Supplementary Table 1. Mutations/sequence variants in *TNFRSF13B* in CVID and IgAD patients [a]

	Origin	Ins204A	R72H	C104R	R122W	A181E	R202H	V220A	P251L
CVID	Sweden	0/230	1/230	1/230	1/228	10/226	0/230	8/228	25/230
Controls	Sweden	0/716	0/1070	8/2038	4/1784	12/1730	0/2082	27/1070	186/1824
P value		-	**0.031**	0.92	0.54	**5.7×10^{-7}**	-	0.40	0.75
OR		-	-	1.11 (0.14-8.89)	1.96 (0.23-16.91)	6.63 (3.16-13.91)	-	1.40 (0.63-3.12)	1.07 (0.69-1.67)
CVID	Germany	1/308	1/308	9/308	0/308	5/308	1/308	3/308	29/308
Controls	Germany	0/636	4/636	4/660	1/636	4/684 [b]	1/636	2/98	22/98
P value		0.15	0.55	**3.5×10^{-3}**	0.49	0.11	0.60	0.40	0.00070
OR		-	0.51 (0.06-4.45)	4.94 (1.69-14.44)	-	2.81 (0.79-9.95)	2.07 (0.14-31.26)	0.47 (0.08-2.75)	0.36 (0.20-0.65)
CVID	USA	1/314	2/306	6/308	NA	7/310	0/314	6/310	29/310
Controls	USA	0/1512	7/1504	5/1510	NA	4/1510	5/1528	33/1514	150/1464
P value		**0.028**	0.67	**8.5×10^{-4}**		**3.7×10^{-5}**	0.31	0.79	0.64
OR		-	1.41 (0.29-6.75)	5.98 (2.09-17.11)		8.70 (3.11-24.32)	-	0.89 (0.37-2.13)	0.90 (0.60-1.37)
CVID all		2/852	4/844	16/846	1/536	22/844	1/852	17/846	83/848
Controls all		0/2864	11/3210	17/4208	5/2420	20/3924	6/4246	62/2682	358/3386
P value [c]		**9.5×10^{-3}** [e]	0.34	**8.2×10^{-5}**	0.45	**3.9×10^{-8}**	0.69	0.45	0.92
Pooled OR [d]		-	1.27 (0.41-3.97)	4.16 (1.98-8.74)	1.14 (0.14-9.35)	5.60 (2.99-10.51)	0.57 (0.06-5.40)	1.04 (0.59-1.83)	0.82 (0.62-1.08)
IgAD	Sweden	0/474	1/476	1/478	1/480	7/464	2/480	17/480	56/480
Controls	Sweden	0/716	0/1070	8/2038	4/1784	12/1730	0/2082	27/1070	186/1824
P value		-	0.13	0.55	0.95	0.09	**3.0×10^{-3}**	0.26	0.35
OR		-	-	0.53 (0.07-4.12)	0.93 (0.10-8.33)	2.19 (0.88-5.47)	-	1.42 (0.77-2.62)	1.16 (0.85-1.60)
IgAD	Sweden	0/474	1/476	1/478	1/480	7/464	2/480	17/480	56/480
Controls all		0/2864	11/3210	17/4208	5/2420	20/3924	6/4246	62/2682	358/3386
P value [c]		-	0.64 [e]	0.72	0.53	0.05 [e]	**1.8×10^{-3}**	0.13	0.18
Pooled OR [d]		-	0.61 [e] (0.08-4.66)	0.53 (0.07-4.26)	0.93 (0.10-8.33)	2.19 [e] (0.86-5.60)	5.91 (1.94-18.07)	1.42 (0.77-2.63)	1.16 (0.85-1.60)

a) Number of mutated alleles/number of tested alleles
b) One control carrying the A181E allele was found to be hypogammaglobulinemic (serum level of IgG = 3.7 g/L)
c) Normal distribution of pooled Mantel-Haenszel OR
d) Mantel-Haenszel test of pooled odds ratios and 95% confidence intervals
e) P-value calculated on pooled case-control data using one-tailed chi-squared test