

S5 Table

Number of expression elements that are deemed to have a causal association with the SLE risk SNP

Lead SNP	Gene	Gene	Transcript	Exon	Junction	Intron
rs2476601	<i>PHTF1</i>	-	-	-	-	1/10
rs1801274	<i>ARHGAP30</i>	-	-	1/12	-	-
rs9782955	<i>LYST</i>	-	-	-	1/34	-
rs3768792	<i>IKZF2</i>	-	-	1/5	-	1/15
rs10028805	<i>BANK1</i>	-	-	2/16	-	-
	<i>BLK</i>	1/1	4/8	13/13	13/14	8/11
rs2736340	<i>FAM167A</i>	1/1	1/1	3/3	2/2	2/4
rs2286672	<i>RABEP1</i>	-	-	1/18	-	-
	<i>TYK2</i>	-	-	1/23	-	1/8
rs2304256	<i>ATG4D</i>	-	-	-	1/8	-
	<i>UBE2L3</i>	-	1/3	2/4	-	-
rs7444	<i>CCDC116</i>	1/1	-	1/1	-	-

This table shows how many expression elements (i.e. number of exons, junctions, introns etc.) that are deemed to have a causal *cis*-eQTL association with the SLE associated SNP (taken from Table 3). A dashed line indicates that no causal association exists at that particular quantification type. For example, rs3768792 is a causal *cis*-eQTL for *IKZF2* at both exon- and intron-level. Out of the five exons of *IKZF2* that are included in the *cis*-eQTL analysis (some may have been dropped from analysis due to low expression etc.), only one shows a causal *cis*-eQTL association with rs3768792. The same is true for one of the fifteen introns of *IKZF2*. For *BANK1*, we were able to resolve to two exons.