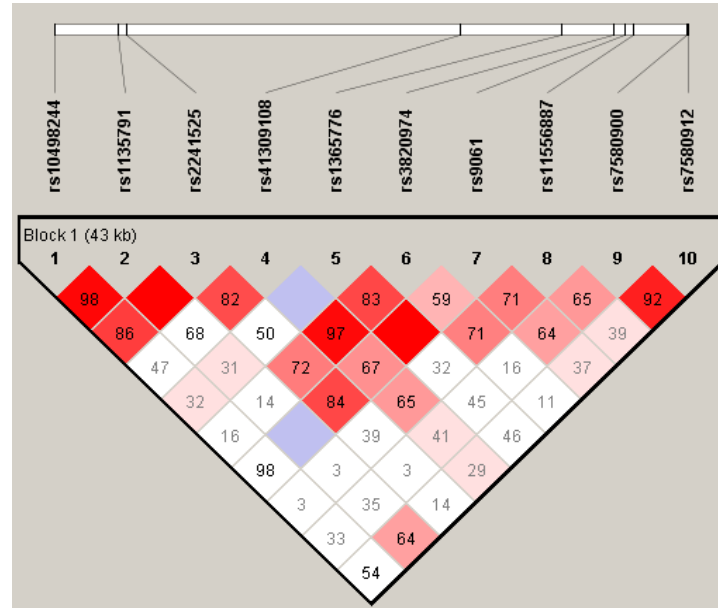


**a**



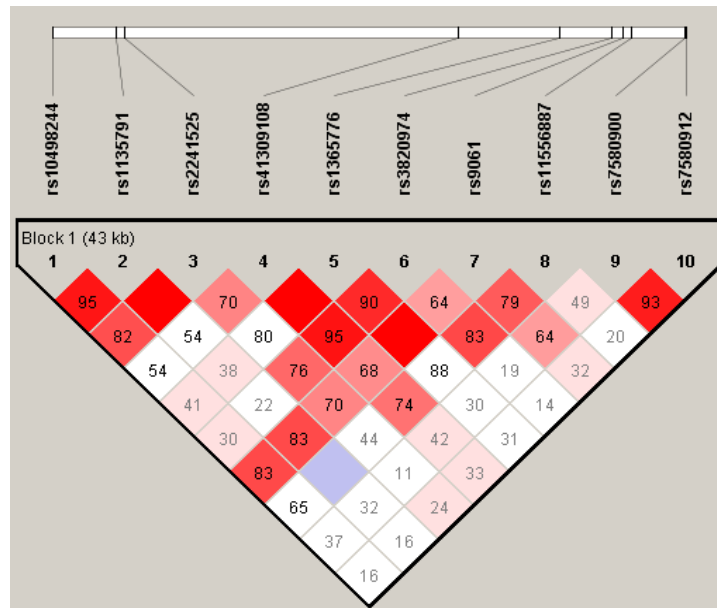
**b**

Haplotypes	Frequencies		Chi Square	OR (95%CI)	P value
	LTBI	Health			
ATGTACGCAA	0.231,	0.281	1.3	0.77 (0.49-1.21)	0.2542
ATATACGCAA	0.049,	0.090	2.256	0.52 (0.22-1.23)	0.1331
ATGTACGCGG	0.099	0.068	1.441	1.50 (0.77-2.94)	0.23
ATATACGCGG	0.122	0.061	5.472	2.11 (1.11-3.99)	<b>0.0193</b>
GCGTACGCAA	0.028	0.060	1.981	0.46 (0.15-1.39)	0.1593
ATGAAAATGG	0.015	0.051	3.191	0.28 (0.06-1.25)	0.074
ATGAAAGCAA	0.025	0.048	1.327	0.50 (0.15-1.64)	0.2493
ATGAAAACGG	0.024	0.045	1.141	0.53 (0.16-1.76)	0.2854
ATGTGAGCAA	0.008	0.042	3.488	0.18 (0.02-1.36)	0.0618
ATGTACGCGA	0.063	0.024	5.206	2.76 (1.12-6.84)	<b>0.0225</b>
ATGAAAGCGG	0.041	0.021	1.73	2.00 (0.69-5.74)	0.1884
GCGTGAGCAA	0.024	0.025	0.008	0.95 (0.27-3.37)	0.9272
ATGTACACGA	0.007	0.020	0.933	0.35 (0.04-3.06)	0.334
ATGAAAATAA	0.010	0.019	0.577	0.48 (0.07-3.24)	0.4477
ATGAAAATGA	0.014	0.017	0.051	0.84 (0.17-4.19)	0.8216
GCGTACGCGA	0.018	0.010	0.563	1.79 (0.38-8.44)	0.4532
ATGTACACGG	0.008	0.011	0.092	0.69 (0.08-5.8)	0.7617

1 OR: odds ratio; CI: confidence interval; ORs are adjusted for gender. The significant ORs are shown in italic.

**Figure S1:** Association of *SP110* SNP haplotypes with LTBI risk in LTBI cases vs. healthy controls. **a** Haplotype block map for *SP110* with 10 SNPs. **b** Association of haplotype frequencies with LTBI risk in LTBI cases and healthy controls.

**a**



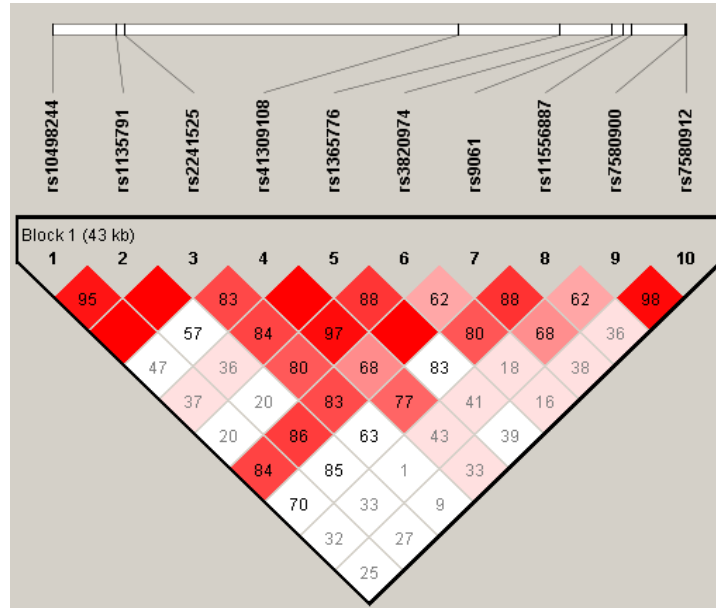
**b**

Haplotypes	Frequencies		Chi Square	OR (95%CI)	P value
	TB	LTBI			
ATGTACGCAA	0.304,	0.235	2.427	1.42 (0.91-2.22)	0.1193
ATATACGCAA	0.076,	0.051	1.03	1.56 (0.66-3.64)	0.3103
ATGTACGCGG	0.062,	0.092	1.554	0.65 (0.33-1.28)	0.2125
ATATACGCGG	0.058,	0.093	2.178	0.60 (0.30-1.19)	0.14
ATGAAAACGG	0.055,	0.024	2.11	2.35 (0.72-7.64)	0.1463
GCGTGAGCAA	0.046,	0.024	1.27	1.98 (0.59-6.63)	0.2598
GCGTACGCGG	0.040,	0.034	0.123	1.20 (0.42-3.41)	0.7257
ATGAAAGCGG	0.030,	0.050	1.351	0.58 (0.23-1.46)	0.2451
ATGTACGCGA	0.024,	0.060	4.708	0.38 (0.16-0.95)	<b>0.03</b>
ATGAAAGCAA	0.030,	0.023	0.204	1.33 (0.38-4.66)	0.6512
GCGTACGCAA	0.029,	0.016	0.67	1.81 (0.43-7.68)	0.413
ATGTGAGCAA	0.028,	0.008	1.844	3.71 (0.49-28.11)	0.1745
ATGTACACGA	0.024,	0.008	1.403	3.17 (0.41-24.25)	0.2362
ATGAAAATAA	0.023,	0.009	0.957	2.47 (0.38-16.13)	0.328
ATGAAAATGG	0.022,	0.014	0.312	1.55 (0.32-7.47)	0.5766
ATGTGAGCGG	0.020,	0.015	0.157	1.38 (0.30-6.43)	0.6921
ATGAAAATGA	0.020,	0.014	0.21	1.44 (0.30-6.99)	0.6468
ATGAAAGCGA	0.007,	0.028	4.576	0.24 (0.06-0.99)	<b>0.0324</b>

1 OR: odds ratio; CI: confidence interval; ORs are adjusted for gender. The significant ORs are shown in italic.

**Figure S2:** Association of *SP110* SNP haplotypes with TB risk in TB cases vs. LTBI individuals. **a** Haplotype block map for *SP110* with 10 SNPs. **b** Association of haplotype frequencies with TB risk in TB cases vs. LTBI individuals.

**a**



**b**

Haplotypes	Frequencies		Chi Square	OR (95%CI)	P value
	TB	Health			
ATGTACGCAA	0.287,	0.280	0.072	1.04 (0.80-1.34)	0.7885
ATATACGCAA	0.081,	0.094	0.588	0.85 (0.56-1.28)	0.4431
ATGTACGCGG	0.070,	0.059	0.576	1.20 (0.75-1.94)	0.4477
ATATACGCGG	0.061,	0.061	0	0.99 (0.61-1.63)	0.9937
GCGTACGCAA	0.047,	0.053	0.217	0.88 (0.52-1.51)	0.6412
ATGAAAACGG	0.051,	0.042	0.55	1.24 (0.71-2.16)	0.4581
ATGTGAGCAA	0.035,	0.045	0.742	0.77 (0.42-1.40)	0.389
ATGAAAGCAA	0.034,	0.045	0.889	0.75 (0.41-1.37)	0.3458
ATGAAAATGG	0.027,	0.047	2.988	0.58 (0.30-1.09)	0.0839
GCGTGAGCAA	0.041,	0.027	1.693	1.54 (0.80-2.98)	0.1932
ATGAAAGCGG	0.033,	0.025	0.706	1.35 (0.67-2.73)	0.4009
ATGTACGCGA	0.025,	0.027	0.026	0.94 (0.45-1.96)	0.8714
ATGAAAATAA	0.023,	0.025	0.061	0.91 (0.42-1.97)	0.8057
ATGTACACGA	0.024,	0.023	0.027	1.07 (0.49-2.30)	0.8702
ATGAAAATGA	0.023,	0.021	0.08	1.12 (0.51-2.49)	0.7774
GCGTACGCGG	0.024,	0.007	5.709	3.81 (1.18-12.31)	<b>0.0169</b>
ATGTGAGCGG	0.019,	0.009	1.695	2.00 (0.69-5.81)	0.1929

1 OR: odds ratio; CI: confidence interval; ORs are adjusted for gender. The significant ORs are shown in italic.

**Figure S3:** Association of *SP110* SNP haplotypes with TB risk in TB cases vs. healthy controls. **a** Haplotype block map for *SP110* with 10 SNPs. **b** Association of haplotype frequencies with TB risk in TB cases and healthy controls.

**Table S1:** Primers for genotype analysis for *SP110*

Gene	SNP	Primer	Sequence	Size (bp)	Allele 1 mass	Allele 2 mass
<i>SP110</i>	rs7580912	Forward	ACGTTGGATGGTCTCAAACCACA AACCACC	99	G, 5353.5	A, 5433.4
		Reverse	ACGTTGGATGCCCCACCTTCTGTG ATAATG			
		Extension	CTGGGCCTTCCAAACTC			
<i>SP110</i>	rs7580900	Forward	ACGTTGGATGGTCTCAAACCACA AACCACC	99	G, 5769.8	A, 5849.7
		Reverse	ACGTTGGATGCCCCACCTTCTGTG ATAATG			
		Extension	TGTGATAATGAACATGCC			
<i>SP110</i>	rs11556887	Forward	ACGTTGGATGATGAATGGCAGAG CAGAGAC	100	C, 6334.2	T, 6414.1
		Reverse	ACGTTGGATGTGGGGTATGGAGG GAGCTT			
		Extension	TGAAGCCCAACTGGCCTAG			
<i>SP110</i>	rs9061	Forward	ACGTTGGATGCTCCTCAGTGACC AATGAC	111	A, 6076	G, 6092
		Reverse	ACGTTGGATGTGCACAGTGCTAG TGAGGAG			
		Extension	TACATCCAAAATGAATGCG			
<i>SP110</i>	rs3820974	Forward	ACGTTGGATGTTTCTCCTCATTCT GGTCCC	98	C, 6872.5	A, 6912.4
		Reverse	ACGTTGGATGTTGTCACCTGGCCA CTGAATG			
		Extension	ACTGAATGGAGGAAGAAAAG			
<i>SP110</i>	rs1365776	Forward	ACGTTGGATGAGATGTATCTGGTC AACTCC	102	G, 5911.9	A, 5991.8
		Reverse	ACGTTGGATGCAGCTCCTCTTGT ACTCTC			
		Extension	TGTACTCTCATCTTACCTC			
<i>SP110</i>	rs41309108	Forward	ACGTTGGATGTCTGGGTCTCTGG GAGATT	106		
		Reverse	ACGTTGGATGAGTGCCATCAATGA TCTCTG			

		Extension	TAGTAAATGCCCTTGGGAAAC		T, 7014.6	A, 7070.5
		Forward	ACGTTGGATGTCCTAGATGAAG GACTCAC			
<i>SP110</i>	rs2241525	Reverse	ACGTTGGATGTAGCTAGCAGGGT CCATTC	98		
		Extension	TCCTGATCAATTACACACA		G, 5962.9	A, 6042.9
		Forward	ACGTTGGATGGAAGGAAAAGGA AGGAACGC			
<i>SP110</i>	rs1135791	Reverse	ACGTTGGATGAATACCTTCAGCAG CTCTCC	103		
		Extension	ACGGAATATACGTTGTGAAGGAA		C, 7407.9	T, 7487.8
		Forward	ACGTTGGATGCAGACTCTCTGCTT GTTGTG			
<i>SP110</i>	rs10498244	Reverse	ACGTTGGATGCAGAGTGGATATCC AAACCC	117		
		Extension	TGTGCCATTTGTCTTGC		A, 5429.6	G, 5445.6

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