Supplemental Information

Table S1. Genotype counts and p-values of the tested SNPs in our samples.

Sample	SNP ID	Position	Genotype	Genotype Counts		p-value	p-value
				Cases	Controls	(nominal)	(corrected)
Yuxi	rs1021042	185453158	GG/GC/CC	33/207/245	26/259/409	**4.0×10^{-3}**	**0.020**
sample	rs11888068	185460295	TT/GT/GG	84/256/150	156/334/204	**0.080**	**0.20**
	rs13026173	185460842	CC/GC/GG	32/214/250	29/266/399	**0.030**	**0.090**
	rs10497655	185462041	CC/CT/TT	109/250/134	172/331/191	**0.49**	**0.94**
	rs359895	185463185	AA/AT/TT	12/133/354	34/237/423	**7.0×10^{-4}**	**2.0×10^{-3}**
	rs1344706	185778428	GG/GT/TT	119/244/125	173/344/177	**0.98**	**1.0**
Kunming	rs1021042	185453158	GG/GC/CC	35/175/163	29/234/311	**1.0×10^{-3}**	**3.0×10^{-3}**
sample	rs359895	185463185	AA/AT/TT	13/112/275	24/219/364	**0.020**	**0.030**
	rs1344706	185778428	GG/GT/TT	88/227/88	137/311/156	**0.26**	**0.60**
Combined	rs1021042	185453158	GG/GC/CC	68/382/408	55/493/720	**7.7×10^{-6}**	**1.8×10^{-5}**
sample	rs359895	185463185	AA/AT/TT	25/245/629	58/456/787	**2.1×10^{-5}**	**2.7×10^{-5}**
	rs1344706	185778428	GG/GT/TT	207/471/213	310/655/333	**0.51**	**0.91**

Note:

Significant p-values ($p<0.05$) were marked in bold and underlined.

Table S2. The result of meta-analyses for rs1344706 in Han Chinese samples

samples(*N* cases/*N* controls)	T-allele frequency in Controls	p-value	OR	95%CI
O'Donovan *et al.*(996/1015)[1]	0.514	0.166	1.06	0.94-1.20
Steinberg *et al.*(439/446)[2]	0.546	0.62	0.95	0.79-1.15
Zhang *et al.*(566/574)[3]	0.457	0.00083	1.32	1.12-1.56
Yuxi sample(488/694)*	0.503	0.876	1.01	0.86-1.19
Kunming sample(403/604)*	0.516	0.489	0.94	0.79-1.12
All samples(2892/3333)	0.507	0.38	1.05	0.94-1.18

Abbreviations: OR, odds ratio; CI, confidence interval.

Test of heterogeneity: χ^2=10.43, df= 4, p-value=0.03.

The result for the combined samples (p=0.38, Z=0.88) was assessed using the Mantel-Haenszel method with the random-effects model.

*Association of rs1344706 with schizophrenia in Yuxi and Kunming sample were genotyped in this study.

Table S3. The result of meta-analyses for rs1344706 in Han Chinese samples when excluding the samples used in Zhang *et al.*

samples(*N* cases/*N* controls)	T-allele frequency in Controls	p-value	OR	95%CI
O'Donovan *et al.*(996/1015)[1]	0.514	0.166	1.06	0.94-1.20
Steinberg *et al.*(439/446)[2]	0.546	0.62	0.95	0.79-1.15
Yuxi sample(488/694)*	0.503	0.876	1.01	0.86-1.19
Kunming sample(403/604)*	0.516	0.489	0.94	0.79-1.12
All samples(2326/2759)	0.517	0.87	1.01	0.93-1.09

Abbreviations: OR, odds ratio; CI, confidence interval.

Test of heterogeneity: χ^2=1.72, df= 3, p-value=0.63.

The result for the combined samples (p=0.87, Z=0.16) was assessed using the Mantel-Haenszel method with the fixed-effects model.

*Association of rs1344706 with schizophrenia in Yuxi and Kunming sample were genotyped in this study.

Table S4. The list of 24 randomly selected SNPs for population stratification analysis

SNP	Chromosome	SNP	Chromosome
rs5177	1	rs4688043	3
rs2297660	1	rs3828611	5
rs2297657	1	rs4704591	5
rs1344706	2	rs362719	7
rs1021042	2	rs6951875	7
rs359895	2	rs2247776	7
rs7597593	2	rs7341475	7
rs3971790	2	rs727709	7
rs3755557	3	rs885995	7
rs6782799	3	rs2874941	8
rs7431209	3	rs2073665	8
rs16830594	3	rs1569198	10

References:

1. O'Donovan MC, Craddock N, Norton N, Williams H, Peirce T, Moskvina V, Nikolov I, Hamshere M, Carroll L, Georgieva L, Dwyer S, Holmans P, Marchini JL, Spencer CC, Howie B, Leung HT, Hartmann AM, Moller HJ, Morris DW, Shi Y, Feng G, Hoffmann P, Propping P, Vasilescu C, Maier W, Rietschel M, Zammit S, Schumacher J, Quinn EM, Schulze TG, Williams NM, Giegling I, Iwata N, Ikeda M, Darvasi A, Shifman S, He L, Duan J, Sanders AR, Levinson DF, Gejman PV, Cichon S, Nothen MM, Gill M, Corvin A, Rujescu D, Kirov G, Owen MJ, Buccola NG, Mowry BJ, Freedman R, Amin F, Black DW, Silverman JM, Byerley WF, Cloninger CR: Identification of loci associated with schizophrenia by genome-wide association and follow-up. Nat Genet 2008; 40:1053-1055
2. Steinberg S, Mors O, Borglum AD, Gustafsson O, Werge T, Mortensen PB, Andreassen OA, Sigurdsson E, Thorgeirsson TE, Bottcher Y, Olason P, Ophoff RA, Cichon S, Gudjonsdottir IH, Pietilainen OP, Nyegaard M, Tuulio-Henriksson A, Ingason A, Hansen T, Athanasiu L, Suvisaari J, Lonnqvist J, Paunio T, Hartmann A, Jurgens G, Nordentoft M, Hougaard D, Norgaard-Pedersen B, Breuer R, Moller HJ, Giegling I, Glenthoj B, Rasmussen HB, Mattheisen M, Bitter I, Rethelyi JM, Sigmundsson T, Fossdal R, Thorsteinsdottir U, Ruggeri M, Tosato S, Strengman E, Kiemeney LA, Melle I, Djurovic S, Abramova L, Kaleda V, Walshe M, Bramon E, Vassos E, Li T, Fraser G, Walker N, Toulopoulou T, Yoon J, Freimer NB, Cantor RM, Murray R, Kong A, Golimbet V, Jonsson EG, Terenius L, Agartz I, Petursson H, Nothen MM, Rietschel M, Peltonen L, Rujescu D, Collier DA, Stefansson H, St Clair D, Stefansson K: Expanding the range of ZNF804A variants conferring risk of psychosis. Mol Psychiatry 2011; 16:59-66
3. Zhang R, Lu SM, Qiu C, Liu XG, Gao CG, Guo TW, Valenzuela RK, Deng HW, Ma J: Population-based and family-based association studies of ZNF804A locus and schizophrenia. Mol Psychiatry 2011; 16:360-361

Figure S1. The LD map of the ZNF804A promoter SNPs downloaded from HapMap database (CHB). The marked SNPs are used in our study. The linkage disequilibrium (LD) of the tested SNPs was calculated using the r^2 algorithm by the Haploview program.

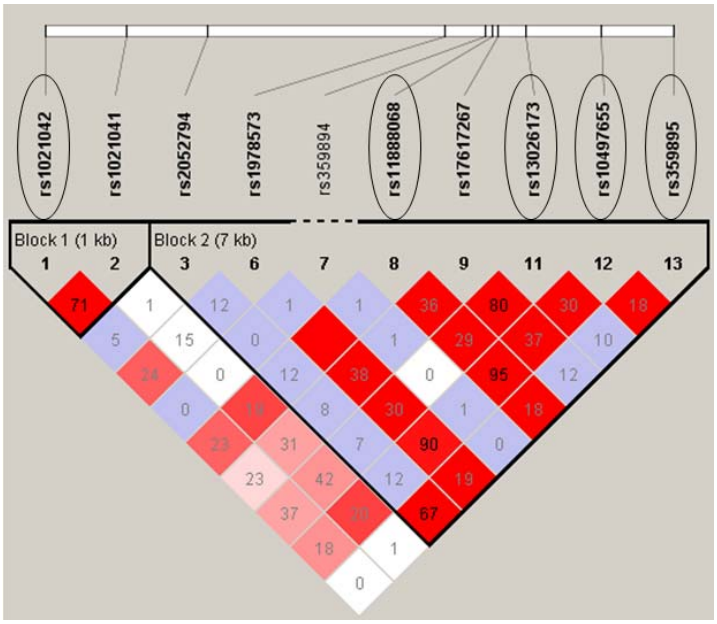


Figure S2. The LD map of ZNF804A promoter region in major populations downloaded from HapMap database. The linkage disequilibrium (LD) of the tested SNPs was calculated using the r^2 algorithm by the Haploview program.

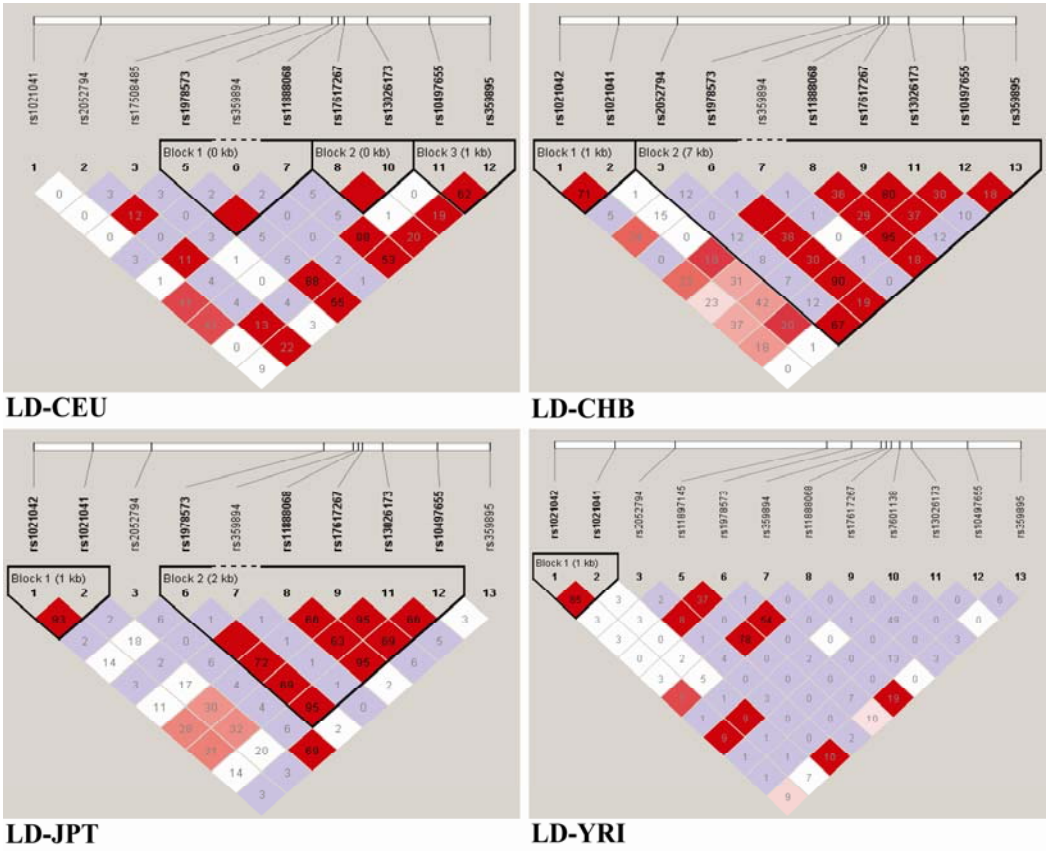
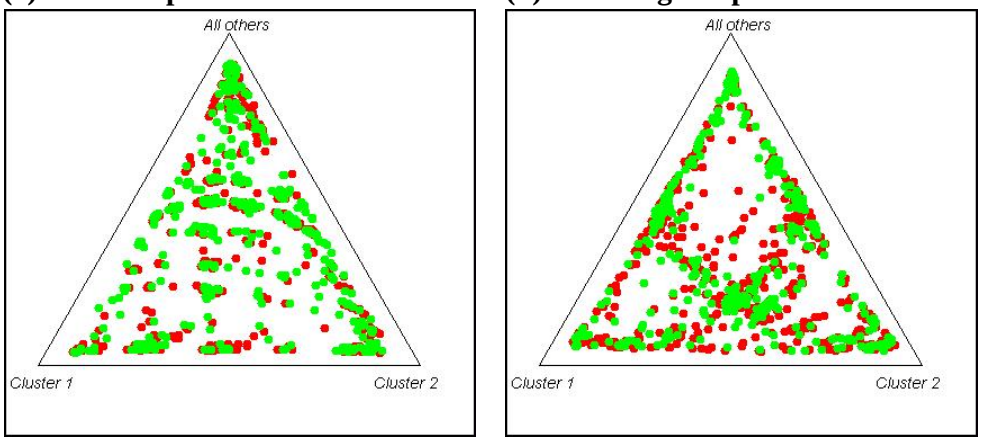


Figure S3. The result of population stratification analysis in Yuxi and Kunming samples. **(a)** Triangle plot for Yuxi sample. **(b)** Triangle plot for Kunming sample. red: controls; green: cases.

(a) Yuxi sample **(b) Kunming sample**



Note: To avoid false positive associations caused by population stratification, we carried out population stratification analysis in our Yuxi and Kunming samples, by using genotyping data of 24 randomly selected SNPs (Table S4), whose genotype distributions were all in Hardy-Weinberg equilibrium in our samples. The Structure software (version 2.3.3) was used. We applied admixture model and independent allelic frequency model and ran from K=2 to K=10, which means the number of potential classification of tested samples, and we showed the triangle plot when K=3 (Figure S3), which is the suggested number of inferring clusters for triangle plots. For all Structure runs, we set the parameters with a burn-in of 10,000 iterations and 10,000 follow-on iterations.