

**Supplementary Table 1. TB association in the Russian GWAS for polymorphisms on chromosomes 11p13 and 18q11 that previously were associated with TB in the African GWAS**

Chr	SNP	Position (hg19)	Gene	Minor allele	MAF cases	MAF controls	OR (95% CI)	P-value
11	rs2057178	32,364,187	<i>WT1</i>	A	0.121	0.136	0.88 (0.81 - 0.95)	0.00068
18	rs4331426	20,190,795	<i>CTAGE1</i>	G	0.028	0.029	0.97 (0.83 - 1.14)	0.71

a - ORs for minor alleles are shown

MAF – minor allele frequency; OR – odds ratio; 95% CI – 95% confidence interval

**Supplementary Table 2. Association of the best SNP in the present GWAS**

**located in candidate genes associated with TB previously**

Chr	Gene	Size (Kb)	N of SNPs	Best_SNP	OR	95%CI	<i>P</i> -value
1	<i>IL10</i>	4.9	18	rs3024498	0.94	0.89 - 1.00	3.23 x 10 <sup>-02</sup>
2	<i>NRAMP1</i>	14.9	20	rs3816560	0.96	0.90 - 1.03	1.13 x 10 <sup>-01</sup>
3	<i>PTX3</i>	6.8	15	rs3816527	1.05	1.00 - 1.11	5.16 x 10 <sup>-02</sup>
4	<i>TLR2</i>	21.8	41	rs5743698	0.73	0.57 - 0.95	1.03 x 10 <sup>-02</sup>
5	<i>IL12B</i>	15.7	34	rs2546892	1.10	1.03 - 1.18	6.65 x 10 <sup>-03</sup>
6	<i>HLA-DQA1</i>	6.2	412	rs28680981	0.88	0.83 - 0.94	3.61 x 10 <sup>-05</sup>
6	<i>HLA-DRB1</i>	11.1	252	rs28724111	0.89	0.82 - 0.96	1.11 x 10 <sup>-03</sup>
6	<i>IFNGR1</i>	21.9	18	rs140855629	0.91	0.76 - 1.09	2.00 x 10 <sup>-01</sup>
6	<i>TNF</i>	2.8	5	rs3093665	1.23	0.97 - 1.56	9.96 x 10 <sup>-02</sup>
10	<i>MBL2</i>	6.3	35	rs1838065	0.94	0.89 - 0.99	2.21 x 10 <sup>-02</sup>
12	<i>IFNG</i>	5	5	rs2069718	0.92	0.87 - 0.97	1.69 x 10 <sup>-03</sup>
12	<i>VDR</i>	63.5	177	12:48267194	1.10	0.97 - 1.25	5.18 x 10 <sup>-02</sup>
15	<i>UBE3A</i>	101.8	224	rs2719878	0.90	0.77 - 1.05	5.88 x 10 <sup>-02</sup>
16	<i>NOD2</i>	35.9	62	rs5743263	1.13	0.97 - 1.31	7.65 x 10 <sup>-02</sup>
17	<i>CCL18</i>	7.2	14	rs2015052	1.09	0.93 - 1.27	4.67 x 10 <sup>-01</sup>
17	<i>MCPI</i>	1.9	3	rs4586	1.04	0.99 - 1.10	2.09 x 10 <sup>-01</sup>
17	<i>CCL4</i>	1.8	12	rs1049807	0.96	0.90 - 1.02	3.65 x 10 <sup>-01</sup>
17	<i>NOS2A</i>	43.8	115	rs2314810	1.10	0.97 - 1.25	5.59 x 10 <sup>-02</sup>
17	<i>STAT5B</i>	77.2	72	rs140935701	1.09	0.97 - 1.23	7.27 x 10 <sup>-02</sup>
19	<i>CD209</i>	7.6	27	rs2287886	1.04	0.99 - 1.10	1.32 x 10 <sup>-01</sup>
19	<i>IL12RB1</i>	27.2	87	rs17882370	1.12	1.01 - 1.25	3.24 x 10 <sup>-03</sup>
20	<i>MC3R</i>	1.1	2	rs3827103	0.99	0.91 - 1.07	8.47 x 10 <sup>-01</sup>

**Supplementary Table 3. TB association in the Russian GWAS for loci that previously were associated with leprosy**

Chr	Locus, start	Locus, end	Gene	Leprosy hit	Leprosy hit		TB hit		TB <i>P</i> -value at
					position	TB hit	position	TB hit <i>P</i> -value	Leprosy hit
8	90,769,975	90,803,291	<i>RIPK2</i>	rs42490	90,778,513	rs188097137	90,793,899	0.059	0.51
9	117,551,600	117,568,406	<i>TNFSF15</i>	rs6478108	117,558,703	rs186553516	117,560,389	0.20	0.54
13	44,398,045	44,453,864	<i>CCDC122</i>	rs3088362	44,433,630	rs184333355	44,424,898	0.11	0.48
13	44,453,420	44,468,068	<i>C13orf31</i>	rs3764147	44,457,925	rs189332232	44,460,369	0.12	0.88
16	50,727,514	50,766,988	<i>NOD2</i>	rs9302752	50,719,103	rs7203344	50,765,376	0.17	0.28
6	31,000,000	33,500,000	MHC region	rs602875	32,681,607	rs6913309	32,339,840	2.53 x 10 <sup>-06</sup>	NA
1	67,632,083	67,725,662	<i>IL23R</i>	rs3762318	67,597,119	rs113084917	67,680,275	0.0092	1.00
6	146,864,829	146,876,101	<i>RAB32</i>	rs2275606	146,918,950	rs78620166	146,871,198	0.064	0.99

**Supplementary Table 5. Association of the *ASAP1* gene polymorphisms with the reduction of the *ASAP1* mRNA expression in dendritic cells infected with *M. tuberculosis***

SNP	Chr 8 position	Genotypes obtained by	<i>P</i> -value
rs1017281	131,247,213	imputation	0.046
rs10956514	131,252,758	direct genotyping (ref <sup>23</sup> )	0.0046
rs1469288	131,226,652	imputation	0.143
rs17285138	131,297,696	imputation	0.160
rs2033059	131,271,216	imputation	0.156
rs4733781	131,296,767	direct genotyping (ref <sup>23</sup> )	0.230
rs12680942	131,264,033	imputation	0.169

## Supplementary Table 6. Taqman genotyping assays

SNP	Alleles	Taqman probe (label dye)	Taqman primer sequences (5' - 3')
rs1017281	G	CTACCATTGTAGGCACCT (VIC)	CTAATACACTGCCTGCCACATAGT
	A	CTACCATTGTAAAGCACCT (FAM)	GAAGGCACTCAAGAATTCATCTAGCT
rs10956514	A	CCTCTGAAATGTCATATATG (VIC)	CCAAACAACAACCTGCAGTGACAT
	G	CTCTGAAATGTCGTATATG (FAM)	CCTATATTATCTACCATTTTCTCTTAGCCCTT
rs1469288	G	TTGAGGTGTGGAAGTTA (VIC)	CCCCCTCAATCCTTGGTCCTA
	A	TTGAGGTGTGAAAGTTA (FAM)	GCAAATCCTAGGCGACTAAAAAGCT
rs17285138	T	TTTAGACCATAAATTTTTTTC (VIC)	GTATGTCGGCCAAAACAAAATGATCT
	A	TAGACCATAAATTTTTTTC (FAM)	TTTTTAAAAAGATACCTCCTGAATAGATAAATATGATCATAATTA
rs2033059	C	TTTGCCCATCGATTC (VIC)	GCAAGTGGTAGGAAGGCCTTTT
	T	TTGCCCATGATTC (FAM)	GGACACATGCTCCTCTGGAATTTAT
rs4733781	A	TGGGCTGAAAATAAA (VIC)	GGTGAGGGAAAACCCATGAAAATTT
	C	TGGGCTGAACATAAA (FAM)	ACTGGGCGCATCCCTTTTAG
rs12680942	T	TCAGTGCAATTGAAATT (VIC)	AAACCGAAAATAGCAAACATATGCAAGT
	C	AGTGCAACTGAAATT (FAM)	AATGCATTTTATTATTGTTCCATGTGGAATTTTAAAC

### Supplementary Table 7. Primer and siRNA sequences

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#### qPCR primers

huASAP1F8: 5'CCAAATGTGCAGTCCAGAGA3'

huASAP1R8: 5'GCCTGGCAGTCATAAATGGT3'

HuB2mF2: 5'GATGAGTATGCCTGCCGTGTG3'

HuB2mR2: 5'CAATCCAAATGCGGCATCT3'

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#### *ASAP1* siRNAs

5'CCCAAUUGGAGAUUUGCCGCCUAA3'

5'GACCAGAUUCUCUGUCUCGGAGUUCA3'

5'CAGCUAACUGCACUCCGAGACUAAA3'

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