

Supplementary Table 1. Association between *CRP* and *IL6* SNPs and Alzheimer's disease based on 2370 controls and 1265 AD cases

<i>Gene/Marker</i>	<i>Genotype</i>	<i>Controls, N (%)</i>	<i>AD cases, N (%)</i>	<i>OR</i>	<i>95%CI</i>		<i>P_{trend}</i>
CRP/ rs2794520	GG	999 (42.2)	534 (42.5)	1	ref		0.80
	AG	1088 (46.0)	573 (45.6)	1.02	0.88	– 1.18	
	AA	279 (11.8)	150 (11.9)	1.02	0.82	– 1.28	
CRP/rs1205	GG	1005 (42.6)	536 (42.6)	1	ref		0.62
	AG	1090 (46.2)	573 (45.6)	1.02	0.88	– 1.17	
	AA	263 (11.2)	148 (11.8)	1.06	0.85	– 1.33	
CRP/rs1800947	GG	2019 (85.2)	1043 (82.7)	1	ref		0.22
	GC	333 (14.1)	203 (16.1)	1.09	0.90	– 1.31	
	CC	17 (0.7)	15 (1.2)	1.57	0.79	– 3.74	
CRP/rs1417938	AA	1097 (46.3)	620 (49.3)	1	ref		0.04
	AT	1063 (44.9)	541 (43.0)	0.90	0.79	– 1.04	
	TT	209 (8.8)	97 (7.7)	0.80	0.62	– 1.03	
CRP/rs3116650	AA	1146 (48.4)	595 (47.5)	1	ref		0.51
	AG	1030 (43.5)	547 (43.7)	1.03	0.90	– 1.18	
	GG	191 (8.1)	111 (8.9)	1.09	0.86	– 1.38	
CRP/rs11265260	AA	2151 (90.9)	1135 (89.9)	1	ref		0.33
	AG	211 (8.9)	122 (9.7)	1.09	0.86	– 1.39	
	GG	5 (0.2)	5 (0.4)	1.87	0.53	– 6.64	
rs11766273	GG	1964 (0.83)	1041 (0.82)	1	ref		0.38
	GA	390 (0.16)	213 (0.17)	1.06	0.88	– 1.27	
	AA	15 (0.006)	9 (0.007)	1.49	0.53	– 4.25	
rs10242595	GG	1308 (0.55)	678 (0.54)	1	ref		0.47
	GA	910 (0.38)	498 (0.39)	1.07	0.93	– 1.22	
	AA	151 (0.06)	85 (0.07)	1.03	0.78	– 1.37	
rs2069861	GG	1954 (0.84)	1076 (0.87)	1	ref		0.04
	GA	367 (0.16)	141 (0.11)	0.74	0.60	– 0.90	
	AA	15 (0.006)	13 (0.01)	1.50	0.76	– 2.99	
rs1554606	AA	617 (0.26)	337 (0.27)	1	ref		0.30
	AC	1179 (0.50)	607 (0.48)	1.00	0.85	– 1.18	
	CC	570 (0.24)	317 (0.25)	1.11	0.91	– 1.35	
rs2069840	CC	1157 (0.49)	594 (0.48)	1	ref		0.52
	CG	973 (0.41)	519 (0.42)	1.01	0.87	– 1.16	
	GG	233 (0.10)	130 (0.10)	1.10	0.87	– 1.39	
rs1474347	AA	654 (0.28)	379 (0.30)	1	ref		0.32
	AC	1159 (0.49)	590 (0.47)	0.90	0.77	– 1.06	
	CC	555 (0.23)	281 (0.22)	0.91	0.75	– 1.11	
rs1800796	GG	2157 (0.91)	1162 (0.93)	1	ref		0.20
	CG	196 (0.08)	90 (0.07)	0.84	0.66	– 1.09	
	CC	10 (0.004)	3 (0.002)	0.82	0.15	– 4.61	
rs2069827	CC	1856 (0.78)	968 (0.77)	1	ref		0.38
	AC	474 (0.20)	277 (0.22)	1.10	0.93	– 1.30	
	AA	37 (0.02)	15 (0.01)	0.95	0.50	– 1.81	
rs12700386	CC	1641 (0.69)	834 (0.67)	1	ref		0.08
	CG	661 (0.28)	374 (0.30)	1.09	0.94	– 1.27	
	GG	65 (0.03)	46 (0.04)	1.39	0.96	– 2.01	
rs2056576	GG	1280 (0.54)	643 (0.52)	1	ref		0.07
	GA	913 (0.39)	490 (0.39)	1.09	0.94	– 1.25	
	AA	173 (0.07)	113 (0.09)	1.25	0.97	– 1.61	
rs10499563	AA	1498 (0.64)	774 (0.62)	1	ref		1.18
	AG	761 (0.32)	410 (0.33)	1.02	0.88	– 1.18	

rs1880241	GG	98 (0.04)	55 (0.04)	1.01	0.71	–	1.42	0.86
	AG	1151 (0.49)	588 (0.48)	1		ref		
	AA	722 (0.31)	372 (0.30)	1.00	0.86	–	1.17	
rs7801617	GG	469 (0.20)	274 (0.22)	1.12	0.92	–	1.37	0.29
	GG	1951 (0.82)	1039 (0.82)	1		ref		
	GA	400 (0.17)	217 (0.17)	1.00	0.84	–	1.20	
rs1546762	AA	19 (0.008)	9 (0.007)	0.88	0.44	–	1.77	0.93
	GG	689 (0.29)	343 (0.27)	1		ref		
	AG	1161 (0.49)	594 (0.47)	1.02	0.88	–	1.20	
	AA	518 (0.22)	319 (0.25)	1.17	0.97	–	1.43	0.12

Odds Ratios (OR) with 95% Confidence Intervals (CI) from Alternating Logistic Regression with the most common homozygote genotype as the reference level. Adjusted for age and sex.

Supplementary Table 2. Haplotypes in CRP and IL6 and their association with AD

Haplotypes in CRP									
	rs1205	rs1800947	rs1417938	rs3116650	rs11265260	Frequency, %	Association with AD		
							Uncorrected p-value	Corrected p-value (1000 perm)	
C1	G	G	T	A	A	30.6	0.11	0.34	
C2	G	G	A	G	A	29.9	0.33	0.77	
C3	A	G	A	A	A	26.2	0.23	0.64	
C4	A	C	A	A	A	8.3	0.03	0.10	

Haplotypes in IL6											
	LD block 1			LD block 2				Frequency, %	Association with AD		
	rs1546762	rs7801617	rs1800796	rs1800795	rs2069837	rs1474347	rs2069840	rs1554606	Uncorrected p-value	Corrected p-value (1000 perm)	
I1	G	G							52.7	0.12	0.50
I2	A	G							30.8	0.46	0.95
I3	A	A							9.3	14.1	0.55
I4			G	C	A	C	C	A	47.1	59.3	0.99
I5			G	G	A	A	G	C	30.8	54.4	0.98
I6			G	G	G	A	C	C	8.0	15.1	0.57
I7			G	G	A	A	C	C	6.2	15.2	0.57

Block structure defined by Confidence Intervals (Gabriel et al, Science, 2002) in HapMap CEU down load data between 15640 & 15660 kb (Chr 1) for CRP and 22530 & 22550 kb (Chr7) for IL6. The association modeled (p-value) is the case-control association between control group and AD cases. Only haplotypes with frequency >5% were included. The corrected p-value is based on 1000 permutations, i.e. the test statistic is also influenced by “chance” and can vary from each time the permutation is done.