	0.298
rs212086	ABCC1	A	0.170	1.096	[0.812,1.478]	0.551	0.656	[0.352,1.224]	0.185	0.599	[0.31,1.155]	0.126	0.309
rs2287623	ABCB11	C	0.389	0.931	[0.729,1.19]	0.569	1.335	[0.872,2.046]	0.184	1.434	[0.903,2.277]	0.126	0.310
rs880303	GJA9	T	0.377	0.716	[0.556,0.922]	0.010	1.038	[0.669,1.611]	0.867	1.449	[0.9,2.333]	0.127	0.031
rs2267669	PPARD	G	0.161	0.767	[0.547,1.076]	0.125	1.214	[0.716,2.059]	0.471	1.583	[0.878,2.854]	0.127	0.201
rs2074087	ABCC1	C	0.162	1.387	[1.019,1.887]	0.037	0.817	[0.427,1.562]	0.541	0.589	[0.298,1.164]	0.128	0.078
rs2286194	HGF	A	0.197	1.177	[0.877,1.577]	0.277	0.721	[0.397,1.31]	0.283	0.613	[0.326,1.151]	0.128	0.262
rs2808630	CRP	C	0.258	1.307	[1.007,1.696]	0.044	0.856	[0.512,1.432]	0.555	0.655	[0.38,1.13]	0.128	0.090
rs10509681	CYP2C8	C	0.087	1.108	[0.743,1.653]	0.615	0.486	[0.174,1.356]	0.168	0.438	[0.151,1.269]	0.128	0.314
rs10017295	BST1	C	0.280	0.800	[0.613,1.043]	0.099	1.180	[0.744,1.87]	0.483	1.475	[0.894,2.433]	0.128	0.167
rs2243267	IL4	C	0.236	1.422	[1.073,1.883]	0.014	0.881	[0.489,1.588]	0.674	0.620	[0.334,1.149]	0.129	0.037
rs11804091	LEPR	G	0.155	1.351	[0.991,1.842]	0.057	0.803	[0.424,1.521]	0.501	0.594	[0.304,1.164]	0.129	0.106
rs872723	SHH	T	0.161	1.179	[0.855,1.626]	0.315	1.840	[1.083,3.125]	0.024	1.560	[0.878,2.774]	0.130	0.063
rs290861	DPYD	G	0.185	1.230	[0.912,1.658]	0.176	0.749	[0.408,1.377]	0.353	0.609	[0.321,1.157]	0.130	0.213
rs993568	DPYD	G	0.481	0.860	[0.682,1.084]	0.201	1.215	[0.8,1.846]	0.361	1.413	[0.902,2.214]	0.131	0.240
rs1799964	LTA	C	0.215	0.934	[0.694,1.258]	0.653	1.396	[0.867,2.248]	0.169	1.495	[0.887,2.518]	0.131	0.311
rs11515	C9orf53	G	0.137	1.109	[0.774,1.59]	0.573	1.812	[1.011,3.251]	0.046	1.634	[0.864,3.091]	0.131	0.132
rs2725362	WRN	T	0.448	1.001	[0.79,1.268]	0.995	0.696	[0.448,1.082]	0.107	0.696	[0.434,1.115]	0.132	0.267
rs1615035	ANKRD29	G	0.353	1.241	[0.977,1.575]	0.076	0.859	[0.549,1.345]	0.508	0.693	[0.43,1.117]	0.132	0.137
rs769224	COMT	A	0.049	1.175	[0.695,1.986]	0.546	0.376	[0.09,1.583]	0.182	0.320	[0.073,1.409]	0.132	0.314
rs405509	APOE	A	0.440	0.862	[0.68,1.092]	0.219	1.218	[0.803,1.848]	0.354	1.413	[0.901,2.216]	0.132	0.254
rs1567868	IL8RA	C	0.093	1.332	[0.901,1.969]	0.150	0.694	[0.31,1.558]	0.376	0.521	[0.223,1.218]	0.133	0.197
rs6003	F13B	G	0.174	1.129	[0.8,1.595]	0.490	0.669	[0.354,1.265]	0.216	0.592	[0.299,1.174]	0.133	0.322
rs216321	VWF	T	0.082	1.066	[0.703,1.617]	0.762	1.829	[0.963,3.471]	0.065	1.715	[0.848,3.469]	0.134	0.182
rs949037	BCL2	T	0.435	0.983	[0.769,1.255]	0.889	1.418	[0.907,2.215]	0.125	1.443	[0.893,2.33]	0.134	0.291
rs7731453	HMMR	A	0.100	0.835	[0.556,1.252]	0.382	1.429	[0.757,2.698]	0.271	1.712	[0.846,3.463]	0.135	0.318

rs1514347	ESR1	A	0.224	0.990	[0.746,1.313]	0.945	0.625	[0.353,1.106]	0.107	0.631	[0.345,1.154]	0.135	0.269
rs4253211	ERCC6	C	0.087	0.891	[0.588,1.349]	0.585	0.395	[0.142,1.101]	0.076	0.443	[0.153,1.288]	0.135	0.193
rs2161811	ALDH1A1	G	0.449	0.976	[0.776,1.228]	0.838	0.689	[0.448,1.059]	0.089	0.705	[0.445,1.117]	0.136	0.236
rs3730849	LIG1	T	0.338	0.902	[0.705,1.154]	0.412	1.285	[0.834,1.979]	0.255	1.425	[0.894,2.271]	0.137	0.320
rs5918	ITGB3	C	0.122	0.810	[0.566,1.159]	0.249	0.411	[0.175,0.966]	0.041	0.508	[0.208,1.24]	0.137	0.079
rs3322	LOC100129773	A	0.070	0.634	[0.386,1.039]	0.071	1.205	[0.565,2.566]	0.629	1.901	[0.816,4.431]	0.137	0.149
rs1105880	UGT1A10	C	0.345	0.911	[0.708,1.171]	0.466	1.310	[0.839,2.045]	0.234	1.439	[0.89,2.325]	0.138	0.328
rs2706358	RAD50	A	0.047	1.136	[0.578,2.232]	0.711	0.384	[0.1,1.469]	0.162	0.338	[0.081,1.415]	0.138	0.326
rs1799809	PROC	G	0.458	0.989	[0.76,1.286]	0.932	1.451	[0.905,2.325]	0.122	1.468	[0.884,2.437]	0.138	0.288
rs751019	PTK2B	C	0.419	1.077	[0.849,1.366]	0.541	1.523	[0.994,2.336]	0.054	1.415	[0.894,2.238]	0.138	0.146
rs2976437	NEFL	G	0.416	0.996	[0.779,1.274]	0.973	1.413	[0.919,2.174]	0.115	1.419	[0.893,2.257]	0.139	0.279
rs888580	ADRB3	A	0.349	0.888	[0.694,1.138]	0.348	1.265	[0.819,1.952]	0.289	1.424	[0.892,2.273]	0.139	0.311
rs2522391	RAD50	A	0.048	1.033	[0.528,2.021]	0.924	0.356	[0.095,1.335]	0.126	0.344	[0.084,1.416]	0.139	0.298
rs3739942	KIAA1984	G	0.268	1.034	[0.797,1.343]	0.799	1.488	[0.952,2.327]	0.081	1.439	[0.888,2.331]	0.139	0.218
rs2585	IGF2	T	0.256	0.842	[0.644,1.102]	0.210	1.236	[0.772,1.979]	0.377	1.468	[0.882,2.442]	0.139	0.259
rs450808	ABCG1	A	0.270	0.891	[0.687,1.158]	0.389	0.595	[0.36,0.983]	0.043	0.667	[0.39,1.141]	0.139	0.106
rs2740574	CYP3A4	G	0.146	1.498	[0.969,2.317]	0.069	0.842	[0.425,1.67]	0.623	0.562	[0.262,1.207]	0.140	0.147
rs2306168	SLCO2B1	T	0.072	1.162	[0.694,1.943]	0.568	0.511	[0.183,1.422]	0.198	0.440	[0.148,1.31]	0.140	0.337
rs299295	HMMR	T	0.248	1.020	[0.781,1.332]	0.882	0.667	[0.391,1.136]	0.136	0.654	[0.371,1.151]	0.140	0.312
rs1137115	CYP2A6	A	0.251	1.127	[0.861,1.476]	0.385	1.630	[1.035,2.569]	0.035	1.447	[0.884,2.367]	0.141	0.093
rs16940	BRCA1	C	0.303	0.848	[0.654,1.1]	0.215	1.223	[0.78,1.917]	0.380	1.442	[0.885,2.349]	0.141	0.265
rs1060915	BRCA1	C	0.303	0.848	[0.654,1.099]	0.213	1.222	[0.78,1.915]	0.381	1.441	[0.885,2.347]	0.141	0.264
rs6873545	GHR	C	0.294	1.056	[0.818,1.365]	0.675	0.714	[0.438,1.166]	0.178	0.676	[0.401,1.14]	0.142	0.337
rs2071048	HNMT	C	0.407	0.786	[0.616,1.004]	0.054	1.116	[0.724,1.719]	0.619	1.419	[0.889,2.264]	0.142	0.117
rs2297595	DPYD	C	0.074	0.785	[0.497,1.239]	0.298	1.388	[0.702,2.743]	0.345	1.769	[0.825,3.791]	0.143	0.315
rs1052369	ANKRD29	A	0.486	1.212	[0.956,1.537]	0.111	0.852	[0.547,1.326]	0.477	0.703	[0.438,1.127]	0.143	0.181
rs1399290	DPYD	G	0.048	2.137	[1.242,3.677]	0.006	0.920	[0.314,2.692]	0.878	0.430	[0.139,1.33]	0.143	0.020
rs2266691	CCNH	G	0.011	0.878	[0.177,4.359]	0.874	3.938	[0.838,18.496]	0.082	4.484	[0.601,33.428]	0.143	0.196
rs2302465	BST1	T	0.102	1.188	[0.828,1.705]	0.349	0.617	[0.265,1.437]	0.263	0.519	[0.216,1.25]	0.143	0.298
rs715948	LRP1	A	0.297	1.120	[0.87,1.441]	0.381	1.591	[1.027,2.463]	0.037	1.421	[0.887,2.275]	0.144	0.097
rs3092906	ATM	G	0.033	0.940	[0.431,2.053]	0.877	0.204	[0.029,1.461]	0.114	0.217	[0.028,1.683]	0.144	0.286
rs7739752	PPARD	T	0.164	0.867	[0.592,1.269]	0.464	1.442	[0.772,2.693]	0.251	1.663	[0.841,3.289]	0.144	0.341
rs3100699	HNMT	C	0.037	1.833	[0.845,3.975]	0.125	0.599	[0.15,2.396]	0.469	0.327	[0.073,1.467]	0.144	0.202
rs2290272	SLC28A1	T	0.358	1.056	[0.831,1.342]	0.655	1.480	[0.971,2.256]	0.068	1.402	[0.891,2.206]	0.144	0.186
rs2544794	SULT2B1	A	0.171	1.016	[0.748,1.381]	0.919	0.606	[0.312,1.174]	0.137	0.596	[0.297,1.196]	0.145	0.319
rs914937	DPYD	A	0.048	2.129	[1.237,3.665]	0.006	0.921	[0.315,2.694]	0.880	0.432	[0.14,1.336]	0.145	0.021
rs10759326	IKBKAP	G	0.259	1.243	[0.949,1.629]	0.114	0.827	[0.493,1.385]	0.470	0.665	[0.384,1.152]	0.145	0.183
rs6063528	PTPN1	A	0.367	1.142	[0.896,1.456]	0.285	1.607	[1.047,2.468]	0.030	1.408	[0.888,2.231]	0.146	0.071
rs2228059	IL15RA	A	0.478	1.059	[0.84,1.334]	0.629	0.756	[0.495,1.155]	0.196	0.714	[0.454,1.124]	0.146	0.347
rs10018622	KLHL5	G	0.445	1.037	[0.813,1.322]	0.773	1.460	[0.95,2.245]	0.084	1.409	[0.887,2.237]	0.146	0.225
rs1800331	FANCA	T	0.071	0.988	[0.628,1.555]	0.960	0.396	[0.12,1.305]	0.128	0.401	[0.117,1.376]	0.146	0.312

rs231775	CTLA4	G	0.410	1.041	[0.823,1.317]	0.735	1.454	[0.956,2.213]	0.080	1.397	[0.89,2.192]	0.147	0.215
rs10018288	Intergenic	G	0.246	1.154	[0.873,1.524]	0.314	0.754	[0.438,1.296]	0.306	0.653	[0.368,1.161]	0.147	0.304
rs2058996	ABCB11	A	0.408	0.787	[0.615,1.007]	0.057	1.113	[0.722,1.717]	0.627	1.415	[0.885,2.26]	0.147	0.124
rs11615	ERCC1	C	0.488	0.948	[0.741,1.213]	0.672	1.350	[0.864,2.109]	0.188	1.424	[0.883,2.297]	0.148	0.347
rs1344642	STK36	A	0.457	1.089	[0.862,1.375]	0.476	0.775	[0.505,1.191]	0.245	0.712	[0.45,1.128]	0.148	0.346
rs1758566		C	0.104	0.628	[0.409,0.963]	0.033	0.281	[0.099,0.794]	0.017	0.447	[0.15,1.331]	0.148	0.009
rs6901410	PPARD	C	0.167	0.816	[0.553,1.206]	0.308	1.368	[0.721,2.594]	0.337	1.676	[0.832,3.375]	0.148	0.318
rs1295686	IL13	A	0.299	1.032	[0.794,1.342]	0.813	0.684	[0.405,1.157]	0.157	0.663	[0.38,1.158]	0.148	0.337
rs3750050	PTPN12	G	0.195	1.006	[0.752,1.347]	0.966	1.489	[0.914,2.427]	0.110	1.480	[0.87,2.517]	0.148	0.274
rs2234997	ATM	A	0.033	0.905	[0.413,1.981]	0.803	0.200	[0.028,1.43]	0.109	0.220	[0.028,1.714]	0.148	0.275
rs3743258	IGF1R	A	0.307	1.000	[0.764,1.308]	0.999	1.441	[0.914,2.272]	0.116	1.441	[0.878,2.366]	0.149	0.284
rs1047840	EXO1	A	0.389	1.024	[0.805,1.303]	0.846	0.718	[0.457,1.127]	0.149	0.701	[0.432,1.136]	0.149	0.329
rs3829888	ABCB11	C	0.054	1.380	[0.817,2.331]	0.228	0.537	[0.156,1.849]	0.324	0.389	[0.108,1.405]	0.150	0.253
rs1799801	ERCC4	C	0.268	0.962	[0.739,1.254]	0.777	1.377	[0.877,2.16]	0.164	1.430	[0.877,2.331]	0.151	0.338
rs189037	ATM	G	0.492	0.986	[0.78,1.247]	0.908	0.706	[0.461,1.08]	0.109	0.716	[0.453,1.13]	0.151	0.275
rs1838066	MBL2	G	0.337	0.926	[0.723,1.186]	0.542	1.306	[0.846,2.015]	0.229	1.410	[0.882,2.255]	0.151	0.357
rs2760501	JUN	G	0.202	1.146	[0.796,1.649]	0.463	0.690	[0.363,1.31]	0.257	0.602	[0.301,1.205]	0.152	0.352
rs836802	MSH3	G	0.244	0.956	[0.726,1.258]	0.748	0.616	[0.35,1.086]	0.094	0.645	[0.354,1.175]	0.152	0.244
rs3817074	BAX	T	0.106	1.087	[0.756,1.563]	0.652	0.589	[0.264,1.312]	0.195	0.542	[0.234,1.253]	0.152	0.358
rs17882248	IL5RA	G	0.352	0.994	[0.783,1.262]	0.958	0.692	[0.434,1.103]	0.121	0.696	[0.424,1.143]	0.152	0.298
rs230521	NFKB1	G	0.404	1.159	[0.913,1.472]	0.227	0.824	[0.534,1.273]	0.383	0.711	[0.446,1.134]	0.152	0.279
rs2687079	CYP3A7	A	0.180	1.273	[0.918,1.765]	0.149	0.793	[0.432,1.456]	0.455	0.623	[0.326,1.192]	0.153	0.223
rs2687084	CYP3A7	G	0.180	1.273	[0.918,1.765]	0.149	0.793	[0.432,1.456]	0.455	0.623	[0.326,1.192]	0.153	0.223
rs1851425	CYP3A7	C	0.180	1.271	[0.917,1.763]	0.151	0.792	[0.431,1.455]	0.453	0.623	[0.326,1.192]	0.153	0.224
rs2687078	CYP3A7	G	0.179	1.272	[0.917,1.764]	0.149	0.793	[0.432,1.456]	0.454	0.623	[0.326,1.193]	0.153	0.223
rs2740565	CYP3A7	A	0.180	1.271	[0.917,1.763]	0.150	0.792	[0.432,1.455]	0.453	0.623	[0.326,1.193]	0.153	0.224
rs2304821	PTPRB	A	0.100	1.001	[0.677,1.48]	0.996	0.520	[0.22,1.226]	0.135	0.519	[0.211,1.277]	0.153	0.322
rs1409986	PTGER3	T	0.064	0.908	[0.555,1.487]	0.703	0.310	[0.074,1.299]	0.109	0.341	[0.078,1.494]	0.154	0.269
rs776742	CYP3A7	A	0.180	1.269	[0.915,1.761]	0.153	0.792	[0.431,1.453]	0.451	0.624	[0.326,1.193]	0.154	0.227
rs1201689	MAPKBP1	G	0.370	0.867	[0.662,1.134]	0.297	1.254	[0.784,2.007]	0.345	1.448	[0.87,2.408]	0.154	0.318
rs838827	IKBKAP	T	0.074	1.090	[0.709,1.676]	0.694	0.496	[0.175,1.405]	0.187	0.455	[0.154,1.344]	0.154	0.363
rs3547	XRCC1	T	0.406	1.106	[0.872,1.403]	0.406	0.785	[0.506,1.219]	0.281	0.710	[0.443,1.138]	0.154	0.346
rs2515363	CNTF	C	0.452	1.001	[0.785,1.276]	0.992	0.703	[0.446,1.109]	0.130	0.702	[0.432,1.143]	0.155	0.310
rs2020902	CASP9	C	0.131	0.762	[0.525,1.107]	0.154	1.233	[0.677,2.247]	0.493	1.618	[0.834,3.139]	0.155	0.245
rs11247367	IGF1R	A	0.081	0.926	[0.589,1.455]	0.740	1.628	[0.806,3.287]	0.174	1.757	[0.808,3.822]	0.155	0.343
rs2272225	SHFM1	A	0.070	0.803	[0.487,1.324]	0.390	1.437	[0.71,2.907]	0.314	1.789	[0.8,3.998]	0.156	0.360
rs1801516	ATM	A	0.110	1.026	[0.711,1.481]	0.889	1.629	[0.907,2.927]	0.103	1.587	[0.838,3.007]	0.156	0.262
rs8177877	GCSH	G	0.024	1.637	[0.74,3.619]	0.224	0.532	[0.122,2.322]	0.401	0.325	[0.069,1.538]	0.156	0.274
rs2068604	PON2	T	0.242	1.204	[0.916,1.582]	0.183	0.806	[0.478,1.358]	0.417	0.669	[0.384,1.167]	0.157	0.251
rs4917636	CYP2C9	G	0.099	1.023	[0.701,1.493]	0.905	0.512	[0.203,1.287]	0.154	0.500	[0.191,1.306]	0.157	0.350
rs28948385	UGT1A8	G	0.052	0.491	[0.225,1.068]	0.073	1.154	[0.436,3.052]	0.773	2.351	[0.719,7.687]	0.157	0.179

rs10475	ATF3	T	0.233	0.976	[0.738,1.292]	0.867	0.626	[0.35,1.122]	0.115	0.641	[0.347,1.187]	0.157	0.290
rs2237586	PON2	T	0.222	1.239	[0.939,1.635]	0.130	0.822	[0.482,1.404]	0.474	0.664	[0.376,1.172]	0.158	0.206
rs2069810	IL5	G	0.057	0.950	[0.522,1.729]	0.867	0.387	[0.121,1.237]	0.110	0.408	[0.117,1.417]	0.158	0.278
rs1471000	HNMT	C	0.026	1.939	[0.865,4.348]	0.108	0.560	[0.11,2.856]	0.485	0.289	[0.051,1.623]	0.158	0.182
rs397589	CBS	G	0.498	0.977	[0.772,1.237]	0.846	0.698	[0.451,1.08]	0.106	0.714	[0.447,1.14]	0.159	0.271
rs160632	RIOK2	G	0.425	1.143	[0.906,1.441]	0.260	0.820	[0.533,1.262]	0.367	0.718	[0.453,1.138]	0.159	0.302
rs1800590	LPL	G	0.084	1.296	[0.809,2.077]	0.280	0.681	[0.297,1.56]	0.364	0.525	[0.215,1.286]	0.159	0.316
rs1061040	SLC7A7	A	0.168	1.022	[0.721,1.446]	0.905	0.603	[0.303,1.199]	0.150	0.591	[0.284,1.228]	0.159	0.339
rs4833095	TLR1	C	0.362	1.150	[0.882,1.5]	0.303	0.790	[0.485,1.285]	0.343	0.687	[0.408,1.158]	0.159	0.322
rs17098707	GRK5	T	0.056	0.502	[0.245,1.029]	0.060	1.087	[0.447,2.644]	0.854	2.166	[0.739,6.35]	0.159	0.157
rs7803574	SHFM1	T	0.070	0.804	[0.487,1.325]	0.391	1.431	[0.707,2.897]	0.319	1.782	[0.797,3.983]	0.159	0.366
rs1364726	XRCC5	T	0.136	1.325	[0.946,1.857]	0.102	0.797	[0.407,1.562]	0.509	0.602	[0.296,1.222]	0.160	0.175
rs11669576	LDLR	A	0.069	0.591	[0.335,1.042]	0.069	1.147	[0.513,2.567]	0.738	1.942	[0.769,4.903]	0.160	0.163
rs4148221	ABCG8	T	0.167	1.270	[0.939,1.718]	0.120	0.799	[0.431,1.479]	0.475	0.629	[0.329,1.202]	0.161	0.193
rs915927	XRCC1	G	0.429	1.135	[0.898,1.434]	0.289	0.814	[0.528,1.255]	0.352	0.717	[0.451,1.141]	0.161	0.318
rs2070682	SERPINE1	C	0.429	1.095	[0.863,1.39]	0.453	0.785	[0.509,1.211]	0.274	0.717	[0.45,1.141]	0.161	0.364
rs7751481	PPARD	A	0.310	0.767	[0.585,1.005]	0.054	1.091	[0.696,1.711]	0.705	1.423	[0.869,2.33]	0.161	0.128
rs2687081	CYP3A7	C	0.180	1.275	[0.919,1.768]	0.145	0.802	[0.437,1.473]	0.477	0.629	[0.329,1.204]	0.162	0.227
rs2299267	PON2	G	0.168	0.913	[0.659,1.264]	0.583	0.546	[0.276,1.08]	0.082	0.598	[0.291,1.229]	0.162	0.207
rs8192707	PLCG1	G	0.139	1.169	[0.849,1.611]	0.338	0.703	[0.357,1.387]	0.309	0.601	[0.295,1.226]	0.162	0.327
rs2241339	ABCB11	T	0.113	1.184	[0.81,1.732]	0.383	0.649	[0.292,1.443]	0.289	0.548	[0.236,1.274]	0.162	0.345
rs1471001	HNMT	G	0.026	1.939	[0.864,4.348]	0.108	0.571	[0.113,2.88]	0.498	0.295	[0.053,1.638]	0.163	0.186
rs4148211	ABCG8	G	0.361	1.050	[0.82,1.344]	0.699	0.728	[0.447,1.184]	0.201	0.693	[0.414,1.161]	0.164	0.377
rs1496496	IGFBP3	G	0.382	0.988	[0.774,1.26]	0.923	0.698	[0.442,1.103]	0.123	0.706	[0.433,1.153]	0.164	0.304
rs17006837	HELQ	G	0.086	1.388	[0.748,2.576]	0.299	0.638	[0.238,1.709]	0.372	0.460	[0.154,1.374]	0.164	0.342
rs12828016	WNK1	T	0.384	1.000	[0.78,1.282]	0.998	0.701	[0.439,1.12]	0.137	0.701	[0.424,1.157]	0.164	0.325
rs2855262	SOD3	T	0.441	1.011	[0.785,1.303]	0.931	0.704	[0.436,1.136]	0.150	0.696	[0.418,1.161]	0.165	0.342
rs35605	ABCC1	T	0.168	1.484	[1.093,2.013]	0.011	0.941	[0.512,1.731]	0.845	0.634	[0.334,1.206]	0.165	0.035
rs769217	CAT	T	0.214	0.935	[0.7,1.251]	0.652	0.596	[0.326,1.088]	0.092	0.637	[0.337,1.205]	0.165	0.234
rs610529	ALDH1A1	C	0.462	0.967	[0.771,1.213]	0.772	1.320	[0.877,1.988]	0.184	1.365	[0.879,2.119]	0.165	0.369
rs316003	SLC22A2	C	0.288	1.039	[0.793,1.361]	0.780	0.699	[0.414,1.182]	0.182	0.673	[0.384,1.178]	0.165	0.371
rs2239185	VDR	C	0.462	1.170	[0.923,1.485]	0.195	0.840	[0.542,1.302]	0.436	0.718	[0.449,1.147]	0.166	0.270
rs17563	BMP4	C	0.496	0.843	[0.672,1.058]	0.140	1.154	[0.762,1.747]	0.499	1.368	[0.878,2.133]	0.166	0.226
rs1057910	CYP2C9	C	0.053	0.484	[0.261,0.9]	0.022	1.023	[0.407,2.573]	0.961	2.113	[0.732,6.093]	0.166	0.069
rs1057911	CYP2C9	T	0.053	0.484	[0.261,0.9]	0.022	1.023	[0.407,2.573]	0.961	2.113	[0.732,6.093]	0.166	0.069
rs9332100	CYP2C9	T	0.096	1.023	[0.697,1.501]	0.906	0.518	[0.205,1.308]	0.164	0.506	[0.193,1.329]	0.167	0.367
rs651852	BHMT	A	0.443	0.969	[0.765,1.228]	0.797	1.336	[0.875,2.039]	0.179	1.378	[0.874,2.172]	0.167	0.367
rs2075685	TMEM167	T	0.470	0.980	[0.773,1.242]	0.866	0.703	[0.452,1.091]	0.116	0.717	[0.447,1.149]	0.167	0.290
rs643788	DPAGT1	C	0.401	1.035	[0.814,1.317]	0.779	0.738	[0.47,1.157]	0.185	0.713	[0.441,1.153]	0.167	0.373
rs8551	DPAGT1	T	0.402	1.035	[0.814,1.317]	0.779	0.738	[0.47,1.157]	0.185	0.713	[0.441,1.153]	0.167	0.373
rs1060463	CYP4F11	G	0.443	1.085	[0.863,1.363]	0.485	0.788	[0.516,1.203]	0.270	0.727	[0.462,1.143]	0.167	0.379

rs20581	LIG1	T	0.405	1.301	[1.032,1.642]	0.026	0.942	[0.613,1.448]	0.787	0.724	[0.458,1.145]	0.168	0.071
rs1536474	RXRA	T	0.332	1.020	[0.76,1.37]	0.894	0.673	[0.388,1.166]	0.158	0.659	[0.365,1.191]	0.168	0.351
rs2295275	TRERF1	A	0.058	0.727	[0.422,1.251]	0.249	1.360	[0.622,2.974]	0.441	1.872	[0.768,4.562]	0.168	0.333
rs1058172	CYP2D6	A	0.128	1.138	[0.779,1.663]	0.503	1.855	[0.974,3.534]	0.060	1.630	[0.814,3.264]	0.168	0.159
rs348457	ALDH1A1	G	0.462	0.968	[0.772,1.214]	0.778	1.319	[0.876,1.987]	0.185	1.363	[0.877,2.117]	0.168	0.373
rs10857971	PPM1J	C	0.017	2.109	[0.821,5.416]	0.121	0.440	[0.052,3.707]	0.450	0.209	[0.022,1.942]	0.169	0.194
rs11765552	LMTK2	A	0.425	0.741	[0.58,0.948]	0.017	1.029	[0.667,1.588]	0.896	1.388	[0.87,2.216]	0.169	0.053
rs529948	NFKBIE	A	0.122	1.524	[1.112,2.089]	0.009	0.933	[0.476,1.828]	0.839	0.612	[0.304,1.232]	0.169	0.027
rs533984	MRE11A	A	0.444	1.082	[0.856,1.369]	0.510	0.784	[0.511,1.203]	0.265	0.725	[0.458,1.147]	0.169	0.384
rs17057718	IL17RD	T	0.157	1.311	[0.952,1.805]	0.097	0.795	[0.403,1.569]	0.509	0.607	[0.297,1.237]	0.169	0.171
rs1137101	LEPR	G	0.482	1.144	[0.905,1.445]	0.262	0.832	[0.546,1.269]	0.394	0.728	[0.462,1.145]	0.169	0.317
rs2279103	CTDP1	T	0.149	1.104	[0.805,1.515]	0.539	1.629	[0.976,2.719]	0.062	1.476	[0.846,2.573]	0.170	0.166
rs7242	SERPINE1	G	0.435	1.062	[0.836,1.347]	0.623	0.767	[0.498,1.182]	0.230	0.723	[0.454,1.15]	0.170	0.391
rs241424	TAP2	T	0.498	1.224	[0.969,1.546]	0.090	1.687	[1.098,2.593]	0.017	1.378	[0.871,2.182]	0.171	0.023
rs2606345	CYP1A1	C	0.457	1.119	[0.88,1.424]	0.358	0.800	[0.511,1.254]	0.331	0.715	[0.443,1.155]	0.171	0.355
rs3756772	FRK	A	0.403	1.112	[0.881,1.405]	0.372	1.530	[0.998,2.346]	0.051	1.376	[0.871,2.172]	0.171	0.123
rs2288087	ALDH1A1	T	0.451	0.963	[0.764,1.216]	0.754	0.697	[0.451,1.076]	0.103	0.723	[0.454,1.151]	0.171	0.264
rs16859180	STK36	T	0.051	1.016	[0.594,1.737]	0.954	0.247	[0.034,1.818]	0.170	0.243	[0.032,1.855]	0.173	0.385
rs2298037	CYP2C9	T	0.146	1.109	[0.802,1.532]	0.532	0.667	[0.332,1.34]	0.255	0.602	[0.29,1.249]	0.173	0.387
rs3748338	RNASE4	T	0.142	0.887	[0.599,1.315]	0.551	0.467	[0.194,1.124]	0.089	0.526	[0.209,1.326]	0.173	0.216
rs2237585	PON2	C	0.476	0.986	[0.779,1.248]	0.909	0.719	[0.47,1.099]	0.127	0.729	[0.462,1.149]	0.173	0.311
rs2790	TYMS	G	0.221	0.803	[0.596,1.081]	0.148	1.169	[0.714,1.914]	0.535	1.456	[0.848,2.502]	0.173	0.250
rs11003125	MBL2	C	0.335	0.949	[0.741,1.215]	0.680	1.316	[0.852,2.032]	0.216	1.386	[0.866,2.218]	0.173	0.392
rs9332093	CYP2C9	G	0.055	0.472	[0.254,0.877]	0.018	0.986	[0.392,2.484]	0.976	2.089	[0.723,6.038]	0.174	0.058
rs513349	BAK1	G	0.466	1.092	[0.865,1.38]	0.459	0.786	[0.503,1.227]	0.289	0.719	[0.447,1.157]	0.174	0.384
rs1020678	HNMT	G	0.398	0.726	[0.568,0.928]	0.010	1.000	[0.653,1.531]	0.999	1.378	[0.868,2.189]	0.174	0.036
rs2074113	AHR	A	0.113	0.902	[0.613,1.329]	0.602	1.427	[0.786,2.59]	0.243	1.581	[0.816,3.064]	0.175	0.396
rs10264715	NPC1L1	A	0.192	0.790	[0.582,1.073]	0.131	1.170	[0.694,1.971]	0.556	1.480	[0.84,2.608]	0.175	0.231
rs6714486	UGT1A10	A	0.078	1.217	[0.788,1.878]	0.375	0.623	[0.247,1.571]	0.316	0.512	[0.194,1.353]	0.177	0.360
rs1799966	BRCA1	G	0.313	0.878	[0.681,1.133]	0.318	1.221	[0.784,1.901]	0.376	1.390	[0.86,2.247]	0.178	0.357
rs1799725	SOD2	C	0.489	1.275	[1.007,1.614]	0.044	0.929	[0.605,1.428]	0.737	0.729	[0.459,1.156]	0.179	0.108
rs2291462	IL17RD	T	0.180	0.848	[0.621,1.157]	0.298	1.239	[0.749,2.051]	0.404	1.462	[0.84,2.544]	0.179	0.357
rs8187755	SLC28A1	T	0.015	0.555	[0.161,1.916]	0.351	1.732	[0.476,6.294]	0.404	3.122	[0.592,16.458]	0.180	0.404
rs910416	ESR1	C	0.494	0.902	[0.716,1.137]	0.384	0.659	[0.43,1.011]	0.056	0.731	[0.462,1.155]	0.180	0.134
rs2974938	PPP1R3A	T	0.020	1.203	[0.535,2.704]	0.655	0.266	[0.032,2.241]	0.223	0.221	[0.024,2.005]	0.180	0.405
rs207440	XDH	A	0.056	1.750	[1.098,2.789]	0.019	0.831	[0.29,2.382]	0.731	0.475	[0.16,1.411]	0.180	0.050
rs2365778	SRD5A2	C	0.483	1.041	[0.822,1.32]	0.737	0.756	[0.488,1.17]	0.210	0.726	[0.454,1.16]	0.180	0.401
rs359974	IHH	C	0.177	0.936	[0.673,1.301]	0.693	1.428	[0.807,2.526]	0.221	1.526	[0.821,2.834]	0.181	0.403
rs7744392	PPARD	G	0.084	0.878	[0.543,1.418]	0.594	1.527	[0.733,3.184]	0.259	1.740	[0.773,3.918]	0.181	0.408
rs158634	DPYD	G	0.190	1.237	[0.922,1.659]	0.156	0.816	[0.458,1.454]	0.489	0.660	[0.358,1.215]	0.182	0.245
rs4646312	COMT	C	0.330	0.891	[0.692,1.146]	0.368	1.238	[0.79,1.94]	0.352	1.390	[0.857,2.256]	0.182	0.378

rs2235040	ABCB1	A	0.114	1.068	[0.727,1.57]	0.736	1.653	[0.926,2.948]	0.089	1.547	[0.814,2.94]	0.183	0.235
rs230496	NFKB1	G	0.400	1.158	[0.912,1.471]	0.229	0.844	[0.547,1.303]	0.444	0.729	[0.457,1.161]	0.183	0.312
rs3218005	CDKN2B	G	0.127	0.886	[0.604,1.301]	0.538	1.403	[0.76,2.588]	0.279	1.582	[0.804,3.114]	0.184	0.414
rs5276	PTGS2	A	0.025	1.366	[0.656,2.847]	0.405	0.341	[0.047,2.464]	0.286	0.250	[0.032,1.936]	0.184	0.368
rs769218	CAT	A	0.205	0.893	[0.663,1.203]	0.457	0.573	[0.309,1.065]	0.078	0.642	[0.333,1.236]	0.185	0.183
rs1800471	TGFB1	C	0.071	1.449	[0.927,2.265]	0.103	0.729	[0.275,1.934]	0.525	0.503	[0.182,1.391]	0.186	0.184
rs17612126	IGHMBP2	A	0.260	1.035	[0.787,1.36]	0.805	1.460	[0.91,2.341]	0.117	1.410	[0.848,2.346]	0.186	0.292
rs734351	IGF2	C	0.386	1.043	[0.826,1.317]	0.721	1.415	[0.928,2.159]	0.107	1.357	[0.864,2.131]	0.186	0.271
rs8827	SPRED2	C	0.255	1.210	[0.923,1.588]	0.168	0.831	[0.492,1.404]	0.488	0.686	[0.393,1.199]	0.186	0.262
rs1799811	GSTP1	T	0.072	0.941	[0.604,1.465]	0.788	0.414	[0.128,1.342]	0.142	0.440	[0.131,1.485]	0.186	0.337
rs689470	PTGS2	T	0.099	1.182	[0.747,1.87]	0.476	0.641	[0.275,1.491]	0.302	0.542	[0.218,1.348]	0.188	0.410
rs2972164	PPARG	T	0.498	1.162	[0.907,1.487]	0.234	0.838	[0.533,1.319]	0.445	0.722	[0.444,1.173]	0.188	0.319
rs212091	ABCC1	G	0.148	1.093	[0.79,1.512]	0.591	0.686	[0.355,1.324]	0.261	0.627	[0.313,1.257]	0.188	0.419
rs12720855	APOB	C	0.017	1.942	[0.816,4.622]	0.133	0.463	[0.058,3.681]	0.466	0.238	[0.028,2.021]	0.189	0.209
rs12713450	APOB	T	0.017	0.509	[0.138,1.879]	0.311	1.679	[0.411,6.866]	0.471	3.297	[0.557,19.524]	0.189	0.408
rs1801105		T	0.091	0.651	[0.418,1.015]	0.058	1.103	[0.544,2.236]	0.785	1.694	[0.772,3.716]	0.189	0.146
rs7663494	DCTD	G	0.331	0.954	[0.745,1.222]	0.709	1.302	[0.848,1.999]	0.228	1.364	[0.858,2.17]	0.189	0.416
rs2305030	LTK	T	0.124	1.300	[0.916,1.844]	0.142	0.787	[0.385,1.606]	0.510	0.605	[0.286,1.282]	0.190	0.233
rs10082466	MBL2	G	0.270	0.999	[0.77,1.297]	0.996	0.698	[0.422,1.155]	0.162	0.698	[0.408,1.196]	0.191	0.371
rs2286233	PON2	T	0.153	0.896	[0.636,1.262]	0.531	1.344	[0.773,2.338]	0.294	1.500	[0.817,2.755]	0.191	0.424
rs348458	ALDH1A1	A	0.466	0.970	[0.774,1.217]	0.794	1.303	[0.864,1.965]	0.207	1.342	[0.863,2.087]	0.191	0.410
rs11574790	IL12B	T	0.115	1.153	[0.814,1.633]	0.425	0.693	[0.335,1.433]	0.323	0.602	[0.281,1.289]	0.191	0.394
rs1045642	ABCB1	T	0.475	0.880	[0.692,1.12]	0.299	0.643	[0.414,0.999]	0.049	0.731	[0.456,1.171]	0.192	0.108
rs730722	CHST3	G	0.093	1.467	[0.999,2.153]	0.051	0.849	[0.391,1.847]	0.681	0.579	[0.255,1.317]	0.193	0.119
rs2153629	CYP2C9	G	0.095	1.024	[0.692,1.516]	0.906	0.538	[0.213,1.36]	0.190	0.526	[0.2,1.383]	0.193	0.410
rs12713675	APOB	A	0.017	1.942	[0.816,4.623]	0.134	0.469	[0.059,3.731]	0.474	0.242	[0.028,2.049]	0.193	0.212
rs1042031	APOB	A	0.174	0.948	[0.695,1.294]	0.738	1.374	[0.824,2.291]	0.224	1.449	[0.829,2.533]	0.193	0.417
rs1060250	SLC7A5	G	0.011	3.077	[1.155,8.201]	0.025	0.707	[0.082,6.134]	0.753	0.230	[0.025,2.115]	0.194	0.063
rs4619	IGFBP1	G	0.384	1.015	[0.799,1.289]	0.906	0.738	[0.471,1.157]	0.185	0.728	[0.45,1.176]	0.194	0.398
rs28899170	UGT1A10	A	0.281	1.019	[0.78,1.33]	0.892	1.408	[0.897,2.21]	0.137	1.382	[0.848,2.254]	0.194	0.330
rs6671692	FMO2	A	0.028	1.346	[0.6,3.021]	0.471	0.323	[0.041,2.55]	0.284	0.240	[0.028,2.077]	0.195	0.406
rs7536646	FMO2	A	0.028	1.347	[0.601,3.023]	0.469	0.324	[0.041,2.553]	0.285	0.240	[0.028,2.077]	0.195	0.406
rs1042580	THBD	G	0.353	1.268	[0.994,1.618]	0.056	0.921	[0.587,1.447]	0.722	0.726	[0.448,1.178]	0.195	0.132
rs1801249	ATP7B	T	0.419	1.307	[1.027,1.664]	0.029	0.959	[0.619,1.485]	0.850	0.733	[0.458,1.173]	0.195	0.082
rs4646091	CASP9	G	0.244	0.899	[0.674,1.199]	0.469	1.279	[0.782,2.091]	0.327	1.422	[0.833,2.43]	0.197	0.426
rs10979601	IKBKAP	T	0.254	1.241	[0.947,1.625]	0.117	0.870	[0.523,1.445]	0.590	0.701	[0.408,1.203]	0.197	0.218
rs2242480	CYP3A4	T	0.218	1.394	[1.006,1.93]	0.046	0.926	[0.518,1.653]	0.794	0.664	[0.356,1.237]	0.197	0.116
rs2299255	PON1	C	0.136	1.376	[0.997,1.899]	0.052	0.890	[0.475,1.668]	0.716	0.647	[0.333,1.255]	0.198	0.123
rs1800469	B9D2	T	0.322	0.979	[0.751,1.276]	0.874	1.375	[0.851,2.22]	0.193	1.405	[0.837,2.356]	0.198	0.406
rs35604	ABCC1	G	0.167	1.445	[1.067,1.957]	0.017	0.948	[0.515,1.744]	0.863	0.656	[0.345,1.247]	0.198	0.052
rs8187758	SLC28A1	A	0.236	0.939	[0.71,1.24]	0.656	1.317	[0.818,2.121]	0.256	1.404	[0.837,2.354]	0.198	0.436

rs3757280	HSP90AB1	C	0.081	0.984	[0.644,1.505]	0.941	0.483	[0.17,1.375]	0.173	0.491	[0.166,1.453]	0.198	0.393
rs11537643	VWF	A	0.034	1.290	[0.62,2.685]	0.496	0.438	[0.092,2.074]	0.298	0.339	[0.065,1.765]	0.199	0.425
rs6886047	GHR	T	0.283	1.040	[0.803,1.347]	0.767	0.736	[0.448,1.209]	0.226	0.708	[0.417,1.201]	0.200	0.433
rs281432	ICAM1	C	0.492	1.051	[0.832,1.329]	0.675	0.782	[0.512,1.194]	0.254	0.744	[0.472,1.17]	0.200	0.439
rs732774	ATP7B	G	0.421	1.310	[1.033,1.661]	0.026	0.965	[0.622,1.495]	0.872	0.736	[0.46,1.177]	0.201	0.074
rs6888011	ADRB2	C	0.350	0.886	[0.688,1.143]	0.352	1.210	[0.778,1.881]	0.397	1.365	[0.847,2.201]	0.201	0.399
rs2243250	IL4	T	0.270	1.277	[0.978,1.667]	0.072	0.886	[0.521,1.505]	0.654	0.694	[0.396,1.216]	0.201	0.156
rs2274419	MUSK	T	0.123	1.434	[1.029,2]	0.033	0.899	[0.453,1.785]	0.761	0.627	[0.306,1.285]	0.202	0.086
rs2049110	DPYD	A	0.017	1.805	[0.716,4.551]	0.211	0.431	[0.052,3.598]	0.437	0.239	[0.026,2.163]	0.203	0.292
rs9306354	XRCC6	T	0.043	0.717	[0.351,1.464]	0.362	0.249	[0.053,1.156]	0.076	0.347	[0.068,1.773]	0.203	0.157
rs1780196	PDSS1	A	0.143	1.005	[0.725,1.393]	0.977	1.456	[0.863,2.458]	0.159	1.450	[0.818,2.569]	0.204	0.364
rs4987310	SELL	T	0.177	0.917	[0.668,1.258]	0.589	1.325	[0.788,2.227]	0.289	1.445	[0.819,2.55]	0.204	0.446
rs1076150	DBH	G	0.482	1.038	[0.822,1.31]	0.755	0.776	[0.511,1.178]	0.234	0.748	[0.477,1.171]	0.204	0.438
rs2120132	MBL2	C	0.269	0.996	[0.767,1.293]	0.977	0.703	[0.424,1.165]	0.171	0.705	[0.412,1.209]	0.204	0.388
rs3761142	GSS	A	0.289	0.908	[0.704,1.172]	0.460	1.234	[0.798,1.911]	0.345	1.359	[0.846,2.183]	0.205	0.435
rs2306508	FNDC8	A	0.395	0.896	[0.706,1.137]	0.368	1.215	[0.783,1.887]	0.385	1.356	[0.847,2.171]	0.205	0.403
rs2072374	NCAPD2	T	0.228	0.623	[0.46,0.842]	0.002	0.905	[0.532,1.54]	0.713	1.454	[0.815,2.593]	0.205	0.009
rs3847262	TPD52L3	T	0.073	0.835	[0.517,1.349]	0.461	0.396	[0.132,1.189]	0.099	0.474	[0.15,1.503]	0.205	0.217
rs1800392	WRN	T	0.438	0.993	[0.785,1.256]	0.951	0.733	[0.473,1.136]	0.165	0.739	[0.462,1.18]	0.205	0.378
rs2856585	ABCC6	A	0.078	1.149	[0.671,1.966]	0.613	0.496	[0.144,1.712]	0.267	0.432	[0.118,1.582]	0.205	0.445
rs1946518	IL18	T	0.395	0.973	[0.768,1.232]	0.818	1.306	[0.853,1.998]	0.219	1.342	[0.85,2.119]	0.206	0.433
rs2020911	MSH6	T	0.353	1.063	[0.828,1.364]	0.634	0.768	[0.478,1.234]	0.275	0.723	[0.437,1.196]	0.207	0.451
rs299290	HMMR	C	0.284	0.954	[0.732,1.242]	0.725	0.670	[0.401,1.121]	0.127	0.703	[0.407,1.215]	0.207	0.308
rs799917	BRCA1	T	0.427	0.916	[0.712,1.179]	0.497	1.253	[0.797,1.97]	0.328	1.368	[0.841,2.223]	0.207	0.442
rs348476	ALDH1A1	C	0.017	1.016	[0.419,2.466]	0.971	2.281	[0.784,6.635]	0.130	2.245	[0.639,7.88]	0.207	0.308
rs3212859	CCND1	T	0.058	1.435	[0.861,2.391]	0.166	0.704	[0.246,2.013]	0.513	0.491	[0.162,1.485]	0.208	0.269
rs2274578	BYSL	G	0.480	1.057	[0.837,1.336]	0.639	1.412	[0.929,2.146]	0.106	1.335	[0.851,2.094]	0.208	0.263
rs3759259	STYK1	A	0.401	1.102	[0.87,1.396]	0.423	0.812	[0.52,1.267]	0.359	0.737	[0.458,1.185]	0.208	0.425
rs274558	SLC22A5	C	0.420	1.094	[0.847,1.413]	0.490	0.798	[0.506,1.259]	0.332	0.730	[0.446,1.193]	0.209	0.444
rs1051332	ATP7B	A	0.409	0.803	[0.626,1.029]	0.083	1.091	[0.701,1.698]	0.700	1.359	[0.842,2.192]	0.209	0.183
rs2598483	STAT6	T	0.099	0.964	[0.653,1.423]	0.854	0.536	[0.223,1.285]	0.162	0.556	[0.223,1.389]	0.209	0.377
rs1042714	ADRB2	G	0.380	1.045	[0.817,1.335]	0.728	1.407	[0.914,2.167]	0.121	1.347	[0.846,2.145]	0.209	0.298
rs1052248	LST1	A	0.248	1.084	[0.826,1.424]	0.561	1.485	[0.942,2.34]	0.088	1.370	[0.838,2.237]	0.209	0.223
rs1799941	SHBG	A	0.224	0.742	[0.548,1.004]	0.053	1.062	[0.638,1.769]	0.817	1.431	[0.818,2.504]	0.209	0.138
rs1341164	CYP2C8	C	0.283	0.804	[0.612,1.056]	0.116	1.118	[0.695,1.797]	0.646	1.391	[0.831,2.328]	0.210	0.232
rs1178027	PTPRA	T	0.179	0.931	[0.657,1.319]	0.688	0.587	[0.299,1.152]	0.122	0.631	[0.307,1.296]	0.210	0.294
rs13141136	HELQ	G	0.380	1.020	[0.799,1.303]	0.872	1.386	[0.886,2.166]	0.152	1.358	[0.841,2.192]	0.210	0.359
rs163081	FAM82A	T	0.224	0.850	[0.624,1.158]	0.302	1.217	[0.728,2.033]	0.454	1.432	[0.817,2.51]	0.210	0.392
rs1378321	HNMT	C	0.201	0.658	[0.483,0.895]	0.008	0.938	[0.568,1.549]	0.803	1.426	[0.818,2.484]	0.211	0.029
rs6902123	PPARD	C	0.166	0.815	[0.552,1.204]	0.305	1.285	[0.668,2.474]	0.453	1.576	[0.773,3.216]	0.211	0.392
rs2076169	PPARD	C	0.085	0.833	[0.535,1.296]	0.418	1.360	[0.68,2.722]	0.384	1.633	[0.757,3.522]	0.211	0.440

rs2778979	PLXDC2	T	0.119	0.841	[0.579,1.221]	0.363	1.293	[0.699,2.39]	0.412	1.537	[0.784,3.015]	0.211	0.420
rs373572	RAD18	G	0.300	1.426	[1.106,1.839]	0.006	1.039	[0.652,1.655]	0.873	0.728	[0.443,1.198]	0.212	0.023
rs4951629	ATF3	C	0.086	1.235	[0.819,1.863]	0.315	0.695	[0.295,1.641]	0.407	0.563	[0.229,1.387]	0.212	0.376
rs40947	THAP5	A	0.296	1.086	[0.843,1.4]	0.523	0.783	[0.482,1.271]	0.322	0.721	[0.43,1.207]	0.213	0.451
rs1677715	PDSS1	A	0.340	1.337	[1.043,1.714]	0.022	0.985	[0.628,1.544]	0.947	0.737	[0.455,1.192]	0.213	0.066
rs757343	VDR	A	0.133	0.908	[0.641,1.286]	0.587	1.341	[0.763,2.357]	0.307	1.477	[0.798,2.735]	0.214	0.462
rs1799998	CYP11B2	C	0.397	1.194	[0.937,1.523]	0.152	0.880	[0.561,1.38]	0.579	0.737	[0.455,1.193]	0.214	0.269
rs1800206	PPARA	G	0.052	1.011	[0.603,1.697]	0.967	0.395	[0.093,1.67]	0.207	0.390	[0.088,1.728]	0.215	0.445
rs2291439	RAD54B	G	0.370	0.994	[0.779,1.269]	0.963	0.730	[0.462,1.153]	0.178	0.735	[0.451,1.197]	0.215	0.399
rs1946519	IL18	A	0.398	0.964	[0.761,1.221]	0.760	1.286	[0.84,1.969]	0.247	1.334	[0.845,2.108]	0.216	0.457
rs4577050	SLC12A6	G	0.392	1.182	[0.924,1.513]	0.183	0.865	[0.544,1.375]	0.540	0.732	[0.446,1.201]	0.216	0.300
rs2267237	LARGE	C	0.134	1.305	[0.929,1.835]	0.125	0.833	[0.425,1.632]	0.594	0.638	[0.313,1.301]	0.216	0.234
rs2239704	LTA	T	0.359	0.808	[0.63,1.036]	0.093	1.090	[0.702,1.693]	0.701	1.349	[0.839,2.17]	0.217	0.202
rs1555026	ID3	C	0.079	1.433	[0.931,2.203]	0.102	0.807	[0.34,1.918]	0.628	0.564	[0.227,1.401]	0.217	0.202
rs743572	CYP17A1	G	0.410	1.077	[0.855,1.358]	0.529	0.804	[0.521,1.243]	0.326	0.747	[0.469,1.187]	0.217	0.459
rs3772173	SKIL	C	0.258	1.046	[0.798,1.369]	0.746	1.426	[0.906,2.244]	0.126	1.363	[0.833,2.232]	0.218	0.308
rs1760944	APEX1	A	0.391	0.976	[0.774,1.23]	0.836	1.286	[0.855,1.935]	0.227	1.318	[0.849,2.046]	0.219	0.448
rs1558093	SMAD5	C	0.329	0.818	[0.63,1.062]	0.131	1.108	[0.709,1.732]	0.652	1.355	[0.834,2.201]	0.219	0.256
rs2069705	IFNG	C	0.373	1.106	[0.875,1.396]	0.399	1.457	[0.967,2.194]	0.072	1.317	[0.848,2.047]	0.220	0.167
rs10017306	SLC39A8	T	0.395	0.970	[0.761,1.238]	0.809	0.714	[0.451,1.13]	0.151	0.736	[0.45,1.202]	0.221	0.356
rs1050891	HNMT	C	0.194	0.661	[0.484,0.903]	0.009	0.943	[0.563,1.581]	0.824	1.427	[0.807,2.522]	0.221	0.034
rs2470146	CYP19A1	C	0.057	1.455	[0.917,2.308]	0.111	0.683	[0.211,2.212]	0.525	0.469	[0.14,1.578]	0.221	0.200
rs1008563	IL8RA	T	0.430	0.936	[0.74,1.183]	0.579	0.699	[0.451,1.083]	0.109	0.747	[0.467,1.193]	0.222	0.260
rs1805087	MTR	G	0.202	0.902	[0.67,1.214]	0.495	1.265	[0.768,2.085]	0.356	1.403	[0.814,2.419]	0.222	0.466
rs1390358	NAT2	C	0.366	1.126	[0.891,1.423]	0.320	0.840	[0.54,1.307]	0.440	0.746	[0.466,1.194]	0.222	0.400
rs20580	LIG1	C	0.495	1.187	[0.947,1.488]	0.137	0.906	[0.604,1.358]	0.631	0.763	[0.494,1.179]	0.223	0.260
rs312016	LRP5	A	0.280	1.076	[0.832,1.392]	0.577	1.451	[0.928,2.267]	0.103	1.348	[0.834,2.18]	0.223	0.251
rs1050900	HNMT	A	0.194	0.660	[0.483,0.901]	0.009	0.939	[0.561,1.571]	0.811	1.423	[0.806,2.511]	0.223	0.033
rs6661174	FMO2	C	0.027	1.232	[0.533,2.847]	0.625	0.321	[0.041,2.529]	0.281	0.261	[0.03,2.274]	0.224	0.474
rs662799	APOA5	G	0.084	1.765	[1.189,2.62]	0.005	2.613	[1.437,4.752]	0.002	1.481	[0.786,2.789]	0.224	0.001
rs2463437	CHST11	C	0.342	1.443	[1.129,1.844]	0.003	1.074	[0.686,1.681]	0.756	0.744	[0.461,1.2]	0.225	0.013
rs4987876	ATM	T	0.094	0.948	[0.627,1.434]	0.800	0.515	[0.202,1.317]	0.166	0.544	[0.203,1.457]	0.225	0.381
rs3770602	ABCB11	A	0.270	0.752	[0.571,0.99]	0.042	1.037	[0.642,1.675]	0.882	1.379	[0.82,2.32]	0.226	0.116
rs698708	KDSR	G	0.292	0.942	[0.722,1.23]	0.663	1.280	[0.81,2.023]	0.290	1.359	[0.827,2.231]	0.226	0.479
rs373496	TNFRSF17	T	0.026	0.860	[0.406,1.82]	0.693	0.233	[0.03,1.8]	0.163	0.271	[0.033,2.244]	0.226	0.364
rs820196	LOC100132011	C	0.226	0.816	[0.599,1.112]	0.198	1.144	[0.696,1.879]	0.597	1.401	[0.811,2.419]	0.226	0.337
rs323870	PARP3	G	0.027	1.097	[0.485,2.48]	0.825	2.351	[0.809,6.83]	0.116	2.143	[0.622,7.384]	0.227	0.291
rs1019731	IGF1	T	0.111	1.066	[0.747,1.522]	0.725	1.585	[0.874,2.874]	0.130	1.487	[0.781,2.83]	0.227	0.315
rs2276299	SLC22A8	T	0.171	0.972	[0.705,1.341]	0.863	1.388	[0.814,2.366]	0.228	1.428	[0.8,2.548]	0.228	0.454
rs6163	CYP17A1	A	0.410	1.065	[0.845,1.343]	0.593	0.801	[0.519,1.237]	0.317	0.752	[0.473,1.196]	0.228	0.482
rs363717	ABCA1	G	0.162	1.254	[0.931,1.688]	0.136	0.849	[0.464,1.555]	0.596	0.677	[0.359,1.277]	0.228	0.248

rs8187799	ABCB4	G	0.123	1.223	[0.851,1.759]	0.277	0.780	[0.392,1.55]	0.478	0.638	[0.306,1.327]	0.229	0.382
rs20551	EP300	G	0.246	0.953	[0.724,1.255]	0.734	0.668	[0.387,1.154]	0.148	0.701	[0.392,1.252]	0.229	0.347
rs3813627	APOA2	T	0.312	0.821	[0.634,1.064]	0.136	1.114	[0.703,1.766]	0.645	1.357	[0.825,2.233]	0.230	0.264
rs2046136	BCL2	C	0.276	1.006	[0.776,1.305]	0.963	0.720	[0.43,1.204]	0.211	0.715	[0.414,1.236]	0.230	0.447
rs5939	PTAFR	G	0.014	1.795	[0.687,4.691]	0.233	0.494	[0.065,3.756]	0.496	0.275	[0.034,2.26]	0.230	0.334
rs10515114	CARTPT	C	0.119	1.260	[0.889,1.787]	0.194	0.809	[0.406,1.612]	0.547	0.642	[0.311,1.324]	0.230	0.310
rs186997	ALDH1A1	G	0.069	0.975	[0.593,1.604]	0.921	1.612	[0.77,3.376]	0.205	1.653	[0.727,3.761]	0.230	0.428
rs2332673	BCL2	C	0.069	0.793	[0.469,1.339]	0.385	1.320	[0.633,2.752]	0.458	1.666	[0.723,3.837]	0.231	0.464
rs348481	ALDH1A1	C	0.235	1.102	[0.832,1.458]	0.499	1.507	[0.938,2.421]	0.090	1.368	[0.819,2.285]	0.232	0.218
rs2404955	CYP3A4	A	0.218	1.242	[0.903,1.708]	0.184	0.853	[0.48,1.513]	0.586	0.687	[0.371,1.272]	0.232	0.315
rs6756629	ABCG5	A	0.062	1.485	[0.962,2.293]	0.074	0.815	[0.316,2.102]	0.672	0.549	[0.205,1.471]	0.233	0.161
rs6673324	LEPR	G	0.484	0.951	[0.749,1.207]	0.678	1.265	[0.816,1.96]	0.293	1.330	[0.832,2.127]	0.233	0.490
rs1042718	ADRB2	A	0.200	0.973	[0.723,1.308]	0.854	1.348	[0.823,2.208]	0.235	1.386	[0.81,2.373]	0.233	0.463
rs2229532	ACP5	A	0.021	1.229	[0.5,3.025]	0.653	0.328	[0.041,2.639]	0.295	0.267	[0.03,2.353]	0.234	0.491
rs1076153	DBH	T	0.202	1.094	[0.822,1.455]	0.538	1.496	[0.927,2.415]	0.099	1.368	[0.816,2.292]	0.234	0.241
rs1799722	BDKRB2	T	0.407	0.891	[0.69,1.149]	0.374	1.197	[0.763,1.877]	0.434	1.344	[0.826,2.186]	0.234	0.445
rs735320	CYP8B1	A	0.160	1.031	[0.759,1.399]	0.846	1.435	[0.869,2.369]	0.158	1.392	[0.807,2.401]	0.234	0.369
rs1861494	IFNG	C	0.271	0.976	[0.753,1.263]	0.851	1.303	[0.837,2.03]	0.241	1.336	[0.828,2.156]	0.235	0.470
rs2306283	SLCO1B1	C	0.465	1.075	[0.847,1.364]	0.551	0.803	[0.51,1.263]	0.342	0.747	[0.461,1.21]	0.235	0.487
rs673548	APOB	A	0.236	0.965	[0.725,1.285]	0.809	0.675	[0.387,1.176]	0.165	0.699	[0.387,1.263]	0.235	0.381
rs1051137	GSTM4	T	0.320	0.812	[0.621,1.062]	0.129	1.102	[0.693,1.754]	0.682	1.357	[0.819,2.248]	0.236	0.261
rs1540339	VDR	A	0.348	1.264	[1,1.598]	0.050	0.952	[0.613,1.478]	0.825	0.753	[0.471,1.204]	0.236	0.130
rs5277	PTGS2	C	0.123	0.981	[0.696,1.384]	0.914	1.423	[0.809,2.502]	0.221	1.450	[0.784,2.68]	0.236	0.452
rs10276036	ABCB1	C	0.403	0.967	[0.76,1.231]	0.786	0.722	[0.459,1.137]	0.160	0.747	[0.46,1.212]	0.237	0.371
rs6971	TSPO	T	0.274	0.903	[0.689,1.183]	0.457	1.223	[0.769,1.947]	0.395	1.355	[0.819,2.243]	0.237	0.477
rs1023244	DPYD	G	0.061	1.291	[0.81,2.058]	0.283	2.083	[0.998,4.346]	0.051	1.613	[0.73,3.563]	0.237	0.115
rs135549	PPARA	G	0.433	0.973	[0.768,1.233]	0.822	0.732	[0.47,1.139]	0.166	0.752	[0.469,1.206]	0.237	0.383
rs2857009	TNXB	G	0.275	1.075	[0.826,1.4]	0.592	1.455	[0.911,2.326]	0.117	1.354	[0.819,2.238]	0.237	0.279
rs2278815	LEP	A	0.473	1.081	[0.847,1.381]	0.531	0.805	[0.509,1.274]	0.355	0.745	[0.457,1.215]	0.238	0.488
rs2412504	PAK6	G	0.111	1.129	[0.761,1.673]	0.547	0.683	[0.311,1.497]	0.341	0.605	[0.263,1.394]	0.238	0.489
rs715147	NFATC2	A	0.456	0.823	[0.649,1.044]	0.108	1.082	[0.71,1.65]	0.713	1.315	[0.834,2.072]	0.238	0.230
rs1799929	NAT2	T	0.383	1.096	[0.866,1.388]	0.446	0.823	[0.527,1.287]	0.394	0.751	[0.467,1.209]	0.238	0.469
rs246234	ABCC1	C	0.349	1.116	[0.861,1.447]	0.406	1.496	[0.951,2.354]	0.082	1.340	[0.823,2.181]	0.239	0.186
rs4724445	IGFBP1	A	0.160	0.962	[0.705,1.314]	0.809	0.635	[0.329,1.227]	0.177	0.660	[0.33,1.321]	0.241	0.401
rs4220	FGB	A	0.159	1.258	[0.923,1.712]	0.146	0.855	[0.463,1.577]	0.615	0.680	[0.356,1.296]	0.241	0.269
rs2227956	HSPA1L	C	0.137	0.684	[0.471,0.994]	0.046	1.032	[0.553,1.927]	0.921	1.509	[0.758,3.002]	0.241	0.130
rs6731242	UGT1A10	G	0.182	1.004	[0.739,1.364]	0.979	0.675	[0.36,1.265]	0.220	0.672	[0.346,1.307]	0.242	0.464
rs1052763	DGCR14	T	0.223	0.958	[0.723,1.271]	0.767	0.678	[0.394,1.166]	0.160	0.707	[0.396,1.263]	0.242	0.370
rs1044250	ANGPTL4	T	0.292	0.807	[0.618,1.055]	0.117	1.086	[0.688,1.712]	0.724	1.344	[0.819,2.207]	0.242	0.248
rs1057335	SERPINF2	A	0.203	0.962	[0.715,1.296]	0.801	0.669	[0.377,1.186]	0.169	0.695	[0.378,1.279]	0.242	0.387
rs1913263	MGST1	G	0.302	1.053	[0.821,1.351]	0.684	0.778	[0.483,1.253]	0.302	0.739	[0.445,1.227]	0.242	0.505

rs3738880	GLI2	C	0.334	0.928	[0.7,1.229]	0.600	1.257	[0.79,1.999]	0.335	1.355	[0.814,2.254]	0.243	0.505
rs10824792	MBL2	C	0.475	1.018	[0.805,1.289]	0.879	0.770	[0.497,1.194]	0.243	0.756	[0.473,1.21]	0.244	0.482
rs3813865	CYP2E1	C	0.050	1.213	[0.702,2.098]	0.489	2.081	[0.917,4.719]	0.079	1.715	[0.693,4.247]	0.244	0.198
rs2243270	IL4	G	0.275	1.353	[1.036,1.766]	0.026	0.974	[0.578,1.642]	0.921	0.720	[0.414,1.251]	0.244	0.078
rs1455158	HNMT	A	0.256	0.716	[0.536,0.957]	0.024	0.984	[0.605,1.602]	0.949	1.374	[0.805,2.344]	0.244	0.076
rs8187710	ABCC2	A	0.075	0.738	[0.444,1.225]	0.240	1.204	[0.587,2.467]	0.612	1.631	[0.715,3.72]	0.245	0.403
rs6945984	CYP3A4	C	0.217	1.237	[0.903,1.696]	0.186	0.862	[0.488,1.52]	0.607	0.696	[0.378,1.281]	0.245	0.325
rs182482	ABCC1	G	0.320	1.145	[0.882,1.486]	0.310	0.839	[0.514,1.371]	0.484	0.733	[0.434,1.237]	0.245	0.418
rs6056	FGB	T	0.160	1.247	[0.916,1.698]	0.161	0.850	[0.461,1.569]	0.603	0.682	[0.357,1.301]	0.245	0.289
rs11226	RAD52	T	0.463	1.016	[0.799,1.293]	0.898	1.340	[0.867,2.07]	0.188	1.319	[0.826,2.104]	0.246	0.420
rs431240	SLC36A2	G	0.431	0.961	[0.759,1.218]	0.744	0.734	[0.481,1.12]	0.152	0.763	[0.484,1.205]	0.246	0.355
rs2239393	COMT	G	0.374	0.915	[0.719,1.165]	0.472	1.203	[0.782,1.852]	0.400	1.315	[0.827,2.089]	0.247	0.490
rs1126579	IL8RB	T	0.414	0.948	[0.746,1.205]	0.663	1.263	[0.8,1.994]	0.317	1.332	[0.82,2.164]	0.247	0.512
rs930507	MBL2	G	0.203	1.048	[0.777,1.413]	0.759	1.432	[0.882,2.324]	0.146	1.366	[0.805,2.319]	0.247	0.347
rs6759892	UGT1A10	G	0.394	0.961	[0.755,1.223]	0.745	1.265	[0.819,1.952]	0.289	1.316	[0.826,2.098]	0.248	0.509
rs1056503	XRCC4	G	0.210	0.953	[0.717,1.268]	0.743	0.668	[0.378,1.181]	0.165	0.701	[0.383,1.283]	0.249	0.377
rs1805377	XRCC4	A	0.210	0.953	[0.717,1.268]	0.743	0.668	[0.378,1.181]	0.165	0.701	[0.383,1.283]	0.249	0.377
rs747659	PARP1	T	0.214	0.988	[0.736,1.326]	0.937	0.692	[0.393,1.22]	0.203	0.700	[0.382,1.284]	0.249	0.444
rs212090	ABCC1	A	0.401	0.950	[0.739,1.22]	0.686	1.263	[0.804,1.982]	0.311	1.329	[0.819,2.159]	0.250	0.515
rs3793345	IGFBP3	C	0.189	0.995	[0.736,1.345]	0.975	0.691	[0.385,1.239]	0.215	0.694	[0.373,1.292]	0.250	0.459
rs6671288	NR1I3	G	0.164	0.756	[0.536,1.066]	0.110	1.079	[0.625,1.862]	0.785	1.428	[0.779,2.619]	0.250	0.248
rs923796	NAT2	G	0.364	1.122	[0.886,1.421]	0.341	0.850	[0.546,1.324]	0.473	0.758	[0.473,1.216]	0.250	0.440
rs3100725	HNMT	T	0.213	0.686	[0.508,0.926]	0.014	0.946	[0.574,1.559]	0.828	1.380	[0.796,2.392]	0.251	0.048
rs7136446	IGF1	C	0.357	1.083	[0.852,1.376]	0.515	0.819	[0.524,1.28]	0.381	0.757	[0.47,1.218]	0.251	0.503
rs2270165	STARD3NL	A	0.150	0.832	[0.59,1.174]	0.294	1.201	[0.677,2.13]	0.532	1.444	[0.771,2.704]	0.252	0.428
rs5743553	TLR1	A	0.033	1.155	[0.596,2.241]	0.670	0.463	[0.104,2.053]	0.311	0.401	[0.084,1.914]	0.252	0.517
rs839763	CDC20	G	0.359	0.820	[0.642,1.047]	0.111	1.075	[0.701,1.65]	0.741	1.311	[0.825,2.085]	0.252	0.242
rs2230399	ICAM3	C	0.103	1.049	[0.714,1.542]	0.807	0.634	[0.28,1.437]	0.275	0.604	[0.255,1.432]	0.252	0.513
rs1051685	XRCC5	G	0.155	1.197	[0.859,1.67]	0.288	0.802	[0.422,1.526]	0.502	0.670	[0.338,1.33]	0.253	0.409
rs6773295	NR1I2	G	0.037	0.900	[0.385,2.106]	0.809	0.254	[0.032,2.008]	0.194	0.282	[0.032,2.469]	0.253	0.426
rs1913262	MGST1	A	0.302	1.047	[0.817,1.343]	0.715	0.779	[0.483,1.255]	0.304	0.744	[0.448,1.236]	0.253	0.519
rs17129772	IL12RB2	G	0.014	1.528	[0.53,4.4]	0.432	0.406	[0.047,3.487]	0.411	0.266	[0.027,2.586]	0.254	0.478
rs10017302	UGT8	G	0.046	1.158	[0.631,2.126]	0.636	0.538	[0.155,1.867]	0.328	0.464	[0.124,1.735]	0.254	0.520
rs348479	ALDH1A1	G	0.232	1.063	[0.804,1.404]	0.668	1.428	[0.893,2.283]	0.137	1.343	[0.809,2.231]	0.254	0.325
rs3778082	ESR1	A	0.173	1.024	[0.737,1.423]	0.886	0.696	[0.374,1.295]	0.253	0.679	[0.349,1.321]	0.255	0.498
rs2239184	VDR	C	0.447	1.147	[0.904,1.456]	0.260	0.874	[0.564,1.354]	0.546	0.762	[0.477,1.217]	0.255	0.394
rs35620	ABCC1	G	0.163	1.452	[1.071,1.97]	0.016	1.000	[0.544,1.839]	0.999	0.689	[0.363,1.309]	0.255	0.053
rs228832	NFATC2	T	0.322	1.072	[0.832,1.38]	0.592	0.798	[0.497,1.283]	0.352	0.745	[0.448,1.237]	0.255	0.520
rs2687127	CYP3A7	C	0.015	1.186	[0.441,3.187]	0.736	2.579	[0.842,7.898]	0.097	2.176	[0.569,8.316]	0.256	0.252
rs7304504	LRP1	A	0.053	1.222	[0.694,2.152]	0.487	0.619	[0.206,1.856]	0.392	0.506	[0.156,1.642]	0.257	0.504
rs2687116	CYP3A4	G	0.139	1.384	[0.906,2.113]	0.133	0.891	[0.446,1.78]	0.745	0.644	[0.301,1.378]	0.257	0.280

rs8192341	BMP1	A	0.221	0.941	[0.712,1.245]	0.671	0.659	[0.368,1.182]	0.162	0.700	[0.378,1.297]	0.257	0.364
rs2020863	FMO2	G	0.096	1.170	[0.806,1.697]	0.409	0.704	[0.302,1.64]	0.417	0.602	[0.25,1.449]	0.258	0.462
UGT2B7_1c	UGT2B7	G	0.129	1.358	[0.971,1.899]	0.074	0.905	[0.464,1.764]	0.769	0.666	[0.33,1.347]	0.258	0.174
rs11401	CCDC101	C	0.180	0.811	[0.592,1.112]	0.194	0.536	[0.271,1.06]	0.073	0.660	[0.321,1.356]	0.258	0.108
rs1530031	CHST10	A	0.495	0.795	[0.633,0.998]	0.048	1.023	[0.681,1.536]	0.913	1.286	[0.831,1.99]	0.258	0.132
rs742350	FMO1	A	0.183	0.957	[0.688,1.331]	0.793	1.334	[0.788,2.257]	0.283	1.394	[0.783,2.482]	0.259	0.513
rs919766	IL12B	C	0.119	1.136	[0.803,1.608]	0.471	0.746	[0.372,1.495]	0.408	0.656	[0.316,1.364]	0.259	0.496
rs1140409	DDX5	G	0.055	0.725	[0.423,1.242]	0.242	0.305	[0.071,1.299]	0.108	0.421	[0.093,1.895]	0.259	0.160
rs12373018	TRAP1	C	0.147	1.171	[0.849,1.614]	0.336	1.631	[0.952,2.795]	0.075	1.394	[0.782,2.483]	0.260	0.164
rs1448905	ADAM23	C	0.404	0.896	[0.705,1.138]	0.367	1.163	[0.762,1.773]	0.484	1.298	[0.824,2.045]	0.261	0.469
rs6577	GSTA2	C	0.155	1.164	[0.797,1.701]	0.432	0.766	[0.39,1.506]	0.440	0.658	[0.317,1.366]	0.261	0.497
rs4292454	GHR	C	0.442	1.081	[0.852,1.371]	0.523	0.825	[0.531,1.282]	0.392	0.763	[0.476,1.224]	0.262	0.520
rs2230748	CD97	A	0.142	0.963	[0.688,1.348]	0.828	1.359	[0.782,2.361]	0.277	1.410	[0.773,2.575]	0.263	0.514
rs1330286	ALDH1A1	G	0.376	1.004	[0.785,1.283]	0.975	1.309	[0.851,2.014]	0.221	1.304	[0.819,2.076]	0.264	0.468
rs1041983	NAT2	T	0.354	0.937	[0.731,1.203]	0.611	0.704	[0.44,1.127]	0.144	0.751	[0.455,1.241]	0.264	0.327
rs603965	CCND1	A	0.442	1.089	[0.862,1.375]	0.477	0.835	[0.539,1.291]	0.417	0.767	[0.481,1.222]	0.264	0.510
rs4986826	AHR	A	0.011	0.296	[0.038,2.329]	0.247	1.288	[0.221,7.49]	0.778	4.358	[0.329,57.724]	0.264	0.474
rs3798343	PPARD	G	0.056	1.215	[0.737,2.004]	0.445	0.637	[0.215,1.882]	0.414	0.524	[0.168,1.635]	0.265	0.491
rs25648	VEGFA	T	0.148	1.081	[0.78,1.5]	0.640	1.515	[0.872,2.631]	0.141	1.401	[0.774,2.537]	0.266	0.329
rs3131637	TNF	T	0.354	0.779	[0.604,1.003]	0.053	1.025	[0.654,1.605]	0.915	1.316	[0.811,2.136]	0.267	0.144
rs6103	SERPINB2	G	0.257	1.380	[1.06,1.797]	0.017	1.820	[1.149,2.881]	0.011	1.319	[0.808,2.153]	0.269	0.005
rs930509	MBL2	C	0.171	0.958	[0.697,1.315]	0.789	1.320	[0.785,2.222]	0.295	1.379	[0.78,2.436]	0.269	0.529
rs2899472	CYP19A1	A	0.206	0.823	[0.608,1.113]	0.205	1.132	[0.672,1.907]	0.642	1.376	[0.781,2.423]	0.269	0.364
rs858521	SAT2	G	0.322	1.020	[0.794,1.311]	0.874	1.338	[0.854,2.094]	0.203	1.311	[0.811,2.119]	0.269	0.445
rs1002153	PARP1	C	0.218	0.915	[0.689,1.214]	0.537	0.654	[0.375,1.142]	0.136	0.715	[0.395,1.296]	0.270	0.297
rs10018287	MGC48628	T	0.338	0.854	[0.663,1.101]	0.223	1.117	[0.721,1.732]	0.621	1.308	[0.812,2.106]	0.270	0.382
rs3793771	WNT8B	G	0.216	0.962	[0.72,1.285]	0.793	1.301	[0.793,2.136]	0.298	1.353	[0.79,2.316]	0.271	0.534
rs3138052	NFKBIA	G	0.275	0.840	[0.638,1.107]	0.217	1.117	[0.702,1.777]	0.640	1.329	[0.801,2.207]	0.271	0.380
rs16944	IL1B	A	0.385	1.112	[0.876,1.412]	0.381	0.852	[0.546,1.329]	0.479	0.766	[0.476,1.232]	0.271	0.482
rs3824874	MTMR2	G	0.325	0.964	[0.732,1.268]	0.792	1.277	[0.806,2.022]	0.298	1.325	[0.803,2.186]	0.271	0.534
rs348485	ALDH1A1	C	0.212	1.086	[0.817,1.443]	0.572	1.450	[0.899,2.339]	0.128	1.336	[0.797,2.239]	0.272	0.297
rs9282682	FANCA	C	0.101	1.000	[0.68,1.47]	0.999	0.621	[0.278,1.388]	0.246	0.621	[0.266,1.453]	0.272	0.505
rs8190955	GSR	T	0.017	1.474	[0.587,3.699]	0.409	0.413	[0.046,3.69]	0.429	0.281	[0.029,2.72]	0.273	0.476
rs12233949	GHR	C	0.251	0.860	[0.651,1.136]	0.287	1.157	[0.707,1.891]	0.562	1.345	[0.791,2.288]	0.273	0.434
rs17110944	PDGFRB	A	0.041	1.375	[0.712,2.655]	0.343	0.654	[0.189,2.259]	0.502	0.475	[0.125,1.802]	0.274	0.467
rs2302538	UGT1A1	G	0.161	1.271	[0.919,1.756]	0.147	0.895	[0.498,1.608]	0.710	0.704	[0.376,1.32]	0.274	0.295
rs1545981	IL17RD	T	0.127	0.980	[0.689,1.394]	0.910	1.387	[0.785,2.451]	0.260	1.416	[0.759,2.64]	0.274	0.509
rs1413228	DPYD	G	0.126	1.340	[0.937,1.916]	0.109	1.889	[1.067,3.346]	0.029	1.410	[0.761,2.612]	0.274	0.044
rs10977171	PTPRD	C	0.050	1.242	[0.745,2.072]	0.405	0.625	[0.191,2.04]	0.436	0.503	[0.147,1.726]	0.275	0.479
rs1805405	PARP1	A	0.216	0.919	[0.692,1.222]	0.563	0.659	[0.376,1.154]	0.145	0.716	[0.394,1.303]	0.275	0.317
rs2072446	NGFR	T	0.044	0.808	[0.455,1.435]	0.467	1.369	[0.594,3.157]	0.461	1.694	[0.657,4.365]	0.275	0.538

rs1799969	ICAM1	A	0.106	0.955	[0.648,1.408]	0.818	1.411	[0.74,2.69]	0.295	1.477	[0.733,2.977]	0.275	0.535
rs6136	SELP	C	0.085	0.822	[0.532,1.269]	0.376	1.263	[0.625,2.552]	0.516	1.537	[0.71,3.327]	0.276	0.497
rs1805388	LIG4	T	0.160	1.197	[0.88,1.629]	0.252	0.830	[0.445,1.549]	0.559	0.694	[0.36,1.339]	0.276	0.393
rs5498	ICAM1	G	0.383	0.881	[0.679,1.143]	0.338	0.657	[0.403,1.073]	0.093	0.746	[0.441,1.263]	0.276	0.184
rs7588635	MERTK	A	0.029	1.417	[0.672,2.987]	0.360	0.576	[0.125,2.656]	0.480	0.407	[0.081,2.051]	0.276	0.469
rs1800797	IL6	A	0.313	1.171	[0.918,1.493]	0.204	0.881	[0.544,1.428]	0.608	0.753	[0.452,1.255]	0.276	0.352
rs215101	ABCC1	C	0.151	1.190	[0.87,1.629]	0.277	0.828	[0.446,1.538]	0.549	0.696	[0.362,1.337]	0.276	0.415
rs268673	PRX	G	0.390	0.833	[0.653,1.062]	0.140	0.633	[0.398,1.007]	0.054	0.761	[0.465,1.245]	0.277	0.074
rs2228083	ALAD	T	0.092	0.978	[0.64,1.494]	0.917	0.592	[0.252,1.389]	0.228	0.605	[0.245,1.496]	0.277	0.483
rs4660	SPP1	A	0.014	0.451	[0.096,2.105]	0.311	1.406	[0.296,6.674]	0.668	3.121	[0.401,24.291]	0.277	0.512
rs2066479	HSD17B3	A	0.064	1.048	[0.647,1.699]	0.848	1.667	[0.774,3.587]	0.191	1.590	[0.688,3.675]	0.278	0.426
rs12680113	ZNF596	T	0.339	0.907	[0.707,1.164]	0.443	1.170	[0.765,1.789]	0.469	1.290	[0.814,2.043]	0.278	0.521
rs3100697	HNMT	C	0.031	2.240	[1.011,4.964]	0.047	0.993	[0.256,3.85]	0.992	0.443	[0.102,1.93]	0.278	0.133
rs454078	IL1RN	T	0.251	1.126	[0.854,1.484]	0.402	0.821	[0.48,1.405]	0.472	0.730	[0.412,1.291]	0.279	0.496
rs7602171	ABCB11	A	0.262	0.769	[0.583,1.014]	0.063	1.027	[0.632,1.667]	0.915	1.336	[0.79,2.258]	0.280	0.167
rs6519270	NHP2L1	A	0.293	1.142	[0.874,1.492]	0.332	0.855	[0.523,1.397]	0.531	0.749	[0.443,1.266]	0.280	0.464
rs1455162	HNMT	C	0.253	0.702	[0.525,0.938]	0.017	0.943	[0.579,1.538]	0.815	1.344	[0.786,2.297]	0.280	0.057
rs2331390	IGFBP1	A	0.473	0.987	[0.779,1.251]	0.915	1.272	[0.828,1.952]	0.272	1.288	[0.813,2.041]	0.281	0.528
rs129116	ABCC1	C	0.310	1.122	[0.864,1.457]	0.389	0.839	[0.512,1.376]	0.488	0.748	[0.442,1.268]	0.281	0.494
rs1137282	KRAS	C	0.207	0.980	[0.742,1.293]	0.885	0.709	[0.407,1.236]	0.225	0.724	[0.402,1.303]	0.281	0.479
rs17473423	KRAS	G	0.207	0.980	[0.742,1.293]	0.885	0.709	[0.407,1.236]	0.225	0.724	[0.402,1.303]	0.281	0.479
rs3769148	ZAK	A	0.408	0.908	[0.71,1.161]	0.441	0.695	[0.44,1.096]	0.117	0.765	[0.47,1.246]	0.282	0.250
rs6098	SERPINB2	G	0.257	1.393	[1.069,1.814]	0.014	1.822	[1.151,2.886]	0.010	1.309	[0.801,2.137]	0.282	0.005
rs5742909	CTLA4	T	0.086	0.721	[0.461,1.129]	0.153	0.401	[0.145,1.111]	0.079	0.556	[0.19,1.624]	0.283	0.096
rs3113199	HNMT	T	0.037	0.975	[0.466,2.038]	0.945	0.414	[0.096,1.783]	0.236	0.424	[0.088,2.036]	0.284	0.495
rs2375005	PON2	A	0.499	0.962	[0.76,1.219]	0.751	0.752	[0.493,1.145]	0.184	0.781	[0.497,1.228]	0.284	0.410
rs1042034	APOB	G	0.227	1.007	[0.755,1.342]	0.963	0.729	[0.417,1.273]	0.266	0.724	[0.4,1.31]	0.285	0.529
rs1202283	ABCB4	A	0.484	0.956	[0.746,1.226]	0.725	0.729	[0.457,1.164]	0.185	0.763	[0.463,1.255]	0.286	0.410
rs348462	ALDH1A1	C	0.344	1.021	[0.794,1.313]	0.872	1.321	[0.852,2.048]	0.214	1.294	[0.806,2.077]	0.287	0.462
rs10018199	SPOCK3	G	0.267	0.840	[0.64,1.1]	0.205	1.105	[0.695,1.756]	0.674	1.316	[0.794,2.18]	0.287	0.376
rs132806	NHP2L1	T	0.302	0.784	[0.601,1.023]	0.073	1.034	[0.645,1.659]	0.888	1.319	[0.791,2.2]	0.288	0.188
rs546382	IGHMBP2	T	0.263	1.210	[0.928,1.578]	0.160	0.905	[0.546,1.498]	0.697	0.748	[0.437,1.279]	0.289	0.313
rs2076167	PPARD	G	0.287	0.807	[0.614,1.062]	0.125	1.061	[0.668,1.686]	0.802	1.315	[0.793,2.179]	0.289	0.278
rs3743261	IGF1R	T	0.033	1.423	[0.792,2.556]	0.238	0.638	[0.152,2.685]	0.540	0.449	[0.102,1.98]	0.290	0.374
rs183374	NFATC1	A	0.431	0.929	[0.732,1.18]	0.546	1.194	[0.775,1.84]	0.422	1.285	[0.807,2.045]	0.290	0.559
rs717620	ABCC2	A	0.162	1.237	[0.904,1.693]	0.184	1.691	[0.985,2.905]	0.057	1.367	[0.766,2.441]	0.290	0.096
rs7804387	MAD1L1	A	0.112	1.404	[0.93,2.119]	0.107	0.889	[0.402,1.97]	0.773	0.634	[0.272,1.479]	0.291	0.240
rs7578587	ABCB11	C	0.028	0.928	[0.394,2.186]	0.865	0.288	[0.036,2.304]	0.241	0.310	[0.035,2.75]	0.293	0.501
rs2241868	HMGCS2	C	0.079	1.379	[0.919,2.067]	0.120	0.856	[0.364,2.014]	0.721	0.621	[0.255,1.511]	0.294	0.250
rs12717	PSMB1	G	0.404	1.031	[0.81,1.313]	0.803	1.322	[0.86,2.031]	0.204	1.282	[0.807,2.036]	0.294	0.444
rs162555	CYP1B1	G	0.194	0.704	[0.51,0.971]	0.032	0.966	[0.563,1.657]	0.900	1.373	[0.76,2.48]	0.294	0.100

rs2301870	LPO	T	0.149	0.858	[0.604,1.218]	0.391	1.196	[0.68,2.104]	0.534	1.395	[0.749,2.595]	0.294	0.522
rs2070874	IL4	T	0.221	1.235	[0.944,1.616]	0.123	0.917	[0.542,1.552]	0.746	0.742	[0.425,1.296]	0.294	0.264
rs1148555	MBD6	G	0.164	0.719	[0.516,1.002]	0.052	0.996	[0.572,1.732]	0.988	1.385	[0.753,2.545]	0.294	0.146
rs15524	CYP3A5	C	0.171	1.178	[0.835,1.661]	0.351	0.824	[0.442,1.537]	0.543	0.700	[0.359,1.364]	0.295	0.489
rs2278294	IMPDH1	A	0.364	0.970	[0.754,1.249]	0.815	1.246	[0.809,1.92]	0.318	1.284	[0.804,2.052]	0.295	0.565
rs17006794	HELQ	T	0.019	0.410	[0.113,1.486]	0.175	1.079	[0.255,4.571]	0.918	2.630	[0.43,16.07]	0.295	0.384
rs3785457	PCGF2	A	0.154	0.964	[0.701,1.327]	0.824	0.659	[0.334,1.297]	0.227	0.683	[0.334,1.396]	0.296	0.481
rs162549	CYP1B1	T	0.201	0.727	[0.528,1]	0.050	0.996	[0.58,1.711]	0.988	1.371	[0.759,2.476]	0.296	0.142
rs11670988	HIPK4	T	0.078	1.410	[0.95,2.093]	0.088	0.872	[0.366,2.076]	0.757	0.618	[0.251,1.524]	0.296	0.200
rs2227564	C10orf55	T	0.222	1.082	[0.82,1.428]	0.578	0.797	[0.463,1.372]	0.412	0.736	[0.414,1.309]	0.297	0.569
rs1061622	TNFRSF1B	G	0.234	0.994	[0.754,1.311]	0.966	1.299	[0.817,2.066]	0.268	1.307	[0.79,2.165]	0.298	0.530
rs1800790	FGB	A	0.168	1.257	[0.923,1.712]	0.147	0.893	[0.486,1.644]	0.717	0.711	[0.374,1.352]	0.298	0.297
rs2302387	ABCB4	A	0.181	0.985	[0.718,1.352]	0.926	1.332	[0.79,2.248]	0.282	1.353	[0.766,2.389]	0.298	0.542
rs2069522	CYP1A2	C	0.050	0.968	[0.562,1.668]	0.906	1.535	[0.705,3.343]	0.280	1.586	[0.665,3.786]	0.299	0.533
rs664393	FLT1	A	0.107	0.952	[0.651,1.392]	0.799	1.384	[0.721,2.658]	0.329	1.454	[0.718,2.948]	0.299	0.573
rs7853758	SLC28A3	A	0.175	1.149	[0.84,1.57]	0.385	0.826	[0.462,1.475]	0.518	0.719	[0.386,1.34]	0.299	0.511
rs1855363	DPYD	A	0.034	2.589	[1.412,4.749]	0.002	1.396	[0.46,4.241]	0.556	0.539	[0.168,1.729]	0.299	0.009
rs13652	FN1	G	0.130	1.143	[0.81,1.612]	0.448	0.789	[0.409,1.522]	0.480	0.691	[0.343,1.389]	0.299	0.537
rs1800451	MBL2	A	0.062	0.998	[0.575,1.733]	0.995	1.594	[0.725,3.505]	0.246	1.597	[0.66,3.864]	0.300	0.500
rs713865	CACNA1I	T	0.409	1.018	[0.804,1.288]	0.883	0.792	[0.508,1.235]	0.304	0.778	[0.485,1.249]	0.300	0.565
rs4149057	SLCO1B1	T	0.463	1.330	[1.053,1.681]	0.017	1.045	[0.682,1.6]	0.841	0.785	[0.497,1.24]	0.300	0.057
rs25882	CSF2	C	0.229	0.852	[0.644,1.128]	0.262	1.117	[0.698,1.788]	0.644	1.312	[0.785,2.19]	0.300	0.439
rs622082	IGHMBP2	G	0.262	1.180	[0.903,1.541]	0.225	0.881	[0.524,1.482]	0.634	0.747	[0.43,1.297]	0.300	0.389
rs248805	SRD5A1	A	0.457	0.882	[0.698,1.114]	0.292	1.123	[0.733,1.719]	0.594	1.273	[0.806,2.012]	0.300	0.455
rs3743260	IGF1R	A	0.032	1.511	[0.832,2.747]	0.175	0.689	[0.163,2.908]	0.612	0.456	[0.103,2.014]	0.300	0.315
rs1799955	BRCA2	G	0.225	1.003	[0.749,1.344]	0.984	1.334	[0.81,2.197]	0.258	1.330	[0.775,2.282]	0.301	0.522
rs2640	EIF2AK1	C	0.058	0.844	[0.507,1.407]	0.516	1.352	[0.603,3.033]	0.464	1.601	[0.656,3.909]	0.301	0.573
rs1040090	DPYD	A	0.153	1.074	[0.779,1.48]	0.663	0.751	[0.396,1.426]	0.382	0.700	[0.355,1.377]	0.301	0.584
rs6413436	RAD52	C	0.392	1.167	[0.912,1.493]	0.219	1.508	[0.956,2.379]	0.077	1.292	[0.794,2.103]	0.302	0.128
rs2269352	UGT1A8	C	0.197	0.933	[0.645,1.351]	0.715	0.620	[0.297,1.293]	0.202	0.664	[0.305,1.444]	0.302	0.436
rs943584	PLEKHG5	T	0.105	1.068	[0.709,1.608]	0.754	0.655	[0.273,1.572]	0.343	0.613	[0.243,1.552]	0.302	0.587
rs1029871	NEK4	G	0.377	0.982	[0.769,1.254]	0.883	0.756	[0.473,1.208]	0.241	0.770	[0.468,1.266]	0.302	0.504
rs8832	IL4R	G	0.489	0.916	[0.721,1.163]	0.472	1.171	[0.758,1.811]	0.477	1.279	[0.801,2.04]	0.302	0.553
rs138056	SULT4A1	A	0.218	1.115	[0.836,1.489]	0.459	1.479	[0.9,2.429]	0.122	1.326	[0.775,2.268]	0.303	0.265
rs4149056	SLCO1B1	C	0.127	1.141	[0.812,1.603]	0.446	1.567	[0.897,2.737]	0.115	1.373	[0.751,2.508]	0.303	0.254
rs1851426	CYP3A4	T	0.150	1.554	[1.006,2.402]	0.047	1.046	[0.529,2.066]	0.897	0.673	[0.317,1.43]	0.303	0.137
rs1469167	ALDH1A1	G	0.089	1.047	[0.677,1.62]	0.836	1.550	[0.786,3.056]	0.206	1.480	[0.701,3.126]	0.304	0.450
rs664982	ATM	G	0.469	0.934	[0.742,1.176]	0.562	0.738	[0.485,1.123]	0.156	0.790	[0.504,1.239]	0.304	0.339
rs500760	PGR	G	0.253	0.852	[0.646,1.122]	0.254	1.114	[0.693,1.79]	0.655	1.308	[0.783,2.185]	0.304	0.430
rs10018280	PDE5A	G	0.308	1.047	[0.814,1.345]	0.722	1.347	[0.86,2.109]	0.193	1.287	[0.795,2.084]	0.305	0.422
rs1520658	DPYD	G	0.128	0.922	[0.653,1.302]	0.645	1.271	[0.722,2.235]	0.406	1.378	[0.746,2.546]	0.306	0.592

rs2217332	HERPUD1	T	0.140	0.991	[0.711,1.38]	0.956	1.349	[0.783,2.324]	0.281	1.362	[0.754,2.46]	0.306	0.545
rs2227631	SERPINE1	G	0.481	0.922	[0.723,1.174]	0.509	1.177	[0.76,1.822]	0.466	1.277	[0.799,2.04]	0.306	0.568
rs5275	PTGS2	C	0.406	1.008	[0.787,1.29]	0.952	0.784	[0.501,1.227]	0.287	0.778	[0.481,1.259]	0.307	0.555
rs6427384	FCRL5	C	0.221	0.798	[0.585,1.088]	0.153	0.575	[0.32,1.034]	0.065	0.720	[0.384,1.352]	0.307	0.087
rs1800391	WRN	A	0.069	0.733	[0.448,1.197]	0.214	0.381	[0.114,1.27]	0.116	0.520	[0.148,1.825]	0.307	0.160
rs6104	SERPINB2	G	0.257	1.400	[1.073,1.827]	0.013	1.810	[1.141,2.87]	0.012	1.292	[0.79,2.114]	0.307	0.005
rs3212723	JAK3	A	0.016	1.276	[0.517,3.153]	0.597	0.410	[0.05,3.326]	0.404	0.321	[0.036,2.852]	0.308	0.579
rs2235048	ABCB1	C	0.475	0.877	[0.691,1.114]	0.283	0.689	[0.447,1.063]	0.092	0.785	[0.493,1.25]	0.308	0.169
rs3125001	NOTCH1	T	0.444	1.210	[0.891,1.643]	0.222	0.903	[0.536,1.521]	0.702	0.747	[0.425,1.31]	0.309	0.402
rs549908	IL18	G	0.290	1.031	[0.802,1.325]	0.813	1.321	[0.846,2.063]	0.220	1.282	[0.794,2.069]	0.309	0.471
rs428073	LOC100130562	C	0.320	0.893	[0.692,1.154]	0.387	1.156	[0.73,1.831]	0.537	1.294	[0.788,2.125]	0.309	0.525
rs2071426	CYP2C8	G	0.272	0.730	[0.552,0.966]	0.028	0.964	[0.589,1.579]	0.884	1.320	[0.773,2.253]	0.309	0.087
rs2066853	AHR	A	0.168	0.876	[0.62,1.239]	0.455	1.204	[0.692,2.096]	0.511	1.374	[0.744,2.538]	0.309	0.565
rs3113224	HNMT	A	0.253	0.713	[0.534,0.952]	0.022	0.941	[0.577,1.535]	0.808	1.320	[0.773,2.256]	0.309	0.071
rs1053046	PPARD	A	0.122	0.900	[0.601,1.348]	0.610	0.586	[0.271,1.27]	0.176	0.651	[0.285,1.489]	0.310	0.377
rs1799949	BRCA1	T	0.288	0.845	[0.653,1.094]	0.200	1.093	[0.689,1.734]	0.705	1.294	[0.786,2.13]	0.311	0.378
rs619487	PGR	G	0.279	1.171	[0.898,1.528]	0.244	0.886	[0.534,1.471]	0.640	0.757	[0.441,1.297]	0.311	0.416
rs502570	ABCB11	T	0.281	1.102	[0.856,1.419]	0.451	1.412	[0.903,2.209]	0.131	1.281	[0.793,2.07]	0.311	0.277
rs2235000	ATM	A	0.012	2.588	[0.96,6.971]	0.060	0.827	[0.099,6.909]	0.861	0.320	[0.035,2.905]	0.311	0.154
rs2641806	CHST5	C	0.409	1.275	[1.003,1.621]	0.047	1.000	[0.644,1.553]	0.999	0.784	[0.49,1.255]	0.311	0.133
rs521102	CHEK1	T	0.467	1.229	[0.965,1.565]	0.095	0.966	[0.626,1.491]	0.876	0.786	[0.493,1.253]	0.312	0.229
rs212087	ABCC1	T	0.389	0.959	[0.748,1.228]	0.738	1.231	[0.783,1.935]	0.369	1.284	[0.791,2.083]	0.312	0.599
rs2301157	SLC10A2	T	0.490	1.255	[0.987,1.597]	0.064	0.986	[0.638,1.525]	0.951	0.786	[0.492,1.254]	0.312	0.170
rs2536512	SOD3	G	0.457	1.060	[0.828,1.357]	0.644	0.829	[0.532,1.292]	0.407	0.782	[0.485,1.26]	0.312	0.599
rs599554	CTDP1	A	0.183	0.899	[0.658,1.227]	0.501	1.201	[0.718,2.012]	0.485	1.337	[0.761,2.35]	0.313	0.580
rs10034373	WHSC1	T	0.021	0.911	[0.355,2.332]	0.845	0.292	[0.036,2.351]	0.247	0.321	[0.035,2.924]	0.313	0.510
rs230533	NFKB1	T	0.309	1.184	[0.92,1.523]	0.190	0.912	[0.567,1.466]	0.704	0.770	[0.464,1.279]	0.313	0.362
rs913118	MGMT	T	0.440	0.866	[0.682,1.101]	0.240	1.098	[0.715,1.688]	0.668	1.268	[0.799,2.013]	0.314	0.420
rs930508	MBL2	G	0.215	1.050	[0.785,1.404]	0.744	1.372	[0.85,2.217]	0.196	1.308	[0.776,2.204]	0.314	0.429
rs2275586	MMS19	G	0.044	0.758	[0.4,1.437]	0.396	0.346	[0.082,1.469]	0.150	0.457	[0.1,2.099]	0.314	0.275
rs7096206	MBL2	G	0.202	0.942	[0.699,1.271]	0.697	1.253	[0.751,2.089]	0.388	1.329	[0.763,2.317]	0.315	0.603
rs1800629	TNF	A	0.169	1.166	[0.848,1.602]	0.345	0.831	[0.446,1.549]	0.560	0.713	[0.369,1.379]	0.315	0.495
rs11572076	CYP2C8	A	0.029	0.395	[0.133,1.171]	0.094	0.896	[0.248,3.245]	0.868	2.267	[0.458,11.219]	0.316	0.246
rs1124	BMP1	A	0.288	1.073	[0.801,1.437]	0.638	0.795	[0.46,1.374]	0.411	0.741	[0.412,1.331]	0.316	0.602
rs1934962	CYP2C9	T	0.026	1.352	[0.562,3.256]	0.501	2.763	[0.808,9.449]	0.105	2.043	[0.504,8.277]	0.317	0.245
rs2275008	OSGEP	G	0.309	1.001	[0.778,1.289]	0.993	0.770	[0.475,1.247]	0.288	0.769	[0.459,1.287]	0.318	0.563
rs2108622	CYP4F2	T	0.266	0.998	[0.77,1.294]	0.990	0.759	[0.458,1.259]	0.286	0.760	[0.444,1.301]	0.318	0.561
rs2270565	UCP1	A	0.067	1.094	[0.692,1.73]	0.699	1.629	[0.799,3.322]	0.180	1.488	[0.682,3.248]	0.318	0.401
rs7563233	ABCB11	C	0.074	1.306	[0.777,2.193]	0.313	0.774	[0.298,2.011]	0.599	0.593	[0.212,1.655]	0.318	0.484
rs12114000	CYP3A4	A	0.032	1.129	[0.524,2.434]	0.757	0.491	[0.106,2.285]	0.365	0.435	[0.085,2.231]	0.318	0.607
rs1799986	LRP1	T	0.116	0.634	[0.424,0.949]	0.027	0.923	[0.474,1.799]	0.814	1.456	[0.695,3.047]	0.319	0.086

rs868891	MON1A	C	0.386	1.115	[0.879,1.413]	0.370	0.877	[0.563,1.364]	0.560	0.787	[0.49,1.262]	0.320	0.520
rs676210	APOB	A	0.228	0.994	[0.745,1.325]	0.965	0.735	[0.42,1.286]	0.281	0.739	[0.408,1.341]	0.320	0.556
rs3797897	MSH3	G	0.088	1.228	[0.833,1.811]	0.300	1.727	[0.92,3.244]	0.089	1.407	[0.718,2.755]	0.320	0.183
rs3752988	CYP2C8	C	0.331	1.152	[0.894,1.485]	0.273	0.895	[0.563,1.424]	0.641	0.777	[0.472,1.279]	0.321	0.453
rs4128474	DPYD	C	0.096	1.058	[0.719,1.557]	0.775	0.674	[0.29,1.571]	0.361	0.638	[0.262,1.553]	0.322	0.611
rs2269429	TNXB	A	0.098	1.111	[0.756,1.632]	0.593	0.731	[0.334,1.599]	0.432	0.658	[0.287,1.508]	0.322	0.600
rs10743597	A2M	G	0.331	0.931	[0.732,1.184]	0.560	1.171	[0.768,1.784]	0.463	1.258	[0.799,1.981]	0.323	0.600
rs11549465	HIF1A	T	0.088	0.817	[0.527,1.266]	0.365	1.192	[0.605,2.349]	0.611	1.460	[0.69,3.091]	0.323	0.537
rs9328764	POLN	A	0.205	0.827	[0.6,1.141]	0.247	1.112	[0.65,1.903]	0.699	1.344	[0.748,2.418]	0.323	0.440
rs2352984	MON1A	C	0.412	1.098	[0.869,1.387]	0.434	0.870	[0.565,1.339]	0.526	0.792	[0.499,1.257]	0.323	0.557
rs1652342	C18orf8	G	0.306	0.809	[0.62,1.055]	0.118	1.045	[0.653,1.673]	0.854	1.292	[0.778,2.145]	0.323	0.272
rs6041759	FKBP1A	C	0.120	1.025	[0.704,1.492]	0.897	0.688	[0.327,1.448]	0.325	0.671	[0.304,1.482]	0.324	0.597
rs1143627	IL1B	C	0.394	1.142	[0.899,1.451]	0.277	0.901	[0.58,1.399]	0.642	0.789	[0.492,1.265]	0.324	0.458
rs196912	ERN1	T	0.305	0.980	[0.749,1.282]	0.882	1.253	[0.798,1.968]	0.327	1.279	[0.784,2.088]	0.325	0.592
rs17829584	PPP3CA	C	0.125	0.844	[0.575,1.24]	0.387	1.195	[0.634,2.251]	0.581	1.416	[0.706,2.838]	0.327	0.549
rs241448	TAP2	C	0.229	0.976	[0.746,1.278]	0.862	0.738	[0.435,1.252]	0.260	0.756	[0.431,1.324]	0.327	0.530
rs2274407	ABCC4	A	0.094	1.105	[0.732,1.67]	0.634	0.734	[0.339,1.589]	0.433	0.664	[0.293,1.507]	0.328	0.614
rs3816540	RPS6KA1	C	0.185	0.817	[0.599,1.115]	0.203	1.096	[0.638,1.881]	0.741	1.340	[0.745,2.412]	0.328	0.393
rs2296241	CYP24A1	G	0.479	1.156	[0.919,1.453]	0.216	1.449	[0.947,2.218]	0.087	1.254	[0.796,1.975]	0.328	0.140
rs2291075	SLCO1B1	T	0.418	1.022	[0.807,1.295]	0.856	0.808	[0.52,1.256]	0.344	0.791	[0.493,1.267]	0.329	0.609
rs1065341	CCL5	G	0.073	0.930	[0.574,1.507]	0.769	0.552	[0.206,1.484]	0.239	0.594	[0.208,1.695]	0.330	0.494
rs2229712	RPS6KA1	C	0.184	0.820	[0.601,1.118]	0.210	1.097	[0.639,1.885]	0.736	1.339	[0.744,2.409]	0.330	0.401
rs3770601	ABCB11	T	0.089	0.809	[0.52,1.258]	0.347	1.190	[0.59,2.401]	0.627	1.471	[0.676,3.198]	0.330	0.531
rs2070673	CYP2E1	A	0.263	0.881	[0.65,1.194]	0.414	1.172	[0.689,1.994]	0.559	1.330	[0.748,2.363]	0.331	0.559
rs932477	ESR1	A	0.122	1.012	[0.709,1.446]	0.946	0.697	[0.343,1.417]	0.319	0.688	[0.324,1.462]	0.331	0.597
rs2109505	ABCB4	A	0.197	0.946	[0.699,1.28]	0.720	1.246	[0.747,2.076]	0.399	1.316	[0.756,2.293]	0.331	0.623
rs1799782	XRCC1	T	0.084	0.785	[0.506,1.22]	0.282	1.145	[0.575,2.282]	0.700	1.458	[0.681,3.122]	0.331	0.482
rs1800610	TNF	T	0.085	0.911	[0.588,1.411]	0.675	1.352	[0.65,2.811]	0.420	1.485	[0.669,3.296]	0.332	0.624
rs5743612	TLR1	T	0.015	1.435	[0.534,3.859]	0.474	0.479	[0.059,3.878]	0.490	0.334	[0.036,3.063]	0.332	0.575
rs1051640	ABCC3	G	0.148	0.952	[0.675,1.343]	0.779	1.303	[0.726,2.342]	0.375	1.369	[0.726,2.584]	0.332	0.620
rs11632814	CYP1A2	A	0.051	1.006	[0.589,1.719]	0.981	1.544	[0.709,3.362]	0.274	1.534	[0.646,3.641]	0.332	0.542
rs3763497	IGFBP1	T	0.318	0.982	[0.765,1.259]	0.883	0.764	[0.474,1.231]	0.268	0.778	[0.468,1.293]	0.333	0.542
rs215073	ABCC1	A	0.066	1.100	[0.684,1.77]	0.693	1.634	[0.787,3.392]	0.188	1.485	[0.667,3.306]	0.333	0.414
rs11875	MGST1	A	0.072	0.750	[0.467,1.205]	0.234	1.131	[0.535,2.394]	0.747	1.509	[0.655,3.476]	0.334	0.440
rs2256974	LST1	T	0.228	1.063	[0.795,1.422]	0.679	0.799	[0.465,1.373]	0.416	0.751	[0.421,1.342]	0.334	0.626
rs4760	PLAUR	C	0.123	1.226	[0.855,1.758]	0.267	0.840	[0.406,1.739]	0.639	0.685	[0.318,1.476]	0.334	0.445
rs2227551	PLAU	G	0.320	1.310	[1.023,1.678]	0.033	1.035	[0.662,1.619]	0.880	0.790	[0.49,1.275]	0.335	0.100
rs1625895	TP53	A	0.145	0.812	[0.572,1.154]	0.246	0.560	[0.277,1.136]	0.108	0.690	[0.325,1.467]	0.335	0.168
rs2070672	CYP2E1	G	0.049	1.079	[0.617,1.887]	0.789	1.721	[0.732,4.044]	0.213	1.594	[0.618,4.115]	0.335	0.459
rs2297322	SLC15A1	T	0.167	1.032	[0.762,1.399]	0.838	0.756	[0.417,1.372]	0.358	0.732	[0.389,1.38]	0.335	0.622
rs4529	TBXAS1	G	0.018	2.357	[0.993,5.598]	0.052	1.026	[0.206,5.105]	0.975	0.435	[0.08,2.367]	0.336	0.145

rs1800787	FGB	T	0.180	1.249	[0.923,1.691]	0.149	0.924	[0.517,1.65]	0.788	0.739	[0.4,1.368]	0.336	0.315
rs1505	CYP2C9	C	0.340	0.951	[0.745,1.214]	0.687	0.744	[0.466,1.188]	0.216	0.783	[0.475,1.289]	0.336	0.452
rs1005658	TSPO	A	0.311	1.115	[0.875,1.421]	0.379	1.395	[0.912,2.133]	0.125	1.251	[0.793,1.974]	0.336	0.248
rs16147	NPY	G	0.488	0.860	[0.675,1.096]	0.222	0.679	[0.433,1.065]	0.092	0.790	[0.489,1.277]	0.336	0.147
rs4150526	GTF2H1	G	0.290	1.220	[0.949,1.569]	0.120	0.954	[0.595,1.529]	0.844	0.782	[0.473,1.292]	0.336	0.273
rs3738099	ALPL	G	0.148	1.000	[0.713,1.402]	0.999	1.341	[0.776,2.318]	0.293	1.341	[0.737,2.439]	0.336	0.568
rs1805386	LIG4	C	0.164	0.937	[0.679,1.293]	0.692	1.254	[0.726,2.165]	0.417	1.338	[0.739,2.423]	0.336	0.630
rs1126667	ALOX12	A	0.409	0.942	[0.741,1.197]	0.624	1.179	[0.771,1.804]	0.447	1.252	[0.792,1.98]	0.337	0.626
rs4713853	PPARD	C	0.199	0.894	[0.635,1.258]	0.519	1.228	[0.673,2.242]	0.504	1.374	[0.718,2.632]	0.338	0.606
rs1805389	LIG4	T	0.047	1.587	[0.948,2.656]	0.079	0.870	[0.264,2.873]	0.820	0.549	[0.16,1.878]	0.339	0.190
rs1881420	ALK	G	0.287	0.953	[0.738,1.231]	0.714	1.206	[0.771,1.888]	0.412	1.265	[0.781,2.05]	0.339	0.634
rs215072	ABCC1	T	0.065	1.156	[0.714,1.872]	0.556	1.718	[0.818,3.611]	0.153	1.487	[0.658,3.356]	0.340	0.339
rs2251660	RDM1	G	0.189	1.013	[0.741,1.384]	0.938	0.741	[0.406,1.353]	0.329	0.732	[0.386,1.39]	0.340	0.608
rs1219663	ACBD3	C	0.224	0.931	[0.705,1.23]	0.617	1.199	[0.744,1.932]	0.457	1.287	[0.766,2.161]	0.340	0.630
rs4531	DBH	T	0.083	1.152	[0.755,1.759]	0.512	1.640	[0.841,3.2]	0.146	1.424	[0.689,2.943]	0.340	0.320
rs2242664	SLC44A4	G	0.445	1.070	[0.845,1.356]	0.573	1.332	[0.877,2.021]	0.179	1.244	[0.794,1.949]	0.341	0.377
rs1799950	BRCA1	G	0.056	0.634	[0.364,1.105]	0.108	1.011	[0.43,2.375]	0.980	1.593	[0.611,4.156]	0.341	0.268
rs6133	SELP	T	0.181	0.966	[0.684,1.364]	0.843	1.305	[0.739,2.304]	0.359	1.351	[0.727,2.511]	0.341	0.620
rs925585	IGF1R	C	0.152	1.084	[0.779,1.507]	0.632	1.439	[0.843,2.459]	0.182	1.328	[0.74,2.382]	0.341	0.395
rs12636461	PPARG	G	0.282	0.950	[0.734,1.229]	0.696	1.203	[0.766,1.888]	0.422	1.266	[0.779,2.059]	0.341	0.636
rs3803036	PTPRR	A	0.274	0.962	[0.724,1.276]	0.786	0.730	[0.43,1.24]	0.244	0.759	[0.43,1.339]	0.342	0.503
rs828063	DPYD	A	0.170	1.107	[0.802,1.528]	0.538	1.461	[0.862,2.478]	0.159	1.321	[0.744,2.343]	0.342	0.343
rs656583	LRP5	C	0.050	0.515	[0.243,1.091]	0.083	0.887	[0.345,2.28]	0.803	1.722	[0.558,5.312]	0.344	0.223
rs13926	TRAP1	G	0.392	0.868	[0.678,1.109]	0.257	1.090	[0.701,1.695]	0.701	1.257	[0.782,2.019]	0.345	0.453
rs2272037	IGF1R	A	0.465	1.074	[0.842,1.371]	0.566	0.851	[0.542,1.336]	0.483	0.792	[0.489,1.284]	0.345	0.623
rs1065780	IGFBP1	A	0.410	0.956	[0.755,1.211]	0.711	0.763	[0.493,1.182]	0.226	0.798	[0.5,1.275]	0.346	0.471
rs1805407	PARP1	G	0.226	0.918	[0.69,1.222]	0.559	0.691	[0.397,1.202]	0.190	0.752	[0.416,1.359]	0.346	0.387
rs1799799	ERCC4	C	0.367	1.100	[0.862,1.403]	0.445	0.871	[0.553,1.371]	0.551	0.792	[0.488,1.286]	0.346	0.582
rs2758346	SOD2	T	0.488	1.269	[1.004,1.605]	0.047	1.019	[0.666,1.56]	0.930	0.803	[0.509,1.267]	0.346	0.135
rs12714192	APOB	A	0.019	0.479	[0.139,1.658]	0.246	1.091	[0.29,4.094]	0.898	2.275	[0.411,12.598]	0.347	0.493
rs1805408	PARP1	G	0.221	0.918	[0.69,1.221]	0.557	0.692	[0.399,1.201]	0.191	0.754	[0.418,1.359]	0.347	0.387
rs241440	TAP2	A	0.215	0.942	[0.716,1.239]	0.668	0.713	[0.413,1.233]	0.227	0.757	[0.424,1.352]	0.348	0.464
rs17064676	NEIL3	G	0.018	1.032	[0.372,2.864]	0.951	2.098	[0.606,7.263]	0.242	2.032	[0.461,8.95]	0.349	0.501
rs1929860	CDC42BPA	A	0.321	1.049	[0.813,1.353]	0.715	1.323	[0.84,2.084]	0.226	1.262	[0.776,2.054]	0.349	0.473
rs2307145	IL12RB2	C	0.047	0.876	[0.503,1.526]	0.640	0.435	[0.106,1.782]	0.247	0.496	[0.114,2.15]	0.349	0.480
rs7195066	FANCA	T	0.393	1.160	[0.914,1.472]	0.223	1.447	[0.939,2.228]	0.094	1.247	[0.785,1.98]	0.349	0.151
rs1983346	NDC80	C	0.216	1.040	[0.779,1.388]	0.790	0.785	[0.451,1.365]	0.391	0.755	[0.419,1.361]	0.350	0.644
rs16963927	CCL5	G	0.071	0.961	[0.591,1.563]	0.873	0.581	[0.215,1.571]	0.285	0.604	[0.21,1.736]	0.350	0.564
rs873301	SUMO3	T	0.138	0.713	[0.492,1.034]	0.074	0.474	[0.21,1.067]	0.071	0.664	[0.281,1.567]	0.350	0.054
rs12954	FMO1	A	0.142	1.140	[0.823,1.58]	0.430	1.503	[0.881,2.564]	0.135	1.318	[0.738,2.352]	0.351	0.281
rs696221	SEC13	C	0.407	1.097	[0.866,1.389]	0.442	0.882	[0.575,1.353]	0.564	0.804	[0.508,1.272]	0.351	0.587

rs8192284	IL6R	C	0.353	1.093	[0.853,1.4]	0.482	0.863	[0.541,1.376]	0.535	0.789	[0.48,1.299]	0.352	0.602
rs885622	DPYD	A	0.306	0.925	[0.72,1.188]	0.541	1.165	[0.742,1.829]	0.508	1.259	[0.775,2.046]	0.352	0.625
rs3741367	CD248	C	0.403	0.975	[0.768,1.239]	0.837	1.213	[0.79,1.864]	0.377	1.244	[0.785,1.973]	0.353	0.641
rs17567	EPS15	C	0.268	1.191	[0.914,1.553]	0.196	0.932	[0.575,1.511]	0.775	0.782	[0.466,1.314]	0.353	0.388
rs1051303	LTBP4	G	0.444	0.983	[0.771,1.253]	0.888	1.240	[0.782,1.966]	0.360	1.262	[0.771,2.064]	0.354	0.636
rs2465811	PTPRB	C	0.307	1.092	[0.846,1.41]	0.498	0.858	[0.532,1.384]	0.530	0.786	[0.471,1.309]	0.354	0.611
rs4918758	CYP2C9	C	0.341	0.937	[0.732,1.198]	0.601	0.739	[0.461,1.183]	0.207	0.789	[0.477,1.303]	0.355	0.423
rs2909430	TP53	G	0.141	0.805	[0.562,1.152]	0.235	0.562	[0.277,1.143]	0.112	0.699	[0.327,1.493]	0.355	0.168
rs2069718	IFNG	T	0.450	1.107	[0.883,1.388]	0.379	1.360	[0.906,2.043]	0.138	1.229	[0.794,1.902]	0.355	0.265
rs3942589	SHFM1	G	0.084	1.004	[0.649,1.552]	0.987	1.430	[0.728,2.809]	0.299	1.425	[0.673,3.015]	0.355	0.578
rs915907	CYP2E1	A	0.168	1.016	[0.742,1.391]	0.921	1.334	[0.783,2.273]	0.288	1.313	[0.737,2.341]	0.355	0.568
rs3218171	E2F2	T	0.427	0.888	[0.692,1.14]	0.352	1.125	[0.703,1.801]	0.624	1.266	[0.768,2.089]	0.355	0.532
rs3736599	SULT1E1	A	0.117	1.139	[0.802,1.619]	0.467	0.805	[0.401,1.615]	0.541	0.707	[0.338,1.476]	0.356	0.595
rs1046515	ADCK2	T	0.098	1.152	[0.776,1.71]	0.482	0.773	[0.345,1.733]	0.532	0.671	[0.287,1.567]	0.357	0.599
rs3824134	ARHGEF10	C	0.234	0.966	[0.729,1.28]	0.809	1.233	[0.763,1.993]	0.393	1.277	[0.759,2.146]	0.357	0.647
rs2470893	CYP1A1	A	0.259	1.186	[0.909,1.547]	0.209	0.919	[0.553,1.528]	0.746	0.775	[0.451,1.332]	0.357	0.402
rs447804	BLM	C	0.345	0.857	[0.662,1.11]	0.242	1.084	[0.682,1.723]	0.733	1.265	[0.767,2.087]	0.357	0.445
rs2260863	EPHX1	G	0.301	1.047	[0.811,1.352]	0.725	1.311	[0.841,2.043]	0.232	1.252	[0.776,2.022]	0.358	0.481
rs10079641	MSH3	G	0.079	0.708	[0.44,1.137]	0.153	1.042	[0.498,2.178]	0.913	1.472	[0.646,3.356]	0.358	0.345
rs1800875	CMA1	A	0.462	1.090	[0.861,1.381]	0.473	0.879	[0.573,1.348]	0.554	0.806	[0.509,1.276]	0.358	0.607
rs2216504	ABCB11	A	0.052	1.306	[0.774,2.203]	0.318	0.765	[0.259,2.264]	0.629	0.586	[0.187,1.833]	0.358	0.500
rs10017297	Intergenic	T	0.055	1.191	[0.648,2.188]	0.573	1.872	[0.798,4.39]	0.150	1.571	[0.599,4.124]	0.359	0.334
rs2229765	IGF1R	A	0.392	1.174	[0.925,1.489]	0.187	0.944	[0.61,1.46]	0.794	0.804	[0.504,1.282]	0.359	0.378
rs10898	LOC100129773	C	0.277	1.027	[0.787,1.34]	0.845	1.296	[0.815,2.061]	0.273	1.262	[0.767,2.078]	0.359	0.547
rs3135506	APOA5	C	0.065	0.802	[0.493,1.305]	0.375	1.205	[0.546,2.66]	0.644	1.502	[0.629,3.585]	0.359	0.567
rs1801244	ATP7B	C	0.446	0.747	[0.579,0.963]	0.025	0.949	[0.588,1.533]	0.831	1.271	[0.761,2.122]	0.359	0.080
rs11572081	CYP2C8	A	0.031	1.370	[0.589,3.186]	0.465	0.657	[0.155,2.791]	0.569	0.479	[0.1,2.309]	0.359	0.609
rs537183	ABCB11	G	0.275	1.092	[0.848,1.406]	0.495	1.366	[0.874,2.135]	0.171	1.251	[0.775,2.02]	0.360	0.349
rs8064946	TP53	C	0.240	1.218	[0.878,1.69]	0.238	0.902	[0.494,1.647]	0.736	0.740	[0.388,1.413]	0.362	0.440
rs7668282	UGT2B7	C	0.020	2.219	[1.036,4.756]	0.040	3.658	[1.319,10.144]	0.013	1.648	[0.563,4.826]	0.362	0.018
rs2369679	AK7	C	0.149	1.166	[0.838,1.622]	0.362	1.540	[0.882,2.688]	0.129	1.320	[0.726,2.402]	0.362	0.253
rs4148553	ABCC4	A	0.432	0.850	[0.671,1.077]	0.179	1.051	[0.686,1.612]	0.818	1.237	[0.782,1.956]	0.363	0.370
rs6457815	PPARD	C	0.109	0.923	[0.604,1.41]	0.710	1.303	[0.661,2.567]	0.445	1.412	[0.671,2.97]	0.363	0.661
rs3092856	ATM	T	0.015	1.822	[0.716,4.638]	0.208	0.659	[0.081,5.384]	0.697	0.361	[0.04,3.245]	0.364	0.391
rs4938016	ANKK1	G	0.372	1.429	[1.112,1.836]	0.005	1.152	[0.749,1.772]	0.520	0.806	[0.506,1.283]	0.364	0.020
rs1424482	ALDH1A1	C	0.409	0.983	[0.771,1.254]	0.889	1.222	[0.789,1.894]	0.369	1.244	[0.777,1.991]	0.364	0.645
rs2242665	SLC44A4	G	0.446	1.085	[0.857,1.373]	0.498	1.335	[0.88,2.026]	0.174	1.231	[0.786,1.928]	0.364	0.353
rs7665103	HELQ	G	0.438	1.013	[0.798,1.284]	0.917	1.254	[0.815,1.929]	0.303	1.238	[0.78,1.967]	0.365	0.587
rs1140616	FASN	T	0.460	0.961	[0.744,1.241]	0.759	1.214	[0.756,1.95]	0.422	1.264	[0.761,2.1]	0.366	0.664
rs11574	ID3	A	0.203	0.801	[0.592,1.083]	0.149	1.046	[0.612,1.787]	0.870	1.306	[0.731,2.332]	0.367	0.331
rs3766934	EPHX1	T	0.091	1.026	[0.689,1.526]	0.901	0.682	[0.293,1.587]	0.375	0.665	[0.275,1.613]	0.367	0.655

rs6131	SELP	A	0.207	0.907	[0.675,1.22]	0.519	1.162	[0.71,1.902]	0.551	1.281	[0.748,2.193]	0.367	0.638
rs6092	SERPINE1	A	0.090	0.775	[0.507,1.186]	0.241	0.489	[0.189,1.269]	0.142	0.631	[0.232,1.717]	0.367	0.202
rs1967120	ABCC1	C	0.333	1.217	[0.955,1.549]	0.112	1.498	[0.981,2.288]	0.061	1.232	[0.783,1.938]	0.367	0.074
rs4905475	BDKRB1	C	0.086	0.954	[0.626,1.452]	0.825	0.607	[0.238,1.55]	0.297	0.637	[0.238,1.701]	0.368	0.577
rs17021877	IKBKE	A	0.019	0.915	[0.372,2.249]	0.847	0.335	[0.041,2.723]	0.307	0.366	[0.041,3.256]	0.368	0.591
rs1049631	IL4R	A	0.476	0.930	[0.731,1.182]	0.551	1.152	[0.746,1.78]	0.524	1.239	[0.777,1.977]	0.368	0.643
rs2104772	TNC	T	0.461	0.993	[0.788,1.25]	0.949	0.807	[0.53,1.23]	0.319	0.813	[0.518,1.277]	0.369	0.607
rs35594	ABCC1	A	0.348	0.929	[0.717,1.204]	0.579	1.163	[0.739,1.831]	0.514	1.251	[0.767,2.043]	0.370	0.654
rs2239995	ABCC1	A	0.172	1.269	[0.938,1.718]	0.123	0.953	[0.527,1.723]	0.874	0.751	[0.402,1.404]	0.370	0.283
rs1042858	RRM1	G	0.092	1.463	[1.013,2.112]	0.042	1.051	[0.528,2.093]	0.887	0.718	[0.349,1.48]	0.370	0.124
rs1062033	CYP19A1	C	0.403	0.931	[0.73,1.187]	0.564	1.150	[0.748,1.767]	0.524	1.235	[0.778,1.96]	0.370	0.649
rs1557044	CYP2C9	C	0.172	1.105	[0.81,1.508]	0.528	0.830	[0.46,1.497]	0.536	0.751	[0.401,1.407]	0.371	0.636
rs2043449	CYP20A1	G	0.074	1.325	[0.824,2.131]	0.246	0.855	[0.347,2.108]	0.734	0.645	[0.247,1.686]	0.372	0.449
rs2228309	FASN	T	0.458	1.019	[0.799,1.299]	0.882	1.262	[0.815,1.955]	0.297	1.239	[0.774,1.982]	0.372	0.581
rs2071214	BIRC5	G	0.043	0.764	[0.413,1.413]	0.390	1.253	[0.47,3.342]	0.652	1.641	[0.552,4.877]	0.372	0.589
rs3748415	APCDD1	T	0.101	0.972	[0.659,1.432]	0.885	1.331	[0.707,2.506]	0.376	1.370	[0.686,2.734]	0.373	0.650
rs1805327	RAD1	G	0.065	1.286	[0.813,2.032]	0.282	1.867	[0.869,4.013]	0.110	1.453	[0.639,3.304]	0.373	0.199
rs769412	MDM2	G	0.065	1.438	[0.909,2.272]	0.120	0.912	[0.352,2.366]	0.850	0.635	[0.233,1.727]	0.373	0.276
rs10018260	Intergenic	T	0.210	0.943	[0.692,1.284]	0.709	1.217	[0.726,2.039]	0.456	1.291	[0.736,2.265]	0.373	0.673
rs1801132	ESR1	G	0.214	0.965	[0.725,1.285]	0.809	0.738	[0.422,1.289]	0.286	0.764	[0.423,1.382]	0.374	0.563
rs854548	PPP1R9A	A	0.284	1.042	[0.81,1.341]	0.750	0.825	[0.509,1.338]	0.436	0.792	[0.474,1.325]	0.374	0.674
rs439132	LIG1	G	0.048	0.946	[0.499,1.794]	0.865	1.495	[0.613,3.643]	0.377	1.580	[0.574,4.346]	0.376	0.644
rs16118	NPY	C	0.409	1.149	[0.903,1.463]	0.259	1.417	[0.92,2.182]	0.114	1.233	[0.776,1.96]	0.376	0.190
rs7847	CHST11	C	0.296	1.333	[1.035,1.717]	0.026	1.065	[0.668,1.699]	0.790	0.799	[0.487,1.313]	0.376	0.084
rs8192719	CYP2B6	T	0.287	1.020	[0.779,1.337]	0.883	1.277	[0.808,2.019]	0.295	1.251	[0.761,2.057]	0.377	0.579
rs348475	ALDH1A1	G	0.450	0.891	[0.706,1.125]	0.332	0.723	[0.468,1.116]	0.143	0.811	[0.51,1.291]	0.377	0.253
rs1805129	CHEK2	G	0.037	1.179	[0.642,2.165]	0.596	0.641	[0.176,2.338]	0.501	0.544	[0.14,2.106]	0.378	0.655
rs3791981	APOB	G	0.156	1.085	[0.769,1.531]	0.643	0.798	[0.421,1.512]	0.489	0.736	[0.372,1.456]	0.378	0.671
rs10018786	POLN	G	0.212	0.815	[0.591,1.124]	0.212	1.064	[0.617,1.835]	0.823	1.306	[0.721,2.364]	0.378	0.424
rs6457813	PPARD	T	0.059	0.731	[0.403,1.325]	0.301	1.151	[0.465,2.847]	0.761	1.574	[0.573,4.323]	0.378	0.528
rs419833	GSTA4	C	0.495	0.929	[0.731,1.18]	0.545	0.755	[0.491,1.159]	0.199	0.813	[0.512,1.29]	0.379	0.398
rs3731680	SULT1C2	C	0.058	0.819	[0.493,1.36]	0.440	0.468	[0.142,1.538]	0.211	0.572	[0.165,1.987]	0.379	0.370
rs1501299	ADIPOQ	A	0.282	0.934	[0.713,1.221]	0.616	0.730	[0.436,1.221]	0.230	0.782	[0.451,1.354]	0.380	0.457
rs701106	SCARB1	A	0.182	1.082	[0.79,1.481]	0.624	1.397	[0.827,2.361]	0.212	1.292	[0.729,2.287]	0.380	0.437
rs7586110	UGT1A10	G	0.349	1.018	[0.796,1.301]	0.889	1.257	[0.809,1.951]	0.309	1.235	[0.77,1.98]	0.381	0.596
rs2048426	PARP1	T	0.420	1.045	[0.826,1.324]	0.712	0.851	[0.554,1.308]	0.463	0.814	[0.513,1.292]	0.383	0.683
rs973013	HNMT	T	0.234	0.712	[0.532,0.953]	0.023	0.908	[0.551,1.495]	0.703	1.275	[0.738,2.202]	0.383	0.074
rs2070959	UGT1A10	G	0.294	0.951	[0.733,1.233]	0.704	1.184	[0.747,1.877]	0.473	1.245	[0.759,2.043]	0.386	0.686
rs3917724	SELP	T	0.012	1.347	[0.463,3.916]	0.585	0.477	[0.051,4.42]	0.514	0.354	[0.034,3.702]	0.386	0.662
rs1063856	VWF	G	0.390	1.081	[0.849,1.375]	0.527	1.323	[0.865,2.025]	0.197	1.224	[0.774,1.935]	0.387	0.393
rs4148551	ABCC4	G	0.424	1.037	[0.817,1.316]	0.766	0.846	[0.549,1.303]	0.448	0.816	[0.513,1.297]	0.389	0.690

rs13436	LIG1	C	0.438	0.896	[0.696,1.153]	0.394	1.097	[0.719,1.673]	0.668	1.224	[0.772,1.941]	0.389	0.597
rs527221	DMPK	C	0.114	0.895	[0.613,1.306]	0.564	1.222	[0.634,2.357]	0.549	1.366	[0.671,2.782]	0.390	0.670
rs348463	ALDH1A1	C	0.287	1.013	[0.78,1.316]	0.923	1.261	[0.794,2.001]	0.326	1.244	[0.756,2.048]	0.390	0.617
rs854556	PON1	T	0.302	0.947	[0.732,1.225]	0.681	0.752	[0.458,1.234]	0.260	0.794	[0.469,1.345]	0.391	0.512
rs7904678	ABCC2	T	0.055	0.837	[0.484,1.448]	0.525	1.253	[0.552,2.846]	0.589	1.497	[0.595,3.767]	0.392	0.670
rs8187694		A	0.054	0.856	[0.494,1.481]	0.577	1.280	[0.563,2.908]	0.555	1.496	[0.595,3.763]	0.392	0.683
rs2070677	CYP2E1	T	0.209	0.866	[0.616,1.217]	0.407	0.640	[0.335,1.224]	0.177	0.739	[0.37,1.477]	0.392	0.323
rs2288550	IMPDH1	C	0.160	0.870	[0.632,1.199]	0.396	1.130	[0.65,1.964]	0.664	1.298	[0.713,2.364]	0.393	0.597
rs436525	ADAMTS1	G	0.336	0.915	[0.722,1.16]	0.462	1.114	[0.733,1.695]	0.613	1.218	[0.775,1.913]	0.393	0.633
rs2706375	RAD50	C	0.017	1.015	[0.339,3.037]	0.979	0.371	[0.043,3.198]	0.367	0.366	[0.036,3.69]	0.394	0.661
rs9640663	PTPN12	G	0.350	1.111	[0.876,1.409]	0.385	0.899	[0.568,1.422]	0.648	0.809	[0.497,1.317]	0.394	0.580
rs1629816	SEC13L1	A	0.424	0.905	[0.716,1.144]	0.405	1.100	[0.726,1.666]	0.654	1.215	[0.776,1.901]	0.395	0.602
rs520354	APOB	G	0.440	0.957	[0.748,1.223]	0.723	1.178	[0.754,1.839]	0.472	1.231	[0.763,1.988]	0.395	0.696
rs2307424	NR1I3	T	0.305	0.816	[0.629,1.059]	0.126	1.015	[0.637,1.618]	0.949	1.244	[0.752,2.059]	0.395	0.300
rs1537514	C1orf167	G	0.103	0.852	[0.578,1.255]	0.417	0.580	[0.251,1.34]	0.202	0.681	[0.281,1.651]	0.395	0.351
rs11550540	TP53RK	G	0.073	1.001	[0.644,1.556]	0.996	1.406	[0.686,2.883]	0.352	1.404	[0.641,3.075]	0.396	0.642
rs3774306	BCL6	G	0.445	1.249	[0.987,1.58]	0.064	1.023	[0.665,1.574]	0.916	0.819	[0.517,1.298]	0.396	0.177
rs1059751	ABCC4	C	0.433	0.846	[0.667,1.071]	0.164	1.031	[0.673,1.579]	0.889	1.219	[0.771,1.927]	0.396	0.359
rs207943	XRCC5	G	0.463	1.265	[1.004,1.594]	0.046	1.043	[0.688,1.581]	0.844	0.824	[0.527,1.289]	0.397	0.136
rs4148733	ABCB1	C	0.163	1.125	[0.806,1.569]	0.488	1.446	[0.85,2.462]	0.174	1.286	[0.719,2.299]	0.397	0.353
rs11582663	FCRL4	T	0.122	0.819	[0.567,1.182]	0.286	0.579	[0.271,1.236]	0.158	0.707	[0.317,1.578]	0.398	0.245
rs1863703	STK36	G	0.099	1.269	[0.854,1.884]	0.238	0.891	[0.412,1.926]	0.769	0.702	[0.309,1.595]	0.398	0.451
rs2685803	ABCB11	A	0.482	1.134	[0.901,1.427]	0.283	0.931	[0.606,1.429]	0.743	0.821	[0.519,1.298]	0.398	0.502
rs2305948	KDR	T	0.131	0.934	[0.644,1.354]	0.720	1.255	[0.668,2.356]	0.480	1.343	[0.677,2.666]	0.399	0.701
rs1131620	LTBP4	G	0.447	0.967	[0.766,1.221]	0.778	1.174	[0.771,1.788]	0.455	1.214	[0.773,1.907]	0.400	0.701
rs2664538	MMP9	G	0.363	0.996	[0.781,1.272]	0.977	0.807	[0.51,1.277]	0.360	0.810	[0.496,1.322]	0.400	0.655
rs11569913	TNFRSF8	G	0.064	1.072	[0.633,1.815]	0.795	0.662	[0.23,1.906]	0.444	0.617	[0.2,1.9]	0.400	0.701
rs6068816	CYP24A1	T	0.113	0.905	[0.631,1.297]	0.586	0.635	[0.291,1.39]	0.256	0.702	[0.309,1.599]	0.400	0.481
rs948516	PGR	G	0.263	1.229	[0.939,1.609]	0.133	0.982	[0.6,1.607]	0.941	0.799	[0.472,1.351]	0.402	0.310
rs4633	COMT	T	0.478	1.134	[0.898,1.432]	0.291	0.928	[0.599,1.438]	0.738	0.818	[0.512,1.308]	0.402	0.511
rs5370	EDN1	T	0.231	1.108	[0.843,1.456]	0.462	0.874	[0.52,1.472]	0.614	0.789	[0.454,1.373]	0.402	0.633
rs228589	ATM	T	0.463	0.960	[0.754,1.222]	0.741	0.788	[0.513,1.21]	0.277	0.821	[0.517,1.303]	0.403	0.545
rs10018064	Intergenic	C	0.401	0.871	[0.685,1.108]	0.260	1.060	[0.691,1.625]	0.789	1.217	[0.768,1.929]	0.403	0.484
rs2227552	C10orf55	C	0.280	1.209	[0.928,1.574]	0.160	0.970	[0.598,1.572]	0.901	0.802	[0.479,1.344]	0.403	0.353
rs3850751	NAT1	C	0.382	1.033	[0.809,1.319]	0.794	1.267	[0.81,1.981]	0.299	1.226	[0.76,1.979]	0.403	0.579
rs1805355	MSH3	A	0.108	1.340	[0.936,1.917]	0.110	0.991	[0.507,1.941]	0.980	0.740	[0.365,1.501]	0.404	0.266
rs3093816	CCNH	C	0.382	1.050	[0.826,1.335]	0.692	1.277	[0.831,1.961]	0.264	1.216	[0.767,1.929]	0.405	0.521
rs903247	CHST11	C	0.375	1.386	[1.092,1.759]	0.007	1.139	[0.739,1.758]	0.555	0.822	[0.518,1.305]	0.406	0.027
rs1926201	FAS	C	0.495	1.034	[0.815,1.312]	0.781	0.848	[0.547,1.315]	0.461	0.820	[0.513,1.31]	0.406	0.708
rs2522390	RAD50	C	0.017	1.014	[0.339,3.034]	0.981	0.381	[0.044,3.278]	0.380	0.376	[0.037,3.788]	0.407	0.675
rs2580874	AICDA	G	0.492	1.010	[0.797,1.28]	0.933	0.830	[0.539,1.278]	0.398	0.822	[0.517,1.306]	0.407	0.686

rs17012739	PLK4	G	0.299	1.014	[0.789,1.302]	0.914	1.240	[0.797,1.928]	0.340	1.223	[0.76,1.967]	0.407	0.635
rs1051992	PRKCDBP	T	0.486	0.936	[0.738,1.186]	0.582	0.768	[0.496,1.188]	0.235	0.821	[0.514,1.31]	0.407	0.457
rs1208	NAT2	G	0.399	1.071	[0.848,1.353]	0.565	0.882	[0.573,1.357]	0.567	0.823	[0.519,1.305]	0.408	0.682
rs884716	SHFM1	A	0.269	1.055	[0.818,1.362]	0.679	1.288	[0.831,1.997]	0.257	1.221	[0.761,1.957]	0.408	0.511
rs632478	MMP3	A	0.487	0.925	[0.732,1.169]	0.513	1.116	[0.739,1.687]	0.602	1.207	[0.773,1.884]	0.408	0.667
rs1467558	CD44	A	0.151	0.717	[0.508,1.013]	0.059	0.939	[0.523,1.684]	0.833	1.309	[0.691,2.479]	0.408	0.168
rs6744284	UGT1A10	T	0.338	1.007	[0.771,1.316]	0.958	1.242	[0.784,1.969]	0.356	1.234	[0.75,2.03]	0.409	0.650
rs398700	RUNDC2A	G	0.220	1.162	[0.864,1.564]	0.321	0.911	[0.531,1.565]	0.737	0.784	[0.44,1.397]	0.409	0.543
rs1514499	DPYD	C	0.020	1.329	[0.589,3]	0.494	0.548	[0.072,4.175]	0.562	0.413	[0.05,3.385]	0.410	0.638
rs2214827	HGF	G	0.191	1.042	[0.778,1.395]	0.781	1.315	[0.786,2.2]	0.297	1.262	[0.726,2.194]	0.410	0.575
rs2857713	LTA	G	0.268	1.178	[0.898,1.546]	0.237	1.458	[0.91,2.336]	0.117	1.237	[0.746,2.053]	0.410	0.186
rs1051741	EPHX1	T	0.104	1.076	[0.734,1.576]	0.709	0.762	[0.351,1.655]	0.493	0.709	[0.312,1.609]	0.410	0.710
rs2165810	MBL2	A	0.274	1.090	[0.836,1.42]	0.524	0.874	[0.534,1.429]	0.591	0.802	[0.473,1.359]	0.411	0.671
rs557462	ABCB11	G	0.263	1.086	[0.84,1.404]	0.528	1.333	[0.845,2.103]	0.216	1.228	[0.753,2.002]	0.411	0.420
rs3795837	ATF3	C	0.136	0.958	[0.68,1.352]	0.809	0.703	[0.35,1.413]	0.323	0.734	[0.35,1.537]	0.412	0.609
rs6196	NR3C1	G	0.151	0.844	[0.606,1.174]	0.314	0.625	[0.317,1.232]	0.174	0.740	[0.36,1.522]	0.413	0.275
rs2242046	SLC28A1	T	0.412	0.854	[0.668,1.091]	0.206	1.042	[0.667,1.627]	0.857	1.221	[0.757,1.968]	0.414	0.421
rs10017301	ZNF827	T	0.087	1.102	[0.708,1.714]	0.668	0.783	[0.367,1.671]	0.527	0.711	[0.313,1.614]	0.414	0.712
rs3842	ABCB1	G	0.140	1.019	[0.73,1.421]	0.913	1.304	[0.755,2.252]	0.341	1.280	[0.707,2.317]	0.415	0.635
rs1799930	NAT2	A	0.293	0.851	[0.654,1.106]	0.227	0.682	[0.416,1.12]	0.130	0.802	[0.472,1.362]	0.415	0.190
rs9282574	ABCG8	A	0.038	1.068	[0.532,2.145]	0.854	0.550	[0.121,2.509]	0.440	0.515	[0.104,2.546]	0.416	0.716
rs4655537	LEPR	A	0.361	0.927	[0.725,1.186]	0.546	0.758	[0.481,1.193]	0.231	0.817	[0.503,1.329]	0.416	0.442
rs7190307	NFATC3	G	0.467	1.053	[0.828,1.337]	0.675	0.867	[0.561,1.341]	0.522	0.824	[0.516,1.315]	0.417	0.714
rs11229545	ZFP91	G	0.224	1.079	[0.814,1.43]	0.596	0.852	[0.499,1.455]	0.558	0.790	[0.446,1.397]	0.417	0.698
rs2518144	AICDA	G	0.483	1.002	[0.791,1.271]	0.985	0.829	[0.541,1.272]	0.391	0.827	[0.523,1.31]	0.418	0.685
rs163077	FAM82A	A	0.246	1.095	[0.838,1.429]	0.506	0.869	[0.513,1.473]	0.602	0.794	[0.453,1.39]	0.419	0.665
rs6941	XRCC5	A	0.112	0.998	[0.687,1.451]	0.994	0.717	[0.336,1.531]	0.391	0.718	[0.322,1.602]	0.419	0.688
rs20432	PTGS2	G	0.230	1.187	[0.876,1.61]	0.268	0.936	[0.547,1.601]	0.808	0.788	[0.441,1.407]	0.420	0.500
rs8192879	CYP7A1	A	0.377	1.228	[0.97,1.553]	0.088	1.017	[0.663,1.56]	0.939	0.828	[0.524,1.31]	0.421	0.229
rs1131532	TNFSF10	T	0.346	0.729	[0.561,0.947]	0.018	0.893	[0.567,1.408]	0.627	1.225	[0.747,2.008]	0.421	0.060
rs2892806	ABCB11	T	0.054	1.448	[0.893,2.349]	0.134	0.953	[0.36,2.521]	0.923	0.658	[0.238,1.823]	0.421	0.308
rs169985	ABCC1	G	0.410	1.138	[0.873,1.484]	0.339	0.914	[0.553,1.509]	0.724	0.803	[0.47,1.371]	0.421	0.563
rs2288648	FASTK	A	0.020	1.497	[0.657,3.411]	0.337	0.623	[0.079,4.879]	0.652	0.416	[0.049,3.529]	0.421	0.542
rs3020411	ESR1	G	0.380	1.205	[0.937,1.549]	0.146	0.984	[0.622,1.559]	0.947	0.817	[0.499,1.337]	0.421	0.335
rs827528	FZD6	G	0.227	0.979	[0.739,1.295]	0.880	0.773	[0.45,1.327]	0.350	0.790	[0.444,1.405]	0.422	0.646
rs1527463	CD36	G	0.028	0.551	[0.237,1.279]	0.165	1.002	[0.276,3.635]	0.998	1.818	[0.423,7.824]	0.422	0.377
rs987539	PON2	C	0.487	1.018	[0.802,1.294]	0.882	1.228	[0.802,1.88]	0.344	1.206	[0.763,1.907]	0.423	0.639
rs3749229	CHRD	A	0.129	0.833	[0.562,1.236]	0.365	1.112	[0.587,2.105]	0.745	1.334	[0.659,2.701]	0.423	0.600
rs4762	AGT	T	0.122	1.229	[0.863,1.751]	0.253	0.905	[0.444,1.841]	0.782	0.736	[0.348,1.557]	0.423	0.473
rs212079	ABCC1	A	0.050	1.402	[0.831,2.363]	0.205	2.012	[0.883,4.585]	0.096	1.436	[0.593,3.477]	0.423	0.158
rs1566439	NLRC5	G	0.377	1.179	[0.923,1.504]	0.187	0.967	[0.615,1.521]	0.884	0.820	[0.505,1.332]	0.423	0.396

rs1803965	MGMT	T	0.141	1.135	[0.801,1.61]	0.477	0.852	[0.441,1.648]	0.634	0.751	[0.372,1.515]	0.423	0.656
rs246218	ABCC1	T	0.145	0.891	[0.645,1.231]	0.485	0.670	[0.345,1.3]	0.236	0.751	[0.373,1.514]	0.424	0.425
rs279942	SLC10A2	G	0.234	1.014	[0.774,1.328]	0.920	0.812	[0.487,1.353]	0.424	0.801	[0.464,1.381]	0.424	0.711
rs11539762	MYEOV	A	0.105	0.916	[0.617,1.358]	0.661	1.216	[0.644,2.295]	0.546	1.328	[0.661,2.669]	0.425	0.724
rs3811740	PLK4	A	0.299	1.017	[0.791,1.306]	0.897	1.234	[0.793,1.92]	0.352	1.214	[0.754,1.954]	0.426	0.648
rs13712	MLH3	A	0.478	0.952	[0.748,1.21]	0.686	0.788	[0.511,1.213]	0.279	0.828	[0.52,1.318]	0.426	0.538
rs7658300	TXK	T	0.318	1.012	[0.771,1.326]	0.934	1.243	[0.778,1.987]	0.363	1.229	[0.74,2.042]	0.426	0.660
rs689453	NQO1	A	0.072	0.902	[0.572,1.424]	0.658	1.256	[0.596,2.648]	0.548	1.393	[0.616,3.147]	0.426	0.724
rs2157930	ABCB1	T	0.202	1.005	[0.727,1.391]	0.974	0.776	[0.43,1.403]	0.402	0.772	[0.409,1.459]	0.426	0.696
rs3729512	LIG1	A	0.150	0.961	[0.681,1.355]	0.819	0.733	[0.396,1.356]	0.323	0.763	[0.392,1.485]	0.426	0.610
rs12917	MGMT	T	0.150	1.124	[0.808,1.564]	0.486	0.859	[0.46,1.603]	0.632	0.764	[0.393,1.485]	0.427	0.663
rs9576175	CSNK1A1L	T	0.498	0.929	[0.734,1.174]	0.537	1.119	[0.73,1.715]	0.607	1.205	[0.761,1.907]	0.427	0.689
rs9286998	ACBD3	C	0.451	0.933	[0.736,1.182]	0.564	0.772	[0.5,1.193]	0.245	0.828	[0.52,1.319]	0.427	0.466
rs1800591	MTTP	T	0.271	0.865	[0.664,1.126]	0.281	1.055	[0.671,1.66]	0.816	1.220	[0.746,1.995]	0.428	0.519
rs776746	CYP3A5	A	0.182	1.301	[0.911,1.857]	0.148	0.998	[0.543,1.834]	0.994	0.767	[0.398,1.479]	0.429	0.342
rs2020865	FMO2	G	0.085	1.025	[0.644,1.63]	0.917	1.413	[0.689,2.895]	0.345	1.378	[0.623,3.052]	0.429	0.640
rs952005	SHFM1	T	0.084	1.036	[0.673,1.594]	0.872	1.400	[0.713,2.752]	0.329	1.352	[0.64,2.853]	0.429	0.620
rs1417938	CRP	A	0.266	1.040	[0.794,1.363]	0.774	1.277	[0.797,2.047]	0.310	1.227	[0.738,2.04]	0.429	0.591
rs914358	AKAP2	G	0.478	1.152	[0.913,1.453]	0.234	0.961	[0.632,1.461]	0.852	0.834	[0.532,1.308]	0.430	0.462
rs10028494	UGT2B7	C	0.142	0.970	[0.642,1.465]	0.883	1.313	[0.654,2.636]	0.444	1.354	[0.637,2.879]	0.431	0.720
rs2233406	NFKBIA	T	0.275	0.815	[0.624,1.066]	0.136	1.003	[0.624,1.611]	0.992	1.229	[0.735,2.055]	0.431	0.322
rs1061047	GPRC5A	C	0.236	1.166	[0.889,1.529]	0.266	0.937	[0.563,1.56]	0.804	0.804	[0.467,1.384]	0.431	0.497
rs3743135	PAK6	G	0.112	1.084	[0.735,1.598]	0.683	0.790	[0.377,1.652]	0.531	0.728	[0.331,1.603]	0.431	0.728
rs1042194	CYP2C18	T	0.149	1.149	[0.831,1.588]	0.402	0.875	[0.462,1.657]	0.682	0.762	[0.387,1.5]	0.431	0.614
rs8187692	ABCC2	T	0.014	0.442	[0.097,2.014]	0.291	1.025	[0.201,5.217]	0.976	2.319	[0.285,18.89]	0.432	0.567
rs9333269	ITGA8	C	0.073	1.010	[0.647,1.577]	0.964	1.390	[0.667,2.9]	0.380	1.376	[0.62,3.056]	0.433	0.677
rs16913653	IKBKAP	T	0.021	1.545	[0.627,3.808]	0.345	0.790	[0.168,3.705]	0.765	0.511	[0.096,2.736]	0.433	0.582
rs3136027	LIG3	T	0.058	0.751	[0.434,1.299]	0.306	1.114	[0.456,2.724]	0.813	1.484	[0.553,3.98]	0.433	0.552
rs3829963	LOC100131484	A	0.176	1.168	[0.85,1.604]	0.338	0.900	[0.489,1.659]	0.736	0.771	[0.402,1.478]	0.433	0.567
rs827423	ESR1	T	0.488	0.947	[0.751,1.194]	0.646	1.133	[0.746,1.721]	0.558	1.196	[0.764,1.874]	0.434	0.725
rs188096	SLC10A2	A	0.119	1.112	[0.78,1.585]	0.557	1.421	[0.805,2.508]	0.225	1.278	[0.691,2.363]	0.434	0.446
rs216867	VWF	A	0.141	0.902	[0.636,1.28]	0.563	0.669	[0.332,1.349]	0.261	0.742	[0.351,1.566]	0.434	0.480
rs1294689	FKBP1A	C	0.289	0.967	[0.746,1.252]	0.797	1.175	[0.745,1.854]	0.487	1.216	[0.745,1.986]	0.435	0.736
rs5030125	WT1	A	0.018	1.402	[0.554,3.547]	0.476	0.601	[0.08,4.505]	0.620	0.429	[0.051,3.598]	0.435	0.658
rs5745325	MSH4	A	0.279	0.728	[0.556,0.953]	0.021	0.889	[0.559,1.414]	0.620	1.222	[0.738,2.022]	0.436	0.068
rs1931072	DPYD	A	0.302	1.003	[0.783,1.285]	0.983	0.825	[0.523,1.303]	0.410	0.823	[0.504,1.343]	0.436	0.706
rs3759217	CDKN1B	T	0.112	0.817	[0.556,1.2]	0.303	1.081	[0.567,2.062]	0.812	1.324	[0.652,2.686]	0.437	0.548
rs234706	CBS	A	0.319	0.929	[0.697,1.238]	0.615	0.730	[0.412,1.293]	0.281	0.786	[0.428,1.443]	0.437	0.521
rs6003071	MCAT	T	0.443	0.900	[0.707,1.146]	0.393	1.083	[0.701,1.672]	0.720	1.203	[0.754,1.917]	0.438	0.617
rs405729	GSTA4	A	0.483	1.092	[0.864,1.381]	0.461	1.309	[0.856,2.002]	0.215	1.198	[0.759,1.891]	0.438	0.393
rs3219090	PARP1	A	0.405	1.012	[0.8,1.281]	0.922	0.843	[0.548,1.297]	0.437	0.833	[0.525,1.322]	0.439	0.724

rs3778893	STARD3NL	A	0.217	1.006	[0.755,1.342]	0.965	0.798	[0.46,1.383]	0.421	0.793	[0.44,1.428]	0.439	0.715
rs1537015	TNC	C	0.383	1.210	[0.95,1.54]	0.123	1.008	[0.657,1.548]	0.969	0.834	[0.526,1.321]	0.439	0.298
rs7895372	ITGA8	G	0.019	0.988	[0.41,2.384]	0.979	1.623	[0.561,4.696]	0.371	1.642	[0.467,5.774]	0.439	0.660
rs3811635	MERTK	A	0.391	1.099	[0.867,1.393]	0.434	1.319	[0.856,2.033]	0.209	1.200	[0.755,1.908]	0.440	0.376
rs514658	TATDN2	T	0.258	0.942	[0.718,1.235]	0.666	1.154	[0.716,1.859]	0.557	1.225	[0.732,2.049]	0.440	0.736
rs3736265	PPARGC1A	A	0.061	0.893	[0.531,1.5]	0.668	1.284	[0.553,2.981]	0.561	1.438	[0.571,3.622]	0.441	0.738
rs710411	NOTCH1	G	0.421	0.842	[0.646,1.098]	0.204	0.673	[0.393,1.154]	0.150	0.799	[0.452,1.414]	0.441	0.194
rs316019	SLC22A2	T	0.117	0.830	[0.562,1.225]	0.348	0.608	[0.29,1.275]	0.187	0.732	[0.331,1.619]	0.441	0.309
rs2243248	IL4	G	0.093	0.687	[0.437,1.079]	0.103	0.945	[0.454,1.967]	0.881	1.377	[0.61,3.106]	0.441	0.264
rs1494961	HELQ	C	0.439	1.059	[0.833,1.347]	0.638	0.880	[0.566,1.369]	0.570	0.830	[0.517,1.333]	0.442	0.730
rs310831	E2F7	T	0.090	0.791	[0.517,1.211]	0.281	1.085	[0.516,2.281]	0.829	1.372	[0.611,3.077]	0.443	0.525
rs993891	HNMT	A	0.276	0.788	[0.592,1.048]	0.101	0.971	[0.595,1.585]	0.906	1.232	[0.722,2.103]	0.443	0.260
rs11673726	UGT1A10	T	0.352	1.095	[0.842,1.423]	0.499	1.329	[0.838,2.107]	0.227	1.214	[0.739,1.993]	0.443	0.424
rs2016347	IGF1R	C	0.497	1.066	[0.839,1.354]	0.601	1.278	[0.829,1.971]	0.267	1.199	[0.753,1.909]	0.444	0.503
rs1805414	PARP1	C	0.405	1.008	[0.797,1.275]	0.946	0.842	[0.549,1.294]	0.434	0.836	[0.527,1.324]	0.445	0.725
rs16480	NPY	C	0.237	1.153	[0.892,1.492]	0.276	1.385	[0.895,2.143]	0.143	1.201	[0.751,1.92]	0.445	0.236
rs2228233	NFATC4	T	0.306	1.163	[0.902,1.498]	0.244	0.956	[0.597,1.531]	0.852	0.822	[0.498,1.358]	0.445	0.476
rs2256327	FAM82A	G	0.208	0.745	[0.547,1.014]	0.062	0.933	[0.55,1.583]	0.796	1.252	[0.703,2.23]	0.445	0.174
rs2275565	MTR	A	0.260	0.930	[0.704,1.23]	0.612	1.141	[0.704,1.851]	0.592	1.227	[0.726,2.073]	0.445	0.730
rs747657	PARP1	G	0.406	1.007	[0.796,1.274]	0.954	0.842	[0.548,1.292]	0.431	0.836	[0.528,1.324]	0.445	0.723
rs2732497	PPP3CA	T	0.459	0.990	[0.778,1.26]	0.937	1.188	[0.77,1.834]	0.437	1.200	[0.752,1.915]	0.445	0.726
rs8191842	IGF2R	T	0.010	2.277	[0.76,6.822]	0.142	0.965	[0.118,7.89]	0.973	0.424	[0.047,3.851]	0.446	0.327
rs4437575	ABCB1	G	0.423	1.015	[0.793,1.298]	0.908	1.210	[0.798,1.836]	0.369	1.193	[0.758,1.878]	0.446	0.668
rs683369	SLC22A1	G	0.194	0.819	[0.602,1.115]	0.205	1.030	[0.596,1.781]	0.915	1.258	[0.697,2.269]	0.446	0.430
rs1047643	FDFT1	C	0.178	1.346	[0.984,1.841]	0.063	1.679	[0.99,2.845]	0.054	1.247	[0.706,2.203]	0.447	0.046
rs2305801	CYP4F11	A	0.230	1.019	[0.768,1.353]	0.895	1.249	[0.771,2.022]	0.366	1.225	[0.726,2.068]	0.447	0.665
rs4426527	AGXT	G	0.166	0.635	[0.453,0.891]	0.009	0.814	[0.452,1.468]	0.494	1.282	[0.676,2.432]	0.447	0.030
rs7071882	MBL2	T	0.271	1.080	[0.83,1.407]	0.566	0.881	[0.54,1.438]	0.613	0.816	[0.483,1.379]	0.447	0.714
rs2214102	ABCB1	A	0.077	0.845	[0.546,1.31]	0.452	0.574	[0.223,1.479]	0.251	0.679	[0.251,1.841]	0.447	0.424
rs2277624	ABCC3	A	0.243	1.029	[0.777,1.362]	0.841	0.830	[0.494,1.394]	0.481	0.806	[0.462,1.405]	0.447	0.746
rs476632	HSP90AB1	A	0.313	0.958	[0.743,1.235]	0.738	1.157	[0.736,1.819]	0.528	1.208	[0.742,1.967]	0.447	0.749
rs25406	PCNA	T	0.403	0.949	[0.75,1.199]	0.659	1.125	[0.748,1.69]	0.572	1.185	[0.764,1.839]	0.448	0.741
rs2440	XRCC5	T	0.386	0.848	[0.667,1.079]	0.180	1.016	[0.659,1.566]	0.942	1.198	[0.752,1.908]	0.448	0.394
rs4918907	PDLIM1	A	0.346	1.121	[0.874,1.438]	0.369	0.931	[0.596,1.455]	0.753	0.831	[0.514,1.342]	0.448	0.605
rs743535	CYP2E1	T	0.115	0.914	[0.634,1.318]	0.630	1.183	[0.641,2.186]	0.591	1.295	[0.664,2.525]	0.449	0.738
rs680055	CYP3A43	C	0.098	0.792	[0.515,1.217]	0.287	0.569	[0.257,1.258]	0.163	0.718	[0.305,1.692]	0.449	0.251
rs11572103	CYP2C8	T	0.031	0.473	[0.181,1.235]	0.126	0.839	[0.244,2.881]	0.780	1.776	[0.402,7.845]	0.449	0.308
rs9282612	BLM	G	0.175	0.827	[0.601,1.14]	0.247	1.040	[0.603,1.793]	0.888	1.257	[0.695,2.272]	0.449	0.488
rs2300703	SRD5A2	T	0.460	1.075	[0.848,1.364]	0.549	1.284	[0.837,1.97]	0.252	1.194	[0.754,1.892]	0.450	0.470
rs741817	CYP8B1	T	0.015	1.339	[0.52,3.446]	0.545	0.717	[0.16,3.207]	0.664	0.536	[0.106,2.706]	0.450	0.714
rs3212860	CCND1	T	0.025	1.674	[0.723,3.874]	0.229	0.932	[0.231,3.766]	0.921	0.557	[0.122,2.546]	0.450	0.466

rs1805403	PARP1	A	0.203	0.969	[0.731,1.284]	0.827	0.770	[0.437,1.354]	0.364	0.794	[0.436,1.445]	0.450	0.658
rs3732379	CX3CR1	T	0.249	0.999	[0.764,1.307]	0.995	1.214	[0.759,1.942]	0.418	1.215	[0.733,2.015]	0.450	0.715
rs2241230	SCARF2	T	0.100	1.021	[0.66,1.579]	0.926	1.374	[0.675,2.797]	0.382	1.346	[0.622,2.912]	0.451	0.681
rs2066457	PMS1	C	0.010	0.911	[0.235,3.525]	0.892	1.925	[0.363,10.204]	0.442	2.113	[0.302,14.807]	0.451	0.715
rs2243290	IL4	A	0.207	1.309	[0.999,1.715]	0.050	1.059	[0.628,1.786]	0.830	0.809	[0.465,1.406]	0.451	0.147
rs2230365	NFKBIL1	T	0.132	0.939	[0.664,1.328]	0.721	1.202	[0.662,2.184]	0.546	1.280	[0.672,2.439]	0.452	0.752
rs8679	PARP1	C	0.202	0.971	[0.733,1.287]	0.840	0.772	[0.439,1.359]	0.370	0.795	[0.437,1.446]	0.452	0.666
rs4337089	SLCO1A2	T	0.107	0.860	[0.591,1.252]	0.432	0.626	[0.285,1.375]	0.243	0.727	[0.316,1.671]	0.453	0.408
rs1381057	POLQ	T	0.312	0.905	[0.704,1.164]	0.438	0.748	[0.47,1.192]	0.222	0.827	[0.502,1.361]	0.454	0.392
rs4150514	ERCC3	G	0.195	0.794	[0.585,1.077]	0.138	0.991	[0.579,1.695]	0.973	1.248	[0.698,2.232]	0.455	0.329
rs3212219	IL12B	T	0.253	1.038	[0.79,1.365]	0.787	0.843	[0.506,1.405]	0.512	0.812	[0.469,1.404]	0.455	0.757
rs182623	GSTA4	A	0.297	0.992	[0.767,1.283]	0.954	1.190	[0.766,1.849]	0.438	1.199	[0.744,1.934]	0.456	0.730
rs6041750	FKBP1A	C	0.392	0.940	[0.738,1.198]	0.618	0.785	[0.504,1.221]	0.283	0.835	[0.519,1.342]	0.456	0.526
rs805657	SLK	A	0.200	0.915	[0.675,1.241]	0.568	1.134	[0.676,1.902]	0.634	1.239	[0.705,2.177]	0.456	0.727
rs11466155	NGFR	T	0.286	1.012	[0.785,1.306]	0.925	1.221	[0.77,1.935]	0.395	1.206	[0.736,1.975]	0.457	0.697
rs2274756	LOC100128028	A	0.161	1.041	[0.754,1.437]	0.807	0.807	[0.43,1.515]	0.504	0.775	[0.396,1.516]	0.457	0.758
rs17162549	MAP3K6	G	0.067	0.934	[0.545,1.599]	0.803	1.312	[0.589,2.923]	0.506	1.406	[0.574,3.444]	0.457	0.753
rs274548	SLC22A5	A	0.213	1.064	[0.793,1.429]	0.678	1.301	[0.799,2.12]	0.290	1.223	[0.72,2.077]	0.457	0.553
rs11632706	CYP1A2	T	0.049	0.956	[0.554,1.649]	0.872	1.345	[0.596,3.036]	0.475	1.407	[0.571,3.467]	0.458	0.744
rs2227973	RAG1	G	0.116	1.301	[0.938,1.803]	0.115	1.006	[0.528,1.919]	0.985	0.774	[0.393,1.523]	0.458	0.281
rs3093873	LOC100132444	T	0.154	0.875	[0.586,1.306]	0.513	0.651	[0.315,1.343]	0.245	0.744	[0.34,1.626]	0.458	0.447
rs1555025	ID3	T	0.436	1.045	[0.816,1.339]	0.726	1.255	[0.799,1.97]	0.325	1.200	[0.74,1.946]	0.459	0.602
rs6808205	PLS1	A	0.378	1.056	[0.831,1.342]	0.656	0.883	[0.567,1.375]	0.583	0.836	[0.521,1.343]	0.460	0.749
rs2082382	ADRB2	G	0.352	1.048	[0.816,1.345]	0.715	1.257	[0.801,1.974]	0.320	1.200	[0.739,1.947]	0.461	0.595
rs3181217	IL12B	A	0.247	0.996	[0.762,1.303]	0.978	0.812	[0.488,1.35]	0.422	0.815	[0.473,1.404]	0.461	0.722
rs3093664	TNF	G	0.077	1.312	[0.856,2.012]	0.212	1.733	[0.873,3.439]	0.116	1.320	[0.63,2.764]	0.461	0.180
rs1822825	PPARG	C	0.419	1.131	[0.891,1.436]	0.313	0.948	[0.611,1.471]	0.813	0.838	[0.524,1.34]	0.462	0.558
rs2270628	IGFBP3	T	0.235	1.012	[0.766,1.337]	0.931	0.821	[0.488,1.383]	0.459	0.811	[0.465,1.416]	0.462	0.747
rs1966265	FGFR4	A	0.203	0.994	[0.74,1.335]	0.969	1.229	[0.727,2.078]	0.441	1.236	[0.702,2.177]	0.462	0.735
rs1050909	FBXO25	T	0.329	1.004	[0.783,1.286]	0.978	0.834	[0.527,1.322]	0.441	0.831	[0.508,1.361]	0.463	0.736
rs3448	GPX1	T	0.254	1.025	[0.786,1.336]	0.856	0.835	[0.5,1.395]	0.491	0.815	[0.472,1.407]	0.463	0.760
rs1801198	TCN2	G	0.399	0.902	[0.708,1.148]	0.401	0.751	[0.475,1.187]	0.220	0.833	[0.51,1.358]	0.463	0.373
rs2107538	CCL5	T	0.220	1.057	[0.791,1.413]	0.706	0.848	[0.489,1.471]	0.558	0.802	[0.446,1.444]	0.463	0.759
rs2229531	ACP5	A	0.094	1.007	[0.672,1.508]	0.975	0.727	[0.32,1.652]	0.447	0.722	[0.303,1.724]	0.464	0.743
rs10916	CYP1B1	G	0.227	1.427	[1.091,1.867]	0.009	1.175	[0.722,1.914]	0.516	0.823	[0.489,1.386]	0.464	0.033
rs3742424	PPP2R5C	C	0.113	1.276	[0.893,1.824]	0.181	0.984	[0.51,1.897]	0.961	0.771	[0.384,1.549]	0.465	0.396
rs769243	CCNA2	A	0.084	0.774	[0.461,1.3]	0.333	1.073	[0.49,2.351]	0.860	1.387	[0.577,3.334]	0.465	0.595
rs2228262	THBS1	G	0.098	1.155	[0.783,1.704]	0.467	1.499	[0.781,2.875]	0.223	1.297	[0.644,2.614]	0.466	0.414
rs2295475	XDH	A	0.270	0.766	[0.583,1.007]	0.056	0.619	[0.36,1.064]	0.083	0.808	[0.455,1.435]	0.467	0.052
rs17274095	BLM	A	0.175	0.830	[0.603,1.142]	0.252	1.033	[0.6,1.777]	0.908	1.244	[0.69,2.244]	0.468	0.500
rs9944225	CYP19A1	A	0.080	0.819	[0.523,1.281]	0.381	1.099	[0.531,2.272]	0.799	1.342	[0.604,2.984]	0.470	0.634

rs956868	WNK1	A	0.158	0.906	[0.657,1.248]	0.545	1.127	[0.653,1.944]	0.668	1.244	[0.687,2.253]	0.471	0.729
rs2281677	SLC7A7	T	0.448	1.025	[0.808,1.301]	0.837	1.211	[0.795,1.844]	0.372	1.181	[0.751,1.858]	0.471	0.669
rs2236379	PRKCQ	T	0.269	1.146	[0.878,1.496]	0.317	0.943	[0.575,1.548]	0.817	0.823	[0.485,1.397]	0.471	0.566
rs17710008	MYCT1	A	0.142	1.254	[0.905,1.738]	0.174	0.970	[0.5,1.884]	0.929	0.774	[0.385,1.554]	0.471	0.382
rs2288831	IL12B	C	0.248	0.988	[0.755,1.293]	0.929	0.809	[0.487,1.344]	0.413	0.819	[0.476,1.411]	0.472	0.716
rs9890721	MYCBPAP	T	0.465	1.100	[0.864,1.402]	0.439	0.924	[0.592,1.442]	0.727	0.840	[0.521,1.352]	0.472	0.667
rs1729409	APOA5	C	0.469	1.067	[0.839,1.357]	0.599	1.270	[0.815,1.979]	0.292	1.190	[0.74,1.915]	0.472	0.532
rs1635498	EXO1	G	0.038	1.094	[0.586,2.045]	0.778	1.589	[0.635,3.974]	0.322	1.452	[0.524,4.023]	0.473	0.608
rs4681	FGB	T	0.149	1.201	[0.873,1.652]	0.261	0.946	[0.51,1.753]	0.860	0.788	[0.41,1.513]	0.474	0.502
rs1800587	IL1A	T	0.303	1.151	[0.894,1.481]	0.276	0.955	[0.592,1.54]	0.851	0.830	[0.499,1.382]	0.474	0.521
rs943975	CYP2E1	C	0.157	1.121	[0.793,1.585]	0.518	1.404	[0.796,2.476]	0.241	1.253	[0.676,2.321]	0.474	0.450
rs187238	IL18	G	0.263	1.017	[0.786,1.317]	0.897	1.216	[0.771,1.92]	0.400	1.196	[0.733,1.951]	0.474	0.702
rs1760216	DPYD	A	0.185	0.916	[0.679,1.235]	0.566	0.730	[0.406,1.312]	0.293	0.797	[0.427,1.486]	0.475	0.521
rs3826705	POU2F2	C	0.106	0.914	[0.616,1.355]	0.655	1.190	[0.611,2.318]	0.609	1.302	[0.631,2.688]	0.475	0.764
rs1051677	XRCC5	C	0.110	0.985	[0.676,1.435]	0.937	0.736	[0.345,1.57]	0.428	0.747	[0.335,1.666]	0.476	0.730
rs11407	LOC390940	A	0.174	1.074	[0.787,1.467]	0.651	0.854	[0.472,1.544]	0.601	0.795	[0.422,1.495]	0.476	0.760
rs9282715	IGF1R	C	0.116	0.986	[0.658,1.478]	0.946	1.285	[0.661,2.498]	0.460	1.303	[0.629,2.7]	0.477	0.750
rs2375744	HNMT	A	0.162	0.938	[0.681,1.292]	0.694	1.164	[0.668,2.028]	0.591	1.242	[0.684,2.256]	0.477	0.771
rs6720173	ABCG5	C	0.192	1.101	[0.823,1.472]	0.519	1.337	[0.812,2.204]	0.254	1.215	[0.71,2.08]	0.477	0.466
rs2508784	MRE11A	G	0.492	1.057	[0.841,1.33]	0.633	0.900	[0.594,1.364]	0.619	0.851	[0.546,1.328]	0.478	0.758
rs1130864	CRP	T	0.284	1.035	[0.801,1.338]	0.791	1.231	[0.79,1.916]	0.358	1.189	[0.736,1.919]	0.479	0.649
rs4722266	STK31	A	0.154	1.038	[0.755,1.427]	0.819	0.820	[0.445,1.511]	0.525	0.790	[0.412,1.516]	0.479	0.778
rs2279344	CYP2B6	G	0.310	1.051	[0.813,1.359]	0.704	0.872	[0.538,1.415]	0.580	0.830	[0.495,1.391]	0.479	0.772
rs2839685	CXCL12	T	0.163	1.075	[0.78,1.482]	0.659	0.851	[0.463,1.563]	0.602	0.791	[0.414,1.514]	0.479	0.764
rs1934961	CYP2C9	A	0.028	1.404	[0.612,3.224]	0.423	2.282	[0.69,7.552]	0.176	1.625	[0.421,6.279]	0.481	0.334
rs2243251	IL4	G	0.030	0.575	[0.231,1.43]	0.234	0.307	[0.063,1.494]	0.144	0.535	[0.094,3.049]	0.481	0.199
rs2243268	IL4	C	0.191	1.352	[1.03,1.773]	0.030	1.108	[0.656,1.871]	0.702	0.820	[0.471,1.426]	0.481	0.094
rs2272611	ARHGEF10	A	0.143	0.855	[0.614,1.189]	0.350	0.661	[0.337,1.298]	0.229	0.774	[0.379,1.581]	0.482	0.353
rs3024491	IL10	T	0.421	0.954	[0.75,1.213]	0.701	0.803	[0.512,1.259]	0.338	0.841	[0.52,1.361]	0.482	0.611
rs10264272	CYP3A5	T	0.017	0.960	[0.363,2.538]	0.934	0.444	[0.06,3.303]	0.428	0.463	[0.054,3.963]	0.482	0.730
rs1800457	CYB5R3	G	0.053	1.530	[0.728,3.214]	0.262	2.411	[0.774,7.512]	0.129	1.576	[0.444,5.601]	0.482	0.207
rs4252596	ERBB2	A	0.120	0.895	[0.615,1.301]	0.561	1.152	[0.6,2.21]	0.671	1.287	[0.637,2.601]	0.482	0.740
rs1284605	MBD6	T	0.175	0.740	[0.537,1.02]	0.066	0.919	[0.529,1.595]	0.763	1.241	[0.679,2.267]	0.483	0.184
rs2023410	ADRB3	G	0.292	0.924	[0.705,1.213]	0.571	0.763	[0.463,1.258]	0.289	0.825	[0.483,1.411]	0.483	0.520
rs6489738	GNB3	T	0.400	0.862	[0.67,1.109]	0.248	1.024	[0.656,1.598]	0.916	1.188	[0.734,1.923]	0.483	0.496
rs7604639	MERTK	G	0.389	1.125	[0.883,1.432]	0.340	1.326	[0.865,2.034]	0.195	1.179	[0.744,1.869]	0.483	0.319
rs4128473	DPYD	C	0.191	1.229	[0.888,1.701]	0.213	1.517	[0.881,2.611]	0.133	1.234	[0.686,2.22]	0.483	0.191
rs1611764	SPRR1A	G	0.442	0.903	[0.709,1.15]	0.409	0.765	[0.496,1.179]	0.225	0.847	[0.532,1.348]	0.483	0.385
rs40401	IL3	T	0.295	1.019	[0.783,1.325]	0.889	1.213	[0.773,1.903]	0.401	1.191	[0.731,1.939]	0.484	0.702
rs6162	CYP17A1	A	0.430	1.041	[0.826,1.313]	0.732	0.884	[0.576,1.357]	0.573	0.849	[0.537,1.342]	0.484	0.780
rs1800849	UCP3	T	0.216	1.015	[0.763,1.352]	0.917	1.230	[0.745,2.032]	0.418	1.212	[0.707,2.078]	0.485	0.720

rs241447	TAP2	G	0.225	0.992	[0.751,1.31]	0.953	0.815	[0.486,1.367]	0.438	0.822	[0.473,1.427]	0.485	0.739
rs1049434	SLC16A1	T	0.379	0.913	[0.716,1.165]	0.465	1.080	[0.696,1.677]	0.731	1.183	[0.738,1.896]	0.486	0.692
rs7169	SLC16A1	C	0.379	0.913	[0.716,1.165]	0.465	1.080	[0.696,1.677]	0.731	1.183	[0.738,1.896]	0.486	0.692
rs13339152	RUNDC2A	C	0.105	1.022	[0.696,1.501]	0.912	0.785	[0.393,1.565]	0.491	0.768	[0.365,1.615]	0.486	0.773
rs7312411	VWF	G	0.399	1.061	[0.83,1.357]	0.636	1.250	[0.816,1.914]	0.304	1.178	[0.743,1.868]	0.486	0.558
rs11632547	CYP1A1	A	0.048	1.043	[0.609,1.787]	0.877	1.435	[0.632,3.257]	0.388	1.375	[0.56,3.374]	0.487	0.689
rs279941	SLC10A2	T	0.120	1.140	[0.801,1.623]	0.467	1.418	[0.802,2.506]	0.230	1.244	[0.672,2.3]	0.487	0.424
rs2039449	DPYD	C	0.289	0.971	[0.748,1.262]	0.828	1.155	[0.734,1.818]	0.532	1.189	[0.729,1.94]	0.487	0.784
rs2020898	CASP9	T	0.393	1.215	[0.955,1.546]	0.113	1.023	[0.649,1.613]	0.922	0.842	[0.518,1.369]	0.488	0.284
rs2275554	AK7	A	0.245	0.827	[0.623,1.097]	0.188	0.997	[0.612,1.624]	0.990	1.205	[0.709,2.049]	0.490	0.415
rs26279	MSH3	G	0.300	0.857	[0.664,1.108]	0.239	1.016	[0.651,1.584]	0.945	1.185	[0.732,1.916]	0.490	0.487
rs1703874	FLJ00290	A	0.250	0.898	[0.684,1.18]	0.439	1.075	[0.67,1.725]	0.765	1.197	[0.718,1.997]	0.491	0.681
rs13035	PYROXD1	C	0.394	1.087	[0.85,1.389]	0.506	1.285	[0.823,2.006]	0.270	1.182	[0.734,1.905]	0.491	0.477
rs1042579	THBD	T	0.162	1.019	[0.74,1.403]	0.909	1.255	[0.724,2.177]	0.418	1.232	[0.681,2.23]	0.491	0.721
rs3795498	STK40	A	0.227	1.110	[0.84,1.468]	0.462	0.909	[0.532,1.553]	0.727	0.819	[0.463,1.448]	0.491	0.689
rs3088440	C9orf53	A	0.116	1.046	[0.723,1.514]	0.812	1.318	[0.716,2.427]	0.375	1.261	[0.651,2.441]	0.492	0.671
rs2280712	PARP1	A	0.157	0.799	[0.576,1.109]	0.179	0.621	[0.315,1.225]	0.169	0.777	[0.378,1.597]	0.492	0.190
rs17057901	PBK	G	0.013	1.233	[0.432,3.52]	0.696	0.562	[0.068,4.614]	0.592	0.456	[0.048,4.308]	0.493	0.782
rs2074900	CYP4F2	A	0.252	0.698	[0.521,0.934]	0.016	0.846	[0.509,1.405]	0.518	1.213	[0.699,2.104]	0.493	0.051
rs6666652	ABCA4	A	0.116	1.030	[0.671,1.583]	0.892	0.775	[0.366,1.641]	0.505	0.752	[0.333,1.699]	0.493	0.781
rs1770810	SLC2A1	T	0.188	0.886	[0.647,1.214]	0.453	1.085	[0.638,1.844]	0.763	1.224	[0.686,2.183]	0.493	0.694
rs12922317	RUNDC2A	G	0.337	0.945	[0.743,1.203]	0.647	1.108	[0.726,1.689]	0.635	1.172	[0.744,1.847]	0.494	0.775
rs2236579	ITGA8	C	0.154	1.013	[0.729,1.407]	0.940	1.255	[0.71,2.217]	0.435	1.239	[0.67,2.292]	0.494	0.736
rs6463524	PMS2	G	0.184	1.299	[0.981,1.721]	0.068	1.065	[0.622,1.825]	0.818	0.820	[0.463,1.451]	0.495	0.189
rs2235033	ABCB1	C	0.493	1.007	[0.796,1.275]	0.951	1.184	[0.768,1.824]	0.445	1.175	[0.739,1.868]	0.495	0.746
rs2069442	CDK5	G	0.304	0.765	[0.59,0.991]	0.042	0.907	[0.577,1.425]	0.671	1.185	[0.727,1.934]	0.496	0.126
rs2665802	GH1	T	0.362	1.034	[0.81,1.321]	0.787	0.876	[0.561,1.368]	0.561	0.847	[0.525,1.366]	0.496	0.793
rs2239360	FANCA	T	0.394	1.369	[1.08,1.736]	0.009	1.604	[1.044,2.464]	0.031	1.172	[0.742,1.851]	0.497	0.007
rs1801376	BUB1B	G	0.285	0.998	[0.773,1.289]	0.988	0.834	[0.513,1.355]	0.464	0.836	[0.498,1.403]	0.497	0.762
rs3181077	CCR1	G	0.221	1.060	[0.8,1.403]	0.685	1.272	[0.779,2.076]	0.336	1.200	[0.708,2.033]	0.497	0.608
rs1514497	DPYD	T	0.300	0.970	[0.748,1.258]	0.820	1.149	[0.73,1.809]	0.548	1.184	[0.726,1.932]	0.498	0.794
rs2071520	TNC	C	0.320	1.174	[0.917,1.503]	0.203	0.991	[0.626,1.568]	0.969	0.844	[0.517,1.377]	0.498	0.435
rs798757	TACC3	G	0.179	1.041	[0.768,1.412]	0.796	1.260	[0.758,2.092]	0.373	1.210	[0.697,2.099]	0.498	0.667
rs1530662	FBXO25	T	0.495	1.034	[0.816,1.312]	0.780	1.215	[0.787,1.874]	0.379	1.174	[0.738,1.87]	0.498	0.671
rs679899	APOB	A	0.438	0.954	[0.746,1.22]	0.705	1.126	[0.719,1.764]	0.604	1.181	[0.73,1.911]	0.498	0.789
rs2304975	PSMB6	T	0.076	0.985	[0.645,1.504]	0.944	0.723	[0.309,1.695]	0.456	0.735	[0.301,1.794]	0.498	0.757
rs592943	MRE11A	T	0.297	0.969	[0.747,1.256]	0.810	1.149	[0.726,1.818]	0.553	1.186	[0.723,1.945]	0.499	0.795
rs2756105	ABCC2	T	0.389	1.272	[0.983,1.647]	0.068	1.072	[0.678,1.698]	0.765	0.843	[0.514,1.383]	0.499	0.188
rs3755160	ABCB11	T	0.340	1.045	[0.819,1.333]	0.725	1.230	[0.79,1.913]	0.359	1.177	[0.733,1.889]	0.500	0.640
rs998075	IGF2R	T	0.484	0.866	[0.682,1.1]	0.239	1.013	[0.663,1.548]	0.951	1.170	[0.742,1.844]	0.500	0.487
rs3794318	AICDA	C	0.131	1.175	[0.817,1.691]	0.385	1.462	[0.817,2.616]	0.201	1.244	[0.659,2.349]	0.501	0.352

rs1491961	CCR1	T	0.220	1.067	[0.806,1.412]	0.650	1.279	[0.784,2.086]	0.325	1.198	[0.708,2.029]	0.501	0.587
rs6410	CYP11B1	A	0.479	0.865	[0.679,1.101]	0.239	1.013	[0.662,1.549]	0.954	1.171	[0.74,1.853]	0.501	0.488
rs2292954	SPG7	C	0.156	0.927	[0.664,1.294]	0.655	1.153	[0.64,2.074]	0.636	1.244	[0.659,2.347]	0.501	0.782
rs2234693	ESR1	C	0.473	1.065	[0.843,1.346]	0.596	0.912	[0.598,1.391]	0.669	0.856	[0.544,1.347]	0.501	0.764
rs2281891	CYP2C18	A	0.146	1.138	[0.823,1.573]	0.435	0.903	[0.479,1.703]	0.753	0.794	[0.405,1.556]	0.502	0.675
rs4986894	CYP2C19	C	0.146	1.138	[0.823,1.573]	0.435	0.903	[0.479,1.703]	0.753	0.794	[0.405,1.556]	0.502	0.675
rs699473	SOD3	C	0.412	1.035	[0.812,1.317]	0.783	0.878	[0.56,1.375]	0.569	0.848	[0.525,1.371]	0.502	0.798
rs1800890	IL10	A	0.353	0.987	[0.769,1.267]	0.919	0.832	[0.522,1.327]	0.440	0.843	[0.512,1.387]	0.502	0.743
rs4244285	CYP2C19	A	0.147	1.133	[0.819,1.566]	0.451	0.900	[0.477,1.696]	0.744	0.794	[0.405,1.557]	0.502	0.686
rs754	LOC729296	G	0.157	1.199	[0.846,1.701]	0.308	1.494	[0.823,2.711]	0.187	1.246	[0.655,2.369]	0.503	0.297
rs1920313	SLC15A2	A	0.012	1.234	[0.425,3.578]	0.699	0.580	[0.072,4.646]	0.608	0.470	[0.052,4.276]	0.503	0.789
rs875120	TTR	T	0.049	0.936	[0.54,1.622]	0.814	0.606	[0.181,2.028]	0.416	0.648	[0.181,2.31]	0.503	0.711
rs2303078	HMMR	A	0.052	0.734	[0.42,1.28]	0.275	0.473	[0.138,1.62]	0.233	0.644	[0.177,2.348]	0.505	0.309
rs1003483	IGF2	G	0.444	1.059	[0.83,1.351]	0.645	1.248	[0.795,1.959]	0.335	1.179	[0.727,1.912]	0.505	0.593
rs2234898	IL4R	T	0.199	0.920	[0.665,1.273]	0.614	1.126	[0.651,1.948]	0.671	1.224	[0.674,2.223]	0.506	0.777
rs31480	IL3	T	0.216	1.024	[0.769,1.362]	0.873	1.225	[0.748,2.005]	0.419	1.197	[0.703,2.037]	0.508	0.721
rs2297881	KIF1B	C	0.034	0.955	[0.503,1.814]	0.889	1.368	[0.521,3.596]	0.525	1.432	[0.494,4.157]	0.509	0.791
rs3766871	RYR2	A	0.054	1.389	[0.849,2.272]	0.191	0.984	[0.374,2.592]	0.975	0.709	[0.255,1.968]	0.509	0.414
rs2972393	GHR	A	0.428	1.174	[0.923,1.492]	0.191	1.374	[0.888,2.124]	0.153	1.170	[0.734,1.867]	0.509	0.194
rs4820889	TCN2	A	0.044	0.623	[0.316,1.228]	0.172	0.911	[0.34,2.442]	0.853	1.462	[0.474,4.509]	0.509	0.393
rs17420378	STK4	A	0.261	1.125	[0.862,1.469]	0.386	0.942	[0.573,1.547]	0.812	0.837	[0.493,1.42]	0.509	0.643
rs9462088	FANCE	A	0.115	0.981	[0.667,1.444]	0.923	0.759	[0.373,1.546]	0.448	0.774	[0.361,1.658]	0.510	0.750
rs2070507	PPM1F	C	0.047	2.144	[1.319,3.485]	0.002	1.539	[0.589,4.019]	0.379	0.718	[0.268,1.923]	0.510	0.008
rs2479717	CCND3	T	0.224	0.847	[0.635,1.129]	0.258	1.016	[0.616,1.678]	0.949	1.200	[0.698,2.062]	0.510	0.515
rs1042157	SULT1A1	T	0.384	1.079	[0.843,1.382]	0.546	1.269	[0.811,1.986]	0.298	1.176	[0.726,1.904]	0.510	0.521
rs1270146	MRE11A	C	0.491	1.055	[0.84,1.325]	0.647	0.909	[0.601,1.374]	0.652	0.862	[0.554,1.341]	0.510	0.785
rs1800795	IL6	C	0.326	1.151	[0.906,1.462]	0.250	0.978	[0.619,1.544]	0.924	0.850	[0.523,1.381]	0.511	0.499
rs3218649	POLQ	C	0.364	0.843	[0.663,1.072]	0.164	0.719	[0.461,1.12]	0.145	0.852	[0.529,1.373]	0.511	0.166
rs3776969	MSH3	A	0.105	1.270	[0.886,1.82]	0.193	1.004	[0.517,1.951]	0.991	0.791	[0.392,1.595]	0.512	0.420
rs2074351	PON1	A	0.296	0.927	[0.722,1.191]	0.555	0.785	[0.493,1.251]	0.308	0.846	[0.514,1.393]	0.512	0.536
rs434455	RUNDC2A	T	0.209	1.129	[0.845,1.509]	0.413	0.935	[0.551,1.585]	0.802	0.828	[0.471,1.457]	0.512	0.667
rs3842787	PTGS1	T	0.079	0.792	[0.49,1.282]	0.343	0.560	[0.212,1.484]	0.244	0.707	[0.251,1.995]	0.513	0.361
rs2020955	ERCC4	C	0.030	1.071	[0.479,2.397]	0.867	0.624	[0.139,2.804]	0.538	0.582	[0.115,2.937]	0.513	0.804
rs1970142	DPYD	T	0.289	0.933	[0.718,1.213]	0.606	1.110	[0.683,1.805]	0.673	1.190	[0.707,2.003]	0.513	0.774
rs2230129	TAF1C	A	0.364	0.832	[0.653,1.06]	0.137	0.973	[0.63,1.503]	0.902	1.169	[0.732,1.866]	0.513	0.331
rs2012199	FCRL5	C	0.150	0.700	[0.497,0.987]	0.042	0.551	[0.281,1.078]	0.082	0.787	[0.383,1.615]	0.513	0.039
rs3014626	PPP1R15B	T	0.012	0.787	[0.231,2.687]	0.702	1.487	[0.279,7.94]	0.642	1.890	[0.28,12.737]	0.513	0.806
rs755622	MIF	G	0.226	1.254	[0.945,1.666]	0.117	1.043	[0.623,1.748]	0.872	0.832	[0.479,1.445]	0.513	0.293
rs9436299	LEPR	C	0.306	1.095	[0.85,1.409]	0.483	1.287	[0.819,2.02]	0.274	1.175	[0.724,1.909]	0.513	0.472
rs1800682	FAS	C	0.496	0.964	[0.761,1.221]	0.762	1.126	[0.728,1.741]	0.593	1.168	[0.733,1.861]	0.513	0.806
rs169758	TPTE	A	0.082	0.919	[0.553,1.529]	0.745	1.241	[0.544,2.827]	0.608	1.350	[0.548,3.323]	0.514	0.807

rs664677	ATM	C	0.393	0.964	[0.759,1.225]	0.766	0.825	[0.532,1.279]	0.389	0.855	[0.534,1.368]	0.514	0.679
rs11569017	EGF	T	0.053	0.841	[0.476,1.488]	0.553	1.187	[0.463,3.047]	0.721	1.411	[0.5,3.984]	0.516	0.763
rs2287498	TP53	A	0.115	1.210	[0.83,1.765]	0.322	0.942	[0.464,1.913]	0.869	0.779	[0.366,1.657]	0.516	0.585
rs568408	IL12A	A	0.145	1.158	[0.833,1.61]	0.382	0.934	[0.508,1.715]	0.825	0.806	[0.421,1.544]	0.516	0.643
rs4148217	ABCG8	A	0.213	0.868	[0.648,1.163]	0.343	1.038	[0.631,1.707]	0.883	1.196	[0.696,2.054]	0.516	0.613
rs7011	CINP	T	0.245	1.015	[0.775,1.33]	0.912	1.201	[0.749,1.925]	0.448	1.183	[0.712,1.965]	0.517	0.749
rs1709409	DPYD	G	0.226	0.952	[0.719,1.261]	0.732	0.788	[0.462,1.346]	0.383	0.828	[0.468,1.466]	0.517	0.666
rs610308	PPP1R15A	C	0.388	1.065	[0.824,1.378]	0.630	0.902	[0.562,1.446]	0.668	0.846	[0.51,1.403]	0.518	0.785
rs4646315	COMT	C	0.172	1.098	[0.807,1.493]	0.552	0.877	[0.459,1.673]	0.689	0.799	[0.404,1.579]	0.518	0.749
rs1051130	CCND3	T	0.414	0.982	[0.779,1.239]	0.881	1.135	[0.756,1.706]	0.541	1.156	[0.745,1.792]	0.518	0.806
rs1263167	APOA5	G	0.169	0.817	[0.59,1.132]	0.225	0.652	[0.341,1.243]	0.194	0.797	[0.401,1.585]	0.518	0.244
rs1870049	CYP19A1	C	0.168	0.906	[0.648,1.267]	0.564	0.731	[0.398,1.342]	0.312	0.807	[0.421,1.547]	0.518	0.545
rs9658655	CHGA	C	0.105	0.880	[0.597,1.296]	0.516	1.103	[0.59,2.063]	0.759	1.254	[0.63,2.496]	0.520	0.747
rs1060896	SLC28A2	C	0.461	1.060	[0.833,1.35]	0.637	0.907	[0.581,1.414]	0.666	0.856	[0.532,1.377]	0.520	0.789
rs2066827	CDKN1B	G	0.311	0.922	[0.683,1.246]	0.598	1.100	[0.67,1.805]	0.706	1.192	[0.697,2.039]	0.520	0.780
rs4149965	EXO1	A	0.201	0.969	[0.725,1.296]	0.832	1.161	[0.696,1.936]	0.567	1.198	[0.69,2.081]	0.521	0.813
rs8058694	ABCC6	T	0.479	0.912	[0.716,1.162]	0.456	1.063	[0.687,1.646]	0.783	1.166	[0.729,1.866]	0.522	0.705
rs4135113	TDG	A	0.052	1.007	[0.554,1.829]	0.982	1.400	[0.558,3.517]	0.473	1.391	[0.506,3.82]	0.522	0.770
rs7709790	GHR	G	0.231	1.113	[0.836,1.482]	0.463	1.322	[0.811,2.155]	0.262	1.188	[0.7,2.015]	0.523	0.452
rs1042821	MSH6	T	0.190	1.091	[0.803,1.481]	0.579	0.898	[0.514,1.566]	0.704	0.823	[0.453,1.496]	0.523	0.771
rs921519	ERICH1	C	0.201	0.897	[0.672,1.196]	0.457	0.738	[0.42,1.295]	0.289	0.823	[0.453,1.497]	0.523	0.473
rs3181218	IL12B	A	0.251	1.012	[0.769,1.332]	0.933	0.846	[0.508,1.411]	0.522	0.836	[0.483,1.447]	0.523	0.804
rs6500452	FANCA	C	0.353	1.304	[1.026,1.657]	0.030	1.513	[0.987,2.32]	0.058	1.160	[0.735,1.833]	0.523	0.027
rs423904	IL1RN	T	0.258	1.113	[0.845,1.465]	0.446	0.932	[0.561,1.548]	0.787	0.838	[0.487,1.443]	0.523	0.697
rs1800947	CRP	C	0.054	0.716	[0.406,1.261]	0.247	1.007	[0.389,2.609]	0.989	1.407	[0.493,4.02]	0.524	0.506
rs557148	MRE11A	C	0.481	1.134	[0.897,1.434]	0.292	0.980	[0.644,1.491]	0.923	0.864	[0.55,1.355]	0.524	0.557
rs7517376	FMO1	G	0.198	1.015	[0.73,1.41]	0.932	1.228	[0.716,2.105]	0.456	1.210	[0.673,2.177]	0.524	0.757
rs4646487	CYP4B1	T	0.138	0.746	[0.519,1.07]	0.112	0.928	[0.501,1.717]	0.812	1.244	[0.635,2.438]	0.524	0.282
rs508078	GSTA4	A	0.086	1.125	[0.736,1.72]	0.587	0.842	[0.362,1.956]	0.689	0.748	[0.307,1.827]	0.524	0.770
rs3770582	ABCB11	A	0.469	1.156	[0.917,1.456]	0.220	0.996	[0.65,1.527]	0.987	0.862	[0.546,1.361]	0.525	0.463
rs7512785	FMO2	T	0.303	0.877	[0.676,1.139]	0.326	1.028	[0.653,1.621]	0.904	1.172	[0.718,1.914]	0.526	0.596
rs3887412	ABCC1	T	0.230	1.172	[0.877,1.565]	0.284	0.975	[0.573,1.657]	0.925	0.832	[0.471,1.47]	0.526	0.547
rs3826573	CTDP1	T	0.403	1.020	[0.788,1.32]	0.879	1.191	[0.766,1.852]	0.438	1.167	[0.723,1.884]	0.526	0.739
rs4646491	CYP4B1	T	0.136	0.808	[0.564,1.158]	0.246	0.630	[0.305,1.299]	0.211	0.779	[0.36,1.687]	0.526	0.270
rs3212227	IL12B	C	0.247	0.960	[0.733,1.258]	0.768	0.805	[0.484,1.339]	0.403	0.839	[0.486,1.446]	0.527	0.693
rs1801280	NAT2	C	0.400	1.081	[0.853,1.371]	0.518	0.931	[0.603,1.438]	0.747	0.861	[0.541,1.371]	0.528	0.744
rs1126643	ITGA2	T	0.384	1.199	[0.944,1.522]	0.137	1.028	[0.658,1.606]	0.903	0.858	[0.533,1.381]	0.528	0.331
rs1800791	FGB	A	0.160	0.883	[0.629,1.239]	0.472	1.084	[0.602,1.953]	0.788	1.227	[0.65,2.319]	0.528	0.720
rs3786187	NFATC1	C	0.439	0.950	[0.75,1.204]	0.673	0.820	[0.536,1.255]	0.361	0.863	[0.546,1.364]	0.528	0.630
rs1760210	DPYD	C	0.178	1.253	[0.928,1.692]	0.141	1.496	[0.894,2.504]	0.125	1.194	[0.687,2.074]	0.529	0.143
rs1801406	BRCA2	G	0.294	1.011	[0.773,1.322]	0.938	1.189	[0.744,1.9]	0.470	1.176	[0.709,1.95]	0.529	0.770

rs3213469	ATF6B	G	0.241	1.159	[0.879,1.527]	0.295	1.374	[0.835,2.263]	0.211	1.186	[0.696,2.02]	0.530	0.314
rs660339	UCP2	T	0.423	1.203	[0.947,1.527]	0.130	1.039	[0.68,1.589]	0.859	0.864	[0.548,1.363]	0.530	0.317
rs4645878	BAX	A	0.107	1.000	[0.687,1.454]	0.999	0.779	[0.376,1.614]	0.502	0.779	[0.358,1.697]	0.530	0.796
rs1062633	MST1R	A	0.477	0.912	[0.721,1.153]	0.442	1.054	[0.693,1.603]	0.806	1.156	[0.735,1.817]	0.530	0.699
rs729940	CHGA	T	0.155	1.147	[0.817,1.609]	0.428	1.416	[0.763,2.626]	0.270	1.235	[0.639,2.386]	0.531	0.444
rs1043720	ADRB3	A	0.274	0.837	[0.642,1.092]	0.189	0.983	[0.616,1.57]	0.944	1.175	[0.709,1.947]	0.531	0.420
rs4364	ACE	A	0.023	1.104	[0.463,2.637]	0.823	0.647	[0.138,3.034]	0.581	0.586	[0.11,3.126]	0.532	0.822
rs10228128	SHFM1	C	0.015	0.942	[0.315,2.814]	0.914	1.537	[0.431,5.49]	0.508	1.633	[0.351,7.599]	0.532	0.784
rs2243289	IL4	G	0.192	1.369	[1.043,1.798]	0.024	1.147	[0.677,1.942]	0.610	0.838	[0.481,1.46]	0.532	0.077
rs998074	IGF2R	A	0.489	0.861	[0.678,1.093]	0.219	0.995	[0.651,1.523]	0.983	1.157	[0.733,1.826]	0.532	0.464
rs440454	RDBP	T	0.265	0.910	[0.696,1.19]	0.491	1.071	[0.666,1.721]	0.777	1.177	[0.705,1.963]	0.533	0.733
rs1129055	CD86	A	0.250	1.161	[0.897,1.504]	0.257	0.984	[0.603,1.606]	0.950	0.848	[0.504,1.426]	0.533	0.513
rs2292245	PTPRG	A	0.156	1.053	[0.765,1.45]	0.751	1.272	[0.733,2.207]	0.392	1.208	[0.666,2.19]	0.533	0.680
rs12450550	EME1	C	0.251	1.032	[0.787,1.352]	0.820	1.215	[0.753,1.962]	0.425	1.178	[0.703,1.973]	0.534	0.723
rs2014800	ABCC1	C	0.454	1.066	[0.843,1.349]	0.594	1.232	[0.805,1.886]	0.337	1.156	[0.732,1.825]	0.535	0.582
rs8191754	IGF2R	G	0.145	0.973	[0.694,1.365]	0.874	0.783	[0.412,1.487]	0.454	0.804	[0.405,1.599]	0.535	0.754
rs4839469	VANGL1	A	0.129	1.170	[0.834,1.641]	0.362	0.938	[0.486,1.811]	0.850	0.802	[0.399,1.61]	0.535	0.628
rs6962039	SLC13A1	A	0.277	0.880	[0.673,1.149]	0.346	1.032	[0.648,1.642]	0.896	1.173	[0.709,1.94]	0.535	0.620
rs8058696	ABCC6	C	0.477	0.879	[0.686,1.127]	0.309	1.024	[0.654,1.603]	0.917	1.165	[0.719,1.887]	0.535	0.579
rs7577677	UGT1A10	A	0.346	1.027	[0.803,1.314]	0.832	1.195	[0.764,1.871]	0.435	1.164	[0.72,1.881]	0.535	0.733
rs1432793	SH3TC2	C	0.482	1.089	[0.865,1.372]	0.467	0.946	[0.625,1.432]	0.793	0.868	[0.556,1.356]	0.535	0.718
rs4886605	CYP1A1	T	0.242	1.115	[0.849,1.464]	0.435	0.941	[0.57,1.553]	0.812	0.844	[0.494,1.442]	0.535	0.694
rs3770603	ABCB11	T	0.104	0.851	[0.564,1.284]	0.442	1.076	[0.547,2.116]	0.833	1.264	[0.601,2.658]	0.536	0.707
rs11003127	MBL2	C	0.274	1.111	[0.853,1.446]	0.435	0.942	[0.58,1.532]	0.811	0.848	[0.504,1.428]	0.536	0.695
rs6892398	RAD50	C	0.016	0.783	[0.241,2.549]	0.685	0.373	[0.043,3.227]	0.370	0.476	[0.045,5.008]	0.536	0.636
rs877518	ID3	A	0.098	1.374	[0.919,2.055]	0.122	1.075	[0.518,2.23]	0.846	0.782	[0.359,1.704]	0.537	0.302
rs426169	GSTA4	T	0.490	0.960	[0.757,1.218]	0.739	0.829	[0.538,1.279]	0.398	0.864	[0.542,1.375]	0.537	0.682
rs17572019	PPARGC1B	A	0.078	1.092	[0.725,1.646]	0.673	0.826	[0.356,1.916]	0.656	0.756	[0.311,1.836]	0.537	0.806
rs2300697	SRD5A2	C	0.396	0.977	[0.768,1.242]	0.848	0.840	[0.536,1.316]	0.446	0.860	[0.532,1.389]	0.537	0.745
rs32950	MSH3	G	0.449	1.245	[0.986,1.571]	0.065	1.079	[0.704,1.651]	0.728	0.866	[0.549,1.368]	0.538	0.182
rs6413420	CYP2E1	T	0.049	0.528	[0.282,0.987]	0.045	0.760	[0.265,2.177]	0.609	1.440	[0.449,4.616]	0.540	0.129
rs1052133	CAMK1	G	0.234	1.148	[0.869,1.517]	0.332	0.968	[0.581,1.614]	0.900	0.843	[0.488,1.456]	0.540	0.602
rs4543	CYP11B2	A	0.105	1.208	[0.826,1.766]	0.329	0.956	[0.474,1.93]	0.901	0.792	[0.374,1.674]	0.541	0.599
rs361525	TNF	A	0.054	1.228	[0.749,2.013]	0.416	1.587	[0.746,3.378]	0.230	1.293	[0.567,2.947]	0.541	0.406
rs135539	PPARA	G	0.465	1.006	[0.797,1.269]	0.959	0.872	[0.569,1.337]	0.531	0.867	[0.548,1.37]	0.541	0.814
rs2011713	PCGF2	A	0.071	0.726	[0.445,1.185]	0.200	0.512	[0.177,1.481]	0.217	0.706	[0.23,2.167]	0.543	0.238
rs5186	AGTR1	C	0.249	0.893	[0.681,1.171]	0.413	0.752	[0.448,1.263]	0.281	0.843	[0.485,1.463]	0.543	0.444
rs1469149	CSF2	C	0.370	0.922	[0.717,1.186]	0.526	1.075	[0.679,1.703]	0.757	1.167	[0.71,1.918]	0.543	0.759
rs1801243	ATP7B	G	0.448	0.791	[0.621,1.008]	0.058	0.915	[0.59,1.42]	0.693	1.157	[0.722,1.855]	0.544	0.164
rs1805011	IL4R	C	0.203	0.944	[0.682,1.307]	0.728	1.136	[0.655,1.971]	0.650	1.204	[0.661,2.193]	0.545	0.828
rs1143634	IL1B	T	0.210	0.974	[0.737,1.287]	0.853	0.819	[0.484,1.387]	0.458	0.841	[0.48,1.474]	0.546	0.756

rs10018284	Intergenic	C	0.337	1.068	[0.833,1.37]	0.603	0.917	[0.577,1.458]	0.715	0.859	[0.523,1.409]	0.546	0.792
rs2305799	ACP5	T	0.101	1.005	[0.68,1.484]	0.981	0.782	[0.363,1.682]	0.529	0.778	[0.345,1.758]	0.546	0.816
rs891507	CDK5	T	0.138	0.896	[0.636,1.261]	0.528	1.097	[0.597,2.015]	0.767	1.224	[0.634,2.363]	0.547	0.761
rs1760209	DPYD	T	0.179	1.202	[0.893,1.618]	0.226	1.421	[0.854,2.365]	0.176	1.183	[0.685,2.042]	0.547	0.241
rs17064	ABCB1	T	0.076	0.888	[0.568,1.389]	0.603	1.122	[0.566,2.226]	0.742	1.263	[0.591,2.702]	0.547	0.803
rs1736565	FMO6	C	0.406	0.884	[0.697,1.121]	0.309	1.019	[0.662,1.568]	0.931	1.153	[0.726,1.832]	0.547	0.581
rs488133	ESR1	T	0.262	0.953	[0.732,1.241]	0.722	1.115	[0.692,1.796]	0.654	1.170	[0.702,1.95]	0.547	0.827
rs2762934	CYP24A1	A	0.171	1.169	[0.865,1.58]	0.309	0.968	[0.543,1.726]	0.913	0.828	[0.449,1.529]	0.547	0.578
rs4792147	ALOX15B	A	0.445	0.835	[0.656,1.063]	0.143	0.966	[0.62,1.506]	0.879	1.157	[0.719,1.863]	0.548	0.341
rs730566	ATRIP	T	0.262	0.883	[0.672,1.161]	0.374	0.746	[0.445,1.25]	0.266	0.844	[0.486,1.466]	0.548	0.407
rs541463	PGR	A	0.135	1.166	[0.832,1.634]	0.372	1.417	[0.782,2.569]	0.251	1.215	[0.643,2.298]	0.548	0.398
rs9529	CCND3	A	0.233	0.966	[0.729,1.28]	0.808	1.136	[0.693,1.863]	0.612	1.177	[0.691,2.004]	0.549	0.835
rs11995670	ADRB3	G	0.319	0.845	[0.653,1.095]	0.202	0.985	[0.619,1.567]	0.949	1.165	[0.707,1.922]	0.549	0.441
rs3790433	LEPR	A	0.352	1.188	[0.92,1.534]	0.186	1.018	[0.633,1.637]	0.943	0.856	[0.516,1.422]	0.549	0.414
rs1413233	DPYD	C	0.013	1.043	[0.266,4.085]	0.952	0.496	[0.055,4.45]	0.531	0.475	[0.042,5.415]	0.549	0.814
rs419129	GSTA4	T	0.487	1.124	[0.887,1.424]	0.335	1.293	[0.842,1.987]	0.240	1.151	[0.726,1.825]	0.549	0.361
rs6911817	PPARD	T	0.063	0.746	[0.425,1.31]	0.308	0.532	[0.192,1.478]	0.226	0.713	[0.236,2.156]	0.549	0.326
rs524	PPP1R15A	A	0.298	0.944	[0.723,1.234]	0.674	0.804	[0.492,1.313]	0.383	0.851	[0.502,1.443]	0.549	0.652
rs173537	HERPUD1	C	0.333	1.115	[0.864,1.44]	0.403	0.959	[0.603,1.524]	0.858	0.860	[0.523,1.412]	0.550	0.674
rs9840993	MYLK	G	0.069	0.961	[0.553,1.67]	0.888	0.705	[0.28,1.78]	0.460	0.734	[0.266,2.024]	0.550	0.760
rs487848	POLQ	A	0.078	0.928	[0.573,1.503]	0.761	1.213	[0.543,2.71]	0.637	1.307	[0.543,3.149]	0.550	0.835
rs1071676	IL1B	C	0.210	0.978	[0.74,1.293]	0.878	0.825	[0.488,1.395]	0.472	0.843	[0.481,1.476]	0.550	0.771
rs610611	MRE11A	A	0.297	0.981	[0.757,1.271]	0.883	1.141	[0.72,1.807]	0.575	1.163	[0.709,1.909]	0.550	0.833
rs3850997	TNFRSF17	T	0.297	1.047	[0.804,1.363]	0.736	1.217	[0.769,1.925]	0.401	1.163	[0.709,1.908]	0.551	0.686
rs1322055	TNFSF8	C	0.121	0.794	[0.548,1.151]	0.224	0.986	[0.513,1.892]	0.965	1.241	[0.611,2.52]	0.551	0.475
rs3093662	TNF	G	0.067	1.354	[0.853,2.152]	0.199	1.711	[0.842,3.476]	0.138	1.263	[0.586,2.723]	0.551	0.198
rs1048804	NRP1	C	0.293	0.978	[0.756,1.266]	0.867	0.839	[0.524,1.343]	0.465	0.858	[0.518,1.42]	0.551	0.764
rs7708626	RAD50	A	0.031	2.004	[0.938,4.278]	0.073	1.352	[0.413,4.434]	0.618	0.675	[0.185,2.467]	0.552	0.196
rs1549758	NOS3	T	0.266	1.195	[0.913,1.565]	0.195	1.016	[0.614,1.681]	0.951	0.850	[0.497,1.454]	0.553	0.428
rs6428830	HSD3B1	A	0.246	1.103	[0.83,1.464]	0.500	0.927	[0.541,1.588]	0.782	0.841	[0.474,1.492]	0.553	0.743
rs10248420	ABCB1	G	0.218	1.205	[0.89,1.632]	0.227	1.422	[0.859,2.356]	0.171	1.180	[0.683,2.04]	0.554	0.236
rs4303	ACE	T	0.019	0.838	[0.29,2.423]	0.744	0.409	[0.044,3.804]	0.432	0.488	[0.046,5.234]	0.554	0.712
rs1202170	ABCB1	G	0.490	1.034	[0.81,1.321]	0.788	1.189	[0.775,1.826]	0.428	1.150	[0.723,1.828]	0.555	0.721
rs17779352	AHR	C	0.077	0.729	[0.453,1.175]	0.195	0.950	[0.426,2.116]	0.899	1.302	[0.542,3.125]	0.555	0.431
rs7514102	PROK1	A	0.422	0.867	[0.682,1.102]	0.245	0.998	[0.646,1.539]	0.991	1.150	[0.722,1.833]	0.557	0.503
rs560096	IGHMBP2	T	0.207	0.882	[0.659,1.182]	0.401	1.038	[0.631,1.709]	0.882	1.177	[0.684,2.025]	0.557	0.679
rs3733549	BMP3	A	0.072	1.173	[0.759,1.812]	0.472	1.474	[0.731,2.973]	0.278	1.257	[0.586,2.695]	0.557	0.477
rs2738258	CYP3A4	A	0.059	1.295	[0.72,2.329]	0.388	0.952	[0.377,2.405]	0.917	0.735	[0.263,2.053]	0.557	0.672
rs3219489	MUTYH	C	0.247	0.872	[0.668,1.139]	0.315	1.013	[0.64,1.601]	0.958	1.161	[0.706,1.91]	0.557	0.592
rs3730477	POLL	T	0.171	0.861	[0.623,1.19]	0.366	1.043	[0.576,1.888]	0.890	1.210	[0.64,2.289]	0.557	0.643
rs165815	ARVCF	C	0.234	1.281	[0.971,1.689]	0.080	1.088	[0.652,1.815]	0.746	0.850	[0.493,1.464]	0.557	0.216

rs2297809	CYP4B1	A	0.152	0.777	[0.548,1.103]	0.158	0.623	[0.311,1.245]	0.180	0.801	[0.382,1.681]	0.558	0.181
rs7805658	SHFM1	A	0.388	0.795	[0.617,1.023]	0.075	0.684	[0.429,1.091]	0.111	0.861	[0.523,1.419]	0.558	0.081
rs776741	CYP3A5	C	0.100	0.985	[0.629,1.541]	0.946	1.237	[0.616,2.483]	0.549	1.257	[0.585,2.697]	0.558	0.824
rs937369	ABCC1	A	0.454	1.075	[0.85,1.359]	0.549	1.232	[0.804,1.887]	0.338	1.146	[0.726,1.81]	0.558	0.566
rs3733182	STK32B	C	0.154	0.972	[0.711,1.329]	0.860	0.803	[0.439,1.469]	0.476	0.826	[0.435,1.568]	0.559	0.773
rs10499926	SHFM1	C	0.388	0.795	[0.618,1.024]	0.076	0.685	[0.43,1.093]	0.112	0.862	[0.523,1.42]	0.559	0.082
rs35592	ABCC1	C	0.280	0.879	[0.672,1.151]	0.350	1.022	[0.643,1.625]	0.927	1.162	[0.702,1.922]	0.559	0.630
rs10261833	SHFM1	C	0.180	1.152	[0.855,1.551]	0.352	0.964	[0.55,1.689]	0.897	0.837	[0.46,1.523]	0.559	0.627
rs506008	GSTM4	A	0.173	0.861	[0.61,1.215]	0.394	1.040	[0.581,1.861]	0.896	1.208	[0.641,2.275]	0.560	0.674
rs2839668	MYO3A	G	0.084	1.000	[0.659,1.517]	0.999	1.267	[0.604,2.656]	0.532	1.267	[0.572,2.808]	0.560	0.819
rs4251710	TAF15	C	0.118	1.021	[0.684,1.524]	0.919	0.808	[0.387,1.685]	0.569	0.791	[0.359,1.743]	0.561	0.837
rs12721613	NR1I2	T	0.020	0.630	[0.238,1.667]	0.352	0.981	[0.273,3.521]	0.977	1.557	[0.35,6.922]	0.561	0.645
rs5987	F13A1	A	0.051	0.794	[0.46,1.369]	0.407	0.550	[0.171,1.768]	0.316	0.693	[0.201,2.39]	0.561	0.462
rs1129923	DUSP23	A	0.080	0.789	[0.502,1.24]	0.305	1.014	[0.465,2.214]	0.971	1.286	[0.55,3.006]	0.562	0.582
rs1130496	PTPRN2	A	0.393	0.752	[0.583,0.969]	0.028	0.866	[0.556,1.35]	0.526	1.153	[0.713,1.862]	0.562	0.084
rs1611755	SPRR1A	T	0.434	0.870	[0.684,1.107]	0.258	0.757	[0.488,1.175]	0.214	0.870	[0.543,1.394]	0.562	0.289
rs3749228	CHRD	G	0.068	1.362	[0.889,2.086]	0.156	1.042	[0.443,2.455]	0.924	0.765	[0.31,1.891]	0.562	0.364
rs608452	MRE11A	T	0.019	0.694	[0.245,1.971]	0.493	0.357	[0.044,2.917]	0.337	0.515	[0.054,4.881]	0.563	0.529
rs2301241	TXN	C	0.396	0.964	[0.759,1.224]	0.762	0.840	[0.544,1.297]	0.432	0.872	[0.547,1.39]	0.564	0.720
rs1004588	DGKG	C	0.485	1.021	[0.811,1.285]	0.861	1.166	[0.765,1.779]	0.475	1.143	[0.726,1.798]	0.564	0.772
rs911605	TNFSF8	G	0.254	0.885	[0.678,1.155]	0.368	0.754	[0.452,1.258]	0.279	0.852	[0.493,1.471]	0.565	0.414
rs3172469	BCL6	C	0.292	1.009	[0.78,1.305]	0.946	1.163	[0.74,1.827]	0.512	1.153	[0.709,1.874]	0.566	0.806
rs2280789	CCL5	C	0.149	1.088	[0.785,1.508]	0.613	0.894	[0.475,1.682]	0.728	0.822	[0.42,1.608]	0.566	0.806
rs4803418	CYP2B6	G	0.288	0.934	[0.713,1.223]	0.618	0.795	[0.474,1.334]	0.385	0.851	[0.491,1.477]	0.567	0.636
rs2295155	CARD10	A	0.092	0.860	[0.568,1.302]	0.475	0.660	[0.282,1.547]	0.340	0.768	[0.311,1.896]	0.567	0.526
rs2228526	ERCC6	G	0.198	0.952	[0.709,1.278]	0.742	1.121	[0.665,1.89]	0.669	1.178	[0.672,2.063]	0.568	0.843
rs1861887	GSTZ1	T	0.183	1.055	[0.784,1.42]	0.723	0.885	[0.502,1.56]	0.672	0.839	[0.458,1.534]	0.568	0.839
rs1045020	SLC22A5	T	0.117	1.017	[0.7,1.478]	0.930	0.809	[0.386,1.695]	0.575	0.796	[0.363,1.743]	0.568	0.843
rs2283512	ABCC1	T	0.374	1.015	[0.79,1.303]	0.909	1.165	[0.751,1.806]	0.496	1.148	[0.715,1.843]	0.568	0.793
rs1801058	GRK4	T	0.378	0.869	[0.681,1.108]	0.257	0.996	[0.643,1.542]	0.984	1.146	[0.716,1.835]	0.570	0.520
rs2234962	BAG3	C	0.163	1.157	[0.847,1.58]	0.360	0.960	[0.524,1.761]	0.896	0.830	[0.437,1.578]	0.570	0.636
rs35599	ABCC1	C	0.111	1.127	[0.784,1.621]	0.519	1.362	[0.743,2.498]	0.318	1.209	[0.627,2.33]	0.571	0.537
rs9282564	ABCB1	G	0.093	0.848	[0.564,1.277]	0.430	0.662	[0.296,1.483]	0.316	0.780	[0.331,1.842]	0.571	0.483
rs1614984	TP53	T	0.437	0.974	[0.768,1.235]	0.828	0.852	[0.555,1.31]	0.466	0.875	[0.552,1.389]	0.572	0.761
rs3176123	THBD	C	0.164	1.058	[0.772,1.45]	0.726	1.258	[0.719,2.2]	0.422	1.189	[0.652,2.165]	0.572	0.705
rs3914142	ACBD3	C	0.459	0.920	[0.728,1.162]	0.485	0.807	[0.527,1.236]	0.324	0.877	[0.555,1.385]	0.573	0.524
rs1873196	TLR1	T	0.028	0.849	[0.398,1.813]	0.672	0.536	[0.12,2.39]	0.414	0.632	[0.128,3.125]	0.573	0.677
rs2107356	IL4R	A	0.365	1.009	[0.791,1.287]	0.941	1.154	[0.747,1.782]	0.518	1.144	[0.717,1.825]	0.574	0.811
rs17780143	MAP4K5	A	0.049	1.377	[0.816,2.325]	0.231	1.787	[0.769,4.153]	0.178	1.297	[0.524,3.214]	0.574	0.252
rs6768093	ATR	A	0.388	0.820	[0.641,1.049]	0.115	0.941	[0.601,1.474]	0.792	1.148	[0.709,1.858]	0.574	0.288
rs2089891	PPP1R15B	G	0.082	0.955	[0.629,1.448]	0.828	0.739	[0.318,1.717]	0.482	0.774	[0.316,1.895]	0.575	0.773

rs6102	SERPINB2	G	0.208	1.434	[1.084,1.897]	0.012	1.662	[1.024,2.697]	0.040	1.159	[0.691,1.943]	0.575	0.011
rs2242578	GLI1	G	0.383	0.929	[0.728,1.186]	0.556	1.062	[0.688,1.64]	0.786	1.143	[0.716,1.824]	0.576	0.788
rs3779620	PBK	G	0.138	0.823	[0.573,1.182]	0.292	0.994	[0.545,1.815]	0.985	1.208	[0.623,2.341]	0.576	0.570
rs11595876	MBL2	C	0.055	1.122	[0.679,1.855]	0.653	0.837	[0.318,2.203]	0.719	0.746	[0.267,2.084]	0.576	0.825
rs2000813	LIPG	T	0.267	1.129	[0.871,1.464]	0.358	0.974	[0.598,1.587]	0.916	0.863	[0.513,1.449]	0.577	0.637
rs6512087	CIB3	C	0.204	0.989	[0.746,1.313]	0.941	0.844	[0.502,1.419]	0.523	0.853	[0.489,1.49]	0.577	0.815
rs215059	ABCC1	T	0.132	1.208	[0.865,1.688]	0.267	0.997	[0.527,1.886]	0.992	0.825	[0.42,1.622]	0.577	0.532
rs947894	GSTP1	G	0.365	1.065	[0.832,1.362]	0.618	0.926	[0.586,1.464]	0.743	0.870	[0.533,1.419]	0.577	0.816
rs164938	TATDN2	T	0.456	1.008	[0.8,1.271]	0.946	1.145	[0.753,1.741]	0.525	1.136	[0.725,1.781]	0.578	0.817
rs3761936	AP4B1	C	0.187	1.394	[1.042,1.865]	0.025	1.178	[0.67,2.07]	0.569	0.845	[0.465,1.533]	0.579	0.079
rs31473	CSF2	T	0.299	1.053	[0.812,1.365]	0.699	1.209	[0.767,1.906]	0.413	1.149	[0.704,1.876]	0.579	0.690
rs917394	NPC2	T	0.374	0.981	[0.769,1.253]	0.879	0.856	[0.545,1.344]	0.499	0.872	[0.538,1.414]	0.580	0.794
rs2072360	FOXM1	G	0.231	1.088	[0.824,1.436]	0.552	0.934	[0.563,1.549]	0.792	0.859	[0.501,1.473]	0.580	0.786
rs3826007	BCL2A1	A	0.238	1.062	[0.811,1.392]	0.661	0.911	[0.547,1.517]	0.720	0.858	[0.498,1.478]	0.580	0.831
rs2075724	CSF2RB	T	0.483	1.197	[0.94,1.524]	0.144	1.052	[0.686,1.612]	0.817	0.878	[0.555,1.391]	0.581	0.343
rs2307492	FMO2	C	0.110	0.940	[0.643,1.374]	0.749	1.141	[0.607,2.142]	0.682	1.214	[0.611,2.413]	0.581	0.854
rs1801279	NAT2	A	0.011	2.003	[0.65,6.174]	0.226	1.046	[0.119,9.228]	0.967	0.522	[0.052,5.23]	0.581	0.477
rs157580	TOMM40	G	0.334	0.921	[0.717,1.181]	0.515	1.052	[0.677,1.636]	0.821	1.143	[0.711,1.836]	0.581	0.768
rs2972388	CDK7	G	0.428	0.976	[0.774,1.231]	0.839	1.109	[0.727,1.69]	0.632	1.136	[0.723,1.785]	0.581	0.859
rs3917991	CSF3R	C	0.040	1.130	[0.589,2.169]	0.713	0.802	[0.26,2.471]	0.700	0.709	[0.209,2.404]	0.581	0.849
rs1056522	CHST13	T	0.337	1.133	[0.891,1.441]	0.310	0.992	[0.638,1.543]	0.972	0.876	[0.547,1.403]	0.582	0.587
rs2853563	VDR	A	0.064	1.285	[0.802,2.059]	0.298	1.002	[0.439,2.288]	0.996	0.780	[0.323,1.887]	0.582	0.574
rs757158	PON1	C	0.482	0.841	[0.656,1.079]	0.173	0.734	[0.467,1.154]	0.181	0.873	[0.537,1.418]	0.582	0.202
rs2227931	ATR	C	0.350	1.199	[0.932,1.541]	0.158	1.374	[0.872,2.164]	0.171	1.146	[0.704,1.865]	0.583	0.184
rs552976	ABCB11	T	0.336	1.147	[0.902,1.458]	0.265	1.304	[0.849,2.004]	0.225	1.138	[0.718,1.803]	0.583	0.305
rs484066	ABCB11	T	0.395	1.118	[0.885,1.413]	0.350	1.267	[0.837,1.919]	0.263	1.133	[0.725,1.772]	0.583	0.392
rs17151919	LEP	A	0.014	1.264	[0.413,3.868]	0.681	0.660	[0.076,5.742]	0.707	0.522	[0.051,5.315]	0.583	0.840
rs5896	F2	T	0.136	1.158	[0.827,1.621]	0.394	1.381	[0.766,2.489]	0.283	1.193	[0.636,2.238]	0.583	0.444
rs4525938	DCK	T	0.119	0.802	[0.503,1.279]	0.353	0.629	[0.286,1.385]	0.250	0.785	[0.33,1.865]	0.583	0.377
rs2037483	HUS1	A	0.496	0.929	[0.734,1.175]	0.537	1.056	[0.688,1.622]	0.803	1.137	[0.718,1.801]	0.584	0.781
rs1962	THBD	C	0.264	1.096	[0.832,1.443]	0.514	1.268	[0.779,2.064]	0.339	1.157	[0.686,1.95]	0.584	0.555
rs584531	MRE11A	G	0.323	1.007	[0.785,1.293]	0.955	1.150	[0.74,1.787]	0.534	1.142	[0.71,1.837]	0.584	0.824
rs828059	DPYD	G	0.179	1.226	[0.912,1.65]	0.177	1.428	[0.858,2.376]	0.170	1.164	[0.675,2.009]	0.585	0.204
rs828057	DPYD	T	0.179	1.224	[0.91,1.646]	0.182	1.425	[0.856,2.371]	0.173	1.164	[0.675,2.01]	0.585	0.209
rs2234900	IL4R	C	0.206	0.875	[0.642,1.192]	0.397	1.028	[0.604,1.75]	0.919	1.175	[0.659,2.094]	0.585	0.682
rs3744644	SCARF1	G	0.055	1.670	[0.925,3.017]	0.089	1.235	[0.452,3.374]	0.681	0.739	[0.249,2.194]	0.586	0.233
rs17197552	PPP2R3A	G	0.268	0.914	[0.706,1.184]	0.497	1.049	[0.664,1.656]	0.839	1.147	[0.701,1.877]	0.586	0.759
rs228851	NFATC2	T	0.416	0.871	[0.683,1.11]	0.264	0.993	[0.638,1.545]	0.976	1.140	[0.71,1.833]	0.587	0.532
rs1014136	STARD3NL	C	0.232	0.956	[0.723,1.264]	0.753	1.110	[0.674,1.827]	0.683	1.160	[0.678,1.987]	0.587	0.858
rs1470414	PASK	A	0.298	0.941	[0.728,1.216]	0.640	1.079	[0.68,1.712]	0.747	1.147	[0.698,1.884]	0.588	0.831
rs1980499	LOC728383	C	0.435	1.113	[0.868,1.426]	0.399	1.272	[0.81,1.997]	0.297	1.143	[0.705,1.854]	0.588	0.452

rs874305	IGF1R	A	0.409	0.858	[0.674,1.093]	0.215	0.975	[0.634,1.499]	0.909	1.137	[0.715,1.808]	0.589	0.463
rs434473	ALOX12	G	0.386	0.939	[0.737,1.198]	0.615	1.068	[0.693,1.648]	0.765	1.137	[0.713,1.813]	0.589	0.822
rs2238783	ARVCF	G	0.397	1.160	[0.916,1.468]	0.217	1.021	[0.662,1.576]	0.925	0.880	[0.554,1.4]	0.590	0.466
rs2515641	CYP2E1	T	0.212	0.826	[0.587,1.164]	0.275	0.687	[0.367,1.284]	0.239	0.831	[0.424,1.629]	0.590	0.320
rs8940	CAV2	G	0.171	1.225	[0.901,1.664]	0.195	1.037	[0.587,1.832]	0.901	0.847	[0.462,1.552]	0.590	0.431
rs8032477	IGF1R	C	0.457	1.012	[0.796,1.287]	0.920	0.888	[0.569,1.387]	0.602	0.877	[0.545,1.413]	0.590	0.860
rs1056663	HUS1	A	0.494	0.935	[0.739,1.184]	0.579	1.062	[0.691,1.631]	0.785	1.135	[0.716,1.799]	0.591	0.806
rs11706052	IMPDH2	G	0.088	0.834	[0.544,1.278]	0.404	0.646	[0.27,1.547]	0.327	0.775	[0.307,1.961]	0.591	0.474
rs2305367	SLC28A1	T	0.388	0.977	[0.77,1.239]	0.848	1.105	[0.728,1.677]	0.640	1.131	[0.721,1.772]	0.592	0.866
rs697221	DDIT3	A	0.177	0.779	[0.568,1.069]	0.122	0.918	[0.528,1.596]	0.763	1.179	[0.646,2.15]	0.592	0.300
rs1884614	HNF4a	T	0.195	0.859	[0.64,1.152]	0.310	1.001	[0.595,1.684]	0.997	1.166	[0.665,2.044]	0.592	0.591
rs10479008	RAD50	A	0.033	1.787	[0.836,3.82]	0.134	1.252	[0.382,4.108]	0.710	0.701	[0.19,2.578]	0.593	0.323
rs3093153	CYP4F2	T	0.058	0.939	[0.574,1.536]	0.802	1.197	[0.526,2.723]	0.669	1.274	[0.524,3.098]	0.593	0.866
rs696217	GHRL	T	0.065	0.814	[0.507,1.309]	0.397	0.607	[0.218,1.69]	0.339	0.745	[0.253,2.195]	0.593	0.479
rs743534	CYP2E1	G	0.209	0.872	[0.624,1.219]	0.424	0.729	[0.395,1.346]	0.312	0.836	[0.432,1.615]	0.593	0.479
rs2299257	PON1	C	0.461	0.895	[0.71,1.128]	0.345	0.791	[0.52,1.205]	0.275	0.885	[0.563,1.389]	0.594	0.400
rs3733890	BHMT	A	0.301	0.949	[0.736,1.225]	0.689	1.085	[0.686,1.718]	0.726	1.143	[0.698,1.873]	0.594	0.849
rs117854	ABCC1	C	0.344	1.104	[0.849,1.436]	0.461	0.960	[0.592,1.556]	0.867	0.869	[0.518,1.458]	0.595	0.734
rs1800822	FMO3	T	0.068	1.152	[0.737,1.8]	0.535	0.887	[0.355,2.214]	0.797	0.770	[0.294,2.018]	0.595	0.778
rs3218012	CDKN2A	T	0.436	1.061	[0.834,1.35]	0.630	0.935	[0.605,1.444]	0.761	0.881	[0.552,1.406]	0.596	0.831
rs4994	ADRB3	C	0.094	0.959	[0.632,1.457]	0.845	1.181	[0.582,2.397]	0.645	1.231	[0.57,2.658]	0.596	0.869
rs1149901	FLJ45983	T	0.229	1.091	[0.838,1.42]	0.517	0.943	[0.567,1.568]	0.820	0.864	[0.503,1.485]	0.597	0.772
rs1358312	PPP3CA	A	0.180	0.932	[0.676,1.287]	0.671	0.787	[0.437,1.417]	0.424	0.844	[0.449,1.586]	0.598	0.691
rs2271010	ATF6	C	0.129	1.170	[0.837,1.634]	0.359	1.379	[0.779,2.44]	0.270	1.179	[0.639,2.174]	0.598	0.412
rs853790	ABCB11	T	0.489	1.137	[0.9,1.436]	0.283	1.006	[0.659,1.536]	0.979	0.885	[0.562,1.394]	0.598	0.558
rs5769	TBXAS1	G	0.010	1.199	[0.382,3.759]	0.756	0.677	[0.094,4.878]	0.699	0.565	[0.067,4.738]	0.599	0.865
rs954619	CCND1	T	0.034	2.125	[1.112,4.061]	0.023	1.556	[0.524,4.621]	0.426	0.732	[0.23,2.336]	0.599	0.069
rs2069830	IL6	T	0.016	0.569	[0.176,1.839]	0.346	0.905	[0.224,3.661]	0.889	1.590	[0.28,9.036]	0.601	0.641
rs483536	NFKBIE	T	0.339	1.070	[0.838,1.367]	0.586	0.942	[0.603,1.473]	0.793	0.880	[0.545,1.42]	0.601	0.813
rs472344	ANKRD49	T	0.490	1.012	[0.805,1.272]	0.918	0.899	[0.594,1.36]	0.615	0.888	[0.57,1.384]	0.601	0.867
rs1800896	IL10	G	0.436	0.945	[0.746,1.197]	0.640	0.834	[0.539,1.292]	0.417	0.883	[0.553,1.41]	0.601	0.674
rs8187737	SLC28A1	T	0.014	1.101	[0.391,3.103]	0.855	0.613	[0.077,4.856]	0.643	0.557	[0.062,5.024]	0.602	0.873
rs6180	GHR	C	0.451	0.874	[0.685,1.116]	0.280	0.774	[0.506,1.183]	0.236	0.885	[0.559,1.401]	0.602	0.323
rs2020924	PLAT	C	0.109	0.735	[0.492,1.096]	0.131	0.900	[0.446,1.818]	0.769	1.225	[0.571,2.632]	0.602	0.318
rs1799999	PPP1R3A	T	0.146	1.006	[0.734,1.379]	0.970	1.176	[0.685,2.019]	0.557	1.169	[0.65,2.104]	0.603	0.841
rs16900023	C6orf26	T	0.032	0.722	[0.341,1.531]	0.396	1.009	[0.334,3.047]	0.987	1.397	[0.396,4.926]	0.603	0.693
rs3731258	CDK6	T	0.031	1.639	[0.811,3.312]	0.168	2.180	[0.816,5.821]	0.120	1.330	[0.455,3.888]	0.603	0.171
rs875740	ABCC1	G	0.373	1.142	[0.898,1.452]	0.279	1.009	[0.651,1.562]	0.969	0.883	[0.553,1.41]	0.603	0.553
rs11818239	BMPR1A	A	0.021	1.789	[0.691,4.629]	0.231	2.663	[0.695,10.2]	0.153	1.489	[0.33,6.711]	0.604	0.226
rs3770596	ABCB11	A	0.445	0.875	[0.688,1.112]	0.274	0.989	[0.642,1.525]	0.960	1.131	[0.71,1.8]	0.605	0.547
rs1133818	MYCBPAP	C	0.260	0.832	[0.634,1.09]	0.181	0.952	[0.592,1.53]	0.839	1.145	[0.685,1.914]	0.606	0.409

rs1319869	IGF1R	C	0.197	1.205	[0.879,1.653]	0.247	1.028	[0.585,1.807]	0.924	0.853	[0.466,1.562]	0.606	0.510
rs3177980	SELL	C	0.227	0.906	[0.69,1.19]	0.477	1.038	[0.643,1.676]	0.878	1.146	[0.682,1.925]	0.607	0.753
rs216902	VWF	A	0.389	1.063	[0.843,1.341]	0.606	1.196	[0.786,1.82]	0.403	1.125	[0.718,1.765]	0.607	0.650
rs12221497	NR1H3	A	0.114	1.092	[0.767,1.554]	0.625	0.895	[0.436,1.838]	0.762	0.819	[0.384,1.749]	0.607	0.828
rs1587241	PPP3CA	G	0.322	0.855	[0.659,1.109]	0.237	0.747	[0.462,1.206]	0.233	0.874	[0.522,1.462]	0.608	0.287
rs17110453	CYP2C8	C	0.119	1.274	[0.903,1.798]	0.167	1.059	[0.54,2.076]	0.868	0.831	[0.409,1.689]	0.608	0.385
rs2017662	TNFRSF17	T	0.087	1.093	[0.704,1.695]	0.692	0.877	[0.4,1.925]	0.744	0.803	[0.346,1.861]	0.608	0.857
rs3760413	EME1	T	0.126	0.938	[0.671,1.311]	0.706	1.110	[0.607,2.03]	0.735	1.184	[0.62,2.261]	0.609	0.861
rs1801274	FCGR2A	C	0.491	1.009	[0.801,1.271]	0.941	1.131	[0.752,1.701]	0.554	1.121	[0.722,1.741]	0.610	0.839
rs585800	BHMT	T	0.234	1.040	[0.782,1.382]	0.790	1.198	[0.719,1.998]	0.488	1.153	[0.667,1.994]	0.611	0.775
rs3743591	TNFRSF17	G	0.088	1.074	[0.693,1.665]	0.748	0.865	[0.394,1.896]	0.717	0.805	[0.347,1.864]	0.612	0.871
rs1634499	CCL3	G	0.229	0.904	[0.683,1.198]	0.484	1.036	[0.637,1.686]	0.885	1.146	[0.676,1.941]	0.613	0.760
rs10407115	PPAP2C	A	0.434	0.980	[0.773,1.241]	0.864	1.103	[0.718,1.696]	0.654	1.126	[0.71,1.786]	0.613	0.880
rs1532268	MTRR	A	0.343	1.108	[0.869,1.414]	0.409	0.980	[0.627,1.531]	0.929	0.884	[0.549,1.425]	0.614	0.696
rs1063147	BLM	T	0.175	0.824	[0.598,1.135]	0.235	0.961	[0.554,1.665]	0.886	1.166	[0.642,2.119]	0.614	0.494
rs3732378	CX3CR1	A	0.157	1.094	[0.789,1.517]	0.589	1.283	[0.723,2.277]	0.395	1.173	[0.632,2.175]	0.614	0.637
rs20579	LIG1	T	0.157	0.771	[0.549,1.084]	0.135	0.648	[0.346,1.213]	0.175	0.840	[0.427,1.652]	0.614	0.162
rs4809957	CYP24A1	G	0.265	0.942	[0.713,1.244]	0.674	1.077	[0.665,1.745]	0.762	1.144	[0.678,1.929]	0.614	0.856
rs776740	CYP3A7	A	0.021	1.010	[0.426,2.397]	0.982	0.663	[0.148,2.97]	0.591	0.656	[0.127,3.381]	0.615	0.862
rs2687080	CYP3A7	C	0.021	1.010	[0.426,2.396]	0.982	0.663	[0.148,2.97]	0.591	0.656	[0.127,3.382]	0.615	0.862
rs5743557	TLR1	T	0.168	0.907	[0.657,1.253]	0.554	1.063	[0.6,1.885]	0.834	1.172	[0.632,2.174]	0.615	0.804
rs907806	IGF1R	G	0.149	1.123	[0.803,1.57]	0.500	1.314	[0.743,2.327]	0.348	1.171	[0.633,2.167]	0.615	0.558
rs9403723	SIM1	G	0.338	0.868	[0.68,1.108]	0.256	0.766	[0.486,1.208]	0.252	0.883	[0.542,1.437]	0.616	0.318
rs6508	WIT1	A	0.122	0.861	[0.578,1.282]	0.461	0.705	[0.343,1.45]	0.342	0.819	[0.375,1.787]	0.616	0.524
rs2062541	ABCC1	C	0.424	1.097	[0.857,1.404]	0.460	1.241	[0.792,1.945]	0.346	1.131	[0.698,1.832]	0.617	0.531
rs11574138	VDR	G	0.017	0.852	[0.277,2.619]	0.779	0.478	[0.059,3.86]	0.488	0.561	[0.058,5.408]	0.617	0.769
rs8034835	CYP19A1	G	0.473	0.944	[0.743,1.199]	0.635	1.062	[0.691,1.631]	0.785	1.125	[0.709,1.785]	0.617	0.843
rs1134921	GAK	A	0.120	1.067	[0.752,1.513]	0.717	0.892	[0.458,1.736]	0.736	0.836	[0.414,1.689]	0.617	0.865
rs2238335	BLM	C	0.051	1.600	[0.935,2.738]	0.086	2.006	[0.88,4.575]	0.098	1.254	[0.516,3.044]	0.618	0.094
rs3743527	ABCC1	T	0.199	0.935	[0.691,1.265]	0.662	1.086	[0.629,1.873]	0.767	1.162	[0.645,2.091]	0.618	0.853
rs268687	SERTAD1	A	0.408	1.261	[0.977,1.627]	0.075	1.430	[0.9,2.272]	0.130	1.134	[0.692,1.86]	0.618	0.091
rs2069832	IL6	A	0.324	1.189	[0.937,1.51]	0.155	1.052	[0.67,1.653]	0.824	0.885	[0.547,1.431]	0.618	0.363
rs6019	F5	C	0.096	1.248	[0.811,1.919]	0.314	1.519	[0.743,3.104]	0.252	1.217	[0.561,2.642]	0.619	0.365
rs1419745	CYP3A5	G	0.101	1.037	[0.665,1.619]	0.871	1.260	[0.625,2.541]	0.518	1.215	[0.565,2.613]	0.619	0.810
rs1709082	CYP2A13	G	0.146	1.180	[0.823,1.692]	0.369	0.991	[0.523,1.877]	0.977	0.840	[0.422,1.671]	0.619	0.659
rs246	OPCML	A	0.221	0.951	[0.718,1.259]	0.724	1.085	[0.67,1.758]	0.740	1.141	[0.677,1.923]	0.620	0.872
rs3097	CYP11B2	A	0.226	0.869	[0.653,1.155]	0.333	1.001	[0.594,1.687]	0.997	1.153	[0.658,2.021]	0.620	0.620
rs11188254	PDLIM1	A	0.345	1.031	[0.799,1.331]	0.814	0.912	[0.58,1.433]	0.689	0.884	[0.544,1.438]	0.620	0.883
rs6330	NGF	T	0.392	0.983	[0.771,1.254]	0.892	1.110	[0.709,1.739]	0.647	1.129	[0.698,1.826]	0.620	0.883
rs1063857	VWF	C	0.384	1.077	[0.848,1.368]	0.543	1.209	[0.79,1.852]	0.382	1.123	[0.71,1.775]	0.621	0.606
rs10836230	CAT	T	0.317	0.810	[0.621,1.057]	0.121	0.708	[0.429,1.168]	0.176	0.874	[0.511,1.493]	0.621	0.152

rs13706	CDC6	A	0.174	1.052	[0.762,1.453]	0.757	1.222	[0.704,2.12]	0.475	1.161	[0.641,2.103]	0.621	0.760
rs2296869	SETX	G	0.263	1.170	[0.888,1.541]	0.264	1.024	[0.624,1.682]	0.924	0.875	[0.515,1.488]	0.623	0.534
rs1514346	IRF4	A	0.185	1.154	[0.847,1.572]	0.363	0.992	[0.565,1.741]	0.977	0.859	[0.47,1.572]	0.623	0.654
rs12680	LOC100129773	C	0.117	1.438	[0.95,2.177]	0.086	1.179	[0.561,2.477]	0.663	0.820	[0.372,1.809]	0.623	0.225
rs9282616	BLM	G	0.063	1.031	[0.625,1.7]	0.906	1.278	[0.589,2.772]	0.535	1.240	[0.526,2.92]	0.623	0.825
rs16945474	PHKB	G	0.054	1.087	[0.64,1.845]	0.757	0.836	[0.314,2.228]	0.720	0.769	[0.269,2.195]	0.624	0.879
rs2282079	LOC100130458	A	0.059	0.855	[0.5,1.463]	0.568	0.644	[0.224,1.855]	0.415	0.753	[0.242,2.341]	0.624	0.637
rs8305	POLI	G	0.251	0.956	[0.727,1.257]	0.748	0.834	[0.5,1.392]	0.488	0.873	[0.506,1.506]	0.624	0.767
rs35596	ABCC1	C	0.299	0.881	[0.671,1.158]	0.365	1.001	[0.625,1.603]	0.996	1.136	[0.682,1.892]	0.625	0.658
rs7871785	PSMB7	G	0.444	0.988	[0.779,1.253]	0.920	1.107	[0.723,1.695]	0.640	1.121	[0.709,1.771]	0.626	0.884
rs17683288	ARHGEF10	G	0.057	0.682	[0.397,1.172]	0.166	0.880	[0.345,2.247]	0.789	1.291	[0.462,3.603]	0.626	0.380
rs215048	ABCC1	A	0.130	1.249	[0.888,1.757]	0.201	1.052	[0.546,2.025]	0.880	0.842	[0.421,1.684]	0.626	0.442
rs17037390	MTHFR	A	0.171	0.855	[0.621,1.176]	0.335	0.726	[0.394,1.338]	0.305	0.850	[0.441,1.637]	0.627	0.412
rs230547	NFKB1	T	0.102	0.949	[0.649,1.389]	0.788	1.125	[0.599,2.114]	0.714	1.185	[0.598,2.351]	0.627	0.886
rs1805075	IGF2R	G	0.058	0.773	[0.459,1.302]	0.333	0.996	[0.387,2.564]	0.993	1.288	[0.464,3.572]	0.627	0.622
rs2228529	ERCC6	G	0.196	0.965	[0.718,1.297]	0.813	1.109	[0.658,1.87]	0.699	1.149	[0.656,2.013]	0.627	0.887
rs1126670	ADH4	G	0.270	0.908	[0.702,1.175]	0.463	1.029	[0.641,1.652]	0.905	1.134	[0.682,1.883]	0.628	0.746
rs163078	FAM82A	T	0.369	1.072	[0.844,1.361]	0.569	0.953	[0.611,1.487]	0.833	0.889	[0.552,1.432]	0.629	0.815
rs2137975	DPYD	C	0.320	1.009	[0.787,1.295]	0.943	0.892	[0.557,1.427]	0.633	0.884	[0.534,1.461]	0.630	0.884
rs504348	ABCC1	G	0.239	1.057	[0.784,1.425]	0.716	1.209	[0.73,2.001]	0.461	1.144	[0.662,1.975]	0.630	0.737
rs954923	DPYD	T	0.019	2.522	[1.144,5.558]	0.022	1.792	[0.479,6.704]	0.387	0.710	[0.176,2.86]	0.630	0.066
rs2292334	SLC22A3	T	0.358	0.853	[0.667,1.091]	0.205	0.757	[0.478,1.197]	0.234	0.887	[0.544,1.447]	0.631	0.265
rs28365094	CYP3A5	G	0.087	1.087	[0.728,1.625]	0.683	0.879	[0.386,2.002]	0.759	0.808	[0.339,1.926]	0.631	0.861
rs1061646	FANCA	T	0.366	1.317	[1.039,1.669]	0.023	1.471	[0.966,2.239]	0.072	1.117	[0.712,1.751]	0.631	0.025
rs1456432	CYP1A1	G	0.233	1.195	[0.906,1.575]	0.207	1.049	[0.64,1.722]	0.849	0.878	[0.517,1.493]	0.631	0.451
rs1801282	PPARG	G	0.105	1.012	[0.694,1.477]	0.949	1.208	[0.619,2.358]	0.580	1.193	[0.58,2.456]	0.632	0.858
rs2266780	FMO3	G	0.157	1.060	[0.78,1.439]	0.712	1.220	[0.71,2.099]	0.472	1.152	[0.644,2.059]	0.633	0.745
rs2020860	FMO2	C	0.080	1.053	[0.663,1.673]	0.826	1.278	[0.623,2.619]	0.504	1.213	[0.549,2.681]	0.634	0.794
rs2070904	CYP2D6	G	0.446	1.142	[0.908,1.438]	0.256	1.028	[0.688,1.538]	0.892	0.900	[0.584,1.388]	0.634	0.524
rs828052	DPYD	T	0.401	0.887	[0.703,1.121]	0.315	0.993	[0.644,1.533]	0.975	1.119	[0.704,1.781]	0.634	0.601
rs9997	KLHL22	C	0.347	1.048	[0.815,1.347]	0.714	1.178	[0.754,1.839]	0.472	1.124	[0.695,1.818]	0.634	0.744
rs9862	SYN3	T	0.434	0.818	[0.641,1.044]	0.107	0.728	[0.464,1.141]	0.166	0.889	[0.549,1.442]	0.634	0.136
rs4443426	MGC42105	C	0.471	0.859	[0.684,1.079]	0.191	0.770	[0.506,1.173]	0.223	0.897	[0.572,1.406]	0.635	0.245
rs2235074	ABCB1	T	0.048	0.539	[0.273,1.062]	0.074	0.724	[0.245,2.143]	0.560	1.343	[0.398,4.534]	0.635	0.188
rs1805016	IL4R	G	0.087	0.638	[0.379,1.077]	0.092	0.788	[0.37,1.677]	0.536	1.234	[0.518,2.935]	0.635	0.222
rs1464645	BCL6	T	0.186	1.125	[0.827,1.53]	0.452	1.286	[0.771,2.143]	0.335	1.143	[0.658,1.986]	0.636	0.523
rs2229032	ATR	A	0.148	0.856	[0.616,1.191]	0.356	0.724	[0.377,1.39]	0.332	0.846	[0.423,1.693]	0.636	0.449
rs854555	PON1	A	0.431	0.788	[0.621,0.999]	0.049	0.880	[0.575,1.345]	0.554	1.116	[0.707,1.764]	0.637	0.137
rs3088142	DUSP13	T	0.491	1.079	[0.854,1.363]	0.524	0.967	[0.633,1.478]	0.878	0.897	[0.569,1.412]	0.638	0.792
rs1329568	LOC100130458	A	0.034	1.040	[0.51,2.119]	0.914	0.747	[0.212,2.635]	0.651	0.719	[0.182,2.842]	0.638	0.891
rs1395119	SIM1	T	0.338	0.862	[0.675,1.1]	0.233	0.767	[0.486,1.209]	0.253	0.890	[0.547,1.448]	0.638	0.301

rs679620	MMP3	A	0.487	0.972	[0.767,1.233]	0.816	1.083	[0.715,1.64]	0.708	1.114	[0.711,1.744]	0.638	0.894
rs2074570	IL4R	G	0.063	0.929	[0.571,1.512]	0.767	0.735	[0.298,1.815]	0.504	0.791	[0.298,2.103]	0.639	0.781
rs25680	CD27	A	0.204	0.981	[0.73,1.319]	0.901	1.122	[0.668,1.884]	0.663	1.143	[0.654,2]	0.639	0.893
rs978458	IGF1	A	0.281	0.801	[0.61,1.051]	0.109	0.907	[0.56,1.468]	0.690	1.133	[0.673,1.907]	0.640	0.273
rs4987131	CYBA	C	0.020	0.602	[0.198,1.829]	0.371	0.350	[0.044,2.799]	0.322	0.581	[0.06,5.655]	0.640	0.439
rs2305706	CYP19A1	G	0.251	1.437	[1.062,1.945]	0.019	1.252	[0.729,2.15]	0.415	0.871	[0.489,1.553]	0.640	0.057
rs2069443	CDK5	C	0.318	0.720	[0.552,0.938]	0.015	0.813	[0.507,1.303]	0.390	1.129	[0.678,1.88]	0.640	0.045
rs2011404	UGT1A10	T	0.127	1.066	[0.749,1.516]	0.723	1.248	[0.673,2.313]	0.482	1.171	[0.604,2.27]	0.640	0.757
rs1064796	CYP4F11	C	0.256	1.040	[0.808,1.339]	0.762	0.920	[0.568,1.491]	0.735	0.885	[0.528,1.481]	0.641	0.888
rs11569046	EGF	C	0.019	0.600	[0.201,1.787]	0.359	0.354	[0.047,2.663]	0.313	0.590	[0.064,5.417]	0.641	0.422
rs887241	ALDH3A1	T	0.331	0.964	[0.746,1.246]	0.782	0.854	[0.529,1.379]	0.518	0.885	[0.53,1.478]	0.642	0.797
rs2303425	MSH2	C	0.108	0.935	[0.639,1.367]	0.727	1.107	[0.575,2.13]	0.761	1.184	[0.581,2.416]	0.642	0.884
rs3218273	IL2RB	T	0.012	0.930	[0.241,3.58]	0.915	1.488	[0.277,7.984]	0.643	1.601	[0.221,11.609]	0.642	0.883
rs1380657	MYCBPAP	G	0.263	0.826	[0.63,1.083]	0.166	0.933	[0.579,1.503]	0.777	1.130	[0.675,1.893]	0.642	0.381
rs2069807	IL5	T	0.033	1.744	[0.833,3.648]	0.140	1.286	[0.396,4.174]	0.676	0.737	[0.204,2.664]	0.642	0.331
rs2193587	DGKG	G	0.202	1.086	[0.813,1.449]	0.578	0.943	[0.54,1.647]	0.837	0.869	[0.481,1.571]	0.642	0.823
rs6717546	UGT1A1	A	0.379	1.193	[0.917,1.55]	0.188	1.062	[0.677,1.666]	0.792	0.891	[0.547,1.451]	0.642	0.419
rs207908	XRCC5	T	0.485	1.128	[0.892,1.427]	0.313	1.016	[0.671,1.538]	0.941	0.900	[0.576,1.407]	0.644	0.600
rs9482	ATF6	A	0.322	1.049	[0.813,1.354]	0.712	1.175	[0.752,1.835]	0.479	1.120	[0.693,1.809]	0.645	0.751
rs1138294	MAP3K6	T	0.325	0.926	[0.72,1.191]	0.549	0.823	[0.516,1.313]	0.414	0.889	[0.54,1.465]	0.645	0.635
rs1144945	MDM2	T	0.020	0.891	[0.353,2.247]	0.807	0.539	[0.073,4.005]	0.546	0.606	[0.072,5.107]	0.645	0.818
rs207906	XRCC5	A	0.124	0.867	[0.603,1.247]	0.441	1.016	[0.543,1.9]	0.961	1.172	[0.595,2.308]	0.647	0.734
rs275652	AGTR1	C	0.186	0.801	[0.584,1.1]	0.170	0.919	[0.536,1.577]	0.760	1.147	[0.637,2.068]	0.647	0.387
rs4072037	MUC1	G	0.419	0.794	[0.631,1]	0.050	0.881	[0.583,1.332]	0.548	1.109	[0.711,1.73]	0.648	0.140
rs448012	FLT4	G	0.389	0.842	[0.653,1.087]	0.187	0.941	[0.607,1.458]	0.785	1.117	[0.694,1.797]	0.649	0.417
rs20541	IL13	T	0.204	1.053	[0.801,1.386]	0.710	0.925	[0.546,1.567]	0.771	0.878	[0.501,1.538]	0.649	0.880
rs6761641	PASK	C	0.194	0.967	[0.712,1.312]	0.828	1.098	[0.662,1.822]	0.718	1.136	[0.656,1.967]	0.650	0.901
rs4757707	PTPN5	C	0.338	1.078	[0.822,1.414]	0.589	1.213	[0.753,1.955]	0.427	1.126	[0.674,1.879]	0.651	0.666
rs848291	FANCL	T	0.334	1.014	[0.789,1.303]	0.916	0.903	[0.566,1.441]	0.669	0.891	[0.54,1.469]	0.651	0.900
rs963981	KIAA1804	C	0.200	1.067	[0.802,1.421]	0.657	0.935	[0.548,1.596]	0.805	0.876	[0.495,1.552]	0.651	0.864
rs7909236	CYP2C8	T	0.212	1.020	[0.761,1.366]	0.895	1.161	[0.687,1.964]	0.577	1.139	[0.649,1.999]	0.651	0.855
rs1801702	APOB	C	0.043	1.067	[0.605,1.882]	0.823	0.796	[0.239,2.652]	0.710	0.746	[0.209,2.659]	0.651	0.900
rs10018297	Intergenic	G	0.015	1.398	[0.506,3.858]	0.518	1.986	[0.509,7.747]	0.323	1.421	[0.309,6.541]	0.652	0.552
rs1017186	GSTZ1	G	0.180	1.026	[0.756,1.392]	0.870	0.888	[0.491,1.604]	0.693	0.865	[0.461,1.623]	0.652	0.903
rs1760217	DPYD	C	0.218	0.920	[0.692,1.222]	0.565	0.806	[0.472,1.377]	0.431	0.876	[0.494,1.554]	0.652	0.654
rs5297	CYP11B1	C	0.112	1.088	[0.735,1.609]	0.674	0.913	[0.45,1.854]	0.801	0.839	[0.392,1.796]	0.652	0.871
rs529126	MRE11A	A	0.279	1.172	[0.905,1.518]	0.228	1.046	[0.659,1.661]	0.847	0.893	[0.545,1.463]	0.653	0.483
rs4148951	CHST3	A	0.033	1.950	[0.949,4.005]	0.069	1.461	[0.456,4.676]	0.523	0.749	[0.213,2.637]	0.653	0.181
rs12022378	AP4B1	T	0.187	1.357	[1.013,1.819]	0.041	1.184	[0.674,2.08]	0.557	0.872	[0.48,1.584]	0.653	0.118
rs2230517	MERTK	A	0.061	1.176	[0.682,2.028]	0.560	1.468	[0.608,3.546]	0.394	1.248	[0.474,3.285]	0.653	0.624
rs1130371	CCL3	T	0.221	0.906	[0.677,1.211]	0.504	1.028	[0.615,1.719]	0.915	1.136	[0.652,1.979]	0.654	0.784

rs1544410	VDR	A	0.366	0.851	[0.667,1.086]	0.196	0.948	[0.612,1.469]	0.811	1.114	[0.695,1.784]	0.654	0.432
rs1057056	CHST10	A	0.078	1.413	[0.86,2.32]	0.172	1.148	[0.495,2.659]	0.748	0.812	[0.327,2.017]	0.654	0.391
rs2072352	BLM	T	0.341	0.873	[0.677,1.127]	0.297	0.782	[0.5,1.224]	0.282	0.896	[0.552,1.452]	0.654	0.375
rs1990277	ARVCF	A	0.371	0.990	[0.773,1.269]	0.938	0.886	[0.561,1.399]	0.603	0.895	[0.549,1.458]	0.655	0.874
rs3740526	MMS19	A	0.368	1.235	[0.965,1.579]	0.094	1.376	[0.881,2.149]	0.160	1.115	[0.691,1.798]	0.655	0.122
rs2241529	DKK1	A	0.435	1.131	[0.89,1.436]	0.314	1.018	[0.66,1.569]	0.936	0.900	[0.567,1.429]	0.656	0.601
rs3747806	ABCB4	C	0.071	1.085	[0.672,1.751]	0.738	0.880	[0.375,2.066]	0.769	0.811	[0.322,2.039]	0.656	0.892
rs7746988	PPARD	C	0.067	0.814	[0.467,1.416]	0.466	1.010	[0.431,2.367]	0.982	1.241	[0.48,3.21]	0.656	0.761
rs13392272	APOB	T	0.419	0.995	[0.778,1.272]	0.968	0.892	[0.568,1.399]	0.618	0.896	[0.554,1.451]	0.656	0.883
rs3138047	NFKBIA	T	0.218	0.803	[0.6,1.075]	0.140	0.913	[0.543,1.533]	0.730	1.136	[0.648,1.992]	0.656	0.333
rs4646316	COMT	T	0.227	0.895	[0.67,1.196]	0.454	0.785	[0.458,1.347]	0.380	0.877	[0.492,1.563]	0.657	0.555
rs1788817	C18orf8	G	0.488	1.107	[0.873,1.402]	0.401	0.999	[0.656,1.52]	0.995	0.902	[0.573,1.42]	0.657	0.698
rs11030918	RRM1	C	0.321	0.860	[0.675,1.095]	0.220	0.955	[0.619,1.475]	0.837	1.111	[0.696,1.774]	0.658	0.471
rs16879427	PSKH2	C	0.058	0.616	[0.315,1.207]	0.158	0.793	[0.299,2.105]	0.642	1.287	[0.422,3.928]	0.658	0.353
rs496190	MRE11A	C	0.496	1.083	[0.861,1.364]	0.495	0.980	[0.646,1.487]	0.924	0.904	[0.579,1.413]	0.659	0.777
rs903880	ABCC1	A	0.308	1.006	[0.758,1.333]	0.969	0.889	[0.534,1.482]	0.652	0.884	[0.511,1.529]	0.660	0.899
rs10895068	PGR	A	0.045	1.645	[0.968,2.796]	0.066	2.007	[0.874,4.611]	0.101	1.220	[0.503,2.957]	0.660	0.081
rs17037102	DKK2	A	0.094	1.120	[0.769,1.632]	0.554	0.938	[0.444,1.981]	0.867	0.837	[0.38,1.847]	0.660	0.814
rs152029	ABCC1	G	0.184	1.247	[0.901,1.728]	0.183	1.086	[0.612,1.927]	0.777	0.871	[0.469,1.615]	0.661	0.411
rs700241	DAB2	A	0.036	1.254	[0.682,2.309]	0.467	0.949	[0.294,3.061]	0.931	0.757	[0.218,2.626]	0.661	0.754
rs939336	ABCC5	A	0.394	1.001	[0.79,1.269]	0.992	1.108	[0.726,1.691]	0.633	1.107	[0.703,1.743]	0.661	0.891
rs1800802	MGP	C	0.173	1.215	[0.903,1.634]	0.198	1.064	[0.611,1.855]	0.826	0.876	[0.485,1.582]	0.661	0.436
rs3783615	VCAM1	T	0.010	0.719	[0.148,3.491]	0.683	1.272	[0.14,11.531]	0.831	1.768	[0.138,22.605]	0.661	0.888
rs1181795	PPARG	T	0.072	1.138	[0.729,1.777]	0.569	1.365	[0.64,2.911]	0.420	1.200	[0.53,2.714]	0.662	0.653
rs11045819	SLCO1B1	A	0.142	0.725	[0.512,1.026]	0.070	0.616	[0.313,1.214]	0.162	0.851	[0.412,1.757]	0.662	0.094
rs13166360	ADCY2	T	0.184	0.788	[0.576,1.078]	0.136	0.904	[0.51,1.604]	0.731	1.147	[0.618,2.129]	0.663	0.326
rs7957203	SLCO1A2	T	0.306	1.027	[0.796,1.324]	0.837	0.917	[0.569,1.478]	0.722	0.893	[0.537,1.486]	0.663	0.908
rs2227306	IL8	T	0.385	0.943	[0.739,1.204]	0.639	1.046	[0.678,1.614]	0.837	1.109	[0.696,1.769]	0.663	0.863
rs3856748	CTNNB1	T	0.016	2.266	[0.805,6.374]	0.121	3.211	[0.756,13.631]	0.114	1.417	[0.295,6.807]	0.663	0.137
rs16975748	LIPE	T	0.018	0.965	[0.343,2.709]	0.945	1.379	[0.342,5.557]	0.651	1.430	[0.286,7.15]	0.663	0.895
rs3217805	CCND2	G	0.351	0.949	[0.74,1.216]	0.680	1.056	[0.674,1.656]	0.811	1.113	[0.687,1.804]	0.664	0.878
rs1669703	ADRB3	T	0.484	0.850	[0.672,1.075]	0.175	0.769	[0.506,1.171]	0.221	0.905	[0.577,1.42]	0.665	0.233
rs3217773	CCNA2	C	0.288	0.997	[0.77,1.291]	0.979	1.114	[0.697,1.78]	0.653	1.117	[0.676,1.847]	0.665	0.900
rs6084	LIPC	G	0.447	0.888	[0.702,1.122]	0.318	0.803	[0.527,1.224]	0.308	0.905	[0.576,1.422]	0.665	0.409
rs3136748	POLB	T	0.081	1.044	[0.659,1.653]	0.856	0.860	[0.385,1.923]	0.714	0.825	[0.344,1.975]	0.665	0.911
rs1051266	SLC19A1	A	0.462	0.975	[0.76,1.25]	0.840	0.875	[0.554,1.381]	0.566	0.898	[0.55,1.465]	0.665	0.841
rs2276078	HSPA8	G	0.017	1.138	[0.475,2.73]	0.772	1.569	[0.419,5.872]	0.503	1.379	[0.321,5.925]	0.666	0.786
rs1138357	BCL2A1	A	0.287	1.003	[0.778,1.292]	0.984	1.115	[0.712,1.748]	0.634	1.112	[0.685,1.806]	0.666	0.892
rs4646453	CYP3A5	T	0.039	0.829	[0.428,1.604]	0.577	1.068	[0.37,3.084]	0.903	1.289	[0.406,4.094]	0.666	0.836
rs1334811	TEK	A	0.055	0.826	[0.476,1.433]	0.496	1.028	[0.417,2.532]	0.953	1.244	[0.461,3.361]	0.667	0.785
rs6874941	CART	C	0.205	0.965	[0.716,1.301]	0.815	0.850	[0.498,1.451]	0.552	0.881	[0.495,1.568]	0.667	0.828

rs2111699	GSTZ1	G	0.308	1.031	[0.804,1.321]	0.811	0.926	[0.587,1.461]	0.741	0.898	[0.551,1.464]	0.667	0.908
rs2069843	IL6	A	0.039	1.106	[0.581,2.104]	0.760	1.403	[0.526,3.738]	0.498	1.269	[0.429,3.752]	0.667	0.779
rs2162679	IGF1	G	0.221	0.905	[0.677,1.211]	0.503	1.019	[0.619,1.679]	0.940	1.126	[0.656,1.933]	0.667	0.788
rs598599	MRE11A	A	0.269	1.163	[0.894,1.512]	0.261	1.037	[0.636,1.691]	0.883	0.892	[0.53,1.501]	0.667	0.532
rs2246176	RAD50	C	0.286	1.080	[0.822,1.42]	0.579	0.959	[0.578,1.593]	0.873	0.888	[0.516,1.527]	0.668	0.833
rs7732671	PPARGC1B	C	0.106	1.171	[0.81,1.694]	0.401	1.003	[0.517,1.946]	0.993	0.856	[0.421,1.741]	0.668	0.698
rs9282718	IGF1R	G	0.062	1.274	[0.806,2.013]	0.299	1.520	[0.719,3.213]	0.273	1.193	[0.533,2.673]	0.668	0.379
rs6271	DBH	T	0.053	1.255	[0.775,2.034]	0.356	1.013	[0.4,2.566]	0.978	0.807	[0.303,2.151]	0.668	0.648
rs2479383	PSMB4	C	0.164	1.028	[0.755,1.4]	0.859	1.170	[0.673,2.036]	0.577	1.138	[0.63,2.057]	0.668	0.852
rs1043424	PINK1	C	0.280	0.789	[0.6,1.036]	0.089	0.882	[0.549,1.419]	0.606	1.119	[0.669,1.872]	0.668	0.225
rs1051061	VRK2	G	0.314	1.040	[0.811,1.333]	0.758	0.935	[0.593,1.474]	0.772	0.899	[0.552,1.464]	0.669	0.901
rs3258	FDFT1	C	0.377	1.018	[0.8,1.296]	0.884	1.129	[0.726,1.754]	0.591	1.108	[0.691,1.778]	0.670	0.863
rs5960	F10	C	0.218	1.032	[0.76,1.4]	0.842	1.169	[0.684,1.999]	0.567	1.134	[0.637,2.019]	0.670	0.843
rs4925	GSTO1	A	0.261	0.802	[0.608,1.059]	0.119	0.710	[0.421,1.199]	0.200	0.885	[0.506,1.55]	0.670	0.164
rs2007231	CSDE1	C	0.307	0.829	[0.639,1.077]	0.161	0.738	[0.447,1.22]	0.236	0.890	[0.521,1.52]	0.670	0.225
rs2069783	IL3	C	0.033	1.041	[0.478,2.267]	0.920	1.370	[0.446,4.21]	0.582	1.317	[0.369,4.697]	0.671	0.859
rs2008691	CYP19A1	G	0.208	1.517	[1.137,2.026]	0.005	1.346	[0.799,2.267]	0.264	0.887	[0.51,1.544]	0.672	0.015
rs2072651	TPP1	T	0.180	1.133	[0.837,1.534]	0.417	1.279	[0.761,2.15]	0.353	1.129	[0.645,1.976]	0.672	0.516
rs2277461	PSMA6	C	0.103	1.114	[0.721,1.722]	0.626	0.928	[0.425,2.029]	0.852	0.833	[0.358,1.938]	0.672	0.861
rs3213195	BLM	G	0.183	0.873	[0.641,1.19]	0.391	0.989	[0.58,1.686]	0.968	1.133	[0.636,2.018]	0.672	0.690
rs7801671	CYP3A4	A	0.037	1.299	[0.603,2.801]	0.504	0.969	[0.28,3.352]	0.961	0.746	[0.191,2.91]	0.673	0.791
rs1333728	DPYD	T	0.077	1.119	[0.73,1.713]	0.606	1.323	[0.638,2.745]	0.452	1.183	[0.542,2.582]	0.673	0.697
rs664143	ATM	T	0.411	0.937	[0.739,1.187]	0.588	0.849	[0.553,1.302]	0.453	0.906	[0.572,1.435]	0.674	0.684
rs1183768	SETX	C	0.270	1.135	[0.859,1.498]	0.372	1.012	[0.616,1.663]	0.961	0.892	[0.524,1.518]	0.674	0.669
rs541731	SPRY2	A	0.407	1.066	[0.843,1.348]	0.594	0.967	[0.634,1.476]	0.877	0.908	[0.577,1.428]	0.675	0.845
rs10846748	SCARB1	T	0.369	0.880	[0.688,1.126]	0.309	0.973	[0.629,1.504]	0.902	1.106	[0.691,1.77]	0.675	0.597
rs329003	PPP4R1	G	0.088	0.712	[0.459,1.104]	0.129	0.579	[0.233,1.436]	0.238	0.813	[0.309,2.143]	0.676	0.185
rs2228570	VDR	T	0.393	1.017	[0.8,1.292]	0.891	0.920	[0.594,1.426]	0.710	0.905	[0.566,1.446]	0.676	0.916
rs3802265	ZHX2	C	0.387	0.969	[0.761,1.233]	0.797	0.876	[0.564,1.361]	0.557	0.905	[0.564,1.451]	0.678	0.828
rs9332	MTRR	T	0.143	0.941	[0.656,1.349]	0.741	1.082	[0.591,1.981]	0.799	1.150	[0.595,2.221]	0.678	0.904
rs1413227	DPYD	A	0.285	0.982	[0.763,1.263]	0.887	1.090	[0.688,1.725]	0.714	1.110	[0.678,1.815]	0.679	0.918
rs3181366	TNFSF8	T	0.397	0.876	[0.689,1.115]	0.283	0.793	[0.51,1.233]	0.303	0.905	[0.565,1.451]	0.679	0.378
rs693	APOB	T	0.435	1.011	[0.793,1.289]	0.929	0.915	[0.588,1.423]	0.693	0.905	[0.564,1.452]	0.679	0.915
rs1530259	PPP3CA	G	0.410	1.108	[0.861,1.425]	0.428	1.230	[0.773,1.956]	0.383	1.110	[0.677,1.821]	0.679	0.545
rs17685	POR	T	0.255	0.801	[0.608,1.056]	0.115	0.714	[0.428,1.191]	0.197	0.891	[0.514,1.542]	0.679	0.159
rs3803390	SLC28A1	A	0.049	1.122	[0.689,1.829]	0.643	0.906	[0.339,2.42]	0.844	0.807	[0.291,2.237]	0.680	0.863
rs1152888	IRAK3	A	0.147	0.885	[0.614,1.276]	0.513	0.762	[0.391,1.482]	0.422	0.860	[0.421,1.76]	0.680	0.622
rs162036	MTRR	G	0.143	0.941	[0.656,1.349]	0.741	1.081	[0.59,1.979]	0.802	1.148	[0.594,2.218]	0.681	0.905
rs2844482	LTA	A	0.121	0.855	[0.594,1.229]	0.397	0.999	[0.501,1.993]	0.997	1.169	[0.556,2.456]	0.681	0.696
rs11574528	MCAT	T	0.223	0.754	[0.556,1.023]	0.069	0.848	[0.509,1.413]	0.527	1.125	[0.642,1.971]	0.681	0.177
rs351855	FGFR4	T	0.301	0.947	[0.72,1.247]	0.699	0.848	[0.518,1.388]	0.512	0.895	[0.527,1.521]	0.682	0.772

rs8190315	BID	G	0.026	1.264	[0.635,2.519]	0.505	0.923	[0.22,3.875]	0.913	0.730	[0.161,3.299]	0.682	0.785
rs12470143	SRD5A2	T	0.441	0.908	[0.713,1.157]	0.437	0.822	[0.525,1.286]	0.391	0.905	[0.56,1.461]	0.683	0.554
rs735943	EXO1	T	0.416	1.264	[1.003,1.592]	0.047	1.151	[0.757,1.749]	0.511	0.911	[0.581,1.426]	0.683	0.129
rs2857605	NFKBIL1	G	0.168	0.778	[0.561,1.081]	0.135	0.889	[0.492,1.607]	0.698	1.143	[0.603,2.165]	0.683	0.321
rs4725387	FASTK	G	0.084	1.128	[0.723,1.76]	0.596	1.343	[0.619,2.91]	0.455	1.190	[0.516,2.747]	0.683	0.691
rs886205	ALDH2	C	0.282	0.968	[0.718,1.304]	0.830	1.085	[0.656,1.795]	0.752	1.121	[0.649,1.936]	0.683	0.919
rs6028	F5	C	0.253	1.083	[0.828,1.418]	0.559	0.967	[0.58,1.613]	0.899	0.893	[0.518,1.539]	0.683	0.825
rs1296028	FDFT1	G	0.234	0.933	[0.701,1.242]	0.634	0.828	[0.484,1.415]	0.490	0.887	[0.5,1.575]	0.683	0.730
rs1805097	IRS2	A	0.295	0.852	[0.649,1.117]	0.246	0.950	[0.584,1.544]	0.835	1.115	[0.66,1.883]	0.684	0.510
rs2286007	WNK1	T	0.053	1.037	[0.624,1.722]	0.890	0.825	[0.292,2.332]	0.717	0.796	[0.265,2.388]	0.684	0.921
rs17680881	TACC3	A	0.240	0.815	[0.61,1.089]	0.166	0.914	[0.549,1.521]	0.729	1.121	[0.646,1.948]	0.684	0.378
rs875119	TTR	G	0.049	0.959	[0.561,1.638]	0.877	0.758	[0.262,2.196]	0.610	0.791	[0.255,2.451]	0.684	0.874
rs4988515	IGFBP1	T	0.072	0.914	[0.568,1.472]	0.712	0.754	[0.318,1.785]	0.520	0.824	[0.325,2.092]	0.684	0.780
rs2850992	PPP3CA	C	0.264	0.904	[0.691,1.184]	0.465	0.809	[0.489,1.338]	0.409	0.895	[0.523,1.53]	0.684	0.586
rs1035130	IL18R1	A	0.251	0.925	[0.705,1.214]	0.574	0.826	[0.497,1.374]	0.462	0.893	[0.518,1.54]	0.685	0.683
rs43037	PON2	C	0.349	1.000	[0.786,1.273]	0.998	1.103	[0.709,1.715]	0.664	1.102	[0.687,1.768]	0.686	0.908
rs3204953	LOC100128477	A	0.111	1.068	[0.741,1.538]	0.725	0.918	[0.461,1.828]	0.808	0.860	[0.413,1.788]	0.686	0.899
rs3813867	CYP2E1	C	0.043	1.099	[0.647,1.867]	0.727	1.335	[0.553,3.224]	0.520	1.215	[0.471,3.137]	0.687	0.789
rs4766003	C12orf32	A	0.412	1.074	[0.843,1.368]	0.563	1.183	[0.762,1.838]	0.454	1.102	[0.688,1.766]	0.687	0.674
rs762623	CDKN1A	A	0.128	0.856	[0.595,1.232]	0.402	0.738	[0.377,1.445]	0.375	0.862	[0.419,1.775]	0.687	0.517
rs348459	ALDH1A1	G	0.067	1.166	[0.727,1.871]	0.524	0.959	[0.392,2.345]	0.927	0.822	[0.317,2.135]	0.688	0.803
rs35597	ABCC1	A	0.436	0.808	[0.635,1.028]	0.083	0.890	[0.575,1.377]	0.601	1.101	[0.688,1.761]	0.688	0.213
rs1058932	CYP2C8	T	0.211	1.140	[0.855,1.52]	0.374	1.016	[0.603,1.713]	0.952	0.892	[0.51,1.56]	0.688	0.672
rs894817	IGF2R	A	0.333	0.757	[0.583,0.983]	0.037	0.838	[0.529,1.33]	0.454	1.107	[0.672,1.825]	0.689	0.101
rs2908004	WNT16	C	0.490	1.095	[0.859,1.394]	0.464	0.995	[0.643,1.54]	0.982	0.909	[0.569,1.451]	0.689	0.759
rs2973015	GHR	G	0.450	0.855	[0.673,1.087]	0.201	0.938	[0.617,1.425]	0.763	1.096	[0.698,1.722]	0.690	0.438
rs737693	MMP12	T	0.117	0.985	[0.68,1.427]	0.936	1.142	[0.582,2.238]	0.700	1.159	[0.561,2.394]	0.690	0.920
rs77905	DBH	T	0.461	1.081	[0.859,1.361]	0.506	0.987	[0.649,1.501]	0.951	0.913	[0.582,1.431]	0.691	0.792
rs12347	MTRR	T	0.142	0.955	[0.666,1.369]	0.801	1.091	[0.596,1.997]	0.779	1.143	[0.592,2.206]	0.691	0.920
rs1395	SLC5A6	G	0.381	1.067	[0.823,1.382]	0.625	1.180	[0.743,1.873]	0.484	1.106	[0.672,1.819]	0.691	0.724
rs4986993	NAT1	T	0.298	0.869	[0.663,1.139]	0.308	0.962	[0.605,1.53]	0.869	1.107	[0.669,1.831]	0.692	0.595
rs639838	PGR	C	0.332	0.961	[0.749,1.234]	0.756	0.870	[0.549,1.379]	0.553	0.905	[0.551,1.485]	0.692	0.815
rs1891073	CYP2C8	C	0.351	0.979	[0.765,1.254]	0.869	0.887	[0.56,1.404]	0.609	0.906	[0.554,1.481]	0.693	0.873
rs1934953	CYP2C8	G	0.350	0.979	[0.765,1.254]	0.869	0.887	[0.56,1.404]	0.609	0.906	[0.554,1.481]	0.693	0.873
rs1048943	CYP1A1	G	0.052	0.935	[0.499,1.754]	0.835	1.166	[0.424,3.208]	0.766	1.247	[0.417,3.723]	0.693	0.924
rs1802904	ATR	G	0.128	1.006	[0.704,1.438]	0.973	1.154	[0.612,2.177]	0.658	1.147	[0.581,2.266]	0.693	0.906
rs7102464	SBF2	T	0.080	0.961	[0.619,1.491]	0.859	0.802	[0.345,1.864]	0.608	0.835	[0.339,2.053]	0.694	0.871
rs1126672	ADH4	T	0.237	0.843	[0.643,1.104]	0.214	0.937	[0.573,1.534]	0.797	1.112	[0.655,1.891]	0.694	0.460
rs7393105	ABCC2	C	0.424	1.154	[0.9,1.48]	0.258	1.050	[0.678,1.628]	0.826	0.910	[0.567,1.459]	0.695	0.526
rs963065	PPP3CA	G	0.493	1.152	[0.903,1.469]	0.256	1.048	[0.675,1.627]	0.835	0.910	[0.567,1.46]	0.695	0.523
rs730365	PON2	T	0.157	1.010	[0.731,1.395]	0.954	1.138	[0.655,1.975]	0.646	1.127	[0.619,2.051]	0.695	0.900

rs543573	SETX	T	0.262	1.129	[0.856,1.488]	0.389	1.016	[0.619,1.667]	0.951	0.900	[0.529,1.529]	0.696	0.689
rs246217	ABCC1	A	0.140	0.881	[0.634,1.223]	0.448	0.769	[0.406,1.457]	0.421	0.873	[0.443,1.723]	0.696	0.582
rs8187706	ABCC2	A	0.022	0.754	[0.286,1.989]	0.568	1.012	[0.291,3.517]	0.985	1.342	[0.306,5.887]	0.697	0.846
rs1884725	XDH	A	0.229	1.201	[0.909,1.587]	0.197	1.078	[0.648,1.794]	0.771	0.898	[0.521,1.548]	0.697	0.432
rs474320	PGR	A	0.130	1.104	[0.783,1.556]	0.574	1.257	[0.681,2.321]	0.464	1.139	[0.59,2.198]	0.698	0.689
rs3738000	NEK11	A	0.382	0.914	[0.711,1.175]	0.481	0.828	[0.523,1.313]	0.423	0.907	[0.553,1.486]	0.698	0.606
rs5082	APOA2	C	0.350	0.952	[0.748,1.211]	0.688	0.867	[0.557,1.349]	0.526	0.910	[0.567,1.463]	0.698	0.777
rs3212218	IL12B	T	0.252	0.918	[0.665,1.267]	0.604	1.035	[0.595,1.8]	0.903	1.127	[0.615,2.065]	0.698	0.859
rs11770116	IMPDH1	T	0.312	1.103	[0.859,1.416]	0.443	1.002	[0.636,1.577]	0.995	0.908	[0.558,1.478]	0.698	0.741
rs5005	ADM	G	0.014	1.013	[0.383,2.68]	0.979	0.672	[0.093,4.835]	0.693	0.663	[0.083,5.314]	0.699	0.922
rs228843	NFATC2	A	0.479	1.065	[0.841,1.35]	0.601	0.974	[0.64,1.483]	0.903	0.915	[0.582,1.438]	0.699	0.855
rs2277448	ALG11	G	0.370	1.199	[0.931,1.543]	0.159	1.317	[0.845,2.051]	0.224	1.098	[0.683,1.767]	0.699	0.222
rs2256871	CYP2C9	C	0.015	0.986	[0.339,2.867]	0.980	1.361	[0.338,5.484]	0.664	1.380	[0.27,7.065]	0.699	0.907
rs2227928	ATR	T	0.400	0.859	[0.676,1.092]	0.215	0.943	[0.606,1.467]	0.795	1.098	[0.684,1.761]	0.699	0.462
rs10409482	VRK3	T	0.030	1.092	[0.51,2.34]	0.820	1.370	[0.506,3.712]	0.536	1.254	[0.398,3.954]	0.699	0.819
rs2260655	DAK	G	0.100	1.263	[0.751,2.124]	0.379	1.056	[0.466,2.393]	0.896	0.837	[0.338,2.069]	0.699	0.680
rs3093056	CSF1	A	0.338	1.002	[0.778,1.29]	0.987	0.908	[0.568,1.452]	0.687	0.906	[0.549,1.497]	0.700	0.920
rs5970	F11	C	0.156	0.989	[0.698,1.403]	0.952	0.863	[0.448,1.661]	0.658	0.872	[0.433,1.755]	0.701	0.907
rs3741883	NUAK1	C	0.198	1.078	[0.796,1.459]	0.629	1.210	[0.697,2.099]	0.498	1.123	[0.622,2.028]	0.701	0.735
rs1799794	XRCC3	G	0.204	1.271	[0.959,1.683]	0.095	1.408	[0.863,2.297]	0.170	1.108	[0.655,1.875]	0.701	0.132
rs1801320	LOC729029	C	0.116	1.220	[0.858,1.736]	0.268	1.068	[0.562,2.027]	0.842	0.875	[0.442,1.733]	0.701	0.541
rs7759	DPAGT1	G	0.327	0.934	[0.724,1.205]	0.600	0.847	[0.532,1.35]	0.485	0.907	[0.55,1.494]	0.701	0.714
rs6005	F5	G	0.014	2.070	[0.709,6.045]	0.183	1.446	[0.272,7.687]	0.665	0.699	[0.112,4.376]	0.702	0.402
rs518276	MRE11A	A	0.406	1.066	[0.844,1.346]	0.592	0.976	[0.641,1.487]	0.911	0.916	[0.583,1.438]	0.703	0.851
rs2230590	MST1R	A	0.482	0.909	[0.714,1.157]	0.438	0.993	[0.652,1.514]	0.975	1.093	[0.693,1.724]	0.703	0.738
rs554715	MRE11A	C	0.322	1.010	[0.786,1.297]	0.941	1.109	[0.709,1.734]	0.651	1.098	[0.679,1.777]	0.703	0.903
rs4647688	CASP3	A	0.151	1.169	[0.859,1.591]	0.322	1.035	[0.572,1.874]	0.909	0.886	[0.473,1.658]	0.704	0.612
rs2145853	ABCC2	A	0.409	1.256	[0.968,1.63]	0.086	1.142	[0.722,1.805]	0.571	0.909	[0.555,1.489]	0.704	0.217
rs2271012	ATF6	T	0.110	1.163	[0.816,1.655]	0.404	1.017	[0.53,1.951]	0.959	0.875	[0.438,1.748]	0.705	0.704
rs2144908	HNF4A	A	0.196	0.881	[0.658,1.181]	0.397	0.982	[0.583,1.657]	0.947	1.115	[0.635,1.957]	0.705	0.698
rs989902	PTPN13	C	0.465	1.101	[0.862,1.407]	0.440	1.205	[0.779,1.865]	0.402	1.095	[0.685,1.749]	0.706	0.567
rs2041049	DBF4	C	0.040	1.120	[0.604,2.077]	0.720	0.871	[0.256,2.967]	0.825	0.778	[0.211,2.866]	0.706	0.905
rs3748022	IKBKE	T	0.199	0.771	[0.572,1.04]	0.089	0.687	[0.39,1.208]	0.192	0.890	[0.487,1.629]	0.706	0.129
rs3136516	F2	A	0.454	1.179	[0.923,1.506]	0.186	1.292	[0.829,2.014]	0.258	1.095	[0.682,1.76]	0.706	0.267
rs3764006	SLCO1B3	C	0.210	1.402	[1.013,1.942]	0.042	1.571	[0.906,2.725]	0.108	1.121	[0.62,2.026]	0.707	0.054
rs4647001	JUN	G	0.405	0.865	[0.677,1.107]	0.249	0.947	[0.613,1.463]	0.806	1.094	[0.685,1.749]	0.707	0.513
rs16880254	TPMT	G	0.051	0.887	[0.515,1.526]	0.664	1.062	[0.455,2.478]	0.890	1.198	[0.466,3.075]	0.708	0.892
rs2069526	CYP1A2	G	0.049	0.972	[0.564,1.674]	0.918	1.164	[0.492,2.756]	0.730	1.198	[0.466,3.078]	0.708	0.930
rs584589	NGFR	G	0.138	1.106	[0.788,1.551]	0.560	1.246	[0.698,2.226]	0.457	1.127	[0.603,2.107]	0.709	0.677
rs2040968	HGF	C	0.242	0.994	[0.755,1.308]	0.963	1.097	[0.677,1.777]	0.706	1.104	[0.656,1.86]	0.709	0.927
rs2228527	ERCC6	G	0.207	0.978	[0.726,1.318]	0.886	1.089	[0.645,1.838]	0.749	1.113	[0.634,1.952]	0.709	0.933

rs16846208	ATF6	T	0.110	1.163	[0.817,1.656]	0.402	1.020	[0.532,1.956]	0.953	0.877	[0.439,1.751]	0.709	0.702
rs10263741	ABCB1	T	0.017	1.407	[0.543,3.647]	0.482	1.818	[0.545,6.063]	0.331	1.292	[0.335,4.977]	0.709	0.553
rs2294038	ARHGEF10	C	0.136	0.857	[0.604,1.217]	0.388	0.972	[0.529,1.785]	0.926	1.134	[0.586,2.193]	0.710	0.689
rs6474491	STAR	C	0.247	0.698	[0.526,0.925]	0.012	0.773	[0.471,1.268]	0.308	1.107	[0.647,1.896]	0.710	0.034
rs1374993	C8orf42	G	0.332	0.982	[0.765,1.261]	0.889	0.894	[0.56,1.426]	0.637	0.910	[0.552,1.498]	0.710	0.892
rs1572983	BAAT	C	0.346	0.910	[0.708,1.171]	0.466	0.829	[0.522,1.315]	0.425	0.910	[0.555,1.494]	0.710	0.597
rs689462	PTGS2	C	0.065	1.096	[0.658,1.825]	0.726	1.287	[0.598,2.772]	0.519	1.175	[0.501,2.755]	0.711	0.786
rs1059293	IFNGR2	C	0.464	0.938	[0.74,1.188]	0.593	0.859	[0.558,1.323]	0.491	0.916	[0.577,1.456]	0.712	0.715
rs1048977	CDA	T	0.330	0.997	[0.774,1.285]	0.982	0.908	[0.571,1.443]	0.684	0.911	[0.555,1.496]	0.712	0.920
rs5936	PROC	G	0.284	0.877	[0.676,1.137]	0.322	0.796	[0.492,1.288]	0.352	0.908	[0.542,1.52]	0.713	0.443
rs7172	PSMB4	G	0.296	1.144	[0.885,1.479]	0.305	1.041	[0.651,1.664]	0.866	0.910	[0.551,1.504]	0.713	0.591
rs3731151	XPC	A	0.267	0.976	[0.749,1.273]	0.860	1.074	[0.668,1.728]	0.767	1.100	[0.66,1.835]	0.714	0.934
rs3749442	ABCC5	T	0.194	0.834	[0.612,1.137]	0.251	0.933	[0.536,1.623]	0.806	1.119	[0.615,2.036]	0.714	0.515
rs1132776	ABCC5	T	0.401	1.000	[0.789,1.267]	1.000	1.088	[0.715,1.656]	0.694	1.088	[0.693,1.707]	0.714	0.924
rs1805061	SLC7A7	C	0.160	1.168	[0.852,1.601]	0.335	1.042	[0.587,1.849]	0.889	0.892	[0.483,1.646]	0.715	0.629
rs2078486	TP53	A	0.124	1.182	[0.823,1.697]	0.366	1.038	[0.544,1.981]	0.910	0.878	[0.438,1.76]	0.715	0.664
rs2147668	RFC3	G	0.173	1.117	[0.806,1.549]	0.506	1.252	[0.709,2.211]	0.438	1.121	[0.608,2.065]	0.715	0.636
rs1776148	EXO1	A	0.347	1.087	[0.855,1.381]	0.496	1.184	[0.772,1.816]	0.439	1.090	[0.688,1.725]	0.715	0.628
rs12254557	MBL2	C	0.023	1.453	[0.643,3.285]	0.370	1.822	[0.622,5.336]	0.274	1.254	[0.372,4.229]	0.715	0.431
rs601391	MRE11A	T	0.324	1.001	[0.779,1.287]	0.992	1.095	[0.7,1.714]	0.690	1.094	[0.676,1.771]	0.715	0.923
rs7525957	FRAP1	C	0.322	1.086	[0.835,1.414]	0.538	0.988	[0.616,1.585]	0.961	0.910	[0.548,1.511]	0.715	0.820
rs7797834	CYP51A1	G	0.389	0.939	[0.741,1.191]	0.605	1.022	[0.67,1.559]	0.920	1.088	[0.69,1.714]	0.716	0.862
rs1061494	TNC	C	0.465	0.946	[0.745,1.2]	0.646	1.030	[0.671,1.58]	0.893	1.089	[0.687,1.726]	0.717	0.882
rs3821207	IL1RL2	G	0.308	0.833	[0.643,1.079]	0.166	0.914	[0.573,1.457]	0.706	1.097	[0.664,1.813]	0.717	0.376
rs3759207	MGST1	G	0.303	1.086	[0.845,1.397]	0.519	1.188	[0.757,1.865]	0.454	1.094	[0.674,1.775]	0.717	0.652
rs3218097	CCND3	T	0.216	0.788	[0.589,1.055]	0.109	0.706	[0.404,1.233]	0.221	0.896	[0.493,1.627]	0.717	0.162
rs1800169	CNTF	A	0.120	0.918	[0.636,1.326]	0.649	1.047	[0.542,2.02]	0.892	1.140	[0.56,2.318]	0.718	0.884
rs916864	PON3	T	0.202	0.760	[0.56,1.032]	0.079	0.849	[0.488,1.476]	0.561	1.116	[0.615,2.027]	0.718	0.200
rs328	LPL	G	0.102	0.768	[0.515,1.145]	0.195	0.883	[0.44,1.771]	0.725	1.149	[0.539,2.449]	0.718	0.424
rs5744934	POLE	G	0.120	1.135	[0.805,1.601]	0.470	1.276	[0.707,2.303]	0.419	1.124	[0.595,2.123]	0.719	0.601
rs865242	DPYD	G	0.254	0.999	[0.77,1.297]	0.994	0.909	[0.562,1.469]	0.697	0.910	[0.544,1.521]	0.719	0.926
rs7689099	NEIL3	G	0.101	0.911	[0.616,1.349]	0.643	0.785	[0.366,1.685]	0.535	0.862	[0.383,1.939]	0.719	0.766
rs743616	ARSA	G	0.486	0.924	[0.734,1.163]	0.500	1.002	[0.663,1.514]	0.991	1.085	[0.696,1.691]	0.719	0.792
rs299284	HMMR	T	0.118	0.873	[0.602,1.265]	0.473	0.761	[0.379,1.526]	0.441	0.872	[0.412,1.844]	0.719	0.609
rs2076655	FRAP1	G	0.373	0.975	[0.753,1.262]	0.845	0.889	[0.556,1.421]	0.623	0.912	[0.552,1.508]	0.720	0.879
rs11547160	TCF7L1	T	0.054	1.819	[1.131,2.926]	0.014	1.532	[0.62,3.783]	0.355	0.842	[0.328,2.159]	0.720	0.042
rs2287620	ABCB11	A	0.403	0.871	[0.683,1.111]	0.265	0.949	[0.613,1.469]	0.813	1.090	[0.681,1.744]	0.721	0.536
rs13418420	UGT1A10	C	0.252	0.857	[0.647,1.136]	0.283	0.774	[0.46,1.303]	0.335	0.903	[0.517,1.579]	0.721	0.398
rs2267131	XBP1	C	0.114	0.812	[0.544,1.211]	0.308	0.936	[0.453,1.934]	0.859	1.153	[0.527,2.523]	0.722	0.594
rs1934954	CYP2C9	G	0.057	0.912	[0.55,1.512]	0.721	0.747	[0.265,2.104]	0.581	0.819	[0.273,2.458]	0.722	0.822
rs2659543	PPP3CA	G	0.105	0.748	[0.457,1.222]	0.246	0.634	[0.275,1.463]	0.285	0.848	[0.341,2.111]	0.723	0.333

rs1800668	GPX1	T	0.276	0.767	[0.585,1.004]	0.054	0.695	[0.419,1.153]	0.159	0.907	[0.528,1.559]	0.724	0.078
rs10176426	UGT1A10	T	0.089	0.792	[0.52,1.206]	0.277	0.913	[0.441,1.892]	0.806	1.153	[0.522,2.547]	0.725	0.550
rs880324	NFATC2	A	0.231	1.301	[0.985,1.718]	0.064	1.179	[0.707,1.968]	0.528	0.907	[0.525,1.566]	0.725	0.168
rs4252228	TAF9	T	0.399	1.012	[0.796,1.287]	0.921	0.929	[0.595,1.452]	0.748	0.918	[0.57,1.478]	0.725	0.940
rs3797896	MSH3	G	0.091	1.346	[0.914,1.982]	0.133	1.522	[0.795,2.912]	0.205	1.131	[0.57,2.245]	0.725	0.199
rs1801133	MTHFR	T	0.286	0.864	[0.665,1.123]	0.275	0.787	[0.483,1.282]	0.336	0.911	[0.54,1.535]	0.725	0.393
rs7903344	CHUK	C	0.457	1.014	[0.796,1.291]	0.910	1.103	[0.712,1.709]	0.661	1.088	[0.68,1.741]	0.726	0.907
rs7802773	ABCB1	A	0.488	1.143	[0.895,1.459]	0.283	1.240	[0.813,1.89]	0.317	1.085	[0.687,1.712]	0.727	0.390
rs3738136	PINK1	A	0.059	0.637	[0.362,1.121]	0.118	0.519	[0.178,1.514]	0.230	0.814	[0.257,2.581]	0.727	0.173
rs1413239	DPYD	T	0.358	0.955	[0.748,1.218]	0.710	0.878	[0.565,1.363]	0.562	0.919	[0.573,1.475]	0.728	0.809
rs1171276	LEPR	G	0.216	0.915	[0.678,1.235]	0.561	1.011	[0.602,1.697]	0.968	1.105	[0.63,1.937]	0.728	0.838
rs2582783	HMGCS2	A	0.271	0.909	[0.69,1.199]	0.500	0.825	[0.497,1.372]	0.459	0.908	[0.526,1.567]	0.729	0.641
rs8044995	NFATC3	A	0.197	0.940	[0.703,1.256]	0.675	1.035	[0.626,1.71]	0.894	1.101	[0.639,1.896]	0.729	0.899
rs144848	BRCA2	G	0.252	1.182	[0.907,1.54]	0.216	1.080	[0.669,1.743]	0.754	0.913	[0.548,1.524]	0.729	0.460
rs12720356	TYK2	G	0.074	0.867	[0.558,1.348]	0.528	1.008	[0.459,2.216]	0.984	1.162	[0.496,2.724]	0.729	0.815
rs2239330	ABCC1	T	0.259	0.941	[0.717,1.236]	0.663	1.033	[0.631,1.69]	0.897	1.098	[0.647,1.86]	0.730	0.892
rs994502	MYO3A	C	0.269	1.032	[0.781,1.364]	0.824	1.134	[0.692,1.858]	0.618	1.098	[0.645,1.871]	0.730	0.873
rs7120118	NR1H3	C	0.331	1.165	[0.911,1.489]	0.224	1.071	[0.685,1.674]	0.764	0.919	[0.57,1.483]	0.730	0.474
rs770087	DUSP6	G	0.233	1.025	[0.768,1.369]	0.867	1.126	[0.686,1.848]	0.639	1.099	[0.643,1.878]	0.731	0.891
rs3177427	GSTZ1	A	0.314	1.041	[0.815,1.329]	0.750	0.956	[0.609,1.502]	0.846	0.919	[0.567,1.49]	0.732	0.924
rs165599	COMT	G	0.401	1.035	[0.808,1.326]	0.783	1.125	[0.725,1.745]	0.600	1.086	[0.677,1.743]	0.732	0.854
rs500079	PPP1R15A	C	0.313	0.961	[0.711,1.299]	0.796	0.870	[0.514,1.47]	0.602	0.905	[0.511,1.601]	0.732	0.857
rs1881421	ALK	G	0.440	1.059	[0.844,1.328]	0.621	1.143	[0.762,1.713]	0.519	1.079	[0.699,1.667]	0.732	0.748
rs1549760	CDK5	T	0.259	0.877	[0.673,1.143]	0.332	0.959	[0.596,1.543]	0.863	1.093	[0.656,1.824]	0.732	0.624
rs8018462	SLC7A7	A	0.462	0.885	[0.698,1.121]	0.311	0.958	[0.625,1.468]	0.845	1.083	[0.685,1.713]	0.733	0.598
rs1405655	NR1H2	C	0.348	1.259	[0.99,1.601]	0.060	1.163	[0.76,1.779]	0.487	0.924	[0.585,1.458]	0.733	0.157
rs1951765	FKBP1A	A	0.232	1.054	[0.804,1.384]	0.702	1.156	[0.703,1.901]	0.567	1.097	[0.645,1.865]	0.734	0.811
rs217434	NPC1L1	G	0.193	0.942	[0.694,1.277]	0.699	0.847	[0.478,1.501]	0.569	0.899	[0.488,1.658]	0.734	0.809
rs1199039	TIE1	C	0.349	0.837	[0.655,1.071]	0.157	0.909	[0.584,1.415]	0.673	1.086	[0.675,1.748]	0.734	0.357
rs2231926	FLJ10213	A	0.464	1.072	[0.842,1.366]	0.572	0.990	[0.645,1.52]	0.963	0.923	[0.581,1.466]	0.734	0.845
rs1361600	F3	G	0.482	0.969	[0.769,1.221]	0.790	1.047	[0.691,1.587]	0.829	1.080	[0.691,1.689]	0.734	0.934
rs1565684	NAT2	C	0.486	1.040	[0.822,1.315]	0.745	0.961	[0.629,1.468]	0.855	0.925	[0.587,1.455]	0.735	0.923
rs2275622	CYP2C8	T	0.349	0.990	[0.773,1.268]	0.936	0.910	[0.575,1.438]	0.685	0.919	[0.563,1.5]	0.735	0.921
rs1802059	MTRR	A	0.343	1.089	[0.853,1.39]	0.495	1.002	[0.639,1.57]	0.993	0.920	[0.569,1.488]	0.735	0.789
rs6737156	DGUOK	C	0.057	1.015	[0.603,1.708]	0.954	0.847	[0.32,2.244]	0.739	0.835	[0.293,2.378]	0.735	0.941
rs853778	ABCB11	A	0.450	1.100	[0.873,1.386]	0.420	1.016	[0.663,1.558]	0.940	0.924	[0.585,1.46]	0.736	0.722
rs25487	XRCC1	A	0.304	0.978	[0.756,1.266]	0.868	1.065	[0.674,1.684]	0.787	1.089	[0.664,1.783]	0.736	0.944
rs941798	PTPN1	G	0.420	1.051	[0.828,1.333]	0.683	0.971	[0.635,1.487]	0.894	0.925	[0.585,1.46]	0.737	0.903
rs2234719	ABCG1	T	0.273	0.816	[0.623,1.069]	0.140	0.745	[0.455,1.219]	0.242	0.913	[0.537,1.552]	0.737	0.206
rs11549147	FDFT1	G	0.068	1.042	[0.667,1.629]	0.856	0.890	[0.373,2.127]	0.793	0.854	[0.339,2.151]	0.738	0.943
rs1805329	RAD23B	T	0.185	1.017	[0.754,1.371]	0.914	0.915	[0.513,1.633]	0.764	0.900	[0.486,1.666]	0.738	0.946

rs5491	ICAM1	T	0.040	1.864	[0.97,3.581]	0.062	2.240	[0.824,6.092]	0.114	1.202	[0.408,3.545]	0.739	0.081
rs2261144	CYP2A7	G	0.299	1.075	[0.841,1.373]	0.563	1.165	[0.749,1.813]	0.498	1.084	[0.675,1.74]	0.739	0.707
rs10017300	Intergenic	C	0.289	0.942	[0.723,1.229]	0.661	1.028	[0.639,1.654]	0.910	1.091	[0.653,1.82]	0.740	0.895
rs10493753	SPATA1	G	0.070	1.028	[0.613,1.724]	0.915	1.199	[0.527,2.723]	0.665	1.165	[0.471,2.885]	0.741	0.910
rs1341160	CYP2C8	A	0.116	1.202	[0.845,1.71]	0.307	1.066	[0.544,2.089]	0.853	0.887	[0.435,1.807]	0.741	0.593
rs1051740	EPHX1	C	0.300	0.998	[0.77,1.292]	0.985	0.915	[0.566,1.479]	0.717	0.917	[0.549,1.533]	0.741	0.936
rs2515644	CYP2E1	A	0.307	0.868	[0.654,1.152]	0.327	0.952	[0.572,1.583]	0.849	1.096	[0.635,1.894]	0.741	0.618
rs3138045	NFKBIA	G	0.218	0.802	[0.6,1.074]	0.138	0.882	[0.526,1.479]	0.634	1.099	[0.627,1.925]	0.741	0.320
rs2231142	ABCG2	A	0.101	1.049	[0.715,1.537]	0.808	0.919	[0.437,1.932]	0.824	0.877	[0.399,1.926]	0.743	0.939
rs2070151	ATF6	T	0.111	1.090	[0.76,1.564]	0.639	0.970	[0.502,1.872]	0.927	0.889	[0.441,1.794]	0.743	0.884
rs1137100	LEPR	G	0.264	1.191	[0.922,1.539]	0.180	1.095	[0.682,1.758]	0.707	0.919	[0.555,1.523]	0.744	0.400
rs133417	MCM5	C	0.072	1.095	[0.669,1.791]	0.718	1.263	[0.576,2.769]	0.559	1.154	[0.489,2.726]	0.744	0.812
rs3824120	MYC	A	0.121	1.210	[0.841,1.739]	0.304	1.074	[0.55,2.1]	0.834	0.888	[0.436,1.811]	0.744	0.589
rs1952467	CYP2E1	T	0.307	0.872	[0.657,1.157]	0.341	0.955	[0.574,1.588]	0.858	1.095	[0.634,1.892]	0.744	0.635
rs2259458	AKR1B1	T	0.284	0.899	[0.691,1.169]	0.425	0.978	[0.61,1.568]	0.926	1.088	[0.654,1.81]	0.745	0.727
rs540199	ANKRD49	G	0.328	1.122	[0.876,1.438]	0.360	1.034	[0.651,1.643]	0.886	0.922	[0.563,1.508]	0.745	0.658
rs1537234	GSTM3	T	0.394	1.023	[0.807,1.298]	0.849	1.104	[0.721,1.691]	0.650	1.078	[0.683,1.704]	0.746	0.895
rs2279238	NR1H3	A	0.207	1.154	[0.863,1.543]	0.333	1.261	[0.769,2.068]	0.359	1.092	[0.64,1.864]	0.746	0.462
rs753381	PLCG1	A	0.374	1.019	[0.794,1.309]	0.880	1.104	[0.705,1.728]	0.666	1.083	[0.669,1.752]	0.746	0.908
rs7218866	PSMB6	T	0.038	0.564	[0.262,1.213]	0.143	0.431	[0.095,1.946]	0.274	0.764	[0.149,3.926]	0.747	0.211
rs398734	CD44	A	0.303	1.287	[0.997,1.66]	0.053	1.185	[0.743,1.891]	0.475	0.921	[0.56,1.515]	0.747	0.140
rs1049897	MGP	T	0.371	0.962	[0.756,1.226]	0.756	1.039	[0.674,1.601]	0.863	1.079	[0.678,1.718]	0.747	0.930
rs1866928	C15orf42	A	0.357	0.963	[0.75,1.236]	0.767	0.888	[0.561,1.406]	0.613	0.922	[0.564,1.509]	0.748	0.857
rs5361	SELE	C	0.085	1.057	[0.707,1.58]	0.788	0.922	[0.421,2.018]	0.839	0.873	[0.38,2.004]	0.748	0.937
rs6949295	IMPDH1	C	0.239	1.006	[0.764,1.325]	0.964	1.096	[0.676,1.776]	0.710	1.089	[0.646,1.835]	0.749	0.933
rs6031	F5	T	0.014	0.829	[0.268,2.562]	0.745	1.115	[0.228,5.44]	0.893	1.344	[0.22,8.213]	0.749	0.933
rs3795375	KIAA1804	T	0.191	1.105	[0.827,1.475]	0.499	1.006	[0.589,1.718]	0.981	0.911	[0.514,1.614]	0.749	0.794
rs1052536	LIG3	T	0.400	1.147	[0.904,1.454]	0.258	1.061	[0.68,1.657]	0.793	0.925	[0.575,1.488]	0.749	0.524
rs1185193	SETX	A	0.210	1.100	[0.826,1.464]	0.514	1.199	[0.733,1.961]	0.471	1.090	[0.643,1.848]	0.750	0.665
rs480562	ABCB11	A	0.461	1.142	[0.906,1.44]	0.261	1.062	[0.702,1.608]	0.775	0.930	[0.596,1.451]	0.750	0.528
rs1405938	CASP3	A	0.158	1.193	[0.88,1.615]	0.256	1.080	[0.607,1.923]	0.794	0.906	[0.492,1.666]	0.750	0.522
rs878201	Intergenic	A	0.309	0.852	[0.657,1.104]	0.225	0.924	[0.578,1.478]	0.742	1.085	[0.655,1.8]	0.751	0.472
rs3775289	DCK	A	0.116	0.685	[0.407,1.153]	0.154	0.586	[0.242,1.418]	0.236	0.856	[0.325,2.251]	0.752	0.217
rs2706338	RAD50	T	0.177	1.091	[0.808,1.473]	0.570	0.987	[0.549,1.774]	0.965	0.905	[0.486,1.683]	0.752	0.845
rs1678339	ABCC4	T	0.080	0.869	[0.557,1.356]	0.536	0.993	[0.463,2.13]	0.986	1.143	[0.498,2.621]	0.753	0.824
rs1799800	ERCC4	A	0.249	0.947	[0.723,1.239]	0.690	1.029	[0.637,1.662]	0.908	1.087	[0.648,1.822]	0.753	0.910
rs2069833	IL6	C	0.323	1.181	[0.931,1.499]	0.171	1.093	[0.693,1.723]	0.702	0.925	[0.571,1.501]	0.753	0.384
rs1272744	MRE11A	C	0.399	1.043	[0.825,1.318]	0.727	0.970	[0.636,1.479]	0.886	0.930	[0.591,1.463]	0.754	0.923
rs1805312	ALAD	C	0.077	0.937	[0.605,1.453]	0.772	0.809	[0.339,1.928]	0.633	0.863	[0.343,2.174]	0.755	0.868
rs7181886	CYP19A1	G	0.110	1.207	[0.828,1.76]	0.328	1.079	[0.56,2.077]	0.821	0.894	[0.441,1.811]	0.755	0.617
rs567754	BHMT	T	0.295	0.891	[0.687,1.157]	0.387	0.967	[0.6,1.56]	0.891	1.085	[0.649,1.813]	0.755	0.688

rs7103126	MYEOV	C	0.300	0.992	[0.747,1.318]	0.957	0.908	[0.541,1.525]	0.717	0.916	[0.526,1.595]	0.755	0.936
rs35683	GHRL	A	0.430	1.138	[0.902,1.435]	0.276	1.059	[0.693,1.616]	0.792	0.930	[0.591,1.465]	0.756	0.549
rs4665766	EFR3B	T	0.269	0.953	[0.73,1.244]	0.722	0.878	[0.543,1.421]	0.597	0.922	[0.55,1.544]	0.757	0.835
rs973874	NAT2	T	0.016	0.878	[0.342,2.259]	0.788	0.633	[0.09,4.442]	0.645	0.720	[0.09,5.791]	0.758	0.877
rs1760212	DPYD	T	0.387	1.006	[0.789,1.282]	0.963	0.934	[0.603,1.448]	0.761	0.929	[0.58,1.488]	0.759	0.951
rs1143623	IL1B	C	0.266	1.107	[0.852,1.439]	0.445	1.021	[0.629,1.658]	0.932	0.922	[0.549,1.548]	0.759	0.747
rs853772	ABCB11	A	0.499	0.855	[0.678,1.079]	0.187	0.917	[0.603,1.394]	0.686	1.073	[0.684,1.683]	0.760	0.408
rs1126671	ADH4	A	0.269	0.925	[0.715,1.198]	0.555	1.001	[0.625,1.605]	0.996	1.082	[0.652,1.796]	0.760	0.837
rs2227930	ATR	T	0.400	0.862	[0.678,1.095]	0.223	0.927	[0.597,1.438]	0.735	1.076	[0.672,1.723]	0.760	0.469
rs1043641	ACBD3	A	0.146	1.122	[0.822,1.531]	0.468	1.020	[0.573,1.814]	0.947	0.909	[0.492,1.678]	0.760	0.768
rs2266782	FMO3	A	0.415	1.119	[0.886,1.415]	0.346	1.200	[0.793,1.815]	0.389	1.072	[0.686,1.674]	0.761	0.490
rs2020869	FMO2	G	0.149	1.145	[0.831,1.576]	0.408	1.041	[0.586,1.847]	0.892	0.909	[0.493,1.677]	0.761	0.710
rs3747258	CERK	A	0.097	1.382	[0.895,2.134]	0.144	1.557	[0.767,3.162]	0.221	1.127	[0.523,2.428]	0.761	0.209
rs864373	ABCB11	T	0.467	1.114	[0.887,1.399]	0.353	1.041	[0.689,1.571]	0.850	0.934	[0.601,1.452]	0.762	0.649
rs1063169	FOS	T	0.138	1.065	[0.746,1.52]	0.729	1.188	[0.614,2.298]	0.610	1.115	[0.551,2.258]	0.762	0.844
rs619824	CYP17A1	T	0.493	1.040	[0.821,1.317]	0.748	0.968	[0.631,1.487]	0.884	0.932	[0.589,1.475]	0.763	0.932
rs3795374	KIAA1804	A	0.201	1.062	[0.798,1.415]	0.679	0.974	[0.577,1.645]	0.922	0.917	[0.523,1.608]	0.763	0.907
rs12500797	PTPN13	A	0.080	1.519	[1.02,2.262]	0.040	1.342	[0.624,2.886]	0.451	0.884	[0.395,1.974]	0.763	0.110
rs17655	ERCC5	G	0.258	1.137	[0.877,1.475]	0.332	1.052	[0.652,1.697]	0.837	0.925	[0.555,1.541]	0.764	0.623
rs2273642	NFATC2	A	0.278	1.272	[0.985,1.642]	0.065	1.179	[0.743,1.872]	0.484	0.927	[0.565,1.52]	0.764	0.165
rs207910	XRCC5	G	0.149	0.943	[0.677,1.313]	0.727	0.854	[0.469,1.556]	0.606	0.906	[0.476,1.725]	0.764	0.842
rs3025039	VEGFA	T	0.144	1.096	[0.786,1.528]	0.588	1.208	[0.668,2.185]	0.531	1.102	[0.584,2.079]	0.764	0.741
rs15922	TAF11	G	0.047	0.876	[0.503,1.526]	0.640	0.724	[0.222,2.355]	0.591	0.826	[0.237,2.878]	0.764	0.795
rs6998760	PSKH2	A	0.317	1.076	[0.839,1.379]	0.563	0.998	[0.627,1.587]	0.992	0.927	[0.565,1.522]	0.765	0.843
rs2847609	TYMS	G	0.369	0.976	[0.758,1.258]	0.853	0.906	[0.577,1.424]	0.670	0.928	[0.57,1.511]	0.765	0.905
rs12441817	CYP1A1	C	0.130	1.093	[0.781,1.529]	0.605	0.987	[0.527,1.848]	0.968	0.903	[0.464,1.761]	0.766	0.869
rs1060584	FLJ10213	C	0.462	1.068	[0.839,1.359]	0.594	0.996	[0.648,1.53]	0.985	0.933	[0.587,1.481]	0.767	0.863
rs2380165	BLM	G	0.342	0.834	[0.645,1.077]	0.164	0.774	[0.492,1.219]	0.269	0.929	[0.569,1.516]	0.768	0.247
rs2464196	HNF1A	T	0.269	1.056	[0.81,1.377]	0.686	1.142	[0.704,1.852]	0.590	1.081	[0.644,1.815]	0.768	0.819
rs3024496	IL10	C	0.447	0.907	[0.716,1.148]	0.416	0.846	[0.549,1.302]	0.447	0.933	[0.587,1.482]	0.768	0.579
rs6945306	STK31	C	0.299	0.865	[0.67,1.118]	0.267	0.933	[0.585,1.488]	0.770	1.078	[0.653,1.782]	0.768	0.535
rs907807	IGF1R	G	0.165	1.151	[0.835,1.588]	0.390	1.259	[0.724,2.189]	0.414	1.094	[0.602,1.986]	0.769	0.543
rs854544	PPP1R9A	T	0.418	0.833	[0.65,1.067]	0.148	0.896	[0.569,1.413]	0.637	1.076	[0.661,1.75]	0.769	0.339
rs2472299	CYP1A1	A	0.312	0.985	[0.763,1.272]	0.911	1.060	[0.672,1.673]	0.801	1.076	[0.658,1.758]	0.770	0.958
rs849526	NRP2	G	0.464	0.927	[0.726,1.184]	0.546	0.995	[0.639,1.548]	0.982	1.073	[0.667,1.724]	0.772	0.832
rs4987164	DMC1	C	0.038	0.988	[0.533,1.83]	0.969	0.823	[0.262,2.586]	0.738	0.833	[0.241,2.874]	0.772	0.946
rs2234721	ABCG1	T	0.329	1.105	[0.855,1.429]	0.447	1.025	[0.639,1.646]	0.917	0.928	[0.56,1.539]	0.772	0.749
rs3218619	FAS	A	0.020	1.631	[0.761,3.495]	0.208	1.944	[0.651,5.809]	0.234	1.192	[0.363,3.92]	0.772	0.291
rs215050	ABCC1	A	0.147	1.079	[0.793,1.469]	0.627	0.988	[0.558,1.749]	0.966	0.915	[0.498,1.681]	0.774	0.883
rs1041163	VCAM1	C	0.173	0.996	[0.73,1.359]	0.980	0.912	[0.522,1.594]	0.748	0.916	[0.503,1.669]	0.774	0.949
rs1010844	CART	C	0.210	0.868	[0.638,1.18]	0.366	0.796	[0.462,1.372]	0.412	0.918	[0.509,1.654]	0.775	0.517

rs462779	REV3L	C	0.284	0.980	[0.755,1.271]	0.876	1.052	[0.668,1.658]	0.826	1.074	[0.657,1.756]	0.775	0.959
rs2606241	C18orf56	T	0.315	1.038	[0.806,1.338]	0.772	1.112	[0.718,1.724]	0.634	1.071	[0.667,1.721]	0.775	0.871
rs1051296	SLC19A1	G	0.434	0.836	[0.651,1.074]	0.161	0.896	[0.577,1.39]	0.624	1.072	[0.666,1.725]	0.775	0.357
rs2069837	IL6	G	0.076	1.344	[0.875,2.064]	0.177	1.507	[0.725,3.131]	0.272	1.121	[0.511,2.459]	0.776	0.270
rs2069824	IL6	C	0.092	0.932	[0.623,1.395]	0.733	0.825	[0.376,1.813]	0.632	0.885	[0.382,2.051]	0.776	0.856
rs4148946	CHST3	C	0.383	0.822	[0.643,1.052]	0.119	0.766	[0.486,1.208]	0.252	0.932	[0.573,1.516]	0.776	0.190
rs7009367	C8orf68	G	0.226	0.858	[0.642,1.147]	0.300	0.928	[0.564,1.528]	0.769	1.082	[0.629,1.861]	0.777	0.578
rs2071421	ARSA	G	0.155	1.118	[0.801,1.561]	0.512	1.230	[0.657,2.305]	0.518	1.101	[0.566,2.142]	0.778	0.691
rs1047768	ERCC5	T	0.395	1.180	[0.941,1.48]	0.152	1.256	[0.836,1.886]	0.272	1.064	[0.688,1.646]	0.779	0.239
rs2227929	ATR	C	0.343	1.231	[0.955,1.587]	0.109	1.320	[0.838,2.079]	0.232	1.072	[0.658,1.746]	0.779	0.172
rs714629	AICDA	G	0.496	0.913	[0.724,1.151]	0.440	0.972	[0.644,1.469]	0.894	1.065	[0.684,1.661]	0.780	0.742
rs1891072	CYP2C8	C	0.347	0.981	[0.766,1.257]	0.880	0.915	[0.578,1.446]	0.703	0.932	[0.571,1.523]	0.780	0.925
rs2401751	PTPN21	T	0.345	0.888	[0.692,1.139]	0.351	0.827	[0.521,1.314]	0.422	0.932	[0.567,1.53]	0.780	0.511
rs540742	GIPC2	C	0.223	1.099	[0.835,1.446]	0.502	1.018	[0.615,1.685]	0.946	0.926	[0.541,1.586]	0.780	0.797
rs662	PON1	G	0.396	0.904	[0.711,1.15]	0.411	0.845	[0.543,1.315]	0.457	0.935	[0.583,1.5]	0.781	0.583
rs2229086		G	0.056	1.430	[0.881,2.32]	0.148	1.623	[0.699,3.768]	0.259	1.135	[0.464,2.776]	0.781	0.237
rs2070180	HCLS1	A	0.244	1.082	[0.832,1.406]	0.556	1.163	[0.724,1.867]	0.533	1.075	[0.647,1.785]	0.781	0.725
rs5982	F13A1	T	0.200	0.920	[0.684,1.239]	0.584	0.846	[0.482,1.483]	0.558	0.919	[0.504,1.676]	0.782	0.752
rs2010963	VEGFA	C	0.309	1.019	[0.796,1.305]	0.879	1.089	[0.703,1.687]	0.703	1.068	[0.667,1.71]	0.783	0.925
rs3212254	ADCY4	A	0.074	1.245	[0.805,1.923]	0.325	1.106	[0.502,2.437]	0.803	0.888	[0.383,2.063]	0.783	0.612
rs2234700	EPHX1	C	0.013	0.411	[0.089,1.906]	0.256	0.586	[0.07,4.908]	0.622	1.425	[0.114,17.795]	0.783	0.483
rs557806	PPP1R15A	G	0.212	0.841	[0.602,1.177]	0.313	0.921	[0.506,1.677]	0.788	1.095	[0.573,2.09]	0.784	0.595
rs1014666	MRE11A	C	0.467	1.031	[0.821,1.296]	0.790	0.970	[0.641,1.467]	0.884	0.940	[0.603,1.465]	0.784	0.949
rs1946235	GPX3	C	0.159	1.047	[0.744,1.475]	0.790	0.955	[0.515,1.769]	0.883	0.912	[0.469,1.772]	0.785	0.949
rs316132	GSTA4	G	0.433	1.246	[0.98,1.584]	0.073	1.169	[0.761,1.796]	0.477	0.938	[0.591,1.489]	0.786	0.179
rs1800286	FANCA	A	0.332	0.867	[0.672,1.119]	0.272	0.809	[0.505,1.294]	0.376	0.933	[0.563,1.544]	0.787	0.415
rs4775936	CYP19A1	T	0.412	0.946	[0.742,1.207]	0.658	1.009	[0.655,1.556]	0.967	1.066	[0.67,1.698]	0.787	0.901
rs2237051	EGF	A	0.472	1.050	[0.825,1.337]	0.692	1.120	[0.723,1.737]	0.612	1.067	[0.666,1.709]	0.787	0.833
rs503931	ABCB11	T	0.500	1.184	[0.942,1.487]	0.148	1.113	[0.736,1.683]	0.610	0.941	[0.604,1.466]	0.787	0.335
rs7089422	CYP17A1	T	0.153	1.080	[0.786,1.484]	0.635	0.992	[0.555,1.771]	0.978	0.918	[0.493,1.709]	0.788	0.889
rs2075800	HSPA1L	A	0.278	0.964	[0.745,1.246]	0.777	1.032	[0.646,1.651]	0.894	1.071	[0.648,1.772]	0.788	0.946
rs3803258	SLC10A2	C	0.179	0.756	[0.551,1.038]	0.084	0.824	[0.46,1.476]	0.515	1.090	[0.582,2.041]	0.789	0.205
rs3176260	FGF17	T	0.106	0.799	[0.539,1.182]	0.261	0.715	[0.336,1.523]	0.385	0.896	[0.399,2.011]	0.790	0.404
rs1566734	PTPRJ	G	0.143	0.858	[0.611,1.203]	0.374	0.779	[0.403,1.506]	0.458	0.909	[0.449,1.839]	0.790	0.548
rs11848612	ADSSL1	G	0.465	1.083	[0.85,1.38]	0.519	1.017	[0.661,1.565]	0.939	0.939	[0.59,1.494]	0.790	0.812
rs551754	ABCB11	A	0.499	0.852	[0.678,1.071]	0.170	0.905	[0.598,1.369]	0.635	1.062	[0.681,1.656]	0.790	0.374
rs2039447	DPYD	C	0.359	0.963	[0.755,1.228]	0.761	0.903	[0.58,1.405]	0.651	0.938	[0.583,1.508]	0.791	0.876
rs4148301	UGT2A1	A	0.085	0.972	[0.634,1.489]	0.895	1.083	[0.515,2.277]	0.834	1.114	[0.5,2.484]	0.792	0.965
rs9606756	TCN2	G	0.123	1.142	[0.814,1.6]	0.442	1.240	[0.699,2.199]	0.462	1.086	[0.587,2.011]	0.792	0.614
rs2137680	IGF1R	T	0.358	1.031	[0.797,1.334]	0.813	1.101	[0.701,1.73]	0.676	1.067	[0.656,1.738]	0.793	0.902
rs7190823	FANCA	C	0.468	1.326	[1.049,1.677]	0.018	1.247	[0.813,1.913]	0.312	0.940	[0.595,1.487]	0.793	0.049

rs17841292	EEF2K	G	0.078	0.918	[0.59,1.428]	0.705	0.810	[0.334,1.967]	0.642	0.882	[0.345,2.257]	0.794	0.852
rs7185307	TNFRSF17	C	0.331	1.083	[0.834,1.407]	0.550	1.013	[0.635,1.618]	0.956	0.936	[0.566,1.545]	0.795	0.836
rs1048691	9-Mar	T	0.251	0.955	[0.71,1.284]	0.759	0.883	[0.51,1.528]	0.656	0.925	[0.512,1.67]	0.795	0.876
rs2384937	ABCC1	C	0.120	1.095	[0.771,1.556]	0.611	1.196	[0.642,2.229]	0.572	1.092	[0.561,2.126]	0.795	0.778
rs10896380	IGHMBP2	G	0.205	0.910	[0.672,1.231]	0.540	0.987	[0.553,1.76]	0.964	1.085	[0.585,2.012]	0.796	0.828
rs3093106	CYP4F2	G	0.202	1.139	[0.856,1.516]	0.372	1.060	[0.638,1.762]	0.821	0.931	[0.54,1.604]	0.796	0.668
rs6463247	PPIA	C	0.295	1.252	[0.96,1.632]	0.098	1.171	[0.726,1.888]	0.517	0.935	[0.563,1.556]	0.797	0.235
rs497692	ABCB11	A	0.499	1.185	[0.943,1.489]	0.144	1.119	[0.74,1.691]	0.595	0.944	[0.606,1.47]	0.798	0.326
rs1130499	PTPRN2	A	0.350	1.313	[1.024,1.683]	0.032	1.399	[0.889,2.2]	0.147	1.065	[0.656,1.73]	0.798	0.051
rs762551	CYP1A2	C	0.316	1.018	[0.789,1.313]	0.892	1.085	[0.686,1.717]	0.726	1.066	[0.651,1.746]	0.799	0.937
rs10520114	RAD50	C	0.181	0.982	[0.728,1.325]	0.906	0.907	[0.509,1.614]	0.739	0.923	[0.5,1.705]	0.799	0.943
rs1573496	ADH7	G	0.081	0.839	[0.545,1.293]	0.426	0.935	[0.435,2.009]	0.862	1.114	[0.487,2.545]	0.799	0.727
rs3742106	ABCC4	C	0.389	0.990	[0.778,1.258]	0.931	0.932	[0.607,1.432]	0.747	0.942	[0.593,1.496]	0.799	0.949
rs2057768	IL4R	A	0.295	0.916	[0.704,1.191]	0.512	0.978	[0.612,1.563]	0.925	1.068	[0.644,1.772]	0.799	0.806
rs288326	FRZB	A	0.094	0.735	[0.478,1.13]	0.161	0.652	[0.274,1.552]	0.333	0.887	[0.351,2.242]	0.800	0.266
rs799923	BRCA1	A	0.179	0.823	[0.6,1.129]	0.227	0.891	[0.504,1.577]	0.693	1.083	[0.585,2.004]	0.800	0.468
rs6597801	LHPP	A	0.100	1.136	[0.781,1.654]	0.505	1.249	[0.629,2.479]	0.525	1.099	[0.53,2.281]	0.800	0.691
rs4646227	SLC15A1	C	0.039	0.748	[0.404,1.388]	0.358	0.869	[0.303,2.493]	0.794	1.161	[0.366,3.682]	0.800	0.648
rs9885672	FIG4	C	0.262	0.932	[0.689,1.263]	0.651	1.004	[0.591,1.705]	0.989	1.076	[0.608,1.906]	0.801	0.900
rs10775648	HUNK	T	0.202	0.801	[0.588,1.092]	0.161	0.865	[0.497,1.506]	0.609	1.080	[0.593,1.967]	0.801	0.354
rs5320	DBH	A	0.076	1.064	[0.677,1.672]	0.788	0.951	[0.421,2.147]	0.904	0.894	[0.373,2.143]	0.802	0.952
rs934197	APOB	A	0.291	1.109	[0.857,1.435]	0.433	1.181	[0.744,1.875]	0.481	1.065	[0.65,1.747]	0.802	0.616
rs2273697	ABCC2	A	0.193	0.881	[0.648,1.197]	0.417	0.949	[0.55,1.637]	0.852	1.078	[0.6,1.938]	0.802	0.717
rs1856908	CYP2C9	T	0.382	1.077	[0.845,1.372]	0.550	1.144	[0.735,1.78]	0.552	1.062	[0.662,1.706]	0.803	0.732
rs2228001	XPC	C	0.365	1.139	[0.896,1.447]	0.288	1.207	[0.785,1.857]	0.391	1.060	[0.669,1.68]	0.803	0.443
rs9282787	MTRR	C	0.183	1.024	[0.757,1.386]	0.876	1.104	[0.64,1.905]	0.723	1.077	[0.6,1.934]	0.803	0.934
rs430397	HSPA5	A	0.092	1.225	[0.815,1.841]	0.330	1.350	[0.661,2.756]	0.410	1.102	[0.513,2.371]	0.803	0.492
rs2285460	BLM	T	0.202	0.860	[0.636,1.162]	0.325	0.924	[0.548,1.558]	0.766	1.075	[0.61,1.892]	0.803	0.609
rs4129472	GHR	G	0.164	1.260	[0.924,1.717]	0.144	1.165	[0.652,2.083]	0.606	0.925	[0.499,1.713]	0.803	0.329
rs1801265	DPYD	C	0.260	0.753	[0.574,0.988]	0.041	0.805	[0.496,1.306]	0.380	1.069	[0.632,1.806]	0.804	0.102
rs700518	CYP19A1	G	0.450	0.935	[0.736,1.187]	0.579	0.990	[0.646,1.518]	0.965	1.060	[0.67,1.676]	0.804	0.857
rs6413419	CYP2E1	A	0.048	1.068	[0.587,1.94]	0.830	0.933	[0.35,2.483]	0.889	0.874	[0.298,2.559]	0.806	0.963
rs1138358	BCL2A1	G	0.344	0.995	[0.776,1.277]	0.971	0.936	[0.595,1.474]	0.776	0.941	[0.578,1.531]	0.806	0.960
rs7778377	STARD3NL	T	0.172	1.016	[0.751,1.375]	0.918	1.092	[0.638,1.868]	0.749	1.075	[0.604,1.911]	0.807	0.949
rs894157	C15orf42	C	0.090	0.942	[0.619,1.432]	0.779	0.845	[0.373,1.914]	0.686	0.897	[0.375,2.145]	0.807	0.897
rs1169288	HNF1A	G	0.286	1.135	[0.856,1.506]	0.379	1.058	[0.621,1.802]	0.836	0.932	[0.528,1.644]	0.807	0.677
rs2227914	DMC1	G	0.024	1.027	[0.422,2.498]	0.953	1.231	[0.342,4.433]	0.750	1.199	[0.28,5.135]	0.807	0.950
rs2072330	ALDH3A1	A	0.344	1.091	[0.856,1.389]	0.482	1.027	[0.65,1.621]	0.910	0.941	[0.579,1.531]	0.807	0.781
rs1126526	ATF3	T	0.176	1.050	[0.771,1.428]	0.758	1.130	[0.645,1.98]	0.668	1.077	[0.593,1.956]	0.808	0.885
rs1396080	CCNA2	C	0.387	1.011	[0.795,1.287]	0.927	1.071	[0.7,1.638]	0.753	1.059	[0.67,1.674]	0.808	0.951
rs905594	ATF6	T	0.461	1.078	[0.843,1.379]	0.548	1.016	[0.647,1.594]	0.946	0.942	[0.582,1.525]	0.808	0.835

rs5888	SCARB1	T	0.416	0.937	[0.737,1.191]	0.595	0.884	[0.573,1.365]	0.579	0.944	[0.593,1.504]	0.808	0.772
rs3743372	C15orf42	A	0.297	0.978	[0.756,1.264]	0.864	1.041	[0.649,1.67]	0.868	1.064	[0.642,1.765]	0.809	0.968
rs139884	SOX10	A	0.331	1.020	[0.793,1.311]	0.879	1.083	[0.685,1.713]	0.732	1.062	[0.65,1.736]	0.809	0.938
rs1800788	FGB	T	0.194	0.963	[0.718,1.291]	0.800	1.034	[0.602,1.776]	0.905	1.074	[0.602,1.916]	0.810	0.957
rs2241280	FGF6	C	0.412	0.901	[0.707,1.149]	0.401	0.954	[0.619,1.47]	0.830	1.058	[0.664,1.686]	0.811	0.699
rs2152092	MMS19	C	0.460	1.106	[0.874,1.4]	0.402	1.168	[0.769,1.776]	0.466	1.056	[0.673,1.659]	0.812	0.581
rs2687074	CYP3A7	C	0.038	0.923	[0.456,1.865]	0.823	0.793	[0.257,2.443]	0.686	0.860	[0.247,2.985]	0.812	0.908
rs2927922	PDSS1	T	0.356	1.064	[0.83,1.363]	0.625	1.002	[0.632,1.588]	0.994	0.942	[0.575,1.542]	0.812	0.886
rs2124459	CBS	C	0.390	1.049	[0.826,1.333]	0.692	0.991	[0.639,1.537]	0.969	0.945	[0.591,1.511]	0.812	0.921
rs3730931	LIG1	G	0.149	0.865	[0.615,1.215]	0.402	0.932	[0.527,1.65]	0.809	1.078	[0.578,2.01]	0.813	0.698
rs853785	ABCB11	G	0.474	1.110	[0.884,1.393]	0.370	1.052	[0.698,1.587]	0.808	0.948	[0.61,1.473]	0.813	0.665
rs10146482	NEK9	T	0.466	1.054	[0.832,1.335]	0.664	1.114	[0.725,1.712]	0.623	1.057	[0.667,1.675]	0.813	0.828
rs982424	MTTP	C	0.097	0.851	[0.558,1.298]	0.453	0.936	[0.449,1.949]	0.860	1.100	[0.496,2.441]	0.814	0.752
rs708155	CD81	A	0.193	1.428	[1.075,1.897]	0.014	1.524	[0.914,2.541]	0.106	1.067	[0.62,1.836]	0.814	0.023
rs2237060	RAD50	C	0.345	1.009	[0.782,1.301]	0.944	1.072	[0.669,1.718]	0.773	1.062	[0.642,1.758]	0.814	0.959
rs6427630	ATF6	G	0.112	1.217	[0.853,1.736]	0.279	1.119	[0.58,2.159]	0.736	0.920	[0.458,1.848]	0.815	0.549
rs1464890	ZC3HC1	T	0.483	0.958	[0.755,1.217]	0.728	0.906	[0.585,1.403]	0.659	0.946	[0.592,1.511]	0.815	0.870
rs1189466	ABCC4	A	0.071	0.862	[0.543,1.367]	0.528	0.957	[0.42,2.183]	0.917	1.111	[0.456,2.706]	0.817	0.819
rs4926	SERPING1	A	0.232	1.168	[0.882,1.547]	0.279	1.094	[0.65,1.842]	0.736	0.937	[0.538,1.631]	0.817	0.547
rs12009	HSPA5	C	0.472	1.054	[0.84,1.322]	0.652	1.000	[0.663,1.51]	0.999	0.949	[0.61,1.476]	0.817	0.901
rs1800796	IL6	C	0.095	0.795	[0.533,1.186]	0.261	0.873	[0.415,1.839]	0.721	1.098	[0.494,2.441]	0.818	0.520
rs1024323	GRK4	A	0.420	0.947	[0.745,1.204]	0.658	1.001	[0.649,1.542]	0.998	1.056	[0.663,1.683]	0.818	0.905
rs2854184	GH1	T	0.368	0.928	[0.721,1.194]	0.559	0.982	[0.625,1.542]	0.937	1.059	[0.651,1.721]	0.818	0.843
rs8645	SUMO3	C	0.183	0.823	[0.595,1.139]	0.240	0.763	[0.421,1.385]	0.374	0.927	[0.487,1.765]	0.818	0.378
rs2272797	FMO6	A	0.162	1.206	[0.897,1.621]	0.214	1.287	[0.768,2.157]	0.339	1.067	[0.614,1.853]	0.819	0.345
rs2725349	WRN	C	0.335	1.009	[0.786,1.294]	0.946	1.067	[0.682,1.67]	0.777	1.058	[0.654,1.711]	0.819	0.960
rs2707466	WNT16	G	0.491	1.093	[0.857,1.394]	0.472	1.035	[0.668,1.603]	0.878	0.947	[0.592,1.514]	0.819	0.771
rs8016621	SALL2	A	0.039	1.814	[0.971,3.389]	0.062	1.602	[0.606,4.236]	0.342	0.884	[0.306,2.548]	0.819	0.143
rs3783408	MAP4K5	A	0.228	0.849	[0.639,1.129]	0.260	0.794	[0.464,1.36]	0.401	0.935	[0.526,1.661]	0.819	0.416
rs10473282	GHR	A	0.332	0.855	[0.664,1.101]	0.225	0.905	[0.574,1.428]	0.669	1.059	[0.648,1.729]	0.819	0.463
rs2276235	ABCG1	A	0.404	1.008	[0.791,1.285]	0.950	0.955	[0.618,1.475]	0.834	0.947	[0.594,1.511]	0.820	0.974
rs16975750	LIPE	G	0.037	1.021	[0.502,2.077]	0.954	0.878	[0.268,2.878]	0.830	0.860	[0.235,3.152]	0.820	0.974
rs7483	GSTM3	A	0.272	1.076	[0.828,1.399]	0.582	1.014	[0.622,1.652]	0.957	0.942	[0.559,1.586]	0.821	0.859
rs235768	BMP2	A	0.325	1.250	[0.96,1.628]	0.097	1.326	[0.821,2.143]	0.249	1.061	[0.635,1.772]	0.822	0.165
rs1800566	NQO1	T	0.205	1.126	[0.851,1.49]	0.405	1.058	[0.635,1.763]	0.827	0.940	[0.545,1.619]	0.823	0.704
rs5742667	IGF1	T	0.280	0.803	[0.612,1.053]	0.113	0.852	[0.524,1.386]	0.520	1.062	[0.628,1.794]	0.823	0.258
rs316133	GSTA4	C	0.432	1.235	[0.972,1.569]	0.084	1.172	[0.763,1.8]	0.469	0.949	[0.598,1.505]	0.824	0.200
rs673197	GSTA4	A	0.432	1.235	[0.972,1.569]	0.084	1.172	[0.763,1.8]	0.469	0.949	[0.598,1.505]	0.824	0.200
rs2269829	PON1	G	0.361	0.906	[0.711,1.155]	0.426	0.956	[0.616,1.482]	0.840	1.055	[0.659,1.688]	0.824	0.725
rs169097	CXCL12	A	0.025	0.975	[0.409,2.322]	0.954	1.141	[0.335,3.887]	0.833	1.170	[0.292,4.689]	0.824	0.974
rs1800287	FANCA	C	0.473	1.362	[1.077,1.723]	0.010	1.293	[0.84,1.991]	0.244	0.949	[0.598,1.505]	0.824	0.026

rs1492078	AGTR1	A	0.444	0.806	[0.625,1.04]	0.097	0.852	[0.537,1.354]	0.498	1.058	[0.644,1.739]	0.825	0.227
rs2980374	CYP3A7	T	0.038	0.893	[0.441,1.81]	0.755	0.776	[0.252,2.394]	0.659	0.869	[0.249,3.027]	0.825	0.878
rs3741378	SIPA1	A	0.159	0.938	[0.672,1.31]	0.707	0.871	[0.472,1.609]	0.660	0.929	[0.481,1.796]	0.827	0.862
rs2227538	IL8	T	0.038	0.760	[0.353,1.637]	0.484	0.877	[0.283,2.723]	0.821	1.154	[0.319,4.18]	0.827	0.775
rs10380	MTRR	T	0.126	1.022	[0.699,1.494]	0.911	1.106	[0.572,2.139]	0.764	1.083	[0.531,2.208]	0.827	0.954
rs2282140	IGF2R	T	0.133	0.835	[0.581,1.2]	0.330	0.770	[0.393,1.511]	0.448	0.923	[0.447,1.905]	0.828	0.506
rs7796976	AHR	A	0.206	1.004	[0.742,1.358]	0.980	0.941	[0.547,1.62]	0.827	0.937	[0.523,1.68]	0.828	0.975
rs11568943	EGF	A	0.098	0.986	[0.653,1.488]	0.945	1.072	[0.536,2.144]	0.845	1.087	[0.51,2.318]	0.828	0.976
rs2227932	ATR	C	0.086	0.869	[0.566,1.332]	0.518	0.790	[0.352,1.77]	0.566	0.909	[0.382,2.161]	0.829	0.717
rs367836	GSTA4	C	0.428	1.264	[0.995,1.607]	0.055	1.202	[0.782,1.847]	0.403	0.950	[0.599,1.509]	0.829	0.135
rs971074	ADH7	A	0.121	0.889	[0.616,1.283]	0.529	0.961	[0.497,1.855]	0.905	1.081	[0.532,2.196]	0.830	0.820
rs1888202	ALDH1A1	G	0.442	0.936	[0.738,1.188]	0.587	0.890	[0.575,1.375]	0.598	0.950	[0.596,1.515]	0.830	0.778
rs5744751	POLE	T	0.098	0.826	[0.557,1.225]	0.342	0.754	[0.343,1.656]	0.481	0.912	[0.394,2.114]	0.830	0.531
rs1407309	TNFSF8	G	0.480	1.026	[0.808,1.302]	0.834	1.079	[0.698,1.667]	0.731	1.052	[0.66,1.676]	0.831	0.930
rs903881	ABCC1	T	0.192	1.474	[1.097,1.98]	0.010	1.386	[0.814,2.36]	0.230	0.940	[0.534,1.657]	0.831	0.026
rs497763	ANKRD49	A	0.436	0.973	[0.772,1.227]	0.817	1.022	[0.668,1.566]	0.919	1.051	[0.666,1.658]	0.831	0.965
rs3817405	PLXDC2	C	0.366	1.028	[0.808,1.307]	0.824	0.978	[0.633,1.51]	0.918	0.951	[0.597,1.516]	0.834	0.967
rs4980999	CAMKK2	A	0.164	0.908	[0.661,1.246]	0.548	0.968	[0.556,1.685]	0.907	1.066	[0.584,1.948]	0.835	0.834
rs1801394	FASTKD3	G	0.496	0.927	[0.731,1.176]	0.533	0.882	[0.569,1.368]	0.576	0.951	[0.595,1.521]	0.835	0.735
rs1043615	DNAJB9	A	0.461	1.055	[0.834,1.336]	0.656	1.006	[0.662,1.53]	0.977	0.954	[0.608,1.496]	0.836	0.905
rs1135148	BNIP2	C	0.327	1.057	[0.826,1.354]	0.660	1.114	[0.701,1.769]	0.649	1.054	[0.643,1.726]	0.836	0.838
rs1751034	ABCC4	C	0.214	1.031	[0.763,1.393]	0.842	0.969	[0.562,1.673]	0.911	0.940	[0.523,1.69]	0.837	0.971
rs2140516	SLC13A1	C	0.313	1.174	[0.915,1.505]	0.207	1.115	[0.706,1.76]	0.641	0.950	[0.583,1.549]	0.837	0.432
rs1801278	IRS1	A	0.057	1.205	[0.744,1.953]	0.449	1.096	[0.468,2.569]	0.832	0.910	[0.369,2.245]	0.837	0.748
rs246241	ABCC1	T	0.138	1.346	[0.969,1.868]	0.076	1.263	[0.716,2.227]	0.420	0.938	[0.511,1.722]	0.837	0.182
rs4648276	PTGS2	C	0.134	1.050	[0.743,1.484]	0.780	1.125	[0.612,2.07]	0.704	1.071	[0.554,2.071]	0.838	0.906
rs2267130	CHEK2	C	0.393	0.932	[0.734,1.184]	0.566	0.888	[0.574,1.373]	0.594	0.952	[0.597,1.52]	0.838	0.763
rs1270764	TSSK4	C	0.025	0.517	[0.197,1.352]	0.178	□.609	[0.154,2.4]	0.478	1.178	[0.243,5.712]	0.839	0.347
rs2363641	POMT2	G	0.326	0.978	[0.765,1.251]	0.862	0.931	[0.593,1.461]	0.755	0.951	[0.587,1.542]	0.839	0.944
rs2074086	ABCC1	C	0.379	1.011	[0.782,1.309]	0.931	1.065	[0.67,1.693]	0.790	1.053	[0.64,1.733]	0.839	0.964
rs4149272	ABCA1	A	0.448	1.117	[0.873,1.431]	0.379	1.063	[0.677,1.669]	0.791	0.951	[0.586,1.544]	0.840	0.672
rs11688	JUN	A	0.073	0.979	[0.608,1.577]	0.931	1.072	[0.478,2.403]	0.866	1.095	[0.455,2.637]	0.840	0.980
rs2320165	CART	C	0.428	0.970	[0.765,1.23]	0.802	1.017	[0.663,1.56]	0.938	1.048	[0.662,1.66]	0.840	0.963
rs2231924	FLJ10213	T	0.462	1.072	[0.843,1.365]	0.569	1.023	[0.664,1.576]	0.918	0.954	[0.599,1.518]	0.842	0.850
rs2608555	GAN	T	0.241	1.037	[0.788,1.366]	0.795	0.982	[0.593,1.624]	0.943	0.946	[0.551,1.625]	0.842	0.961
rs4149180	SLC22A8	A	0.116	1.174	[0.718,1.918]	0.523	1.075	[0.494,2.341]	0.855	0.916	[0.388,2.164]	0.842	0.812
rs759845	ADAM23	C	0.387	0.981	[0.77,1.249]	0.875	1.028	[0.666,1.588]	0.900	1.048	[0.658,1.67]	0.842	0.977
rs4149117	SLCO1B3	T	0.213	1.470	[1.089,1.984]	0.012	1.554	[0.934,2.585]	0.090	1.057	[0.612,1.827]	0.842	0.018
rs2250889	MMP9	G	0.087	0.873	[0.565,1.348]	0.539	0.951	[0.432,2.094]	0.901	1.090	[0.465,2.553]	0.842	0.827
rs2253635	CYP2C9	G	0.384	1.079	[0.847,1.376]	0.537	1.132	[0.727,1.763]	0.582	1.049	[0.653,1.686]	0.843	0.740
rs2277119	CYP39A1	A	0.233	0.982	[0.741,1.3]	0.897	1.036	[0.631,1.699]	0.889	1.055	[0.619,1.798]	0.843	0.979

rs2860840	CYP2C18	T	0.300	0.970	[0.749,1.258]	0.821	1.022	[0.635,1.643]	0.930	1.053	[0.633,1.751]	0.843	0.968
rs2069762	IL2	G	0.269	0.857	[0.653,1.125]	0.267	0.905	[0.549,1.492]	0.696	1.056	[0.617,1.807]	0.843	0.524
rs611251	PPP1R15A	G	0.187	0.963	[0.693,1.34]	0.824	1.026	[0.574,1.834]	0.930	1.065	[0.569,1.996]	0.843	0.969
rs1048013	CYP20A1	T	0.497	0.951	[0.752,1.202]	0.675	0.908	[0.592,1.392]	0.659	0.955	[0.604,1.509]	0.844	0.850
rs2681417	CD86	G	0.117	0.966	[0.641,1.456]	0.870	0.897	[0.453,1.776]	0.755	0.928	[0.44,1.957]	0.844	0.945
rs2020895	CASP9	T	0.438	1.211	[0.957,1.534]	0.111	1.156	[0.749,1.785]	0.512	0.955	[0.599,1.521]	0.845	0.254
rs585890	SRD5A2	T	0.465	0.941	[0.742,1.195]	0.620	0.986	[0.64,1.518]	0.949	1.047	[0.659,1.665]	0.845	0.884
rs5988	F13A1	C	0.163	1.101	[0.817,1.485]	0.527	1.165	[0.686,1.977]	0.572	1.058	[0.6,1.864]	0.846	0.731
rs7496	GSTA4	A	0.155	1.052	[0.782,1.415]	0.736	0.996	[0.59,1.679]	0.987	0.946	[0.54,1.658]	0.846	0.943
rs2241279	FGF6	C	0.419	0.866	[0.679,1.105]	0.246	0.907	[0.588,1.398]	0.657	1.047	[0.657,1.669]	0.846	0.490
rs2287395	GSTZ1	G	0.297	0.925	[0.718,1.193]	0.550	0.880	[0.55,1.41]	0.596	0.951	[0.574,1.577]	0.847	0.754
rs3770	ABCC4	A	0.413	1.034	[0.816,1.31]	0.780	0.989	[0.651,1.504]	0.960	0.957	[0.61,1.501]	0.847	0.958
rs207878	XRCC5	G	0.417	1.031	[0.811,1.311]	0.803	0.985	[0.639,1.518]	0.946	0.955	[0.601,1.518]	0.847	0.964
rs3784932	CHST5	C	0.185	1.191	[0.887,1.598]	0.245	1.126	[0.66,1.92]	0.663	0.946	[0.537,1.667]	0.847	0.493
rs8191613	NEIL2	A	0.028	0.967	[0.477,1.961]	0.925	1.096	[0.345,3.477]	0.877	1.133	[0.318,4.037]	0.847	0.981
rs3130618	BAT4	A	0.224	1.023	[0.772,1.355]	0.876	1.078	[0.656,1.771]	0.767	1.054	[0.617,1.801]	0.847	0.951
rs2069849	IL6	T	0.045	1.330	[0.745,2.373]	0.334	1.201	[0.457,3.154]	0.710	0.903	[0.319,2.556]	0.847	0.613
rs10794486	IGF1R	G	0.368	1.100	[0.854,1.417]	0.460	1.048	[0.663,1.658]	0.840	0.953	[0.583,1.558]	0.848	0.758
rs1042482	DPYD	A	0.081	1.113	[0.724,1.711]	0.625	1.024	[0.461,2.277]	0.953	0.920	[0.393,2.154]	0.848	0.887
rs305968	CYP2F1	A	0.359	0.978	[0.758,1.26]	0.861	1.025	[0.652,1.612]	0.914	1.049	[0.645,1.707]	0.848	0.976
rs17273563	BLM	A	0.176	0.978	[0.713,1.342]	0.892	0.921	[0.516,1.643]	0.780	0.941	[0.506,1.75]	0.848	0.957
rs1048201	FGF2	T	0.164	0.872	[0.634,1.201]	0.402	0.927	[0.522,1.647]	0.796	1.062	[0.572,1.975]	0.848	0.696
rs833061	VEGFA	C	0.468	1.080	[0.856,1.363]	0.514	1.129	[0.743,1.714]	0.570	1.045	[0.667,1.636]	0.848	0.720
rs4680	COMT	A	0.452	1.085	[0.847,1.389]	0.519	1.034	[0.654,1.635]	0.886	0.953	[0.584,1.556]	0.848	0.811
rs3771342	UGT1A1	A	0.147	0.965	[0.686,1.357]	0.837	0.904	[0.49,1.67]	0.748	0.937	[0.483,1.818]	0.848	0.937
rs6457816	PPARD	C	0.164	0.892	[0.616,1.291]	0.545	0.831	[0.419,1.646]	0.595	0.931	[0.448,1.937]	0.849	0.751
rs1056836	CYP1B1	G	0.483	1.068	[0.836,1.364]	0.599	1.020	[0.655,1.589]	0.929	0.955	[0.594,1.537]	0.851	0.871
rs1063743	TACC3	A	0.239	0.877	[0.665,1.158]	0.355	0.924	[0.558,1.53]	0.759	1.053	[0.612,1.812]	0.852	0.641
rs2671272	EPHX1	T	0.267	0.969	[0.737,1.274]	0.822	0.922	[0.564,1.507]	0.745	0.951	[0.56,1.616]	0.853	0.933
rs2684773	IGF1R	G	0.180	1.139	[0.825,1.573]	0.428	1.076	[0.607,1.905]	0.803	0.944	[0.511,1.745]	0.854	0.723
rs1052576	CASP9	A	0.444	1.238	[0.978,1.567]	0.077	1.293	[0.841,1.986]	0.242	1.044	[0.658,1.657]	0.854	0.134
rs4148380	ABCC1	A	0.053	1.198	[0.73,1.966]	0.475	1.090	[0.422,2.815]	0.858	0.910	[0.333,2.484]	0.854	0.772
rs215060	ABCC1	G	0.117	1.136	[0.799,1.615]	0.478	1.063	[0.547,2.067]	0.857	0.936	[0.462,1.897]	0.854	0.775
rs1611753	SPRR1A	C	0.455	0.947	[0.748,1.2]	0.653	0.908	[0.593,1.388]	0.655	0.958	[0.607,1.513]	□.855	0.838
rs7921	CD79B	T	0.252	1.033	[0.793,1.347]	0.808	0.986	[0.619,1.572]	0.953	0.954	[0.578,1.576]	0.855	0.967
rs2072671	CDA	C	0.284	1.009	[0.777,1.311]	0.946	0.960	[0.584,1.579]	0.873	0.952	[0.56,1.617]	0.855	0.983
rs2241228	GPRC5A	A	0.450	1.043	[0.818,1.33]	0.734	0.998	[0.643,1.55]	0.993	0.957	[0.597,1.534]	0.855	0.942
rs2854455	EPHX1	C	0.266	0.919	[0.696,1.215]	0.554	0.966	[0.594,1.569]	0.887	1.050	[0.621,1.777]	0.855	0.838
rs2274736	PTPN21	C	0.367	0.901	[0.701,1.157]	0.413	0.943	[0.596,1.493]	0.803	1.047	[0.639,1.715]	0.855	0.708
rs246214	ABCC1	T	0.142	0.993	[0.709,1.391]	0.968	1.054	[0.577,1.927]	0.863	1.062	[0.557,2.024]	0.855	0.983
rs6021275	NFATC2	G	0.417	0.850	[0.671,1.077]	0.178	0.887	[0.583,1.349]	0.574	1.043	[0.663,1.639]	0.856	0.376

rs2953983	POLB	C	0.176	0.898	[0.617,1.309]	0.577	0.842	[0.442,1.606]	0.602	0.937	[0.465,1.89]	0.856	0.773
rs3814058	NR1I2	C	0.240	1.043	[0.775,1.405]	0.781	0.990	[0.59,1.662]	0.971	0.950	[0.541,1.665]	0.857	0.960
rs13027171	MERTK	A	0.253	0.852	[0.647,1.122]	0.254	0.896	[0.535,1.501]	0.677	1.052	[0.606,1.828]	0.857	0.502
rs730821	SIRT1	G	0.232	1.305	[0.994,1.713]	0.055	1.243	[0.756,2.045]	0.391	0.953	[0.561,1.619]	0.858	0.134
rs2032349	ADH4	T	0.033	1.528	[0.838,2.787]	0.166	1.379	[0.471,4.035]	0.557	0.902	[0.292,2.792]	0.858	0.363
rs543304	BRCA2	C	0.179	1.280	[0.957,1.714]	0.097	1.217	[0.721,2.055]	0.463	0.950	[0.543,1.663]	0.859	0.223
rs7775	FRZB	G	0.114	0.848	[0.567,1.268]	0.422	0.791	[0.389,1.608]	0.517	0.932	[0.432,2.015]	0.859	0.622
rs1200314	CYP2C9	C	0.047	1.121	[0.652,1.925]	0.680	1.022	[0.398,2.626]	0.963	0.912	[0.33,2.522]	0.859	0.918
rs1341162	CYP2C8	A	0.244	1.167	[0.883,1.543]	0.279	1.113	[0.68,1.822]	0.671	0.954	[0.561,1.621]	0.861	0.536
rs17012064	PTPN13	C	0.012	0.509	[0.11,2.349]	0.387	0.638	[0.074,5.5]	0.683	1.254	[0.1,15.784]	0.861	0.650
rs4148949	CHST3	T	0.376	0.838	[0.654,1.073]	0.162	0.802	[0.507,1.269]	0.346	0.957	[0.586,1.564]	0.861	0.282
rs731236	VDR	C	0.362	0.887	[0.687,1.144]	0.356	0.849	[0.54,1.336]	0.480	0.958	[0.587,1.562]	0.862	0.549
rs3093105	CYP4F2	G	0.189	1.124	[0.837,1.509]	0.438	1.069	[0.633,1.807]	0.803	0.951	[0.542,1.669]	0.862	0.733
rs4149963	EXO1	T	0.085	0.900	[0.594,1.365]	0.620	0.968	[0.453,2.069]	0.932	1.075	[0.475,2.434]	0.862	0.884
rs9935059	EEF2K	G	0.124	1.082	[0.747,1.569]	0.677	1.151	[0.606,2.184]	0.668	1.063	[0.531,2.129]	0.862	0.855
rs6644	ADSSL1	T	0.457	0.796	[0.619,1.023]	0.074	0.762	[0.484,1.2]	0.241	0.958	[0.589,1.559]	0.863	0.132
rs6220	IGF1	G	0.304	0.830	[0.638,1.081]	0.168	0.869	[0.541,1.396]	0.561	1.046	[0.627,1.744]	0.863	0.357
rs9808232	ROCK2	T	0.492	0.905	[0.71,1.153]	0.418	0.943	[0.608,1.462]	0.793	1.042	[0.65,1.671]	0.864	0.712
rs2306134	PPP4R1	T	0.184	0.962	[0.709,1.306]	0.804	1.012	[0.587,1.746]	0.964	1.052	[0.586,1.889]	0.864	0.967
rs4983543	ADSSL1	T	0.457	0.793	[0.617,1.019]	0.069	0.760	[0.483,1.196]	0.235	0.958	[0.589,1.559]	0.864	0.123
rs2389603	ABCB11	T	0.067	1.306	[0.795,2.146]	0.292	1.204	[0.504,2.874]	0.676	0.922	[0.361,2.351]	0.864	0.554
rs7736656	UBLCP1	A	0.177	1.096	[0.81,1.483]	0.553	1.152	[0.674,1.971]	0.605	1.051	[0.591,1.871]	0.865	0.762
rs1805059	SLC7A7	G	0.417	1.019	[0.8,1.298]	0.879	1.060	[0.693,1.623]	0.788	1.041	[0.658,1.646]	0.865	0.958
rs569143	MRE11A	G	0.450	1.025	[0.815,1.29]	0.830	1.065	[0.705,1.61]	0.763	1.039	[0.668,1.617]	0.865	0.941
rs2392221	VCAM1	T	0.146	0.956	[0.681,1.341]	0.794	1.011	[0.554,1.844]	0.972	1.058	[0.553,2.021]	0.866	0.964
rs16938893	GDAP1	G	0.301	1.168	[0.904,1.507]	0.235	1.119	[0.705,1.777]	0.634	0.958	[0.584,1.572]	0.866	0.471
rs2293616	SLC15A2	T	0.442	0.973	[0.77,1.229]	0.816	1.011	[0.664,1.539]	0.959	1.040	[0.662,1.634]	0.866	0.970
rs1673026	POLD1	T	0.104	1.163	[0.785,1.723]	0.453	1.235	[0.649,2.348]	0.520	1.062	[0.527,2.141]	0.866	0.653
rs1024611	CCL2	C	0.281	1.193	[0.93,1.532]	0.165	1.244	[0.791,1.957]	0.345	1.042	[0.643,1.691]	0.867	0.289
rs2472304	CYP1A2	G	0.488	1.047	[0.82,1.338]	0.713	1.091	[0.698,1.705]	0.703	1.042	[0.646,1.681]	0.867	0.884
rs7081	SLC5A6	G	0.141	1.017	[0.673,1.536]	0.938	1.084	[0.542,2.169]	0.819	1.067	[0.499,2.281]	0.868	0.973
rs1805313	ALAD	C	0.386	0.990	[0.775,1.265]	0.936	1.030	[0.665,1.597]	0.894	1.041	[0.649,1.668]	0.869	0.986
rs2237582	PON1	G	0.402	0.926	[0.728,1.178]	0.533	0.890	[0.576,1.378]	0.602	0.961	[0.602,1.535]	0.869	0.748
rs3136820	APEX1	G	0.464	0.915	[0.723,1.158]	0.459	0.950	[0.628,1.436]	0.807	1.038	[0.664,1.622]	0.869	0.752
rs1136410	PARP1	C	0.164	1.252	[0.92,1.705]	0.153	1.315	[0.759,2.28]	0.329	1.050	[0.585,1.885]	0.869	0.272
rs5743611	TLR1	C	0.081	0.882	[0.569,1.367]	0.574	0.950	[0.414,2.179]	0.903	1.077	[0.445,2.609]	0.870	0.853
rs10429965	NEK2	C	0.139	0.932	[0.673,1.29]	0.670	0.980	[0.557,1.726]	0.945	1.052	[0.572,1.937]	0.870	0.913
rs3828942	LEP	A	0.404	1.000	[0.785,1.275]	0.998	0.961	[0.613,1.506]	0.862	0.961	[0.594,1.553]	0.870	0.985
rs11572073	CYP2C8	T	0.021	1.400	[0.517,3.789]	0.508	1.220	[0.274,5.432]	0.794	0.871	[0.167,4.543]	0.870	0.794
rs2421047	IL12B	A	0.246	0.948	[0.724,1.241]	0.698	0.907	[0.556,1.48]	0.696	0.957	[0.564,1.622]	0.870	0.874
rs1805411	PARP1	A	0.174	1.146	[0.844,1.557]	0.383	1.204	[0.693,2.09]	0.510	1.050	[0.584,1.89]	0.870	0.595

rs17561	IL1A	T	0.275	1.040	[0.803,1.346]	0.767	0.997	[0.623,1.596]	0.990	0.959	[0.579,1.588]	0.871	0.956
rs442332	RUNDC2A	C	0.107	0.984	[0.663,1.461]	0.937	1.045	[0.536,2.04]	0.897	1.062	[0.515,2.189]	0.871	0.987
rs35629	ABCC1	T	0.176	1.186	[0.839,1.677]	0.335	1.122	[0.605,2.082]	0.716	0.946	[0.485,1.845]	0.871	0.611
rs914959	DPYD	A	0.320	0.867	[0.679,1.108]	0.254	0.833	[0.522,1.329]	0.442	0.960	[0.583,1.58]	0.873	0.429
rs1143671	SLC15A2	T	0.441	0.976	[0.773,1.233]	0.840	1.013	[0.665,1.541]	0.953	1.037	[0.66,1.63]	0.873	0.976
rs1044141	STK17A	A	0.193	0.819	[0.605,1.11]	0.199	0.779	[0.436,1.392]	0.399	0.951	[0.511,1.77]	0.874	0.345
rs2582790	HMGCS2	T	0.315	0.863	[0.669,1.114]	0.259	0.829	[0.523,1.314]	0.426	0.961	[0.586,1.576]	0.874	0.428
rs3851294	RIPK5	A	0.076	1.128	[0.728,1.749]	0.589	1.050	[0.457,2.416]	0.908	0.931	[0.384,2.256]	0.874	0.864
rs1346044	WRN	C	0.239	1.015	[0.773,1.332]	0.916	0.971	[0.585,1.613]	0.910	0.957	[0.557,1.645]	0.874	0.986
rs3783613	VCAM1	C	0.018	0.435	[0.123,1.54]	0.197	0.359	[0.044,2.961]	0.341	0.826	[0.077,8.881]	0.874	0.302
rs7515157	FMO2	T	0.330	0.916	[0.709,1.185]	0.505	0.953	[0.605,1.502]	0.837	1.040	[0.638,1.696]	0.875	0.796
rs9282626	CAT	C	0.046	1.034	[0.597,1.791]	0.904	1.123	[0.436,2.89]	0.811	1.085	[0.391,3.015]	0.875	0.968
rs2185379	PRDM1	A	0.039	0.997	[0.522,1.902]	0.992	1.095	[0.376,3.188]	0.868	1.098	[0.339,3.56]	0.876	0.986
rs7987433	SLC10A2	C	0.146	1.227	[0.883,1.705]	0.223	1.288	[0.732,2.265]	0.380	1.050	[0.571,1.93]	0.876	0.372
rs308394	FGF2	C	0.031	0.983	[0.472,2.044]	0.963	0.883	[0.258,3.026]	0.843	0.899	[0.234,3.449]	0.876	0.980
rs5030737	MBL2	T	0.065	1.080	[0.679,1.718]	0.744	1.005	[0.423,2.383]	0.992	0.930	[0.369,2.341]	0.877	0.947
rs1051298	SLC19A1	T	0.446	0.903	[0.711,1.147]	0.401	0.936	[0.612,1.43]	0.759	1.037	[0.657,1.636]	0.877	0.691
rs2066870	FGG	C	0.016	1.262	[0.46,3.464]	0.651	1.422	[0.377,5.363]	0.603	1.127	[0.247,5.132]	0.877	0.817
rs617219	BHMT	C	0.352	0.971	[0.761,1.237]	0.810	1.007	[0.65,1.56]	0.974	1.038	[0.649,1.66]	0.877	0.969
rs2288378	IGF1	A	0.231	0.910	[0.686,1.208]	0.514	0.871	[0.519,1.462]	0.601	0.957	[0.549,1.669]	0.878	0.733
rs1052637	DDX18	C	0.394	1.005	[0.786,1.283]	0.971	1.043	[0.67,1.623]	0.853	1.038	[0.646,1.667]	0.878	0.983
rs2292305	THBS1	C	0.186	1.257	[0.92,1.718]	0.152	1.200	[0.691,2.085]	0.518	0.955	[0.528,1.727]	0.878	0.325
rs289747	NLRC5	A	0.395	0.948	[0.742,1.211]	0.669	0.913	[0.584,1.427]	0.690	0.963	[0.596,1.556]	0.878	0.861
rs669674	GSTA4	T	0.093	0.943	[0.641,1.388]	0.767	0.888	[0.43,1.834]	0.748	0.941	[0.433,2.046]	0.878	0.919
rs1799977	MLH1	G	0.259	1.117	[0.858,1.456]	0.411	1.073	[0.656,1.755]	0.779	0.960	[0.569,1.621]	0.879	0.704
rs854569	PON1	T	0.319	0.970	[0.745,1.264]	0.823	0.933	[0.581,1.498]	0.773	0.961	[0.578,1.599]	0.879	0.943
rs1413229	DPYD	A	0.312	0.906	[0.709,1.158]	0.429	0.872	[0.548,1.387]	0.562	0.962	[0.586,1.579]	0.879	0.652
rs10046	CYP19A1	T	0.475	1.017	[0.8,1.292]	0.892	0.981	[0.639,1.506]	0.931	0.965	[0.609,1.529]	0.880	0.985
rs2489581	PDSS1	G	0.444	1.125	[0.884,1.432]	0.339	1.085	[0.703,1.675]	0.712	0.965	[0.605,1.538]	0.880	0.615
rs3808553	FZD6	G	0.445	1.049	[0.831,1.326]	0.687	1.013	[0.66,1.553]	0.953	0.965	[0.61,1.526]	0.880	0.922
rs588701	MRE11A	A	0.328	1.134	[0.884,1.454]	0.323	1.092	[0.687,1.736]	0.710	0.963	[0.588,1.577]	0.881	0.598
rs2033178	IGF1	T	0.061	0.964	[0.594,1.564]	0.882	0.893	[0.348,2.293]	0.814	0.926	[0.339,2.533]	0.881	0.966
rs4919682	CYP17A1	T	0.266	1.132	[0.877,1.461]	0.343	1.090	[0.684,1.737]	0.718	0.963	[0.587,1.581]	0.881	0.623
rs2020870	FMO2	G	0.074	0.630	[0.38,1.045]	0.073	0.677	[0.284,1.616]	0.380	1.076	[0.413,2.799]	0.881	0.159
rs2295298	NFATC4	A	0.494	1.041	[0.82,1.321]	0.742	1.079	[0.695,1.674]	0.735	1.036	[0.648,1.658]	0.882	0.907
rs410509	EDEM1	C	0.048	1.313	[0.769,2.242]	0.318	1.414	[0.574,3.488]	0.452	1.077	[0.406,2.859]	0.882	0.505
rs6919734	PPARD	A	0.032	0.614	[0.281,1.34]	0.221	0.545	[0.126,2.346]	0.415	0.887	[0.183,4.292]	0.882	0.374
rs2159499	STARD3NL	G	0.451	0.924	[0.728,1.174]	0.519	0.892	[0.578,1.377]	0.607	0.965	[0.606,1.538]	0.882	0.741
rs1157745	PON1	T	0.396	0.905	[0.712,1.151]	0.417	0.874	[0.564,1.352]	0.545	0.965	[0.604,1.542]	0.882	0.635
rs2426157	PTPN1	G	0.269	1.116	[0.859,1.45]	0.410	1.159	[0.727,1.849]	0.535	1.038	[0.629,1.713]	0.883	0.627
rs7867504	SLC28A3	C	0.384	1.207	[0.939,1.551]	0.143	1.251	[0.801,1.953]	0.325	1.037	[0.642,1.673]	0.883	0.252

rs1260326	GCKR	T	0.344	0.924	[0.708,1.207]	0.564	0.888	[0.542,1.457]	0.639	0.961	[0.566,1.632]	0.883	0.783
rs376618	FGFR4	G	0.247	0.981	[0.745,1.291]	0.891	0.942	[0.57,1.556]	0.816	0.961	[0.56,1.646]	0.884	0.968
rs596104	PHGDH	A	0.421	0.938	[0.737,1.194]	0.605	0.906	[0.587,1.399]	0.656	0.966	[0.606,1.539]	0.884	0.815
rs1271079	MRE11A	G	0.257	1.175	[0.902,1.531]	0.231	1.131	[0.693,1.845]	0.623	0.962	[0.572,1.618]	0.884	0.465
rs215095	ABCC1	C	0.116	1.200	[0.844,1.707]	0.310	1.139	[0.586,2.212]	0.701	0.949	[0.469,1.92]	0.884	0.580
rs3091336	IL3	A	0.065	0.962	[0.54,1.714]	0.896	0.892	[0.356,2.236]	0.808	0.927	[0.336,2.561]	0.884	0.966
rs1503185	PTPRJ	T	0.170	0.858	[0.621,1.184]	0.350	0.898	[0.505,1.599]	0.716	1.048	[0.561,1.957]	0.884	0.626
rs2239359	FANCA	T	0.470	1.026	[0.812,1.298]	0.827	1.061	[0.697,1.616]	0.781	1.034	[0.658,1.624]	0.884	0.947
rs7164902	SLC12A6	A	0.256	1.137	[0.861,1.501]	0.366	1.093	[0.666,1.793]	0.725	0.961	[0.565,1.636]	0.884	0.648
rs3211892	CD36	A	0.059	1.069	[0.611,1.87]	0.814	0.988	[0.364,2.679]	0.980	0.924	[0.314,2.717]	0.885	0.971
rs909530	FMO3	T	0.287	1.175	[0.912,1.514]	0.213	1.134	[0.72,1.785]	0.588	0.965	[0.593,1.569]	0.885	0.432
rs523349	SRD5A2	G	0.287	1.008	[0.782,1.301]	0.949	1.046	[0.656,1.668]	0.850	1.037	[0.629,1.711]	0.886	0.981
rs3136717	POLB	C	0.215	0.916	[0.655,1.282]	0.608	0.960	[0.534,1.725]	0.890	1.048	[0.555,1.975]	0.886	0.875
rs9350	EXO1	T	0.179	0.751	[0.544,1.036]	0.081	0.785	[0.443,1.393]	0.408	1.046	[0.563,1.944]	0.887	0.181
rs699947	VEGFA	A	0.437	1.066	[0.844,1.347]	0.593	1.102	[0.715,1.7]	0.659	1.034	[0.651,1.644]	0.887	0.809
rs3918226	NOS3	T	0.070	1.235	[0.793,1.924]	0.350	1.159	[0.505,2.659]	0.727	0.938	[0.391,2.251]	0.887	0.634
rs11155472	SIM1	T	0.489	1.006	[0.799,1.268]	0.957	0.974	[0.64,1.483]	0.903	0.968	[0.617,1.519]	0.888	0.990
rs215106	ABCC1	G	0.115	1.039	[0.729,1.482]	0.831	0.987	[0.498,1.953]	0.969	0.949	[0.46,1.959]	0.888	0.975
rs2938395	PPARG	C	0.339	0.902	[0.7,1.163]	0.427	0.934	[0.592,1.476]	0.771	1.036	[0.634,1.692]	0.888	0.717
rs4251545	IRAK4	A	0.136	0.762	[0.522,1.112]	0.158	0.724	[0.376,1.393]	0.333	0.950	[0.465,1.943]	0.889	0.268
rs12338	CTSB	G	0.361	1.340	[1.048,1.715]	0.020	1.387	[0.886,2.171]	0.152	1.035	[0.641,1.67]	0.889	0.036
rs6817280	HELQ	A	0.053	1.032	[0.523,2.035]	0.928	1.115	[0.427,2.908]	0.824	1.080	[0.363,3.214]	0.889	0.974
rs3112831	ABCA4	G	0.294	0.978	[0.764,1.251]	0.857	1.012	[0.643,1.59]	0.960	1.035	[0.638,1.679]	0.890	0.981
rs853783	ABCB11	T	0.467	1.075	[0.852,1.355]	0.543	1.109	[0.733,1.676]	0.625	1.032	[0.662,1.609]	0.890	0.765
rs4341514	IGF2	T	0.422	0.983	[0.774,1.249]	0.891	0.952	[0.612,1.479]	0.825	0.968	[0.604,1.551]	0.891	0.970
rs2228226	ARHGAP9	G	0.325	0.944	[0.735,1.213]	0.653	0.977	[0.618,1.544]	0.921	1.035	[0.633,1.692]	0.891	0.903
rs1805331	RAD23B	A	0.067	1.115	[0.681,1.824]	0.665	1.041	[0.413,2.626]	0.931	0.934	[0.348,2.507]	0.892	0.910
rs2069812	IL5	T	0.394	0.913	[0.708,1.179]	0.487	0.946	[0.588,1.522]	0.819	1.036	[0.623,1.721]	0.892	0.778
rs1165678	HSP90B1	G	0.363	1.112	[0.877,1.411]	0.382	1.076	[0.691,1.676]	0.744	0.968	[0.603,1.553]	0.892	0.667
rs4073	IL8	T	0.470	1.046	[0.822,1.332]	0.714	1.081	[0.698,1.673]	0.728	1.033	[0.646,1.651]	0.893	0.894
rs7311358	SLCO1B3	G	0.215	1.501	[1.112,2.027]	0.008	1.559	[0.937,2.595]	0.088	1.038	[0.601,1.795]	0.893	0.013
rs578430	MUSK	T	0.058	1.239	[0.715,2.146]	0.445	1.323	[0.55,3.186]	0.532	1.068	[0.409,2.788]	0.893	0.656
rs5742671	IGF1	T	0.143	0.822	[0.581,1.164]	0.270	0.861	[0.452,1.64]	0.649	1.048	[0.524,2.093]	0.895	0.517
rs1805034	TNFRSF11A	C	0.444	0.821	[0.648,1.04]	0.102	0.796	[0.522,1.215]	0.291	0.970	[0.616,1.528]	0.896	0.186
rs667565	DPYD	G	0.395	1.147	[0.909,1.447]	0.248	1.181	[0.784,1.778]	0.426	1.030	[0.663,1.598]	0.896	0.420
rs2228224	GLI1	G	0.471	0.962	[0.753,1.228]	0.754	0.993	[0.636,1.55]	0.974	1.032	[0.64,1.665]	0.896	0.952
rs5742666	IGF1	G	0.232	0.892	[0.67,1.186]	0.430	0.859	[0.512,1.442]	0.566	0.964	[0.552,1.682]	0.896	0.655
rs3828855	BYSL	A	0.097	1.274	[0.864,1.879]	0.222	1.336	[0.682,2.617]	0.398	1.049	[0.511,2.152]	0.897	0.383
rs709816	NBN	G	0.451	1.032	[0.815,1.306]	0.795	1.001	[0.651,1.538]	0.997	0.970	[0.611,1.539]	0.897	0.966
rs2252784	PTPRB	A	0.464	1.259	[0.995,1.594]	0.055	1.298	[0.844,1.997]	0.235	1.031	[0.65,1.635]	0.897	0.104
rs1367117	APOB	A	0.288	1.102	[0.852,1.427]	0.460	1.139	[0.716,1.812]	0.583	1.033	[0.629,1.699]	0.897	0.689

rs4342522	SHFM1	A	0.296	1.228	[0.937,1.609]	0.136	1.187	[0.732,1.924]	0.487	0.967	[0.576,1.623]	0.898	0.293
rs1063742	TACC3	T	0.244	0.911	[0.689,1.204]	0.512	0.878	[0.519,1.485]	0.626	0.964	[0.548,1.695]	0.898	0.741
rs11989	Magmas	T	0.077	1.235	[0.781,1.953]	0.367	1.307	[0.576,2.963]	0.522	1.058	[0.441,2.539]	0.899	0.585
rs2232642	LIG4	A	0.024	1.636	[0.731,3.661]	0.231	1.498	[0.436,5.147]	0.521	0.916	[0.236,3.562]	0.899	0.441
rs9932251	NFATC3	A	0.171	1.023	[0.758,1.381]	0.883	1.060	[0.624,1.801]	0.828	1.037	[0.586,1.835]	0.901	0.970
rs3798134	RAD50	T	0.238	1.069	[0.811,1.41]	0.634	1.033	[0.62,1.72]	0.901	0.966	[0.56,1.667]	0.901	0.891
rs3735481	PPIA	A	0.279	1.227	[0.942,1.598]	0.129	1.266	[0.797,2.012]	0.318	1.032	[0.629,1.694]	0.901	0.236
rs2072501	ZNF71	A	0.191	0.968	[0.69,1.358]	0.850	1.010	[0.537,1.902]	0.975	1.044	[0.531,2.052]	0.901	0.981
rs2269800	ABCC1	G	0.135	0.963	[0.675,1.372]	0.833	0.923	[0.494,1.723]	0.801	0.958	[0.488,1.882]	0.902	0.953
rs275704	Intergenic	G	0.317	0.828	[0.624,1.1]	0.193	0.857	[0.513,1.432]	0.557	1.035	[0.596,1.798]	0.902	0.392
rs1054875	POLG	T	0.436	0.975	[0.764,1.245]	0.841	0.947	[0.606,1.479]	0.811	0.971	[0.602,1.566]	0.903	0.958
rs1538660	IKBKAP	T	0.200	0.866	[0.637,1.177]	0.358	0.899	[0.515,1.567]	0.706	1.038	[0.57,1.888]	0.904	0.634
rs2066534	FMO3	G	0.226	1.084	[0.833,1.412]	0.548	1.118	[0.704,1.775]	0.637	1.031	[0.628,1.694]	0.904	0.775
rs1934951	CYP2C8	A	0.201	1.121	[0.838,1.501]	0.442	1.084	[0.645,1.82]	0.762	0.967	[0.554,1.687]	0.905	0.731
rs8058690	NFATC3	G	0.171	1.022	[0.757,1.38]	0.888	1.058	[0.623,1.797]	0.835	1.035	[0.585,1.833]	0.905	0.972
rs2953993	POLB	A	0.179	0.860	[0.588,1.257]	0.435	0.824	[0.432,1.571]	0.556	0.958	[0.474,1.936]	0.905	0.655
rs581002	MRE11A	T	0.246	1.219	[0.935,1.59]	0.142	1.258	[0.772,2.05]	0.356	1.032	[0.615,1.732]	0.906	0.266
rs3204145	IKBKAP	A	0.201	0.856	[0.629,1.163]	0.320	0.887	[0.508,1.548]	0.674	1.037	[0.569,1.888]	0.906	0.585
rs2069391	CDK2	T	0.076	1.025	[0.666,1.578]	0.911	0.976	[0.453,2.1]	0.950	0.952	[0.419,2.163]	0.906	0.990
rs2274760	GSTA4	C	0.098	1.219	[0.843,1.762]	0.293	1.271	[0.65,2.485]	0.483	1.043	[0.513,2.123]	0.907	0.498
rs8252	GADD45G	A	0.046	1.323	[0.802,2.182]	0.274	1.393	[0.618,3.137]	0.424	1.053	[0.442,2.507]	0.907	0.459
rs6544718	ABCG8	T	0.189	0.872	[0.643,1.184]	0.380	0.904	[0.51,1.603]	0.730	1.036	[0.562,1.913]	0.909	0.662
rs2686184	FDFT1	A	0.408	0.866	[0.676,1.109]	0.254	0.842	[0.534,1.327]	0.458	0.972	[0.596,1.584]	0.909	0.438
rs4774584	CYP19A1	A	0.450	0.951	[0.757,1.194]	0.665	0.975	[0.651,1.46]	0.903	1.026	[0.664,1.584]	0.909	0.909
rs6802898	PPARG	T	0.218	1.144	[0.837,1.562]	0.399	1.183	[0.688,2.036]	0.543	1.035	[0.575,1.862]	0.909	0.619
rs2979895	POLB	C	0.174	0.880	[0.601,1.287]	0.509	0.844	[0.441,1.615]	0.609	0.960	[0.474,1.944]	0.909	0.735
rs1870377	KDR	A	0.228	1.134	[0.853,1.506]	0.387	1.097	[0.644,1.868]	0.734	0.968	[0.548,1.708]	0.910	0.671
rs16845759	TNFSF10	T	0.013	1.507	[0.486,4.669]	0.477	1.355	[0.261,7.049]	0.718	0.899	[0.144,5.617]	0.910	0.754
rs186556	SLC29A1	T	0.014	1.533	[0.526,4.467]	0.434	1.697	[0.348,8.283]	0.513	1.107	[0.19,6.456]	0.910	0.638
rs11700112	PAK7	G	0.099	1.121	[0.78,1.612]	0.537	1.168	[0.598,2.282]	0.649	1.042	[0.51,2.128]	0.910	0.772
rs3176878	VCAM1	T	0.160	0.878	[0.625,1.232]	0.451	0.912	[0.496,1.677]	0.766	1.038	[0.537,2.007]	0.911	0.738
rs2303929	SLC4A2	A	0.229	0.856	[0.65,1.127]	0.268	0.883	[0.529,1.475]	0.635	1.032	[0.596,1.785]	0.911	0.514
rs10264952	STK31	A	0.155	0.898	[0.645,1.251]	0.524	0.864	[0.46,1.623]	0.650	0.963	[0.491,1.887]	0.912	0.761
rs1009373	CD40	T	0.215	1.272	[0.959,1.687]	0.096	1.233	[0.736,2.064]	0.426	0.969	[0.56,1.678]	0.912	0.215
rs207905	XRCC5	G	0.139	0.932	[0.662,1.313]	0.686	0.967	[0.529,1.768]	0.912	1.037	[0.542,1.986]	0.912	0.921
rs1046428	GSTZ1	T	0.177	1.044	[0.767,1.422]	0.784	1.008	[0.565,1.8]	0.978	0.966	[0.52,1.793]	0.912	0.963
rs1801426	BRCA2	G	0.022	1.303	[0.594,2.855]	0.509	1.205	[0.335,4.332]	0.775	0.925	[0.232,3.689]	0.912	0.792
rs2270132	BLM	G	0.384	1.120	[0.877,1.431]	0.365	1.091	[0.697,1.706]	0.704	0.974	[0.603,1.571]	0.913	0.642
rs10018625	TLR3	T	0.258	0.918	[0.699,1.206]	0.540	0.892	[0.546,1.456]	0.647	0.971	[0.572,1.647]	0.914	0.771
rs2071336	TNFRSF17	T	0.040	1.039	[0.594,1.817]	0.893	1.098	[0.439,2.747]	0.842	1.056	[0.393,2.841]	0.914	0.975
rs2228088	TNF	T	0.014	0.493	[0.139,1.744]	0.273	0.561	[0.07,4.503]	0.587	1.138	[0.109,11.906]	0.914	0.494

rs3730017	NOS2	T	0.062	0.903	[0.523,1.561]	0.716	0.856	[0.352,2.083]	0.732	0.948	[0.357,2.514]	0.914	0.896
rs2303400	XRCC5	C	0.402	0.926	[0.728,1.178]	0.533	0.950	[0.62,1.456]	0.814	1.026	[0.647,1.625]	0.914	0.814
rs1805404	PARP1	T	0.171	1.122	[0.822,1.533]	0.469	1.159	[0.666,2.019]	0.602	1.033	[0.57,1.871]	0.914	0.705
rs7175052	IGF1R	A	0.221	1.038	[0.785,1.372]	0.795	1.008	[0.612,1.658]	0.976	0.971	[0.568,1.66]	0.915	0.967
rs532411	POLQ	T	0.084	0.936	[0.597,1.469]	0.775	0.979	[0.46,2.084]	0.956	1.046	[0.458,2.388]	0.916	0.960
rs2645444	FDFT1	G	0.182	0.882	[0.655,1.188]	0.409	0.910	[0.534,1.55]	0.728	1.031	[0.58,1.834]	0.916	0.691
rs3218634	POLQ	G	0.083	0.949	[0.605,1.491]	0.822	0.992	[0.466,2.109]	0.983	1.045	[0.458,2.383]	0.918	0.975
rs1801275	IL4R	G	0.302	0.947	[0.722,1.243]	0.695	0.973	[0.602,1.573]	0.912	1.027	[0.613,1.723]	0.918	0.925
rs11547883	VRK3	G	0.030	1.379	[0.673,2.823]	0.380	1.462	[0.536,3.991]	0.458	1.061	[0.343,3.282]	0.919	0.568
rs10501815	MRE11A	A	0.092	0.813	[0.54,1.222]	0.319	0.848	[0.394,1.824]	0.673	1.044	[0.458,2.376]	0.919	0.582
rs2229113	IL10RA	A	0.291	1.168	[0.908,1.501]	0.227	1.138	[0.723,1.793]	0.576	0.975	[0.599,1.587]	0.919	0.447
rs2308327	LOC100129103	G	0.100	0.742	[0.494,1.116]	0.152	0.775	[0.356,1.687]	0.520	1.044	[0.453,2.406]	0.920	0.320
rs8659	MTRR	T	0.368	1.005	[0.772,1.308]	0.972	0.979	[0.607,1.578]	0.930	0.974	[0.584,1.625]	0.921	0.995
rs2053098	SLCO1B3	A	0.216	1.503	[1.114,2.027]	0.008	1.545	[0.928,2.571]	0.094	1.028	[0.595,1.776]	0.921	0.013
rs2241766	ADIPOQ	G	0.104	0.907	[0.628,1.31]	0.604	0.875	[0.438,1.746]	0.704	0.964	[0.46,2.019]	0.923	0.832
rs1757095	TNC	T	0.067	1.089	[0.678,1.751]	0.724	1.138	[0.494,2.621]	0.761	1.045	[0.426,2.56]	0.924	0.910
rs1536826	CYP2E1	A	0.305	0.901	[0.673,1.206]	0.481	0.876	[0.51,1.502]	0.630	0.972	[0.546,1.733]	0.924	0.723
rs2434470	ALKBH3	G	0.222	1.048	[0.792,1.386]	0.743	1.076	[0.645,1.795]	0.779	1.027	[0.594,1.774]	0.925	0.922
rs2069456	CDK5	C	0.250	0.949	[0.73,1.234]	0.696	0.972	[0.605,1.563]	0.908	1.025	[0.616,1.705]	0.925	0.925
rs512535	APOB	G	0.487	0.856	[0.669,1.096]	0.218	0.876	[0.557,1.379]	0.568	1.023	[0.63,1.661]	0.925	0.432
rs10733103	HSD3B1	G	0.332	1.169	[0.908,1.505]	0.226	1.142	[0.73,1.789]	0.560	0.977	[0.604,1.582]	0.925	0.441
rs609636	CYP4F12	T	0.061	0.380	[0.202,0.713]	0.003	0.404	[0.123,1.324]	0.135	1.064	[0.289,3.919]	0.925	0.005
rs609290	CYP4F12	T	0.061	0.380	[0.202,0.714]	0.003	0.404	[0.123,1.325]	0.135	1.064	[0.289,3.918]	0.926	0.005
rs2470890	CYP1A2	C	0.488	1.058	[0.829,1.35]	0.651	1.082	[0.692,1.69]	0.730	1.023	[0.634,1.649]	0.927	0.867
rs7889839	FMO6	G	0.165	1.226	[0.915,1.644]	0.173	1.258	[0.75,2.111]	0.384	1.026	[0.591,1.782]	0.927	0.318
rs2073618	TNFRSF11B	C	0.460	0.790	[0.613,1.017]	0.068	0.772	[0.489,1.219]	0.267	0.977	[0.598,1.597]	0.927	0.130
rs1800686	CD40	A	0.215	1.258	[0.947,1.671]	0.113	1.227	[0.73,2.062]	0.441	0.975	[0.561,1.695]	0.929	0.246
rs2255235	B2M	T	0.159	1.248	[0.895,1.739]	0.191	1.213	[0.686,2.147]	0.506	0.972	[0.526,1.797]	0.929	0.381
rs6046	F7	T	0.113	1.028	[0.711,1.487]	0.882	1.062	[0.55,2.049]	0.858	1.033	[0.509,2.096]	0.929	0.976
rs3740469	SLK	A	0.204	0.880	[0.657,1.18]	0.393	0.904	[0.526,1.551]	0.713	1.027	[0.575,1.833]	0.929	0.671
rs7886938	FMO6	A	0.165	1.230	[0.917,1.649]	0.167	1.261	[0.752,2.115]	0.380	1.025	[0.59,1.78]	0.930	0.309
rs2544773	RIOK2	C	0.360	0.943	[0.737,1.208]	0.643	0.923	[0.586,1.454]	0.729	0.978	[0.602,1.59]	0.930	0.863
rs389480	BLM	T	0.470	1.143	[0.907,1.44]	0.258	1.166	[0.769,1.768]	0.470	1.020	[0.653,1.595]	0.930	0.449
rs1800871	IL10	T	0.281	0.971	[0.746,1.264]	0.827	0.993	[0.622,1.586]	0.977	1.023	[0.618,1.693]	0.930	0.976
rs1800378	VWF	A	0.429	1.032	[0.808,1.319]	0.800	1.054	[0.675,1.646]	0.815	1.022	[0.634,1.647]	0.930	0.949
rs2363642	GSTZ1	T	0.291	0.883	[0.683,1.141]	0.341	0.863	[0.54,1.379]	0.538	0.978	[0.591,1.618]	0.930	0.563
rs165974	ABCC1	T	0.144	1.017	[0.726,1.424]	0.924	1.046	[0.569,1.926]	0.884	1.029	[0.536,1.979]	0.931	0.987
rs2300095	FRAP1	T	0.320	1.127	[0.872,1.456]	0.361	1.151	[0.729,1.82]	0.546	1.022	[0.625,1.669]	0.932	0.588
rs1061302	NBN	G	0.309	1.147	[0.901,1.461]	0.265	1.171	[0.753,1.821]	0.483	1.021	[0.636,1.638]	0.933	0.461
rs1885472	SIRT1	G	0.361	1.197	[0.943,1.519]	0.139	1.221	[0.794,1.878]	0.364	1.020	[0.644,1.616]	0.933	0.264
rs1348161	PPP3CA	A	0.398	1.154	[0.898,1.484]	0.263	1.130	[0.713,1.791]	0.602	0.979	[0.599,1.6]	0.933	0.501

rs6334	NTRK1	A	0.198	1.043	[0.766,1.42]	0.789	1.017	[0.586,1.766]	0.952	0.975	[0.538,1.767]	0.934	0.965
rs2230806	ABCA1	A	0.331	0.854	[0.654,1.116]	0.248	0.836	[0.523,1.338]	0.455	0.979	[0.59,1.624]	0.934	0.432
rs5974	F11	G	0.157	1.031	[0.75,1.417]	0.850	1.005	[0.565,1.787]	0.986	0.975	[0.526,1.808]	0.936	0.982
rs2072351	BLM	T	0.326	0.857	[0.664,1.104]	0.233	0.840	[0.537,1.313]	0.444	0.980	[0.605,1.588]	0.936	0.408
rs4073054	NR1I3	G	0.346	0.930	[0.73,1.184]	0.557	0.912	[0.589,1.412]	0.681	0.981	[0.614,1.569]	0.936	0.796
rs1938484	LEPR	A	0.205	1.189	[0.901,1.57]	0.222	1.215	[0.739,1.998]	0.443	1.022	[0.601,1.739]	0.937	0.399
rs459552	APC	A	0.198	0.856	[0.629,1.165]	0.323	0.877	[0.502,1.532]	0.645	1.025	[0.562,1.869]	0.937	0.580
rs3217772	CCNA2	C	0.350	0.910	[0.71,1.167]	0.458	0.928	[0.583,1.478]	0.754	1.020	[0.621,1.676]	0.937	0.742
rs17112809	MMS19	T	0.030	1.651	[0.809,3.37]	0.169	1.735	[0.556,5.413]	0.343	1.051	[0.305,3.625]	0.937	0.297
rs2165627	PTPRB	G	0.137	0.902	[0.64,1.271]	0.555	0.878	[0.475,1.624]	0.679	0.974	[0.501,1.891]	0.937	0.793
rs11862958	TNFRSF17	T	0.311	0.859	[0.667,1.107]	0.240	0.876	[0.548,1.403]	0.583	1.020	[0.616,1.691]	0.938	0.462
rs12456560	NDC80	T	0.124	1.330	[0.945,1.872]	0.102	1.295	[0.69,2.434]	0.421	0.974	[0.499,1.902]	0.938	0.225
rs680695	MRE11A	G	0.304	1.123	[0.872,1.447]	0.370	1.145	[0.721,1.819]	0.567	1.020	[0.623,1.67]	0.939	0.606
rs2069835	IL6	C	0.070	0.828	[0.517,1.327]	0.433	0.858	[0.367,2.005]	0.724	1.037	[0.412,2.606]	0.939	0.710
rs1341163	CYP2C8	A	0.388	1.032	[0.809,1.317]	0.797	1.052	[0.675,1.639]	0.824	1.019	[0.633,1.64]	0.939	0.950
rs1934985	CYP2C8	G	0.388	1.032	[0.809,1.317]	0.797	1.052	[0.675,1.639]	0.824	1.019	[0.633,1.64]	0.939	0.950
rs2275620	CYP2C8	T	0.388	1.032	[0.809,1.317]	0.797	1.052	[0.675,1.639]	0.824	1.019	[0.633,1.64]	0.939	0.950
rs1544094	LOC100130458	C	0.191	1.179	[0.846,1.643]	0.331	1.208	[0.676,2.158]	0.524	1.024	[0.547,1.918]	0.940	0.548
rs9503893	PRPF4B	A	0.311	0.898	[0.691,1.168]	0.423	0.881	[0.548,1.416]	0.601	0.981	[0.589,1.634]	0.941	0.665
rs1736557	FMO3	A	0.072	0.605	[0.36,1.015]	0.057	0.581	[0.22,1.533]	0.273	0.961	[0.337,2.74]	0.941	0.110
rs1800738	TPP1	T	0.468	1.095	[0.858,1.399]	0.465	1.115	[0.72,1.727]	0.626	1.018	[0.636,1.628]	0.941	0.711
rs894469	FMO5	G	0.082	0.779	[0.502,1.21]	0.266	0.755	[0.35,1.628]	0.473	0.969	[0.42,2.237]	0.942	0.455
rs16876805	PSKH2	C	0.032	1.359	[0.683,2.705]	0.382	1.418	[0.508,3.959]	0.505	1.043	[0.337,3.225]	0.942	0.597
rs2269112	BRPF1	T	0.158	0.995	[0.718,1.378]	0.975	1.018	[0.566,1.831]	0.951	1.024	[0.546,1.921]	0.942	0.997
rs2066530	FMO3	C	0.011	1.012	[0.302,3.391]	0.984	0.934	[0.133,6.536]	0.945	0.922	[0.103,8.264]	0.942	0.997
rs2480452	PPP2R4	A	0.062	0.862	[0.532,1.399]	0.549	0.894	[0.349,2.291]	0.816	1.037	[0.38,2.829]	0.943	0.825
rs3740066	ABCC2	A	0.347	1.259	[0.981,1.615]	0.070	1.280	[0.815,2.011]	0.284	1.017	[0.628,1.648]	0.945	0.139
rs4764883	IGF1	C	0.329	0.849	[0.655,1.1]	0.215	0.864	[0.541,1.379]	0.539	1.017	[0.615,1.682]	0.946	0.420
rs3087243	CTLA4	A	0.378	0.984	[0.766,1.264]	0.901	0.968	[0.619,1.513]	0.887	0.984	[0.608,1.591]	0.946	0.985
rs3897933	DPYD	A	0.276	0.940	[0.726,1.216]	0.636	0.924	[0.583,1.464]	0.736	0.983	[0.599,1.615]	0.947	0.861
rs246240	ABCC1	G	0.146	1.053	[0.752,1.474]	0.764	1.030	[0.56,1.895]	0.925	0.978	[0.509,1.879]	0.947	0.955
rs10018618	C1QTNF7	C	0.047	1.264	[0.648,2.465]	0.492	1.313	[0.476,3.621]	0.599	1.039	[0.337,3.204]	0.947	0.721
rs3204141	ZHX2	A	0.284	1.050	[0.8,1.378]	0.726	1.069	[0.647,1.766]	0.795	1.018	[0.596,1.74]	0.947	0.919
rs6935443	ESR1	G	0.279	1.226	[0.929,1.619]	0.150	1.248	[0.76,2.05]	0.381	1.018	[0.597,1.734]	0.948	0.282
rs2307340	MCM5	G	0.068	0.590	[0.35,0.995]	0.048	0.569	[0.203,1.597]	0.284	0.964	[0.317,2.933]	0.948	0.095
rs3791878	GAD1	A	0.252	0.889	[0.679,1.164]	0.392	0.905	[0.547,1.496]	0.696	1.018	[0.595,1.741]	0.949	0.667
rs1548216	IL6	C	0.055	1.295	[0.764,2.195]	0.337	1.334	[0.573,3.106]	0.504	1.030	[0.41,2.586]	0.949	0.552
rs1805415	PARP1	A	0.174	1.141	[0.842,1.545]	0.396	1.162	[0.675,2]	0.588	1.019	[0.57,1.819]	0.950	0.639
rs1063045	NBN	T	0.324	1.181	[0.931,1.498]	0.170	1.164	[0.758,1.786]	0.488	0.985	[0.622,1.56]	0.950	0.343
rs2575875	ABCA1	A	0.440	1.149	[0.899,1.469]	0.267	1.132	[0.734,1.747]	0.575	0.985	[0.617,1.573]	0.950	0.497
rs2966245	HSD17B2	C	0.401	1.113	[0.876,1.413]	0.381	1.096	[0.71,1.692]	0.678	0.985	[0.619,1.569]	0.951	0.652

rs10895065	PGR	A	0.332	0.731	[0.557,0.958]	0.023	0.743	[0.461,1.198]	0.222	1.016	[0.606,1.704]	0.951	0.050
rs1236913	PTGS1	T	0.059	0.929	[0.558,1.546]	0.776	0.897	[0.318,2.533]	0.838	0.966	[0.32,2.912]	0.951	0.946
rs3764340	WWOX	G	0.065	0.931	[0.568,1.525]	0.777	0.905	[0.39,2.099]	0.816	0.972	[0.391,2.415]	0.951	0.943
rs2235041	ABCB1	T	0.013	2.012	[0.654,6.185]	0.222	2.125	[0.423,10.678]	0.360	1.056	[0.181,6.173]	0.952	0.378
rs6540964	FRAP1	C	0.361	1.005	[0.769,1.314]	0.972	1.021	[0.631,1.652]	0.934	1.016	[0.606,1.702]	0.953	0.996
rs1801701	APOB	A	0.076	1.059	[0.694,1.615]	0.791	1.085	[0.508,2.319]	0.833	1.025	[0.454,2.315]	0.953	0.951
rs2272615	POLB	G	0.211	0.926	[0.665,1.288]	0.648	0.909	[0.507,1.628]	0.747	0.981	[0.523,1.842]	0.953	0.870
rs4646421	CYP1A1	T	0.173	1.151	[0.848,1.563]	0.367	1.171	[0.692,1.982]	0.556	1.017	[0.576,1.795]	0.953	0.599
rs2257212	SLC15A2	A	0.441	0.970	[0.767,1.226]	0.797	0.957	[0.625,1.464]	0.838	0.986	[0.625,1.558]	0.953	0.954
rs10515783	UBLCP1	T	0.289	0.859	[0.662,1.116]	0.255	0.872	[0.544,1.397]	0.570	1.015	[0.611,1.685]	0.954	0.479
rs1143672	SLC15A2	A	0.440	0.968	[0.766,1.224]	0.788	0.981	[0.645,1.492]	0.929	1.013	[0.645,1.592]	0.955	0.963
rs8353	KLHL22	T	0.200	0.956	[0.715,1.278]	0.762	0.940	[0.545,1.621]	0.824	0.983	[0.549,1.763]	0.955	0.939
rs16932374	VWF	T	0.029	1.232	[0.579,2.618]	0.588	1.275	[0.425,3.829]	0.665	1.035	[0.305,3.517]	0.956	0.814
rs1060253	SLC7A5	G	0.256	0.976	[0.748,1.273]	0.859	0.990	[0.616,1.593]	0.968	1.014	[0.609,1.689]	0.956	0.984
rs5759197	TSPO	C	0.426	1.353	[1.066,1.718]	0.013	1.371	[0.89,2.11]	0.152	1.013	[0.639,1.606]	0.957	0.026
rs2228638	NRP1	A	0.098	0.976	[0.66,1.443]	0.903	0.956	[0.478,1.911]	0.899	0.980	[0.466,2.059]	0.957	0.987
rs2235047	ABCB1	G	0.051	1.644	[0.955,2.829]	0.073	1.602	[0.666,3.856]	0.293	0.975	[0.384,2.474]	0.957	0.158
rs2242048	SLC28A1	T	0.111	1.123	[0.771,1.636]	0.544	1.101	[0.558,2.175]	0.781	0.980	[0.473,2.032]	0.957	0.817
rs1805335	RAD23B	A	0.445	1.029	[0.815,1.298]	0.811	1.016	[0.665,1.553]	0.940	0.988	[0.627,1.557]	0.958	0.971
rs7214723	CAMKK1	C	0.402	1.088	[0.859,1.378]	0.484	1.075	[0.701,1.649]	0.741	0.988	[0.625,1.561]	0.959	0.762
rs2066494	RAD9A	C	0.024	1.646	[0.815,3.327]	0.165	1.591	[0.472,5.37]	0.454	0.967	[0.264,3.54]	0.959	0.333
rs1639	PON2	G	0.206	0.819	[0.606,1.107]	0.194	0.807	[0.461,1.411]	0.451	0.985	[0.54,1.795]	0.959	0.361
rs1520664	DPYD	T	0.386	0.994	[0.782,1.264]	0.961	0.982	[0.638,1.511]	0.935	0.988	[0.622,1.57]	0.960	0.996
rs2278293	IMPDH1	A	0.465	1.054	[0.828,1.342]	0.668	1.042	[0.679,1.599]	0.852	0.988	[0.622,1.57]	0.960	0.905
rs871514	UGT1A10	G	0.493	1.044	[0.821,1.328]	0.726	1.056	[0.692,1.611]	0.799	1.012	[0.642,1.595]	0.960	0.921
rs1135961	PSMA7	T	0.134	0.873	[0.616,1.238]	0.447	0.858	[0.443,1.663]	0.650	0.982	[0.482,2]	0.961	0.700
rs2288548	IMPDH1	A	0.237	1.034	[0.794,1.346]	0.803	1.048	[0.647,1.696]	0.850	1.013	[0.604,1.699]	0.961	0.957
rs1962589	IGF1R	C	0.186	1.159	[0.842,1.596]	0.365	1.177	[0.673,2.059]	0.569	1.015	[0.556,1.854]	0.961	0.601
rs13428823	EFR3B	G	0.399	0.978	[0.773,1.237]	0.852	0.967	[0.635,1.472]	0.876	0.989	[0.63,1.553]	0.961	0.974
rs17773251	CSNK1A1L	G	0.090	0.921	[0.607,1.397]	0.699	0.939	[0.453,1.948]	0.866	1.020	[0.463,2.247]	0.962	0.921
rs5496	ICAM1	A	0.016	0.340	[0.076,1.519]	0.158	0.361	[0.046,2.855]	0.334	1.061	[0.091,12.417]	0.962	0.254
rs1805794	NBN	G	0.309	1.164	[0.915,1.481]	0.217	1.151	[0.743,1.783]	0.529	0.989	[0.619,1.58]	0.962	0.419
rs2229362	BCL6	A	0.189	1.111	[0.816,1.515]	0.503	1.096	[0.643,1.87]	0.736	0.986	[0.555,1.752]	0.963	0.777
rs3762412	DPYD	T	0.308	0.904	[0.707,1.155]	0.419	0.893	[0.561,1.422]	0.634	0.988	[0.602,1.624]	0.963	0.673
rs12448860	FANCA	A	0.454	1.326	[1.05,1.673]	0.018	1.340	[0.877,2.048]	0.176	1.011	[0.642,1.592]	0.963	0.035
rs4883263	CD163	T	0.102	0.901	[0.588,1.383]	0.635	0.885	[0.44,1.78]	0.733	0.982	[0.456,2.115]	0.963	0.859
rs1570070	IGF2R	G	0.347	0.789	[0.613,1.017]	0.068	0.799	[0.503,1.267]	0.340	1.012	[0.616,1.663]	0.963	0.145
rs183484	RRM1	T	0.454	0.982	[0.773,1.246]	0.879	0.993	[0.635,1.552]	0.974	1.011	[0.627,1.63]	0.963	0.988
rs1063311	MAPK1	A	0.393	0.934	[0.728,1.198]	0.589	0.944	[0.598,1.491]	0.806	1.012	[0.619,1.652]	0.964	0.851
rs5742714	IGF1	C	0.095	0.741	[0.487,1.127]	0.161	0.755	[0.353,1.616]	0.469	1.019	[0.446,2.331]	0.964	0.318
rs1709182	ESR1	C	0.316	0.920	[0.715,1.185]	0.520	0.910	[0.567,1.46]	0.695	0.988	[0.597,1.637]	0.964	0.775

rs2070150	ATF6	C	0.095	1.197	[0.823,1.739]	0.347	1.216	[0.617,2.397]	0.571	1.017	[0.496,2.085]	0.964	0.589
rs348472	ALDH1A1	A	0.098	0.982	[0.64,1.507]	0.934	1.000	[0.478,2.092]	1.000	1.018	[0.457,2.269]	0.965	0.996
rs1800925	IL13	T	0.233	1.057	[0.801,1.396]	0.694	1.070	[0.641,1.786]	0.795	1.012	[0.585,1.751]	0.965	0.906
rs4646034	CASP9	A	0.444	1.233	[0.977,1.557]	0.078	1.221	[0.796,1.872]	0.361	0.990	[0.625,1.567]	0.965	0.168
rs1139488	ALAD	C	0.365	1.029	[0.807,1.312]	0.818	1.018	[0.659,1.574]	0.935	0.990	[0.62,1.58]	0.966	0.973
rs638456	DPYD	C	0.388	1.149	[0.905,1.458]	0.255	1.160	[0.762,1.767]	0.490	1.010	[0.643,1.587]	0.966	0.455
rs1520663	DPYD	T	0.385	1.000	[0.786,1.272]	0.999	0.990	[0.644,1.524]	0.964	0.990	[0.623,1.574]	0.967	0.999
rs4986791	TLR4	T	0.043	0.821	[0.458,1.47]	0.506	0.000	[0,5.770474E256]	0.966	0.000	[0,7.033067E256]	0.967	0.801
rs12806698	RRM1	A	0.241	0.914	[0.688,1.214]	0.534	0.903	[0.536,1.523]	0.703	0.988	[0.564,1.73]	0.967	0.787
rs2302524	PLAUR	C	0.176	0.839	[0.608,1.157]	0.284	0.850	[0.474,1.522]	0.584	1.013	[0.541,1.899]	0.967	0.517
rs3740955	RAG1	G	0.418	1.074	[0.846,1.363]	0.558	1.064	[0.686,1.649]	0.783	0.990	[0.619,1.584]	0.968	0.826
rs2296239	CYP24A1	T	0.274	1.014	[0.782,1.314]	0.915	1.025	[0.64,1.639]	0.919	1.010	[0.611,1.67]	0.968	0.991
rs4947324	TNF	T	0.102	1.431	[0.995,2.057]	0.053	1.412	[0.756,2.638]	0.279	0.987	[0.507,1.922]	0.969	0.115
rs7201683	WWOX	G	0.031	0.517	[0.238,1.126]	0.097	0.000	[0,2.470432E271]	0.968	0.000	[0,4.778227E271]	0.969	0.251
rs35766	IGF1	G	0.246	0.844	[0.632,1.126]	0.249	0.853	[0.51,1.427]	0.545	1.011	[0.581,1.758]	0.969	0.465
rs35621	ABCC1	T	0.113	1.302	[0.915,1.853]	0.142	1.286	[0.691,2.39]	0.427	0.987	[0.508,1.917]	0.970	0.290
rs1800872	IL10	A	0.281	0.969	[0.744,1.26]	0.812	0.959	[0.602,1.529]	0.862	0.990	[0.599,1.638]	0.970	0.962
rs2303428	MSH2	C	0.106	0.739	[0.499,1.095]	0.132	0.751	[0.353,1.596]	0.456	1.015	[0.452,2.281]	0.970	0.272
rs2071724	TTLL12	A	0.418	0.971	[0.77,1.225]	0.807	0.963	[0.634,1.463]	0.861	0.992	[0.633,1.553]	0.971	0.961
rs419029	TNFRSF17	A	0.016	1.712	[0.732,4.007]	0.215	1.666	[0.409,6.782]	0.476	0.973	[0.224,4.229]	0.971	0.420
rs478333	ABCB11	C	0.500	1.170	[0.931,1.47]	0.179	1.160	[0.767,1.756]	0.482	0.992	[0.636,1.546]	0.971	0.353
rs2286940	MLH1	T	0.390	0.976	[0.766,1.245]	0.845	0.985	[0.631,1.535]	0.945	1.009	[0.627,1.623]	0.972	0.980
rs16944831	BLM	T	0.085	1.141	[0.731,1.781]	0.560	1.125	[0.551,2.298]	0.746	0.986	[0.45,2.163]	0.972	0.819
rs1496499	IGFBP3	T	0.487	1.023	[0.811,1.289]	0.850	1.031	[0.678,1.567]	0.887	1.008	[0.643,1.58]	0.972	0.976
rs11571117	REN	A	0.011	0.828	[0.232,2.963]	0.772	0.795	[0.101,6.293]	0.828	0.960	[0.095,9.693]	0.973	0.942
rs2074085	ABCC1	G	0.133	0.941	[0.656,1.348]	0.739	0.929	[0.495,1.745]	0.820	0.988	[0.5,1.952]	0.973	0.930
rs3219484	MUTYH	A	0.052	1.420	[0.868,2.323]	0.163	1.396	[0.564,3.459]	0.471	0.984	[0.379,2.555]	0.973	0.336
rs2794520	CRP	T	0.320	0.816	[0.636,1.049]	0.113	0.810	[0.513,1.278]	0.365	0.992	[0.608,1.619]	0.973	0.223
rs2310235	IL1RL2	T	0.299	0.858	[0.661,1.115]	0.253	0.851	[0.525,1.378]	0.512	0.991	[0.591,1.662]	0.974	0.458
rs16931996	DUSP13	C	0.022	0.761	[0.293,1.978]	0.576	0.000	[0,.]	0.974	0.000	[0,.]	0.975	0.855
rs8191448	GSTP1	T	0.023	0.415	[0.137,1.257]	0.120	0.000	[0,.]	0.973	0.000	[0,.]	0.975	0.298
rs983101	DPYD	C	0.009	2.096	[0.612,7.171]	0.238	0.000	[0,.]	0.977	0.000	[0,.]	0.976	0.499
rs915909	CYP2E1	T	0.018	0.994	[0.38,2.601]	0.991	0.000	[0,.]	0.976	0.000	[0,.]	0.976	0.999
rs3793524	PTPN3	C	0.378	1.205	[0.947,1.533]	0.129	1.214	[0.787,1.872]	0.381	1.007	[0.633,1.602]	0.976	0.253
rs2228065	ALOX5	A	0.016	1.626	[0.7,3.778]	0.258	0.000	[0,.]	0.977	0.000	[0,.]	0.976	0.528
rs552926	DPYD	G	0.390	1.138	[0.898,1.444]	0.285	1.146	[0.754,1.743]	0.524	1.007	[0.642,1.58]	0.976	0.502
rs2227307	IL8	G	0.484	0.945	[0.746,1.197]	0.640	0.939	[0.617,1.428]	0.768	0.993	[0.632,1.561]	0.976	0.873
rs3739927	SETX	G	0.055	0.967	[0.545,1.716]	0.909	0.952	[0.353,2.568]	0.922	0.984	[0.337,2.87]	0.977	0.990
rs11879620	VRK3	C	0.031	1.494	[0.742,3.008]	0.261	1.519	[0.557,4.143]	0.414	1.017	[0.333,3.105]	0.977	0.437
rs6763816	TNFSF10	T	0.009	0.599	[0.124,2.889]	0.524	0.000	[0,.]	0.976	0.000	[0,.]	0.977	0.816
rs16905649	PTPRJ	A	0.016	1.181	[0.461,3.021]	0.729	0.000	[0,.]	0.977	0.000	[0,.]	0.977	0.941

rs4987875	ATM	T	0.013	1.016	[0.304,3.393]	0.980	0.000	[0,.]	0.977	0.000	[0,.]	0.977	0.999
rs13815	MCAT	C	0.403	0.832	[0.645,1.073]	0.156	0.838	[0.521,1.347]	0.466	1.007	[0.606,1.675]	0.977	0.315
rs2020873	MLH1	T	0.015	0.642	[0.178,2.312]	0.498	0.663	[0.087,5.075]	0.693	1.034	[0.102,10.494]	0.978	0.749
rs2230592	MST1R	G	0.015	1.512	[0.582,3.928]	0.396	0.000	[0,.]	0.979	0.000	[0,.]	0.978	0.697
rs2270423	GSTZ1	A	0.296	0.906	[0.699,1.175]	0.457	0.913	[0.555,1.501]	0.719	1.007	[0.592,1.712]	0.979	0.732
rs2229653	SPN	T	0.013	0.882	[0.282,2.756]	0.828	0.000	[0,.]	0.979	0.000	[0,.]	0.979	0.976
rs3136664	CCR1	A	0.015	0.914	[0.332,2.517]	0.861	0.000	[0,.]	0.979	0.000	[0,.]	0.979	0.985
rs28900388	UGT1A10	C	0.013	1.919	[0.611,6.032]	0.265	0.000	[0,.]	0.980	0.000	[0,.]	0.979	0.537
rs874401	LOC729734	T	0.209	0.964	[0.728,1.277]	0.800	0.957	[0.58,1.58]	0.865	0.993	[0.58,1.701]	0.979	0.959
rs6868365	RAD50	T	0.010	0.621	[0.127,3.031]	0.555	0.642	[0.071,5.817]	0.694	1.035	[0.079,13.484]	0.979	0.796
rs1056932	BCL6	C	0.413	1.173	[0.922,1.493]	0.194	1.180	[0.765,1.82]	0.454	1.006	[0.633,1.599]	0.980	0.368
rs663530	MRE11A	T	0.249	1.202	[0.921,1.568]	0.175	1.194	[0.734,1.943]	0.475	0.993	[0.592,1.666]	0.980	0.350
rs496550	ABCB11	A	0.491	1.141	[0.907,1.435]	0.259	1.147	[0.758,1.737]	0.515	1.006	[0.645,1.569]	0.980	0.467
rs169547	BRCA2	A	0.012	1.023	[0.324,3.224]	0.969	0.000	[0,.]	0.980	0.000	[0,.]	0.980	0.999
rs5742980	PMS1	C	0.012	1.169	[0.352,3.877]	0.799	0.000	[0,.]	0.981	0.000	[0,.]	0.981	0.968
rs2230635	CHAF1A	G	0.014	2.054	[0.742,5.688]	0.166	0.000	[0,.]	0.982	0.000	[0,.]	0.981	0.383
rs4253199	ERCC6	T	0.011	2.038	[0.733,5.668]	0.173	0.000	[0,.]	0.982	0.000	[0,.]	0.981	0.394
rs12072582	FMO3	C	0.014	1.529	[0.542,4.314]	0.422	0.000	[0,.]	0.982	0.000	[0,.]	0.981	0.724
rs8178318	LPO	T	0.012	1.587	[0.513,4.904]	0.423	0.000	[0,.]	0.982	0.000	[0,.]	0.981	0.725
rs4765181	SCARB1	A	0.365	1.124	[0.878,1.438]	0.355	1.117	[0.702,1.778]	0.641	0.994	[0.605,1.634]	0.981	0.614
rs3917974	CSF3R	G	0.015	0.127	[0.016,0.998]	0.050	0.000	[0,.]	0.979	0.000	[0,.]	0.982	0.146
rs9332485	F5	A	0.009	1.179	[0.33,4.215]	0.800	0.000	[0,.]	0.982	0.000	[0,.]	0.982	0.968
rs12659	SLC19A1	T	0.424	0.896	[0.707,1.135]	0.362	0.891	[0.584,1.36]	0.593	0.995	[0.632,1.566]	0.982	0.607
rs6416668	ABCC6	T	0.018	1.105	[0.447,2.727]	0.829	0.000	[0,.]	0.983	0.000	[0,.]	0.982	0.977
rs3136430	F2	T	0.014	0.523	[0.117,2.344]	0.397	0.000	[0,.]	0.982	0.000	[0,.]	0.983	0.698
rs246220	ABCC1	G	0.176	0.870	[0.634,1.194]	0.387	0.864	[0.486,1.537]	0.618	0.993	[0.535,1.844]	0.983	0.639
rs16839100	FCRL2	T	0.010	1.412	[0.473,4.215]	0.536	0.000	[0,.]	0.984	0.000	[0,.]	0.983	0.826
rs2410478	NAT1	C	0.010	0.661	[0.154,2.845]	0.579	0.000	[0,.]	0.983	0.000	[0,.]	0.983	0.857
rs2142694	CYP2D6	A	0.463	0.943	[0.741,1.2]	0.633	0.948	[0.616,1.459]	0.807	1.005	[0.632,1.597]	0.983	0.878
rs16836266	NEK11	C	0.110	1.521	[1.041,2.221]	0.030	1.509	[0.779,2.926]	0.223	0.993	[0.491,2.007]	0.984	0.066
rs3808600	ZHX2	T	0.287	1.041	[0.792,1.367]	0.774	1.047	[0.632,1.732]	0.859	1.006	[0.587,1.722]	0.984	□□□□
rs3886641	GARS	A	0.010	0.576	[0.127,2.621]	0.476	0.000	[0,.]	0.983	0.000	[0,.]	0.984	0.775
rs2292566	EPHX1	A	0.143	1.120	[0.815,1.538]	0.484	1.113	[0.634,1.955]	0.709	0.994	[0.543,1.82]	0.984	0.754
rs673	TNF	A	0.011	0.259	[0.034,2.003]	0.196	0.000	[0,.]	0.983	0.000	[0,.]	0.984	0.433
rs5490	ICAM1	C	0.038	1.646	[0.842,3.218]	0.145	1.662	[0.603,4.584]	0.326	1.010	[0.335,3.042]	0.986	0.268
rs1049007	BMP2	A	0.340	1.239	[0.961,1.597]	0.099	1.233	[0.783,1.942]	0.366	0.996	[0.612,1.619]	0.986	0.205
rs2472680	NR1I2	T	0.082	0.831	[0.465,1.484]	0.531	0.839	[0.298,2.364]	0.740	1.010	[0.327,3.121]	0.987	0.794
rs472614	ABCB11	A	0.444	1.074	[0.855,1.348]	0.540	1.078	[0.714,1.626]	0.722	1.004	[0.645,1.561]	0.987	0.799
rs3136682	CCL1	T	0.033	1.265	[0.67,2.389]	0.469	1.253	[0.412,3.807]	0.691	0.990	[0.302,3.25]	0.987	0.739
rs1801020	F12	T	0.305	1.086	[0.844,1.398]	0.521	1.082	[0.687,1.703]	0.734	0.996	[0.612,1.62]	0.988	0.789
rs8187858	ABCC1	T	0.080	0.992	[0.646,1.524]	0.971	0.986	[0.452,2.15]	0.971	0.993	[0.43,2.298]	0.988	0.999

rs3021094	IL10	C	0.086	0.796	[0.511,1.24]	0.314	0.791	[0.346,1.805]	0.577	0.993	[0.408,2.417]	0.988	0.546
rs2802269	CDC42BPA	G	0.089	0.911	[0.609,1.361]	0.648	0.916	[0.442,1.899]	0.814	1.006	[0.458,2.207]	0.988	0.887
rs3024944	STAT6	C	0.014	1.259	[0.403,3.935]	0.692	1.276	[0.28,5.816]	0.753	1.013	[0.177,5.794]	0.988	0.895
rs1934963	CYP2C9	C	0.180	0.833	[0.608,1.139]	0.252	0.836	[0.466,1.502]	0.550	1.005	[0.534,1.889]	0.989	0.465
rs725349	HGF	T	0.238	1.038	[0.78,1.38]	0.800	1.042	[0.628,1.727]	0.875	1.004	[0.582,1.732]	0.989	0.961
rs759853	AKR1B1	A	0.386	0.979	[0.768,1.248]	0.866	0.982	[0.637,1.514]	0.936	1.003	[0.63,1.598]	0.990	0.984
rs3093057	CSF1	T	0.329	0.996	[0.772,1.285]	0.976	0.999	[0.624,1.601]	0.998	1.003	[0.606,1.661]	0.990	1.000
rs10521092	IKBKAP	T	0.038	1.586	[0.768,3.275]	0.213	1.598	[0.542,4.709]	0.396	1.008	[0.302,3.361]	0.990	0.369
rs3136794	POLB	G	0.210	0.919	[0.659,1.284]	0.622	0.923	[0.514,1.658]	0.789	1.004	[0.533,1.891]	0.990	0.867
rs2236654	IGHMBP2	A	0.216	0.877	[0.652,1.181]	0.389	0.881	[0.507,1.529]	0.651	1.004	[0.555,1.815]	0.991	0.650
rs592792	GSTM2	A	0.143	0.980	[0.692,1.387]	0.910	0.976	[0.525,1.817]	0.940	0.996	[0.509,1.949]	0.991	0.992
rs4252749	CCNI	C	0.026	1.210	[0.551,2.661]	0.635	1.201	[0.357,4.047]	0.767	0.992	[0.258,3.824]	0.991	0.870
rs43038	PON2	G	0.162	1.049	[0.76,1.448]	0.771	1.052	[0.594,1.866]	0.861	1.003	[0.541,1.859]	0.992	0.950
rs4766002	C12orf32	T	0.434	1.101	[0.865,1.401]	0.434	1.099	[0.708,1.705]	0.675	0.998	[0.623,1.598]	0.993	0.701
rs773902	F2RL3	A	0.245	0.877	[0.65,1.184]	0.392	0.875	[0.505,1.516]	0.634	0.998	[0.552,1.803]	0.993	0.647
rs2020903	CASP9	C	0.444	1.223	[0.968,1.544]	0.091	1.225	[0.799,1.878]	0.353	1.002	[0.633,1.585]	0.994	0.187
rs699517	ENOSF1	T	0.370	0.940	[0.736,1.199]	0.616	0.941	[0.605,1.464]	0.788	1.002	[0.624,1.609]	0.994	0.864
rs1005230	VEGFA	T	0.437	1.049	[0.829,1.327]	0.690	1.051	[0.676,1.632]	0.826	1.001	[0.625,1.603]	0.995	0.911
rs1822017	DCBLD2	T	0.157	0.931	[0.668,1.296]	0.670	0.932	[0.514,1.691]	0.818	1.002	[0.528,1.903]	0.995	0.899
rs6041884	FKBP1A	G	0.290	1.030	[0.804,1.32]	0.815	1.029	[0.653,1.621]	0.903	0.999	[0.614,1.623]	0.996	0.969
rs610899	MRE11A	G	0.421	0.998	[0.789,1.263]	0.988	0.997	[0.65,1.531]	0.990	0.999	[0.632,1.58]	0.997	1.000
rs4646032	CASP9	C	0.444	1.218	[0.965,1.538]	0.097	1.219	[0.795,1.869]	0.363	1.001	[0.633,1.584]	0.997	0.198
rs1866389	LOC100129870	G	0.194	0.953	[0.709,1.28]	0.748	0.954	[0.559,1.626]	0.862	1.001	[0.565,1.775]	0.997	0.942
rs1205	CRP	T	0.313	0.814	[0.632,1.048]	0.111	0.813	[0.513,1.289]	0.378	0.999	[0.609,1.638]	0.997	0.224
rs757081	NUCB2	C	0.293	1.102	[0.85,1.429]	0.461	1.104	[0.686,1.775]	0.685	1.001	[0.602,1.665]	0.997	0.728
rs10410075	VRK3	A	0.031	1.457	[0.723,2.936]	0.292	1.456	[0.53,3.997]	0.466	0.999	[0.324,3.077]	0.998	0.493
rs7006788	C8orf42	T	0.340	1.005	[0.784,1.287]	0.972	1.005	[0.643,1.571]	0.983	1.000	[0.619,1.616]	0.999	0.999
rs26312	GHRL	A	0.150	0.847	[0.597,1.201]	0.351	0.847	[0.455,1.578]	0.601	1.000	[0.51,1.964]	0.999	0.595