Appendix 1 to Yin X, Wineinger NE, Wang K, et al. Common susceptibility variants are shared between schizophrenia and psoriasis in the Han Chinese population. *J Psychiatry Neurosci* 2016.

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Common susceptibility variants are shared between schizophrenia and psoriasis in the Han Chinese population

Xianyong Yin, Nathan E. Wineinger, Kai Wang, Weihua Yue, Nina Norgren, Ling Wang, Weiyi Yao, Xiaoyun Jiang, Bo Wu, Yong Cui, Changbing Shen, Hui Cheng, Fusheng Zhou, Gang Chen, Xianbo Zuo, Xiaodong Zheng, Xing Fan, Hongyan Wang, Lifang Wang, Jimmy Lee, Max Lam, E Shyong Tai, Zheng Zhang, Qiong Huang, Liangdan Sun, Jinhua Xu, Sen Yang, Kirk C. Wilhelmsen, Jianjun Liu, Nicholas J. Schork and Xuejun Zhang

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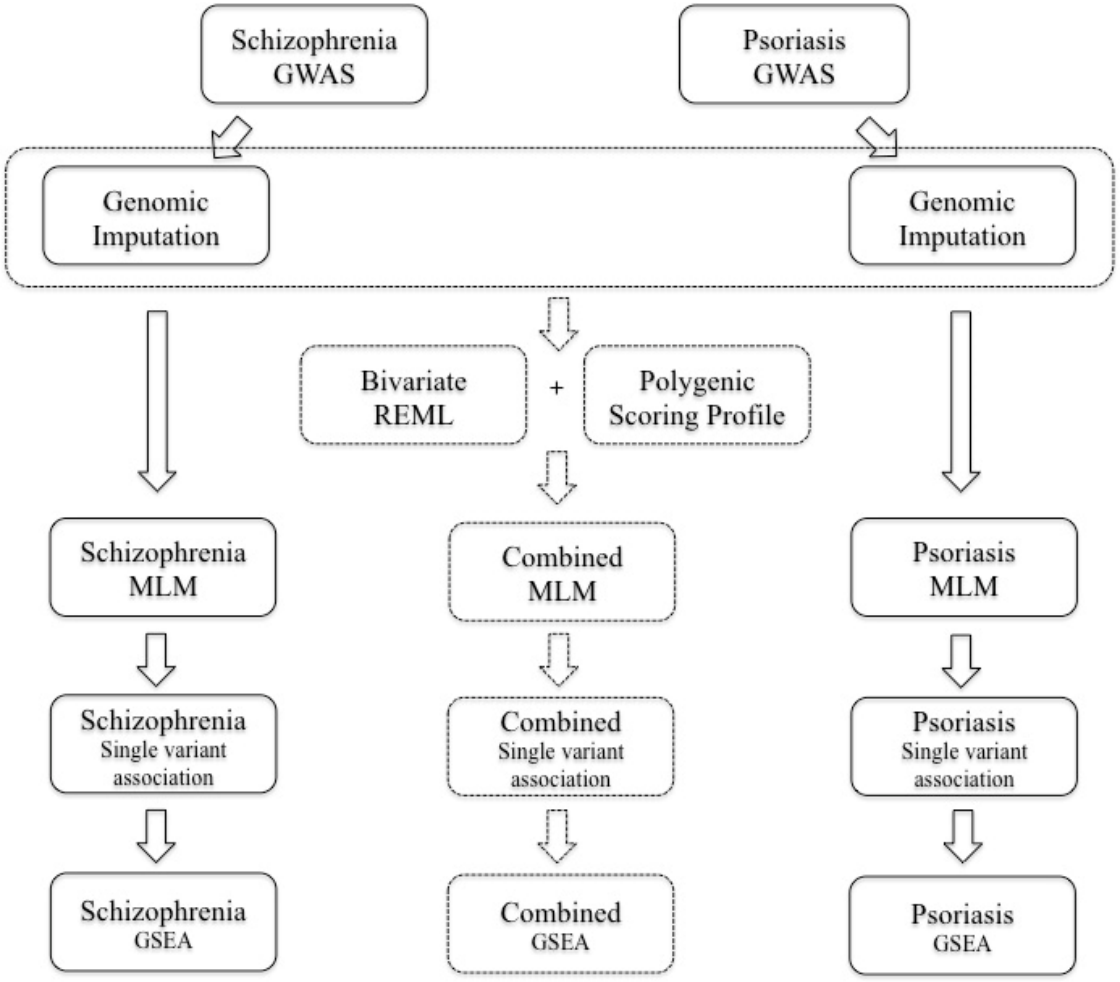
Fig. S1 The research strategy of this study



We implemented single marker, marker-based co-heritability and gene set enrichment analyses in the schizophrenia cohort, psoriasis cohort and the combined cohort respectively. REML: Restricted Maximum Likelihood analysis; MLM: mixed linear model analysis; GSEA: Gene Set Enrichment Analysis.

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Fig. S2 The lambda selection of LASSO model in HLA region in the combined cohort

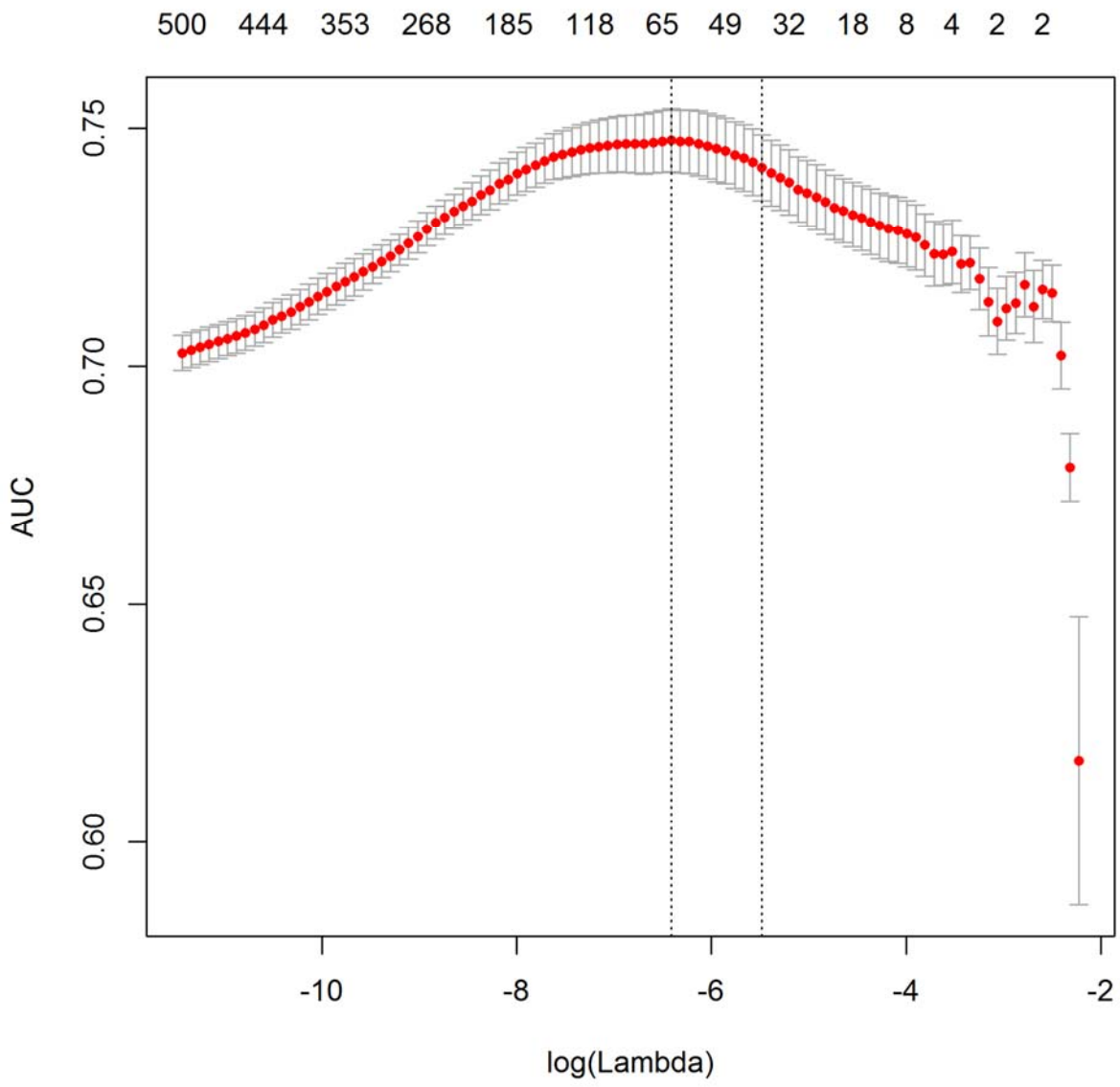

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Fig. S3 Principal component plot of the combined cohort

All 3,494 GWAS samples plotted on the first two principal components, colored by phenotypic status.

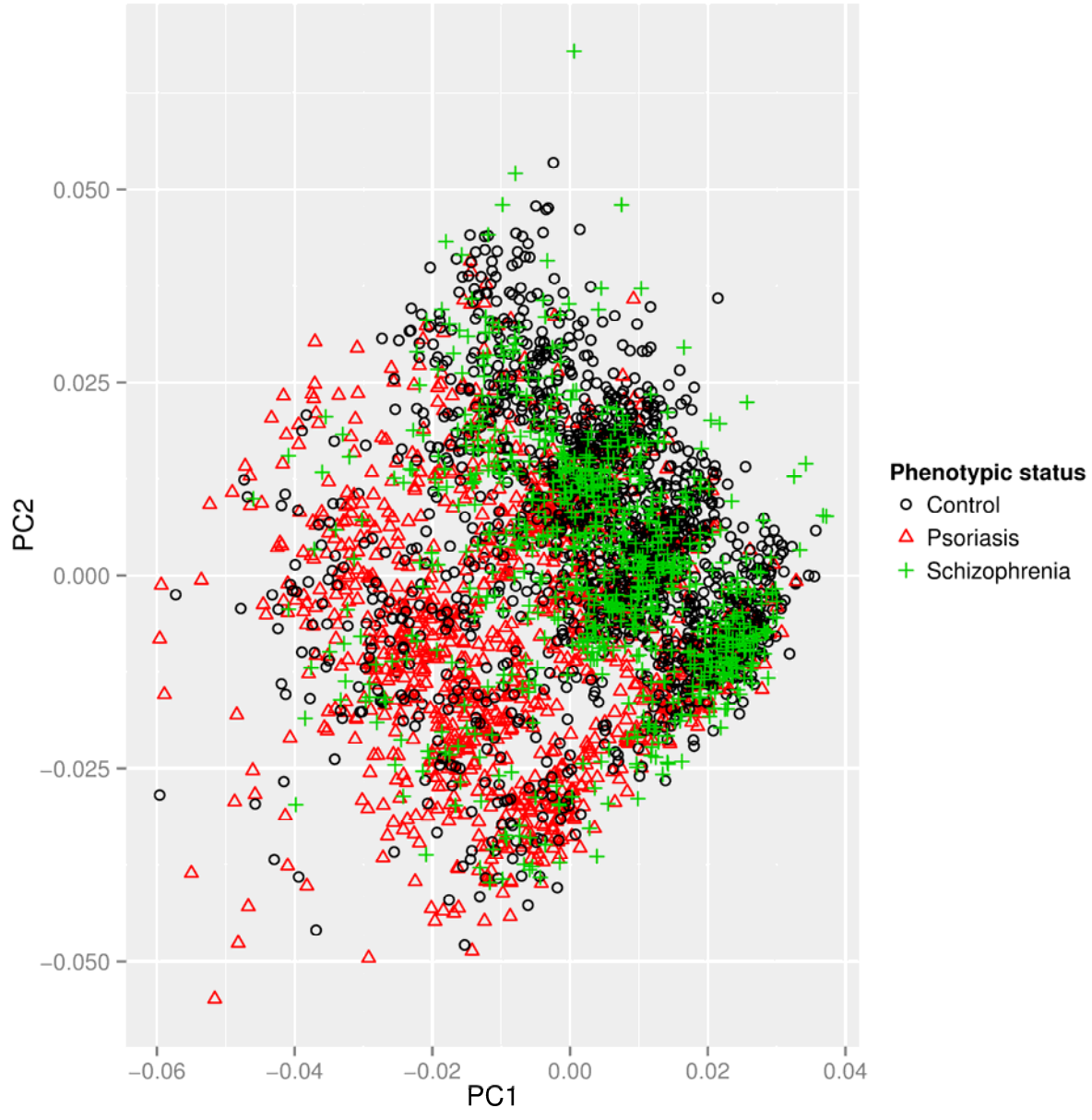

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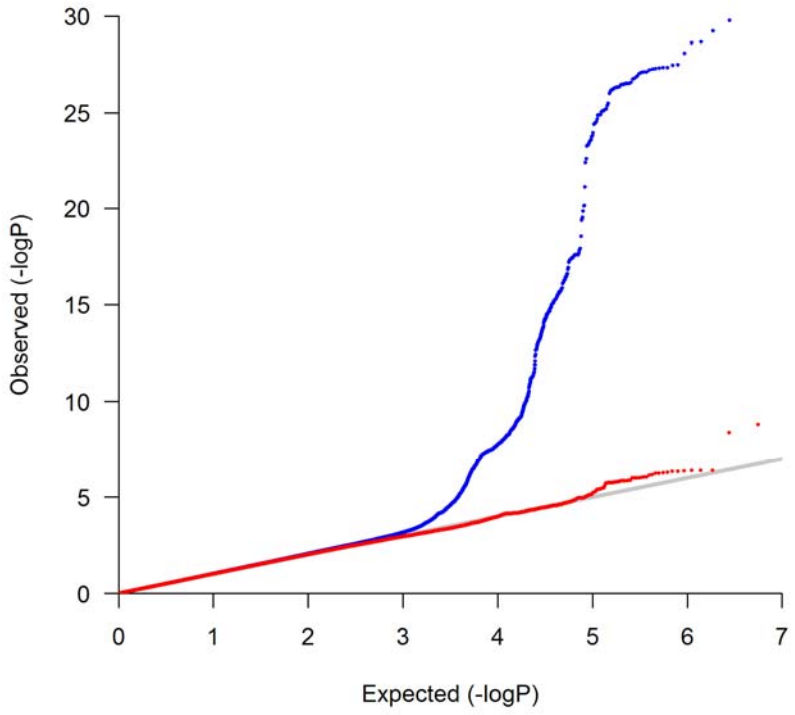
Fig. S4 Quantile-quantile plot of single variant test in the combined dataset



The blue curve shows the distribution of association p value for all SNPs passed quality control in our combined cohort, while the red one without SNPs in HLA region (Chr6: 29,700kb – 33,300kb).

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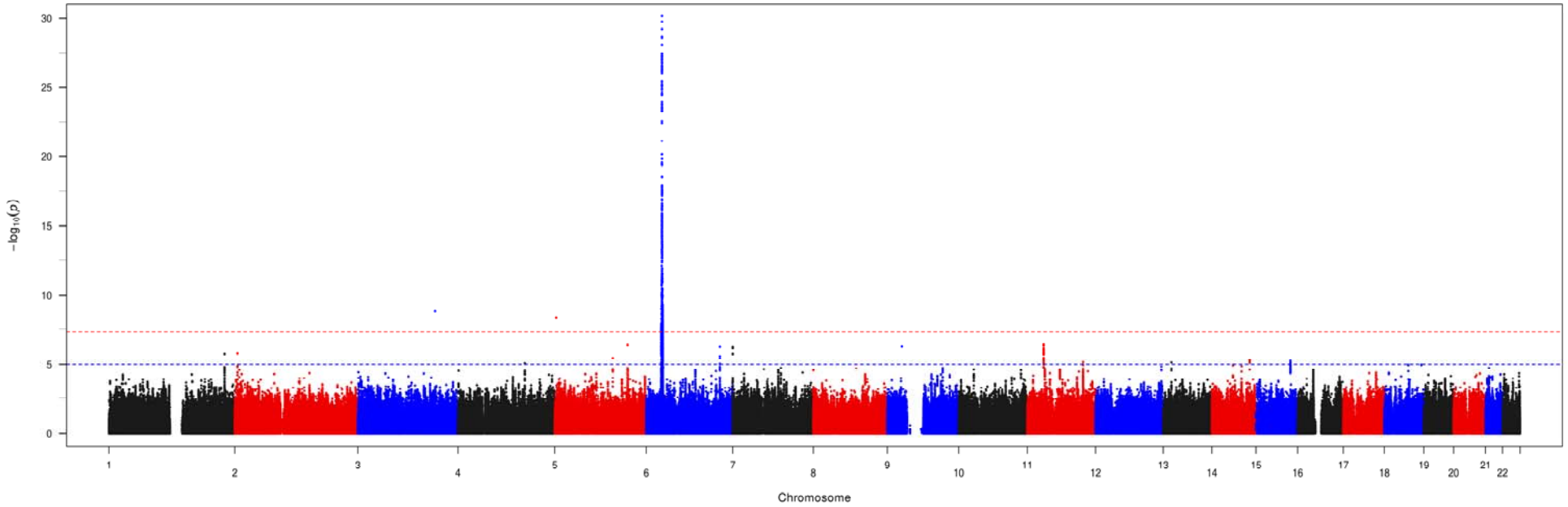
Fig. S5a Manhattan plot of single variant test in the combined dataset



The blue dash line shows suggestive association p value 10^{-5}, the red dash line shows genome wide significant association p value: $5\square10^{-8}$. The $-\log_{10}$ (P value) is shown.

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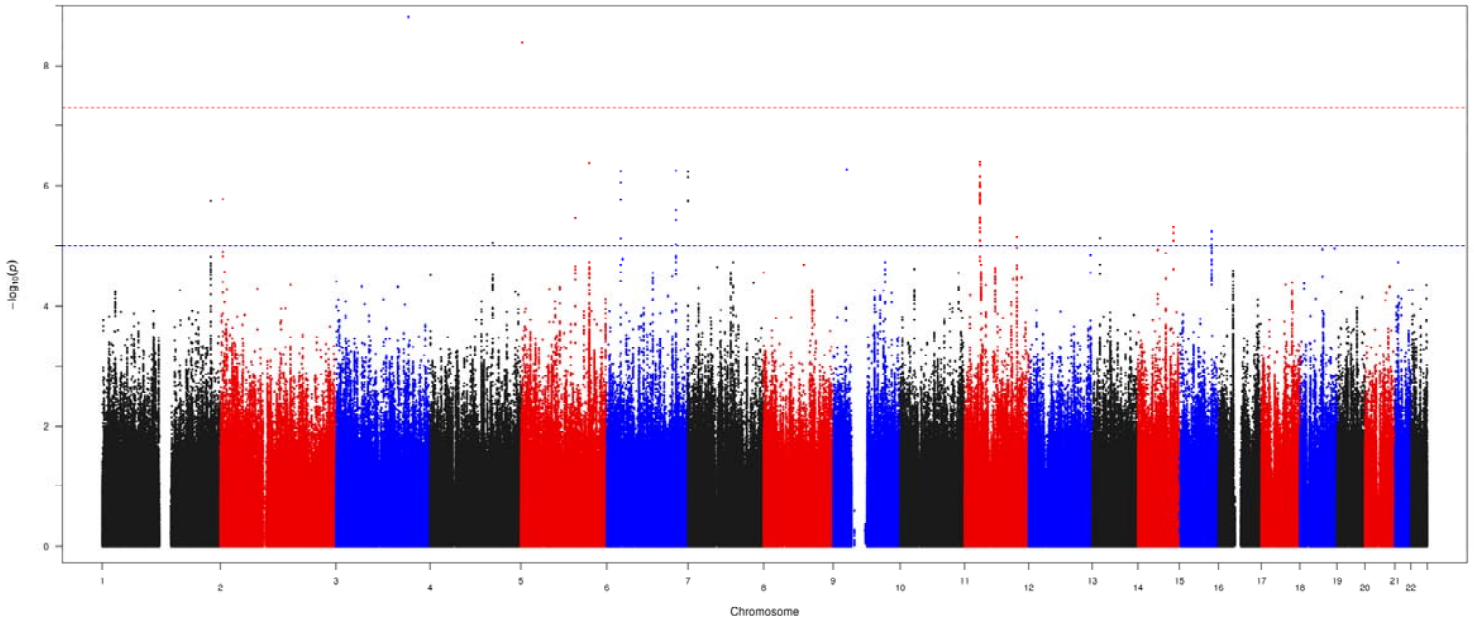
Fig. S5b Manhattan plot of single variant test in the combined dataset without HLA region



The blue dash line shows suggestive association p value 10^{-5}, the red dash line shows genome wide significant association p value: 5×10^{-8}. The $-\log_{10}$ (P value) is shown. The SNPs in HLA region (Chr6:29,700kb – 33,300kb) were excluded in this analysis.

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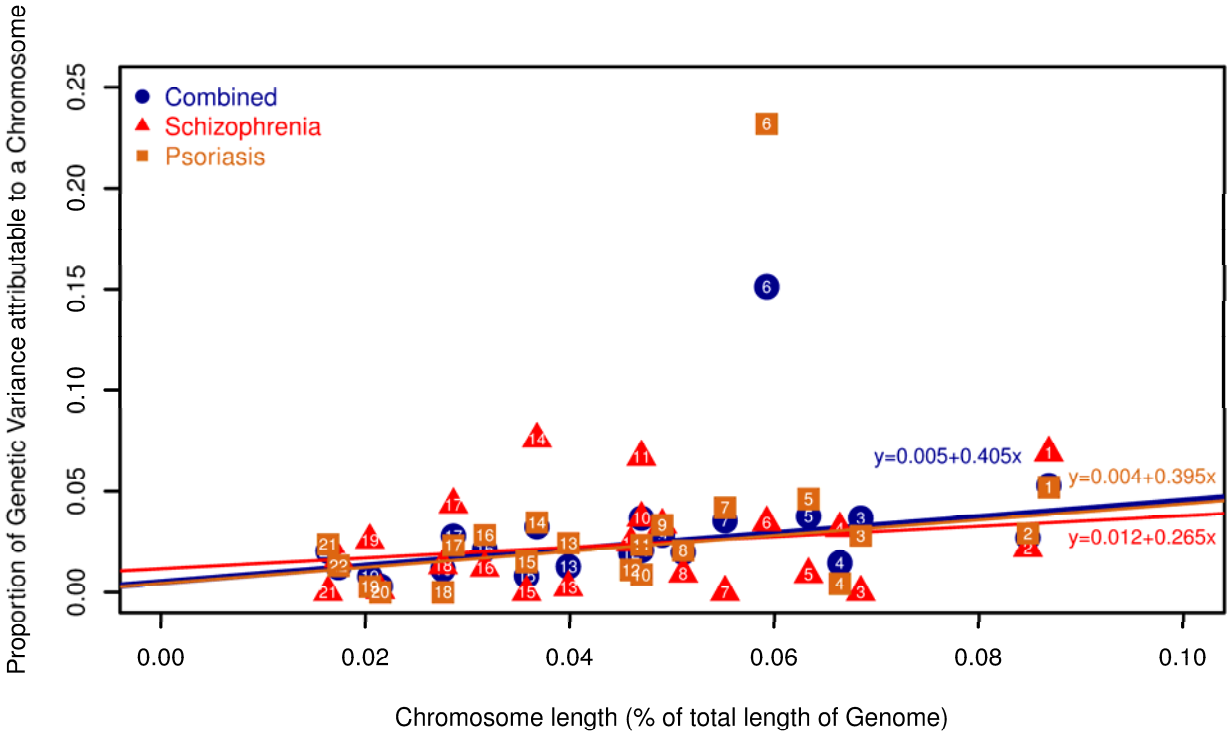
Fig. S6 Genomic partitioning explained by each chromosome in separate analysis in three cohorts



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The x axis denotes the length proportion of each individual chromosome in the whole genome. The y axis denotes the proportion of total genetic variation. The results in schizophrenia, psoriasis and combined cohorts are depicted in red triangles, brown squares and blue circles respectively. The numbers in the circles/squares/triangles are the chromosome numbers. The linear correlation between the chromosome length proportion and proportion of total genetic variation is described using three equations in different colors (red: schizophrenia; brown: psoriasis; blue: combined phenotype).

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Fig. S7a Genomic partitioning explained by MAF Bin in separate analysis in three cohorts

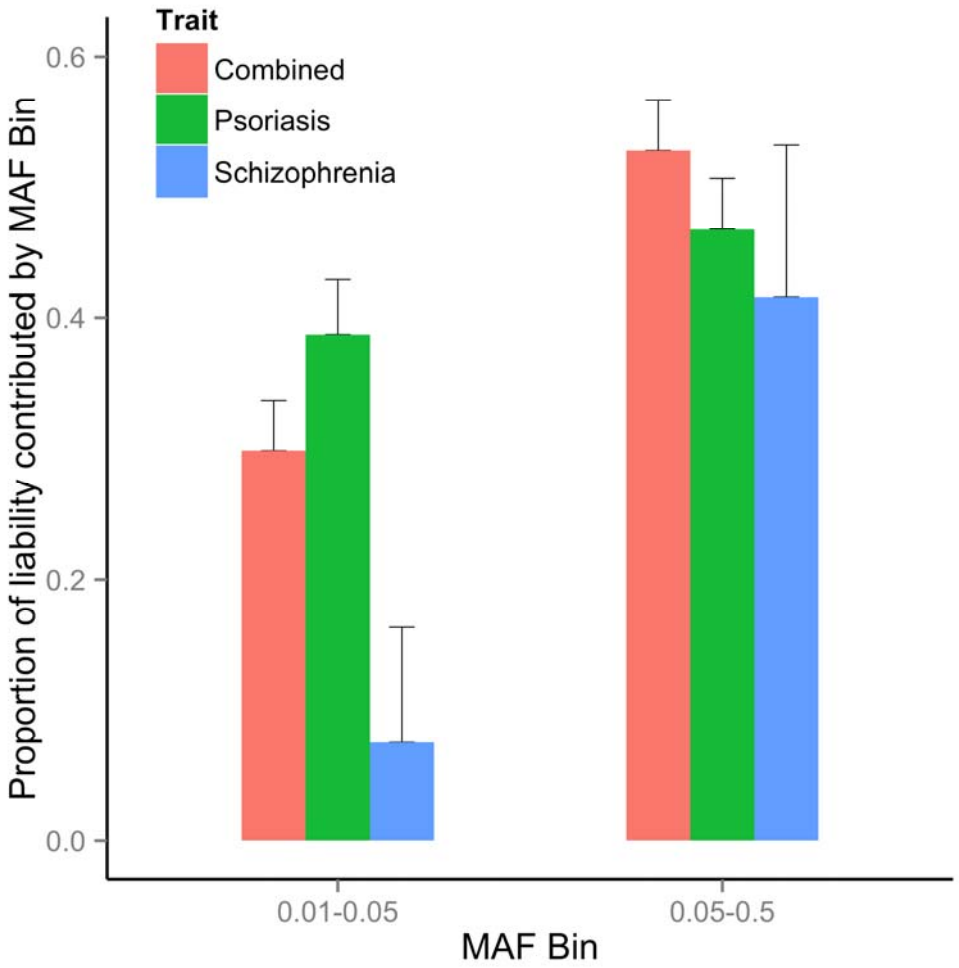

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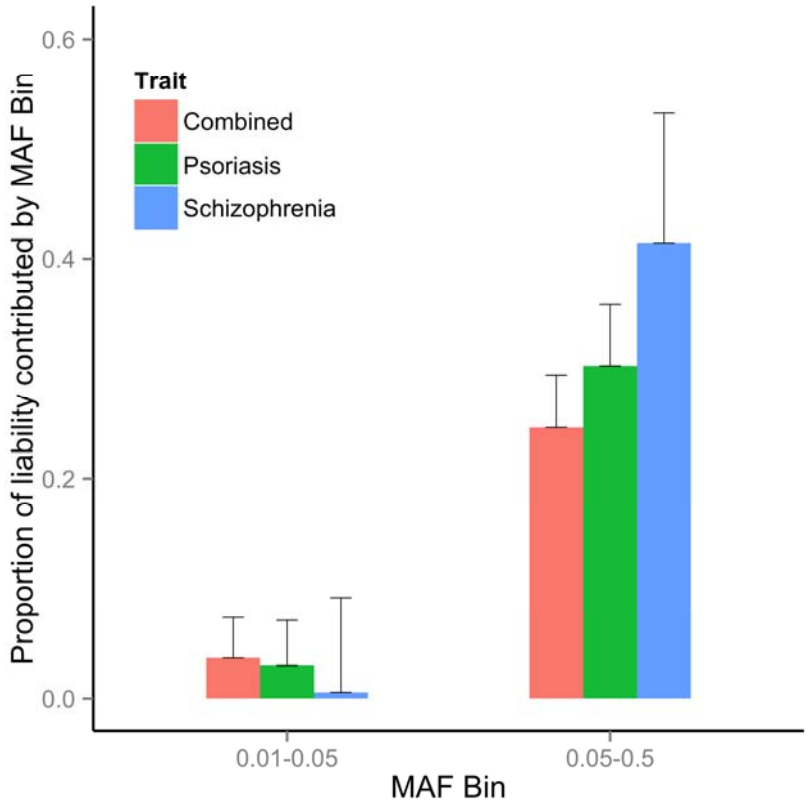
Fig. S7b The Distribution of genetic variance explained by MAF Bin in joint analysis



Notes: In these analysis, none kinds of prevalence were included. So the y axis represented the proportion of genetic variance explained. Error bar was plotted in black and only the high boundary was plotted out.

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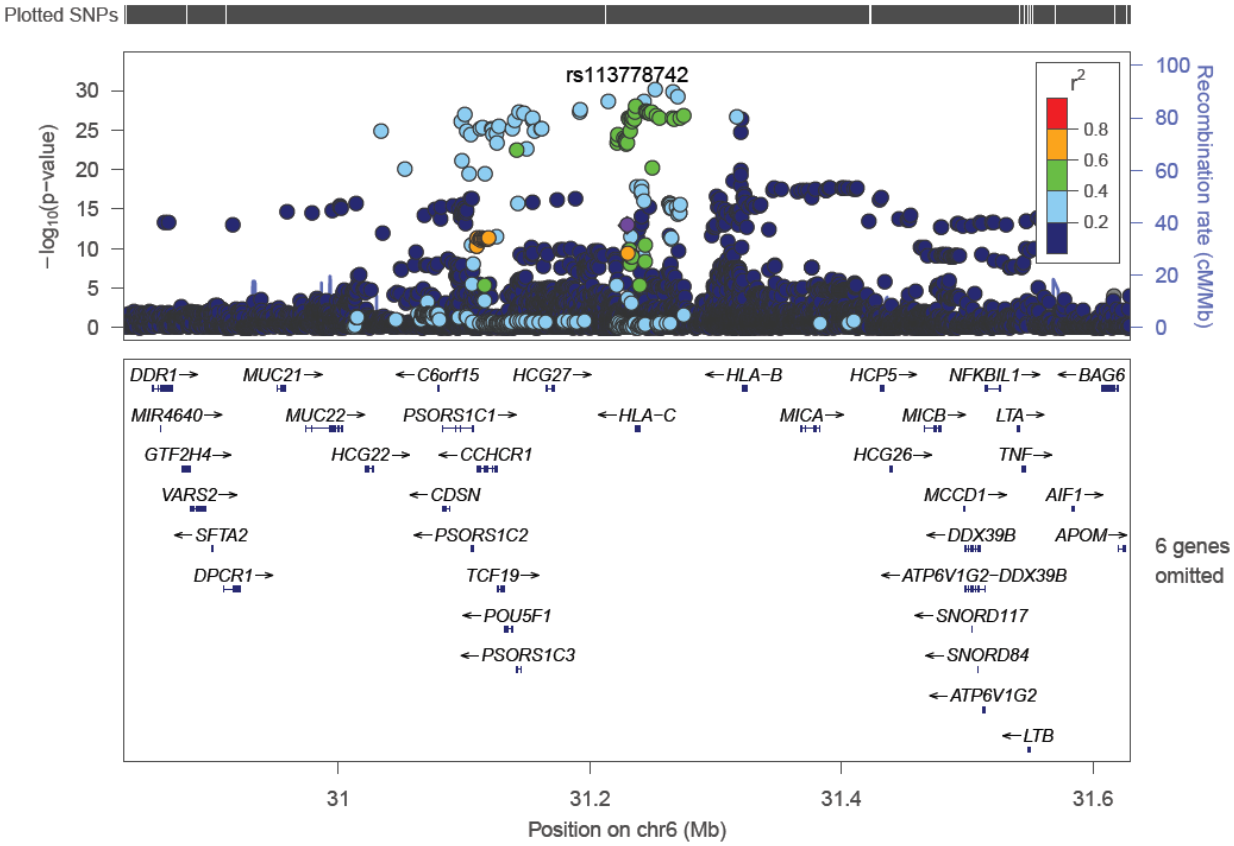
Fig. S8a Annotated regional Association plot of rs113778742 in the combined cohort



The relative location of annotated genes and the direction of transcription are shown in the lower portion of the figure, and the chromosomal position is shown on the *x* axis. The blue line shows the recombination rate (estimated from HapMap data of CHB population) across the region (right *y* axis), and the left *y* axis shows the significance of the associations.

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Fig. S8b Annotated regional association plot of rs115328826 in the combined cohort

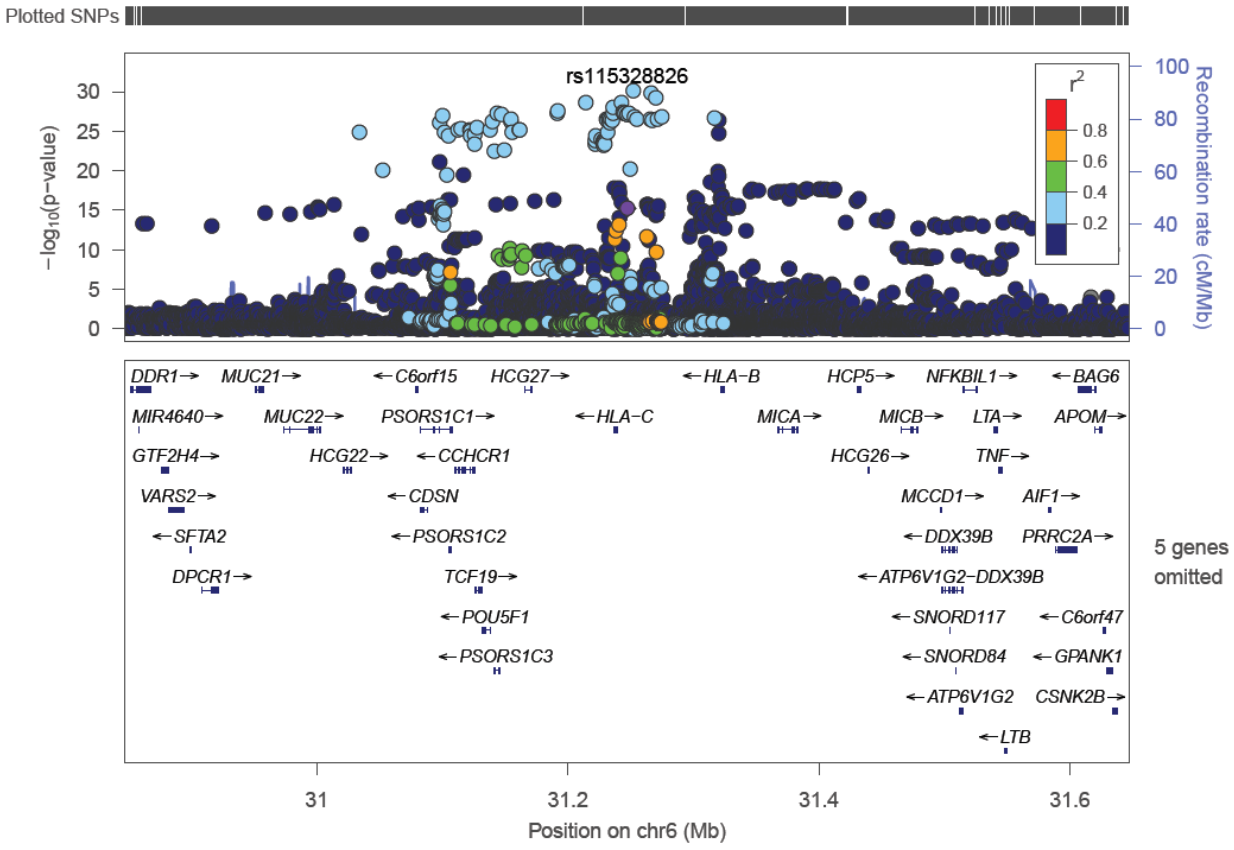

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Fig. S8c Annotated regional association plot of rs116743258 in the combined cohort

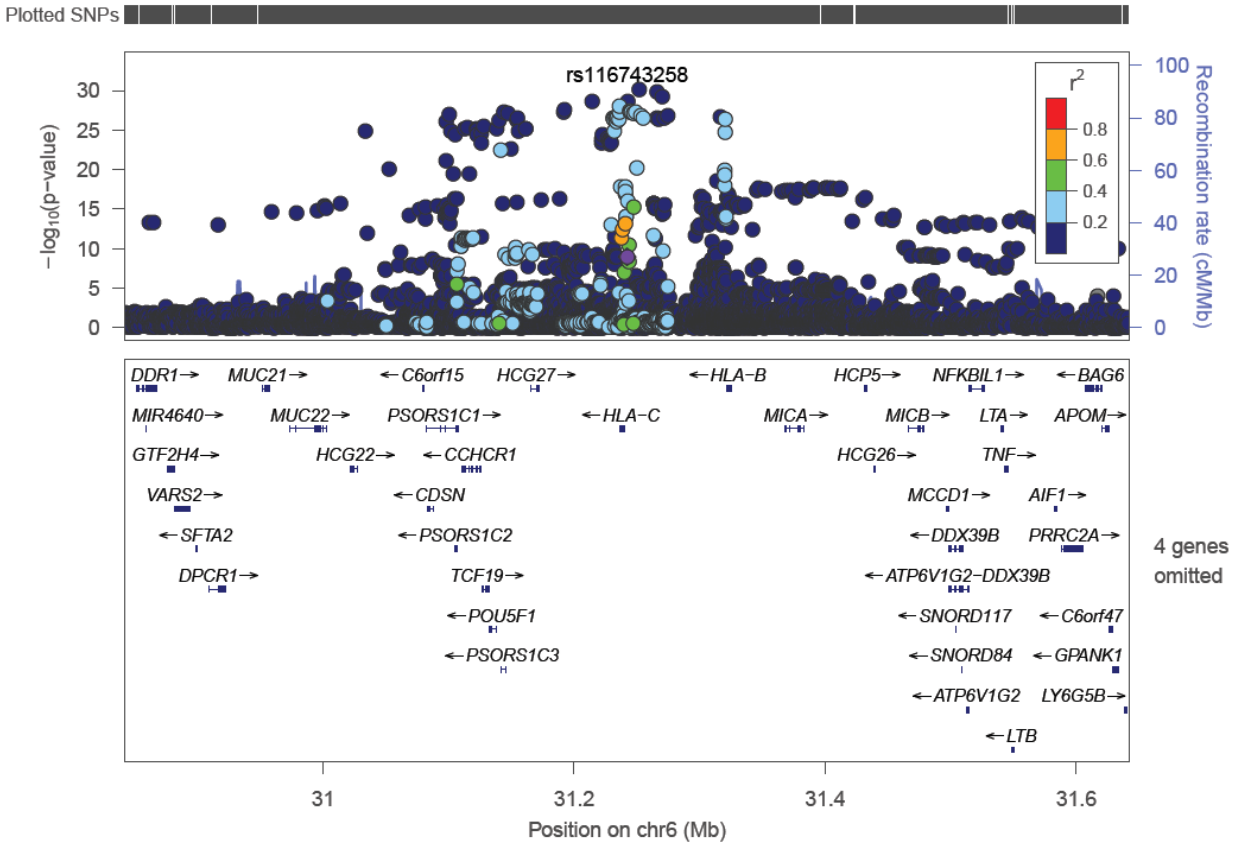

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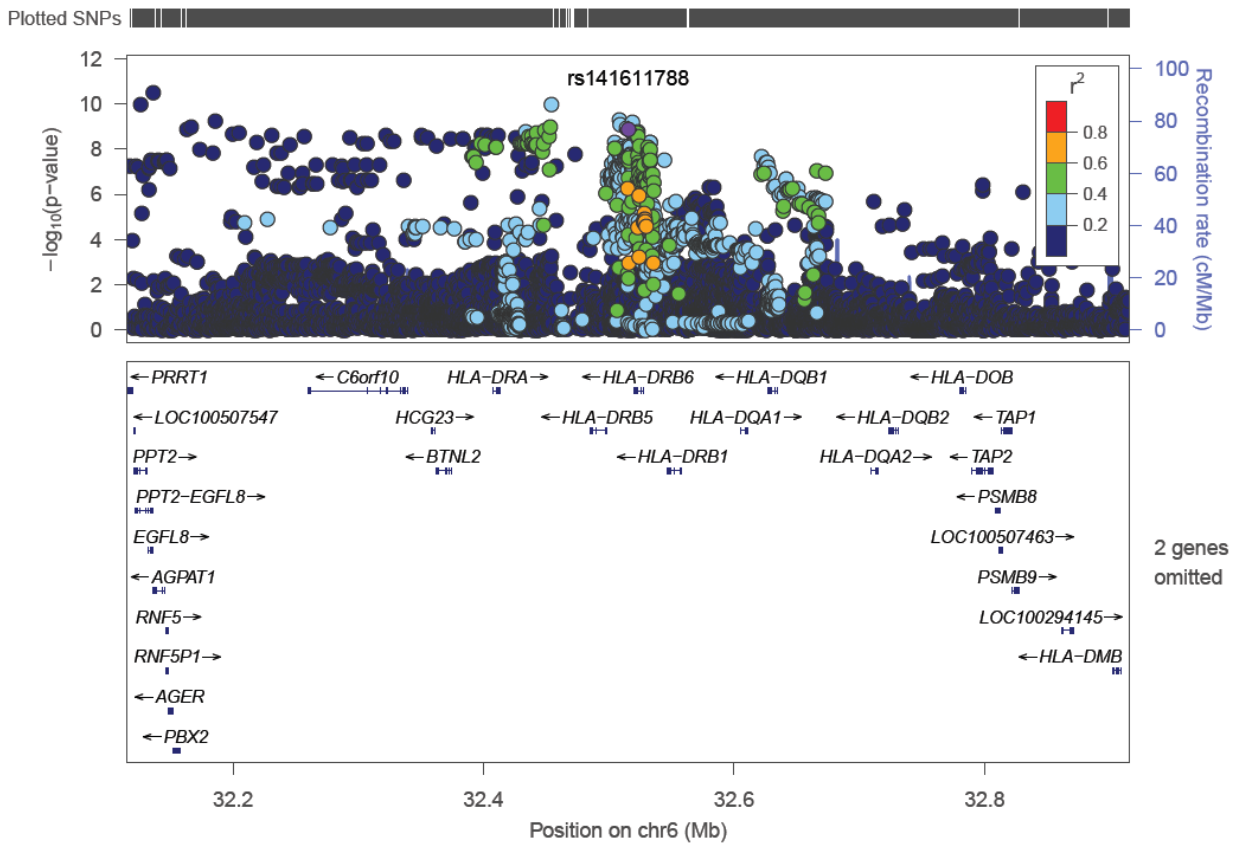
Fig. S8d Annotated regional association plot of rs141611788 in the combined cohort



Appendix 1 to Yin X, Wineinger NE, Wang K, et al. Common susceptibility variants are shared between schizophrenia and psoriasis in the Han Chinese population. *J Psychiatry Neurosci* 2016.

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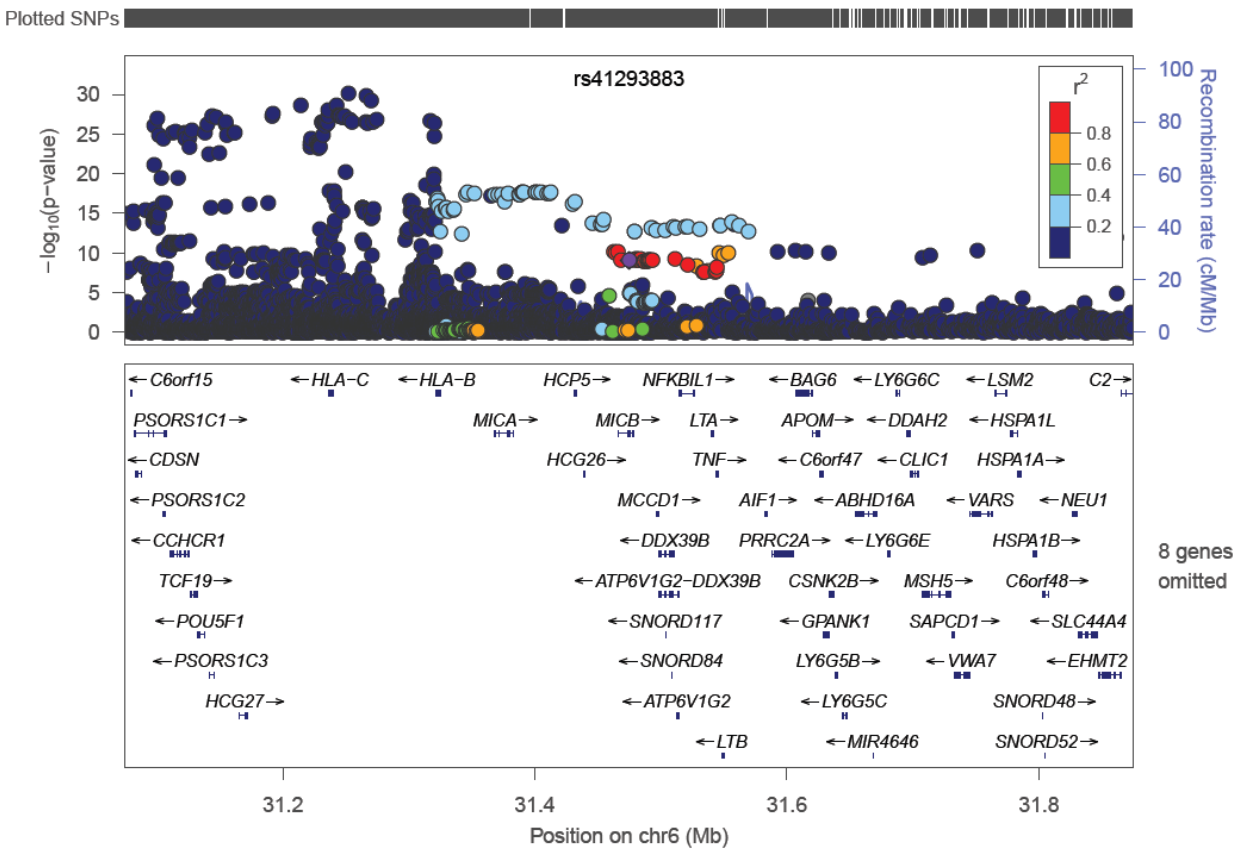
Fig. S8e Annotated regional association plot of rs41293883 in the combined cohort



Appendix 1 to Yin X, Wineinger NE, Wang K, et al. Common susceptibility variants are shared between schizophrenia and psoriasis in the Han Chinese population. *J Psychiatry Neurosci* 2016.

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Table S1 Genomic partitioning result in Schizophrenia samples by MAF Bin

Sample Size	Type	No. of SNPs	MAF	h^2	s.e.
1,276	separate	1,239,647	0.01-0.05	0.07	9.0%
	separate	4,379,725	0.05-0.50	0.42	12.0%
	joint	1,239,647	0.01-0.05	0.01	9.0%
	joint	4,379,725	0.05-0.50	0.41	12.0%

Type: partitioning analysis type, separate: separate analysis; joint: joint analysis. MAF: minor allele frequency. h^2: proportion of liability to schizophrenia. s.e.: standard error.

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Table S2 The genetic variance explained by autosomal variants in combined dataset

Sample Size	No. of autosomal SNPs	Prevalence	h^2	s.e.	P value
3,494	5,604,467	1.47%	0.29	5.0%	2.00E-08

h^2: Proportion of genetic variance explained by autosomal SNPs or proportion of liability to shared phenotype explained by autosomal SNPs. s.e.: standard error.

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Table S3 The Co-heritability between Schizophrenia and Psoriasis in Bivariate Model

schizophrenia	psoriasis	h^2_{sch} (se)	h^2_{pso} (se)	Cov. (s.e.)	$r_{g\ SNP}$(s.e.)	P($r_{g\ SNP}$=0)
1244	2250	0.37 (15.0%)	0.35 (6.0%)	0.03(3.0%)	0.21(20.0%)	0.1

h^2_{Sch}: proportion of liability to schizophrenia. h^2_{Pso}: proportion of liability to psoriasis. r_{gSNP}: SNP correlation. P(r_{gSNP}=0): likelihood test p value when r_{gSNP} fixed at 0. P(r_{gSNP}=1): likelihood test p value when r_{gSNP} fixed at 1. s.e.: standard error.

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Table S4 Bivariate analysis with chromosome exclusion in combined dataset

chr. excluded	Sch h^2 (s.e.)	Pso h^2(s.e.)	$r_{g\ SNP}$(s.e.)	P(r_{gSNP}=0)
1	0.34(14.0%)	0.33(6.0%)	0.18(20.0%)	0.2
2	0.36(14.0%)	0.36(6.0%)	0.25(19.0%)	0.09
3	0.34(14.0%)	0.33(6.0%)	0.16(21.0%)	0.2
4	0.36(14.0%)	0.36(6.0%)	0.23(19.0%)	0.1
5	0.37(14.0%)	0.33(6.0%)	0.21(20.0%)	0.1
6	0.37(14.0%)	0.11(6.0%)	0.26(35.0%)	0.2
7	0.39(14.0%)	0.32(6.0%)	0.26(20.0%)	0.09
8	0.35(14.0%)	0.35(6.0%)	0.27(21.0%)	0.08
9	0.35(14.0%)	0.36(6.0%)	0.19(20.0%)	0.2
10	0.32(14.0%)	0.36(6.0%)	0.19(20.0%)	0.2
11	0.32(14.0%)	0.35(6.0%)	0.14(20.0%)	0.2
12	0.35(14.0%)	0.35(6.0%)	0.22(20.0%)	0.1
13	0.37(14.0%)	0.35(6.0%)	0.22(19.0%)	0.1
14	0.31(14.0%)	0.34(6.0%)	0.24(22.0%)	0.1
15	0.38(14.0%)	0.35(6.0%)	0.18(19.0%)	0.2
16	0.39(14.0%)	0.34(6.0%)	0.19(19.0%)	0.2
17	0.33(14.0%)	0.34(6.0%)	0.22(21.0%)	0.1
18	0.35(14.0%)	0.36(6.0%)	0.21(20.0%)	0.1
19	0.36(14.0%)	0.35(6.0%)	0.21(20.0%)	0.1
20	0.38(14.0%)	0.36(6.0%)	0.20(19.0%)	0.1
21	0.40(14.0%)	0.34(6.0%)	0.18(19.0%)	0.2
22	0.36(14.0%)	0.36(6.0%)	0.20(20.0%)	0.2

chr. excluded: chromosome excluded in the analysis. Sch h^2: proportion of liability to schizophrenia. Pso h^2: proportion of liability to psoriasis. r_{gSNP}: SNP correlation. P(r_{gSNP}=0): likelihood test p value when r_{gSNP} fixed at 0. P(r_{gSNP}=1): likelihood test p value when r_{gSNP} fixed at 1. s.e.: standard error.

Appendix 1 to Yin X, Wineinger NE, Wang K, et al. Common susceptibility variants are shared between schizophrenia and psoriasis in the Han Chinese population. *J Psychiatry Neurosci* 2016.

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Table S5 Genomic partition of liability of HLA region in the combined dataset

sample size	No. of SNPs	Prevalence	h^2	s.e.	P value
3,494	49,332	1.47%	0.07	1.0%	$<10^{-8}$

No. of SNPs: number of SNPs in HLA region. Prevalence means the prevalence setting of the shared phenotype between psoriasis and schizophrenia. h^2: proportion of liability to schizophrenia. s.e.: standard error.

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Table S6 Genomic partition of liability by MAF bin in the combined dataset

Prevalence	Type	MAF	No. of SNPs	h^2	s.e.	P
1.47%	separate	0.01-0.05	1,229,334	0.30	4.0%	$<10^{-8}$
1.47%	separate	0.05-0.50	4,375,366	0.53	4.0%	$<10^{-8}$
1.47%	joint	0.01-0.05	1,229,334	0.04	4.0%	0.2
1.47%	joint	0.05-0.50	4,375,366	0.25	5.0%	

Prevalence means the prevalence setting of the shared phenotype between psoriasis and schizophrenia. Type: partitioning analysis type, separate: separate analysis; joint: joint analysis. MAF: minor allele frequency. h^2: proportion of liability to schizophrenia. s.e.: standard error.

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Table S7: The 12 suggested association results in the combined dataset

CHR	SNP	BP	Gene_symbol	Effect Allele	Combined Dataset		Psoriasis Dataset		Schizophrenia Dataset	
					OR(95%CI)	P	OR(95%CI)	P	OR(95%CI)	P
1	rs78442485	229052124	RHOU	T	0.51(0.38-0.67)	1.77E-06	0.49(0.33-0.72)	3.58E-04	0.62(0.39-0.97)	3.56E-02
2	rs6707203	5303541	SOX11	C	0.66(0.55-0.78)	1.64E-06	0.68(0.54-0.87)	1.79E-03	0.66(0.50-0.87)	2.96E-03
4	rs10776509	131861223	C4orf33	G	1.28(1.15-1.43)	8.77E-06	1.32(1.13-1.54)	4.11E-04	1.22(1.02-1.45)	2.79E-02
5	rs2925180	114676772	CCDC112	T	1.40(1.21-1.61)	3.47E-06	1.46(1.19-1.78)	2.02E-04	1.37(1.09-1.72)	6.76E-03
5	rs79299789	143867204	KCTD16	T	2.50(1.75-3.56)	4.27E-07	2.54(1.53-4.23)	3.22E-04	1.81(1.08-3.06)	2.55E-02
9	rs4879265	28771619	LINGO2	T	1.64(1.35-1.99)	5.30E-07	1.49(1.10-2.00)	9.31E-03	1.77(1.33-2.35)	8.71E-05
11	rs7950535	32548278	EIF3M	C	3.70(2.19-6.25)	9.97E-07	4.08(1.90-8.76)	3.07E-04	2.91(1.37-6.18)	5.45E-03
11	rs2155569	110275001	FDX1	A	0.45(0.32-0.64)	7.12E-06	0.33(0.20-0.55)	1.30E-05	0.49(0.29-0.84)	9.85E-03
13	rs60298977	35345292	NBEA	C	1.34(1.18-1.52_	7.42E-06	1.26(1.05-1.51)	1.22E-02	1.39(1.14-1.70)	1.08E-03
14	rs72692881	94950066	SERPINA12	A	1.27(1.14-1.40)	8.13E-06	1.24(1.07-1.43)	4.37E-03	1.29(1.10-1.51)	2.28E-03
14	rs11160185	94950617	SERPINA12	T	1.27(1.15-1.41)	4.97E-06	1.25(1.08-1.44)	3.32E-03	1.30(1.11-1.53)	1.58E-03
14	rs11626701	94954368	SERPINA12	G	1.27(1.15-1.41)	6.02E-06	1.23(1.07-1.43)	4.99E-03	1.31(1.11-1.54)	1.09E-03

CHR: chromosome; SNP: single nucleotide polymorphism; BP: physical position; OR: odds ratio; 95%CI: 95% confidence interval.

Appendix 1 to Yin X, Wineinger NE, Wang K, et al. Common susceptibility variants are shared between schizophrenia and psoriasis in the Han Chinese population. *J Psychiatry Neurosci* 2016.

DOI: 10.1503/jpn.150210

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Table S8: The summary consistent results with significance of gene enrichment analysis across three datasets

See the Excel spreadsheet in Appendix 2.

Table S9: Regulatory effect of 12 SNPs within HLA region in ENCODE Project

See the Excel spreadsheet in Appendix 2.

Table S10: Regulatory effect of 12 suggested associated SNPs in ENCODE Project

See the Excel spreadsheet in Appendix 2.

Chr: chromosome. Pos.: genomic position. Ref: reference allele. Alt: alternative allele. ASN freq: The allele frequency in 1000 Genomes Project Phase 1 ASN population. GERP cons: conserved regions by GERP tool. SiPhy cons: conserved regions by SiPhy tool. Enhancer histone marks: cell type as enhancer histone marks in. DNAse: cell type as DNAse in. Proteins Bound: Proteins bounds with. Motif change: putative transcription factor binding motifs that are altered by the variant. GENCODE gene: gene implied and position distance away in GENCODE Project. Refseq gene: gene implied and position distance away in UCSC database.

Appendix 1 to Yin X, Wineinger NE, Wang K, et al. Common susceptibility variants are shared between schizophrenia and psoriasis in the Han Chinese population. *J Psychiatry Neurosci* 2016.

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Table S11: The overlapping analysis between schizophrenia and psoriasis in Singapore GWAS datasets

P Threshold	No. of Overlapped	No. of consistent	Proportion	P
P≤0.10	828	591	71.38%	2.20E-16
P≤0.09	684	496	72.51%	2.20E-16
P≤0.08	540	397	73.52%	2.32E-12
P≤0.07	225	159	70.67%	2.45E-10
P≤0.05	211	156	73.94%	1.09E-12
P≤0.03	92	69	75.00%	8.35E-07
P≤0.01	12	8	66.67%	1.90E-01

* **P Threshold**: the P value threshold P for the single variant association in each individual GWAS in Singapore schizophrenia and psoriasi GWAS datasets; **No of Overlapped**: The number of overlapping SNPs between the two validation GWASs by the P value threshold; **No of consistent**: the number of SNPs in each individual GWAS with the consistent effect direction in each bin of SNPs; **Proportion**: the proportion of SNPs with consistent effect in the total overlapped SNPs; **P**: the binomial test P value.

Appendix 1 to Yin X, Wineinger NE, Wang K, et al. Common susceptibility variants are shared between schizophrenia and psoriasis in the Han Chinese population. *J Psychiatry Neurosci* 2016.

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Table S12: The significant variants with consistent effect in the HLA region between schizophrenia and psoriasis in Singapore GWAS datasets

				Psoriasis GWAS		Schizophrenia GWAS	
chr	**SNP**	**BP**	**A1/A2**	**P**	**OR**	**P**	**OR**
6	rs113039233	27430126	T/A	1.45E-02	1.31	4.14E-02	1.55
6	rs185599622	28204376	G/A	9.50E-03	2.08	3.23E-02	1.38
6	rs2844673	30961926	T/A	4.44E-10	1.83	2.39E-02	1.38
6	rs2523897	30993958	A/G	8.51E-10	1.64	3.26E-02	1.51
6	rs189418663	31470107	A/T	4.13E-02	1.38	7.95E-03	1.43
6	rs17576984	32212985	A/T	4.22E-04	1.37	3.71E-02	1.11
6	rs6457796	34828553	C/T	1.60E-02	1.29	1.33E-02	1.77

chr: chromosome; SNP: single nucleotide polymorphism; BP: physical position; A1: the effect allele; A2: the alternative allele; P: the single variant association P value; OR: odds ratio.