

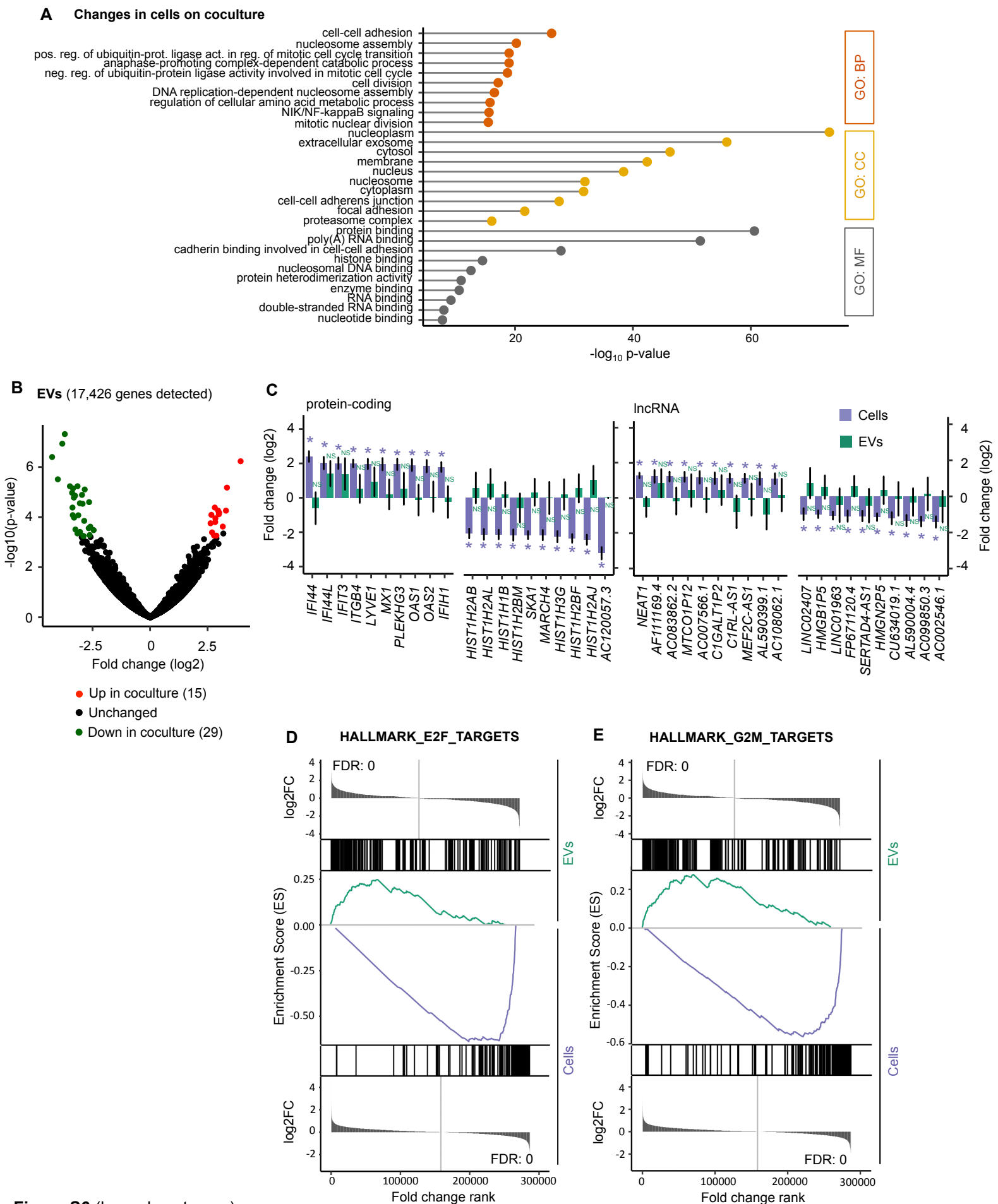


Figure S6 (legend next page)

**Figure S6:** (A) Gene Ontology analysis of protein-coding genes altered in cells by coculture. For each category the top 10 most significantly enriched GO terms (FDR < 0.05) are displayed. BP = Biological Process, CC = Cellular Compartment, MF = Molecular Function. Individual values can be found in Additional file 17. (B) Volcano plot of log<sub>2</sub> fold changes by RNA-Seq of mRNA and lncRNA genes (combined) in EVs derived from tumor-exposed cells vs. EVs derived from unexposed cells. (C) Log<sub>2</sub> fold change in tumor-exposed cells vs. unexposed cells and in EVs derived from tumor-exposed cells vs. EVs derived from unexposed cells for the most increased (left) and decreased (right) mRNA and lncRNA genes significantly changed in cells. Error bars represent standard error of log<sub>2</sub> fold change. Individual values can be found in Additional file 17. (D-E) Depletion of E2F\_TARGETS\_V1 gene set (D) and G2M\_TARGETS gene set (E) in tumor-exposed vs. unexposed cells and enrichment of the same gene set in EVs derived from tumor-exposed vs. unexposed cells. All analyses were performed using 3 EV and 3 cell samples.