

Supplementary Table 2: Association of HapMap phase II variants to IRF-5 expression levels

Marker ^a	Chr	Position ^b	MAF ^c	r ² to rs2280714 ^d	P ^e
rs729302	7	128,122,922	0.32	0.09	0.2
rs2004640	7	128,132,263	0.49	0.68	6.0 x 10 ⁻⁸
rs752637	7	128,133,382	0.45	0.83	2.8 x 10 ⁻⁹
rs2280714	7	128,148,687	0.42	-	1.0 x 10 ⁻¹⁰
rs7789423	7	128,175,166	0.42	1.00	1.0 x 10 ⁻¹⁰
rs6948928	7	128,177,059	0.42	1.00	1.0 x 10 ⁻¹⁰
rs3857852	7	128,211,235	0.42	1.00	2.6 x 10 ⁻¹⁰
rs13221560	7	128,217,133	0.39	1.00	7.4 x 10 ⁻¹⁰
rs921403	7	128,230,682	0.43	0.97	4.0 x 10 ⁻¹⁰
rs10279821	7	128,237,505	0.41	0.97	4.9 x 10 ⁻¹⁰
rs10156169	7	128,238,529	0.42	0.93	3.4 x 10 ⁻¹⁰

^a HapMap Phase II markers with P < 1.0 x 10⁻⁹ are shown, in addition to the results for IRF-5 region markers genotyped in the SLE families (rs729302, rs2004640, rs752637)

^b Position in HG16 (Build 34).

^c Minor Allele Frequency in HapMap CEPH (CEU) population.

^d Correlation to rs2280714.

^e P calculated using conditional linear regression, testing variants for association to IRF-5 expression in EBV-transformed B cells from CEPH individuals.