Multiple functional SNPs in differentially expressed genes modify risk and survival of non-small cell lung cancer in chinese female non-smokers

Supplementary Materials

Supplementary Table 1: Distribution of genotypes and ORs for different types of NSCLC and controls

SNP	Genotype	Controls (%) N = 395	Adenocarcinoma (%) N = 322	Adjusted OR[a]	95% CI	P	Squamous cell carcinoma N = 66	Adjusted OR[a]	95% CI	P
Rs4754	CC	183 (46.3)	163 (50.6)	Ref			42 (63.6)	Ref		
	CT	167 (42.3)	136 (42.2)	0.915	0.671,1.246	0.572	20 (30.3)	0.526	0.297,0.933	0.028*
	TT	45 (11.4)	23 (7.1)	0.566	0.328,0.978	0.042*	4 (6.1)	0.383	0.130,1.124	0.081
Dominant model				0.842	0.627,1.130	0.252		0.495	0.289,0.849	0.011*
Recessive model				0.597	0.353,1.011	0.055		0.494	0.171,1.424	0.191
Additive model	T allele			0.817	0.651,1.025	0.080		0.558	0.358,0.869	0.010*
Rs959173	TT	348 (88.1)	295 (91.6)	Ref			64 (97.0)	Ref		
	TC+CC	47 (11.9)	27 (8.4)	0.678	0.412,1.115	0.126	2 (3.0)	0.238	0.056,1.003	0.051
Additive model	C allele			0.702	0.435,1.133	0.148		0.239	0.057,0.996	0.049*
Rs2069837	AA	264 (66.8)	211 (65.5)	Ref			40 (60.6)	Ref		
	AG	120 (30.4)	96 (29.8)	1.001	0.724,1.384	0.994	22 (33.3)	1.213	0.690,2.130	0.503
	GG	11 (2.8)	15 (4.7)	1.705	0.767,3.792	0.190	4 (6.1)	2.356	0.714,7.774	0.159
Dominant model				1.061	0.777,1.448	0.710		1.311	0.767,2.243	0.322
Recessive model				1.705	0.772,3.766	0.187		2.220	0.684,7.201	0.184
Additive model	G allele			1.110	0.851,1.449	0.441		1.341	0.859,2.095	0.197
Rs2066992	TT	201 (50.9)	150 (46.6)	Ref			28 (42.4)	Ref		
	TG	159 (40.3)	137 (42.5)	1.154	0.845,1.576	0.369	30 (45.5)	1.357	0.778,2.365	0.282
	GG	35 (8.9)	35 (10.9)	1.361	0.813,2.279	0.241	8 (12.1)	1.571	0.660,3.742	0.307
Dominant model				1.190	0.886,1.599	0.247		1.403	0.828,2.376	0.208
Recessive model				1.256	0.767,2.058	0.365		1.389	0.612,3.150	0.432
Additive model	G allele			1.162	0.972,1.457	0.193		1.303	0.882,1.924	0.184
Rs2239144	GG	169 (42.8)	105 (32.6)	Ref			18 (27.3)	Ref		
	GT	171 (43.3)	147 (45.7)	1.384	0.996,1.922	0.053	32 (48.5)	1.734	0.933,3.223	0.082
	TT	55 (13.9)	70 (21.7)	2.063	1.342,3.171	0.001*	16 (24.2)	2.730	1.302,5.723	0.008*
Dominant model				1.548	1.139,2.103	0.005*		1.989	1.116,3.543	0.020*
Recessive model				1.721	1.166,2.540	0.006*		1.992	1.059,3.747	0.033*
Additive model	T allele			1.458	1.178,1.804	0.001*		1.705	1.176,2.472	0.005*
Rs7306706	GG	154 (39.0)	137 (42.5)	Ref			27 (40.9)	Ref		
	GA	171 (43.3)	139 (43.2)	0.920	0.667,1.268	0.610	33 (50.0)	1.109	0.637,1.929	0.715
	AA	70 (17.7)	46 (14.3)	0.727	0.470,1.125	0.152	6 (9.1)	0.484	0.191,1.226	0.126
Dominant model				0.862	0.639,1.163	0.332		0.922	0.542,1.568	0.764
Recessive model				0.761	0.508,1.139	0.185		0.451	0.187,1.086	0.076
Additive model	A allele			0.857	0.691,1.062	0.159		0.789	0.536,1.163	0.232
Rs3181385	TT	355 (89.9)	272 (84.5)	Ref			60 (90.9)	Ref		
	TC + CC	40 (10.1)	50 (15.5)	1.771	1.125,2.789	0.014*	6 (9.1)	0.945	0.382,2.339	0.902
Additive model	A allele			1.464	0.960,2.232	0.076		0.823	0.343,1.974	0.662
Rs423490	GG	323 (81.8)	274 (85.1)	Ref			59 (89.4)	Ref		
	GA + AA	72 (18.2)	48 (14.9)	0.786	0.527,1.171	0.237	7 (10.6)	0.540	0.237,1.232	0.143
Additive model	A allele			0.809	0.554,1.180	0.271		0.550	0.247,1.222	0.142