



Figure 1. LncRHOXF2B expression profiling analysis. (A) Heatmap and clustering of 162 differentially expressed genes in TetON-IncRHOXF2B huES9 clone 28 cells treated with or without dox to induce overexpression. Also included is huES9 treated with dox. **(B)** Cluster 2 (bottom cluster in 1A) was isolated for Gene Ontology analysis in TetON-IncRHOXF2B huES9 clone 28 cells. **(C)** Gene Ontology analysis was performed on cluster 2 using the DAVID functional annotation tool **(D)** Gene set enrichment analysis was performed on the entire array dataset (10403 genes). The enrichment plot shows genes upregulated in huES9 clones overexpressing IncRHOXF2B.