Online supplement to: Variants of the *IFI16* Gene Affecting the Levels of Expression of mRNA Are Associated with Susceptibility to Behçet Disease.
The Journal of Rheumatology, doi:10.3899/jrheum.140949

Table S1. Tag single-nucleotide polymorphisms (SNP) included in this study.

Gen	CHR	Tag SNP	SNP Identified	Genotyping
IFI16	1	rs9887904	rs9887904	SEQUENOM
		rs1417806	rs1417806	SEQUENOM
		rs2276404	rs2276404	SEQUENOM
		rs12727764	rs12727764	SEQUENOM
		rs1361564	rs12738378, rs1361565, rs1361564	SEQUENOM
		rs866484	rs866484, rs856064	SEQUENOM
		rs856046	rs856049, rs856046, rs11265131, rs7535856	SEQUENOM
		rs1057024	rs1057024	SEQUENOM
		rs12093523	rs12094741, rs1101991, rs12093523, rs11265133, rs856054, rs2106095, rs1101995, rs1101996, rs1101998, rs1101993	SEQUENOM
		rs1772408	rs855865, rs12124059, rs2570916, rs1772408, rs1772405, rs1057028, rs861318, rs856055, rs856052, rs856053, rs1633265, rs1772414, rs856058, rs1057027, rs1772415, rs1614182, rs1633256	SEQUENOM
		rs3754459	rs3754459	TaqMan
		rs7532207	rs7532207	SEQUENOM
		rs6940	rs6940, rs1772407, rs3018316, rs3737522, rs2814770, rs3768513, rs2814771, rs1616024, rs1633266, rs12098223, rs1633267, rs3754460, rs3768515	SEQUENOM
AIM2	1	rs855871	rs855871	SEQUENOM
		rs855873	rs855873	SEQUENOM
IFIH1	2	rs1990760	rs1990760	TaqMan
		rs3747517*	rs3747517	SEQUENOM
		rs13023380	rs13023380	SEQUENOM
		rs17715343	rs17715343	SEQUENOM
TLR9		rs352140	rs352140, rs352139	SEQUENOM
		rs187084	rs187084	SEQUENOM
TLR3	4	rs5743305	rs5743305	SEQUENOM
		rs11721827	rs11721827, rs11730143, rs11732384	SEQUENOM
		rs13126816	rs13126816, rs6552950	SEQUENOM
		rs13108688	rs13108688, rs7657186	SEQUENOM
		rs5743312	rs3775296, rs5743312, rs5743303	SEQUENOM
		rs7668666	rs7668666	SEQUENOM
		rs3775292	rs3775292	SEQUENOM
		rs3775291	rs3775291	SEQUENOM

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Table S1, part 2.

DDX58	9	rs12006123	rs17289116, rs1133071, rs7045087, rs12555727, rs12006123	SEQUENOM
		rs7865082	rs7865082, rs3205166	TaqMan
		rs10738890	rs10738890, rs10738889	TaqMan
		rs9650702	rs6476362, rs9650702	SEQUENOM
		rs9695310	rs9695310	TaqMan
		rs944581	rs944581 ,rs639949, rs6476363, rs868608	SEQUENOM
		rs944582	rs944582	SEQUENOM
		rs17289402	rs17289402	SEQUENOM
		rs17289627	rs17289627, rs3824456, rs17290242	SEQUENOM
		rs944583	rs7037171, rs944583, rs4384073	SEQUENOM
		rs592515	rs10813821, rs7855688, rs10511907, rs10971001, rs592515, rs10813825, rs7848849	SEQUENOM
		rs13286888	rs13286888, rs13290848, rs13300627, rs13300238, rs11549548, rs7034650, rs17289655, rs12554841, rs13288658, rs17217280, rs17289927, rs669260	SEQUENOM
		rs10813826	rs10813826, rs582509, rs10970997	SEQUENOM
		rs608227	rs10738891, rs7026407, rs659527, rs668559, rs4633144, rs621277, rs1622531, rs613645, rs10813829, rs12340133, rs680471, rs3739674, rs10813827, rs608227, rs660819, rs2777729, rs7023269, rs7044989, rs605383, rs658253, rs7022323	SEQUENOM
		rs11795343	rs11795343	SEQUENOM
		rs10813831*	rs4013911, rs10970990, rs4013910, rs10813831	SEQUENOM
ZBP1	20	rs4811885*	rs4811885	SEQUENOM
		rs6064572	rs6064572, rs6123711	TaqMan
		rs8118279	rs8118279	TaqMan
		rs4811887	rs4811887, rs6070180, rs6025653	SEQUENOM
		rs4811888*	rs4811888	SEQUENOM
		rs742724	rs742724	SEQUENOM
		rs2073145	rs2073145	SEQUENOM
		rs16981188	rs16981188	SEQUENOM
		rs4811890	rs2865395, rs4811890	SEQUENOM
TLR7	X	rs5741880	rs5743733, rs5741880, rs5935436	TaqMan
		rs179021	rs179018, rs179021	SEQUENOM
		rs179019	rs179019, rs179014	SEQUENOM
		rs1731479	rs1634322, rs1731479	SEQUENOM
		rs179016	rs179016	SEQUENOM
		rs5743749	rs5743749	SEQUENOM
		rs1638596	rs1638596, rs1634321, rs1634320, rs1634323, rs1731478, rs1620233, rs1638597, rs1638595, rs1638594	SEQUENOM
		rs179013	rs179011, rs179009, rs179013, rs179008	SEQUENOM

		rs179012	rs179012	SEQUENOM
		rs179010	rs179010	SEQUENOM
		rs1634319	rs1634319	SEQUENOM
		rs864058	rs850633, rs864058	SEQUENOM
TLR8	X	rs5741883	rs5741883	SEQUENOM
		rs3764880	rs3761624, rs3764879, rs4830805, rs3764880	SEQUENOM
		rs17256081	rs17256081	SEQUENOM
		rs2109134	rs2109134	SEQUENOM
		rs1548731	rs1548731	SEQUENOM
		rs5744067	rs4830808, rs5744067, rs2159377, rs3827469	SEQUENOM
		rs2407992	rs5741886, rs5744069, rs2407992, rs3747414, rs4830807, rs1013151, rs5744080	SEQUENOM
		rs5744088	rs5744055, rs1013150, rs5744088, rs5744068	SEQUENOM

* Genotyping assay failure or not meet the threshold of quality control.

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Table S2. Genetic models of inheritance of the risk (A) and the protective (B) haplotypes.

A

Model	β	Wald Test (p)	AIC	LR (p)
Dominant	0.41577	2.3766 (0.017472)	2349.67	5.5011 (0.019004)
Recessive	0.48185	0.9571 (0.338539)	2354.34	0.8302 (0.362215)
Multiplicative	**0.38289**	**2.4318 (0.015023)**	**2349.45**	**5.7241 (0.016734)**
General	0.40130	2.2575 (0.023979)	2351.40	5.7731 (0.055768)

B

Model	β	Wald Test (p)	AIC	LR (p)
Dominant	–0.67269	–2.5915 (0.009555)	2346.58	7.5896 (0.005871)
Recessive	–15.3711	–0.0093 (0.992577)	2351.92	3.2560 (0.071163)
Multiplicative	**–0.68408**	**–2.7237 (0.006455)**	**2346.57**	**8.6007 (0.003360)**
General	–0.62145	–2.4028 (0.016270)	2347.44	9.7301 (0.007712)

β: Estimated haplotype effect. Wald statistic for testing whether $\beta = 0$ and the associated p value. Subjects with 1 copy of the risk haplotype have in the recessive model the same risk as those subjects with no copies; in the dominant model, the same risk as those subjects with 2 copies; in the multiplicative model, an intermediate risk on log scale with respect to those subjects with 0 or 2 copies; and in the general model a general change in risk compared to those with 0 or 2 copies. AIC: Akaike information criteria; LR: likelihood-ratio statistic for testing the global null hypothesis.

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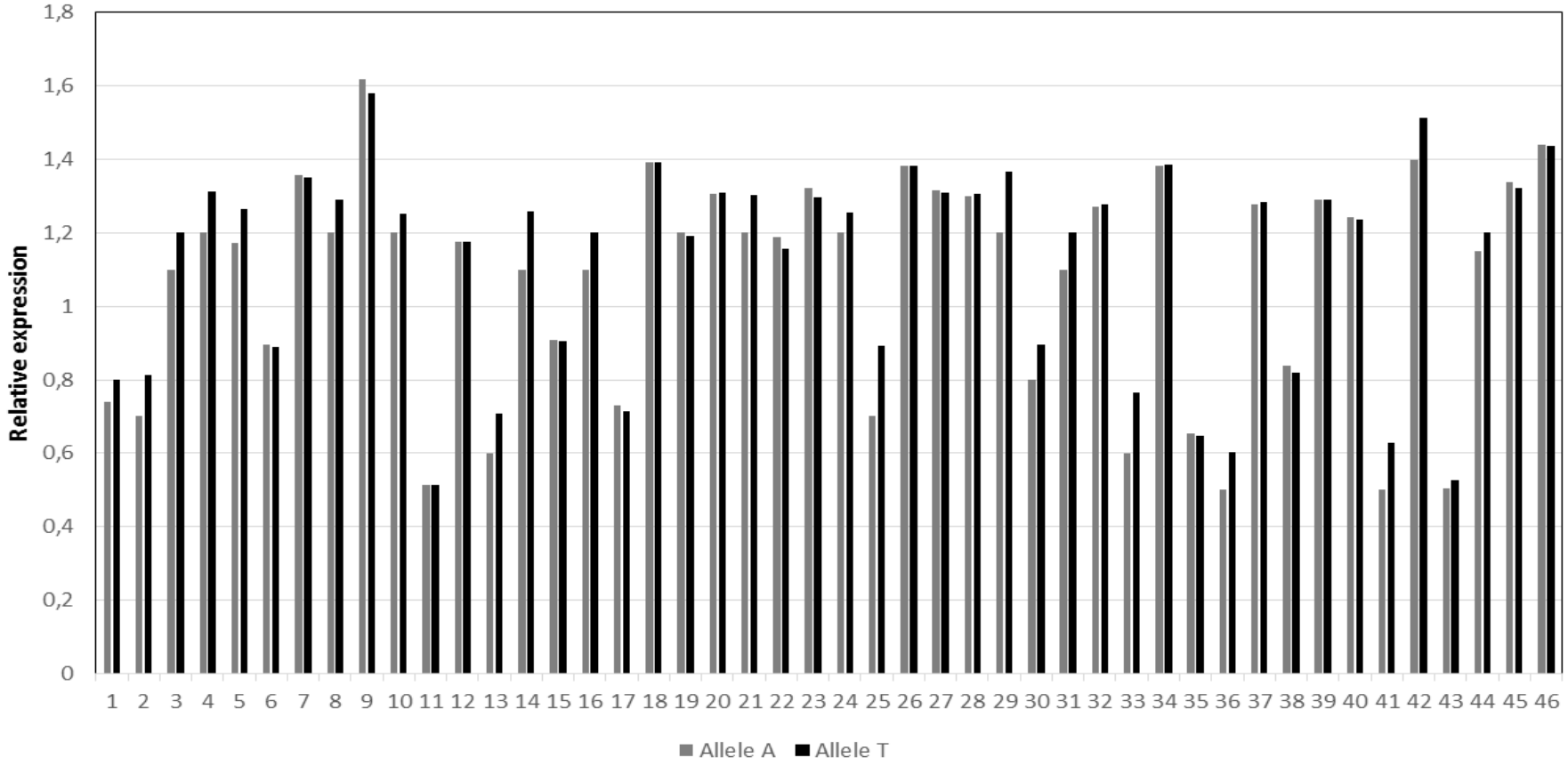
Figure S1. Relative expression levels of the alleles A versus T of the single-nucleotide polymorphism nonsynonymous rs6940.



The relative quantification was performed in samples from 46 heterozygous healthy donors. Ratio A/T = 0.97 ± 0.08; p = 0.027.