

Table 7. Association of genotype with *IRF5* expression in 233 transformed B cell lines

Marker	Chromosome	Position <sup>*</sup>	Location	MAF <sup>†</sup>	Nominal <i>P</i> <sup>‡</sup>	<i>P</i> conditional on rs10954213 <sup>§</sup>	<i>P</i> conditional on rs2004640 and rs10954213 <sup>¶</sup>
rs729302	7	128,162,911	Promoter	0.32	0.02	0.34	0.201
rs2004640	7	128,172,252	Exon 1B splice site	0.49	$1.9 \times 10^{-17}$	0.0016	-
rs752637	7	128,173,371	intron	0.45	$1.2 \times 10^{-9}$	0.11	0.809
rs2070197	7	128,182,951	3' UTR	0.09	0.004	0.74	0.649
rs10954213	7	128,183,378	3' UTR	0.43	$1.7 \times 10^{-38}$	-	-
rs11770589	7	128,183,439	3' UTR	0.48	$2.4 \times 10^{-25}$	1.00	0.487
rs10954214	7	128,183,584	3' UTR	0.37	$1.5 \times 10^{-34}$	0.0018	NA <sup>  </sup>
rs2280714	7	128,188,676	5 kb 3' of <i>IRF5</i>	0.42	$1.4 \times 10^{-35}$	0.0012	NA <sup>  </sup>

<sup>\*</sup> Position of marker in the HG17 assembly of the human genome.

<sup>†</sup> Minor Allele Frequency.

<sup>‡</sup> Uncorrected *P* value for association of the indicated marker to *IRF5* mRNA levels in 233 CEPH EBV-transformed B cells (15).

<sup>§</sup> Association of the indicated marker under the model that rs10954213 fully explains all the variance in *IRF5* expression.

<sup>¶</sup> Association of the indicated marker under the model that rs10954213 and rs2004640 fully explain all the variance in *IRF5* expression.

<sup>||</sup> NA indicates that the association to *IRF5* expression cannot be calculated because it is statistically indistinguishable from the proposed model.