Supplementary Table S1. Characteristics of the SLE patients included in the exploratory and confirmatory genetic studies.

	n	Females (%)	Age (mean±SD)	Renal involvement (%)	Positive anti-Ro/SSA antibodies (%)
Belgium	153	92%	39.2 ± 11.8	31%	60%
Spain	596	92%	28.7 ± 12.3	35%	26%
Grece	194	89%	30.9 ± 12.2	64%	22%
Milan	208	90%	30.5 ± 11.7	31%	29%
Netherlands	97	87%	29.3 ± 12.9	43%	44%
Portugal	116	97%	34.5 ± 14.7	28%	26%
Hungary	90	90%	33.8 ± 14.0	31%	39%
Germany	79	87%	32.4 ± 12.2	24%	28%

Supplementary Table S2. PCR Primers.

Tag SNP / gene	Forward primer	Reverse primer
IFI27	5'-ACCTCATCAGCAGTGACCAGT-3'	5'-ACATCATCTTGGCTGCTATGG-3'
IFI44	5'-GAGAGATGTGAGCCTGTGAGG-3'	5'-TTTTCCTTGTGCACAGTTGAT-3'
β-actin	5'-TCACCCACACTGTGCCCATCTACGA-3'	5'-CAGCGGAACCGCTCATTGCCAATGG-3'
rs4862632	5'-TGCTCTCAGGGAATTTAACCA-3'	5'-TCAGAAGCAGCCAACAAACTT-3'
rs4862633	5'-TGCAACTCTCTAGCCTTGCTC-3'	5'-CACCTGCCCTTGAATTTCTTT-3'
rs5743305	5'-TCTCTTTCATTGAAGGCCAAA-3'	5'-TGAAATATCACAATTGGAAGGAA-3'
rs10025405	5'-ATTTGGCTTTGTGGAAACAGA-3'	5'-CAAGGCGAGAGGATCACTTG-3'
rs6857595	5'-CTGTGCAGCTGGAGGAATAAG-3'	5'-CTGGCCTTGAGACTAGGGTTT-3'
rs1519309	5'-TTAGCCGGGTGTAGTGGTGTA-3'	5'-TAAGGCATTGACTGGTGTTCC-3'
rs3775292	5'-AATCTTCCAATTGCGTGAAAA-3'	5'-TAAGCTGAGGCTGTGAATGCT-3'
rs4608848	5'-GCTCCACTGTCCTGTTTATGG-3'	5'-CACCTGCCCTTGAATTTCTTT-3'
rs3775291	5'-TTTCCAGAGCCGTGCTAAGT-3'	5'-TGGCTAAAATGTTTGGAGCA-3'

Supplementary Table S3. Primers used to identify *TLR3* Tag SNP allelic variations (ABI Prism® SnaPshot™ Multiplex Kit).

Tag SNP	SNaPshot Primer
rs4862632	5'-CAAAATGGCACTAGTACTCCC-3'
rs4862633	5'-AAAAAATTTTGTTTGAGGACTTCTGGG-3'
rs5743305	5'-AAAAAAAAAAAAAGCCCAGTAACTATAAAGCGG-3'
rs10025405	5'-AAAAAAAAAAAAAAAAAAAGACTCAGGAGATGGCGTTGGC-3'
rs6857595	5'-TGGGTCGAGCCGTTATTTATC-3'
rs1519309	5'-AAAAAAGTTGGTTTGGCAACTGACTCA-3'
rs3775292	5'-AAAAAAAAAAAAAGAGCATTTCTCCCCCTTCCT-3'
rs4608848	5'-AAAAAAAAAAAAAAAAAAAAAGTGAGTGAAATAAGCTGGAT-3'
rs3775291	5'-ACTTGCTCATTCTCCCTTACACATA-3'

Supplementary Table S4. Genetic variations observed in 8 Tag SNPs in the sequence of the human *TLR3* gene in Caucasian SLE patients *vs*. healthy controls.

SNP		Western-European SLE population: All (n=153)		Western-European SLE population: >Ro/SSA + (n=68)		Controls (n=105) %
		%	Odds ratio (95% C.I.)	%	Odds ratio (95% C.I.)	
rs4862632	Major allele A	70.9%	0.99 (0.68 – 1.47)	64.2%	0.73 (0.46 – 1.16)	71.0%
	AA	51.0%	1.10 (0.67 – 1.81)	43.3%	0.81 (0.44 – 1.50)	48.6%
	GG	9.3%	-	14.9%	-	6.6%
	AG	39.7%	-	41.8%	-	44.8%
rs4862633	Major allele C	72.3%	0.90 (0.61 – 1.35)	70.5%	0.83 (0.51 – 1.34)	74.3%
	CC	54.0%	0.95 (0.58 – 1.57)	50.0%	0.81 (0.44 – 1.50)	55.2%
	TT	9.3%	-	9.1%	-	6.7%
	CT	36.7%	-	40.9%	-	38.1%
rs5743305	**Major allele T**	70.3%	1.45 (0.99 – 2.11)	**76.1%****	**1.95 (1.20 – 3.17)**	**62.0%**
	TT	**57.4%****	**2.07 (1.24 – 3.45)**	**65.7%*****	**2.94 (1.55 – 5.57)**	**39.4%**
	AA	16.9%	-	13.4%	-	15.4%
	TA	25.7%	-	20.9%	-	45.2%
rs10025405	Major allele A	56.8%	0.98 (0.69 – 1.41)	62.7%	1.26 (0.81 – 1.96)	57.1%
	AA	33.8%	1.23 (0.74 – 2.20)	**43.3%***	**1.91 (1.00 – 3.63)**	**28.6%**
	GG	20.3%	-	17.9%	-	14.3%
	AG	45.9%	-	38.8%	-	57.1%
rs6857595	Major allele C	70.4%	0.91 (0.62 – 1.35)	73.9%	1.08 (0.66 – 1.76)	72.4%
	CC	48.3%	0.92 (0.56 – 1.51)	55.2%	1.21 (0.65 – 2.24)	50.5%
	TT	7.4%	-	7.5%	-	5.7%
	CT	44.3%	-	37.3%	-	43.8%
rs1519309	Major allele A	55.7%	1.00 (0.70 – 1.43)	47.0%	0.70 (0.46 – 1.09)	55.8%
	AA	40.5%	1.14 (0.68 – 1.9)	32.8%	0.81 (0.43 – 1.55)	37.5%
	GG	29.1%	-	38.8%	-	26.0%
	AG	30.4%	-	28.4%	-	36.5%
rs3775292	Major allele C	74.2%	0.76 (0.50 – 1.16)	77.6%	0.92 (0.54 – 1.55)	79.0%
	CC	58.4%	0.83 (0.50 – 1.38)	62.7%	0.99 (0.53 – 1.87)	62.8%
	GG	10.1%	-	7.5%	-	4.8%
	CG	31.5%	-	29.8%	-	32.4%
rs4608848	Major allele T	61.3%	0.92 (0.64 – 1.32)	58.1%	0.80 (0.52 – 1.25)	63.3%
	TT	38.4%	1.06 (0.63 – 1.76)	33.8%	0.71 (0.38 – 1.32)	37.1%
	CC	15.9%	-	17.6%	-	10.5%
	TC	45.7%	-	48.6%	-	52.4%

Tag SNPs were selected using the Tagger-multiMarkerTaging algorithm in the HapMap Data Rel 24/phase II database (r2 cut-off >0.8; minor allele frequency >0.2, CEU population). Odds ratios were calculated for the major allele frequencies and the frequencies of individuals homozygous for the major allele in the SLE populations *vs*. healthy controls. The distribution of all genotypes are in Hardy-Weinberg equilibrium in the control population. C.I. Confidence Interval. *p<0.05; **p<0.01; ***p<0.001 using Fisher's exact test.