

S4 Table. Around a third of the GWAS variants residing in the SIP PIR regions disrupt the transcript factor binding motifs.

Cell type	# Variants in SIP PIRs	#(%) disrupting motifs
Ery	369	132 (35.8%)
MacMon	149	59 (39.6%)
MK	249	88 (35.3%)
nCD4	222	57(25.7%)
Neu	208	69 (33.2%)