

**Influence of elevated-CRP level-related polymorphisms in non-rheumatic Caucasians on the risk of subclinical atherosclerosis and cardiovascular disease in rheumatoid arthritis**

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**Supplementary Table S1.** Association between *CRP* polymorphisms and CRP serum levels in

RA patients.

	Allele	CRP serum levels at RA diagnosis mean ± SD (mg/l) (n=1,662)	p	CRP serum levels at the time of carotid US study mean ± SD (mg/l) (n=1,193)	p
<i>CRP</i> rs1417938	T	9.80 ± 19.39	0.0002	5.64 ± 14.56	0.029
	A	12.66 ± 25.32		7.15 ± 19.16	
<i>CRP</i> rs1800947	C	10.95 ± 21.91	0.06	6.17 ± 16.33	0.83
	G	7.87 ± 1.01		5.85 ± 17.94	
<i>CRP</i> rs1205	C	11.44 ± 22.82	0.06	6.71 ± 17.70	0.018
	T	9.92 ± 19.43		5.02 ± 12.81	

CRP: C-reactive protein; RA: rheumatoid arthritis; SD: standard deviation; US: ultrasound.

**Supplementary Table S2.** Association between *CRP* haplotypes and CRP serum levels in RA patients.

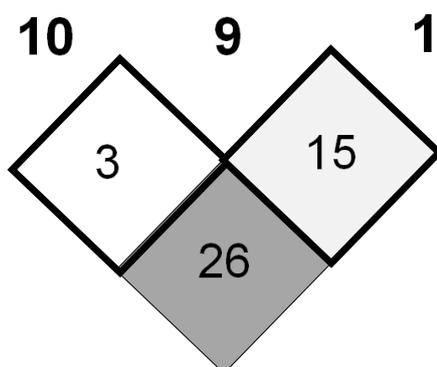
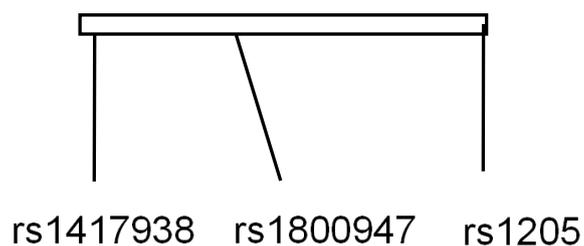
Haplotypes			CRP serum levels at RA diagnosis mean ± SD (mg/l)	p	CRP serum levels at the time of carotid US study mean ± SD (mg/l)	p
<b>rs1417938</b>	<b>rs1800947</b>	<b>rs1205</b>				
T	C	C	10.23 ± 19.90	Ref.	6.14 ± 16.46	Ref.
A	C	C	14.08 ± 28.28	0.0002	7.73 ± 20.13	0.11
T	C	T	9.76 ± 20.18	0.64	4.34 ± 7.75	0.023
A	C	T	11.55 ± 21.11	0.26	6.32 ± 19.22	0.89

CRP: C-reactive protein; RA: rheumatoid arthritis; SD: standard deviation; US: ultrasound.

**Supplementary Table S3.** Association between *HNF1A*, *LEPR*, *GCKR*, *NLRP3*, *IL1F10*, *PPP1R3B*, *ASCL1*, *HNF4A*, *SALL1* polymorphisms and CRP serum levels in RA patients.

	Allele	CRP serum levels at RA diagnosis mean $\pm$ SD (mg/l) (n=1,662)	p	CRP serum levels at the time of carotid US study mean $\pm$ SD (mg/l) (n=1,193)	p
<i>HNF1A</i> rs1183910	G	10.86 $\pm$ 21.33	0.39	6.43 $\pm$ 16.86	0.14
	A	10.19 $\pm$ 21.51		5.38 $\pm$ 14.63	
<i>LEPR</i> rs4420065	C	10.85 $\pm$ 21.79	0.52	6.41 $\pm$ 16.03	0.33
	T	10.37 $\pm$ 21.18		5.75 $\pm$ 16.82	
<i>GCKR</i> rs1260326	C	10.60 $\pm$ 21.15	0.64	5.91 $\pm$ 15.99	0.42
	T	10.94 $\pm$ 22.30		6.44 $\pm$ 16.73	
<i>NLRP3</i> rs12239046	C	10.48 $\pm$ 20.37	0.55	6.35 $\pm$ 17.71	0.51
	T	10.93 $\pm$ 23.31		5.91 $\pm$ 13.99	
<i>IL1F10</i> rs6734238	A	10.77 $\pm$ 21.54	0.94	6.07 $\pm$ 15.67	0.75
	G	10.82 $\pm$ 21.72		6.29 $\pm$ 17.43	
<i>PPP1R3B</i> rs9987289	G	10.79 $\pm$ 21.81	0.21	6.24 $\pm$ 16.32	0.96
	A	9.07 $\pm$ 18.58		6.17 $\pm$ 17.24	
<i>ASCL1</i> rs10745954	A	10.62 $\pm$ 21.60	0.78	6.40 $\pm$ 16.85	0.41
	G	10.83 $\pm$ 20.62		5.85 $\pm$ 15.70	
<i>HNF4A</i> rs1800961	C	10.55 $\pm$ 21.09	0.48	6.32 $\pm$ 16.56	0.11
	T	11.95 $\pm$ 2.71		3.29 $\pm$ 5.14	
<i>SALL1</i> rs10521222	C	10.77 $\pm$ 21.79	0.46	6.23 $\pm$ 16.57	0.97
	T	9.61 $\pm$ 19.29		6.17 $\pm$ 14.07	

CRP: C-reactive protein; RA: rheumatoid arthritis; SD: standard deviation; US: ultrasound.



**Supplementary Fig. Linkage disequilibrium (LD) pattern of the *CRP* polymorphisms (*CRP* rs1417938, *CRP* rs1800947, *CRP* rs1205) analyzed in our study measured by  $r^2$  coefficient.**

Data obtained by HapMap Project phase I, II and III and Haploview (v.4.2) software. The LD between the *CRP* polymorphisms studied is shown in a scale from minimum (white) to maximum (black).