Data supplement to Zhang et al. evidence for complement factor H conferring susceptibility to major depressive disorder in Han Chinese. Br J Psychiatry doi: 10.1192/bjp.bp.115.163790

Table DS1 Demographics of MDD cases and controls for expression analyses

	Cases	Controls	*P*
Number of subjects (n)	53	55	
Age (years), mean (SD)	29.0 (5.9)	31.0 (6.8)	0.41
Gender, male n (%)	18 (34.0)	22 (40.0)	0.33
Smoking status, n (%)	14 (26.4)	17 (30.9)	0.38
Alcoholic misuse, n (%)	0 (0)	0 (0)	
Duration of illness (month) a, mean (SD)	2.9 (1.0)	N/A	
HRSD-17 b, mean (SD)	25.2 (2.1)	N/A	
Number of episodes, mean (SD)	1.4 (0.3)	N/A	
Family history of mood disorders, n (%)	3 (5.6)	N/A	

Note: [a] Duration of illness prior to admission

[b] HRSD-17 on admission

Table DS2 Information of selected SNPs genotyped in this study

#	SNP ID	Allele	MAF [a]	Position (Chr. 1)	Note
1	rs800292	C/T	0.329	194908856	tag, V62I
2	rs10801555	A/G	0.122	194926884	tag
3	rs10922096	C/T	0.232	194929082	tag
4	rs10733086	A/T	0.158	194943558	tag
5	rs10737680	A/C	0.329	194946078	tag
6	rs11582939	C/T	0.500	194976780	tag
7	rs2019727	A/T	0.110	194941337	tag
8	rs1410996	C/T	0.433	194963556	tag
9	rs1061170	C/T	0.067	194925860	Y402H
10	rs460184	A/G	0.000	194982960	V1197L
11	rs426736	C/T	0.467	195027040	tag, located in CFHR3

[a] MAF - minor allele frequency, in dbSNP CHB dataset (http://www.ncbi.nlm.nih.gov/SNP/).

Table DS3 Primers for genotyping the *CFH* SNPs

SNP ID	Primer	Primer sequences (5'>3')
rs800292	PCRU	TTAATGGATTAAGAGCAACCCA
	PCRL	AGGCTATCTATAAATGCCGCC
	SNP	TCTCCCTTCCTGCATACCATTATTA
rs10801555	PCRU	TTAAAAGGAAAAACCTTATCAAGGA
	PCRL	TCAAATGATTGATTCCAATGTACA
	SNP	gactCTGTACCCTCATTATCTGCCTAAAC
rs10922096	PCRU	GCTGTAGTTTCCTTTAAAATAGTCATTT
	PCRL	AATCATTCAGATGGCACTAGTAATT
	SNP	t$(gact)_2$CCAGATAAATCACAGAATATCAATT
rs10733086	PCRU	GAGGAAAAATATCAGATAAGTAACTTTAATG
	PCRL	TATAATAACAAACATTCCTGTTATGCTC
	SNP	ct$(gact)_3$TAGACAAAACATATGTCTTCTTGAC
rs10737680	PCRU	CCTTGTGTTGATTAAAGCCT
	PCRL	TTATAAGACTATCAGGTTCACATGC
	SNP	act$(gact)_4$TCTTTGCTGCAAACCCTACTGTCTC
rs11582939	PCRU	AAATTAGTTCATTTTCACATCATCTTG
	PCRL	ATGAGTAGAGGCAGCTGTGC
	SNP	$(gact)_6$TTAAGCATCCTCTGATGTATATTCT
rs2019727	PCRU	CTCATGATATTCCCCAAGTCTT
	PCRL	TAAGTAAAAATTACTAATGGATCTGGC
	SNP	$(gact)_7$TAAACCCATCCCTTCTCTCTCATGT
rs1410996	PCRU	ATGAGATTTACAGTGTGAAGTCCG
	PCRL	AGGGTTGGTGGGCCACAG
	SNP	$(gact)_8$TGACTCAGTCCCTGACTACCTCATG
rs1061170	PCRU	TTATGGTCCTTAGGAAAATGTTATTT
	PCRL	ATGGCAGGCAACGTCTATAG
	SNP	$(gact)_9$TTTGGAAAATGGATATAATCAAAAT
rs460184	PCRU	AATGTGTGAGAACGTGATGAAA
	PCRL	TTTTTTATTTTCAGATCCGTGTG
	SNP	$(gact)_{10}$ATATCCCCGTTTACACACAAATTCA
rs426736	PCRU	CCATAATCATTGTGGCTTATATTTT
	PCRL	AAGCCAGTAATATAGGTATACTTCCAGA
	SNP	t$(gact)_{11}$GAGTTGTGTTGCTTCAAGTTCATAG

Note: PCR amplification primers were marked by "PCRU" and "PCRL", whereas SNP-specific oligonucleotide primer was marked by "SNP". In the "$(gact)_n$", n means the number of "gact" repeats.

Table DS4 Plasma C3, C4 and AP activity in MDD cases and healthy controls

	Cases	Controls	*P* [a]	*P* [b]	Power [c] (%)
C3 (pg/ml)	2735.3 (964.8)	2225.1 (726.3)	0.002	0.004	82.4
C4 (pg/ml)	1619.3 (754.3)	1352.5 (503.4)	0.032	0.016	77.3
AP activity (%)	82.1 (20.3)	73.9 (21.8)	0.046	0.078	23.5

[a] Raw *P* values

[b] The *P* values were adjusted for age, sex and smoking status

[c] Observed power

Table DS5 Distributions of genotypes and alleles of *CFH* variants in stage 1 study (sample set 1: 1012 MDD cases and 1196 controls)

#	SNP	Sample	Genotype, n (%)			*P*	Allele, n (%)		*P*	Odds ratio (95%CI)
1	rs800292		T/T	T/C	C/C		T	C		
		Cases	156 (15.4)	520 (51.4)	336 (33.2)	0.60	832 (41.1)	1192 (58.9)	0.39	1.04 (0.92-1.17)
		Controls	185 (15.5)	591 (49.4)	420 (35.1)		961 (40.2)	1431 (59.8)		
2	rs1061170		C/C	C/T	T/T		C	T		
		Cases	6 (0.6)	139 (13.7)	867 (85.7)	**0.004** [a]	151 (7.5)	1873 (92.5)	**0.001** [a]	1.50 (1.17-1.92)
		Controls	2 (0.2)	118 (9.9)	1076 (90.0)		122 (5.1)	2270 (94.9)		
3	rs10801555		A/A	A/G	G/G		A	G		
		Cases	7 (0.7)	135 (13.3)	870 (86.0)	0.03	149 (7.4)	1875 (92.6)	0.009	1.38 (1.08-1.76)
		Controls	5 (0.4)	120 (10.0)	1071 (89.5)		130 (5.4)	2262 (94.6)		
4	rs10922096		T/T	T/C	C/C		T	C		
		Cases	36 (3.6)	255 (25.2)	721 (71.2)	0.04	327 (16.2)	1697 (83.8)	0.03	1.20 (1.02-1.42)
		Controls	23 (1.9)	285 (23.8)	888 (74.2)		331 (13.8)	2061 (86.2)		
5	rs2019727		T/T	T/A	A/A		T	A		
		Cases	8 (0.8)	167 (16.5)	837 (82.7)	0.94	183 (9.0)	1841 (91.0)	0.07	1.03 (0.83-1.26)
		Controls	10 (0.8)	191 (16.0)	995 (83.2)		211 (8.8)	2181 (91.2)		
6	rs10733086		A/A	A/T	T/T		A	T		
		Cases	15 (1.5)	161 (15.9)	836 (82.6)	0.03	191 (9.4)	1833 (90.6)	0.008	1.34 (1.08-1.66)
		Controls	8 (0.7)	157 (13.1)	1031 (86.2)		173 (7.2)	2219 (92.8)		
7	rs10737680		C/C	C/A	A/A		C	A		
		Cases	172 (17.0)	512 (50.6)	328 (32.4)	0.96	856 (42.3)	1168 (57.7)	0.87	1.00 (0.90-1.14)
		Controls	204 (17.1)	598 (50.0)	394 (32.9)		1006 (42.1)	1386 (57.9)		
8	rs1410996		T/T	T/C	C/C		T	C		
		Cases	167 (16.5)	515 (50.9)	330 (32.6)	0.68	849 (41.9)	1175 (58.1)	0.48	1.04 (0.93-1.18)
		Controls	193 (16.1)	592 (49.5)	411 (34.4)		978 (40.9)	1414 (59.1)		
9	rs11582939		T/T	T/C	C/C		T	C		
		Cases	228 (22.5)	513 (50.7)	271 (26.8)	0.09	969 (47.9)	1055 (52.1)	0.05	0.89 (0.79-1.00)
		Controls	293 (24.5)	630 (52.7)	273 (22.8)		1216 (50.8)	1176 (49.2)		
11	rs426736		C/C	C/T	T/T		C	T		
		Cases	218 (21.5)	521 (51.5)	273 (27.0)	0.04	957 (47.3)	1067 (52.7)	0.03	0.88 (0.78-0.99)
		Controls	313 (26.2)	581 (48.6)	302 (25.3)		1207 (50.5)	1185 (49.5)		

Note: [a] *P* values were presented after Bonferroni correction
Significance was presented in bold

Table DS6 Sliding window haplotype analysis covering 10 *CFH* variants in stage 1 samples

	SNP1	SNP2	SNP3	SNP4	SNP5	SNP6	SNP7	SNP8	SNP9	SNP11
2 SNPs	WIN1	WIN2	WIN3	WIN4	WIN5	WIN6	WIN7	WIN8	WIN9	
P-value	3.0E-04	2.5E-05	4.8E-04	1.4E-02	6.4E-02	4.6E-03	6.5E-01	4.1E-02	6.8E-08	
3 SNPs	WIN10	WIN11	WIN12	WIN13	WIN14	WIN15	WIN16	WIN17		
P-value	3.2E-05	2.1E-04	1.2E-04	3.9E-04	2.0E-02	3.4E-03	6.9E-03	5.9E-07		
4 SNPs	WIN18	WIN19	WIN20	WIN21	WIN22	WIN23	WIN24			
P-value	1.2E-04	3.4E-04	4.2E-04	4.2E-04	1.6E-02	2.0E-03	1.4E-07			
5 SNPs	WIN25	WIN26	WIN27	WIN28	WIN29	WIN30				
P-value	1.0E-03	1.2E-03	3.9E-04	3.0E-04	7.5E-03	1.1E-07				
6 SNPs	WIN31	WIN32	WIN33	WIN34	WIN35					
P-value	1.3E-03	1.2E-03	2.7E-04	7.3E-04	3.7E-06					
7 SNPs	WIN36	WIN37	WIN38	WIN39						
P-value	1.1E-02	8.7E-04	4.3E-04	8.8E-08						
8 SNPs	WIN40	WIN41	WIN42							
P-value	1.2E-02	9.9E-04	9.1E-08							
9 SNPs	WIN43	WIN44								
P-value	2.4E-03	3.2E-07								
10 SNPs	WIN45									
P-value	2.5E-07									

Fig. DS1 Ct values of *GAPDH* between MDD patients and controls. Ct values representing the expression levels of the *GAPDH* gene in human whole blood samples. MDD, major depressive disorder; CTL, controls; ns, no significance

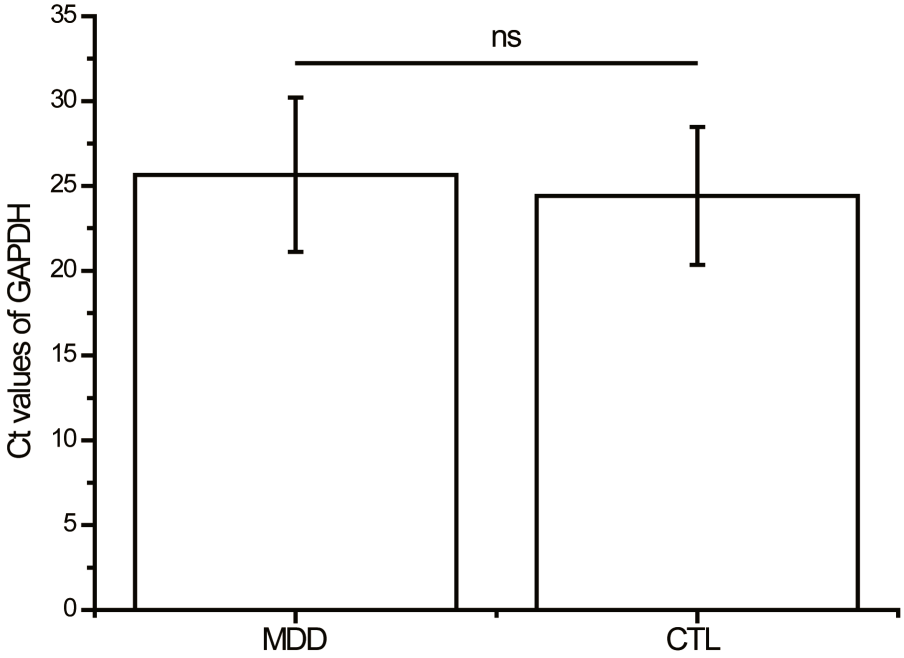

Fig. DS2 Linkage disequilibrium plot consisting of 10 SNPs at the *CFH* gene and its region plot. Pairwise linkage disequilibrium (LD) was computed for all possible combinations of the 10 SNPs using the values of D' and r^2. The individual square showed the 100 × D' (or r^2) value for each SNP pair. Rs460184 was not included due to the deviation from HWE.