**Supplementary Materials and Methods**

**Gene Expression Profiling and Pathway Analysis**

The Affymetrix GeneChip Mouse Gene 2.0 ST Array was used for gene expression profiling, and Affymetrix Expression Console was used for data processing and normalization. Gene expression microaaray data has been submitted the Gene Expression Omnibus (GEO) database under accession GSE 88828. Hierarchical clustering was performed with the R package heatmap on the top 1% variant genes (n=414)(2,3). Genes with more than 2-fold change were selected for pathway analysis by DAVID (4,5).

References:

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