Genome-wide DNA methylation analysis in obsessive-compulsive disorder patients

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Supplementary Figure 1. The principal component analysis (PCA) plots of the first five components of our sample. Plots of PC2-PC5 *v.s.* PC1, respectively, for methylation analysis of individuals with OCD included in the present study. Then we found that the genomic control factor (λ_{GC}) was about 1.094.
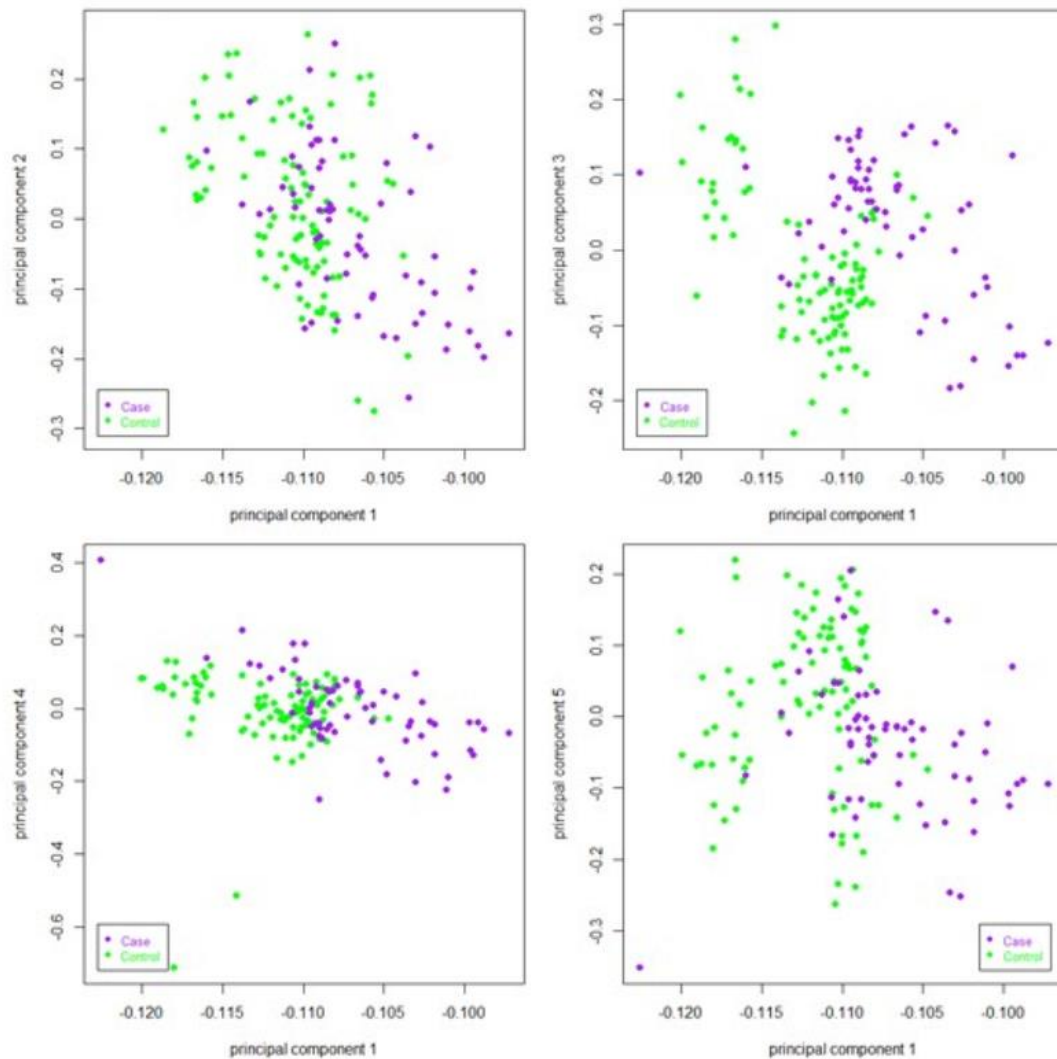
Supplementary Figure 2. Clustering profiles for selected methylation probes.

The clustering profiles for selected methylation probes (*diffscore* ≥ 20, delta *β*

values > 0.1). Unsupervised clustering analysis of the top significant methylation

probes revealed two distinct groups with significantly more people with OCD in

cluster one compared with controls (67.74% cases *v.s.* 27.13% controls, *df* = 1, *P* =

3.41E-07). The abscissa axis represents id numbers of all the 65 OCD cases and 96

healthy control subjects and related clusters. The vertical axis represents clusters of

the methylation probes. The color key represents Z-scores, from Green to Red as from

-4 to 4.