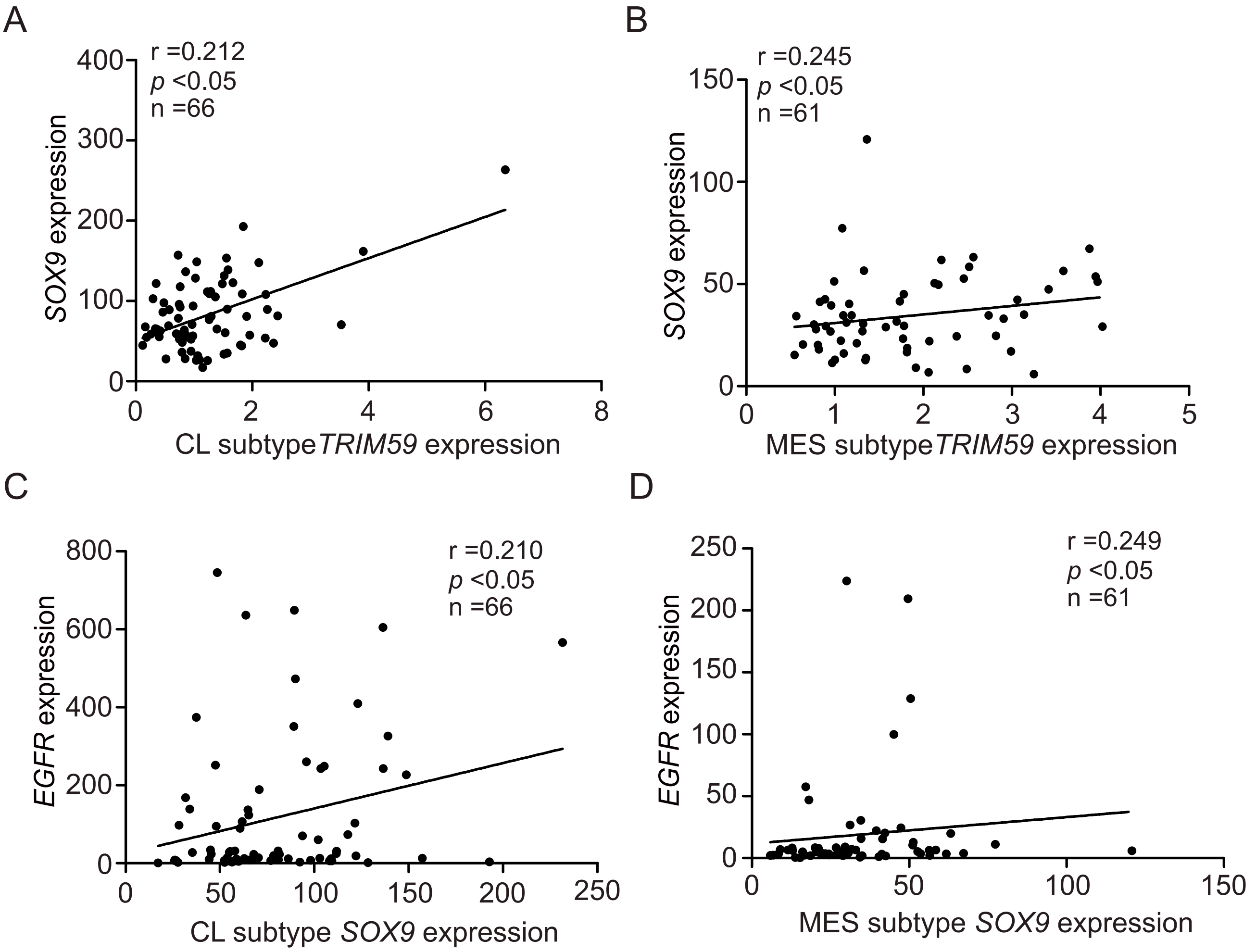

Supplementary Figure 2. Spearman's correlation analysis of expression of *TRIM59* and *SOX9* (A and B), and *SOX9* and *EGFR* (C and D) in human clinical classical (CL) and mesenchymal (MES) subtype glioma specimens using RNA-Seq analysis. Expression data of *TRIM59*, *SOX9* and *EGFR* mRNAs were downloaded from the CGGA dataset of Grade III tumors and GBM (www.cgga.org.cn/).