Supp. Table S1. Predicted effect of non-synonymous SNVs on IL-12Rβ1 protein function

SNPid	amino acid change	minor allele frequency[a]	SIFT score	SIFT prediction	Polyphen2 score	Polyphen2 prediction	Condel score	Condel prediction
rs17884651	p.Pro3Gln	0.00-0.021	0[b]	damaging	0.001	benign	0.694	deleterious
rs200783433	p.Arg25Lys	n.a.	0.86	tolerated	0.118	benign	0.000	neutral
rs202206502	p.Pro34Ser	0.001	0.32	tolerated	0.818	possibly damaging	0.024	neutral
rs113524129	p.Pro34Leu	n.a.	0.64	tolerated	0.663	possibly damaging	0.022	neutral
rs142484991	p.Pro37Leu	0.001	0.89	tolerated	0.994	probably damaging	0.917	deleterious
rs189309495	p.Ser43Leu	0.001	0.01	damaging	0.538	possibly damaging	0.017	neutral
rs150070244	p.Ser45Leu	0.000	0.4	tolerated	0.002	benign	0.000	neutral
rs17887176	p.Pro47Ser	0.010-0.067	0	damaging	1.000	probably damaging	0.990	deleterious
rs150816599	p.Arg51Thr	0.000	0.48	tolerated	0.019	benign	0.002	neutral
rs142273743	p.Arg59His	0.000	0.12	tolerated	0.043	benign	0.406	neutral
rs140770932	p.Tyr60Cys	0.000	0.05	damaging	0.998	probably damaging	0.893	deleterious
rs117720235	p.Glu61Lys	0.008	0.86	tolerated	0.961	probably damaging	0.017	neutral
rs138859377	p.Arg85Cys	0.000	0.03	damaging	0.004	benign	0.009	neutral
rs144128347	p.Ala90Thr	0.000	0.51	tolerated	0.585	possibly damaging	0.081	neutral
rs150285174	p.Val107Ala	0.000	0.02	damaging	0.104	benign	0.871	deleterious
rs200328413	p.Leu183Ser	n.a.	0.06	tolerated	0.883	possibly damaging	0.754	deleterious
rs201652727	p.Pro199Arg	n.a.	0.78	tolerated	1.000	probably damaging	0.922	deleterious
rs139505765	p.Glu201Ala	0.006	0.07	tolerated	0.952	possibly damaging	0.766	deleterious

SNPid	amino acid change	minor allele frequency[a]	SIFT score	SIFT prediction	Polyphen2 score	Polyphen2 prediction	Condel score	Condel prediction
rs182250241	p.Met202Arg	n.a.	0.62	tolerated	0.000	benign	0.001	neutral
rs148994509	p.Gln218Pro	0.000	0.25	tolerated	0.000	benign	0.001	neutral
rs140762977	p.Val231Ile	0.000	0.42	tolerated	0.774	possibly damaging	0.007	neutral
rs201567666	p.Pro232Ser	n.a.	0.18	tolerated	1.000	probably damaging	0.990	deleterious
rs147436538	p.Pro232Leu	0.001	0.03	damaging	1.000	probably damaging	0.990	deleterious
rs200977237	p.Gln238Glu	0.001	0.32	tolerated	0.067	benign	0.057	neutral
rs200203598	p.Ser244Leu	0.001	0.33	tolerated	0.074	benign	0.001	neutral
rs138189707	p.Leu258Val	0.000	0.01	damaging	0.910	possibly damaging	0.681	deleterious
rs200508693	p.Leu267Pro	0.001	0.34	tolerated	1.000	probably damaging	0.828	deleterious
rs150555147	p.Leu274Gln	0.000	0.63	tolerated	0.229	benign	0.002	neutral
rs201831465	p.Ala275Val	0.001	0.32	tolerated	0.701	possibly damaging	0.256	neutral
rs201223132	p.Thr278Met	n.a.	0.22	tolerated	0.052	benign	0.011	neutral
rs117511121	p.Arg283Gln	0.004-0.017	0.7	tolerated	0.019	benign	0.006	neutral
rs149896994	p.Pro292Leu	0.000	0.85	tolerated	0.987	probably damaging	0.327	neutral
rs112658457	p.Thr298Ala	n.a.	0.86	tolerated	0.011	benign	0.024	neutral
rs192185254	p.Tyr308Cys	n.a.	0.19	tolerated	0.913	possibly damaging	0.051	neutral
rs34844088	p.Val316Met	0.000	0.02	damaging	0.974	probably damaging	0.255	neutral
rs141507253	p.Ser320Pro	0.000	0.01	damaging	0.998	probably damaging	0.736	deleterious
rs147766868	p.Ser321Leu	0.000	0.63	tolerated	0.531	possibly damaging	0.019	neutral
rs144612211	p.Gly325Ser	0.000	0.01	damaging	1.000	probably	0.990	deleterious

SNPid	amino acid change	minor allele frequency[a]	SIFT score	SIFT prediction	Polyphen2 score	Polyphen2 prediction	Condel score	Condel prediction
						damaging		
rs137983313	p.Asp337Glu	0.000	1	tolerated	0.031	benign	0.004	neutral
rs17884957	p.His339Gln	0.002-0.022	0.3	tolerated	0.156	benign	0.010	neutral
rs200811721	p.Gly350Arg	0.002	0.33	tolerated	0.999	probably damaging	0.774	deleterious
rs111768826	p.Gly353Glu	n.a.	1	tolerated	0.868	possibly damaging	0.023	neutral
rs150261140	p.Arg361Gly	0.000	0.23	tolerated	0.826	possibly damaging	0.052	neutral
rs191062711	p.Ala387Val	n.a.	0.65	tolerated	0.231	benign	0.000	neutral
rs140254802	p.Pro391Leu	0.000	0.28	tolerated	0.014	benign	0.058	neutral
rs202048215	p.Arg403Gln	n.a.	0.52	tolerated	0.019	benign	0.003	neutral
rs199504990	p.Gly406Glu	n.a.	0.96	tolerated	0.745	possibly damaging	0.893	deleterious
rs201548803	p.Ser421Phe	n.a.	0.17	tolerated	0.938	possibly damaging	0.962	deleterious
rs200875188	p.Thr432Met	n.a.	0.03	damaging	0.998	probably damaging	1.000	deleterious
rs190491500	p.Asn442Lys	n.a.	0.4	tolerated	0.954	possibly damaging	0.932	deleterious
rs150767749	p.Ser444Leu	n.a.	0.11	tolerated	0.999	probably damaging	0.950	deleterious
rs142884929	p.Val477Ile	0.000	0.77	tolerated	1.000	probably damaging	0.772	deleterious
rs199661046	p.Arg484His	n.a.	0.59	tolerated	1.000	probably damaging	0.952	deleterious
rs11575932	p.Pro534Ser	n.a.	0.37	tolerated	1.000	probably damaging	0.827	deleterious
rs186935027	p.Ile590Phe	n.a.	0.11	tolerated	0.838	possibly damaging	0.030	neutral
rs201846511	p.Ile590Met	n.a.	0.12	tolerated	0.838	possibly	0.051	neutral

SNPid	amino acid change	minor allele frequency[a]	SIFT score	SIFT prediction	Polyphen2 score	Polyphen2 prediction	Condel score	Condel prediction
						damaging		
rs145590794	p.Val605Leu	n.a.	0.22	tolerated	0.118	benign	0.011	neutral
rs111662740	p.Ser612Phe	n.a.	0.69	tolerated	0.316	benign	0.024	neutral
rs143367415	p.Glu627Lys	0.001-0.002	0.56	tolerated	0.886	possibly damaging	0.192	neutral
rs202106699	p.Asp654Asn	n.a.	0[b]	damaging	0.948	possibly damaging	0.890	deleterious

[a] data from dbSNP, [b] low confidence prediction, n.a. = not available. SIFT scores and predictions are based on amino acid sequence homology [Kumar et al., 2009]. Polyphen2 scores and predictions are based on amino acid sequence conservation, structure and SWISS-PROT annotation [Adzhubei et al., 2010]. Condel scores and predictions are based on the weighted average of scores of five different prediction tools (a.o. SIFT and Polyphen2) [Gonzalez-Perez and Lopez-Bigas, 2011].

Supp. Table S2. Associations of *IL12RB1* polymorphisms with disease

Cohort	allele or haplotype	in patients n (%)	in controls n (%)	p-value	reference
98 TB patients	QMG	104 (53%)	252 (64%)		[Akahoshi et
197 controls,	RTR	92 (47%)	142 (36%)	<0.013[a]	al., 2003]
Southern Japan					
86 TB patients	QMG	93 (48.3%)	298 (59.8%)	<0.0063[b]	[Kusuhara et
249 controls,	RTR	85 (49.4%)	182 (36.5%)		al., 2007]
Southern Japan	other	4 (2.3%)	18 (3.7%)		
101 TB families,	-2C	n.a.	n.a.		[Remus et al.,
Morocco	-2T	n.a.	n.a.	0.013	2004]
	-111A	n.a.	n.a.		
	-111T	n.a.	n.a.	0.019	
	QMG[c]	n.a.	n.a.	0.4-0.9	
	RTR	n.a.	n.a.		
115 TB patients	QMG	160 (69.6%)	193 (63.9%)	0.94	[Lee et al.,
151 controls,	RTR	69 (30%)	102 (33.8%)		2005]
Korea	other	1 (0.4%)	7 (2.3%)		
	1573G[d]	223 (97.0)	291 (96.3)	0.81	
	1573A	7 (3.0)	11 (3.7)		
382 TB patients	-2C	590 (94.9%)	587 (94.4%)	0.71	[Sahiratmadja
437 controls,	-2T	32 (5.1%)	35 (5.6%)		et al., 2007]
Indonesia					
	641A[e]	377 (66.1%)	400 (66.4%)	0.91	
	641G	193 (33.9%)	202 (33.6%)		
	1573G[d]	590 (96.4)	578 (96.0)	0.72	
	1573A	22 (3.6)	24 (4.0)		
382 AD patients	-111A	573 (75.0%)	1034 (78.6%)	0.00044[f]	[Takahashi et
658 controls,	-111T	191 (25.0%)	282 (21.4%)		al., 2005]

Cohort	**allele or haplotype**	**in patients n (%)**	**in controls n (%)**	**p-value**	**reference**
Japan	-2C	592 (77.5%)	1067 (81.1%)	0.00075[f]	
	-2T	172 (22.5%)	249 (18.9%)		
304 CA patients	-111A	438 (72.0%)	1034 (78.6%)	0.0020[g]	
658 controls,	-111T	170 (28.0%)	282 (21.4%)		
Japan					
1946 NHL	rs2305742 A	2849 (79.6%)	3140 (81.8%)	0.013[h]	[Lan et al.,
patients, 1808	rs2305742 C	729 (20.4%)	698 (18.2%)		2011]
controls, USA					
and Australia					
115 SARS	QMGP[i]	111 (59.0%)	131 (58.0%)		[Tang et al.,
patients, 141	RTRS	50 (26.6%)	25 (11.1%)	0.011[j]	2008]
potentially	RTRP	15 (7.9%)	52 (23.0%)	0.017[k]	
exposed, China	other	12 (6.4%)	18 (8.0%)		

TB = tuberculosis, AD = atopic dermatitis, CA = childhood asthma, NHL = non-Hodgkin lymphoma, SARS = severe acute respiratory syndrome. [a] p-value for homozygosity of RTR/RTR, [b] protects from TB, [c] two polymorphisms representing the QMG/RTR haplotypes were tested separately, [d] the 1573G>A polymorphism results in the A525T amino acid substitution, [e] the 641A>G polymorphism represents the QMG/RTR haplotype, [f] p-value for comparison of genotypes AA/AT versus TT, [g] p-value for comparison of genotypes, [h] p-value for comparison of genotypes AC/CC versus AA, [i] the P534S substitution is analyzed in combination with the QMG/RTR haplotypes, [j] P534S in the RTR background increases susceptibility to SARS, [k] the RTRP haplotype protects from SARS. n.a.= not available.

Supp. References

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