

Supplementary Table 1. Genotype and allele frequency of four main ethnic groups and relative risk estimation for homozygous variant and heterozygous genotype

Gene polymorphism	Population	Genotype Frequency			High Risk	Moderate Risk	Allele frequency	
		Homozygous wild type	Homozygous variant	Heterozygous	Homozygous variant Population/All	Heterozygous Population/All	Major allele	Minor allele
NRF2 rs6721961 C617A (in the promoter)		GG	TT	GT	TT	GT	G	T
	African	0.887	0.002	0.112	0.069	0.483	0.943	0.057
	East Asian	0.577	0.063	0.359	2.172	1.547	0.757	0.243
Oxidative Stress	South Asian	0.726	0.031	0.243	1.069	1.047	0.848	0.152
	European	0.763	0.014	0.223	0.483	0.961	0.875	0.125
	All	0.739	0.029	0.232			0.855	0.145
NRF2 rs35652124 A653G (in the promoter)		TT	CC	CT	CC	CT	T	C
	African	0.720	0.015	0.265	0.091	0.626	0.852	0.148
	East Asian	0.208	0.312	0.480	1.902	1.135	0.448	0.552
Oxidative Stress	South Asian	0.207	0.286	0.507	1.744	1.199	0.460	0.540
	European	0.479	0.091	0.429	0.555	1.014	0.694	0.306
	All	0.413	0.164	0.423			0.624	0.376
NQO1 rs1800566 C609T or C559T (base transition in exon 6) (Pro ¹⁸⁷ Ser)		GG	AA	AG	AA	AG	G	A
	African	0.675	0.026	0.300	0.295	0.748	0.825	0.175
	East Asian	0.319	0.157	0.524	1.784	1.307	0.581	0.419
Oxidative Stress	South Asian	0.411	0.127	0.462	1.443	1.152	0.642	0.358
	European	0.626	0.048	0.326	0.545	0.813	0.789	0.211
	All	0.510	0.088	0.401			0.711	0.289
NQO1 rs1131341 C465T(Arg ¹³⁹ Trp)		GG	AA	AG	AA	AG	G	A
	African	0.994	0	0.006	0	0	0.997	0.003
	East Asian	0.960	0	0.040	0	1	0.980	0.020
Oxidative Stress	South Asian	0.910	0.010	0.080	5	2.051	0.950	0.050
	European	0.950	0	0.050	0	1.282	0.975	0.025
	All	0.959	0.002	0.039			0.979	0.021

HO-1 rs2071746 -413A>T		AA	TT	AT	TT	AT	T	A
	African	0.098	0.474	0.428	1.596	0.926	0.688	0.312
	East Asian	0.242	0.288	0.470	0.970	1.017	0.523	0.477
Oxidative Stress	South Asian	0.190	0.309	0.501	1.040	1.084	0.559	0.441
	European	0.306	0.187	0.507	0.630	1.097	0.440	0.560
	All	0.241	0.297	0.462			0.528	0.472
SOD2 rs4880G/A (exon 2) (Ala ¹⁶ Val)		AA	GG	AG	GG	AG	A	G
	African	0.333	0.180	0.487	0.923	1.127	0.576	0.424
	East Asian	0.764	0.014	0.222	0.072	0.514	0.875	0.125
	South Asian	0.245	0.262	0.493	1.344	1.141	0.492	0.508
Oxidative Stress	European	0.294	0.227	0.479	1.164	1.109	0.534	0.466
	All	0.373	0.195	0.432			0.589	0.411
GST-A1 rs3957357 C69T (non coding)		GG	AA	AG	AA	AG	G	A
	African	0.470	0.103	0.427	0.972	1.062	0.684	0.316
	East Asian	0.740	0.018	0.242	0.170	0.601	0.861	0.139
Detoxification	South Asian	0.440	0.131	0.429	1.236	1.067	0.654	0.346
	European	0.318	0.177	0.505	1.670	1.256	0.571	0.429
	All	0.492	0.106	0.402			0.693	0.307
GST-M1 rs366631							Positive	Null
	African						0.684	0.316
	East Asian						0.479	0.521
Detoxification	South Asian						0.597	0.403
	European						0.488	0.512
	All						0.520	0.480* (no Americans were included)
GST-T1 rs17856199							Positive	Null
	African						0.629	0.371
Detoxification	East Asian						0.524	0.476
	South						0.755	0.245

Asian								
European							0.867	0.183
All							0,736	0.264* (no Americans were included)
GST-P1(319A>G) rs1695 Ile ¹⁰⁵ Val (missense mutation)		AA	GG	AG	GG	AG	A	G
African		0.265	0.225	0.510	1.619	1.194	0.520	0.480
East Asian		0.673	0.030	0.298	0.216	0.698	0.821	0.179
Detoxification	South Asian	0.513	0.102	0.384	0.734	0.899	0.706	0.294
	European	0.445	0.107	0.447	0.770	1.047	0.669	0.331
	All	0.434	0.139	0.427			0.647	0.353
EPHX1 Ex_3 rs1051740 Tyr ¹¹³ His (slow allele)		TT	CC	TC	CC	TC	T	C
African		0.744	0.026	0.230	0.222	0.585	0.859	0.141
East Asian		0.272	0.236	0.492	2.017	1.252	0.518	0.482
Detoxification	South Asian	0.384	0.139	0.476	1.188	1.211	0.623	0.377
	European	0.487	0.095	0.417	0.812	1.061	0.696	0.304
	All	0.490	0.117	0.393			0.687	0.313
EPHX1 Ex_4 rs2234922 His ¹³⁹ Arg(fast allele)		AA	GG	AG	AA	AG	A	G
African		0.421	0.127	0.452	0,673	1.426	0.647	0.353
East Asian		0.780	0.016	0.204	1,246	0.644	0.882	0.118
Detoxification	South Asian	0.605	0.074	0.321	0,966	1.013	0.766	0.234
	European	0.686	0.014	0.300	1,096	0.946	0.836	0.164
	All	0.626	0.057	0.317			0.785	0.215
CYP1A1_2A rs4646903 (T> C mutation at 3' UTR)		AA	GG	AG	GG	AG	A	G
African		0.589	0.057	0.354	0.523	0.959	0.766	0.234
East Asian		0.329	0.188	0.482	1.725	1.306	0.570	0.430
Detoxification	South Asian	0.446	0.125	0.429	1.147	1.163	0.661	0.339
	European	0.793	0.008	0.199	0.073	0.539	0.893	0.107
	All	0.522	0.109	0.369			0.707	0.293

CYP1A1_2C rs1048943 Ile ⁴⁶² Val		TT	CC	TC	CC	TC	T	C
	African	0.986	0	0.014	0	0.07	0.993	0.007
	East Asian	0.562	0.065	0.373	1.625	1.995	0.748	0.252
Detoxification	South Asian	0.765	0.018	0.217	0.45	1.16	0.873	0.127
	European	0.930	0	0.070	0	0.374	0.965	0.035
	All	0.773	0.040	0.187			0.867	0.133
CYP2E1*6 rs6413432 (7632 T>A)(intron mutation)		TT	AA	AT	TT	AT	T	A
	African	0.855	0.009	0.136	1.199	0.538	0.923	0.077
	East Asian	0.536	0.079	0.385	0.752	1.522	0.728	0.272
Detoxification	South Asian	0.628	0.043	0.329	0.881	1.300	0.792	0.208
	European	0.805	0.016	0.179	1.129	0.708	0.895	0.105
	All	0.713	0.034	0.253			0.839	0.161
CYP2E1*5B rs3813867 (in the 5' UTR)		GG	CC	CG	GG	CG	G	C
	African	0.871	0.005	0.124	1.032	0.873	0.933	0.067
	East Asian	0.651	0.056	0.294	1	2	0.798	0.202
Detoxification	South Asian	0.982	0	0.018	1	0	0.991	0.009
	European	0.920	0.002	0.078	1.090	0.549	0.959	0.041
	All	0.844	0.014	0.142			0.915	0.085
MPO rs2333227 G463A (in the promoter region)		CC	TT	CT	CC	CT	C	T
	African	0.415	0.145	0.440	0.675	1.375	0.635	0.365
	East Asian	0.734	0.02	0.246	1.193	0.769	0.857	0.143
Detoxification	South Asian	0.763	0.016	0.221	1.241	0.691	0.873	0.127
	European	0.588	0.064	0.348	0.956	1.088	0.762	0.238
	All	0.615	0.065	0.320			0.775	0.225
XRCC3 rs1799782 Arg ¹⁹⁴ Trp		GG	AA	AG	AA	AG	G	A

DNA repair	African	0.858	0.002	0.141	0.091	0.691	0.928	0.072
	East Asian	0.518	0.081	0.401	3.682	1.966	0.718	0.282
	South Asian	0.783	0.004	0.213	0.182	1.044	0.890	0.110
	European	0.907	0.010	0.083	0.455	0.407	0.948	0.052
	All	0.774	0.022	0.204			0.876	0.124
XRCC3 rs861539								
Thr ²⁴¹ Met (C/T transition at codon 241)		GG	AA	AG	AA	AG	G	A
DNA repair	African	0.657	0.038	0.306	0.603	0.994	0.809	0.191
	East Asian	0.855	0.002	0.143	0.032	0.464	0.927	0.073
	South Asian	0.630	0.049	0.321	0.778	1.042	0.790	0.210
	European	0.378	0.165	0.457	2.619	1.484	0.606	0.394
	All	0.629	0.063	0.308			0.783	0.217
XPD rs1799793								
Asp ³¹² Asn (XPD G312A)		CC	TT	CT	TT	CT	C	T
DNA repair	African	0.858	0.005	0.138	0.098	0.481	0.927	0.073
	East Asian	0.903	0.002	0.095	0.039	0.331	0.950	0.050
	South Asian	0.440	0.110	0.450	2.157	1.568	0.665	0.335
	European	0.406	0.123	0.471	2.412	1.641	0.641	0.359
	All	0.662	0.051	0.287			0.806	0.194
XRCC1								
rs 25487 Arg ³⁹⁹ Gln		CC	TT	CT	TT	CT	C	T
DNA repair	African	0.787	0.008	0.206	0.103	0.564	0.890	0.110
	East Asian	0.587	0.058	0.355	0.744	0.973	0.765	0.235
	South Asian	0.436	0.123	0.442	1.577	1.211	0.656	0.344
	European	0.402	0.133	0.465	1.705	1.274	0.634	0.366
	All	0.557	0.078	0.365			0.740	0.260
hOGG1 rs1052133								
Ser ³²⁶ Cys		CC	GG	CG	GG	CG	C	G
DNA repair	African	0.726	0.036	0.238	0.313	0.638	0.845	0.155
	East Asian	0.220	0.315	0.464	2.739	1.243	0.452	0.548
	South Asian	0.415	0.127	0.458	1.104	1.228	0.644	0.356

	European	0.624	0.030	0.346	0.261	0.928	0.797	0.203
	All	0.511	0.115	0.373			0.698	0.302
XPD rs13181 Lys ⁷⁵¹ Gln (T > G)		TT						
			GG	GT	GG	GT	T	G
	African	0.651	0.035	0.315	0.530	0.924	0.808	0.192
	East Asian	0.851	0.004	0.145	0.061	0.425	0.924	0,076
DNA repair	South Asian	0.421	0.115	0.464	1,742	1.361	0.653	0,347
	European	0.417	0.145	0.437	2.197	1.282	0.636	0.364
	All	0.593	0.066	0.341			0.763	0.237
XRCC1 rs25487 Arg ¹⁹⁴ Trp		TT						
			CC	CT	CC	CT	C	T
	African	0.008	0.787	0.206	1.413	0.564	0.890	0.110
	East Asian	0.058	0.587	0.355	1.054	0.973	0.765	0.235
	South Asian	0.123	0.436	0.442	0.783	1.211	0.656	0.344
	European	0.133	0.402	0.465	0.722	1.274	0.634	0.366
	All	0.078	0.557	0.365			0.740	0.260

All the genes conferring a specific (unfavourable) susceptibility are those listed in the homozygous variant genotype column.

Four genes highlighted in bold *Italics* i.e. EPHX1 rs2234922, MPO rs2333227, CYP2E1*6 rs6413432, CYP2E1*5B rs3813867 indicate polymorphisms whose homozygous wild-type genotype might confer a disadvantageous condition in the enzymatic function.