

S4 Table. Gene-based association results, restricted to nonsense and missense variants with MAF<0.5% and predicted to be possibly or probably damaging in PolyPhen-2 and SIFT.

Gene	N variants	Burden		FRQWGT		VT		SKAT-O
		direction	P	direction	P	direction	P	P
<i>CDC37</i>	3	risk	0.5	Protect	0.5	Protect	0.69	1
<i>ICAM1</i>	9	risk	0.4	Protect	0.36	Protect	0.1	0.18
<i>ICAM3</i>	11	risk	0.5	risk	0.46	risk	0.49	1
<i>ICAM4</i>	2	Protect	0.015	Protect	0.015	Protect	0.015	0.06
<i>ICAM5</i>	3	Protect	0.31	Protect	0.31	Protect	0.31	1
<i>PDE4A</i>	10	Protect	0.12	Protect	0.20	Protect	0.17	0.24
<i>RAVER1</i>	14	Protect	0.41	Protect	0.5	risk	0.39	0.46
<i>S1PR5</i>	6	risk	0.31	risk	0.37	risk	0.5	0.91
<i>TYK2</i>	22	Protect	0.12	Protect	0.15	Protect	0.18	0.38