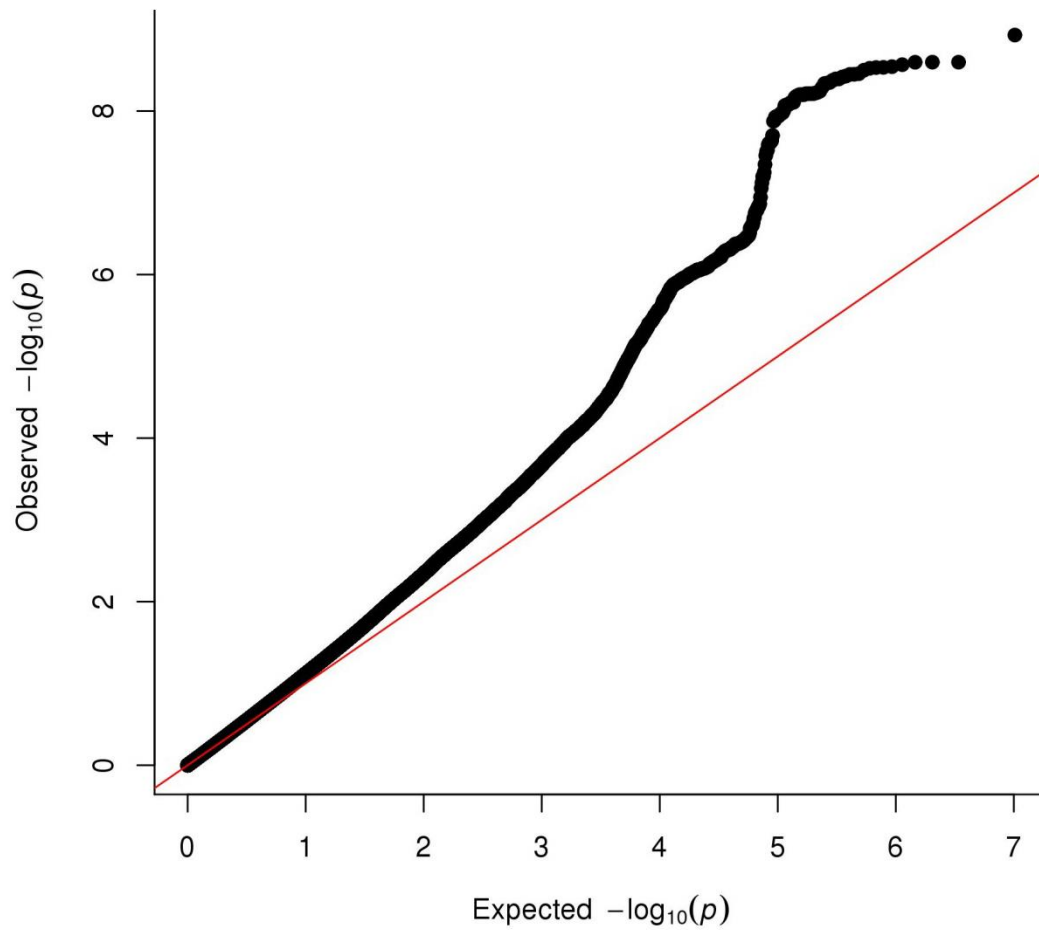


**Supplementary Figure 1**

PCA of the Chinese GWAS sample with the HapMap3 sample.

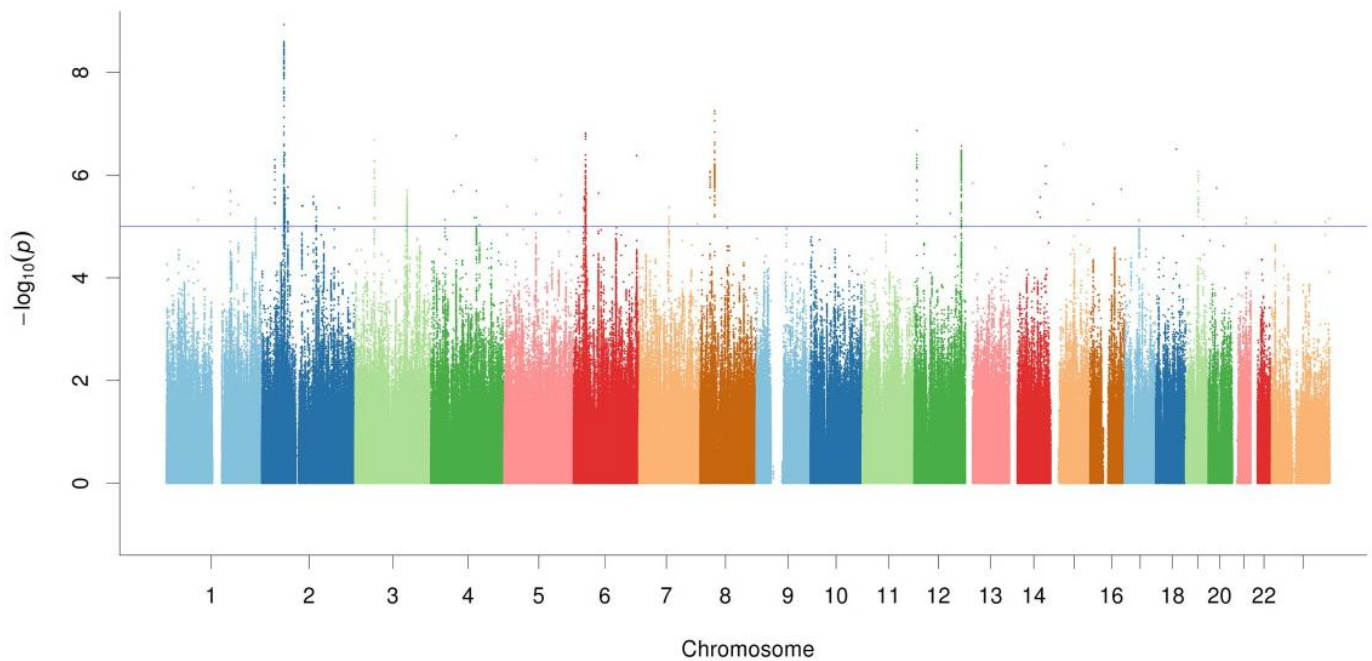
**a)** GWAS Set 1, **b)** GWAS Set 2, **c)** GWAS Set 3. Plot of the first two principal components (C1 and C2) from principal components analysis (PCA) of Chinese GWAS sample with HapMap3 sample. The enlarged area is for the Aisan sample, including our cases and controls.



## Supplementary Figure 2

Quantile–quantile (Q–Q) plot of the GWAS analysis of Chinese individuals.

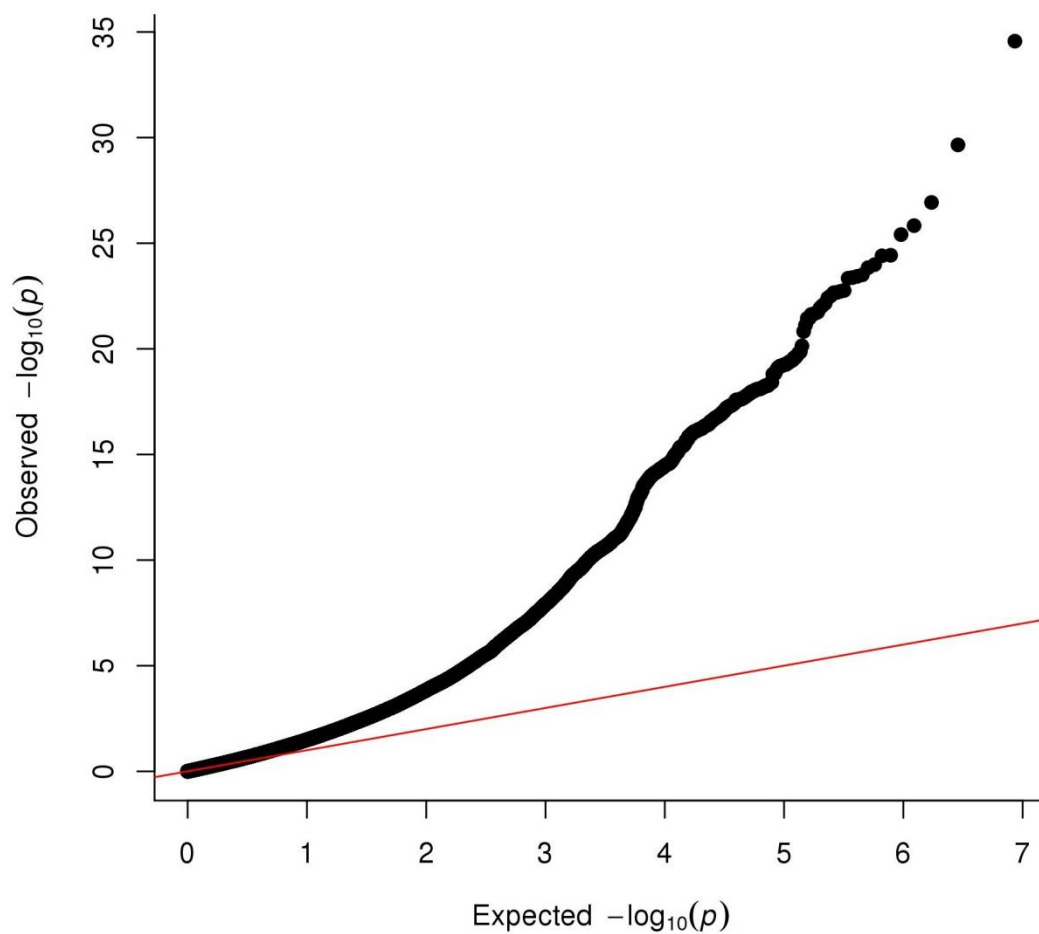
The Q–Q plot representative of observed (y axis) vs. expected (x axis) SNP  $P$  values distribution. Expected  $P$  values are those expected under the null hypothesis, and the uniform null distribution is marked with a red line.



### Supplementary Figure 3

Manhattan plot of the GWAS analysis of Chinese individuals.

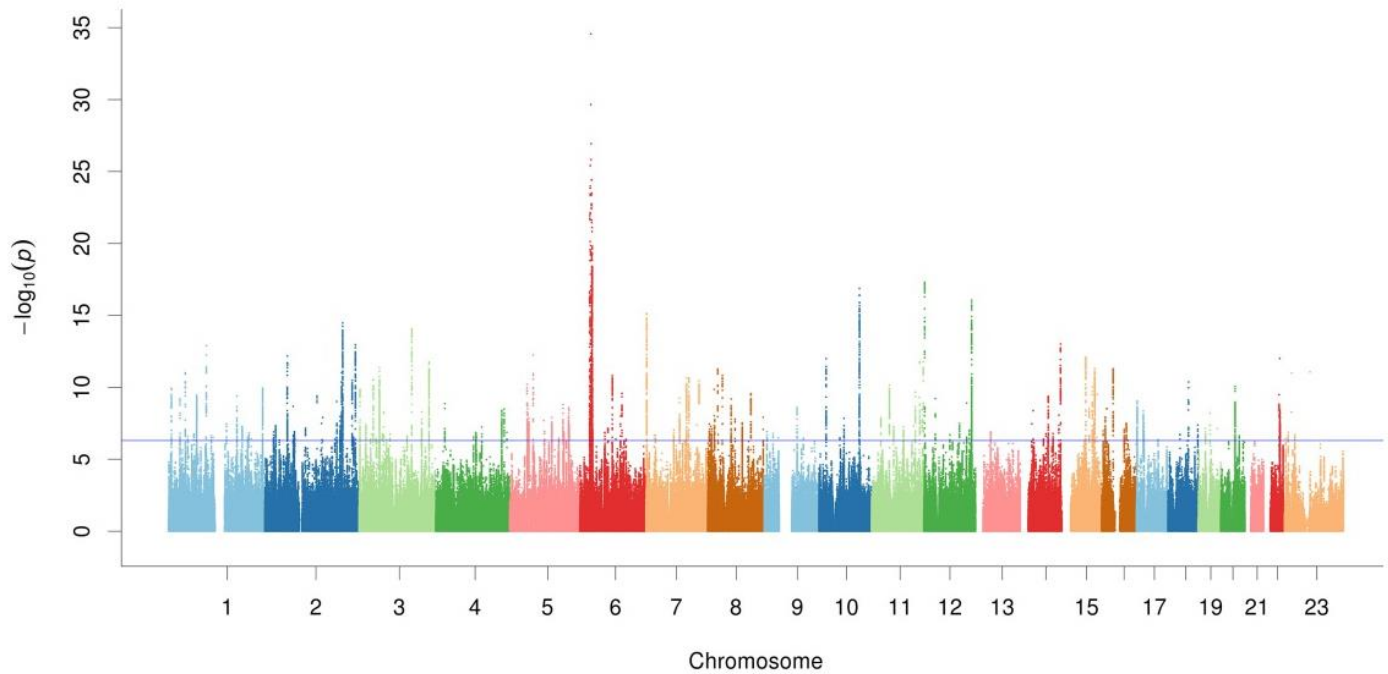
Genome-wide P-values ( $-\log_{10} P$ , y axis) plotted against their respective chromosomal positions (x axis). The blue line is the suggestive significance level ( $1 \times 10^{-5}$ ).



#### Supplementary Figure 4

Quantile–quantile plot of the Chinese and PGC2 GWAS meta-analysis.

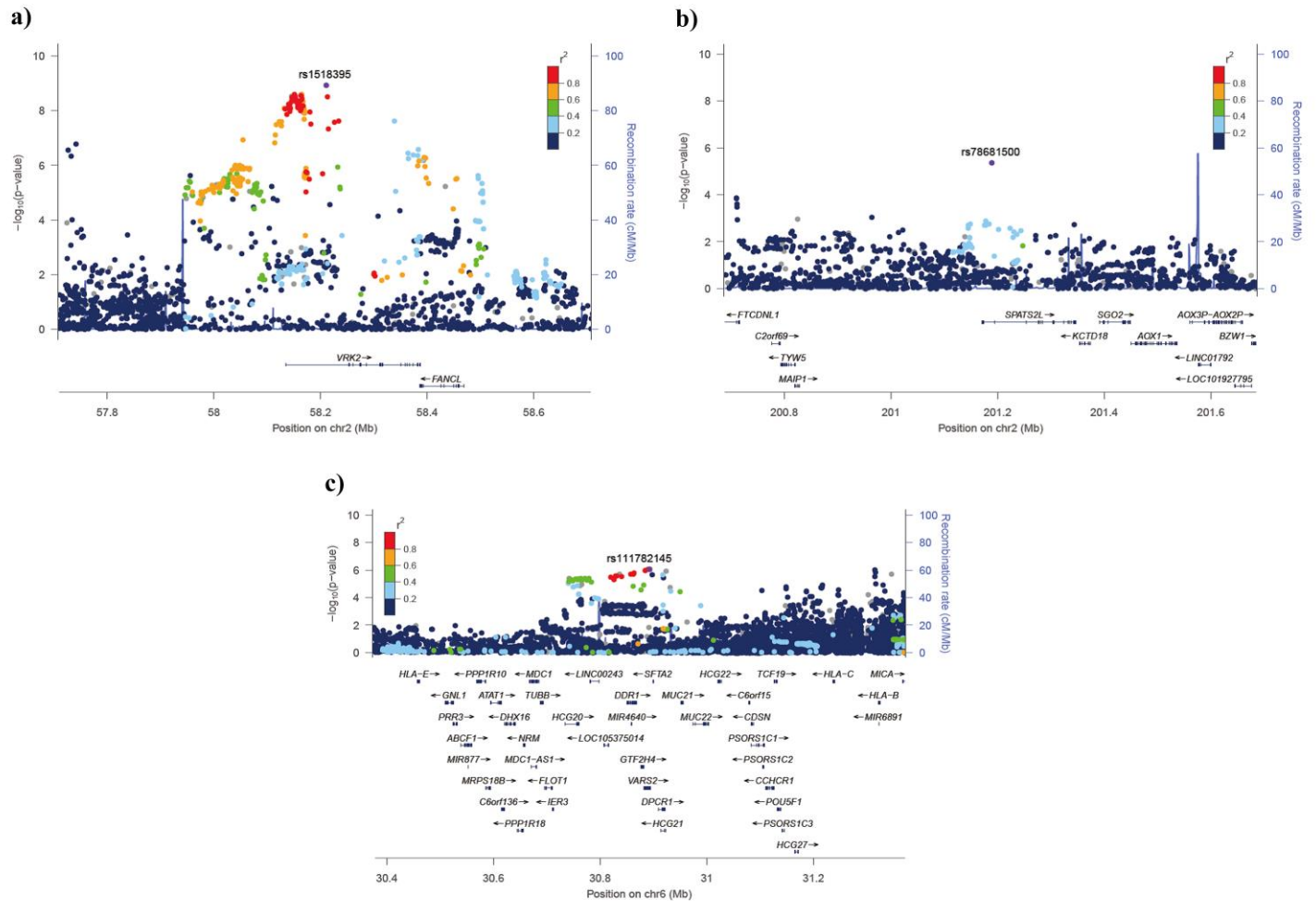
The Q-Q plot representative of observed (y axis) vs. expected (x axis) SNP  $P$  values distribution. Expected  $P$  values are those expected under the null hypothesis, and the uniform null distribution is marked with a red line.



### Supplementary Figure 5

Manhattan plot of the Chinese and PGC2 GWAS meta-analysis.

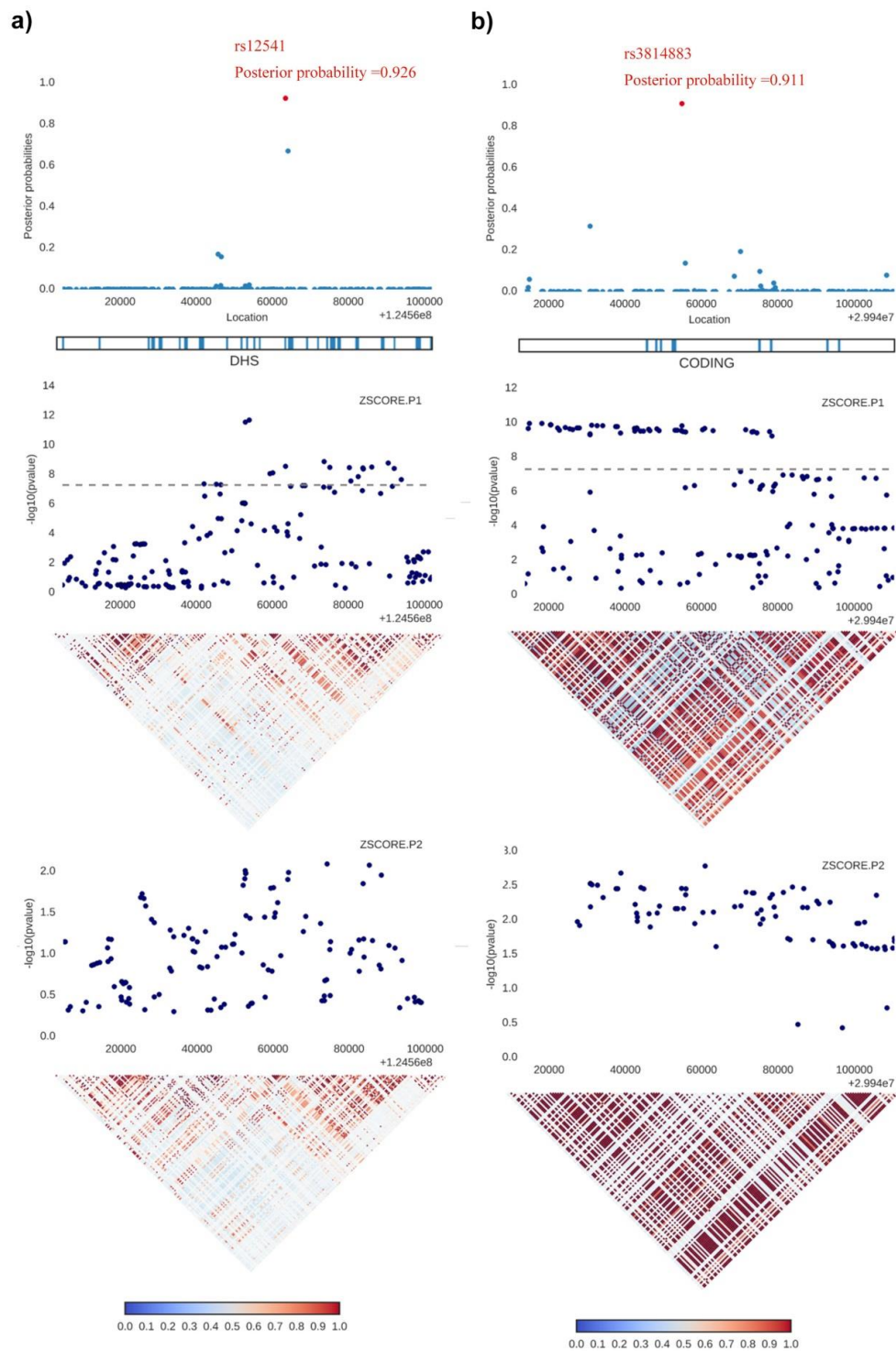
Genome-wide P-values ( $-\log_{10} P$ , y axis) plotted against their respective chromosomal positions (x axis). The blue line is the suggestive significance level ( $5 \times 10^{-7}$ ).



## Supplementary Figure 6

Regional plots of the GWS loci from the Chinese GWAS and replication meta-analysis.

**a)** rs1518395 at 2p16.1, **b)** rs78681500 at 2q33.1, **c)** rs111782145 at eMHC.  $-\log_{10} P$  values are shown for SNPs for the region 500 kb on either side of the marker SNPs. The index SNP is shown in purple, and the  $r^2$  values of the other SNPs are indicated by color. The  $r^2$  values are established based on the 1000 Genome data. The genes within the relevant regions are annotated and shown as arrows.



**Supplementary Figure 7**

Fine-mapping analyses for GWS loci nos. 80 and 103 with PAINTOR.

**Supplementary Table 1. Description of Chinese samples**

Stage	Platform <sup>a</sup>	Regions	Cases, N (BIOX1)	Controls, N (BIOX1)
GWAS set 1	SNP6.0	Northern China	1,623 (1,517)	3,690 (1,567)
GWAS set 1	SNP6.0	Central China	1,606 (1,226)	5,732 (2,832)
GWAS set 1	SNP6.0	Southern China	946 (905)	1,048 (970)
GWAS set 2	CHB1	Central China	1,734	2,391
GWAS set 2	CHB1	Northern China	738	3,537
GWAS set 3	CHB1 or 1M	Southern China	1,052	1,929
<b>GWAS</b>			<b>7,699</b>	<b>18,327</b>
Replication	Illumina+	Central & Northern China	4,384	5,770
<b>GWAS &amp; Replication</b>			<b>12,083</b>	<b>24,097</b>

<sup>a</sup>SNP6.0 = Affymetrix Genome-Wide Human SNP Array 6.0; CHB1 = Affymetrix Axiom™ Genome-Wide CHB1 Array Plate; 1M = illumina 1M Array; Illumina+ = Illumina HumanHap610-Quad, Human660W-Quad and Human OmniZhongHua BeadChips; Exome = Affymetrix Axiom myDesign Human Genotyping Array (based on Axiom® Exome 319 Array). For the GWAS set 1, BIOX1 indicates the number of sample in the discovery phase of our prior GWAS analysis (Shi *et al*, Nat Genet, 2011).



**Supplementary Table 7. Concordance in the direction of effect of schizophrenia risk alleles**

<b><i>P</i> value threshold</b>	<b>CHN into PGC2</b>			<b>PGC2 into CHN</b>		
	<b>Concordant SNPs/total SNPs</b>	<b>%</b>	<b>Binomial test <i>P</i></b>	<b>Concordant SNPs/total SNPs</b>	<b>%</b>	<b>Binomial test <i>P</i></b>
$P \leq 0.0001$	136/201	67.7%	3.06E-07	684/1022	66.9%	5.90E-28
$0.0001 < P \leq 0.001$	513/898	57.1%	1.09E-05	1044/1747	59.8%	1.67E-16
$0.001 < P \leq 0.01$	2776/4769	58.2%	3.74E-30	3498/6191	56.5%	7.09E-25
$0.01 < P \leq 0.05$	6960/12578	55.3%	2.60E-33	6970/13034	53.5%	1.09E-15
$0.05 < P \leq 0.5$	23961/45916	52.2%	4.05E-21	25726/49695	51.8%	1.66E-15
$0.5 < P \leq 1$	24687/49125	50.3%	1.32E-01	23892/47710	50.1%	3.69E-01

The Chinese (CHN) data set was comprised of 7,699 cases and 18,327 controls. The PGC2 data set was comprised of 35,476 cases and 46,839 controls. For each comparison, we first identified independent SNPs with evidence of association for schizophrenia from the discovery data set, and then aligned the effect of the schizophrenia risk allele into the other data set.