Table 3. Variants discovered by resequencing all IRF5 exons and introns and 1 Kb upstream of exon 1A in 40 SLE cases and 8 controls from Sweden.

Internal ID	RS number*	Chromosome	Position†	MAF‡	Minor allele	No. of chromosomes§	No. of chromosomes with minor allele	Description
UUmolmed_IRF5_01	rs3757386	7	128,171,248	0.15/0.04	T/G	46	7/2	Promoter
UUmolmed_IRF5_02	rs3757385	7	128,171,255	0.24	A	46	11	Promoter
UUmolmed_IRF5_03	rs3834330	7	128171273-5	0.16	"TG" deletion	44	7	Promoter
UUmolmed_IRF5_04	rs3807134	7	128,171,289	0.15	G	46	7	Promoter
UUmolmed_IRF5_05	rs3807135	7	128,171,568	0.26	A	46	12	Promoter
UUmolmed_IRF5_06	rs6968563	7	128,171,682	0.04	A	46	2	Promoter
UUmolmed_IRF5_07		7	128,172,086	0.06	G	72	4	Promoter
UUmolmed_IRF5_08		7	128171882-7	0.37	"GCCCC" insertion	86	32	Promoter
UUmolmed_IRF5_09	rs6953165	7	128,172,161	0.04	G	28	1	Intron
UUmolmed_IRF5_10	rs2004640	7	128,172,252	0.49	G	90	44	Intron
UUmolmed_IRF5_11	rs3807307	7	128,173,153	0.46	A	46	21	Intron
UUmolmed_IRF5_12		7	128,173,233	0.01	A	76	1	Intron
UUmolmed_IRF5_13		7	128,173,283	0.01	T	76	1	Intron
UUmolmed_IRF5_14	rs752637	7	128,173,371	0.33	A	82	27	Intron
UUmolmed_IRF5_15	rs3823536	7	128,173,617	0.46	T	54	25	Intron
UUmolmed_IRF5_16	rs3778753	7	128,173,993	0.44	A	64	28	Intron
UUmolmed_IRF5_17	rs3778752	7	128,173,998	0.38	G	26	10	Intron
UUmolmed_IRF5_18	rs3778751	7	128,173,999	0.44	T	50	22	Intron
UUmolmed_IRF5_19		7	128,174,126	0.04	C	28	1	Intron
UUmolmed_IRF5_20		7	128,174,377	0.04	C	28	1	Intron
UUmolmed_IRF5_21	rs3807306	7	128,174,631	0.44	C	72	32	Intron
UUmolmed_IRF5_22	rs11767834	7	128,175,227	0.02	A	46	1	Intron
UUmolmed_IRF5_23		7	128,175,684	0.02	A	46	1	Intron
UUmolmed_IRF5_24		7	128,175,305	0.02	C	46	1	Intron
UUmolmed_IRF5_25		7	128,175,281	0.02	G	46	1	Intron
UUmolmed_IRF5_26	rs11761199	7	128,175,786	0.50	G	42	21	Intron
UUmolmed_IRF5_27		7	128,175,834	0.18	A	44	8	Intron
UUmolmed_IRF5_28		7	128,178,156	0.02	G	46	1	Intron
UUmolmed_IRF5_29	rs1874328	7	128,179,055	0.36	G	80	29	Intron
UUmolmed_IRF5_30	rs1874327	7	128,179,327	0.27	A	56	15	Intron
UUmolmed_IRF5_31		7	128,179,567	0.23	C	56	13	Intron
UUmolmed_IRF5_32		7	128,179,704	0.03	A	30	1	Intron
UUmolmed_IRF5_33		7	128,180,368	0.02	A	48	1	Intron
UUmolmed_IRF5_34		7	128,180,688	0.07	A	30	2	Intron
UUmolmed_IRF5_35		7	128181324-54	0.45	30nt deletion	76	34	In-frame deletion
UUmolmed_IRF5_36		7	128182387-8	0.18	"G" insertion	84	15	Intron
UUmolmed_IRF5_37	rs2070197	7	128,182,951	0.32	G	44	14	3'UTR
UUmolmed_IRF5_38	rs10954213	7	128,183,378	0.24	T	50	12	3'UTR
UUmolmed_IRF5_39	rs11770589	7	128,183,439	0.42	C	52	22	3'UTR
UUmolmed_IRF5_40	rs10954214	7	128,183,584	0.24	T	34	8	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.