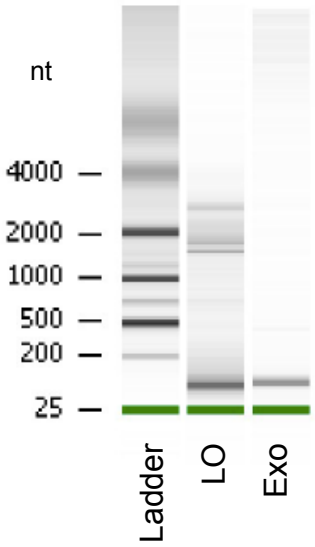
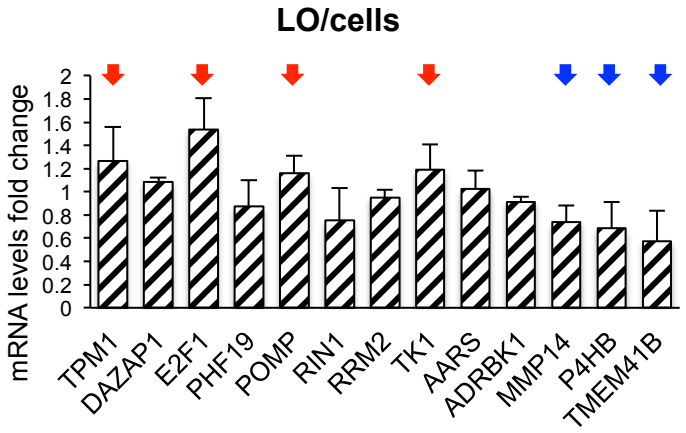
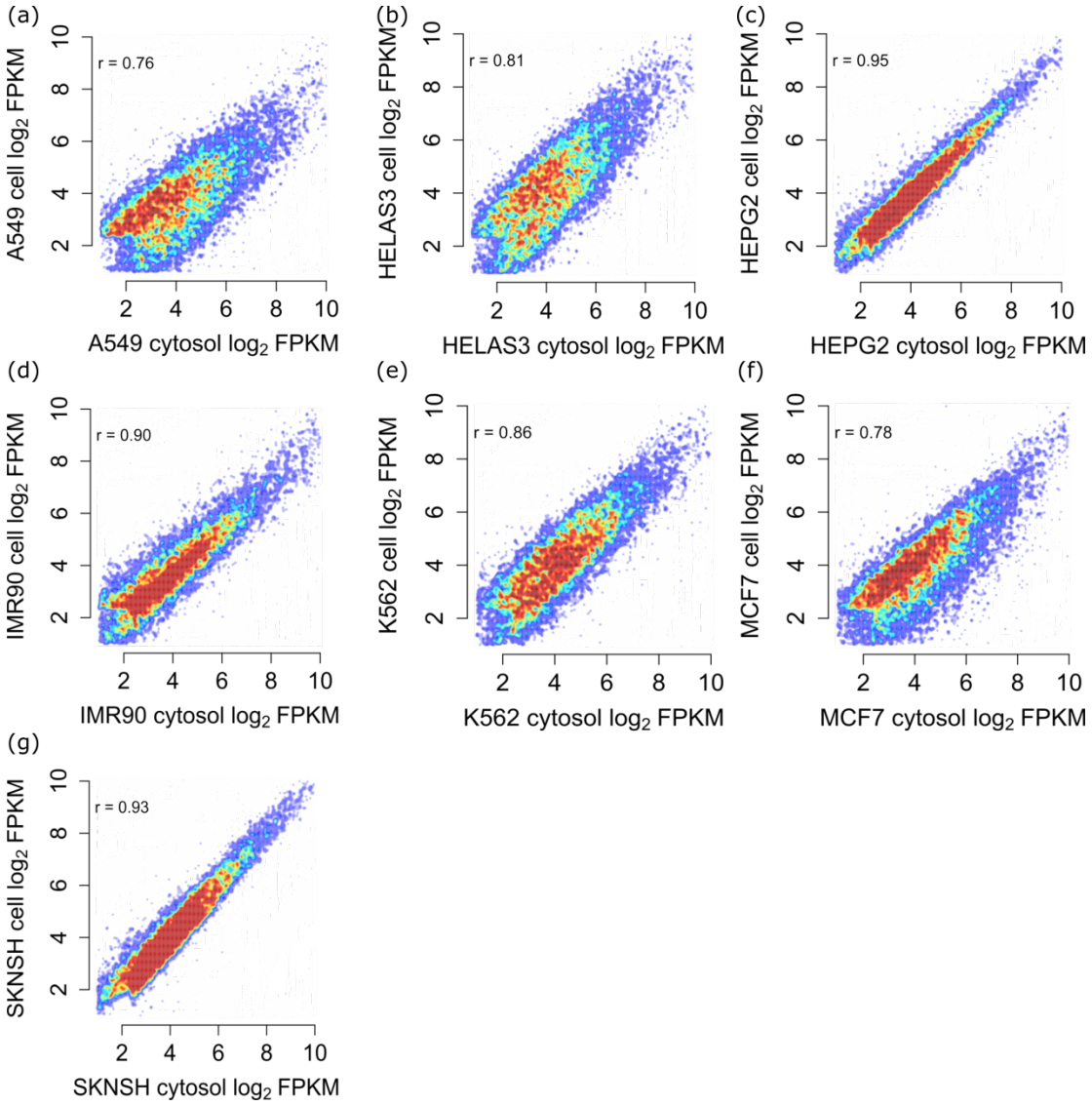


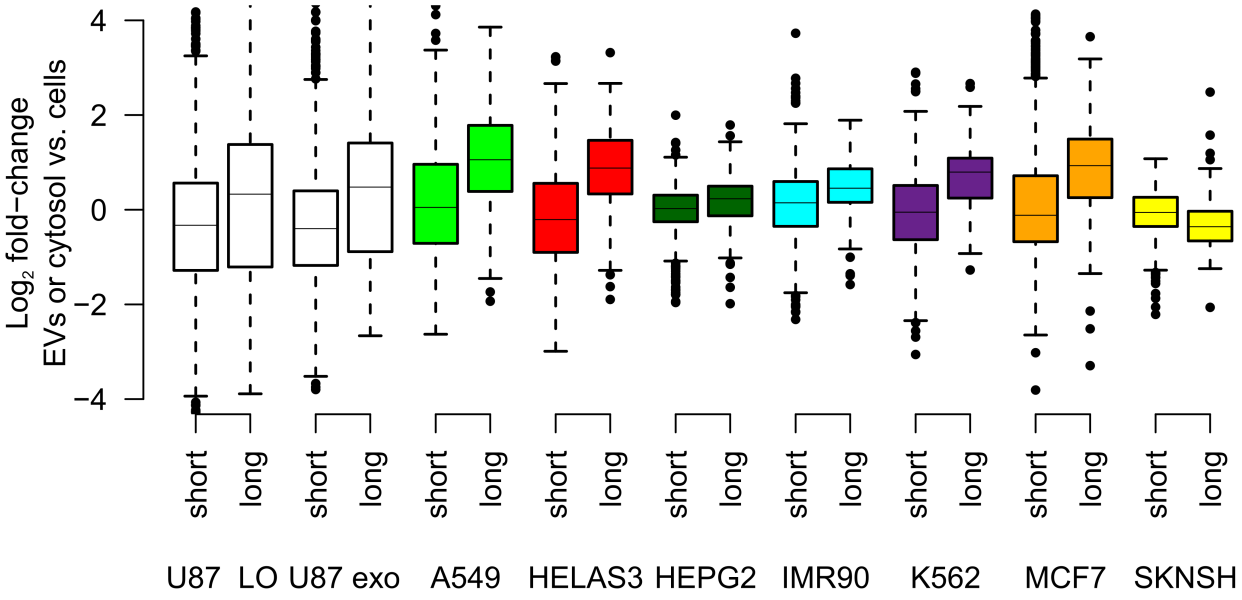
Supplementary Figure S1. Electropherograms showing the size distribution of total RNA in LO and Exo.



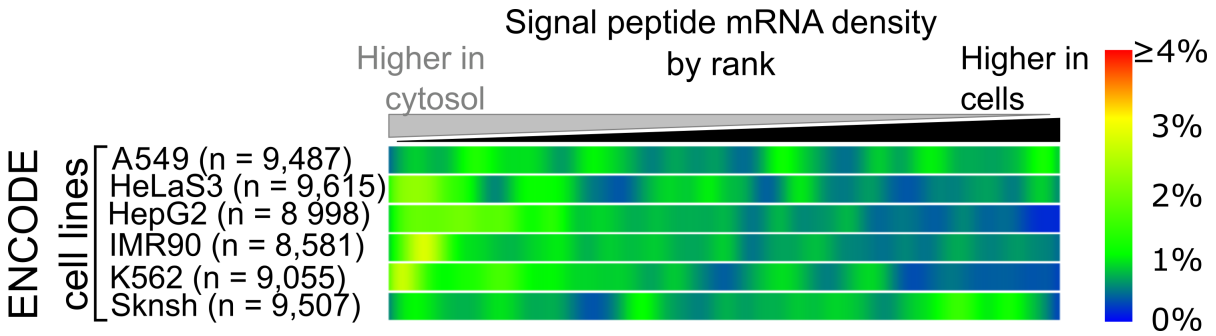
Supplementary Figure S2. Ratio of RNA expression for the indicated genes in LO versus U87 cells as measured by Fluidigm. ASL and TSNARE were used as normalizers. The mRNAs identified as enriched or depleted in EVs by both RNA-Seq and PCR are indicated with red and blue arrows, respectively.



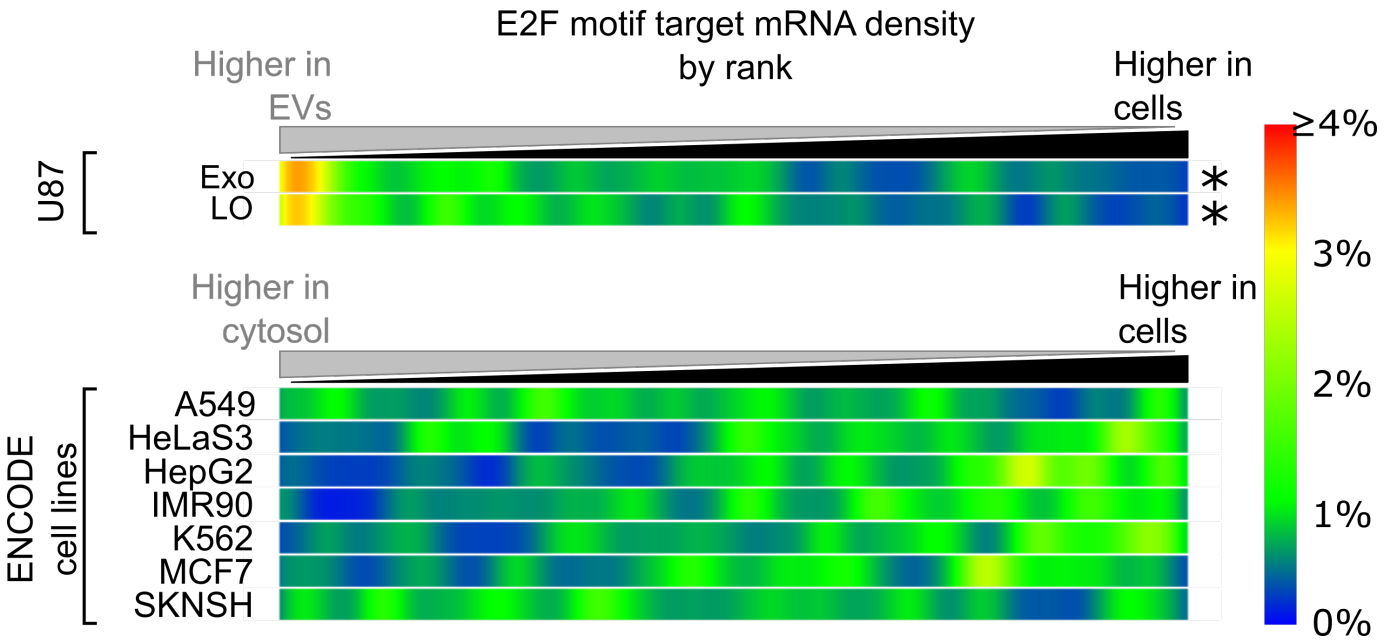
Supplementary Figure S3. Correlation between cytosol and cell mRNA in ENCODE cell types.



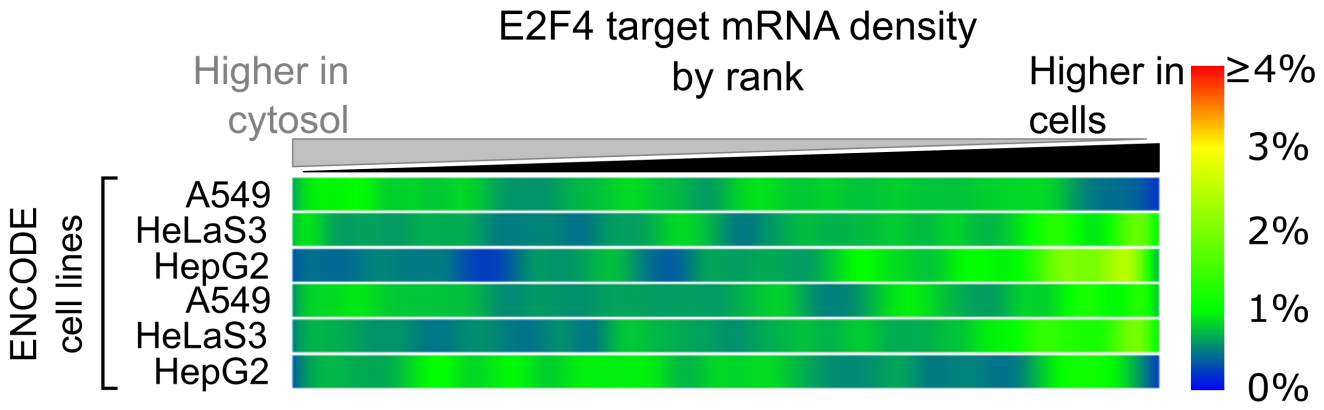
Supplementary Figure S4. Short half-life mRNAs are depleted from U87 EVs and ENCODE cytosol profiles. The fold-change between U87 EVs and cells, and between ENCODE cytosol and cells, was found for short (<= 4 hours) and long (>-= 12 hours) half-life mRNAs. * - $p < 1e^{-4}$.



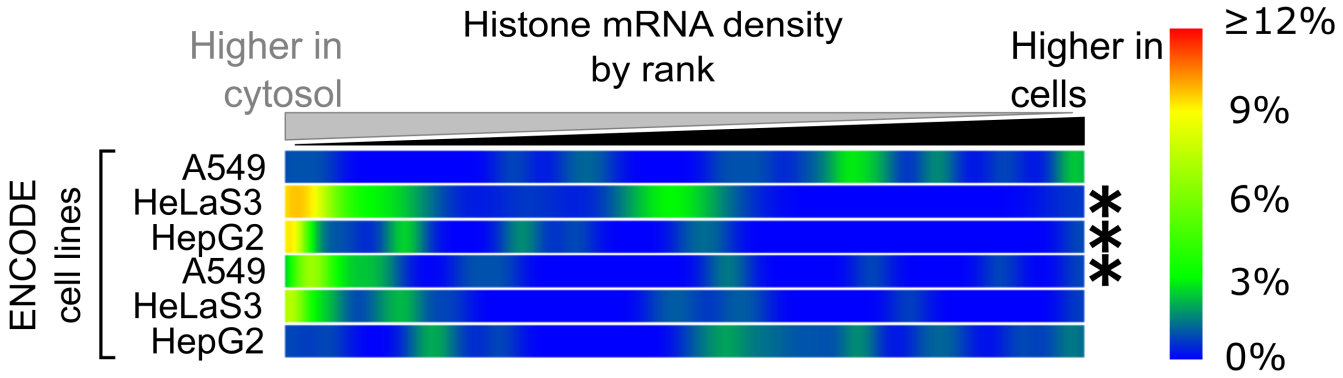
Supplementary Figure S5. Signal peptide encoding mRNAs were characterized using the SignalP utility, and the fold-change in mRNA abundance found between ENCODE cytosol and whole-cells. * - $p < 0.001$



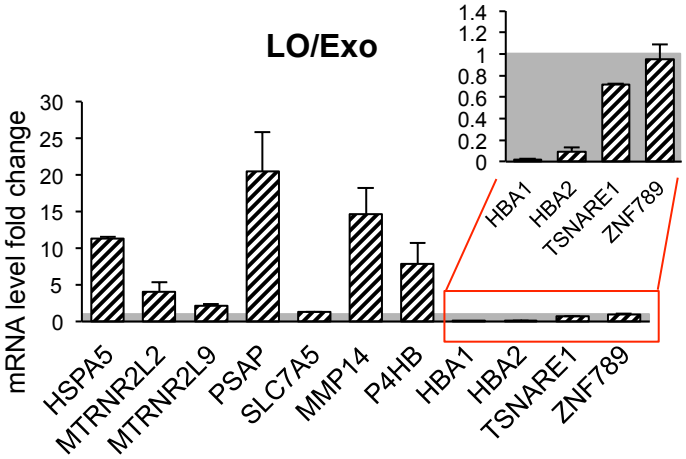
Supplementary Figure S6. E2F transcriptional targets were identified as those having and E2F motif within 2.5 kb of their promoter, and the fold-change found between U87 EVs and cells and between ENCODE cytosol and whole-cells. * - $p < 0.001$



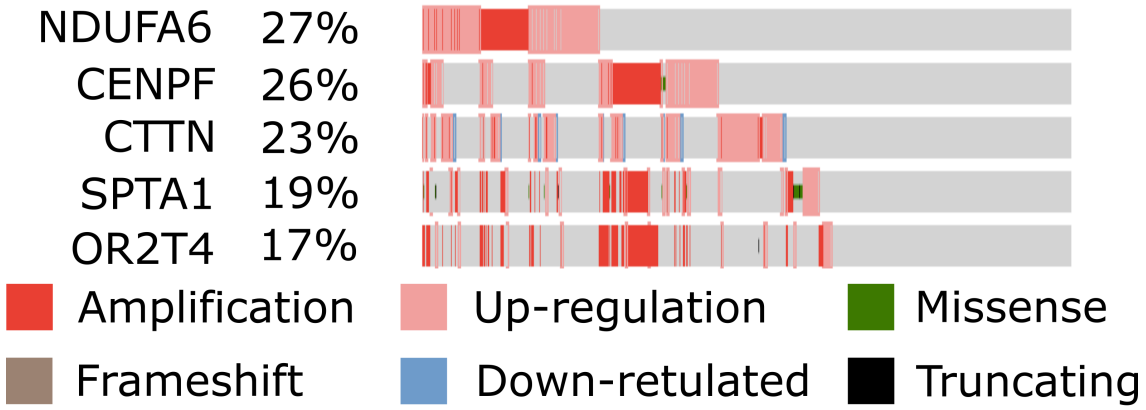
Supplementary Figure S7. E2F4 transcriptional targets were identified via ChIP-seq data targeting the E2F4 protein. For these targets, the fold-change in mRNA abundance was found between ENCODE cytosol and whole-cells.



Supplementary Figure S8. For annotated histone genes, the fold-change in mRNA abundance was found between ENCODE cytosol and whole-cells. * - $p < 0.001$



Supplementary Figure S9. Ratio of mRNA expression for the indicated genes In LO and Exo as measured by Fluidigm. Three mRNAs (TPM1, RRM2, AARS) that resulted unvaried at RNA-Seq were used as normalizers.



Supplementary Figure S10. mRNAs enriched in tumor compared to normal EVs that have been found altered in a high percentage of cases according to the TCGA database.