

Supplementary Tables

Supplementary Table 1. Genotype and allele frequencies distribution of *TRAF1* rs10818488 polymorphism among CCP-positive rheumatoid arthritis (RA) patients and controls

<i>TRAF1</i> rs10818488	CCP-positive RA patients (<i>n</i> = 214)		<i>p</i> -value	OR (95% CI)
	<i>n</i>	(%)		
Genotype				
G/G	69	(32.2)	118 (26.5)	0.25
A/G	91	(42.5)	217 (48.7)	
A/A	54	(25.2)	111 (24.9)	
Allele				
G	229	(53.5)	453 (50.8)	0.36
A	199	(46.5)	439 (49.2)	
Dominant model				
G/G + A/G	160	(74.8)	335 (75.1)	0.84
A/A	54	(25.2)	111 (24.9)	
Recessive model				
G/G	69	(32.2)	118 (26.5)	0.11
A/G + A/G	145	(67.8)	328 (73.5)	

Regarding the genotype comparison and associations under the genetic models (dominant model and recessive model), the *p* values and corresponding ORs (95% CIs) were calculated with the adjustment for age and sex, and the *p* values were not corrected for multiple comparison

Supplementary Table 2. Genotype and allele frequencies distribution of *TRAF1* rs10818488 polymorphism among CCP-negative rheumatoid arthritis (RA) patients and controls

<i>TRAF1</i> rs10818488	CCP-negative RA patients (<i>n</i> = 53)		<i>p</i> -value	OR (95% CI)
	<i>n</i> (%)	<i>n</i> (%)		
Genotype				
G/G	14 (26.4)	118 (26.5)	0.80	
A/G	23 (43.4)	217 (48.7)		
A/A	16 (30.2)	111 (24.9)		
Allele				
G	51 (48.1)	453 (50.8)	0.60	0.90 (0.60-1.35)
A	55 (51.9)	439 (49.2)		
Dominant model				
G/G + A/G	37 (69.8)	335 (75.1)	0.58	0.83 (0.43-1.61)
A/A	16 (30.2)	111 (24.9)		
Recessive model				
G/G	14 (26.4)	118 (26.5)	0.87	1.06 (0.53-2.10)
A/G + A/G	39 (73.6)	328 (73.5)		

Regarding the genotype comparison and associations under the genetic models (dominant model and recessive model), the *p* values and corresponding ORs (95% CIs) were calculated with the adjustment for age and sex, and the *p* values were not corrected for multiple comparison

Supplementary Table 3. Genotype and allele frequencies distribution of *TRAF1* rs10818488 polymorphism among RF-positive rheumatoid arthritis (RA) patients and controls

<i>TRAF1</i> rs10818488	RF-positive RA patients (<i>n</i> = 198)		<i>p</i> -value	OR (95% CI)
	<i>n</i>	(%)		
Genotype				
G/G	59	(29.8)	118 (26.5)	0.67
A/G	90	(45.5)	217 (48.7)	
A/A	49	(24.7)	111 (24.9)	
Allele				
G	208	(52.5)	453 (50.8)	0.56
A	188	(47.5)	439 (49.2)	
Dominant model				
G/G + A/G	149	(75.3)	335 (75.1)	0.94
A/A	49	(24.7)	111 (24.9)	
Recessive model				
G/G	59	(29.8)	118 (26.5)	0.39
A/G + A/G	139	(70.2)	328 (73.5)	

Regarding the genotype comparison and associations under the genetic models (dominant model and recessive model), the *p* values and corresponding ORs (95% CIs) were calculated with the adjustment for age and sex, and the *p* values were not corrected for multiple comparison

Supplementary Table 4. Genotype and allele frequencies distribution of *TRAF1* rs10818488 polymorphism among RF-negative rheumatoid arthritis (RA) patients and controls

<i>TRAF1</i> rs10818488	RF-negative RA patients (<i>n</i> = 104)		<i>p</i> -value	OR (95% CI)
	<i>n</i> (%)	<i>n</i> (%)		
Genotype				
G/G	35 (33.7)	118 (26.5)	0.16	
A/G	42 (40.4)	217 (48.7)		
A/A	27 (26.0)	111 (24.9)		
Allele				
G	112 (53.8)	453 (50.8)	0.43	1.13 (0.84-1.53)
A	96 (46.2)	439 (49.2)		
Dominant model				
G/G + A/G	77 (74.0)	335 (75.1)	0.86	1.05 (0.62-1.78)
A/A	27 (26.0)	111 (24.9)		
Recessive model				
G/G	35 (33.7)	118 (26.5)	0.07	1.61 (0.97-2.67)
A/G + A/G	69 (66.3)	328 (73.5)		

Regarding the genotype comparison and associations under the genetic models (dominant model and recessive model), the *p* values and corresponding ORs (95% CIs) were calculated with the adjustment for age and sex, and the *p* values were not corrected for multiple comparison

Supplementary Table 5. Genotype and allele frequencies distribution of *TRAF1* rs3761847 polymorphism among CCP-positive rheumatoid arthritis (RA) patients and controls

<i>TRAF1</i> rs3761847	CCP-positive RA patients (<i>n</i> = 207)		<i>p</i> -value	OR (95% CI)
	<i>n</i>	(%)		
Genotype				
A/A	66	(31.9)	130 (29.2)	0.80
A/G	98	(47.3)	216 (48.5)	
G/G	43	(20.8)	99 (22.2)	
Allele				
A	230	(55.6)	476 (53.5)	0.48
G	184	(44.4)	414 (46.5)	
Dominant model				
A/A + A/G	164	(79.2)	346 (77.8)	0.73
G/G	43	(20.8)	99 (22.2)	
Recessive model				
A/A	66	(31.9)	130 (29.2)	0.51
A/G + G/G	141	(68.1)	315 (70.8)	

Regarding the genotype comparison and associations under the genetic models (dominant model and recessive model), the *p* values and corresponding ORs (95% CIs) were calculated with the adjustment for age and sex, and the *p* values were not corrected for multiple comparison

Supplementary Table 6. Genotype and allele frequencies distribution of *TRAF1* rs3761847 polymorphism among CCP-negative rheumatoid arthritis (RA) patients and controls

<i>TRAF1</i> rs3761847	CCP-negative RA patients (<i>n</i> =52)		<i>p</i> -value	OR (95% CI)
	<i>n</i>	(%)		
Genotype				
A/A	14	(26.9)	130 (29.2)	0.58
A/G	23	(44.2)	216 (48.5)	
G/G	15	(28.8)	99 (22.2)	
Allele				
A	51	(49.0)	476 (53.5)	0.39
G	53	(51.0)	414 (46.5)	
Dominant model				
A/A + A/G	37	(71.2)	346 (77.8)	0.30
G/G	15	(28.8)	99 (22.2)	
Recessive model				
A/A	14	(26.9)	130 (29.2)	0.79
A/G + G/G	38	(73.1)	315 (70.8)	

Regarding the genotype comparison and associations under the genetic models (dominant model and recessive model), the *p* values and corresponding ORs (95% CIs) were calculated with the adjustment for age and sex, and the *p* values were not corrected for multiple comparison

Supplementary Table 7. Genotype and allele frequencies distribution of *TRAF1* rs3761847 polymorphism among RF-positive rheumatoid arthritis (RA) patients and controls

<i>TRAF1</i> rs3761847	RF-positive RA patients (<i>n</i> = 192)		<i>p</i> -value	OR (95% CI)
	<i>n</i>	(%)		
Genotype				
A/A	58	(30.2)	130 (29.2)	0.98
A/G	92	(47.9)	216 (48.5)	
G/G	42	(21.9)	99 (22.2)	
Allele				
A	208	(54.2)	476 (53.5)	0.82
G	176	(45.8)	414 (46.5)	
Dominant model				
A/A + A/G	150	(78.1)	346 (77.8)	0.87
G/G	42	(21.9)	99 (22.2)	
Recessive model				
A/A	58	(30.2)	130 (29.2)	0.92
A/G + G/G	134	(69.8)	315 (70.8)	

Regarding the genotype comparison and associations under the genetic models (dominant model and recessive model), the *p* values and corresponding ORs (95% CIs) were calculated with the adjustment for age and sex, and the *p* values were not corrected for multiple comparison

Supplementary Table 8. Genotype and allele frequencies distribution of *TRAF1* rs3761847 polymorphism among RF-negative rheumatoid arthritis (RA) patients and controls

<i>TRAF1</i> rs3761847	RF-negative RA patients (<i>n</i> = 102)		<i>p</i> -value	OR (95% CI)
	<i>n</i>	(%)		
Genotype				
A/A	34	(33.3)	130 (29.2)	0.53
A/G	46	(45.1)	216 (48.5)	
G/G	22	(21.6)	99 (22.2)	
Allele				
A	114	(55.9)	476 (53.5)	0.54
G	90	(44.1)	414 (46.5)	
Dominant model				
A/A + A/G	80	(78.4)	346 (77.8)	0.86
G/G	22	(21.6)	99 (22.2)	
Recessive model				
A/A	34	(33.3)	130 (29.2)	0.27
A/G + G/G	68	(66.7)	315 (70.8)	

Regarding the genotype comparison and associations under the genetic models (dominant model and recessive model), the *p* values and corresponding ORs (95% CIs) were calculated with the adjustment for age and sex, and the *p* values were not corrected for multiple comparison

Supplementary Table 9. Distribution of the *TRAF1* rs10818488 polymorphism genotype and allele frequencies among rheumatoid arthritis (RA) patients and controls

Author	Year	Case			Control			Case		Control	
		G/G	A/G	A/A	G/G	A/G	A/A	G	A	G	A
The present study	2017	100	145	82	118	217	111	345	309	453	439
Moaaz <i>et al.</i>	2016	27	57	21	27	40	8	111	99	94	56
Fodil <i>et al.</i>	2015	34	69	7	66	92	38	137	83	224	168
Liang <i>et al.</i>	2015	90	144	66	75	153	72	324	276	303	297
Ahmadvand <i>et al.</i>	2014	150	160	52	195	180	47	460	264	570	274
Fakhfakh <i>et al.</i>	2012	23	56	29	53	83	25	102	114	189	133
Mohamed <i>et al.</i>	2012	74	71	27	89	55	16	219	125	233	87
El-Gabalawy <i>et al.</i>	2011	155	142	36	257	193	40	452	214	707	273
Nishimoto <i>et al.</i> (1)	2010	320	757	405	152	389	199	1397	1567	693	787
Nishimoto <i>et al.</i> (2)	2010	190	422	217	132	320	202	802	856	584	724
Nishimoto <i>et al.</i> (3)	2010	238	575	298	191	476	271	1051	1171	858	1018
Nishimoto <i>et al.</i> (4)	2010	217	448	277	82	263	154	882	1002	427	571
Stark <i>et al.</i>	2009	186	240	85	116	134	50	612	410	366	234
Zervou <i>et al.</i>	2008	99	179	33	175	148	21	377	245	498	190
Barton <i>et al.</i>	2008	734	1687	988	552	1514	968	3155	3663	2618	3450
Palomino-Morales <i>et al.</i>	2008	114	117	43	147	197	77	345	203	491	351
Kurreeman <i>et al.</i> (1)	2007							255	247	289	193
Kurreeman <i>et al.</i> (2)	2007							425	387	304	220
Kurreeman <i>et al.</i> (3)	2007							1500	1500	984	840
Kurreeman <i>et al.</i> (4)	2007							513	427	582	356
WTCCC	2007	369	911	578	595	1419	920	1649	2067	2609	3259

Supplementary Table 10. Distribution of the *TRAF1* rs3761847 polymorphism genotype and allele frequencies among rheumatoid arthritis (RA) patients and controls

Author	Year	Case			Control			Case		Control	
		A/A	A/G	G/G	A/A	A/G	G/G	A	G	A	G
The present study	2017	98	153	69	130	216	99	349	291	476	414
Liang <i>et al.</i>	2015	69	156	75	90	147	63	294	306	327	273
Danoy <i>et al.</i>	2011							1056	1014	1838	1566
El-Gabalawy <i>et al.</i>	2011	155	142	36	257	193	40	452	214	707	273
Zhu <i>et al.</i>	2011	192	282	102	171	369	149	666	486	711	667
Nishimoto <i>et al.</i> (1)	2010	331	747	387	162	388	191	1409	1521	712	770
Nishimoto <i>et al.</i> (2)	2010	201	418	211	137	322	193	820	840	596	708
Nishimoto <i>et al.</i> (3)	2010	248	573	289	198	475	266	1069	1151	871	1007
Nishimoto <i>et al.</i> (4)	2010	227	442	274	85	264	152	896	990	434	568
Han <i>et al.</i>	2009	341	657	303	249	509	238	1339	1263	1007	985
Stark <i>et al.</i>	2009	186	243	87	117	133	49	615	417	367	231
Barton <i>et al.</i>	2008	733	1612	1073	628	1607	1102	3078	3758	2863	3811
Plenge <i>et al.</i> (1)	2007							935	791	1487	877
Plenge <i>et al.</i> (2)	2007							628	636	727	579
Plenge <i>et al.</i> (3)	2007							521	449	1587	977
Plenge <i>et al.</i> (4)	2007							600	536	569	463
WTCCC	2007	348	902	608	565	1410	960	1598	2118	2540	3330