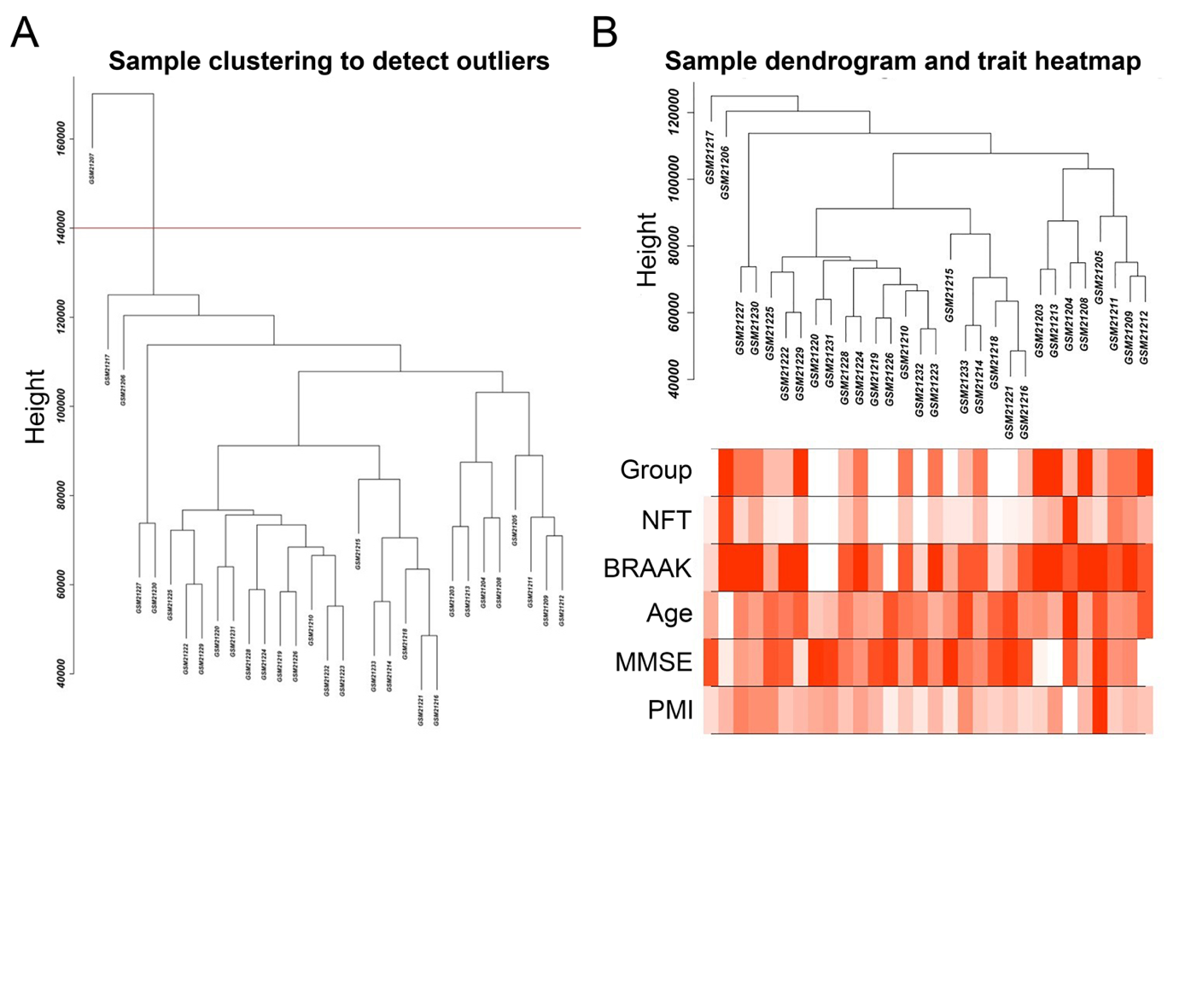
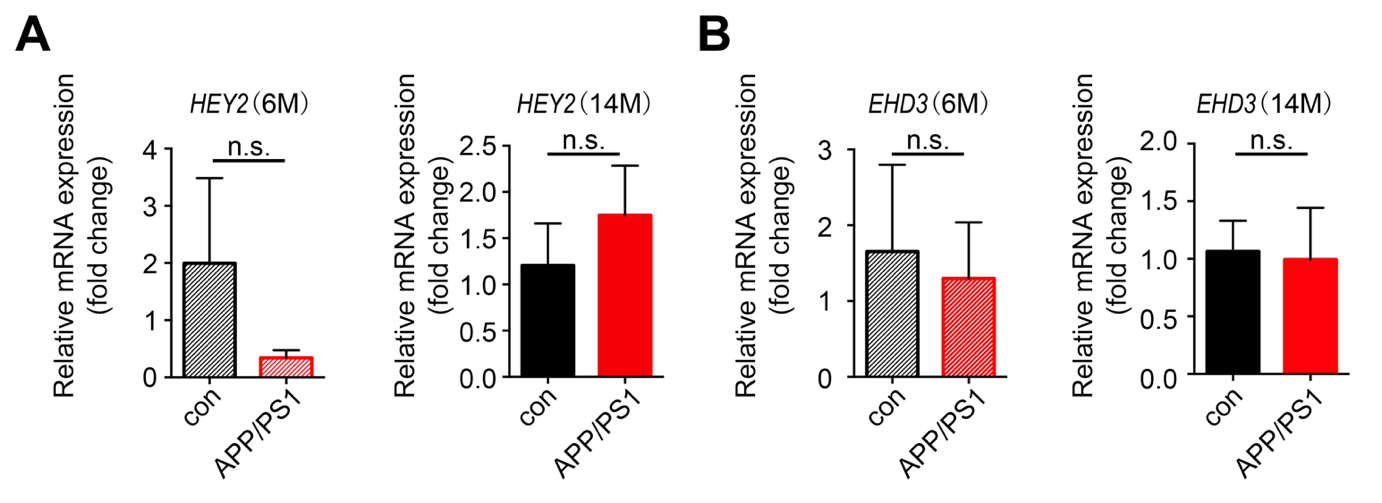
**Supplementary Material**



**Supplementary Fig. 1.** Preprocessing of the mRNA expression data. A) Gene expression database GSE1297 including 31 groups of samples were read by R software, clustered, and one outlier sample (GSM21207) with significantly high average expression level was removed. B) The mRNA expression data of the remaining 30 groups of samples were matched to clinical data.

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**Supplementary Fig. 2.** Validation of the key genes in AD transgenic mice. Total RNAs were isolated from hippocampal tissues of APP/PS-1 transgenic mice and wild type control mice for qRT-PCR analysis of the expression of key genes identified in WGCNA. A, B) Expression of *HEY2, EHD3* in 6-month-old and 14-month-old mice; n = 3 per group. \*p<0.05, \*\*p<0.01, \*\*\*p<0.001 versus Con. Data are mean±SEM.