

## VDR polymorphisms and tuberculosis susceptibility

**Table S1.** Meta-regression analysis results

	N	t vs. T		tt vs. TT		tt vs. Tt + TT		Tt vs. TT		tt + Tt vs. TT	
		95% CI	P	95% CI	P	95% CI	P	95% CI	P	OR	P
Publication years	38	-50, 82, 23.22	0.45	-87.42, 38.08	0.43	-83.56, 40.63	0.49	-52.32, 27.24	0.53	-50.82, 23.22	0.45
Ethnicities	38	-0.33, 0.58	0.58	-1.11, 0.70	0.65	-1.11, 0.70	0.65	-0.27, 0.68	0.39	-0.33, 0.58	0.58
Sample size	38	-0.05, 0.19	0.27	-0.12, 0.31	0.38	-0.13, 0.30	0.43	-0.06, 0.20	0.27	-0.05, 0.19	0.27
Genotyping method	38	-0.07, 0.12	0.60	-0.07, 0.26	0.26	-0.08, 0.25	0.29	-0.08, 0.11	0.77	-0.07, 0.12	0.60
Source of controls	38	-0.15, 0.20	0.75	-0.30, 0.40	0.77	-0.30, 0.40	0.77	-0.16, 0.20	0.81	-0.15, 0.20	0.75
HWE	38	-0.07, 0.10	0.75	-0.15, 0.17	0.89	-0.16, 0.16	0.94	-0.07, 0.11	0.67	-0.07, 0.10	0.75
The type of tuberculosis	38	-0.16, 0.28	0.59	-0.36, 0.56	0.67	-0.36, 0.56	0.67	-0.18, 0.28	0.67	-0.16, 0.28	0.59

**Table S2.** Sensitivity analyses of study with controls not in HWE excluded

	N	t vs. T		tt vs. TT		tt vs. Tt + TT		Tt vs. TT		tt + Tt vs. TT	
		OR (95% CI)	Heterogeneity (I <sup>2</sup> , P <sub>Q</sub> )	OR (95% CI)	Heterogeneity (I <sup>2</sup> , P <sub>Q</sub> )	OR (95% CI)	Heterogeneity (I <sup>2</sup> , P <sub>Q</sub> )	OR (95% CI)	Heterogeneity (I <sup>2</sup> , P <sub>Q</sub> )	OR (95% CI)	Heterogeneity (I <sup>2</sup> , P <sub>Q</sub> )
Total	38	1.05 (0.94, 1.17)	54.9%; 0.000	1.14 (0.87, 1.48)	53.9%, 0.000	0.97 (0.84, 1.12) <sup>F</sup>	43.3%, 0.008	1.05 (0.96, 1.15) <sup>F</sup>	34.9%, 0.034	1.04 (0.95, 1.13) <sup>F</sup>	45.1%, 0.005
Ethnicities											
ES Asians	7	0.97 (0.77, 1.22) <sup>F</sup>	0%; 0.541	1.10 (0.49, 2.48) <sup>F</sup>	0%, 0.997	1.09 (0.48, 2.44) <sup>F</sup>	0%, 0.993	0.94 (0.73, 1.22) <sup>F</sup>	23.2%, 0.252	0.96 (0.75, 1.23) <sup>F</sup>	8.9%, 0.361
SW Asians	11	1.33 (1.04, 1.72) <sup>+</sup>	70.4%; 0.000	1.72 (1.03, 2.86) <sup>*F</sup>	65.4%, 0.001	1.40 (1.08, 1.82) <sup>+,F</sup>	46.2%, 0.046	1.29 (1.06, 1.56) <sup>+,F</sup>	40.3%, 0.080	1.41 (1.03, 1.91) <sup>+</sup>	61.6%, 0.004
Africans	8	0.95 (0.87, 1.03) <sup>F</sup>	0%; 0.432	0.86 (0.64, 1.16)	51.2%, 0.045	0.86 (0.64, 1.15)	51.9%, 0.042	0.98 (0.88, 1.10) <sup>F</sup>	0%, 0.927	0.96 (0.86, 1.07) <sup>F</sup>	0%, 0.884
Americans	1	0.59 (0.28, 1.22)	-	0.62 (0.03, 15.48) <sup>F</sup>	-	0.67 (0.03, 16.47) <sup>F</sup>	-	0.91 (0.43, 1.91) <sup>F</sup>	-	0.59 (0.28, 1.25) <sup>F</sup>	-
Europeans	2	0.94 (0.70, 1.27) <sup>F</sup>	0%; 0.894	0.32 (0.03, 3.85)	66.2%, 0.086	0.20 (0.01, 6.66)	82.5%, 0.017	1.70 (0.61, 4.74)	79.9%, 0.026	1.39 (0.66, 2.95)	65.1%, 0.091
Sample size											
Large <sup>a</sup>	7	0.93 (0.85, 1.01) <sup>F</sup>	11.8%; 0.339	0.81 (0.65, 1.01) <sup>F</sup>	47.9%, 0.074	0.82 (0.67, 1.02) <sup>F</sup>	49.6%, 0.064	0.96 (0.85, 1.08) <sup>F</sup>	0%, 0.971	0.93 (0.84, 1.04) <sup>F</sup>	0%, 0.849
Small <sup>b</sup>	22	1.14 (0.97, 1.33)	54.3%; 0.001	1.28 (1.04, 1.59) <sup>*,F</sup>	48.7%, 0.007	1.13 (0.92, 1.38) <sup>*,F</sup>	34.9%, 0.059	1.18 (1.03, 1.36) <sup>*,F</sup>	42.9%, 0.018	1.19 (1.05, 1.35) <sup>*,F</sup>	49.0%, 0.005
Genotyping method											
PCR-RFLP	20	1.11 (0.96, 1.29)	62.4%; 0.000	1.30 (0.95, 1.79)	53.1%, 0.003	1.15 (0.96, 1.37) <sup>F</sup>	31.7%, 0.092	1.06 (0.95, 1.19) <sup>F</sup>	34.3%, 0.067	1.11 (0.94, 1.32)	52.3%, 0.003
Other methods	9	0.92 (0.83, 1.03) <sup>F</sup>	0%; 0.594	0.73 (0.56, 0.95) <sup>*,F</sup>	36.6%, 0.126	0.69 (0.54, 0.90) <sup>*,F</sup>	45.6%, 0.065	1.03 (0.89, 1.19) <sup>F</sup>	42.8%, 0.082	0.97 (0.85, 1.12) <sup>F</sup>	19.4%, 0.270
Source of controls											
Contacts <sup>c</sup>	10	1.03 (0.90, 1.18) <sup>F</sup>	0.0%; 0.674	1.15 (0.83, 1.60) <sup>F</sup>	0%, 0.927	1.09 (0.79, 1.49) <sup>F</sup>	0%, 0.915	1.01 (0.85, 1.21) <sup>F</sup>	0%, 0.591	1.03 (0.86, 1.22) <sup>F</sup>	0%, 0.620
Healthy <sup>d</sup>	19	1.08 (0.93, 1.25)	67.5%; 0.000	1.20 (0.84, 1.73)	67.4%, 0.000	1.07 (0.79, 1.46)	59%, 0.001	1.06 (0.96, 1.17) <sup>F</sup>	49.2%, 0.008	1.11 (0.94, 1.32)	58.9%, 0.001
Tuberculosis type											
pulmonary	21	1.00 (0.93, 1.07)	62.4%; 0.000	1.16 (0.83, 1.60)	61.5%, 0.000	1.05 (0.79, 1.38)	51.4%, 0.004	1.04 (0.94, 1.15) <sup>F</sup>	47.7%, 0.008	1.08 (0.92, 1.27)	55.2%, 0.001
Extra and pulmonary	6	1.13 (0.95, 1.33) <sup>F</sup>	30%; 0.21	1.29 (0.84, 1.96) <sup>F</sup>	39.6%, 0.141	1.22 (0.81, 1.82) <sup>F</sup>	35.7%, 0.169	1.12 (0.90, 1.39) <sup>F</sup>	0%, 0.545	1.14 (0.93, 1.41) <sup>F</sup>	0.9%, 0.410
extra	2	0.97 (0.70, 1.36) <sup>F</sup>	0%; 0.855	1.00 (0.49, 2.04) <sup>F</sup>	0%, 0.876	1.06 (0.55, 2.06) <sup>F</sup>	0%, 0.915	0.90 (0.55, 1.46) <sup>F</sup>	0%, 0.873	0.92 (0.58, 1.46) <sup>F</sup>	0%, 0.855

Abbreviations: N: number of studies included; OR: odds ratio; Ph: p value for heterogeneity; P<sub>Q</sub>: Cochran's Q statistics; I<sup>2</sup>: Higgin's I<sup>2</sup> statistics. F: Results derived using Fixed effects for analysis. Random effects were used for all other calculations. \*OR with statistical significance; a: studies with more than 500 participants; b: studies with less than 5000 participants; c: studies with controls from patient contacts; d: studies with controls from healthy person.