Table 4. Variants discovered by resequencing all *IRF5* exons and 1kb of upstream of exon 1A in 96 SLE cases from the USA.

Internal ID	RS number [*]	Chromosome	Position [†]	MAF [‡]	Minor Allele	Total chromosomes [§]	Number of chromosomes with minor allele	Description	Frequency in HapMap CEU
Broad11429372	rs3757388	7	128,169,974	0.27	G	166	44	promoter	failed_design
Broad11429376	rs4639458	7	128,170,037	0.42	T	166	69	promoter	failed_QC
Broad11374596		7	128,170,524	0.03	A	176	6	promoter	
Broad11374705		7	128,170,965	0.01	A	190	2	promoter	
Broad11374729		7	128,171,076	0.01	A	190	1	promoter	
Broad11374811		7	128,171,232	0.02	A	190	3	promoter	
Broad11374827	rs3757386	7	128,171,248	0.12/0.02	T/G	192	22/3	promoter	failed_design
Broad11374834	rs3757385	7	128,171,255	0.26	T	184	47	promoter	failed_design
Broad11374851	rs3840553	7	128,171,277	0.11	A	188	21	promoter	failed QC
Broad11374863	rs3807134	7	128,171,289	0.12	C	190	23	promoter	failed_design
Broad11374900	rs3807135	7	128,171,568	0.27	T	172	46	promoter	0.44
Broad11374958	rs6968563	7	128,171,682	0.03	C	164	5	promoter	0.05
Broad11374970		7	128,171,699	0.01	C	166	1	promoter	
Broad11880969		7	128,174,987	0.01	T	190	1	intronic	
Broad11880979	rs3807305	7	128,175,084	0.01	A	192	2	intronic	
Broad11880984		7	128,175,162	0.01	G	192	2	intronic	
Broad11375359		7	128,179,704	0.01	A	192	2	intronic	
Broad11375713		7	128,180,096	0.01	A	192	1	intronic	
Broad11375787		7	128,180,663	0.01	T	192	1	intronic	
Broad11375788		7	128,180,688	0.02	A	192	3	intronic	0.01
Broad11376007		7	128,180,986	0.01	T	192	1	intronic	
Exon6_Deletion		7	128,181,324-54	0.48	30nt deletion	190	92	In-frame deletion	0.48
Broad11376731	rs2230117	7	128,181,996	0.01	G	192	1	synonomous	0.00
Broad11376908		7	128,182,399	0.13	G	166	22	intronic	
Broad11376919		7	128,182,426	0.03	A	174	5	intronic	0.04
Broad11376973		7	128,182,546	0.02	G	176	4	intronic	
Broad11376984		7	128,182,561	0.02	G	192	3	intronic	0.02
Broad11376997		7	128,182,579	0.01	G	182	1	missense	
Broad11377186	rs2070197	7	128,182,951	0.18	C	190	35	3'UTR	0.17
Broad11377207		7	128,182,978	0.01	G	192	1	3'UTR	
Broad11377253		7	128,183,044	0.02	C	178	4	3'UTR	0.00
Broad11377330	rs10954213	7	128,183,378	0.36	G	192	69	3'UTR	0.46
Broad11377356	rs11770589	7	128,183,439	0.40	G	192	77	3'UTR	0.38
Broad11377358		7	128,183,459	0.01	A	192	1	3'UTR	
Broad11429458	rs10954214	7	128,183,584	0.22	C	192	43	3'UTR	0.42
Broad11429530		7	128,184,089	0.01	T	192	1	3'UTR	

[*] Number assigned to variant by dbSNP (http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=snp).

[†] Position in the HG17 assembly of the Human Genome.

[‡] Minor Allele Frequency.

[§] Number of chromosomes with high quality data.