

S5 Table. Description of the 26 missense variants predicted to be damaging identified in *TYK2* by sequencing of 1,118 RA cases and 1,118 controls.

CHR	hg19	rsID	Counts		Ref	Alt	Substitution	Protein domain
			cases	controls				
chr19	10488926	rs55762744	14	27	C	T	A53T	FERM
chr19	10488904	.	1	0	A	G	I60T	FERM
chr19	10478825	.	0	1	C	T	R124H	FERM
chr19	10477229	.	0	1	C	T	A165T	FERM
chr19	10475595	.	1	0	G	A	R381W	FERM
chr19	10475333	.	0	1	G	A	R442W	-
chr19	10473232	.	1	0	C	T	R490H	SH2
chr19	10472988	.	0	1	C	T	G541R	-
chr19	10472760	.	1	0	G	C	I589M	Kinase1
chr19	10472598	rs140594440	1	0	C	T	V603M	Kinase1
chr19	10469975	rs12720356	133	174	A	C	I684S	Kinase1
chr19	10469919	rs55882956	1	3	G	A	R703W	Kinase1
chr19	10468777	.	0	1	C	T	R738Q	Kinase1
chr19	10468759	.	0	1	C	T	R744Q	Kinase1
chr19	10468732	.	0	1	G	A	P753L	Kinase1
chr19	10468708	.	1	2	C	A	G761V	Kinase1
chr19	10468526	.	0	1	C	T	A794T	Kinase1
chr19	10468465	rs143743593	0	1	G	A	P814L	Kinase1
chr19	10467283	.	1	0	G	A	R860C	Kinase1
chr19	10464892	.	0	1	T	C	S912G	Kinase2
chr19	10464843	rs35018800	7	13	G	A	A928V	Kinase2
chr19	10464730	.	1	0	A	C	C966G	Kinase2
chr19	10463121	.	1	0	T	C	S1103G	Kinase2
chr19	10463118	rs34536443	48	70	G	C	P1104A	Kinase2
chr19	10461517	.	1	0	A	C	V1186G	-
chr19	10461514	.	0	1	C	T	C1187Y	-