

Supplemental Table 1: Description of Candidate Genes

Gene Name (Abbreviation)	Functional Group	Gene Length (kb)	LDU across Gene		SNP*	NS SNP**
			Blacks	Whites		
Catalase (CAT)	Catalase	33	1.16	0.06	7	0
Gamma-glutamyl Transferase 1 (GGT1)	GSH Synthesis	45	2.05	1.83	3	0
Glucose-6-Phosphate Dehydrogenase (G6PD)	Reducing Equivalents	16	0	0	1	0
Glutamate-cysteine ligase (catalytic subunit) (GCLC)	GSH Synthesis	48	3.85	1.71	15	0
Glutamate-cysteine ligase (modulatory subunit) (GCLM)	GSH Synthesis	22	0.16	0.18	6	0
Glutaredoxin (GLRX)	Disulfide Reductase	9	0.74	0.21	5	0
Glutaredoxin 2 (GLRX2)	Disulfide Reductase	10	0	0	6	0
Glutathione Peroxidase 1 (GPX1)	Peroxidase Activity	1.2	0.02	0	3	0
Glutathione Peroxidase 2 (GPX2)	Peroxidase Activity	3.7	0.12	0	5	0
Glutathione Peroxidase 3 (GPX3)	Peroxidase Activity	8.5	1.11	0.45	4	0
Glutathione Peroxidase 4 (GPX4)	Peroxidase Activity	2.9	0.78	0.14	5	0
Glutathione Peroxidase 7 (GPX7)	Peroxidase Activity	6.7	0	0	5	0
Glutathione Reductase (GSR)	Disulfide Reductase	49	1.96	0.10	9	1
Glutathione S-Transferase A1 (GSTA1)	Glutathione S-Transferase	12	0.01	0	3	0
Glutathione S-Transferase A2 (GSTA2)	Glutathione S-Transferase	13	1.19	0.19	3	1
Glutathione S-Transferase A3 (GSTA3)	Glutathione S-Transferase	13	0	0.03	6	1
Glutathione S-Transferase A4 (GSTA4)	Glutathione S-Transferase	17	0	0.48	6	0
Glutathione S-Transferase A5 (GSTA5)	Glutathione S-Transferase	14	0.18	0	7	1
Glutathione S-Transferase K1 (GSTK1)	Glutathione S-Transferase	5.6	0.15	0.01	1	0
Glutathione S-Transferase M2 (GSTM2)	Glutathione S-Transferase	7.2	0	0.55	3	0
Glutathione S-Transferase M3 (GSTM3)	Glutathione S-Transferase	6.5	0.283	0.089	6	1
Glutathione S-Transferase M4 (GSTM4)	Glutathione S-Transferase	9.4	0.235	0.664	4	0
Glutathione S-Transferase O1 (GSTO1)	Glutathione S-Transferase	13	0	0.005	4	0
Glutathione S-Transferase O2 (GSTO2)	Glutathione S-Transferase	31	0.863	0.082	9	1
Glutathione S-Transferase P1 (GSTP1)	Glutathione S-Transferase	2.8	0.055	0.083	8	2
Glutathione S-Transferase Z1 (GSTZ1)	Glutathione S-Transferase	8.1	0	0	6	2
Glutathione Synthetase (GSS)	GSH Synthesis	11	0.199	0.147	7	0
Heme-Oxygenase 1 (HMOX1)	Heme-Oxygenase	13	0.234	0.206	5	0

Gene Name (Abbreviation)	Functional Group	Gene Length (kb)	LDU across Gene		SNP*	NS SNP**
Heme-Oxygenase 2 (HMOX2)	Heme-Oxygenase	34	0	0.099	6	0
Isocitrate Dehydrogenase 1 (IDH1)	Reducing Equivalents	19	1.188	0.443	7	1
Isocitrate Dehydrogenase 2 (IDH2)	Reducing Equivalents	19	0.849	2.134	7	0
Isocitrate Dehydrogenase 3A (IDH3A)	Reducing Equivalents	21	0	0.192	5	0
Isocitrate Dehydrogenase 3B (IDH3B)	Reducing Equivalents	5.8	0.571	0.116	4	0
Isocitrate Dehydrogenase 3G (IDH3G)	Reducing Equivalents	8.7	0	0.236	5	0
Microsomal Glutathione S-Transferase 1 (mGST1)	Glutathione S-Transferase	17	1.151	2.013	8	0
Microsomal Glutathione S-Transferase 2 (mGST2)	Glutathione S-Transferase	39	8.838	1.303	11	0
Microsomal Glutathione S-Transferase 3 (mGST3)	Glutathione S-Transferase	24	3.25	1.293	11	0
Peroxiredoxin 1 (PRDX1)	Peroxidase Activity	11	0	0	3	0
Peroxiredoxin 2 (PRDX2)	Peroxidase Activity	5	0.005	0	6	0
Peroxiredoxin 3 (PRDX3)	Peroxidase Activity	11	0.271	0.107	6	0
Peroxiredoxin 4 (PRDX4)	Peroxidase Activity	19	0.218	0.039	6	0
Peroxiredoxin 5 (PRDX5)	Peroxidase Activity	3.7	0.145	0	6	1
Peroxiredoxin 6 (PRDX6)	Peroxidase Activity	11	0.0047	0	6	0
Selenoprotein P 1 (SEPP1)	Selenoprotein	12	0.154	0.312	6	1
Selenoprotein W 1 (SEPW1)	Selenoprotein	6.1	0.032	0.131	7	0
Superoxide Dismutase 1 (SOD1)	Superoxide Dismutase	9.3	0	0	6	0
Superoxide Dismutase 2 (SOD2)	Superoxide Dismutase	14	0.074	0.143	6	1
Superoxide Dismutase 3 (SOD3)	Superoxide Dismutase	6.4	2.603	2.277	10	1
Thioredoxin 1 (TXN)	Thioredoxin	12	1.524	1.078	5	0
Thioredoxin 2 (TXN2)	Thioredoxin	15	1.031	0.308	5	0
Thioredoxin Reductase 1 (TXNRD1)	Disulfide Reductase	63	0	0	8	0
Thioredoxin Reductase 2 (TXNRD2)	Disulfide Reductase	66	3.599	3.071	12	1

Gene Name (Abbreviation)	Functional Group	Gene Length (kb)	LDU across Gene		SNP*	NS SNP**
Thioredoxin Reductase 3 (TXNRD3)	Disulfide Reductase	52	0.892	0.356	4	0

*SNP, single nucleotide polymorphism;

**NS SNP, non-synonymous single nucleotide polymorphism

Supplemental Table 2: Single Nucleotide Polymorphisms Studied, by Gene

Gene	Single Nucleotide Polymorphism	Minor Allele Frequency		Type
		European Americans	African Americans	
Catalase	rs564250	22%	20%	5' region
	rs769214	33%	41%	5' region
	rs484214	29%	29%	Intron
	rs7933285	27%	18%	Intron
	rs769217	23%	16%	Intron
	rs2420388	23%	18%	Intron
	rs475043	38%	10%	3' region
Glucose-6-Phosphate Dehydrogenase	rs2472394	10%	13%	Intron
Glutamate-cysteine ligase (catalytic subunit)	rs742528	26%	38%	3' region
	rs6458939	25%	42%	3' region
	rs7742367	19%	31%	3' region
	rs2066511	26%	25%	Intron
	rs16883894	9%	35%	Intron
	rs1555903	9%	27%	Intron
	rs622447	20%	17%	Intron
	rs600033	45%	36%	Intron
	rs4715407	8%	25%	Intron
	rs4712035	19%	34%	Intron
	rs2397147	37%	24%	Intron
	rs606548	6%	34%	Intron
	rs2284650	5%	6%	Intron
	rs510088	31%	18%	Intron
	rs17883901	8%	3%	5' region
Glutamate-cysteine ligase (modulatory subunit)	rs7549683	35%	36%	3' region
	rs769211	26%	24%	Intron
	rs7517826	35%	36%	Intron
	rs3827715	26%	25%	Intron
	rs2301022	31%	47%	Intron
	rs41303970	18%	19%	5' region
Gamma-glutamyl Transferase 1	rs16978740	3%	10%	Intron
	rs2154611	28%	32%	Intron
	rs6519519	26%	39%	Intron
Glutaredoxin	rs1047420	38%	15%	3' region
	rs4561	41%	32%	Synonymous
	rs3822751	25%	47%	Intron
	rs9314160	43%	42%	Intron
	rs3756704	47%	32%	5' region
Glutaredoxin 2	rs34552619	0%	8%	3' region
	rs35358794	1%	6%	Intron
	rs4657845	26%	25%	Intron
	rs10801174	32%	48%	Intron
	rs912071	27%	27%	5' region
Glutathione Peroxidase 1	rs7547615	32%	48%	5' region
	rs8179172	0%	9%	3' region
	rs3811699	33%	29%	5' region
Glutathione Peroxidase 2	rs3448	25%	27%	5' region
	rs10133054	22%	42%	3' region
	rs4902346	22%	41%	Intron

Gene	Single Nucleotide Polymorphism	Minor Allele Frequency		Type
		European Americans	African Americans	
Glutathione Peroxidase 3	rs2412065	22%	41%	Intron
	rs2737844	31%	21%	Intron
	rs17102360	7%	10%	5' region
	rs1946234	14%	20%	5' region
	rs3828599	25%	43%	Intron
Glutathione Peroxidase 4	rs8177435	39%	30%	Intron
	rs8177447	17%	33%	Intron
	rs757228	45%	41%	5' region
	rs3746165	45%	42%	5' region
	rs4807542	18%	4%	Synonymous
Glutathione Peroxidase 7	rs8178977	23%	30%	Intron
	rs2074451	50%	29%	3' region
	rs6588431	39%	40%	5' region
	rs3753753	26%	13%	Intron
	rs946154	33%	41%	Intron
Glutathione Reductase	rs1047635	45%	38%	3' region
	rs7529595	31%	12%	3' region
	rs3594	39%	18%	3' region
	rs2250192	21%	35%	Intron
	rs8190996	43%	32%	Intron
Glutathione Synthetase	rs8190955	0%	8%	Nonsynonymous
	rs2978662	19%	34%	Intron
	rs2978296	19%	29%	Intron
	rs10088455	0%	35%	Intron
	rs8190907	0%	38%	Intron
	rs1002149	17%	24%	5' region
	rs725521	39%	46%	3' region
	rs6087651	39%	45%	Intron
	rs6087653	39%	46%	Intron
	rs2273684	45%	30%	Intron
Glutathione S-Transferase A1	rs6060127	29%	20%	Intron
	rs6088659	19%	4%	Intron
	rs3761144	41%	24%	5' region
	rs6920039	0%	9%	3' region
	rs6917325	44%	31%	Intron
Glutathione S-Transferase A2	rs3756982	44%	31%	5' region
	rs2180314	43%	33%	Nonsynonymous
	rs2180319	33%	7%	Intron
Glutathione S-Transferase A3	rs2608629	37%	14%	Intron
	rs10214816	3%	18%	3' region
	rs557135	37%	35%	Intron
	rs1052661	0%	13%	Nonsynonymous
	rs2281594	4%	40%	Intron
Glutathione S-Transferase A4	rs614765	4%	43%	Intron
	rs563464	3%	33%	5' region
	rs405729	45%	45%	3' region
	rs316133	39%	48%	Intron
	rs3756980	20%	11%	Intron
Glutathione S-Transferase A5	rs6904771	2%	24%	Intron
	rs11967816	8%	7%	Intron
	rs13207376	8%	10%	Intron
	rs4236107	0%	15%	3' region

Gene	Single Nucleotide Polymorphism	Minor Allele Frequency		Type
		European Americans	African Americans	
	rs10948726	40%	9%	3' region
	rs7755335	4%	13%	Intron
	rs2397118	4%	13%	Nonsynonymous
	rs4715353	44%	38%	Intron
	rs4715354	46%	16%	Intron
	rs7749576	6%	42%	Intron
Glutathione S-Transferase K1	rs7803893	0%	4%	Intron
Glutathione S-Transferase M2	rs638820	48%	50%	5' region
	rs625456	14%	17%	Intron
	rs673151	6%	3%	Intron
Glutathione S-Transferase M3	rs1927328	31%	12%	3' region
	rs1537236	49%	41%	3' region
	rs7483	30%	12%	Nonsynonymous
	rs1571858	30%	15%	Intron
	rs10735234	43%	16%	Intron
	rs1332018	44%	19%	5' region
Glutathione S-Transferase M4	rs560018	36%	14%	Intron
	rs535537	13%	12%	Intron
	rs627365	14%	3%	Intron
	rs670439	14%	13%	Intron
Glutathione S-Transferase O1	rs2164624	34%	13%	5' region
	rs12259337	0%	25%	Intron
	rs17116741	0%	25%	Intron
	rs1147611	38%	28%	Intron
Glutathione S-Transferase O2	rs12264844	0%	25%	5' region
	rs7089730	0%	25%	Intron
	rs7070750	0%	34%	Intron
	rs157077	46%	25%	Intron
	rs156697	35%	29%	Nonsynonymous
	rs276203	35%	29%	Intron
	rs157076	32%	33%	Intron
	rs157080	32%	31%	Intron
	rs3740466	29%	24%	3' region
Glutathione S-Transferase P1	rs6591256	39%	38%	5' region
	rs4147581	49%	16%	Intron
	rs8191446	0%	12%	Intron
	rs1695	32%	45%	Nonsynonymous
	rs749174	33%	26%	Intron
	rs743679	0%	12%	Intron
	rs1138272	8%	1%	Nonsynonymous
	rs947895	33%	26%	3' region
Glutathione S-Transferase Z1	rs2111699	32%	31%	Intron
	rs2363643	32%	31%	Splice Site Donor
	rs2270422	39%	15%	Intron
	rs3177427	34%	29%	Nonsynonymous
	rs1046428	20%	9%	Nonsynonymous
	rs1017186	20%	11%	3' region
Heme-Oxygenase 1	rs6518952	0%	32%	Intron
	rs2071749	46%	12%	Intron
	rs5755720	35%	20%	Intron
	rs2285112	41%	34%	Intron

Gene	Single Nucleotide Polymorphism	Minor Allele Frequency		Type
		European Americans	African Americans	
Heme-Oxygenase 2	rs17883419	6%	11%	3' region
	rs11639998	26%	22%	Intron
	rs8055559	4%	26%	Intron
	rs11643057	28%	35%	Intron
	rs1362626	27%	48%	Intron
	rs2270366	32%	25%	Intron
Isocitrate Dehydrogenase 1	rs1051308	31%	25%	3' region
	rs7593466	21%	35%	3' region
	rs7565247	8%	42%	Intron
	rs34218846	7%	8%	Nonsynonymous
	rs6435435	7%	13%	Intron
	rs12612631	0%	14%	Intron
	rs1437410	42%	22%	Intron
	rs10207062	42%	22%	5' region
Isocitrate Dehydrogenase 2	rs7176347	0%	12%	3' region
	rs9972549	2%	43%	Intron
	rs11073899	17%	20%	Intron
	rs8030346	41%	28%	Intron
	rs8028234	25%	35%	Intron
	rs4932279	44%	24%	Intron
	rs7182369	25%	34%	Intron
Isocitrate Dehydrogenase 3A	rs11631100	42%	47%	Intron
	rs8032618	50%	33%	Intron
	rs7180781	1%	11%	Intron
	rs3816253	44%	48%	Intron
	rs17674205	8%	2%	3' region
Isocitrate Dehydrogenase 3B	rs6037255	26%	41%	Intron
	rs6115381	7%	37%	Intron
	rs6107100	7%	37%	Intron
	rs2073192	7%	5%	5' region
Isocitrate Dehydrogenase 3G	rs2071122	28%	35%	Intron
	rs2071123	28%	34%	Intron
	rs2071124	7%	10%	Intron
	rs17429	0%	22%	Intron
	rs2283753	7%	10%	Intron
	rs4898445	35%	26%	Intron
Microsomal Glutathione S-Transferase 1	rs7970208	47%	29%	5' region
	rs7294985	24%	36%	Intron
	rs2975149	25%	42%	Intron
	rs2075237	20%	15%	Intron
	rs4149197	31%	46%	Intron
	rs9332939	50%	31%	Intron
	rs3852576	49%	22%	Intron
	rs7135371	49%	31%	3' region
Microsomal Glutathione S-Transferase 2	rs8191997	16%	26%	5' region
	rs8192004	9%	6%	5' region
	rs1000222	39%	48%	Intron
	rs795594	47%	23%	Intron
	rs8192047	26%	9%	Intron
	rs795590	2%	9%	Intron
	rs795589	42%	49%	Intron
	rs8192066	0%	7%	Intron

Gene	Single Nucleotide Polymorphism	Minor Allele Frequency		Type
		European Americans	African Americans	
Microsomal Glutathione S-Transferase 3	rs7664313	21%	39%	Intron
	rs2646076	22%	28%	Intron
	rs2646035	17%	42%	3' region
	rs7549530	16%	19%	5' region
	rs10737515	47%	20%	5' region
	rs9333378	38%	36%	Intron
	rs10800120	40%	20%	Intron
	rs7554034	21%	46%	Intron
	rs957644	26%	46%	Intron
	rs9333471	29%	44%	Intron
	rs4147602	31%	43%	Intron
	rs2297765	44%	36%	Intron
	rs7533986	30%	26%	Intron
Peroxiredoxin 1	rs10494446	14%	29%	Intron
	rs4660306	35%	19%	Intron
	rs2152077	35%	41%	Intron
	rs713358	22%	25%	5' region
Peroxiredoxin 2	rs10404253	1%	23%	3' region
	rs35866106	1%	5%	Intron
	rs10413408	3%	18%	Intron
Peroxiredoxin 3	rs1205171	18%	5%	Intron
	rs10422248	3%	16%	Intron
	rs8107906	3%	18%	5' region
	rs7068937	47%	19%	3' region
	rs7768	33%	44%	3' region
	rs11198808	13%	16%	Intron
	rs4752257	13%	19%	Intron
	rs11198811	32%	48%	Intron
	rs1553850	42%	23%	5' region
	rs557914	40%	37%	Intron
Peroxiredoxin 4	rs513573	40%	38%	Intron
	rs528960	9%	24%	Intron
	rs518329	40%	38%	Intron
	rs795489	42%	32%	Intron
	rs1548734	40%	38%	Intron
	rs477233	42%	41%	3' region
	rs9787810	32%	7%	5' region
Peroxiredoxin 5	rs7938623	0%	19%	Nonsynonymous
	rs7941847	0%	12%	Intron
	rs566049	0%	13%	Intron
	rs1047206	15%	5%	3' region
	rs4930702	14%	25%	3' region
	rs34619706	10%	2%	5' region
Peroxiredoxin 6	rs34977864	0%	7%	5' region
	rs7540065	25%	38%	Intron
	rs9425725	0%	20%	Intron
	rs34308867	0%	10%	Intron
	rs6702835	24%	41%	3' region
	rs230813	46%	45%	3' region
	rs6413428	25%	34%	3' region
Selenoprotein P 1	rs3877899	24%	27%	Nonsynonymous
	rs1046068	29%	15%	Intron

Gene	Single Nucleotide Polymorphism	Minor Allele Frequency		Type
		European Americans	African Americans	
Selenoprotein W 1	rs230820	45%	45%	Intron
	rs6865453	26%	7%	Intron
	rs11670990	33%	43%	5' region
	rs1862485	31%	25%	Intron
	rs3815751	33%	46%	Intron
	rs10412896	36%	42%	Intron
	rs10427074	0%	12%	Intron
Superoxide Dismutase 1	rs3786777	48%	11%	Intron
	rs2042286	42%	42%	3' region
	rs11910115	0%	12%	5' region
	rs4998557	11%	39%	Intron
	rs2070424	6%	19%	Intron
Superoxide Dismutase 2	rs1041740	32%	10%	Intron
	rs4342445	22%	15%	3' region
	rs2758329	50%	41%	3' region
	rs8031	49%	34%	Intron
	rs2758331	49%	25%	Intron
Superoxide Dismutase 3	rs4880	48%	44%	Nonsynonymous
	rs2758346	49%	44%	5' region
	rs2284659	37%	18%	5' region
	rs8192287	7%	2%	5' region
	rs699474	2%	9%	Intron
	rs17885542	1%	13%	Intron
	rs17878863	8%	1%	Intron
	rs7655372	1%	8%	Intron
	rs1007991	34%	22%	Intron
	rs1799895	1%	0%	Nonsynonymous
Thioredoxin 1	rs2855262	37%	18%	3' region
	rs2695234	9%	50%	3' region
	rs2026312	42%	35%	3' region
	rs1964889	34%	25%	Intron
	rs2418076	27%	44%	Intron
	rs4135191	2%	10%	Intron
	rs4135168	25%	28%	Intron
Thioredoxin 2	rs5995291	11%	34%	Intron
	rs8139906	18%	40%	Intron
	rs2283965	19%	24%	Intron
	rs2267337	19%	22%	Intron
Thioredoxin Reductase 1	rs2281082	20%	22%	Intron
	rs11111979	46%	32%	5' region
	rs4523760	24%	26%	Intron
	rs5018287	46%	37%	Intron
	rs4595619	46%	32%	Intron
	rs17202060	34%	17%	Intron
	rs7138318	32%	39%	Intron
	rs11610799	8%	13%	Intron
Thioredoxin Reductase 2	rs4964785	46%	38%	3' region
	rs7285948	16%	38%	3' region
	rs1139795	17%	45%	Synonymous
	rs1139793	26%	10%	Nonsynonymous
	rs2073750	23%	44%	Intron
	rs9606173	15%	18%	Intron

Gene	Single Nucleotide Polymorphism	Minor Allele Frequency		Type
		European Americans	African Americans	
Thioredoxin Reductase 3	rs5992493	18%	50%	Intron
	rs3788314	48%	28%	Intron
	rs756661	44%	25%	Intron
	rs5748469	36%	24%	Nonsynonymous
	rs5748471	44%	23%	Intron
	rs9306229	22%	15%	Intron
	rs737866	29%	14%	5' region
	rs9834240	35%	38%	Intron
	rs1520850	34%	46%	Intron
	rs777238	12%	50%	Intron
rs9637365	42%	27%	Intron	

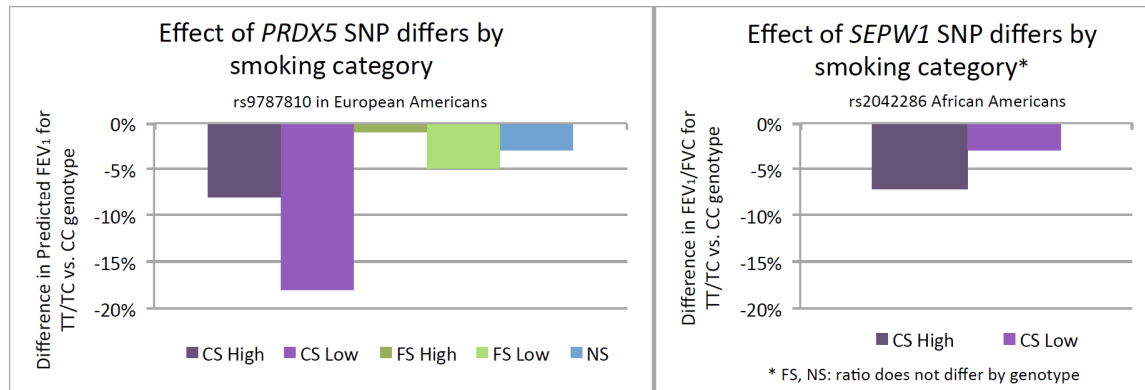
Online Supporting Material

Supplemental Table 3: Statistically Significant Associations in Models with Small Numbers in Genotype/Smoking Subgroups^a

Population	Outcome	SNP (*smoking parameter)	Gene	Function	P-value ^b	SNP Type
Whites	% Pred FEV ₁ FEV ₁ /FVC	Rs2066511*Dose	<i>GCLC</i>	GSH Synthesis	0.00008	Intron
		Rs2154611*Dose ^c	<i>GGT1</i>	GSH Synthesis	0.0004	Intron
		Rs6519519*Dose ^c	<i>GGT1</i>	GSH Synthesis	0.0004	Intron
		Rs17102360*Dose	<i>GPX2</i>	Peroxidase Activity	0.002	5' region
		Rs3828599*Dose	<i>GPX3</i>	Peroxidase Activity	0.001	Intron
		Rs8177447*Dose	<i>GPX3</i>	Peroxidase Activity	0.0003	Intron
		rs10214816*Dose	<i>GSTA3</i>	Glutathione S-Transferase	0.002	Intron
		Rs7749576*Dose	<i>GSTA5</i>	Glutathione S-Transferase	0.001	Intron
		Rs1046428*Dose ^d	<i>GSTZ1</i>	Glutathione S-Transferase	0.0006	NonSynonymous
		Rs1017186*Dose ^d	<i>GSTZ1</i>	Glutathione S-Transferase	0.0004	3' region
		Rs2071749*Dose	<i>HMOX1</i>	Heme-Oxygenase	0.002	Intron
		Rs11631100*Dose	<i>IDH3A</i>	Reducing Equivalents	0.0001	Intron
		Rs3816253*Dose	<i>IDH3A</i>	Reducing Equivalents	0.0002	Intron
		Rs8032618*Dose	<i>IDH3A</i>	Reducing Equivalents	0.001	Intron
		Rs2071124*Dose	<i>IDH3G</i>	Reducing Equivalents	0.0009	Intron
		Rs2283753*Dose	<i>IDH3G</i>	Reducing Equivalents	0.001	Intron
		Rs4898445*Dose	<i>IDH3G</i>	Reducing Equivalents	0.001	Intron
		Rs2646035*Dose	<i>mGST2</i>	Glutathione S-Transferase	0.003	3' region
		Rs795590*Dose	<i>mGST2</i>	Glutathione S-Transferase	0.002	Intron
		Rs4342445*Dose	<i>SOD2</i>	Superoxide Dismutase	0.0009	3' region
Blacks	FEV ₁ /FVC	Rs2284650*Status	<i>GCLC</i>	Glutathione Synthesis	0.0000009	Intron
		Rs2071749*Status	<i>HMOX1</i>	Heme-Oxygenase	0.0008	Intron
		Rs3786777*Status	<i>SEPWI</i>	Selenoprotein	0.0006	Intron
		Rs4135191*Status	<i>TXN</i>	Disulfide Reductase	0.0004	Intron
		Rs2284650*Dose	<i>GCLC</i>	Glutathione Synthesis	0.000002	Intron
		Rs17674205*Dose	<i>IDH3A</i>	Reducing Equivalents	0.0009	3' region

^aAll results with nominal p-value <0.002^bNominal p-values shown^cStrong LD observed between these SNPs (R²=0.93)^dStrong LD observed between these SNPs (R²=0.90)

Online Supporting Material



Graphical abstract

*abbreviations: FEV₁, forced expiratory volume in the first second; CS High, cigarette smokers at higher dose; CS Low, cigarette smokers lower dose; FS High, former smokers at higher dose; FS Low, former smokers at lower dose; NS, never smokers.

Online Supporting Material***Highlights***

- We evaluated polymorphisms in genes with antioxidant function and lung function phenotypes.
- Interactions between variants and cigarette smoking parameters were investigated.
- Without consideration of smoking, no variant was associated with lung function.
- Results highlight *IDH3A*, *IDH3B*, *IDH2*, and *PRDX5* for further investigation.