

Table 6. Association with *IRF5* mRNA expression in transformed B cells from 210 samples from HapMap CEU, CHB, JPT and YRI populations.

Variant	Chromosome	Position [*]	<i>P</i> [†]
rs7780972	7	128,113,113	0.66
rs4731523	7	128,124,227	0.45
rs6948542	7	128,141,463	0.90
rs1495461	7	128,145,691	0.57
rs960633	7	128,154,711	0.0036
rs6968225	7	128,157,557	6.0 x 10 ⁻²⁵
rs729302	7	128,162,910	0.0075
rs4728142	7	128,167,917	6.5 x 10 ⁻²¹
rs2004640	7	128,172,251	4.2 x 10 ⁻¹⁴
rs1874328	7	128,179,054	1.3 x 10 ⁻²²
Exon6 indel	7	128,181,324	2.0 x 10 ⁻³¹
rs2070197	7	128,182,950	8.7 x 10 ⁻⁷
rs10954213	7	128,183,377	3.5 x 10 ⁻⁵⁵
rs11770589	7	128,183,438	3.7 x 10 ⁻³³
rs10954214	7	128,183,583	1.7 x 10 ⁻⁴⁰
rs10488631	7	128,188,133	7.9 x 10 ⁻⁷
rs2280714	7	128,188,675	1.7 x 10 ⁻⁴⁰
rs3847098	7	128,189,099	2.0 x 10 ⁻¹¹
rs11761242	7	128,189,556	0.0011
rs12539741	7	128,190,755	2.1 x 10 ⁻⁶
rs17166351	7	128,191,754	7.4 x 10 ⁻³⁴
rs6966125	7	128,192,475	1.8 x 10 ⁻²⁴

^{*} Position of variant in the HG17 assembly of the human genome.

[†] Association of variant to *IRF5* mRNA levels in 210 unrelated EBV-transformed B cell lines derived from the HapMap samples (GENEVAR dataset, www.sanger.ac.uk/humgen/genevar/).