**Supplementary Figure S1: Examples of gene set enrichment analysis (GSEA) result**

Positive label (red color) is MES-phenotype enriched genes and negative label (blue color) is ADRN-phenotype enriched genes. Normalized enrichment scores (NES) and Folse discovery rate q-values (FDR *q*-val) are shown. Both example gene sets, "SANA_TNF_SIGNALING_UP" and "NAGASHIMA_EGF_SIGNALING_UP", are significantly enriched in MES-phenotype.
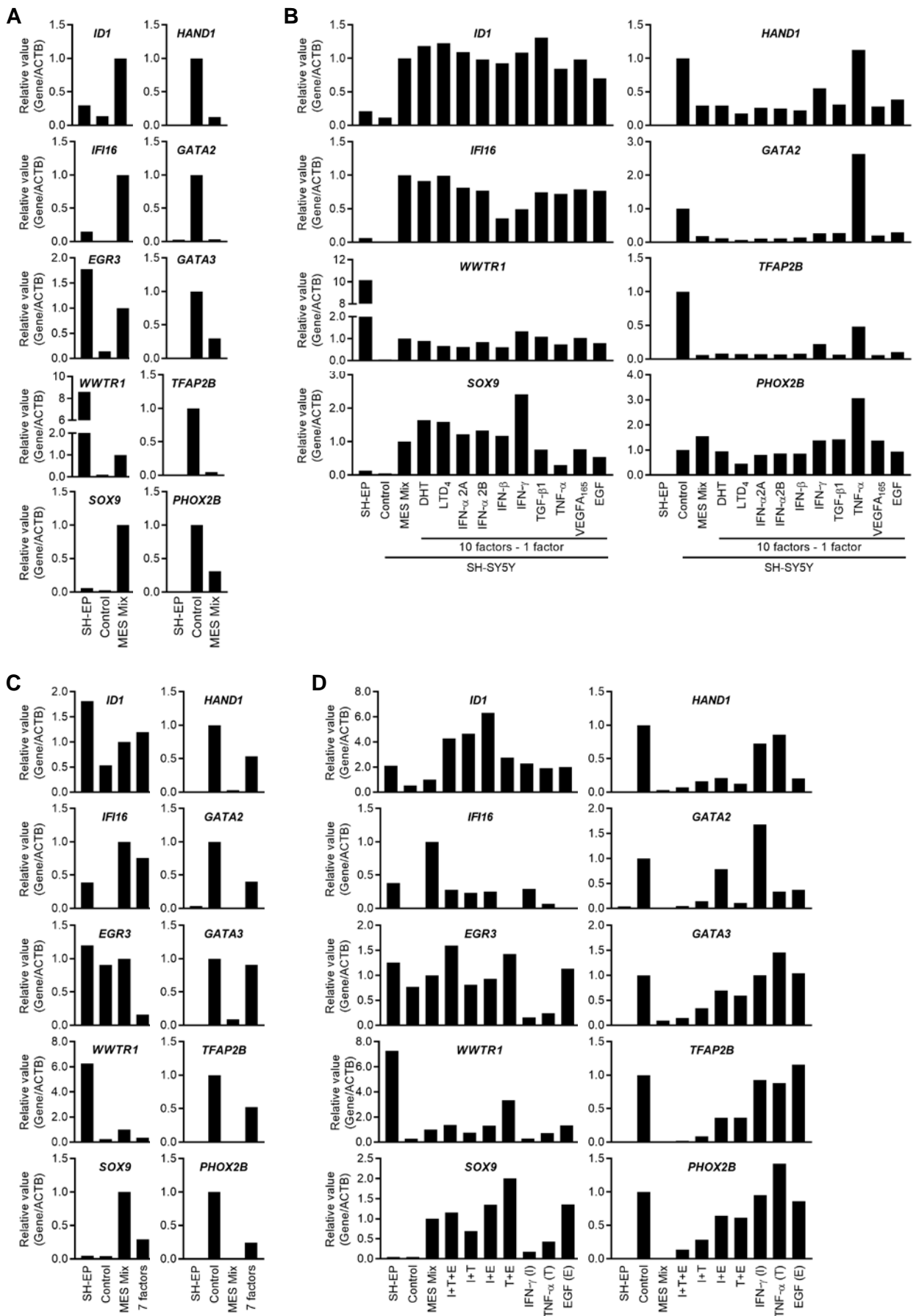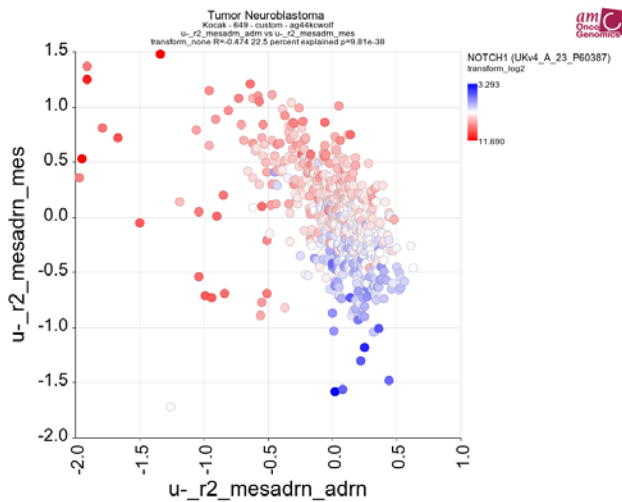
Supplementary Figure S2: qPCR experiment (repeated)

Repeated qPCR experiment results. A, Repeat for Figure 1C. B, Repeat for Figure 2A. C, Repeat for Figure 2B. D, Repeat for Figure 2C.
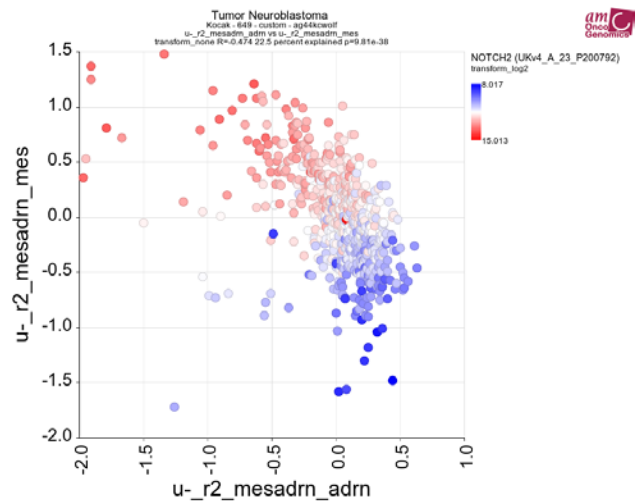
NOTCH1 expression

vs MES score: r = 0.698

vs ADRN score: r = -0.563

NOTCH2 expression

vs MES score: r = 0.832

vs ADRN score: r = -0.573

Supplementary Figure S3: Expressions of *NOTCH1* and *NOTCH2* and their association with MES or ADRN signature scores

Expression of *NOTCH1* and *NOTCH2* in 649 human neuroblastoma cohort ("Kocak - 649 - custom - ag44kcwolf" in R2 platform). X-axis shows the ADRN signature scores and Y-axis shows the MES signature scores. Color indicates log2 transformed expression levels. Correlation coefficients between gene expressions and signature scores were shown.