

## Supplementary Information

### **Common variants of *HTR3* genes are associated with obsessive-compulsive disorder and its phenotypic expression**

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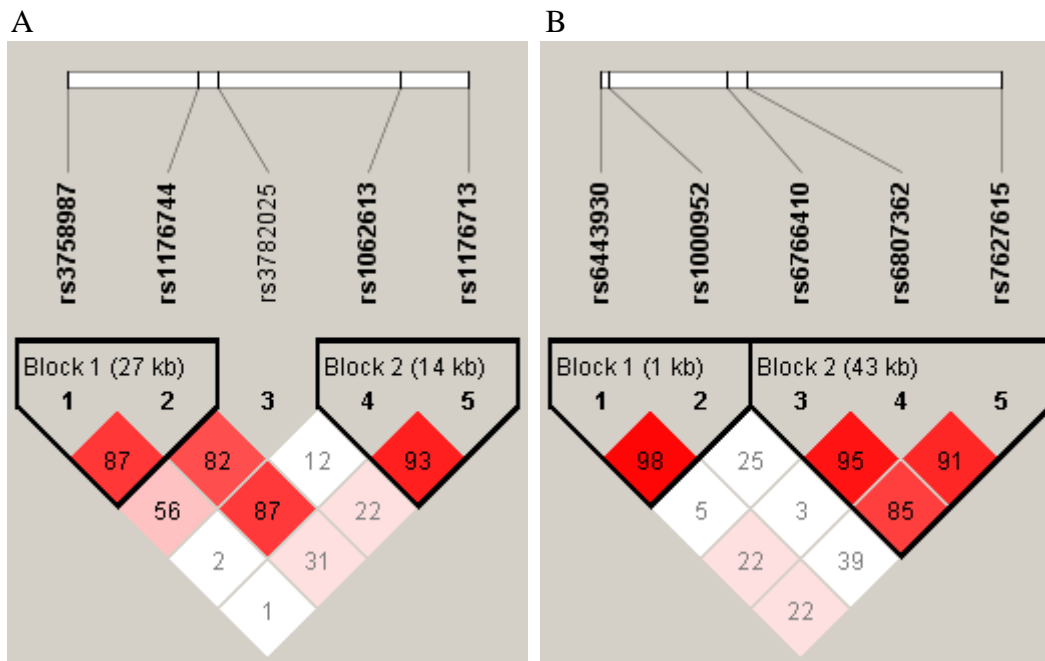
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**Supplementary Figure S1.** Linkage disequilibrium patterns and haplotype blocks estimated with markers that were examined in this study. All numbers in the square represent the pairwise  $D'$  value as a percentile. (A) *HTR3A* (rs1062613, rs1176713) and *HTR3B* (rs3758987, rs1176744, rs3782025). (B) *HTR3C* (rs6766410, rs6807362), *HTR3D* (rs6443930, rs1000952), and *HTR3E* (rs7627615).

**Supplementary Table S1. Conditional association results for rs6766410 and rs6443930 and the cleaning dimension**

| Model        | SNP       | covariate | rs6766410                   |                             |   | rs6443930                   |   |                 |
|--------------|-----------|-----------|-----------------------------|-----------------------------|---|-----------------------------|---|-----------------|
|              |           |           | Total subjects              | Male subjects               | Female subjects                                       | Total subjects              | Male subjects   | Female subjects |
|              |           |           | OR (95% CI); <i>P</i> value |                             |   | OR (95% CI); <i>P</i> value |   |                 |
| Dominant     | rs6766410 | –         | –                           | –                           | 0.61 (0.40–0.92);<br>0.0155                           | 0.83 (0.51–1.37);<br>0.4747 | 0.31 (0.14–0.69);<br>0.0021                           |                 |
|              | rs6443930 | –         | 1.12 (0.76–1.67);<br>0.5643 | 1.62 (1.01–2.60);<br>0.0460 | 0.47 (0.21–1.05);<br>0.0548                           | –                           | –   |                 |
| Recessive    | rs6766410 | –         | –                           | –                           | 0.79 (0.47–1.31);<br>0.3689                           | 0.68 (0.38–1.23);<br>0.2100 | 1.33 (0.46–3.86);<br>0.5863                           |                 |
|              | rs6443930 | –         | 0.66 (0.42–1.04);<br>0.0771 | 0.95 (0.54–1.68);<br>0.8674 | 0.30 (0.13–0.69);<br>0.0050                           | –                           | –   |                 |
| Overdominant | rs6766410 | –         | –                           | –                           | 0.74 (0.51–1.07);<br>0.1079                           | 1.07 (0.68–1.68);<br>0.7856 | <b>0.33 (0.17–0.67);</b><br><b>0.0013<sup>a</sup></b> |                 |
|              | rs6443930 | –         | 1.44 (0.99–2.09);<br>0.0529 | 1.61 (1.01–2.56);<br>0.0420 | 1.17 (0.61–2.24);<br>0.6398                           | –                           | –   |                 |
| Additive     | rs6766410 | –         | –                           | –                           | 0.73 (0.56–0.97);<br>0.0297                           | 0.81 (0.58–1.14);<br>0.2355 | 0.61 (0.36–1.01);<br>0.0529                           |                 |
|              | rs6443930 | –         | 0.92 (0.71–1.20);<br>0.5367 | 1.22 (0.89–1.69);<br>0.2159 | <b>0.46 (0.27–0.78);</b><br><b>0.0031<sup>a</sup></b> | –                           | –   |                 |

SNP, single nucleotide polymorphism; OR, odds ratio; CI, confidence interval.

<sup>a</sup>Significant *P* values under a genetic model with the lowest Akaike information criteria are highlighted in bold.

**Supplementary Table S2. Primer sets and assay IDs used in the experiment**

| rs number | Primer sequence   |
|-----------|---|
| rs3782025 | Forward: CAGGAAACAGCTATGACCgtggcacatccctgtaa<br>Reverse: TGTA AACGACGGCCAGTAAACTGCCCTACCTACA<br>SNP primer: AGGCAAYTACAGGCTAACCTTGG |
| rs number | Assay ID  |
| rs1062613 | C__7488465_10   |
| rs1176713 | C__1372122_10   |
| rs3758987 | C__27512451_10  |
| rs1176744 | C__7488596_1_   |
| rs6766410 | C__26004660_10  |
| rs6807362 | C__28948667_10  |
| rs6443930 | C__28960641_10  |
| rs1000952 | C__109464_10  |
| rs7627615 | C__28960643_10  |

SNP, single nucleotide polymorphism