Supplemental Table 1: *CRP* SNPs, their minor allele frequencies.

rs number (SNP location)	SNP pseudonyms	Genotype count (genotype frequency %)		95% CI of genotype frequency (%)	MAF (%) [1000 Genomes Project MAF% for Africans / Europeans]	HW p-value
rs7553007[Φ] (159728759)	Promotor	GG GA AA	923 (57.90) 583 (36.57) 88 (5.52)	55.4 – 60.3 34.2 – 39.0 4.43 – 6.70	A = 23.8 [19.8 / 30.9]	0.05
rs1341665[Φ] (159721769)	-7180C>T Promotor	GG GA AA	931 (58.44) 577 (36.22) 85 (5.34)	55.9 – 60.8 33.9 – 38.6 4.27 – 6.49	A = 23.5 [19.0 / 31.6]	0.53
rs2027471[Φ] (159719598)	Promotor	TT TA AA	932 (58.47) 577 (36.20) 85 (5.33)	55.9 – 60.8 33.9 – 38.6 4.26 – 6.49	A = 23.5 [18.8 / 31.7]	0.73
rs3093058[§] (159715525)	-790A>T Promotor (conserved region predicted to alter a transcription factor E box binding element)	AA AT TT	1101 (69.25) 458 (28.81) 31 (1.95)	67.1 – 71.6 26.5 – 31.0 1.23 – 2.58	A = 19.4 [18.4 / 0.0]	0.84
rs3093062[§] (159714894)	-409G>A Promotor	GG (CC) GA (CT) AA (TT)	1102 (69.26) 458 (28.79) 31 (1.95)	67.1 – 71.7 26.5 – 30.9 1.23 – 2.58	T = 16.4 [18.5 / 0.0]	0.76
rs1417938 (159714396)	IVS1+29A>T, i178T>A; 1919A>T intron (position + 29) close to splice site junction	AA TA	1509 (95.03) 79 (4.97)	94.0 – 96.2 3.82 – 5.96	A = 2.49 [8.50 / 32.6]	0.27
rs1800947 (159713648)	Leu184Leu (L184L) or silent/synonymous mutation or +1059C>G; 2667G>C Exon 2	CC CG	1587 (99.56) 7 (0.44)	99.2 – 99.9 0.12 – 0.77	G = 0.22 [0.20 / 0.51]	0.62
rs1130864 (159713301)	3u1273C>T or +1444G>A or 3014G>A 3′ UTR	CC (GG) CT (GA) TT (AA)	1189 (74.59) 382 (23.96) 23 (1.44)	72.4 – 76.7 21.9 – 26.1 0.86 – 2.05	A = 13.4 [13.2 / 32.7]	0.05
rs1205[Φ] (159712443)	3u2131C>T or 3872A>G/C>T or +1846G>A Distal 3′ UTR ('3 flanking region) in the MLT1K repeat	CC CT TT	945 (59.32) 570 (35.78) 78 (4.90)	56.9 – 61.7 33.4 – 38.2 3.81 – 5.94	T = 22.8 [17.0 / 31.0]	0.73
rs3093068 (159711574)	+2911C>G; 4741G>C 3′ UTR	GG GC CC	610 (38.32) 769 (48.30) 213 (13.38)	35.9 – 40.7 46.1 – 51.0 11.5 – 14.8	C = 37.5 [29.9 / 7.10]	0.29
rs2808630 (159711078)	+5237A>G 3′ UTR	TT TC CC	1173 (73.59) 387 (24.28) 34 (2.13)	71.4 – 75.7 22.2 – 26.4 1.43 – 2.87	C = 14.3 [14.8 / 28.4]	0.73
rs2794520[Φ] (159709026)	3′ UTR	CC CT TT	923(58.27) 574 (36.24 87 (5.49)	55.8 – 60.7 33.9 – 38.7 4.34 – 6.60	T = 23.6 [18.3 / 31.1]	1.00

Several SNP aliases are the complement alleles of those given on Ensembl or published elsewhere. At rs3093058 we report our raw BeadXpress data even though it differs from that of Ensembl and previously reported by our group. Major/minor allele frequency is based Homo Sapiens GRCh38.p5.