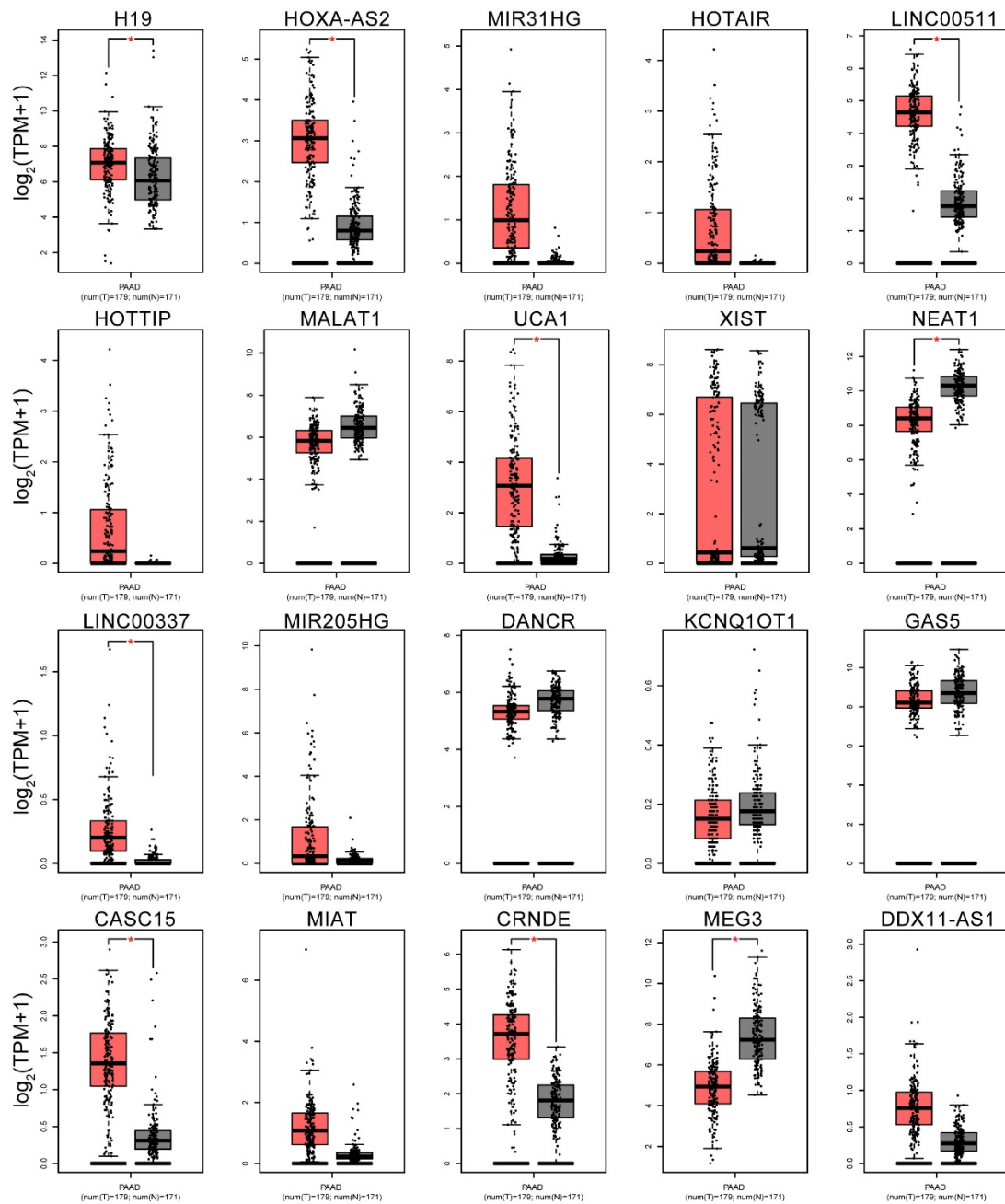


# 1 Supplementary figures



2

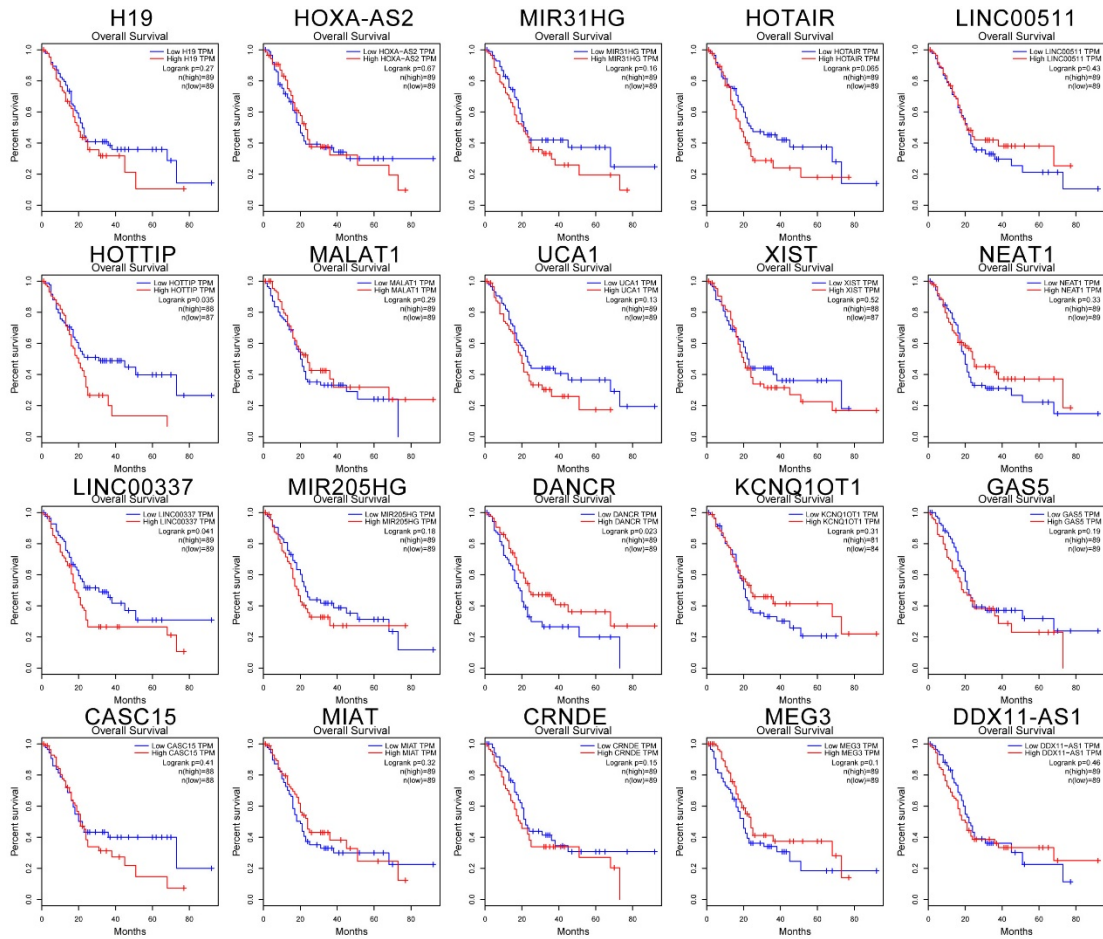
3 **Figure S1.** Related to Figure 1

4 Box plots depicting the expression of 20 cancer-associated lncRNAs in PDAC and  
5 normal tissues. TCGA data was analyzed using the GEPIA website ([http://gepia.cancer-](http://gepia.cancer-pku.cn/index.html)  
6 [pku.cn/index.html](http://gepia.cancer-pku.cn/index.html)).

7

8

9

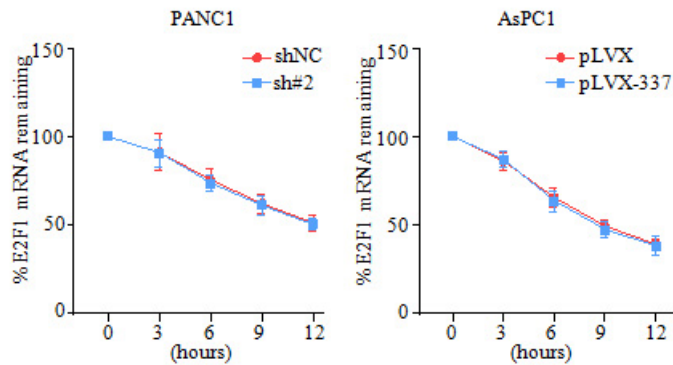


10

11 **Figure S2.** Related to Figure 1

12 Overall survival analysis of the expression of 20 cancer-associated lncRNAs in PDAC.  
 13 TCGA data was analyzed using the GEPIA website ([http://gepia.cancer-](http://gepia.cancer-pku.cn/index.html)  
 14 [pku.cn/index.html](http://gepia.cancer-pku.cn/index.html)).

15

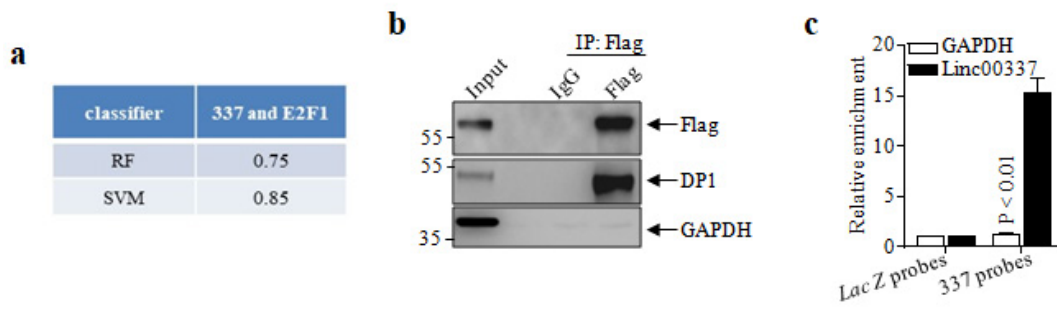


16

17 **Figure S3.** Related to Figure 4

18 RNA decay curves depicting the degradation of mRNAs. 18S was used as a reference  
 19 gene and no significant alterations were observed following Actinomycin D treatment.

20 Data represent the mean  $\pm$  SD of three independent experiments.



21

22 **Figure S4.** Related to Figure 5

23 a, RPISeq prediction parameters of Linc00337 and E2F1 binding.

24 b, western blot analysis of Flag-E2F1 immunoprecipitation, DP1 as positive control and  
25 GAPDH as negative control.

26 c, qRT-PCR analysis of Linc00337 and GAPDH enrichment in PANC1 cells by *Lac Z*  
27 and 337.

28