Supplementary tables for the paper

"Genome-wide significant association between a sequence variant at 15q15.2 and lung cancer risk"

Thorunn Rafnar et al.

Supplementary table 1 - Association of rs748404-T with different histological subtypes of lung cancer

	OR	95%CI	P	Cases (N)	Cases (F)	Phet	I^2
Adenocarcinoma							
ICELAND	1.31	(1.11,1.53)	0.0010	538	0.837		
USA	1.05	(0.72,1.54)	0.79	67	0.776		
NETHERLAND	1.09	(0.84,1.41)	0.52	167	0.781		
SPAIN	0.87	(0.61,1.23)	0.42	82	0.713		
COMBINED[a]	1.17	(1.04,1.32)	0.0095	854	0.776	0.16	42.7
::::::::::::::							
SMCC							
ICELAND	1.17	(0.93,1.48)	0.19	223	0.822		
NETHERLANDS	0.8	(0.50,1.27)	0.34	47	0.723		
SPAIN	0.93	(0.63,1.37)	0.72	70	0.729		
COMBINED[a]	1.05	(0.87,1.26)	0.63	340	0.758	0.28	20.7
::::::::::::::							
SQCC							
ICELAND	1.24	(1.01,1.53)	0.04	309	0.83		
USA	0.87	(0.55,1.38)	0.55	52	0.741		
NETHERLANDS	1.06	(0.82,1.38)	0.64	177	0.777		
SPAIN	1.29	(0.96,1.73)	0.097	134	0.787		
COMBINED[a]	1.16	(1.02,1.33)	0.030	672	0.783	0.42	0

The frequency of rs748404-T in cases was compared with the frequency of the variant in control populations. The frequencies in controls are as follows: Iceland= 0.797, USA=0.766, Netherlands=0.766, Spain=0.742.

[a]For the combined study populations, the reported control frequency was the average, unweighted control frequency of the individual populations, while the OR and the P value were estimated using the Mantel-Haenszel model.

Supplementary table 2 - Association results for 5 SNPs reported by Landi *et al.* in chip-typed Icelandic lung cancer cases and controls

SNP	P	# cases	# controls	Overall freq	Information	Allele tested
rs2277532	0.000203258	839	36,606	0.683693	0.997003	G
rs12050604	0.000124821	837	36,550	0.686415	1.000000	C
rs504417	0.0344518	839	36,558	0.300492	1.000000	G
rs471122	0.0317988	839	36,606	0.300853	0.999991	G
rs506120	0.403561	839	36,606	0.291453	0.996399	T

Supplementary table 3 - LD between rs748404 and the 5 SNPs reported by Landi *et al.*

SNP	D'	r2	Chr	Pos	P*
rs12050604	0.42	0.13	C15	41,144,698	9.75×10^{-6}
rs2277532	0.43	0.14	C15	41,031,991	3.55×10^{-6}
rs471122	1.00	0.69	C15	41,345,866	1.59×10^{-5}
rs504417	1.00	0.69	C15	41,341,518	1.92×10^{-5}
rs506120	0.85	0.51	C15	41,589,316	4.25×10^{-5}

* P value reported in meta-analysis by Landi *et al*.

Supplementary table 4 - Association between rs12050604-C and lung cancer in case control sample sets

POPULATIONS	P	OR	CI	cases (N)	cases (F)	controls (N)	controls (F)	Phet	I2
Results from meta-analysis[a]	9.7×10^{-6}	1.09	(1.05, 1.13)	13,300		19,666			
Follow-up sample sets:									
USA	0.482	1.1	(0.84, 1.44)	177	0.718	823	0.697		
The Netherlands	0.485	1.06	(0.90, 1.23)	506	0.710	1832	0.699		
Spain	0.289	1.12	(0.91, 1.37)	497	0.742	503	0.721		
COMBINED follow up	0.17	1.08	(0.97, 1.21)	1,180	0.723	3,158	0.706	0.91	0
ALL COMBINED	**3.6×10^{-6}**	**1.09**	**(1.05, 1.13)**	**14,480**		**22,824**		**0.98**	**0**

[a] The meta-analysis reported by Landi et al. includes data from 719 cases and 6,030 controls from the Icelandic population, therefore Icelandic samples are not included among the follow-up datasets for this SNP.

Supplementary table 5 - Joint analysis of rs748404(T) and rs12050604(C)

	rs748404(T) adjusted for rs12050604(C)				rs12050604(C) adjusted for rs748404(T)		
Population	**OR**	**95% CI**	***P* value**		**OR**	**95% CI**	***P* value**
USA	1.22	(0.92, 1.62)	0.17		1.07	(0.82, 1.39)	0.62
The Netherlands	1.05	(0.89, 1.24)	0.56		1.04	(0.88, 1.23)	0.64
Iceland	1.12	(0.98, 1.28)	0.085		1.16	(1.05, 1.28)	0.003
Spain	1.05	(0.88,1.25)	0.59		1.11	(0.91, 1.36)	0.31
COMBINED	**1.09**	**(1.01,1.19)**	**0.037**		**1.12**	**(1.04, 1.21)**	**0.0028**
	Phet=0.76, $I^2 = 0$				Phet=0.71, $I^2 = 0$		

Supplementary table 6 - Association between the *TP53BP1* missense variant rs2602141-T and lung cancer

POPULATIONS	P	OR	CI95	cases (N)	cases (F)	controls (N)	controls (F)	Phet	I^2
Iceland[a]	0.011	1.11	(1.02, 1.20)	1,417	0.72	36,260	0.70		
USA	0.329	1.13	(0.88, 1.46)	187	0.74	845	0.71		
The Netherlands	0.131	1.12	(0.97, 1.30)	531	0.7	1,829	0.68		
Spain	0.019	1.2	(1.03, 1.40)	542	0.68	1,087	0.64		
4 groups COMBINED[b]	**0.00015**	**1.13**	**(1.06, 1.20)**					0.84	0
Results from Truong et al.	0.001	1.08	(1.03, 1.13)	15,719	-	19,305	-		
Results from Rudd et al.	0.0009	1.18	(1.07, 1.30)	1,529	-	2,707	-		
ALL COMBINED[b]	**8.6×10^{-9}**	**1.11**	**(1.07, 1.15)**					0.56	0

Shown are the P values, allelic odds-ratio (OR) and 95% CI based on the multiplicative model, the number (N) and the allelic frequency (F) of the variant in cases and controls. All P values are two-sided.

[a] Results for the Icelandic population were adjusted by the method of genomic control.

[b] For the combined study populations, the reported control frequency was the average, unweighted control frequency of the individual populations, while the OR and the P value were estimated using the Mantel-Haenszel model.

Supplementary table 7 - Joint analysis of rs748404(T) and rs2602141(T)

	rs748404(T) adjusted for rs2602141(T)				rs2602141(T) adjusted for rs748404(T)		
Population (# cases/# controls)	**OR**	**95% CI**	***P* value**		**OR**	**95% CI**	***P* value**
USA (195/867)	1.22	(0.84, 1.76)	0.30		1.03	(0.74, 1.44)	0.86
The Netherlands (533/1,832)	0.97	(0.78, 1.21)	0.80		1.14	(0.94, 1.39)	0.19
Iceland (959/36,277)	1.27	(1.09, 1.47)	0.0017		0.90	(0.79, 1.03)	0.12
Spain (552/1,442)	0.97	(0.78, 1.21)	0.79		1.19	(0.97, 1.46)	0.098
COMBINED (2,239/40,418	**1.12**	**(1.01, 1.24)**	**0.027**		**1.02**	**(0.93, 1.11)**	**0.74**
	Phet=0.10, I^2 = 51.3				Phet=0.079, I^2 = 55.8		