Table S1.1: Imputed SNP associations from the case-control analysis of all lung cancer histologies in African-Americans (P<0.01)

SNP Position[a]	Allele 1	Allele 2	Imputation QC Metric (Info)	Allele 2 Frequency (Cases)	Allele 2 Frequency (Controls)	P-value	OR[b]	$\mathrm{OR}_{\mathrm{Lower}}$[c]	$\mathrm{OR}_{\mathrm{Upper}}$[c]
Chr15:78849034	T	C	0.93394	0.29672	0.24395	2.82E-05	1.34	1.17	1.53
Chr15:78857986	C	G	0.95081	0.29411	0.23996	5.55E-05	1.31	1.15	1.50
Chr15:78894339	G	A	0.96958	0.15115	0.11019	5.79E-05	1.43	1.20	1.70
Chr15:78857939	T	G	0.93269	0.11156	0.080758	8.87E-05	1.50	1.23	1.84
Chr15:78886198	C	T	0.97529	0.088065	0.060655	1.31E-04	1.56	1.24	1.97
Chr15:78906177	A	T	0.8527	0.10913	0.079998	1.33E-04	1.52	1.23	1.89
Chr15:78886947	G	A	0.97071	0.090201	0.06235	1.46E-04	1.55	1.24	1.95
Chr15:78877381	C	A	0.98512	0.13596	0.10104	1.69E-04	1.41	1.18	1.69
Chr15:78862453	C	A	0.9799	0.13584	0.10166	2.29E-04	1.40	1.17	1.68
Chr15:78862064	C	T	0.96336	0.088475	0.062756	2.40E-04	1.53	1.22	1.93
Chr15:78868636	G	A	0.96942	0.088043	0.062471	2.62E-04	1.53	1.22	1.92
Chr15:78900647	A	G	0.8439	0.18107	0.14156	2.94E-04	1.36	1.15	1.61
Chr15:78900650	C	T	0.85059	0.18396	0.14416	3.23E-04	1.35	1.15	1.59
Chr5:1290319	T	G	0.70422	0.4863	0.45193	3.74E-04	0.78	0.68	0.89
Chr15:78720915	T	A	0.93913	0.071154	0.049101	4.95E-04	1.57	1.22	2.03
Chr15:78938771	T	C	0.81847	0.0232	0.013295	5.01E-04	2.29	1.44	3.65
Chr15:78866445	G	A	0.98081	0.14456	0.11218	6.01E-04	1.36	1.14	1.61
Chr15:78849779	C	T	0.93864	0.14359	0.11305	6.39E-04	1.36	1.14	1.62
Chr5:1292983	C	A	0.97868	0.44015	0.47895	8.28E-04	0.82	0.73	0.92
Chr15:78922638	G	A	0.94485	0.091049	0.067593	8.31E-04	1.47	1.17	1.85
Chr15:78898932	C	G	0.97361	0.19706	0.15634	8.88E-04	1.29	1.11	1.49
Chr15:78926445	T	C	0.94848	0.091588	0.068493	1.06E-03	1.45	1.16	1.82
Chr15:78783277	G	A	0.90046	0.08463	0.062853	1.25E-03	1.47	1.16	1.86
Chr15:78899003	C	A	0.95299	0.2084	0.16787	1.55E-03	1.27	1.10	1.47
Chr15:78972145	A	G	0.76472	0.050348	0.069303	1.59E-03	0.64	0.48	0.84
Chr15:78804144	G	C	0.87901	0.031674	0.019562	1.78E-03	1.84	1.25	2.69
Chr5:1243850	T	A	0.76128	0.033903	0.021577	2.17E-03	1.85	1.25	2.74
Chr15:78973356	C	T	0.72352	0.058847	0.077052	2.38E-03	0.66	0.50	0.86
Chr6:31004786	G	A	0.86973	0.012966	0.023561	2.59E-03	0.49	0.31	0.78
Chr5:1325803	A	G	0.95551	0.45982	0.41863	2.68E-03	0.83	0.74	0.94
Chr6:29903991	G	A	0.76612	0.10388	0.083034	2.72E-03	1.41	1.13	1.76
Chr15:78812949	G	C	0.932	0.039057	0.023788	2.82E-03	1.65	1.19	2.30
Chr15:78833584	G	A	0.9104	0.053863	0.036573	2.91E-03	1.53	1.16	2.03
Chr15:78965209	G	A	0.76261	0.066745	0.087819	2.93E-03	0.69	0.54	0.88
Chr5:1330253	T	C	0.97474	0.46217	0.42103	2.93E-03	0.84	0.74	0.94
Chr5:1330840	T	C	0.97502	0.46215	0.42107	2.96E-03	0.84	0.74	0.94
Chr15:78892661	C	T	0.98346	0.4332	0.47935	2.97E-03	1.19	1.06	1.34
Chr5:1323212	C	T	0.93587	0.5047	0.46243	2.98E-03	0.84	0.74	0.94
Chr15:78924040	A	G	0.93421	0.2303	0.26212	3.03E-03	0.81	0.70	0.93
Chr15:78883813	A	G	0.98042	0.4623	0.50615	3.09E-03	0.84	0.75	0.94
Chr15:78805036	G	A	0.9291	0.038667	0.023782	3.13E-03	1.65	1.18	2.29
Chr5:1325767	A	G	0.96159	0.45842	0.41751	3.20E-03	0.84	0.74	0.94
Chr5:1325590	T	C	0.95977	0.45683	0.41608	3.22E-03	0.84	0.74	0.94
Chr15:78801394	A	C	0.95171	0.19891	0.16503	3.30E-03	1.26	1.08	1.47

Chr5:1322468	G	A	0.93405	0.47913	0.52051	3.34E-03	0.84	0.74	0.94
Chr15:78900701	T	G	0.84755	0.17674	0.1428	3.42E-03	1.28	1.09	1.52
Chr6:29903993	T	C	0.76926	0.1039	0.083394	3.43E-03	1.40	1.12	1.75
Chr6:31080606	A	G	0.87962	0.019218	0.030399	3.48E-03	0.56	0.37	0.82
Chr5:1356450	C	T	0.81446	0.47663	0.44078	3.52E-03	0.83	0.73	0.94
Chr15:78809338	G	A	0.91112	0.029434	0.018373	3.57E-03	1.78	1.21	2.63
Chr15:78800925	G	T	0.90634	0.037657	0.023173	3.59E-03	1.65	1.18	2.32
Chr15:78739763	A	G	0.97223	0.077149	0.057934	3.68E-03	1.42	1.12	1.81
Chr6:32212568	T	G	0.86205	0.075113	0.095099	3.87E-03	0.72	0.58	0.90
Chr15:78752188	C	G	0.97878	0.076169	0.057133	3.98E-03	1.42	1.12	1.80
Chr5:1311708	C	T	0.86794	0.1385	0.16462	4.02E-03	0.78	0.66	0.92
Chr6:31079695	G	C	0.90358	0.01571	0.026598	4.03E-03	0.54	0.36	0.82
Chr15:78964464	G	A	0.77715	0.078132	0.099557	4.05E-03	0.72	0.57	0.90
Chr6:29903961	C	T	0.814	0.10759	0.086505	4.06E-03	1.37	1.11	1.70
Chr5:1327851	C	T	0.88871	0.46823	0.50786	4.11E-03	0.84	0.74	0.94
Chr5:1356944	C	T	0.78502	0.46649	0.43201	4.25E-03	0.83	0.73	0.94
Chr15:78962803	C	T	0.76839	0.071163	0.090925	4.29E-03	0.71	0.56	0.90
Chr15:78861349	T	C	0.73754	0.018434	0.011611	4.34E-03	2.20	1.28	3.78
Chr15:78746698	T	G	0.75572	0.036283	0.048616	4.44E-03	0.62	0.45	0.86
Chr5:1328527	A	G	0.9437	0.21338	0.24638	4.60E-03	0.82	0.71	0.94
Chr6:29903979	T	C	0.78008	0.10335	0.083392	4.63E-03	1.38	1.10	1.72
Chr15:78880385	C	T	0.8371	0.016352	0.0095649	5.07E-03	2.19	1.27	3.79
Chr15:78886692	C	T	0.82864	0.016437	0.0096866	5.09E-03	2.19	1.27	3.80
Chr6:31275289	A	C	0.76511	0.49108	0.45527	5.09E-03	1.20	1.06	1.36
Chr6:30995894	A	T	0.75786	0.017897	0.027865	5.15E-03	0.53	0.34	0.83
Chr6:29819601	G	A	0.85648	0.050006	0.03577	5.19E-03	1.55	1.14	2.10
Chr6:30996354	C	T	0.75872	0.017883	0.027836	5.22E-03	0.53	0.34	0.83
Chr5:1333077	A	G	0.90694	0.4512	0.41425	5.29E-03	0.84	0.74	0.95
Chr6:31000005	T	A	0.76449	0.01774	0.027648	5.37E-03	0.53	0.34	0.83
Chr6:30999438	C	T	0.76371	0.017762	0.027669	5.39E-03	0.53	0.34	0.83
Chr6:30997517	A	T	0.76078	0.017848	0.027761	5.39E-03	0.53	0.34	0.83
Chr6:31037322	A	T	0.78556	0.015352	0.02483	5.42E-03	0.51	0.32	0.82
Chr6:31002205	C	A	0.76827	0.017633	0.027515	5.51E-03	0.54	0.34	0.83
Chr6:30993719	A	G	0.80098	0.01267	0.021915	5.60E-03	0.50	0.30	0.82
Chr15:78720923	T	G	0.95475	0.08	0.061187	5.65E-03	1.39	1.10	1.76
Chr15:78970542	C	G	0.76482	0.015763	0.0098276	5.68E-03	2.23	1.26	3.92
Chr6:30809469	C	T	0.7611	0.012422	0.021587	5.73E-03	0.50	0.30	0.82
Chr6:30929766	G	A	0.78885	0.013341	0.023185	5.73E-03	0.51	0.32	0.82
Chr6:30807578	C	T	0.76102	0.012424	0.021587	5.74E-03	0.50	0.30	0.82
Chr5:1355058	C	T	0.82156	0.4759	0.44203	5.76E-03	0.84	0.74	0.95
Chr6:30872557	G	C	0.74929	0.012747	0.022173	5.77E-03	0.50	0.30	0.82
Chr6:30861789	G	A	0.74929	0.012747	0.022173	5.77E-03	0.50	0.30	0.82
Chr15:78977370	G	A	0.7443	0.037506	0.050934	5.82E-03	0.63	0.45	0.87
Chr15:78914265	G	A	0.81099	0.014876	0.008909	5.82E-03	2.26	1.27	4.03
Chr6:29902254	C	T	0.88909	0.08151	0.062739	6.09E-03	1.38	1.10	1.75
Chr6:29819599	T	C	0.85602	0.049093	0.035289	6.29E-03	1.54	1.13	2.09
Chr5:1354462	G	T	0.7939	0.45199	0.41758	6.29E-03	0.84	0.74	0.95

Chr5:1336243	A	G	0.81606	0.41569	0.38158	6.55E-03	0.84	0.73	0.95
Chr15:78869754	C	T	0.86197	0.015735	0.0091926	6.79E-03	2.14	1.23	3.72
Chr15:78937489	G	A	0.84955	0.41682	0.44372	6.81E-03	0.84	0.74	0.95
Chr15:78719832	G	C	0.95589	0.080925	0.062356	6.91E-03	1.38	1.09	1.74
Chr6:29910558	T	C	0.75754	0.43732	0.41108	6.93E-03	0.83	0.73	0.95
Chr5:1336459	T	C	0.81056	0.41351	0.37986	7.13E-03	0.84	0.73	0.95
Chr5:1302145	G	A	0.81264	0.091228	0.11326	7.28E-03	0.75	0.61	0.93
Chr6:29876635	A	G	0.736	0.071502	0.057091	7.28E-03	1.46	1.11	1.92
Chr6:29897860	C	A	0.78594	0.066485	0.050479	7.45E-03	1.44	1.10	1.89
Chr6:31094261	G	C	0.87791	0.08418	0.10226	7.49E-03	0.74	0.60	0.92
Chr5:1337106	T	A	0.80812	0.41176	0.37833	7.84E-03	0.84	0.74	0.95
Chr6:31096561	G	A	0.87089	0.10177	0.12456	7.86E-03	0.77	0.63	0.93
Chr15:78961421	G	A	0.74028	0.069712	0.088411	7.94E-03	0.72	0.56	0.92
Chr6:29821982	C	T	0.89373	0.17184	0.14841	8.07E-03	1.25	1.06	1.47
Chr6:30005305	G	A	0.96076	0.15083	0.12919	8.08E-03	1.25	1.06	1.48
Chr6:29819602	C	T	0.91403	0.053326	0.038894	8.12E-03	1.47	1.11	1.96
Chr6:30008003	C	G	0.96016	0.15082	0.1292	8.13E-03	1.25	1.06	1.48
Chr6:30045199	G	A	0.91912	0.16501	0.1435	8.19E-03	1.25	1.06	1.47
Chr6:31073367	C	T	0.78333	0.010046	0.017529	8.41E-03	0.47	0.27	0.83
Chr6:31074316	G	C	0.78333	0.010046	0.017529	8.41E-03	0.47	0.27	0.83
Chr6:30011581	T	C	0.95593	0.15072	0.12927	8.47E-03	1.25	1.06	1.48
Chr6:29924831	T	C	0.9204	0.079758	0.061833	8.53E-03	1.37	1.08	1.72
Chr15:78712119	A	T	0.87779	0.46619	0.49955	8.68E-03	1.18	1.04	1.34
Chr15:78907527	A	G	0.82898	0.015126	0.0091717	8.75E-03	2.14	1.21	3.78
Chr6:29968426	C	T	0.96369	0.14938	0.12789	8.80E-03	1.25	1.06	1.48
Chr5:1312962	G	A	0.97438	0.23415	0.26632	8.97E-03	0.84	0.73	0.96
Chr6:29819325	C	T	0.96598	0.057259	0.042424	9.02E-03	1.43	1.09	1.88
Chr6:30980685	A	G	0.77412	0.017677	0.027266	9.13E-03	0.56	0.36	0.87
Chr6:29825415	A	G	0.89776	0.037361	0.025401	9.15E-03	1.59	1.12	2.24
Chr6:29821270	G	A	0.89842	0.037358	0.025397	9.18E-03	1.59	1.12	2.24
Chr6:29819541	C	A	0.96735	0.05723	0.042465	9.20E-03	1.43	1.09	1.87
Chr5:1309168	T	C	0.87709	0.3866	0.41929	9.22E-03	1.18	1.04	1.34
Chr5:1312020	T	C	0.85809	0.40842	0.4423	9.23E-03	1.18	1.04	1.34
Chr6:29819741	A	G	0.96762	0.057223	0.042472	9.25E-03	1.43	1.09	1.87
Chr6:29819695	G	C	0.96757	0.057221	0.04247	9.25E-03	1.43	1.09	1.87
Chr6:29819813	G	A	0.96772	0.05722	0.042475	9.26E-03	1.43	1.09	1.87
Chr6:30984527	C	T	0.76419	0.018016	0.027595	9.26E-03	0.56	0.36	0.87
Chr5:1308865	T	C	0.8357	0.11958	0.14278	9.35E-03	0.78	0.65	0.94
Chr6:29874575	G	A	0.73205	0.051434	0.039434	9.47E-03	1.54	1.11	2.13
Chr15:78970474	A	G	0.78815	0.013935	0.0088654	9.50E-03	2.19	1.21	3.96
Chr5:1338554	C	T	0.8241	0.12164	0.14488	9.85E-03	0.78	0.65	0.94
Chr6:29902109	G	A	0.749	0.24971	0.22135	9.98E-03	1.23	1.05	1.43
Chr6:31082081	G	A	0.88492	0.084719	0.10231	9.98E-03	0.75	0.61	0.93

[a] SNPs are ordered by P-value; [b] OR for each additional copy of allele 2, estimated in a logistic regression model adjusted for: age, sex, study site, % sub-Saharan African Ancestry, %European ancestry, and number of pack-years smoked; [c] Standard errors account for additional uncertainty inherent in analysis of imputed genotypes

Table S1.2: Imputed SNP associations from the case-control analysis of lung adenomcarcinoma in African-Americans (P<0.01)

SNP Position[a]	Allele 1	Allele 2	Imputation QC Metric (Info)	Allele 2 Frequency (Cases)	Allele 2 Frequency (Controls)	P-value	OR[b]	$\mathrm{OR}_{\mathrm{Lower}}$[c]	$\mathrm{OR}_{\mathrm{Upper}}$[c]
Chr5:1292983	C	A	0.97882	0.41608	0.47895	5.98E-05	0.74	0.64	0.86
Chr5:1283312	A	G	0.90451	0.50806	0.44499	7.91E-05	0.73	0.63	0.86
Chr5:1283104	T	C	0.88285	0.49055	0.43081	1.66E-04	0.74	0.63	0.87
Chr5:1243850	T	A	0.75505	0.04014	0.021577	6.15E-04	2.38	1.45	3.92
Chr15:78906177	A	T	0.84336	0.11173	0.079998	1.49E-03	1.56	1.19	2.06
Chr5:1299379	C	G	0.77115	0.36199	0.40768	1.88E-03	1.31	1.10	1.55
Chr6:31034896	T	A	0.83066	0.44327	0.39156	2.11E-03	1.29	1.10	1.52
Chr5:1285162	C	T	0.83945	0.3064	0.34856	2.47E-03	0.77	0.65	0.91
Chr15:78922638	G	A	0.94173	0.096976	0.067593	2.49E-03	1.56	1.17	2.09
Chr15:78926445	T	C	0.94676	0.097501	0.068493	2.92E-03	1.54	1.16	2.05
Chr15:78720915	T	A	0.93212	0.075035	0.049101	2.94E-03	1.64	1.18	2.28
Chr5:1351248	C	T	0.75408	0.020816	0.010403	3.09E-03	3.09	1.46	6.52
Chr6:33039535	A	T	0.92869	0.15192	0.11423	3.16E-03	1.41	1.12	1.77
Chr5:1328527	A	G	0.94682	0.20187	0.24638	3.22E-03	0.77	0.64	0.92
Chr15:78962803	C	T	0.77142	0.064831	0.090925	3.29E-03	0.64	0.48	0.86
Chr15:78938771	T	C	0.80254	0.023632	0.013295	3.41E-03	2.62	1.38	5.00
Chr15:78886198	C	T	0.97345	0.088552	0.060655	3.48E-03	1.55	1.16	2.08
Chr6:29273612	C	G	0.83024	0.10714	0.13985	3.55E-03	0.70	0.56	0.89
Chr6:29272761	G	A	0.82733	0.10679	0.13933	3.67E-03	0.70	0.56	0.89
Chr6:29859460	G	A	0.77377	0.020095	0.010224	3.80E-03	3.02	1.43	6.38
Chr6:30103009	A	G	0.809	0.30446	0.26544	3.80E-03	1.31	1.09	1.57
Chr6:29272420	T	A	0.8309	0.10721	0.13971	3.81E-03	0.71	0.56	0.89
Chr6:29272301	C	T	0.83094	0.10722	0.1397	3.84E-03	0.71	0.56	0.89
Chr6:29272316	A	T	0.83094	0.10722	0.13969	3.84E-03	0.71	0.56	0.89
Chr6:29272046	C	T	0.83103	0.10722	0.13969	3.85E-03	0.71	0.56	0.89
Chr6:33044956	T	C	0.90183	0.15131	0.11428	3.89E-03	1.41	1.12	1.77
Chr6:29271126	G	T	0.83119	0.10723	0.13965	3.91E-03	0.71	0.56	0.89
Chr6:29270827	A	G	0.83128	0.10724	0.13965	3.93E-03	0.71	0.56	0.90
Chr6:29270038	C	T	0.83146	0.10725	0.13962	3.99E-03	0.71	0.56	0.90
Chr6:29269781	T	A	0.83149	0.10725	0.13961	4.01E-03	0.71	0.56	0.90
Chr6:33028349	G	A	0.81091	0.10943	0.078451	4.05E-03	1.51	1.14	2.00
Chr5:1331271	C	T	0.98278	0.22079	0.26555	4.22E-03	0.78	0.66	0.93
Chr6:33082109	C	T	0.77369	0.045963	0.028404	4.27E-03	1.94	1.23	3.05
Chr5:1326122	A	G	0.98055	0.2205	0.265	4.40E-03	0.78	0.66	0.93
Chr5:1279964	G	C	0.88209	0.36858	0.41076	4.58E-03	1.25	1.07	1.47
Chr6:31081065	T	C	0.87308	0.40885	0.45548	4.71E-03	0.80	0.69	0.93
Chr5:1312962	G	A	0.97526	0.22189	0.26632	4.78E-03	0.78	0.66	0.93
Chr5:1287340	A	G	0.76864	0.24769	0.21536	4.78E-03	0.75	0.61	0.92
Chr6:31080704	T	G	0.8722	0.23976	0.20044	4.92E-03	1.32	1.09	1.60
Chr6:33037474	A	G	0.95547	0.12234	0.088502	5.35E-03	1.42	1.11	1.82
Chr15:78817929	C	T	0.88167	0.50688	0.45591	5.65E-03	0.81	0.69	0.94
Chr15:78886947	G	A	0.97001	0.089162	0.06235	5.75E-03	1.51	1.13	2.02
Chr15:78972145	A	G	0.77006	0.048301	0.069303	5.84E-03	0.62	0.44	0.87

Chr6:33024224	G	A	0.74208	0.46723	0.51129	5.95E-03	0.79	0.66	0.93
Chr6:33083884	A	G	0.81293	0.046106	0.066761	6.23E-03	0.63	0.45	0.88
Chr6:29343355	C	T	0.74194	0.21318	0.24882	6.27E-03	0.76	0.63	0.93
Chr6:33093821	T	C	0.834	0.046845	0.029349	6.31E-03	1.83	1.19	2.81
Chr15:78900647	A	G	0.83834	0.17759	0.14156	6.40E-03	1.34	1.09	1.66
Chr6:33094825	T	C	0.83526	0.04677	0.029339	6.51E-03	1.82	1.18	2.80
Chr15:78956032	A	C	0.84288	0.042597	0.063955	6.54E-03	0.63	0.45	0.88
Chr6:33085591	G	A	0.85818	0.05771	0.080861	6.57E-03	0.66	0.49	0.89
Chr6:33085578	G	A	0.85827	0.057709	0.080851	6.58E-03	0.66	0.49	0.89
Chr15:78880385	C	T	0.83069	0.017439	0.0095649	6.68E-03	2.89	1.34	6.21
Chr15:78857939	T	G	0.93349	0.10929	0.080758	6.79E-03	1.44	1.11	1.88
Chr15:78965209	G	A	0.76725	0.063597	0.087819	6.83E-03	0.66	0.49	0.89
Chr15:78862064	C	T	0.96281	0.0886	0.062756	6.83E-03	1.50	1.12	2.01
Chr6:33085033	T	G	0.8628	0.057368	0.080376	6.85E-03	0.66	0.49	0.89
Chr5:1271714	T	C	0.88731	0.2006	0.16908	6.96E-03	1.32	1.08	1.61
Chr6:33087564	T	C	0.83113	0.06065	0.083764	7.03E-03	0.66	0.49	0.89
Chr6:33087519	G	A	0.8312	0.060644	0.08375	7.04E-03	0.66	0.49	0.89
Chr15:78886692	C	T	0.82222	0.017466	0.0096866	7.06E-03	2.87	1.33	6.20
Chr6:33084460	A	G	0.8676	0.057048	0.079915	7.15E-03	0.66	0.49	0.89
Chr5:1282194	C	T	0.78325	0.094897	0.072822	7.16E-03	1.51	1.12	2.04
Chr6:33082692	A	C	0.87108	0.056179	0.078939	7.24E-03	0.66	0.49	0.89
Chr5:1282319	C	A	0.94412	0.234	0.20064	7.39E-03	1.28	1.07	1.54
Chr6:30070275	C	G	0.79048	0.037963	0.023723	7.54E-03	1.99	1.20	3.29
Chr6:33083574	C	T	0.85567	0.058701	0.081061	7.63E-03	0.66	0.49	0.90
Chr15:78868636	G	A	0.9688	0.087925	0.062471	7.68E-03	1.49	1.11	2.00
Chr6:33681603	G	A	0.98993	0.055388	0.037391	7.70E-03	1.65	1.14	2.38
Chr6:30296071	C	T	0.8483	0.1588	0.13051	7.85E-03	0.73	0.58	0.92
Chr5:1284135	C	T	0.88949	0.23479	0.20226	7.89E-03	1.29	1.07	1.55
Chr6:33114527	C	T	0.91487	0.044423	0.027535	7.90E-03	1.79	1.16	2.74
Chr15:78900650	C	T	0.84531	0.17973	0.14416	8.00E-03	1.33	1.08	1.64
Chr15:78869754	C	T	0.85502	0.016843	0.0091926	8.12E-03	2.82	1.31	6.07
Chr5:1311708	C	T	0.87323	0.13342	0.16462	8.21E-03	0.75	0.61	0.93
Chr6:33083816	G	C	0.8311	0.047514	0.068146	8.22E-03	0.64	0.46	0.89
Chr15:78935661	G	C	0.85863	0.15786	0.18702	8.24E-03	0.76	0.61	0.93
Chr6:33202640	C	T	0.71241	0.37857	0.33702	8.28E-03	0.79	0.66	0.94
Chr6:31060362	G	T	0.965	0.14507	0.17862	8.32E-03	0.76	0.62	0.93
Chr6:31078804	G	A	0.95434	0.14624	0.17963	8.48E-03	0.76	0.62	0.93
Chr6:33083936	T	G	0.84474	0.055016	0.076734	8.55E-03	0.66	0.48	0.90
Chr6:31069476	T	A	0.95944	0.14576	0.17907	8.62E-03	0.76	0.62	0.93
Chr15:78977370	G	A	0.75201	0.033861	0.050934	8.64E-03	0.59	0.39	0.87
Chr15:78943291	T	C	0.86728	0.043685	0.065412	8.70E-03	0.64	0.46	0.89
Chr6:31071231	C	T	0.96086	0.14542	0.17864	8.86E-03	0.76	0.62	0.93
Chr6:31076397	T	A	0.9605	0.14546	0.17865	8.92E-03	0.76	0.62	0.93
Chr6:33679807	A	G	0.91547	0.050772	0.034388	9.15E-03	1.70	1.14	2.54
Chr15:78964464	G	A	0.78488	0.075436	0.099557	9.23E-03	0.69	0.53	0.91
Chr6:33676556	G	A	0.98023	0.05552	0.03792	9.25E-03	1.63	1.13	2.35
Chr6:33663055	G	A	0.97628	0.0554	0.037853	9.25E-03	1.63	1.13	2.35

Chr6:33657494	T	C	0.9721	0.055283	0.037794	9.26E-03	1.63	1.13	2.36
Chr6:33182517	C	T	0.84331	0.046828	0.029689	9.33E-03	1.75	1.15	2.68
Chr6:33183730	T	C	0.9179	0.19979	0.16563	9.57E-03	0.77	0.63	0.94
Chr6:33124587	C	A	0.90335	0.044517	0.027696	9.68E-03	1.76	1.15	2.71
Chr6:31048516	G	A	0.94911	0.49074	0.44322	9.76E-03	1.22	1.05	1.42
Chr6:29907270	G	A	0.81443	0.31499	0.35152	9.80E-03	0.80	0.68	0.95

[a]SNPs are ordered by P-value; [b]OR for each additional copy of allele 2, estimated in a logistic regression model adjusted for: age, sex, study site, % sub-Saharan African Ancestry, %European ancestry, and number of pack-years smoked; [c]Standard errors account for additional uncertainty inherent in analysis of imputed genotypes

Table S1.3: Imputed SNP associations from the case-control analysis of squamous cell lung cancer in African-Americans (P<0.01)

SNP Position[a]	Allele 1	Allele 2	Imputation QC Metric (Info)	Allele 2 Frequency (Cases)	Allele 2 Frequency (Controls)	P-value	OR[b]	OR_{Lower}[c]	OR_{Upper}[c]
Chr6:31738343	C	T	0.96733	0.29166	0.36147	5.86E-04	0.71	0.59	0.86
Chr6:32121932	C	T	0.74012	0.15554	0.11004	6.78E-04	1.74	1.27	2.40
Chr6:31878006	A	G	0.8987	0.14345	0.095881	8.32E-04	1.70	1.25	2.32
Chr6:31941390	A	G	0.80907	0.15161	0.10555	9.84E-04	1.70	1.24	2.34
Chr6:31924880	G	A	0.82154	0.2761	0.21408	1.01E-03	1.48	1.17	1.88
Chr6:31794592	C	T	0.92377	0.42385	0.36571	1.13E-03	0.72	0.59	0.88
Chr6:31811850	T	C	0.90869	0.3218	0.2647	1.16E-03	0.70	0.56	0.87
Chr6:31928306	A	G	0.82103	0.27309	0.21167	1.25E-03	1.47	1.16	1.87
Chr6:31938635	G	C	0.80553	0.15219	0.10661	1.30E-03	1.68	1.23	2.31
Chr6:31937037	C	T	0.80612	0.15217	0.10659	1.30E-03	1.68	1.22	2.31
Chr6:31783208	A	C	0.91218	0.32079	0.26539	1.39E-03	0.70	0.57	0.87
Chr6:31882354	T	C	0.88494	0.16881	0.12146	1.50E-03	1.59	1.19	2.11
Chr6:31885930	C	T	0.89936	0.26015	0.20494	1.64E-03	0.69	0.55	0.87
Chr6:31883957	A	G	0.90006	0.26004	0.20484	1.65E-03	0.69	0.55	0.87
Chr5:1322468	G	A	0.93482	0.53826	0.47949	1.68E-03	0.74	0.61	0.89
Chr6:31881731	G	A	0.89932	0.26016	0.20507	1.69E-03	0.70	0.55	0.87
Chr6:32029929	C	T	0.74199	0.14607	0.10348	1.71E-03	1.70	1.22	2.37
Chr6:31667028	C	A	0.99283	0.53856	0.47156	1.73E-03	0.74	0.62	0.90
Chr6:32009284	G	A	0.73302	0.15131	0.1102	1.74E-03	1.70	1.22	2.36
Chr6:31881878	C	T	0.89145	0.16756	0.12058	1.74E-03	1.58	1.19	2.09
Chr6:31881223	G	C	0.89191	0.16753	0.12057	1.75E-03	1.57	1.19	2.09
Chr6:31745518	A	G	0.92565	0.088912	0.12688	1.96E-03	0.64	0.48	0.85
Chr6:31629211	C	T	0.96634	0.069612	0.1047	2.04E-03	0.62	0.45	0.84
Chr6:31923997	C	T	0.82694	0.27091	0.21211	2.05E-03	1.45	1.14	1.83
Chr6:31920687	C	T	0.82711	0.2709	0.2121	2.05E-03	1.45	1.14	1.83
Chr6:31916951	T	C	0.82724	0.27088	0.21209	2.05E-03	1.45	1.14	1.83
Chr6:31919956	T	C	0.82712	0.27089	0.2121	2.05E-03	1.45	1.14	1.83
Chr6:31919917	T	C	0.82713	0.27089	0.2121	2.05E-03	1.45	1.14	1.83
Chr6:31622893	T	C	0.96605	0.06969	0.10475	2.06E-03	0.62	0.45	0.84
Chr5:1327851	C	T	0.88546	0.45195	0.50786	2.13E-03	0.74	0.61	0.90
Chr6:31916062	A	G	0.84885	0.14821	0.10384	2.19E-03	1.63	1.19	2.22
Chr6:31910456	G	T	0.85001	0.14813	0.10377	2.21E-03	1.63	1.19	2.22
Chr5:1323212	C	T	0.93833	0.52091	0.46243	2.21E-03	0.75	0.62	0.90
Chr6:31908224	C	T	0.851	0.14806	0.10371	2.22E-03	1.62	1.19	2.22

Chr6:31585692	A	G	0.97649	0.082315	0.11948	2.41E-03	0.64	0.48	0.85
Chr6:31762843	G	C	0.87894	0.27627	0.22286	2.42E-03	1.44	1.14	1.81
Chr6:31688200	C	T	0.98403	0.14337	0.19223	2.51E-03	0.70	0.55	0.88
Chr6:31623873	G	A	0.99212	0.081847	0.11863	2.61E-03	0.65	0.49	0.86
Chr6:31605167	G	A	0.99404	0.081773	0.11842	2.62E-03	0.65	0.49	0.86
Chr6:31638178	A	C	0.98994	0.081844	0.11859	2.63E-03	0.65	0.49	0.86
Chr6:31888869	T	G	0.88771	0.1559	0.11003	2.63E-03	1.57	1.17	2.11
Chr6:32735311	A	G	0.84301	0.1595	0.20803	2.65E-03	1.46	1.14	1.87
Chr6:31641386	G	T	0.98854	0.081899	0.11854	2.65E-03	0.65	0.49	0.86
Chr6:31598293	G	A	0.99486	0.081646	0.11827	2.66E-03	0.65	0.49	0.86
Chr6:31106409	A	G	0.8815	0.36219	0.29954	2.66E-03	1.37	1.12	1.69
Chr6:32121659	T	C	0.74679	0.15738	0.11589	2.67E-03	1.62	1.18	2.22
Chr6:31644090	C	G	0.98749	0.081946	0.11851	2.67E-03	0.65	0.49	0.86
Chr6:32123345	G	A	0.7468	0.15738	0.1159	2.67E-03	1.62	1.18	2.22
Chr6:32128186	G	T	0.74688	0.15739	0.11592	2.68E-03	1.62	1.18	2.22
Chr6:32132590	A	G	0.74699	0.15741	0.11595	2.68E-03	1.62	1.18	2.22
Chr5:1325803	A	G	0.95775	0.47697	0.41863	2.69E-03	0.75	0.62	0.91
Chr6:32140003	C	T	0.74685	0.15747	0.11604	2.71E-03	1.62	1.18	2.22
Chr6:32136930	G	T	0.7469	0.15747	0.11603	2.71E-03	1.62	1.18	2.22
Chr6:31930462	G	A	0.80885	0.29422	0.2348	2.74E-03	1.43	1.13	1.80
Chr15:78812949	G	C	0.93864	0.04741	0.023788	2.74E-03	2.22	1.32	3.74
Chr6:31628113	A	C	0.9708	0.076615	0.1116	2.74E-03	0.64	0.47	0.86
Chr6:31596675	A	G	0.98207	0.083573	0.12022	2.79E-03	0.65	0.49	0.86
Chr6:31605278	C	T	0.97243	0.076643	0.11143	2.79E-03	0.64	0.47	0.86
Chr6:31887058	G	A	0.90144	0.15393	0.10832	2.80E-03	1.57	1.17	2.11
Chr6:31886442	C	T	0.90191	0.1539	0.1083	2.80E-03	1.57	1.17	2.11
Chr6:31887076	C	G	0.90137	0.15382	0.10824	2.80E-03	1.57	1.17	2.11
Chr6:31783507	G	C	0.90411	0.32871	0.27529	2.87E-03	0.72	0.59	0.90
Chr6:31870873	C	A	0.92062	0.14854	0.10236	2.87E-03	1.57	1.17	2.11
Chr6:32151420	G	C	0.78356	0.1199	0.15848	2.87E-03	0.65	0.49	0.86
Chr6:32092207	T	C	0.74689	0.15552	0.11355	2.91E-03	1.62	1.18	2.23
Chr6:31854543	C	T	0.92788	0.14836	0.10216	2.94E-03	1.57	1.17	2.10
Chr6:31853858	C	T	0.92795	0.14835	0.10216	2.95E-03	1.57	1.17	2.10
Chr6:31762844	G	T	0.89121	0.28781	0.23391	3.02E-03	1.41	1.12	1.77
Chr6:31906505	C	T	0.83084	0.25921	0.20135	3.03E-03	1.43	1.13	1.82
Chr15:78805036	G	A	0.93959	0.046949	0.023782	3.14E-03	2.20	1.30	3.71
Chr5:1325767	A	G	0.96393	0.47518	0.41751	3.19E-03	0.76	0.63	0.91
Chr15:78800925	G	T	0.9186	0.046045	0.023173	3.20E-03	2.23	1.31	3.80
Chr6:32073913	G	C	0.74274	0.15789	0.11588	3.20E-03	1.62	1.17	2.22
Chr5:1325590	T	C	0.96181	0.47366	0.41608	3.21E-03	0.76	0.63	0.91
Chr6:31907168	C	T	0.83249	0.25957	0.20193	3.23E-03	1.43	1.13	1.81
Chr6:31907147	T	C	0.83249	0.25957	0.20193	3.24E-03	1.43	1.13	1.81
Chr6:31906334	T	A	0.83275	0.25954	0.20191	3.24E-03	1.43	1.13	1.81
Chr6:31906865	C	T	0.83261	0.25955	0.20192	3.24E-03	1.43	1.13	1.81
Chr6:32102231	C	T	0.7442	0.15584	0.11425	3.25E-03	1.61	1.17	2.22
Chr6:31905328	G	T	0.833	0.25948	0.20189	3.26E-03	1.43	1.13	1.81
Chr6:31905130	G	A	0.83308	0.25947	0.20188	3.26E-03	1.43	1.13	1.81

Chr6:31908761	T	C	0.8315	0.25975	0.20209	3.30E-03	1.43	1.13	1.81
Chr6:33074750	T	C	0.8396	0.034942	0.017458	3.31E-03	2.79	1.41	5.54
Chr6:31792174	A	G	0.89418	0.14952	0.10436	3.32E-03	1.57	1.16	2.13
Chr6:32106931	C	T	0.74422	0.15586	0.11435	3.33E-03	1.61	1.17	2.22
Chr6:31910929	G	A	0.83089	0.25993	0.20234	3.41E-03	1.43	1.12	1.81
Chr6:31910938	G	T	0.83089	0.25993	0.20234	3.41E-03	1.43	1.12	1.81
Chr6:31910162	G	A	0.83103	0.2599	0.20232	3.42E-03	1.43	1.12	1.81
Chr6:31805600	T	C	0.90173	0.14047	0.095972	3.44E-03	1.59	1.16	2.16
Chr6:31807148	A	G	0.90142	0.14047	0.095989	3.45E-03	1.59	1.16	2.16
Chr6:31914180	G	A	0.81945	0.26346	0.20668	3.46E-03	1.43	1.12	1.81
Chr6:32149883	C	T	0.74347	0.17919	0.13643	3.60E-03	1.55	1.15	2.08
Chr6:31219982	G	A	0.87575	0.31694	0.25979	3.70E-03	1.38	1.11	1.73
Chr6:31810266	C	T	0.87624	0.15562	0.11075	3.90E-03	1.55	1.15	2.09
Chr5:1330253	T	C	0.97613	0.47732	0.42103	3.97E-03	0.76	0.63	0.92
Chr5:1330840	T	C	0.97646	0.47721	0.42107	4.05E-03	0.76	0.63	0.92
Chr6:32074518	C	G	0.74835	0.15713	0.11628	4.07E-03	1.59	1.16	2.19
Chr6:31818279	A	G	0.87377	0.15563	0.11099	4.08E-03	1.55	1.15	2.08
Chr6:31852617	G	T	0.91279	0.13699	0.093353	4.15E-03	1.57	1.15	2.14
Chr6:32800221	C	T	0.75978	0.049892	0.025916	4.16E-03	2.26	1.29	3.95
Chr6:31713566	A	G	0.98801	0.1531	0.1979	4.18E-03	0.71	0.57	0.90
Chr6:32798243	G	A	0.74299	0.050975	0.026882	4.28E-03	2.25	1.29	3.94
Chr6:30054087	C	G	0.8053	0.088226	0.063722	4.34E-03	1.82	1.21	2.74
Chr6:30053144	G	A	0.80533	0.088228	0.063724	4.34E-03	1.82	1.21	2.74
Chr6:32023903	G	C	0.74634	0.15312	0.1131	4.58E-03	1.59	1.15	2.19
Chr6:31900232	A	C	0.87675	0.15606	0.11183	4.63E-03	1.53	1.14	2.06
Chr6:31471324	G	A	0.79444	0.021694	0.012005	4.64E-03	3.72	1.50	9.24
Chr6:31471767	A	C	0.79444	0.021694	0.012005	4.64E-03	3.72	1.50	9.24
Chr6:32070838	T	C	0.7482	0.15766	0.11738	4.65E-03	1.58	1.15	2.17
Chr6:31467303	C	G	0.79438	0.02169	0.012004	4.66E-03	3.72	1.50	9.24
Chr6:31472704	T	C	0.7944	0.021691	0.012006	4.66E-03	3.72	1.50	9.24
Chr6:31653120	G	A	0.98378	0.52182	0.46388	4.73E-03	0.77	0.64	0.92
Chr6:31630241	C	T	0.99553	0.51737	0.45996	4.73E-03	0.77	0.64	0.92
Chr6:32105512	G	A	0.73582	0.16414	0.12309	4.73E-03	1.57	1.15	2.15
Chr6:32108362	C	G	0.73596	0.16412	0.12312	4.81E-03	1.57	1.15	2.14
Chr6:31900468	G	A	0.87572	0.15509	0.11193	4.87E-03	1.53	1.14	2.06
Chr6:31629096	T	C	0.996	0.5176	0.46022	4.90E-03	0.77	0.64	0.92
Chr6:31643251	A	T	0.99634	0.51753	0.46008	4.93E-03	0.77	0.64	0.92
Chr6:31462545	C	T	0.79216	0.021558	0.011975	4.94E-03	3.69	1.49	9.19
Chr6:31648403	C	T	0.99605	0.51755	0.46021	4.99E-03	0.77	0.64	0.92
Chr6:31700657	G	T	0.99103	0.1515	0.19598	5.00E-03	0.72	0.57	0.90
Chr6:31783863	G	C	0.89172	0.40796	0.45941	5.03E-03	0.76	0.62	0.92
Chr6:31654732	T	A	0.99631	0.51757	0.46039	5.06E-03	0.77	0.64	0.92
Chr6:31657754	C	G	0.99669	0.51758	0.46048	5.10E-03	0.77	0.64	0.92
Chr6:31664219	A	G	0.99643	0.51781	0.46077	5.14E-03	0.77	0.64	0.92
Chr6:31661489	T	C	0.99734	0.51759	0.46058	5.14E-03	0.77	0.64	0.92
Chr6:31662229	A	G	0.9975	0.51759	0.4606	5.15E-03	0.77	0.64	0.92
Chr6:31702710	C	T	0.9936	0.15184	0.1962	5.16E-03	0.72	0.57	0.91

Chr5:1320136	G	A	0.81702	0.39798	0.34742	5.21E-03	0.74	0.60	0.92
Chr6:31740003	A	G	0.93959	0.24043	0.29261	5.27E-03	0.75	0.61	0.92
Chr6:32823393	C	T	0.73504	0.058166	0.032596	5.30E-03	2.11	1.25	3.56
Chr6:31704934	C	T	0.99421	0.1518	0.19605	5.30E-03	0.72	0.57	0.91
Chr6:31900253	T	C	0.8583	0.15895	0.11587	5.33E-03	1.52	1.13	2.05
Chr6:32823948	G	A	0.73516	0.058184	0.032616	5.37E-03	2.11	1.25	3.56
Chr6:32827356	G	A	0.73519	0.058183	0.032617	5.38E-03	2.11	1.25	3.56
Chr6:31903121	G	A	0.87345	0.15686	0.11366	5.41E-03	1.52	1.13	2.04
Chr6:31659731	T	G	0.99605	0.51185	0.45607	5.42E-03	0.77	0.64	0.93
Chr6:31204315	T	C	0.84062	0.23143	0.28418	5.48E-03	1.37	1.10	1.70
Chr6:31902645	A	G	0.87611	0.15666	0.11351	5.52E-03	1.52	1.13	2.04
Chr6:31902289	C	G	0.87822	0.15653	0.1134	5.56E-03	1.52	1.13	2.04
Chr6:31900570	A	G	0.8818	0.15627	0.11311	5.59E-03	1.52	1.13	2.04
Chr6:32827916	T	C	0.76876	0.052066	0.028145	5.63E-03	2.16	1.25	3.72
Chr6:31517797	T	G	0.85838	0.044308	0.02665	5.66E-03	2.26	1.27	4.04
Chr6:33048532	G	C	0.78975	0.052219	0.032018	5.66E-03	2.13	1.25	3.63
Chr6:33048641	A	G	0.7899	0.052206	0.032013	5.68E-03	2.13	1.25	3.63
Chr6:31710968	T	A	0.99639	0.15169	0.19563	5.70E-03	0.72	0.57	0.91
Chr6:31898285	A	G	0.88365	0.15617	0.11311	5.75E-03	1.51	1.13	2.03
Chr6:31897543	G	A	0.8842	0.15614	0.11309	5.76E-03	1.51	1.13	2.03
Chr6:32085598	C	T	0.73437	0.14841	0.1101	5.79E-03	1.59	1.14	2.20
Chr6:31597753	G	A	0.98174	0.47487	0.41969	5.85E-03	0.77	0.64	0.93
Chr6:31892592	G	A	0.88798	0.1559	0.1129	5.88E-03	1.51	1.13	2.03
Chr6:31891662	T	C	0.88867	0.15586	0.11287	5.90E-03	1.51	1.13	2.03
Chr6:31891487	C	G	0.88883	0.15584	0.11286	5.91E-03	1.51	1.13	2.03
Chr6:31203074	T	G	0.8425	0.23102	0.2835	5.92E-03	1.36	1.09	1.70
Chr6:31203217	G	C	0.84246	0.23102	0.2835	5.92E-03	1.36	1.09	1.70
Chr6:31890158	T	G	0.88986	0.1558	0.11281	5.92E-03	1.51	1.13	2.03
Chr6:31203744	T	C	0.84228	0.23104	0.2835	5.93E-03	1.36	1.09	1.70
Chr6:31205754	T	C	0.84168	0.23109	0.28351	5.94E-03	1.36	1.09	1.70
Chr6:31820643	A	G	0.87942	0.38726	0.33549	5.95E-03	0.75	0.61	0.92
Chr6:32842691	T	G	0.73959	0.057953	0.03258	6.29E-03	2.07	1.23	3.50
Chr5:1356450	C	T	0.80945	0.48749	0.44078	6.29E-03	0.76	0.62	0.92
Chr6:31445156	G	A	0.7898	0.021133	0.011904	6.35E-03	3.56	1.43	8.88
Chr6:31667202	A	G	0.96488	0.079427	0.1097	6.38E-03	0.66	0.49	0.89
Chr5:1327101	C	G	0.84428	0.39815	0.34861	6.38E-03	0.75	0.61	0.92
Chr6:31640518	T	G	0.99544	0.47928	0.42511	6.55E-03	0.77	0.64	0.93
Chr15:78985317	G	A	0.74574	0.2126	0.1758	6.57E-03	1.45	1.11	1.90
Chr6:31616366	G	A	0.99287	0.47897	0.42446	6.62E-03	0.77	0.64	0.93
Chr6:31620020	A	G	0.99346	0.47896	0.42471	6.73E-03	0.77	0.64	0.93
Chr6:31634193	A	G	0.9943	0.47368	0.42075	6.79E-03	0.77	0.64	0.93
Chr6:31734890	T	A	0.96788	0.16163	0.20493	6.90E-03	0.73	0.58	0.92
Chr6:32045226	T	A	0.74806	0.15528	0.11671	6.97E-03	1.55	1.13	2.13
Chr6:32059400	C	T	0.7476	0.15526	0.11678	7.13E-03	1.55	1.13	2.12
Chr6:31145416	C	G	0.85212	0.10472	0.075828	7.14E-03	1.64	1.14	2.35
Chr6:31213583	T	C	0.75903	0.43858	0.38603	7.16E-03	1.34	1.08	1.66
Chr5:1320247	G	A	0.92088	0.47296	0.42172	7.32E-03	0.77	0.64	0.93

Chr6:31150350	G	A	0.85271	0.10459	0.075883	7.44E-03	1.63	1.14	2.34
Chr6:31736570	G	A	0.97131	0.053166	0.07878	7.67E-03	0.62	0.44	0.88
Chr6:31674639	G	A	0.98317	0.028853	0.014501	7.83E-03	2.54	1.28	5.05
Chr6:30066358	G	T	0.78164	0.0899	0.066506	7.88E-03	1.73	1.15	2.60
Chr6:32286685	A	G	0.88585	0.01884	0.0087562	7.91E-03	3.44	1.38	8.55
Chr5:1315343	G	A	0.88655	0.40665	0.45429	7.99E-03	1.30	1.07	1.59
Chr6:32726838	C	T	0.76312	0.21134	0.25284	8.01E-03	1.39	1.09	1.77
Chr6:32853605	A	C	0.78589	0.049175	0.026583	8.07E-03	2.12	1.22	3.68
Chr6:30063087	G	A	0.78172	0.090333	0.067048	8.12E-03	1.73	1.15	2.58
Chr5:1356944	C	T	0.78177	0.47805	0.43201	8.15E-03	0.76	0.62	0.93
Chr6:32009279	T	C	0.71644	0.15986	0.12521	8.16E-03	1.54	1.12	2.12
Chr6:31834317	G	A	0.91856	0.17994	0.22431	8.16E-03	0.74	0.59	0.92
Chr6:32227556	G	A	0.89532	0.018988	0.0088461	8.17E-03	3.40	1.37	8.40
Chr6:32721392	G	A	0.95366	0.12756	0.17205	8.17E-03	1.41	1.09	1.81
Chr6:32721510	A	C	0.95365	0.12756	0.17205	8.17E-03	1.41	1.09	1.81
Chr6:32721502	G	T	0.95366	0.12756	0.17205	8.17E-03	1.41	1.09	1.81
Chr6:32719028	G	A	0.96917	0.12709	0.17178	8.22E-03	1.40	1.09	1.80
Chr6:32716022	G	A	0.96887	0.12708	0.17174	8.26E-03	1.40	1.09	1.80
Chr15:78833584	G	A	0.91514	0.062388	0.036573	8.28E-03	1.82	1.17	2.85
Chr6:30065152	A	G	0.77887	0.090655	0.067419	8.28E-03	1.72	1.15	2.58
Chr6:32289808	G	A	0.88594	0.018902	0.0088521	8.35E-03	3.39	1.37	8.39
Chr6:31114597	T	A	0.85166	0.10392	0.075487	8.43E-03	1.63	1.13	2.34
Chr6:32277509	A	C	0.9014	0.018851	0.0088247	8.48E-03	3.37	1.36	8.34
Chr6:31463832	T	C	0.75731	0.039751	0.026165	8.50E-03	2.33	1.24	4.38
Chr6:31601022	T	C	0.99402	0.47698	0.42469	8.51E-03	0.78	0.64	0.94
Chr5:1355058	C	T	0.81647	0.48682	0.44203	8.62E-03	0.76	0.63	0.93
Chr5:1314009	C	T	0.87335	0.40198	0.44765	8.74E-03	1.30	1.07	1.59
Chr5:1354462	G	T	0.78875	0.46342	0.41758	8.78E-03	0.76	0.62	0.93
Chr15:78849034	T	C	0.9386	0.29381	0.24395	8.78E-03	1.33	1.08	1.65
Chr6:31735631	C	T	0.98665	0.24431	0.29642	8.80E-03	0.77	0.63	0.94
Chr6:31480511	T	G	0.76607	0.040078	0.026269	8.84E-03	2.30	1.23	4.30
Chr5:1313701	A	G	0.87197	0.40122	0.44667	8.97E-03	1.30	1.07	1.59
Chr6:31776604	G	A	0.94868	0.053955	0.078998	9.02E-03	0.63	0.44	0.89
Chr15:78961880	C	T	0.81406	0.01812	0.008417	9.17E-03	3.55	1.37	9.23
Chr6:31105413	A	G	0.86927	0.4571	0.39822	9.29E-03	1.29	1.07	1.57
Chr6:31820469	C	A	0.92344	0.18059	0.224	9.32E-03	0.74	0.59	0.93
Chr6:31820174	T	C	0.92355	0.18061	0.22399	9.35E-03	0.74	0.59	0.93
Chr6:31780594	C	A	0.95211	0.17977	0.22483	9.37E-03	0.74	0.60	0.93
Chr6:31819421	T	A	0.92379	0.18063	0.22399	9.40E-03	0.74	0.59	0.93
Chr6:32097891	A	G	0.73729	0.16498	0.12627	9.43E-03	1.51	1.11	2.06
Chr6:31777077	C	T	0.95262	0.1798	0.22483	9.44E-03	0.74	0.60	0.93
Chr6:32299173	G	T	0.8461	0.019488	0.0094625	9.45E-03	3.32	1.34	8.21
Chr15:78914265	G	A	0.8116	0.018159	0.008909	9.67E-03	3.66	1.37	9.77
Chr6:31763942	G	C	0.95436	0.17994	0.2248	9.68E-03	0.75	0.60	0.93
Chr6:31806598	G	A	0.93615	0.1742	0.21725	9.68E-03	0.74	0.59	0.93
Chr5:1312020	T	C	0.86497	0.39759	0.4423	9.69E-03	1.30	1.07	1.59
Chr15:78975468	C	T	0.81662	0.017908	0.0083336	9.83E-03	3.52	1.35	9.17

Chr15:78977579	T	C	0.81662	0.017899	0.0083328	9.87E-03	3.52	1.35	9.17
Chr6:29196418	G	A	0.79879	0.016512	0.0077397	9.94E-03	4.13	1.41	12.14
Chr6:29205077	G	A	0.79917	0.0165	0.0077333	9.95E-03	4.13	1.40	12.14

[a]SNPs are ordered by P-value; [b]OR for each additional copy of allele 2, estimated in a logistic regression model adjusted for: age, sex, study site, % sub-Saharan African Ancestry, %European ancestry, and number of pack-years smoked; [c]Standard errors account for additional uncertainty inherent in analysis of imputed genotypes

Table S1.4: Imputed SNP associations from the case-control analysis of small-cell lung cancer in African-Americans (P<0.01)

SNP Position[a]	Allele 1	Allele 2	Imputation QC Metric (Info)	Allele 2 Frequency (Cases)	Allele 2 Frequency (Controls)	P-value	OR[b]	OR_{Lower}[c]	OR_{Upper}[c]
Chr6:31519775	T	C	0.81077	0.099191	0.047315	1.34E-04	5.37	2.27	12.74
Chr6:31521302	G	C	0.81256	0.099415	0.047399	1.36E-04	5.33	2.26	12.60
Chr6:31533606	C	T	0.81891	0.10086	0.04821	1.61E-04	5.04	2.17	11.67
Chr6:31077239	C	T	0.90613	0.1009	0.045481	6.49E-04	3.79	1.76	8.14
Chr6:31553468	A	G	0.86798	0.10918	0.055394	9.78E-04	3.35	1.63	6.87
Chr6:31560670	C	T	0.85708	0.053552	0.020389	1.02E-03	7.05	2.20	22.63
Chr6:31565648	G	A	0.89109	0.11011	0.056067	1.23E-03	3.17	1.58	6.39
Chr6:32107139	T	C	0.76463	0.3321	0.45145	1.34E-03	1.83	1.27	2.65
Chr6:31558978	G	C	0.89126	0.11142	0.057338	1.41E-03	3.08	1.54	6.14
Chr15:78778953	A	G	0.98383	0.49528	0.37255	1.45E-03	1.70	1.23	2.37
Chr15:78778972	A	G	0.98801	0.49686	0.37377	1.45E-03	1.70	1.23	2.36
Chr6:31564728	G	A	0.86784	0.11282	0.060612	2.25E-03	2.88	1.46	5.68
Chr6:31557226	G	A	0.8629	0.11119	0.059793	2.26E-03	2.93	1.47	5.84
Chr15:78765122	G	T	0.98684	0.32906	0.22683	2.29E-03	1.78	1.23	2.57
Chr6:31080103	T	C	0.96238	0.050368	0.015801	2.34E-03	5.99	1.89	18.96
Chr6:31558720	G	A	0.86369	0.11151	0.060387	2.47E-03	2.88	1.45	5.73
Chr6:31560702	A	G	0.86497	0.1116	0.060417	2.47E-03	2.88	1.45	5.72
Chr6:31559900	G	A	0.86425	0.11156	0.060428	2.48E-03	2.88	1.45	5.72
Chr6:31561639	G	A	0.86536	0.11162	0.060446	2.49E-03	2.88	1.45	5.71
Chr15:78742579	A	G	0.99217	0.32715	0.2263	2.72E-03	1.76	1.22	2.54
Chr15:78735438	G	C	0.99201	0.326	0.22624	3.00E-03	1.75	1.21	2.53
Chr15:78735269	C	T	0.99233	0.32571	0.22613	3.05E-03	1.75	1.21	2.52
Chr15:78733390	A	T	0.99308	0.3252	0.22633	3.26E-03	1.74	1.20	2.52
Chr15:78726577	G	A	0.96855	0.21122	0.13595	3.48E-03	1.98	1.25	3.13
Chr6:31272553	G	A	0.87439	0.38857	0.29099	3.51E-03	1.75	1.20	2.55
Chr6:30374408	T	C	0.83212	0.080593	0.040943	3.54E-03	3.65	1.53	8.73
Chr6:30374481	G	A	0.83212	0.080593	0.040943	3.54E-03	3.65	1.53	8.73
Chr6:31080718	T	C	0.94561	0.051926	0.017329	3.55E-03	5.14	1.71	15.46
Chr6:31080367	C	G	0.95757	0.051783	0.017164	3.61E-03	5.11	1.70	15.33
Chr6:31327861	C	T	0.79917	0.07032	0.14974	3.66E-03	2.05	1.26	3.34
Chr6:31093505	G	A	0.85883	0.050764	0.01886	3.69E-03	5.61	1.75	17.97
Chr6:30384604	G	A	0.8319	0.080546	0.041024	3.73E-03	3.62	1.52	8.63
Chr6:31140008	C	T	0.90429	0.54646	0.43669	3.75E-03	1.63	1.17	2.27
Chr6:31078160	A	G	0.97681	0.051724	0.017078	3.86E-03	4.98	1.68	14.82
Chr6:31078836	G	A	0.97674	0.051724	0.017079	3.86E-03	4.98	1.68	14.82
Chr6:31079242	A	G	0.9767	0.051724	0.01708	3.86E-03	4.98	1.68	14.82

Chr6:31079264	C	T	0.9767	0.051724	0.01708	3.86E-03	4.98	1.68	14.82
Chr6:31079371	C	G	0.97668	0.051724	0.01708	3.87E-03	4.98	1.68	14.81
Chr6:32708118	T	C	0.92138	0.26044	0.17907	3.94E-03	0.54	0.36	0.82
Chr6:31058178	T	C	0.95241	0.050569	0.017245	4.01E-03	5.23	1.69	16.15
Chr6:31055018	G	A	0.95227	0.050563	0.017248	4.02E-03	5.23	1.69	16.15
Chr6:32683055	C	T	0.81731	0.21549	0.14481	4.04E-03	2.00	1.25	3.22
Chr6:31077046	C	T	0.96787	0.051489	0.017249	4.06E-03	4.98	1.67	14.90
Chr6:32709363	G	A	0.94039	0.25211	0.17089	4.10E-03	0.54	0.35	0.82
Chr15:78712364	C	A	0.83705	0.14351	0.087466	4.12E-03	2.54	1.34	4.79
Chr6:31076199	A	T	0.9624	0.05131	0.017391	4.25E-03	4.97	1.66	14.92
Chr6:31075718	T	C	0.96231	0.051305	0.017392	4.26E-03	4.97	1.66	14.92
Chr6:31074148	G	T	0.96212	0.051293	0.017398	4.27E-03	4.97	1.65	14.92
Chr6:31074455	C	T	0.96214	0.051293	0.017398	4.27E-03	4.97	1.65	14.92
Chr6:31070522	G	A	0.95836	0.050862	0.017371	4.28E-03	5.06	1.66	15.38
Chr6:31070524	C	T	0.95836	0.050862	0.017371	4.28E-03	5.06	1.66	15.38
Chr6:31070548	C	T	0.95836	0.050863	0.017371	4.28E-03	5.06	1.66	15.38
Chr6:31073537	T	A	0.96206	0.051288	0.0174	4.28E-03	4.97	1.65	14.92
Chr6:31073337	T	G	0.96204	0.051287	0.017401	4.28E-03	4.97	1.65	14.91
Chr6:31073369	G	T	0.96204	0.051287	0.017401	4.28E-03	4.97	1.65	14.91
Chr6:31072685	C	T	0.96202	0.051287	0.017403	4.28E-03	4.97	1.65	14.91
Chr6:31071453	G	A	0.96194	0.051282	0.017406	4.29E-03	4.96	1.65	14.91
Chr6:31074128	C	T	0.95836	0.051345	0.017477	4.30E-03	4.96	1.65	14.89
Chr6:30410988	G	C	0.81882	0.081013	0.041969	4.34E-03	3.52	1.48	8.34
Chr6:32698686	A	T	0.96513	0.253	0.17118	4.34E-03	0.55	0.36	0.83
Chr6:32694710	G	A	0.95759	0.25336	0.17185	4.40E-03	0.55	0.36	0.83
Chr6:32702498	C	T	0.95981	0.25171	0.17043	4.41E-03	0.55	0.36	0.83
Chr6:32699751	A	T	0.96309	0.2523	0.1708	4.43E-03	0.55	0.36	0.83
Chr6:31051553	C	T	0.93588	0.050644	0.017575	4.44E-03	5.12	1.66	15.75
Chr6:31049655	G	A	0.93575	0.050644	0.017577	4.45E-03	5.11	1.66	15.74
Chr6:32687102	G	A	0.95748	0.25319	0.17177	4.45E-03	0.55	0.36	0.83
Chr6:32693428	C	T	0.95809	0.25318	0.17174	4.45E-03	0.55	0.36	0.83
Chr6:32685911	T	A	0.95574	0.25314	0.17178	4.45E-03	0.55	0.36	0.83
Chr6:32693570	A	G	0.95791	0.25312	0.17171	4.45E-03	0.55	0.36	0.83
Chr6:32695960	G	T	0.96036	0.25312	0.17163	4.46E-03	0.55	0.36	0.83
Chr6:32692122	C	T	0.95742	0.2531	0.17174	4.46E-03	0.55	0.36	0.83
Chr6:32703206	A	G	0.96184	0.25188	0.17058	4.48E-03	0.55	0.36	0.83
Chr6:32703021	G	A	0.96201	0.25193	0.17062	4.48E-03	0.55	0.36	0.83
Chr6:32695783	A	G	0.95956	0.25314	0.17173	4.49E-03	0.55	0.36	0.83
Chr6:32695790	T	C	0.95955	0.25314	0.17173	4.49E-03	0.55	0.36	0.83
Chr6:32697382	T	C	0.96197	0.25312	0.17162	4.49E-03	0.55	0.36	0.83
Chr6:30420778	G	A	0.8176	0.080963	0.042053	4.53E-03	3.49	1.47	8.26
Chr6:31070960	A	T	0.95797	0.05108	0.017561	4.54E-03	4.94	1.64	14.90
Chr6:32705152	G	A	0.94942	0.24562	0.16547	4.55E-03	0.54	0.35	0.83
Chr6:32703591	C	T	0.96044	0.25139	0.17033	4.55E-03	0.55	0.36	0.83
Chr6:32704683	A	G	0.96038	0.25136	0.17031	4.55E-03	0.55	0.36	0.83
Chr6:32706234	G	A	0.96028	0.25134	0.1703	4.56E-03	0.55	0.36	0.83
Chr6:32704326	A	T	0.96039	0.25137	0.17032	4.56E-03	0.55	0.36	0.83

Chr6:32706334	A	G	0.96028	0.25134	0.1703	4.56E-03	0.55	0.36	0.83
Chr6:31223293	C	T	0.70923	0.20197	0.29639	4.58E-03	1.78	1.19	2.64
Chr6:32687960	A	T	0.95634	0.25319	0.17203	4.58E-03	0.55	0.36	0.83
Chr6:32688273	A	G	0.95636	0.25319	0.17203	4.58E-03	0.55	0.36	0.83
Chr6:31325030	T	C	0.72289	0.088649	0.16563	4.62E-03	2.03	1.24	3.31
Chr6:32699054	G	C	0.96102	0.25232	0.17128	4.65E-03	0.55	0.36	0.83
Chr6:32706441	A	T	0.95727	0.25161	0.17086	4.69E-03	0.55	0.36	0.83
Chr6:32706478	C	T	0.95727	0.2516	0.17086	4.69E-03	0.55	0.36	0.83
Chr6:32706480	C	T	0.95727	0.2516	0.17086	4.69E-03	0.55	0.36	0.83
Chr6:31324742	T	C	0.73888	0.085317	0.16207	4.70E-03	2.02	1.24	3.30
Chr6:32705419	T	C	0.95766	0.25158	0.17075	4.73E-03	0.55	0.36	0.83
Chr6:32708338	T	C	0.95684	0.25006	0.16961	4.75E-03	0.55	0.36	0.83
Chr6:32708467	T	A	0.95669	0.24999	0.16958	4.77E-03	0.55	0.36	0.83
Chr6:32708504	C	G	0.95665	0.24996	0.16957	4.77E-03	0.55	0.36	0.83
Chr6:30448017	T	C	0.80577	0.080656	0.041975	4.80E-03	3.46	1.46	8.22
Chr6:32708736	T	C	0.95548	0.24949	0.16931	4.85E-03	0.55	0.36	0.83
Chr6:32708774	A	G	0.95528	0.24941	0.16927	4.86E-03	0.55	0.36	0.83
Chr6:31073007	G	T	0.90227	0.37396	0.27919	4.93E-03	1.68	1.17	2.42
Chr6:31058975	G	A	0.94805	0.05061	0.017826	4.95E-03	4.95	1.62	15.10
Chr6:31072300	T	C	0.90264	0.37403	0.27929	4.95E-03	1.68	1.17	2.42
Chr6:32709309	A	G	0.95348	0.24874	0.16892	4.99E-03	0.55	0.36	0.83
Chr6:32709370	T	C	0.95361	0.24868	0.16887	5.00E-03	0.55	0.36	0.83
Chr6:32735311	A	G	0.84594	0.29163	0.20803	5.12E-03	0.56	0.37	0.84
Chr6:31225708	G	A	0.72328	0.19068	0.2843	5.12E-03	1.75	1.18	2.60
Chr6:32705002	C	T	0.94826	0.24563	0.16601	5.13E-03	0.55	0.36	0.83
Chr6:32704982	A	C	0.94825	0.24563	0.16601	5.13E-03	0.55	0.36	0.83
Chr6:31227506	A	G	0.76131	0.18305	0.27818	5.23E-03	1.74	1.18	2.56
Chr6:31231234	G	A	0.80644	0.17213	0.26816	5.26E-03	1.73	1.18	2.55
Chr6:32449478	A	G	0.80159	0.059747	0.024546	5.27E-03	4.58	1.57	13.33
Chr6:31313714	G	A	0.72703	0.32885	0.42529	5.38E-03	1.71	1.17	2.49
Chr6:32446682	T	C	0.78837	0.057109	0.025554	5.44E-03	4.70	1.58	13.99
Chr15:78766208	A	T	0.97478	0.21057	0.13802	5.44E-03	1.90	1.21	3.00
Chr6:31051008	G	A	0.9315	0.050678	0.018168	5.48E-03	4.84	1.59	14.73
Chr6:31035038	G	A	0.8167	0.26244	0.18456	5.49E-03	1.92	1.21	3.03
Chr6:31141209	A	G	0.86584	0.068433	0.14323	5.65E-03	1.98	1.22	3.22
Chr6:31227494	C	A	0.80707	0.16454	0.25829	5.65E-03	1.73	1.17	2.55
Chr6:31241838	T	C	0.87992	0.069704	0.14922	5.67E-03	1.96	1.22	3.16
Chr6:31086849	A	G	0.98451	0.10578	0.1936	5.79E-03	1.76	1.18	2.62
Chr6:31044027	C	T	0.86709	0.17737	0.11599	5.81E-03	2.15	1.25	3.70
Chr6:31225907	G	T	0.76038	0.18253	0.2764	5.82E-03	1.73	1.17	2.54
Chr6:32453387	C	T	0.77581	0.064834	0.028605	5.87E-03	4.14	1.51	11.36
Chr6:32449764	A	G	0.79673	0.058374	0.024086	5.90E-03	4.60	1.55	13.62
Chr6:31227577	C	T	0.76723	0.18195	0.27573	5.93E-03	1.73	1.17	2.56
Chr6:31022822	C	G	0.86234	0.17833	0.11596	5.94E-03	2.14	1.24	3.67
Chr15:78792398	T	C	0.99285	0.41445	0.30999	6.22E-03	1.60	1.14	2.25
Chr6:32713188	C	T	0.94926	0.24665	0.16824	6.24E-03	0.56	0.37	0.85
Chr15:78793921	C	T	0.98949	0.41314	0.30921	6.25E-03	1.61	1.14	2.26

Chr15:78767346	G	A	0.98129	0.41283	0.30883	6.33E-03	1.60	1.14	2.25
Chr15:78751961	C	T	0.9862	0.41466	0.31022	6.35E-03	1.60	1.14	2.25
Chr6:32507621	C	T	0.77318	0.18237	0.12182	6.50E-03	2.14	1.24	3.71
Chr15:78754000	A	G	0.9892	0.41531	0.31101	6.51E-03	1.60	1.14	2.24
Chr15:78789223	G	A	0.99323	0.41392	0.31007	6.52E-03	1.60	1.14	2.25
Chr15:78779510	T	A	0.99343	0.41408	0.31034	6.61E-03	1.60	1.14	2.24
Chr6:32427581	C	G	0.83676	0.06104	0.025388	6.64E-03	4.10	1.48	11.38
Chr6:31073656	T	A	0.91202	0.051931	0.019156	6.65E-03	4.45	1.51	13.08
Chr15:78782095	C	T	0.99266	0.41375	0.31026	6.71E-03	1.60	1.14	2.24
Chr6:32428917	G	A	0.83656	0.061231	0.025526	6.72E-03	4.08	1.48	11.29
Chr6:32429077	T	C	0.79154	0.059977	0.02708	6.78E-03	4.10	1.48	11.39
Chr6:32404135	A	G	0.85978	0.23767	0.15896	6.94E-03	1.86	1.19	2.92
Chr6:32421327	C	T	0.90163	0.057172	0.022575	6.95E-03	4.14	1.48	11.61
Chr6:32454153	T	C	0.82035	0.061599	0.026312	6.95E-03	4.01	1.46	11.01
Chr6:32404043	A	G	0.85985	0.23764	0.15896	6.97E-03	1.86	1.18	2.92
Chr15:78774374	A	G	0.99267	0.41559	0.31216	6.98E-03	1.59	1.14	2.23
Chr6:32403934	C	T	0.85988	0.23763	0.15897	6.98E-03	1.86	1.18	2.92
Chr6:31242695	G	T	0.93505	0.061707	0.13859	7.05E-03	1.94	1.20	3.13
Chr6:30424655	C	G	0.85846	0.11531	0.069062	7.05E-03	2.50	1.28	4.87
Chr6:32418722	G	A	0.90208	0.057195	0.022619	7.06E-03	4.12	1.47	11.53
Chr6:32416799	T	G	0.90245	0.057185	0.022614	7.07E-03	4.12	1.47	11.52
Chr6:32512745	G	A	0.76116	0.20005	0.13678	7.08E-03	2.06	1.22	3.49
Chr15:78765290	T	G	0.99034	0.41603	0.31267	7.09E-03	1.59	1.13	2.23
Chr6:32407433	G	C	0.86119	0.23799	0.15936	7.09E-03	1.86	1.18	2.91
Chr6:32407440	T	C	0.86117	0.23798	0.15935	7.09E-03	1.86	1.18	2.91
Chr6:32395835	A	G	0.86498	0.23701	0.15895	7.10E-03	1.86	1.18	2.92
Chr6:32407153	A	T	0.86139	0.23795	0.15936	7.11E-03	1.85	1.18	2.91
Chr6:32406887	C	T	0.86154	0.23792	0.15937	7.13E-03	1.85	1.18	2.91
Chr6:31227588	G	T	0.78088	0.18042	0.27232	7.13E-03	1.71	1.16	2.53
Chr6:32397712	A	C	0.86165	0.23648	0.15866	7.17E-03	1.86	1.18	2.93
Chr6:32406412	C	G	0.86187	0.23787	0.15939	7.18E-03	1.85	1.18	2.91
Chr15:78769130	A	G	0.99244	0.41591	0.31272	7.18E-03	1.59	1.13	2.22
Chr6:32437896	G	A	0.83492	0.061437	0.025793	7.20E-03	4.00	1.46	11.01
Chr6:32412114	C	T	0.90722	0.057034	0.022518	7.20E-03	4.09	1.46	11.45
Chr6:32438896	C	T	0.83497	0.061448	0.025802	7.22E-03	4.00	1.45	11.00
Chr6:32405076	G	C	0.86223	0.23778	0.15941	7.25E-03	1.85	1.18	2.90
Chr6:32405062	G	T	0.86222	0.23777	0.15941	7.25E-03	1.85	1.18	2.90
Chr15:78766194	T	A	0.99064	0.41546	0.31251	7.25E-03	1.59	1.13	2.22
Chr6:32396506	A	G	0.86405	0.23726	0.1592	7.26E-03	1.86	1.18	2.91
Chr6:32397049	G	A	0.86401	0.23728	0.15921	7.26E-03	1.85	1.18	2.91
Chr6:32404878	T	G	0.86227	0.23777	0.15941	7.26E-03	1.85	1.18	2.90
Chr15:78766629	C	T	0.99082	0.41543	0.31252	7.27E-03	1.59	1.13	2.22
Chr6:32398648	G	A	0.86395	0.2373	0.15924	7.29E-03	1.85	1.18	2.91
Chr6:32398872	T	G	0.86391	0.23731	0.15925	7.30E-03	1.85	1.18	2.91
Chr6:32398975	C	T	0.86389	0.23732	0.15926	7.31E-03	1.85	1.18	2.91
Chr15:78767850	C	T	0.99155	0.41535	0.31252	7.32E-03	1.59	1.13	2.22
Chr6:32404213	C	T	0.86252	0.23769	0.15943	7.33E-03	1.85	1.18	2.90

Chr6:32399022	A	G	0.86367	0.23735	0.15932	7.34E-03	1.85	1.18	2.91
Chr6:32403655	T	G	0.86287	0.23766	0.15943	7.35E-03	1.85	1.18	2.90
Chr6:31029282	G	A	0.8627	0.17744	0.11664	7.40E-03	2.09	1.22	3.59
Chr6:32399261	C	G	0.8636	0.23749	0.15942	7.41E-03	1.85	1.18	2.90
Chr6:32399785	A	G	0.86356	0.2375	0.15945	7.45E-03	1.85	1.18	2.90
Chr6:32400520	G	A	0.86356	0.23752	0.15946	7.45E-03	1.85	1.18	2.90
Chr6:32401534	C	T	0.86349	0.23753	0.15947	7.46E-03	1.85	1.18	2.90
Chr6:32399842	T	C	0.86332	0.23718	0.15936	7.53E-03	1.85	1.18	2.90
Chr6:31227219	G	A	0.76572	0.18431	0.27536	7.58E-03	1.70	1.15	2.51
Chr6:32406549	C	T	0.90598	0.057057	0.022714	7.59E-03	4.04	1.45	11.25
Chr6:32702421	T	C	0.85398	0.2735	0.19711	7.60E-03	0.57	0.38	0.86
Chr6:30453795	G	A	0.84043	0.11716	0.070764	7.68E-03	2.45	1.27	4.73
Chr6:31035552	C	T	0.86306	0.17727	0.11675	7.69E-03	2.08	1.21	3.57
Chr6:32401237	G	A	0.90676	0.057086	0.022787	7.71E-03	4.02	1.44	11.18
Chr6:33026110	A	C	0.92026	0.38741	0.30224	7.72E-03	1.63	1.14	2.33
Chr6:33045934	G	A	0.94718	0.35799	0.27036	7.73E-03	1.63	1.14	2.33
Chr6:33046662	T	C	0.94209	0.35551	0.26824	7.74E-03	1.64	1.14	2.35
Chr6:32427361	C	T	0.77379	0.10963	0.059984	7.79E-03	2.57	1.28	5.16
Chr6:32396384	A	G	0.90699	0.057086	0.022838	7.82E-03	4.00	1.44	11.13
Chr6:31231591	C	T	0.76202	0.18451	0.27419	7.89E-03	1.72	1.15	2.57
Chr6:31230319	C	A	0.78481	0.18346	0.27463	7.95E-03	1.70	1.15	2.51
Chr6:32684387	A	G	0.85586	0.2218	0.15355	8.05E-03	1.86	1.17	2.93
Chr6:30761486	T	C	0.76991	0.1673	0.11094	8.11E-03	2.11	1.21	3.65
Chr6:32684257	A	G	0.85468	0.22169	0.15357	8.12E-03	1.86	1.17	2.93
Chr6:31038966	C	A	0.86384	0.17697	0.11692	8.21E-03	2.07	1.21	3.55
Chr6:31227151	C	T	0.76152	0.19286	0.2841	8.27E-03	1.69	1.14	2.49
Chr6:31086617	C	T	0.97343	0.10633	0.18895	8.27E-03	1.73	1.15	2.60
Chr6:32391527	G	A	0.90997	0.057082	0.023027	8.30E-03	3.94	1.42	10.93
Chr6:32399158	C	T	0.86077	0.23526	0.15883	8.31E-03	1.84	1.17	2.90
Chr6:32390820	G	A	0.91002	0.057077	0.023031	8.31E-03	3.94	1.42	10.92
Chr6:31089125	A	G	0.99142	0.10324	0.18681	8.36E-03	1.72	1.15	2.58
Chr6:31227146	T	C	0.76818	0.18918	0.27889	8.37E-03	1.69	1.14	2.50
Chr6:32684272	T	A	0.85466	0.22139	0.15352	8.37E-03	1.85	1.17	2.92
Chr6:32698285	A	G	0.8673	0.271	0.19536	8.38E-03	0.58	0.38	0.87
Chr6:31080704	T	G	0.87171	0.27847	0.20044	8.42E-03	1.80	1.16	2.79
Chr6:31088232	A	G	0.99312	0.10332	0.18687	8.45E-03	1.72	1.15	2.57
Chr6:31088241	C	T	0.99312	0.10332	0.18687	8.45E-03	1.72	1.15	2.57
Chr6:31088856	T	C	0.99457	0.10351	0.1871	8.50E-03	1.72	1.15	2.57
Chr6:31088325	A	G	0.99469	0.10352	0.18711	8.50E-03	1.72	1.15	2.57
Chr6:31087908	T	G	0.99476	0.10353	0.18712	8.50E-03	1.72	1.15	2.57
Chr6:31087934	G	A	0.99476	0.10353	0.18712	8.50E-03	1.72	1.15	2.57
Chr6:31088037	T	C	0.99474	0.10353	0.18712	8.50E-03	1.72	1.15	2.57
Chr6:31087496	G	A	0.99484	0.10354	0.18713	8.51E-03	1.72	1.15	2.57
Chr6:31086402	G	A	0.99482	0.10355	0.18713	8.52E-03	1.72	1.15	2.57
Chr6:32449705	T	C	0.80864	0.059782	0.025758	8.52E-03	4.05	1.43	11.50
Chr6:31027516	G	A	0.90066	0.31141	0.22637	8.56E-03	1.68	1.14	2.48
Chr6:31029685	C	T	0.90068	0.31139	0.22637	8.58E-03	1.68	1.14	2.48

Chr6:32683763	G	A	0.85181	0.22107	0.15356	8.59E-03	1.85	1.17	2.92
Chr6:31085882	A	G	0.99014	0.10374	0.18713	8.64E-03	1.72	1.15	2.57
Chr6:32451012	C	A	0.82188	0.061588	0.026431	8.65E-03	3.82	1.40	10.40
Chr6:30993880	G	C	0.74308	0.11476	0.070623	8.67E-03	2.60	1.27	5.31
Chr6:32451550	T	A	0.82162	0.061594	0.026445	8.68E-03	3.82	1.40	10.39
Chr6:32451419	T	G	0.82164	0.061594	0.026445	8.68E-03	3.82	1.40	10.39
Chr6:32451979	C	T	0.8216	0.061594	0.026447	8.68E-03	3.82	1.40	10.39
Chr6:32452300	C	G	0.82156	0.061593	0.026447	8.68E-03	3.82	1.40	10.39
Chr6:32452178	A	T	0.82158	0.061593	0.026447	8.68E-03	3.82	1.40	10.39
Chr6:32453054	T	A	0.82149	0.061599	0.026451	8.69E-03	3.82	1.40	10.38
Chr6:32453769	G	A	0.82144	0.061604	0.026456	8.69E-03	3.82	1.40	10.38
Chr6:30451515	G	A	0.84295	0.11425	0.069352	8.71E-03	2.45	1.25	4.77
Chr6:31225292	T	C	0.71105	0.20448	0.29185	8.77E-03	1.69	1.14	2.51
Chr6:32702422	G	A	0.83111	0.27707	0.20206	8.78E-03	0.58	0.38	0.87
Chr6:32450257	T	G	0.77271	0.054138	0.022665	8.89E-03	4.50	1.46	13.90
Chr6:33041226	C	T	0.98897	0.3926	0.49263	8.90E-03	0.65	0.47	0.90
Chr6:31222610	G	A	0.81767	0.16136	0.2512	8.90E-03	1.67	1.14	2.46
Chr6:32684105	C	T	0.85209	0.22135	0.15385	8.91E-03	1.84	1.17	2.91
Chr6:32449662	G	A	0.80596	0.059835	0.025925	9.03E-03	3.99	1.41	11.27
Chr6:32450103	A	G	0.80578	0.05984	0.025934	9.05E-03	3.99	1.41	11.26
Chr5:1243427	T	G	0.97037	0.58008	0.47873	9.07E-03	1.52	1.11	2.07
Chr6:31562150	G	A	0.82775	0.11631	0.069234	9.15E-03	2.34	1.23	4.44
Chr6:33045949	G	A	0.94487	0.358	0.27228	9.17E-03	1.61	1.13	2.31
Chr6:33048921	A	G	0.97923	0.55868	0.45875	9.20E-03	0.64	0.46	0.90
Chr6:33037891	C	T	0.97582	0.26122	0.35068	9.25E-03	0.64	0.46	0.90
Chr6:32716022	G	A	0.96933	0.24795	0.17174	9.27E-03	0.58	0.39	0.87
Chr6:32719028	G	A	0.96964	0.24797	0.17178	9.30E-03	0.58	0.39	0.88
Chr6:31038048	A	G	0.90261	0.30996	0.22599	9.34E-03	1.67	1.14	2.47
Chr6:32688529	T	G	0.89404	0.29206	0.21423	9.41E-03	0.59	0.40	0.88
Chr6:32721502	G	T	0.95549	0.24794	0.17205	9.43E-03	0.58	0.38	0.88
Chr6:32721510	A	C	0.95549	0.24794	0.17205	9.43E-03	0.58	0.38	0.88
Chr6:32721392	G	A	0.95549	0.24794	0.17205	9.43E-03	0.58	0.38	0.88
Chr6:30884251	G	A	0.87962	0.14369	0.086907	9.49E-03	2.16	1.21	3.86
Chr6:32406100	C	T	0.85447	0.23297	0.15821	9.49E-03	1.83	1.16	2.89
Chr6:31139452	T	C	0.91619	0.38061	0.48329	9.52E-03	1.54	1.11	2.13
Chr6:32507480	C	T	0.75122	0.20428	0.1453	9.65E-03	1.99	1.18	3.35
Chr6:31227142	G	T	0.7861	0.18486	0.27438	9.90E-03	1.67	1.13	2.46

[a] SNPs are ordered by P-value; [b] OR for each additional copy of allele 2, estimated in a logistic regression model adjusted for: age, sex, study site, % sub-Saharan African Ancestry, %European ancestry, and number of pack-years smoked; [c] Standard errors account for additional uncertainty inherent in analysis of imputed genotypes