

Data supplement to Chen et al. Role played by the *SP4* gene in schizophrenia and major depressive disorder in the Han Chinese population. *Br J Psychiatry*
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| Table DS1 Single site association analysis | | | |
|---|-----------------|--------------|--------------|
| Marker | Position | Function | Polymorphism |
| rs2073534 | Chr 7: 21465942 | 5' near gene | C/T |
| rs40245 | Chr 7: 21470536 | intron | A/T |
| rs10255890 | Chr 7: 21483246 | intron | A/C |
| rs2107448 | Chr 7: 21485102 | intron | C/T |
| rs10233357 | Chr 7: 21490045 | intron | A/C |
| rs6461563 | Chr 7: 21496397 | intron | G/T |
| rs1018954 | Chr 7: 21549891 | intron | A/T |
| rs3735440 | Chr 7: 21551070 | 3' UTR | A/G |
| rs2285941 | Chr 7: 21553621 | 3' UTR | G/T |

| Table DS2 SNP analysis in men | | | | | | | | | |
|-------------------------------|---------------|------------------|-------|-------------|------------------------------|--------------------|-------------|-------------|--------------------------------|
| SNP | | Allele frequency | OR | 95% CI | P_{allele} value | Genotype frequency | | | P_{genotype} value |
| rs2073534 | | C | | | | CC | CT | TT | |
| | Schizophrenia | 309 (0.195) | 1.043 | 0.87–1.26 | 0.656 | 41 (0.052) | 227 (0.287) | 523 (0.661) | 0.911 |
| | MDD | 263 (0.183) | 0.960 | 0.79–1.16 | 0.681 | 31 (0.043) | 201 (0.279) | 436 (0.678) | 0.857 |
| | Control | 237 (0.189) | | | | 32 (0.049) | 181 (0.279) | 436 (0.672) | |
| rs40245 | | A | | | | AA | AT | TT | |
| | Schizophrenia | 218 (0.141) | 1.548 | 1.23–1.96 | 0.0002 | 17 (0.022) | 184 (0.238) | 572 (0.740) | 0.001 |
| | MDD | 142 (0.101) | 1.055 | 0.82–1.36 | 0.681 | 5 (0.007) | 132 (0.187) | 569 (0.806) | 0.272 |
| | Control | 125 (0.096) | | | | 9 (0.014) | 107 (0.164) | 536 (0.822) | |
| rs1025589 0 | | C | | | | AA | AC | CC | |
| | Schizophrenia | 409 (0.262) | 0.968 | 0.98–1.14 | 0.697 | 421 (0.538) | 313 (0.400) | 48 (0.061) | 0.649 |
| | MDD | 372 (0.262) | 0.970 | 0.82–1.15 | 0.724 | 377 (0.531) | 294 (0.414) | 39 (0.055) | 0.309 |
| | Control | 351 (0.268) | | | | 352 (0.537) | 255 (0.389) | 48 (0.073) | |
| rs1023335 7 | | C | | | | AA | AC | CC | |
| | Schizophrenia | 596 (0.302) | 0.889 | 0.77–1.03 | 0.125 | 303 (0.384) | 376 (0.477) | 110 (0.139) | 0.178 |
| | MDD | 620 (0.435) | 1.130 | 0.99 – 1.32 | 0.116 | 236 (0.363) | 332 (0.466) | 144 (0.202) | 0.305 |
| | Control | 529 (0.406) | | | | 237 (0.363) | 301 (0.462) | 114 (0.175) | |
| rs6461563 | | G | | | | GG | GT | TT | |
| | Schizophrenia | 512 (0.350) | 1.241 | 1.06–1.46 | 0.0088 | 93 (0.127) | 326 (0.446) | 312 (0.427) | 0.0306 |
| | MDD | 408 (0.313) | 1.048 | 0.89–1.24 | 0.583 | 58 (0.089) | 292 (0.448) | 302 (0.463) | 0.695 |
| | Control | 381 (0.303) | | | | 57 (0.091) | 267 (0.424) | 305 (0.485) | |

| | | | | | | | | | |
|---|---------------|-------------|-------|-------------|-------|-------------|-------------|-------------|-------|
| rs1018954 | | A | | | | AA | AT | TT | |
| | Schizophrenia | 123 (0.078) | 1.073 | 0.81–1.42 | 0.619 | 4 (0.005) | 115 (0.146) | 667 (0.849) | 0.518 |
| | MDD | 113 (0.081) | 1.113 | 0.88 – 1.03 | 0.545 | 4 (0.006) | 105 (0.150) | 589 (0.844) | 0.418 |
| | Control | 95 (0.073) | | | | 1 (0.002) | 93 (0.144) | 554 (0.855) | |
| rs3735440 | | G | | | | AA | AG | GG | |
| | Schizophrenia | 157 (0.101) | 0.837 | 0.66–1.06 | 0.139 | 630 (0.810) | 139 (0.179) | 9 (0.012) | 0.169 |
| | MDD | 123 (0.088) | 0.723 | 0.56–0.93 | 0.011 | 580 (0.833) | 109 (0.157) | 7 (0.010) | 0.016 |
| | Control | 153 (0.118) | | | | 500 (0.773) | 141 (0.218) | 6 (0.009) | |
| rs2285941 | | G | | | | GG | GT | TT | |
| | Schizophrenia | 464 (0.294) | 1.131 | 0.96–1.33 | 0.139 | 69 (0.087) | 326 (0.413) | 395 (0.500) | 0.321 |
| | MDD | 390 (0.272) | 1.016 | 0.86–1.20 | 0.850 | 57 (0.079) | 276 (0.385) | 384 (0.536) | 0.977 |
| | Control | 351 (0.269) | | | | 50 (0.077) | 251 (0.384) | 352 (0.539) | |
| SNP, single-nucleotide polymorphism; OR, odds ratio; CI, confidence interval; MDD, major depressive disorder. | | | | | | | | | |

Table DS3 SNP analysis in women

| SNP | | Allele frequency | OR | 95% CI | P_{allele} value | Genotype frequency | | | P_{genotype} value |
|------------|---------------|------------------|-----------|-------------|------------------------------|--------------------|-------------|-------------|--------------------------------|
| | | C | | | | CC | CT | TT | |
| rs2073534 | Schizophrenia | 162 (0.190) | 1.099 | 0.87–1.38 | 0.422 | 12 (0.028) | 138 (0.323) | 277 (0.649) | 0.454 |
| | MDD | 83 (0.133) | 0.723 | 0.55–0.95 | 0.022 | 3 (0.010) | 77 (0.248) | 231 (0.743) | 0.040 |
| | Control | 196 (0.176) | | | | 18 (0.032) | 160 (0.287) | 380 (0.681) | |
| rs40245 | | A | | | | AA | AT | TT | |
| | Schizophrenia | 106 (0.130) | 1.156 | 0.88–1.52 | 0.300 | 13 (0.032) | 80 (0.196) | 316 (0.773) | 0.062 |
| | MDD | 82 (0.131) | 1.171 | 0.87–1.57 | 0.297 | 4 (0.013) | 74 (0.236) | 235 (0.751) | 0.562 |
| Control | 128 (0.114) | | | | 6 (0.011) | 116 (0.207) | 439 (0.783) | | |
| rs10255890 | | C | | | | AA | AC | CC | |
| | Schizophrenia | 234 (0.275) | 0.963 | 0.79 – 1.18 | 0.713 | 217 (0.511) | 182 (0.428) | 26 (0.061) | 0.556 |
| | MDD | 148 (0.241) | 0.805 | 0.64 – 1.01 | 0.060 | 176 (0.573) | 114 (0.371) | 17 (0.055) | 0.168 |
| Control | 319 (0.283) | | | | 289 (0.512) | 231 (0.410) | 44 (0.078) | | |
| rs10233357 | | C | | | | AA | AC | CC | |
| | Schizophrenia | 329 (0.389) | 0.965 | 0.80–1.16 | 0.700 | 161 (0.381) | 195 (0.461) | 67 (0.158) | 0.908 |
| | MDD | 269 (0.430) | 1.123 | 0.94–1.39 | 0.190 | 101 (0.323) | 155 (0.495) | 57 (0.182) | 0.398 |
| Control | 442 (0.397) | | | | 204 (0.367) | 262 (0.471) | 90 (0.162) | | |
| rs6461563 | | G | | | | GG | GT | TT | |
| | Schizophrenia | 259 (0.327) | 1.133 | 0.93–1.38 | 0.213 | 48 (0.121) | 163 (0.412) | 185 (0.467) | 0.211 |
| MDD | 170 (0.293) | 0.967 | 0.78–1.21 | 0.770 | 22 (0.076) | 126 (0.434) | 142 (0.490) | 0.879 | |

| | | | | | | | | | |
|---|---------------|-------------|-------|-----------|-------|-------------|-------------|-------------|-------|
| | Control | 321 (0.300) | | | | 46 (0.086) | 229 (0.428) | 260 (0.486) | |
| | | A | | | | AA | AT | TT | |
| rs1018954 | Schizophrenia | 69 (0.082) | 1.313 | 0.93–1.85 | 0.120 | 4 (0.007) | 63 (0.149) | 356 (0.844) | 0.292 |
| | MDD | 49 (0.078) | 1.239 | 0.85–1.81 | 0.265 | 1 (0.003) | 47 (0.149) | 491 (0.848) | 0.352 |
| | Control | 71 (0.064) | | | | 3 (0.005) | 65 (0.116) | 491 (0.878) | |
| | | G | | | | AA | AG | GG | |
| rs3735440 | Schizophrenia | 67 (0.081) | 0.677 | 0.50–0.92 | 0.013 | 349 (0.845) | 61 (0.148) | 3 (0.007) | 0.034 |
| | MDD | 63 (0.104) | 0.891 | 0.64–1.22 | 0.461 | 244 (0.803) | 57 (0.188) | 3 (0.010) | 0.680 |
| | Control | 128 (0.115) | | | | 432 (0.778) | 118 (0.213) | 5 (0.009) | |
| | | G | | | | GG | GT | TT | |
| rs2285941 | Schizophrenia | 270 (0.318) | 1.125 | 0.93–1.36 | 0.233 | 51 (0.120) | 168 (0.396) | 205 (0.483) | 0.490 |
| | MDD | 147 (0.239) | 0.755 | 0.60–0.95 | 0.014 | 20 (0.065) | 107 (0.347) | 181 (0.588) | 0.058 |
| | Control | 331 (0.293) | | | | 56 (0.099) | 219 (0.388) | 289 (0.512) | |
| SNP, single-nucleotide polymorphism; OR, odds ratio; CI, confidence interval; MDD, major depressive disorder. | | | | | | | | | |

Fig. DS1 Relationship between tag SNPs and the *SP4* gene.

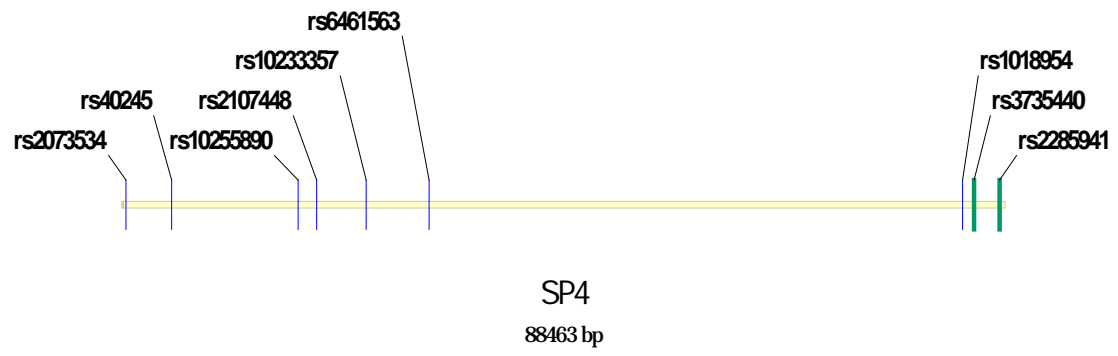


Fig. DS2 Population stratification analysis when $K=3$. (a) Stratification result from combined population: the red dots represent HapMap CEU (Utah residents with ancestry from Northern and Western Europe) population; the green dots represent CHB (Han Chinese in Beijing, China); and the blue dots represent YRI (Yoruba, in Ibadan, Nigeria). (b) Our samples from the two disorders and healthy controls: the blue dots represent schizophrenia; the green dots represent major depressive disorder; and the red dots represent the healthy controls.

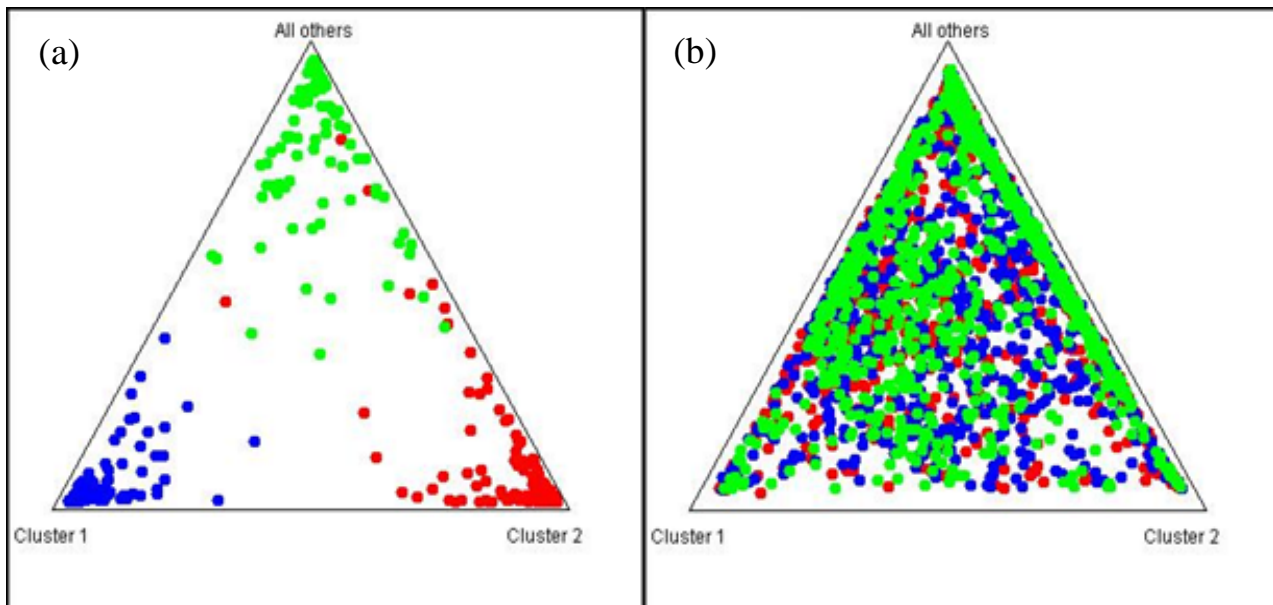


Fig. DS3 Linkage disequilibrium pattern of the human *SP4* gene in the CHB population.



Fig. DS4 Linkage disequilibrium pattern of the human *SP4* gene in the control population.

