

Figure S1A

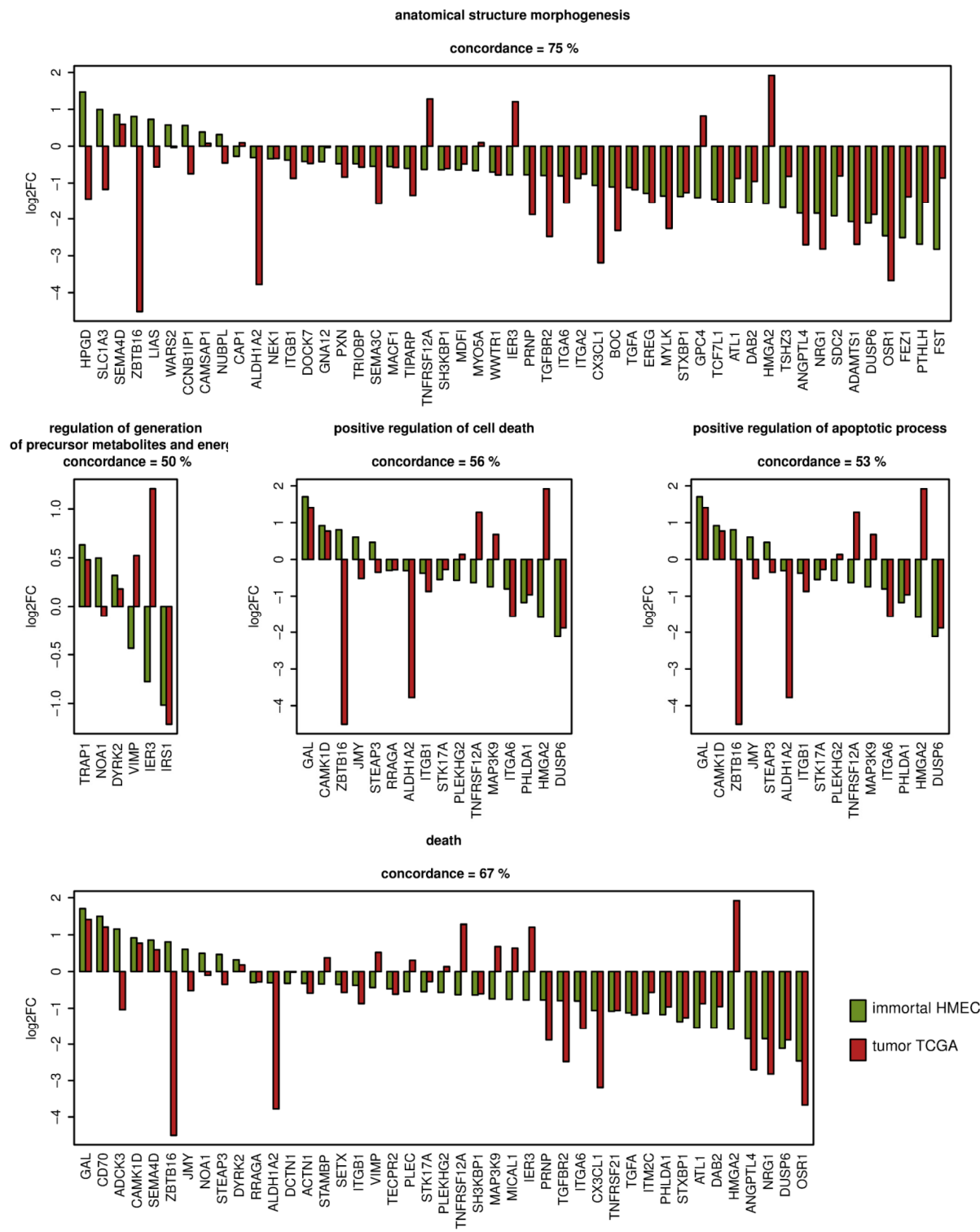


Figure S1B

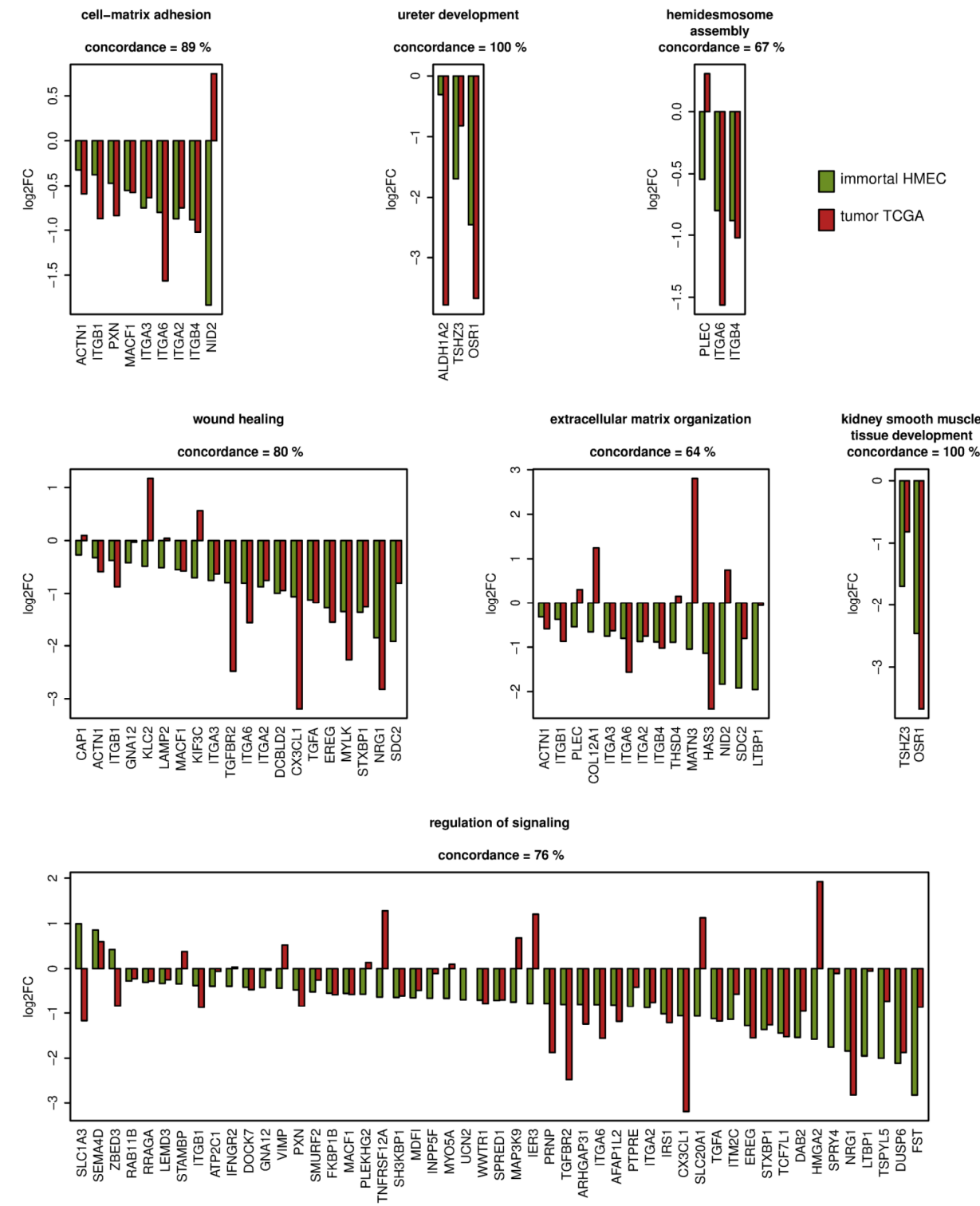


Figure S1C

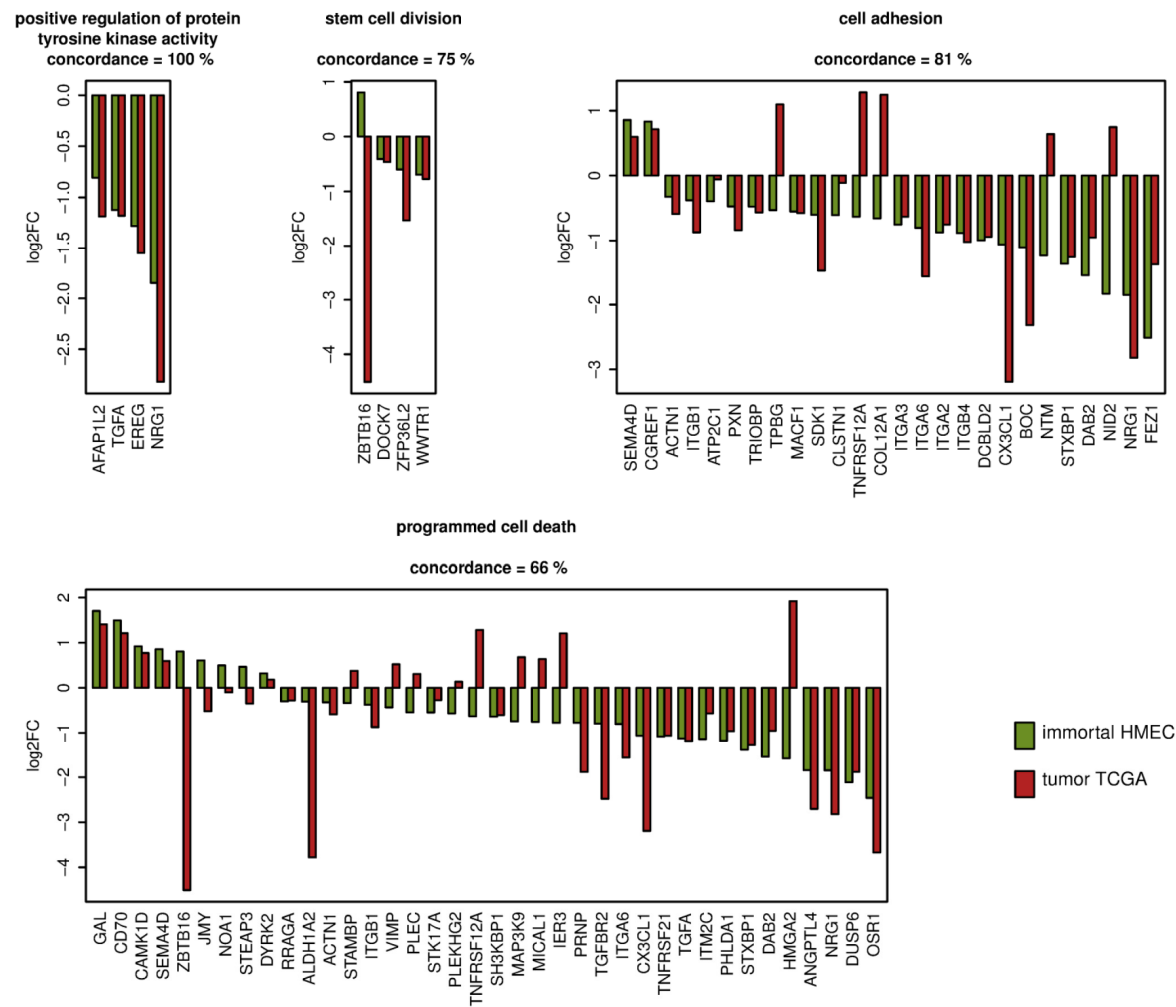


Figure S1. Comparison of gene expression changes in individual enriched GO categories in the in vitro immortalization model with those in the TCGA breast invasive carcinoma samples relative to non-tumor samples.

Figure S2

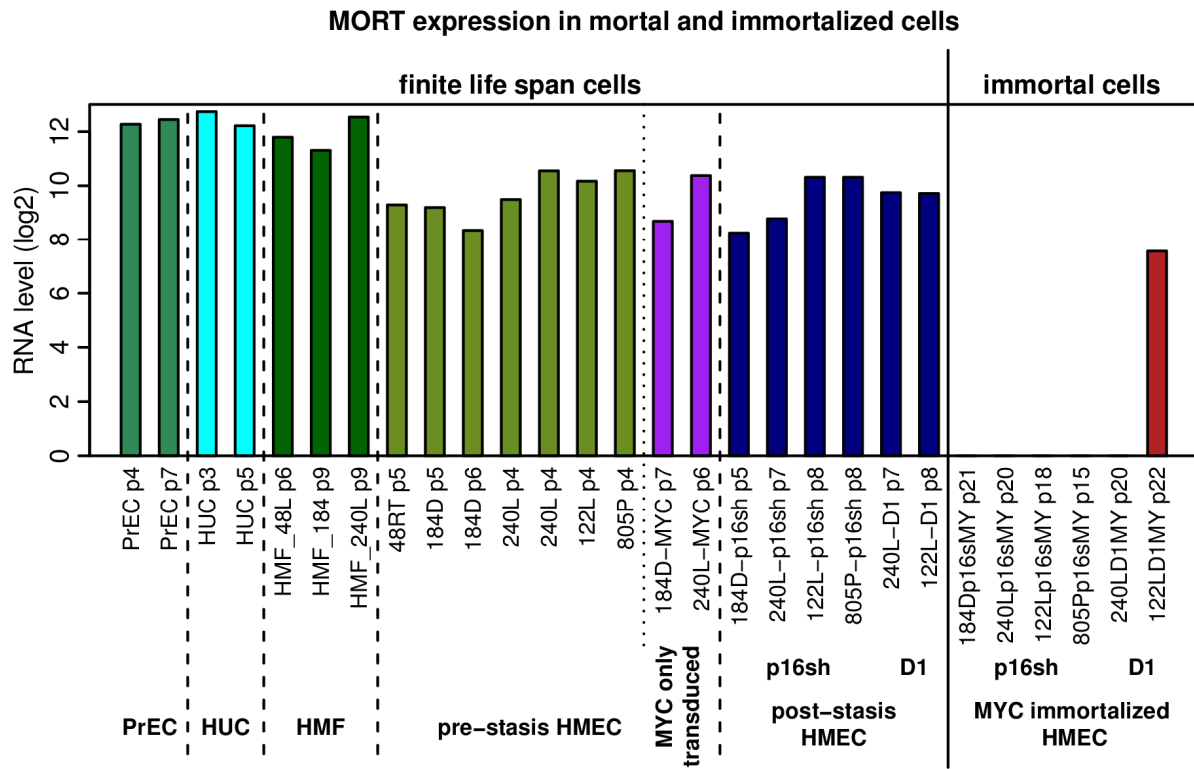


Figure S2. MORT expression in HMEC immortalization model cultures, additional primary cell types, and additional controls. Primary cell types - prostate epithelial cells (PrEC), human urothelial cells (HUC), human mammary fibroblasts (HMF) and human mammary epithelial cells (HMEC), as well as MYC only transduced HMEC and post-stasis HMEC do express MORT. MYC alone likely has a little to no effect on MORT expression. MYC immortalized p16 or D1 cells have MORT either completely silenced or substantially reduced (122LD1MY).

Figure S3

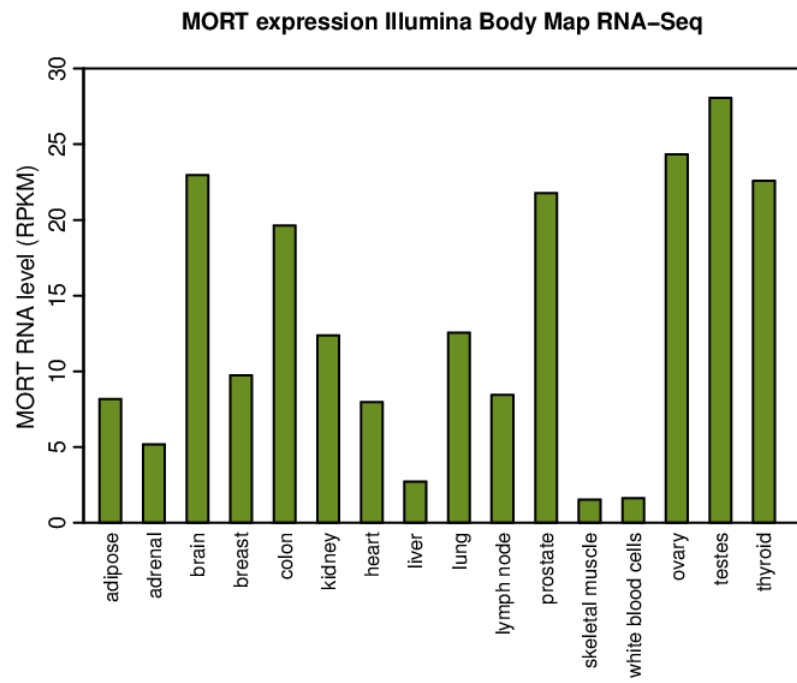


Figure S3. MORT expression across 16 tissues of Illumina Body Map.

Figure S4

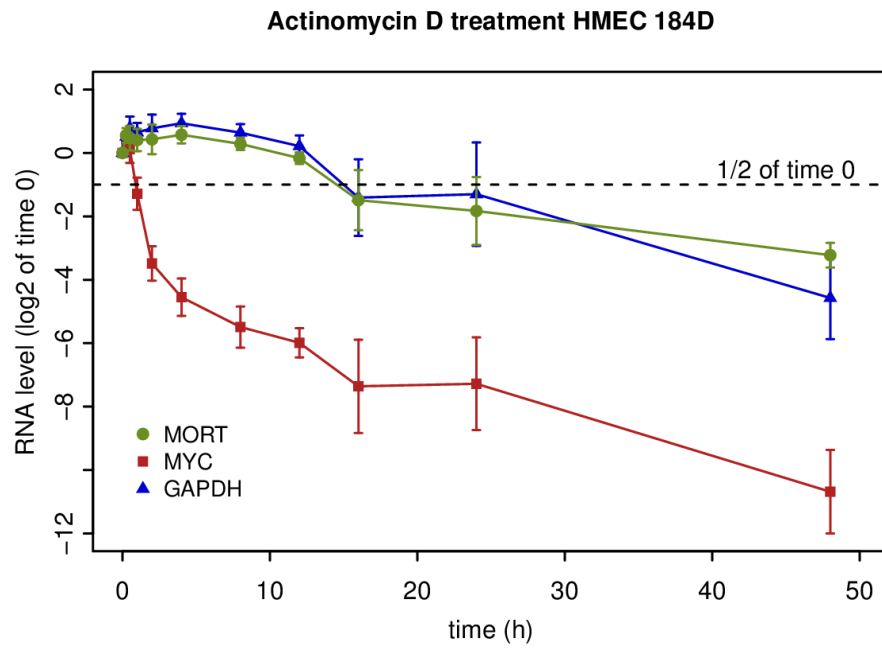


Figure S4. Determination of MORT transcript half-life using actinomycin D (1 μ g/ml) treatment. MYC was used as a short half-life reference gene and GAPDH was used as a long half-life reference gene (Yang et al. 2003). The results indicate that MORT has a long half-life of ~15 hrs comparable to GAPDH. The error bars show the SEM of 3 independent experiments.

Figure S5

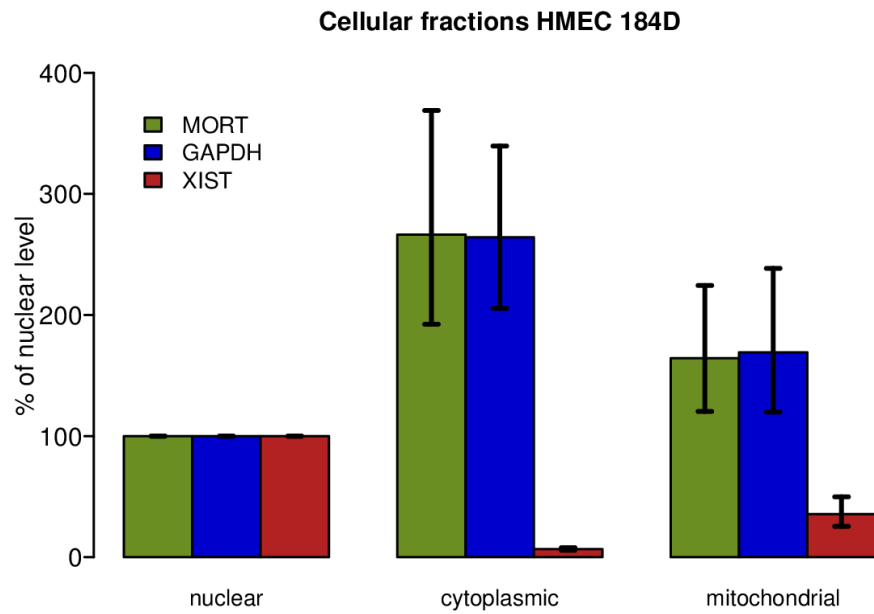


Figure S5. Cellular localization of MORT. HMEC cells were lysed in hypotonic conditions using a Dounce homogenizer and the lysate was separated by differential centrifugation to nuclear, mitochondrial and cytoplasmic fractions. Relative representation of MORT, GAPDH (cytoplasmic) and XIST (nuclear) transcripts was determined by real-time PCR. All data are displayed relative to the nuclear fraction, which is set to 100 %. The error bars show the SEM of 3 independent experiments. MORT is localized predominantly in the cytoplasmic fraction, similar to GAPDH.

Figure S6

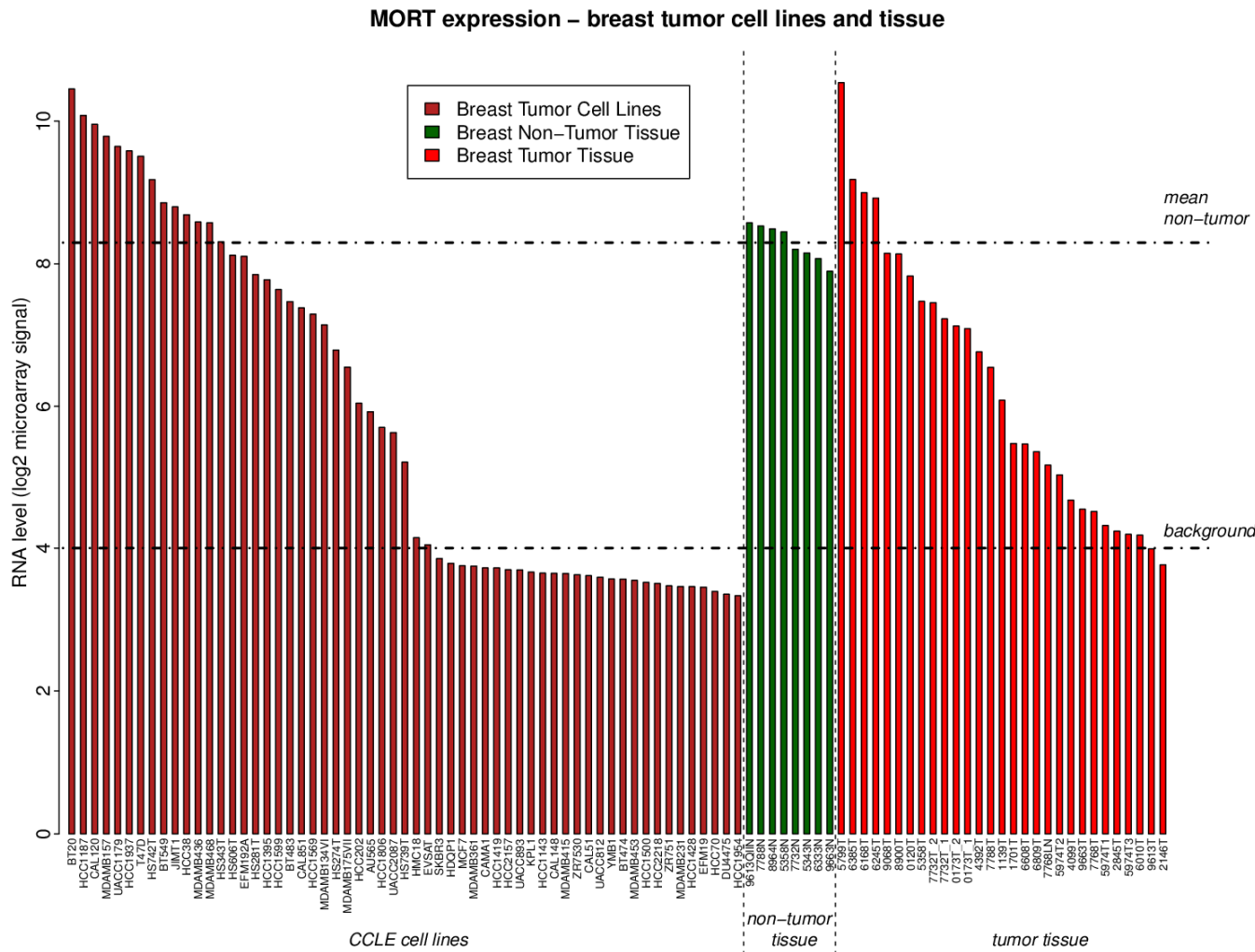


Figure S6. MORT expression level across breast cancer cell lines from cancer cell line encyclopedia (CCLE) and a set of 8 breast non-tumor samples and 27 breast carcinomas.

Figure S7

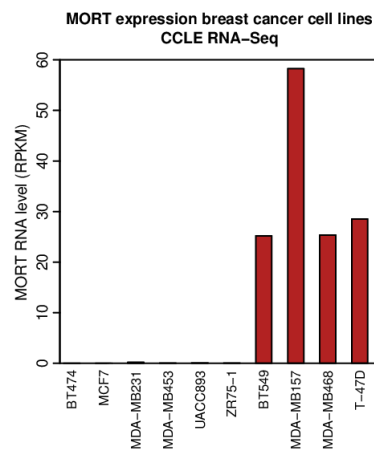


Figure S7. MORT expression level across 10 breast cancer cell lines from cancer cell line encyclopedia (CCLE) as determined by RNA-seq

Figure S8A

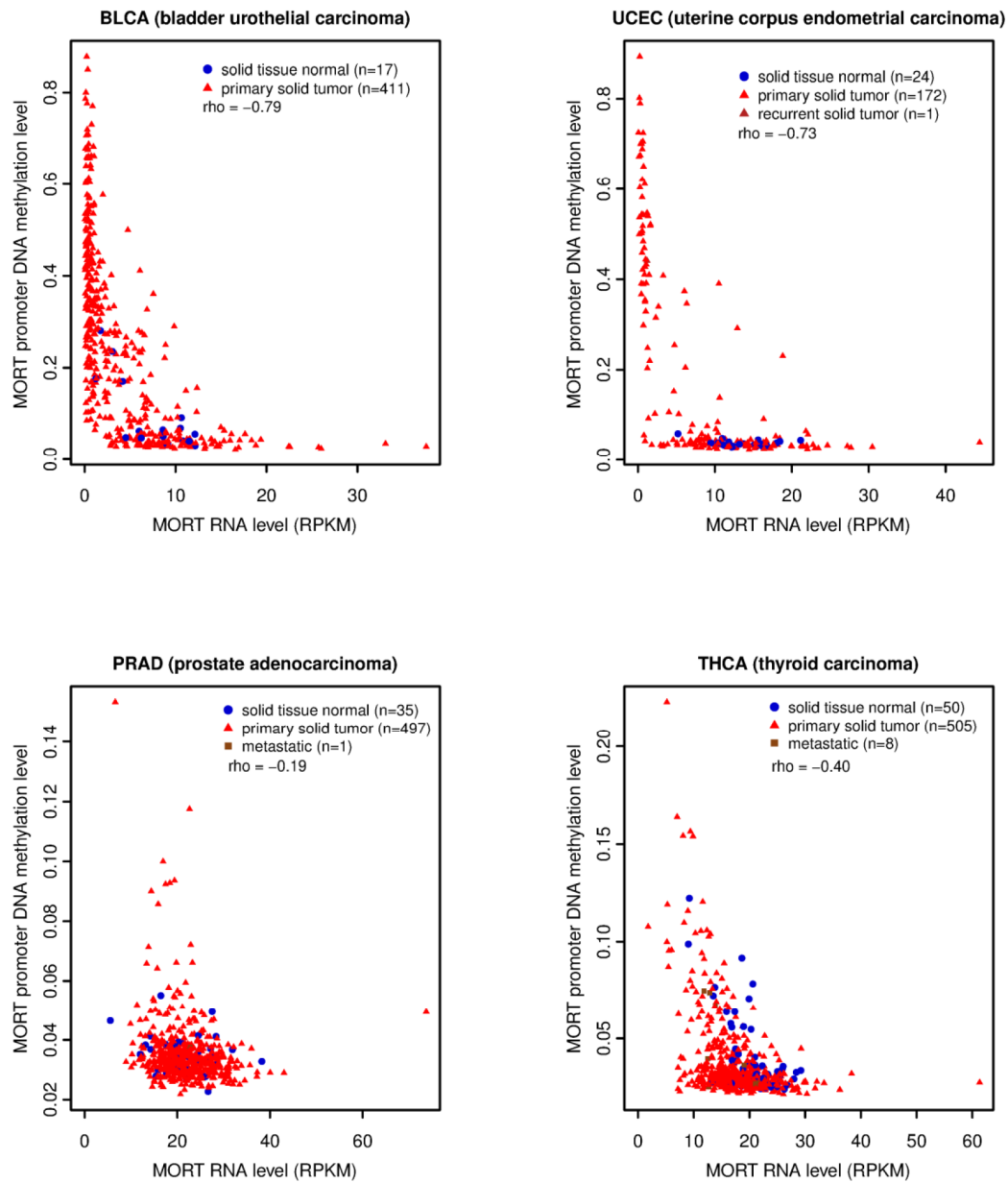


Figure S8B

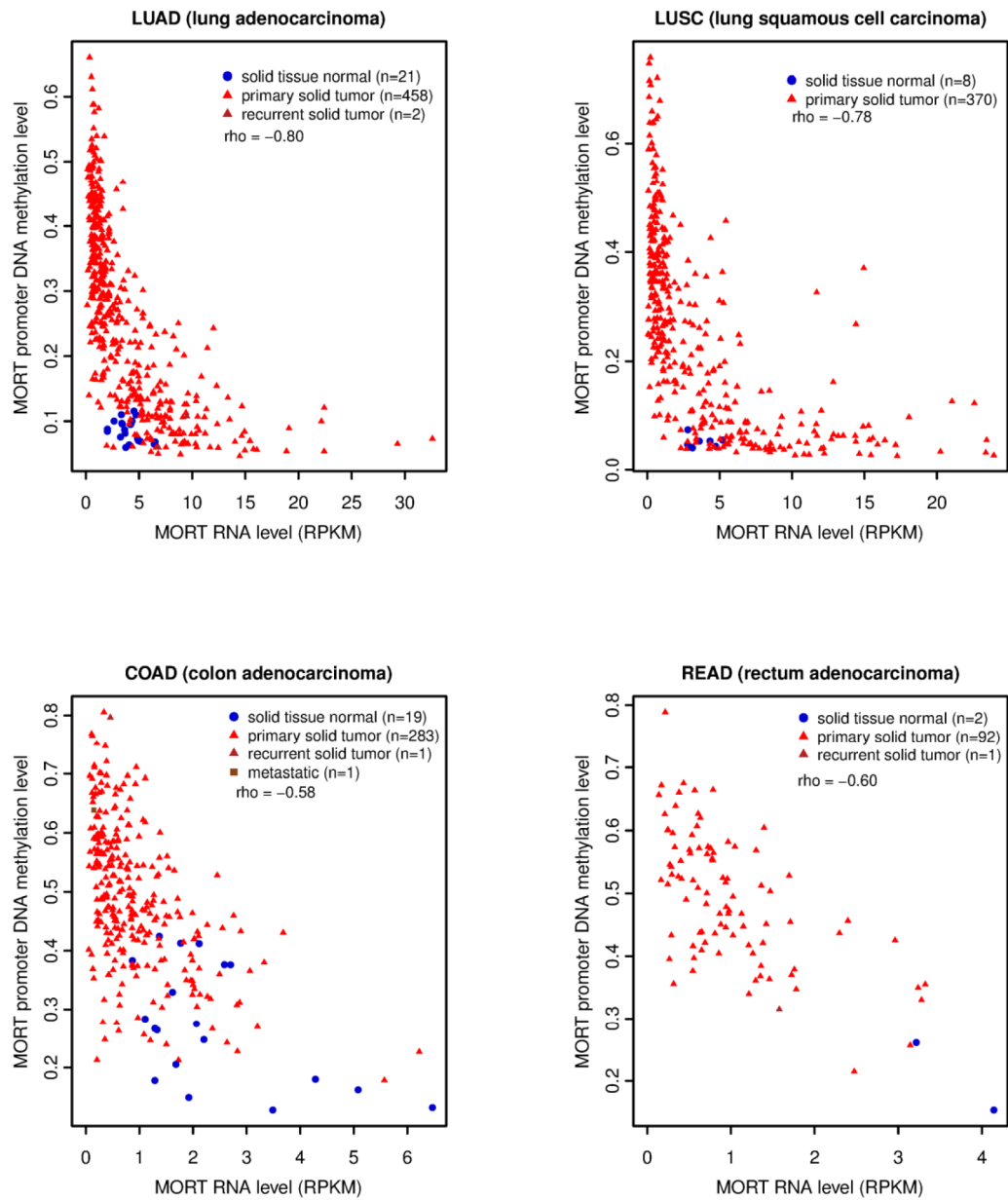


Figure S8C

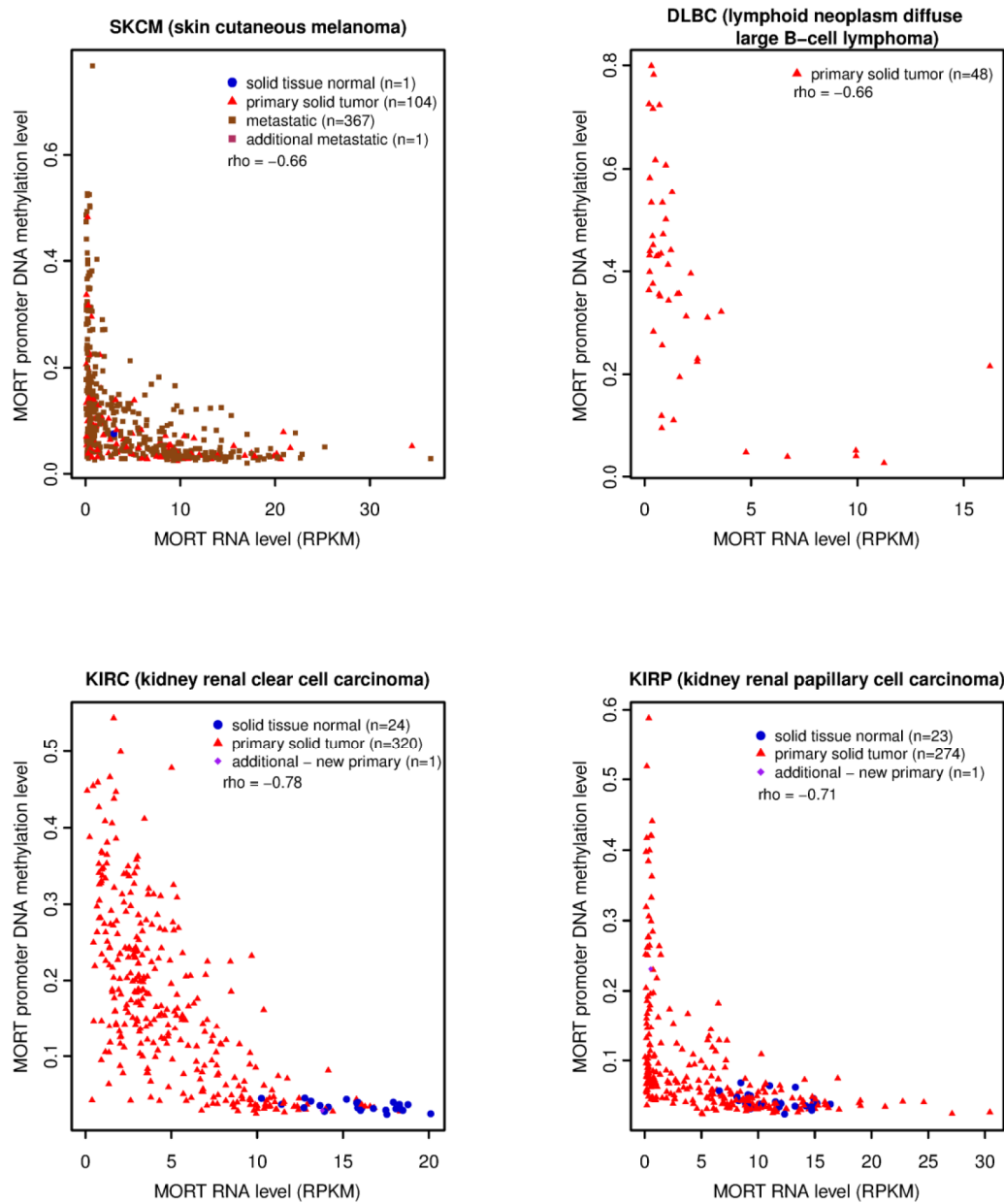


Figure S8D

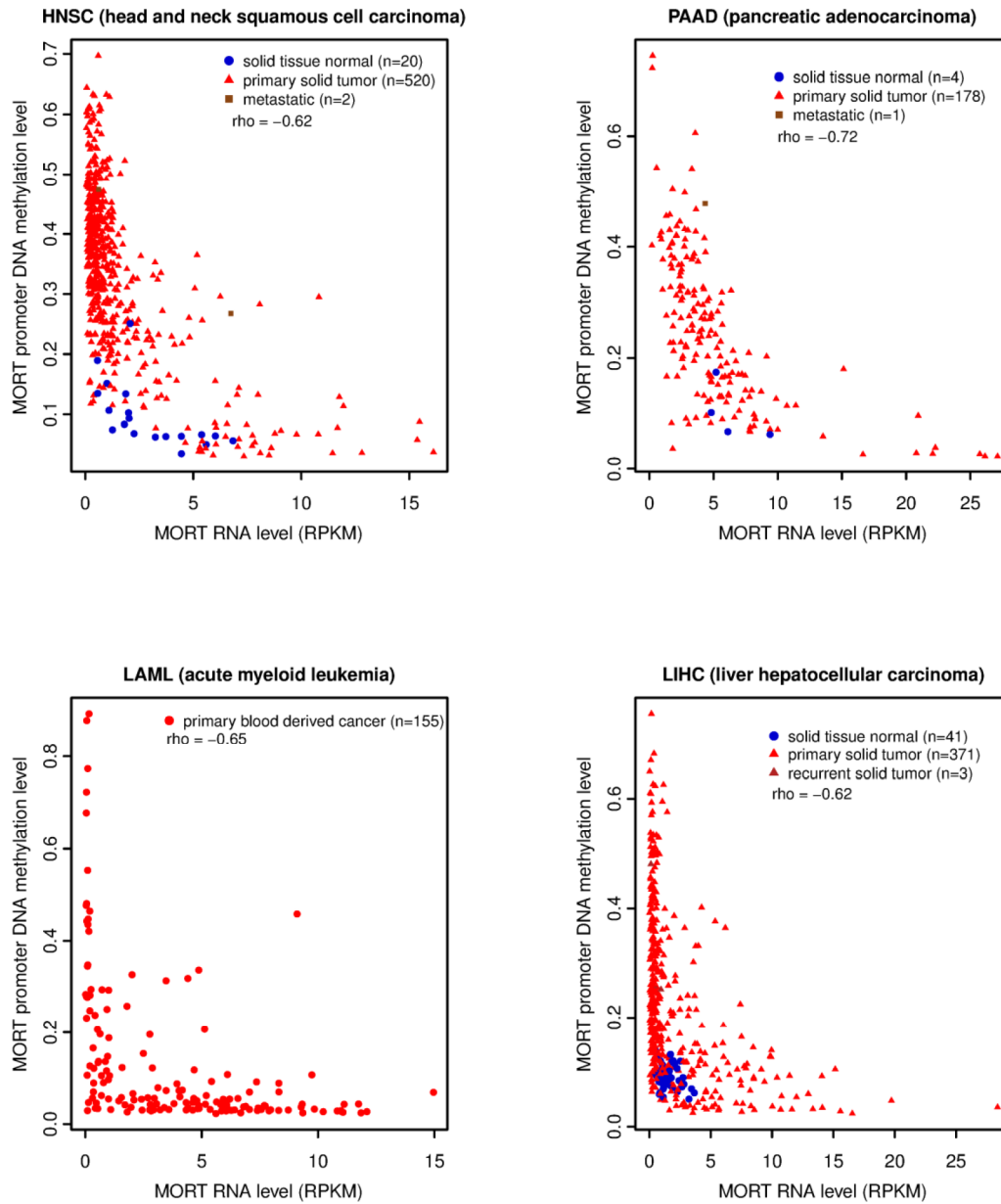


Figure S8. Integration of MORT expression and DNA methylation TCGA data for 16 additional TCGA tumor types. The x-axis shows MORT expression level according to RNA-seq and y-axis shows the level of MORT promoter methylation according to Illumina HumanMethylation450 microarray. The correlation coefficient ρ between MORT expression and promoter methylation for each tumor type is displayed.

Figure S9

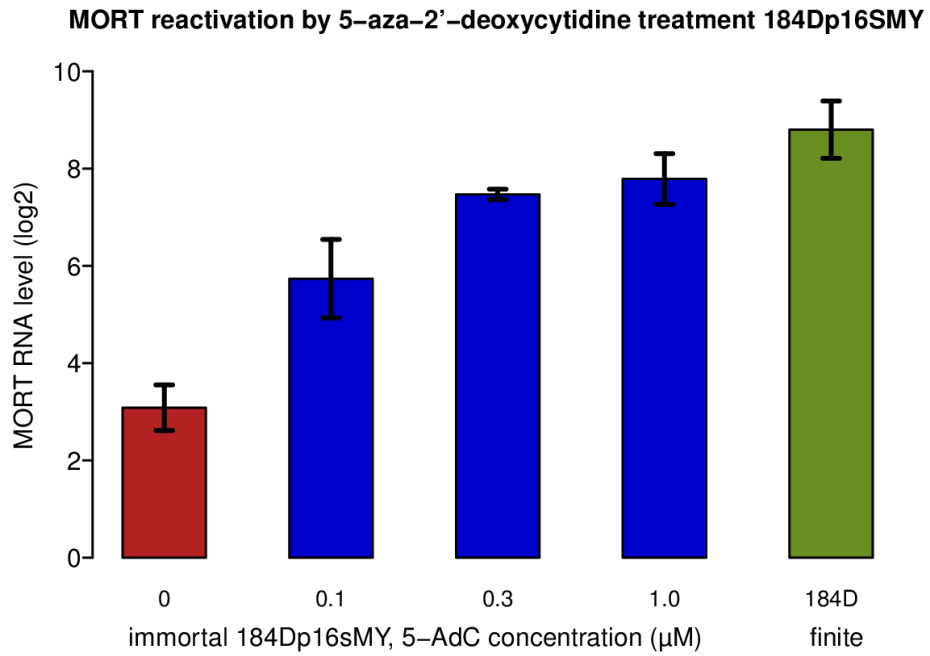


Figure S9. MORT is reactivated by 5-AdC treatment of immortalized HMEC 184Dp16SMY. The figure shows MORT transcript level in untreated 184Dp16SMY (red), an increased MORT level after 96 h treatment with three concentrations of 5-AdC (blue) and the MORT level in untreated finite parental 184D HMEC (green). The error bars show the SEM of 3 independent experiments.

Supplemental References

Yang E, van Nimwegen E, Zavolan M, Rajewsky N, Schroeder M, Magnasco M, Darnell JE, Jr. 2003. Decay rates of human mRNAs: correlation with functional characteristics and sequence attributes. *Genome Res* **13**(8): 1863-1872.