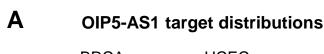
## **Supplemental Information**

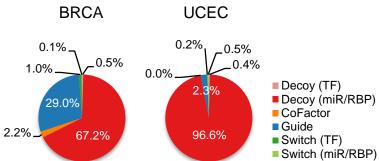
**Pan-Cancer Analysis of IncRNA Regulation** 

**Supports Their Targeting of Cancer** 

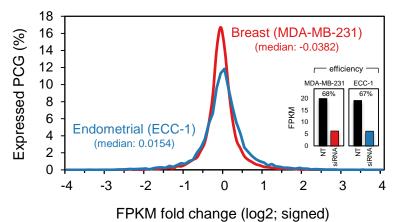
**Genes in Each Tumor Context** 

Hua-Sheng Chiu, Sonal Somvanshi, Ektaben Patel, Ting-Wen Chen, Vivek P. Singh, Barry Zorman, Sagar L. Patil, Yinghong Pan, Sujash S. Chatterjee, The Cancer Genome Atlas Research Network, Anil K. Sood, Preethi H. Gunaratne, and Pavel Sumazin

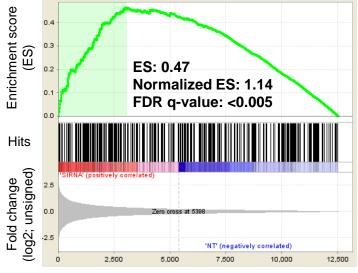




## B siOIP5-AS1 vs. NT fold changes by RNA-seq

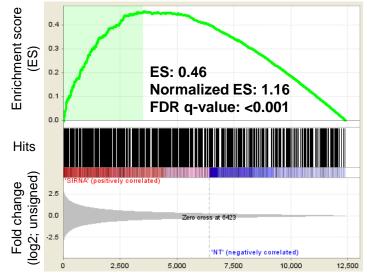


## C Predicted post-transcriptional decoy targets of OIP5-AS1 in MDA-MB-231



Fold-change rank of expressed genes in descending order

## D Predicted post-transcriptional decoy targets of OIP5-AS1 in ECC-1



Fold-change rank of expressed genes in descending order

**Figure S1.** The majority of the predicted and expressed OIP5-AS1 post-transcriptional targets were downregulated following siOIP5-AS1 transfections in MDA-MB-231 and ECC-1. (**A**) OIP5-AS1 was inferred to regulate most of its targets as a post-transcriptional decoy in BRCA and UCEC. (**B**) Fold changes after siOIP5-AS1 and NT transfections of expressed PCGs (FPKM>0.1 in both siOIP5-AS1 and NT, and nonzero MAD score in TCGA tumor data) were near 0. The oip5-as1 expression is inset to demonstrate its silencing. (**C**) GSEA analysis of expressed predicted post-transcriptional decoy targets in MDA-MB-231 and (**D**) ECC-1; all expressed genes were sorted by siOIP5-AS1 to NT absolute fold changes, GSEA used weighted enrichment statistics and ratio of classes, with p-values computed using 1k gene-set permutations. Related to Figure 6.