Supplementary Figures

Regional association plots for all regions containing a SNP associated $p < 5 \times 10^{-5}$ and INFO > 0.3. The regional association plots are based on a concept developed by Paul de Bakker for the genome-wide association study by the Diabetes Genetics Initiative (1).

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For each top SNP region there are two plots:

- 1Mb region about the most associated SNP, plotting $-\log_{10}(p)$ for each SNP, the position of genes in the region and the recombination rate across the region that bound haplotype blocks. The plotted SNPs are colour coded by the number of analysis sets in which they are imputed (legend). The size of the diamonds reflects the magnitude of $r^2$ linkage disequilibrium between the SNP and the labelled top associated SNP of the region. Genes within 50kb of these SNPs are listed. Colour coding for SNPs: number of sets in which the SNP was imputed (0 = imputed in all analysis sets, 4= genotyped in all analysis sets).

- Forest plots showing Odds Ratios (OR) and their 95% Confidence Intervals ($L95$-$U95$) for each contributing analysis set. I/G: I=Imputed, G=Genotyped. INFO: ratio of observed genotypic variance calculated from dosage scores, to expected genotypic variance based on mean dosage score, a measure of imputation quality. Fcon, Fcas: minor allele frequency in controls and cases.
Major depressive disorder genome-wide association

Wray et al.
8q24.23–q24.3 Both Sex analysis Rank 4 Not included in Table 3 because of low INFO

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Odds Ratio
Major depressive disorder genome-wide association

Wray et al

![Graph showing the association of rs10815615 in major depressive disorder genome-wide association study.](image-url)
Major depressive disorder genome-wide association

12q22-23 Both Sex analysis Rank 3

Chromosome 12 position (kb)

rs2638463

Set | I/G | INFO | P | Fcon | Fcas | OR | L95 | U95
---|-----|------|---|------|------|----|-----|-----
I317 | I   | 0.95 | 0.55 | 0.281 | 0.294 | 1.14 | 0.74 | 1.78
I370 | I   | 0.91 | 0.21 | 0.302 | 0.308 | 1.10 | 0.95 | 1.28
I610 | G   | 0.9 | 0.036 | 0.315 | 0.381 | 1.36 | 1.02 | 1.82
A6.0 | I   | 1.02 | 8.7e-06 | 0.296 | 0.338 | 1.30 | 1.16 | 1.45
All   |     | 0.97 | 2.9e-06 | 0.299 | 0.330 | 1.22 | 1.12 | 1.33

Odds Ratio
Major depressive disorder genome-wide association

7q35–36 Male only analysis Rank 6

Chromosome 7 position (kb)

rs826824
Set  I/G INFO    P  Fcon  Fcas OR L95 U95
I370  I  1  0.00017 0.482 0.397 0.68 0.55 0.83
I610  I  0.89  0.036 0.424 0.290 0.49 0.25 0.96
A6.0  G  0.97  0.032 0.477 0.432 0.83 0.70 0.98
All   -  0.98  9.2e-06 0.475 0.412 0.76 0.67 0.86
Major depressive disorder genome-wide association

Wray et al

13q14.13 Male only analysis Rank 2

rs7318876

Set I/G INFO P Fcon Fcas OR L95 U95
1370 G 0.97 6.2e-05 0.133 0.0750 0.49 0.34 0.69
1610 G 0.91 0.019 0.148 0.0530 0.22 0.06 0.78
A6.0 I 0.99 0.012 0.119 0.0990 0.71 0.54 0.93
All - 0.98 1.8e-06 0.127 0.0879 0.61 0.50 0.75

Odds Ratio
Major depressive disorder genome-wide association

Wray et al.

13q21.2 Male only analysis Rank 5

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Odds Ratio
13q31.1 Male only analysis Rank 1

rs7490744

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Major depressive disorder genome-wide association

3q28 Female only analysis Rank 7

rs695884

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Odds Ratio

rs695884
**Major depressive disorder genome-wide association**

Wray et al

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**4q26 Female only analysis Rank 3**

Observed (~logP)

Recombination rate (cM/Mb)

Chromosome 4 position (kb)

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Major depressive disorder genome-wide association

7q32 Female only analysis Rank 8

rs7797729

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Major depressive disorder genome-wide association

rs10815615
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I370  G   0.97  0.14  0.452  0.419  0.87  0.71  1.05
I610  I   1.04  0.014 0.476  0.389  0.68  0.51  0.93
A6.0  I   0.95  0.00035 0.507  0.436  0.76  0.65  0.88
All   -   0.97  4.2e-06 0.478  0.427  0.78  0.71  0.87
Major depressive disorder genome-wide association

Wray et al

13q22 Female only analysis Rank 1

rs9564791

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Odds Ratio
14q23 Female only analysis Rank 5

Chromosome 14 position (kb)

rs2253168

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Odds Ratio
Major depressive disorder genome-wide association

Wray et al

19q13.2-q13.4 Female only analysis Rank 2 Not included in Table 3 because of low INFO

rs11666105

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<th>U95</th>
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Odds Ratio
Major depressive disorder genome-wide association

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4q35.1 Recurrent Early Onset analysis Rank 1

rs4478240

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Odds Ratio
### rs715217

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Odds Ratio
rs1317640
Set I/G INFO P Fcon Fcas OR L95 U95
I317 I 2 0.88 0.059 0.056 0.88 0.17 4.61
I370 I 1 0.59 0.062 0.063 1.13 0.73 1.74
I610 I 1 0.13 0.043 0.071 2.19 0.79 6.10
A6.0 G 1 0.0031 0.072 0.104 1.32 1.10 1.58
All - 3 8.5e-06 0.064 0.092 1.44 1.23 1.69
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Reference