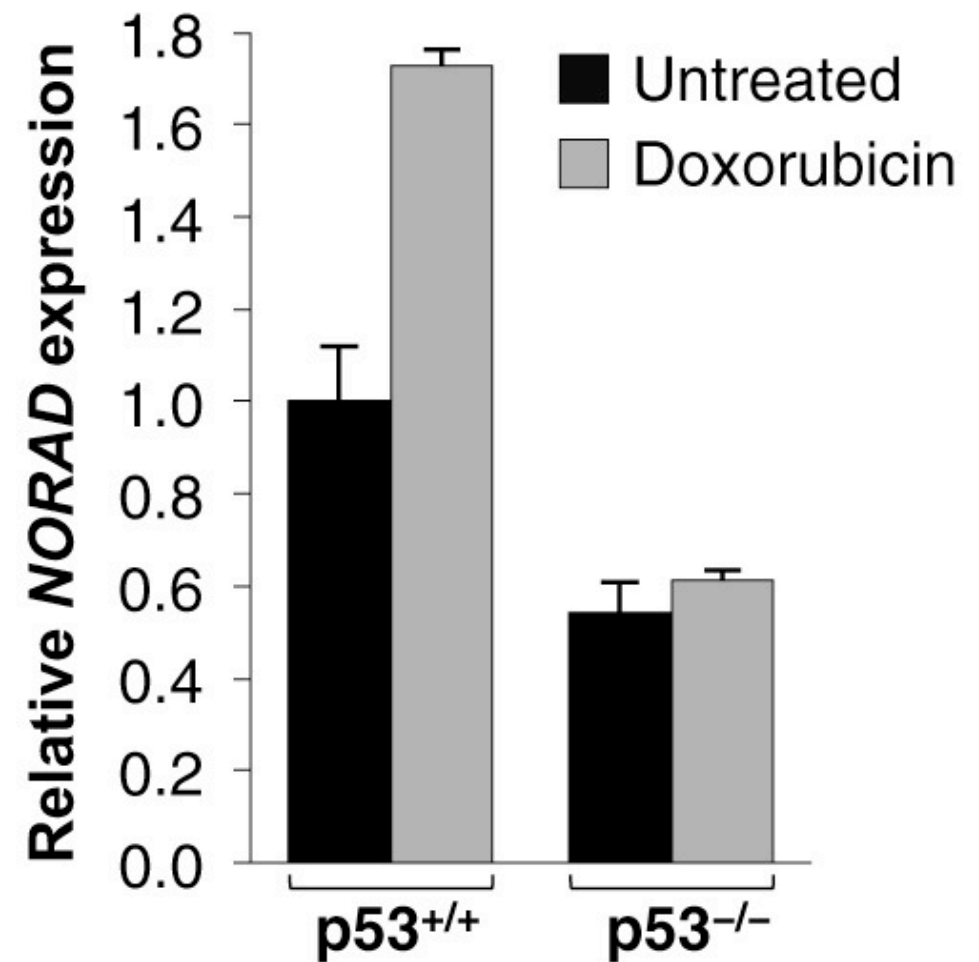
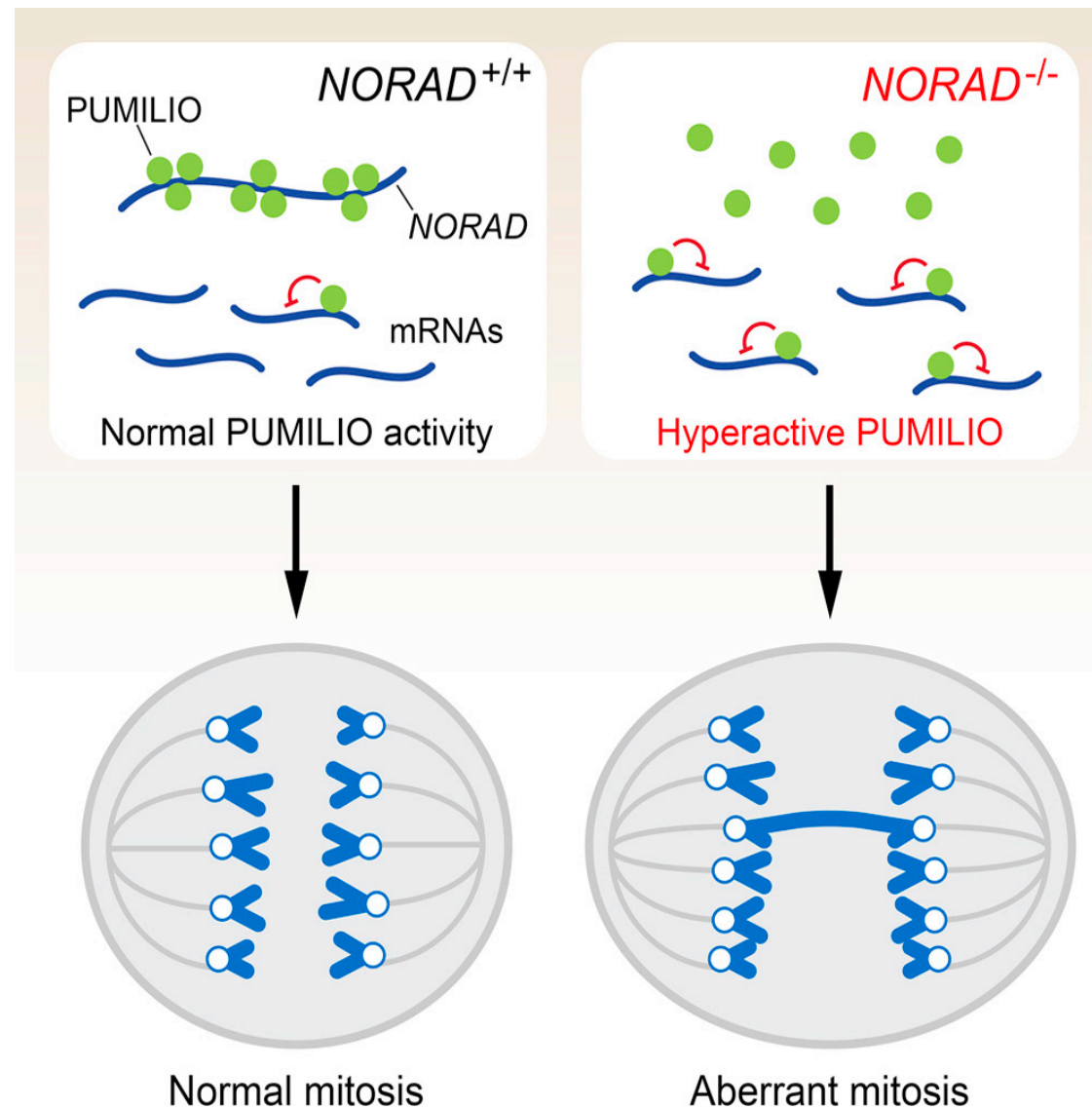


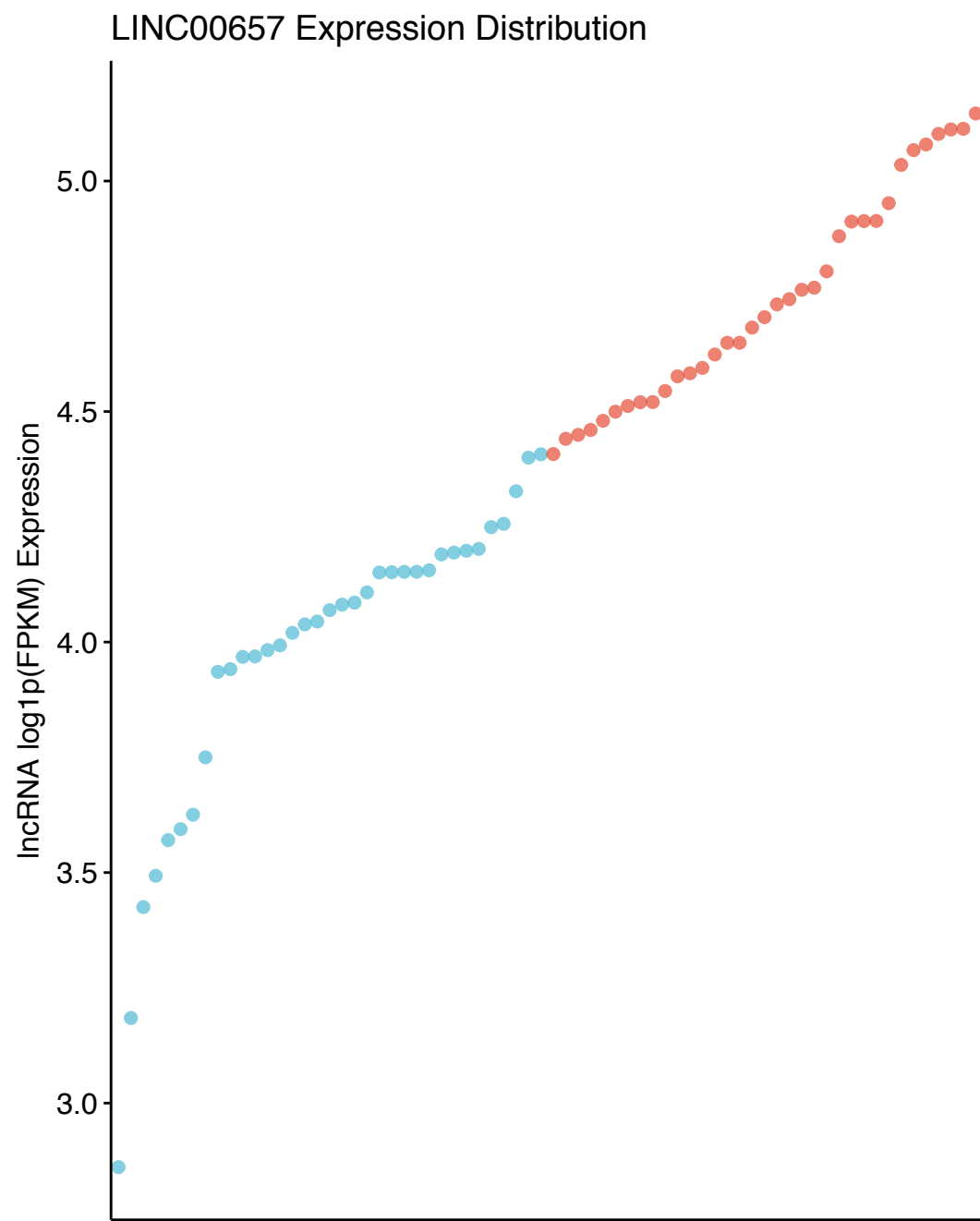
Updated Slides

LINC00657 = NORAD

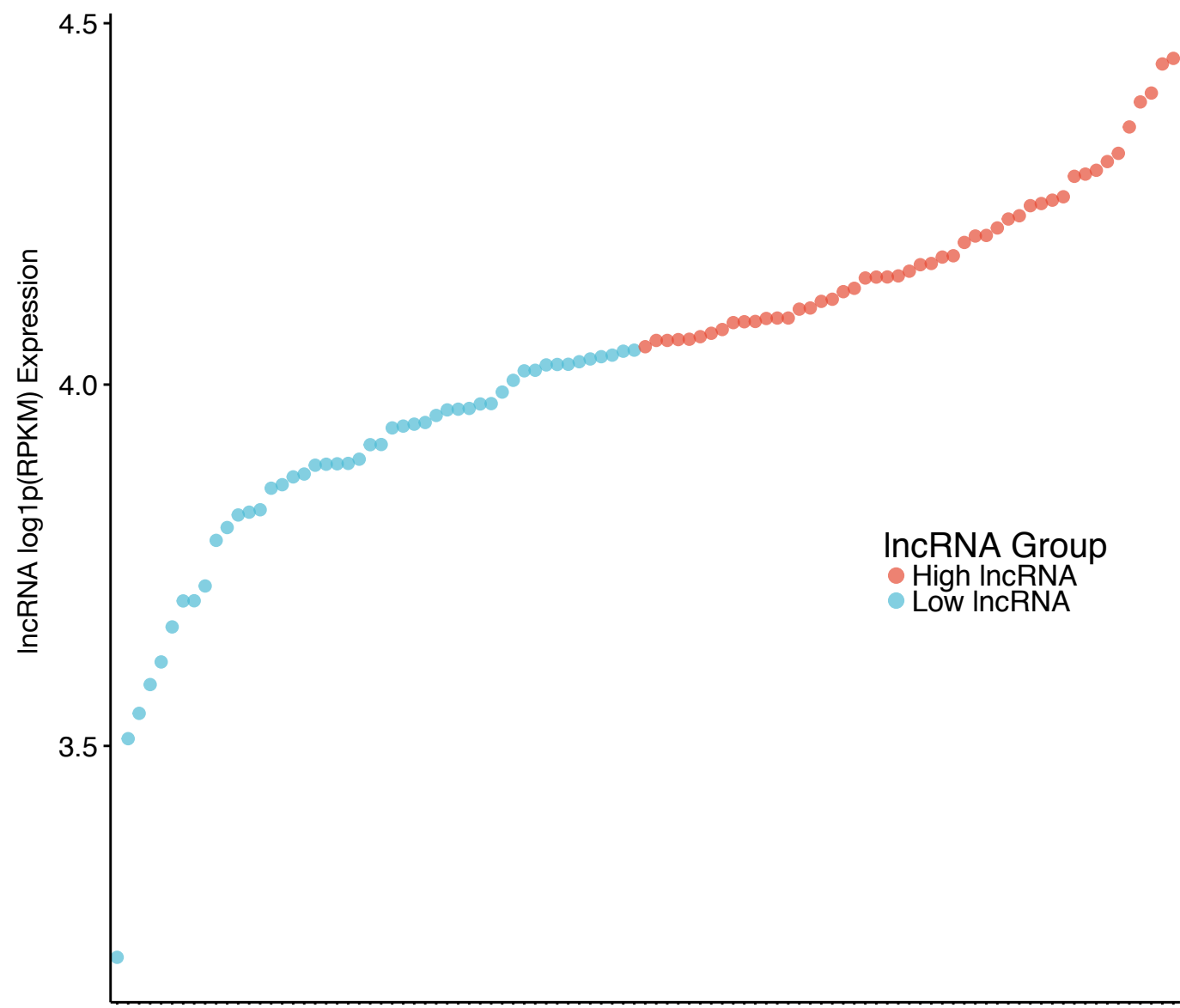


Lee et al. (2016) found that **DNA damage induced NORAD expression in a p53 (TP53; 191170)-dependent manner** in HCT116 human colon cancer cells. Conditional knockout or knockdown of NORAD expression caused multiple mitotic errors, including anaphase bridges, mitotic slippage, and significant aneuploidy.

Expression Distribution of NORAD between Normal and Tumour Tissues



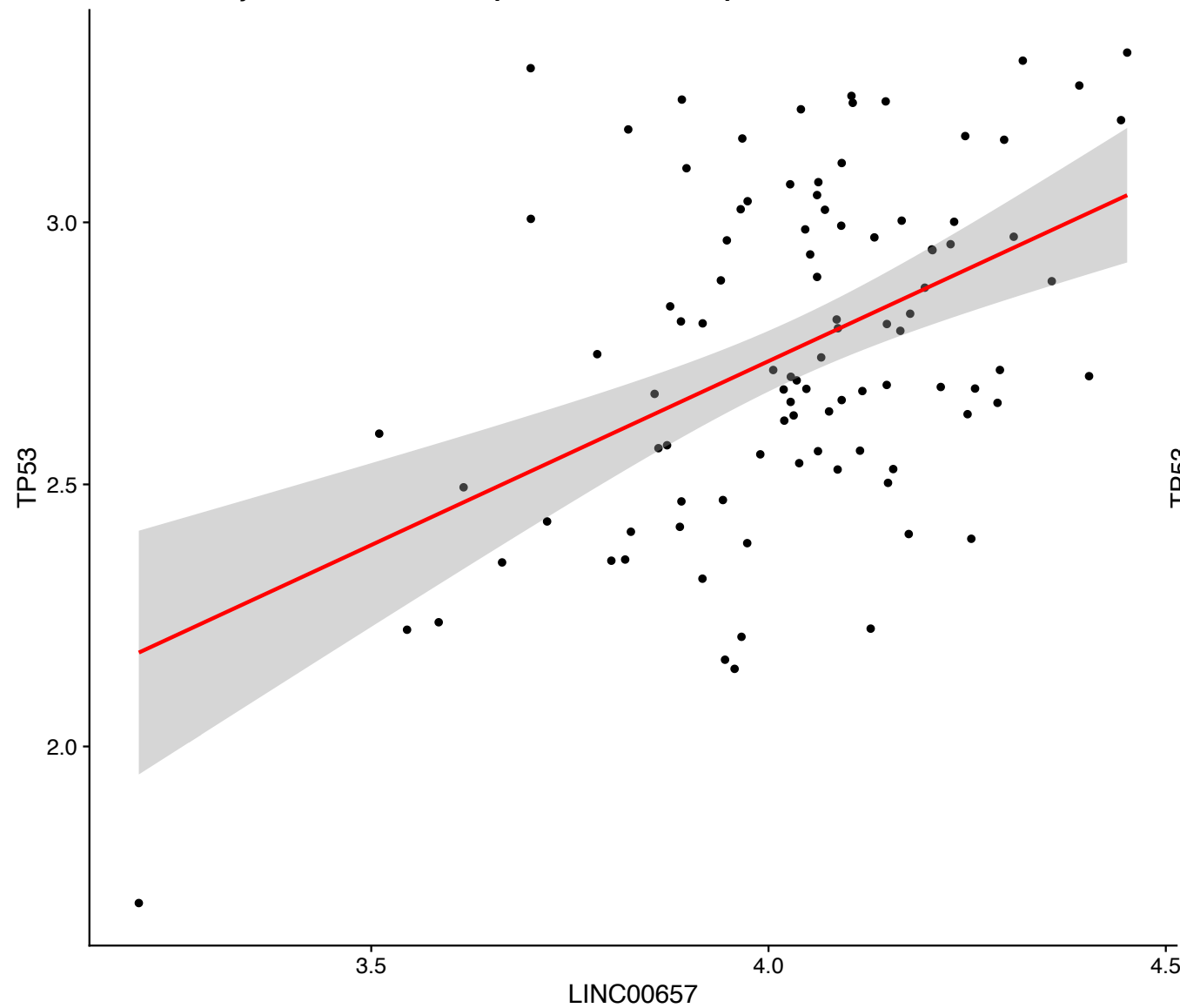
PCAWG, n = 70



GTEx, n = 97

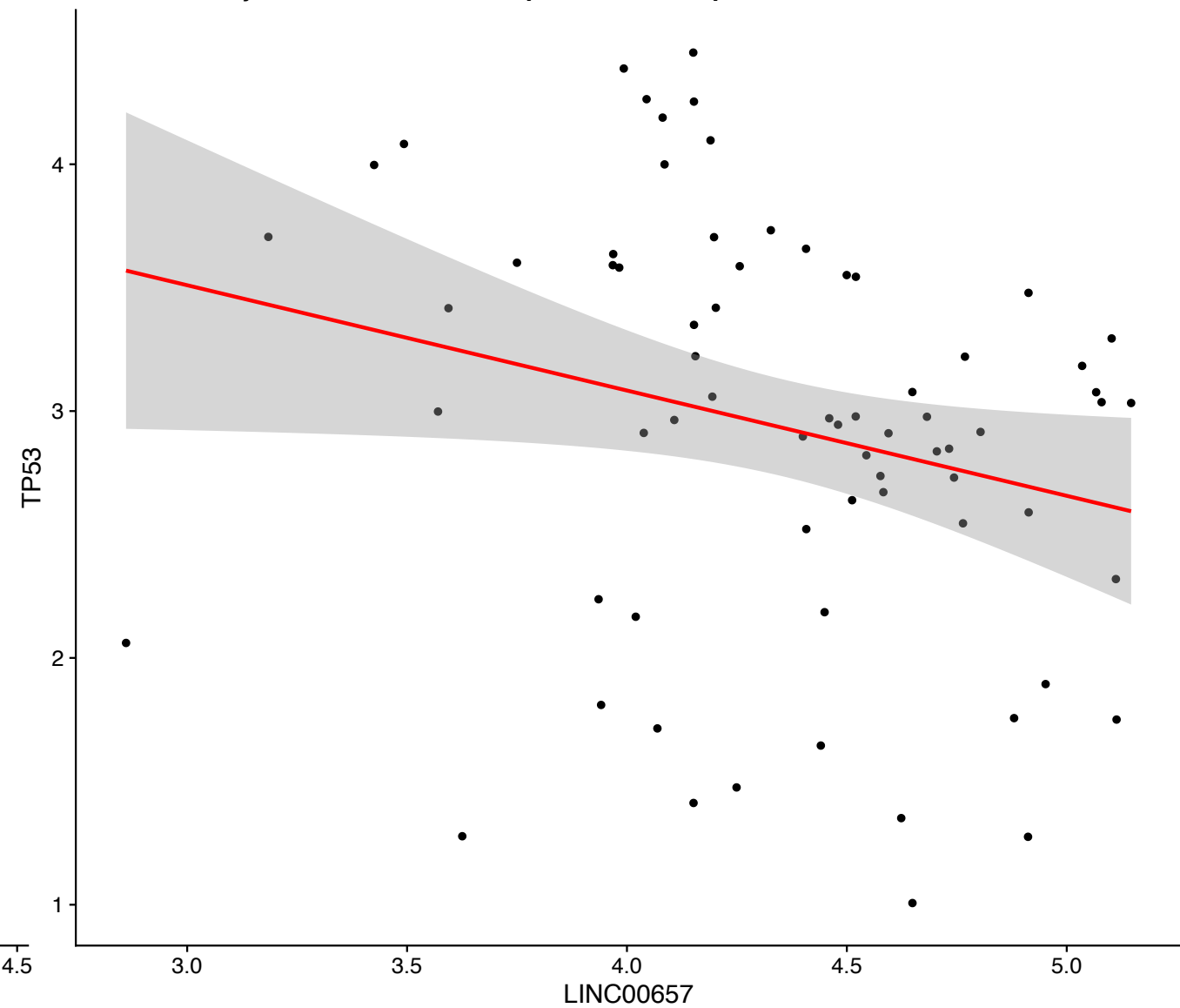
NORAD-TP53 Co-Expression in 97 Normal Ovary Samples

Adj R2 = 0.2062 Intercept = -0.071258 Slope = 0.7016 P = 1.7836e-06

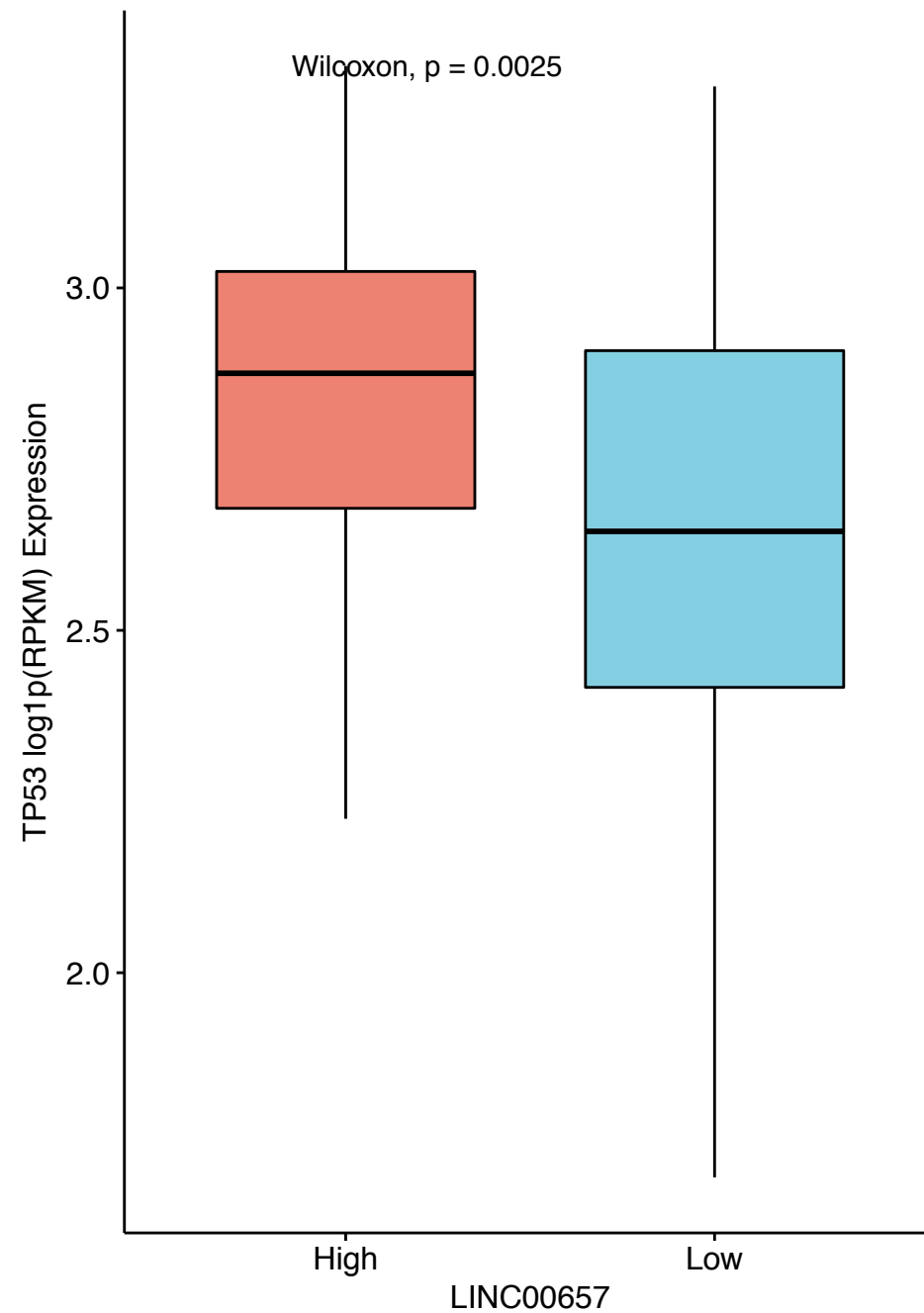


NORAD-TP53 Co-Expression in 70 Tumour Ovary Samples

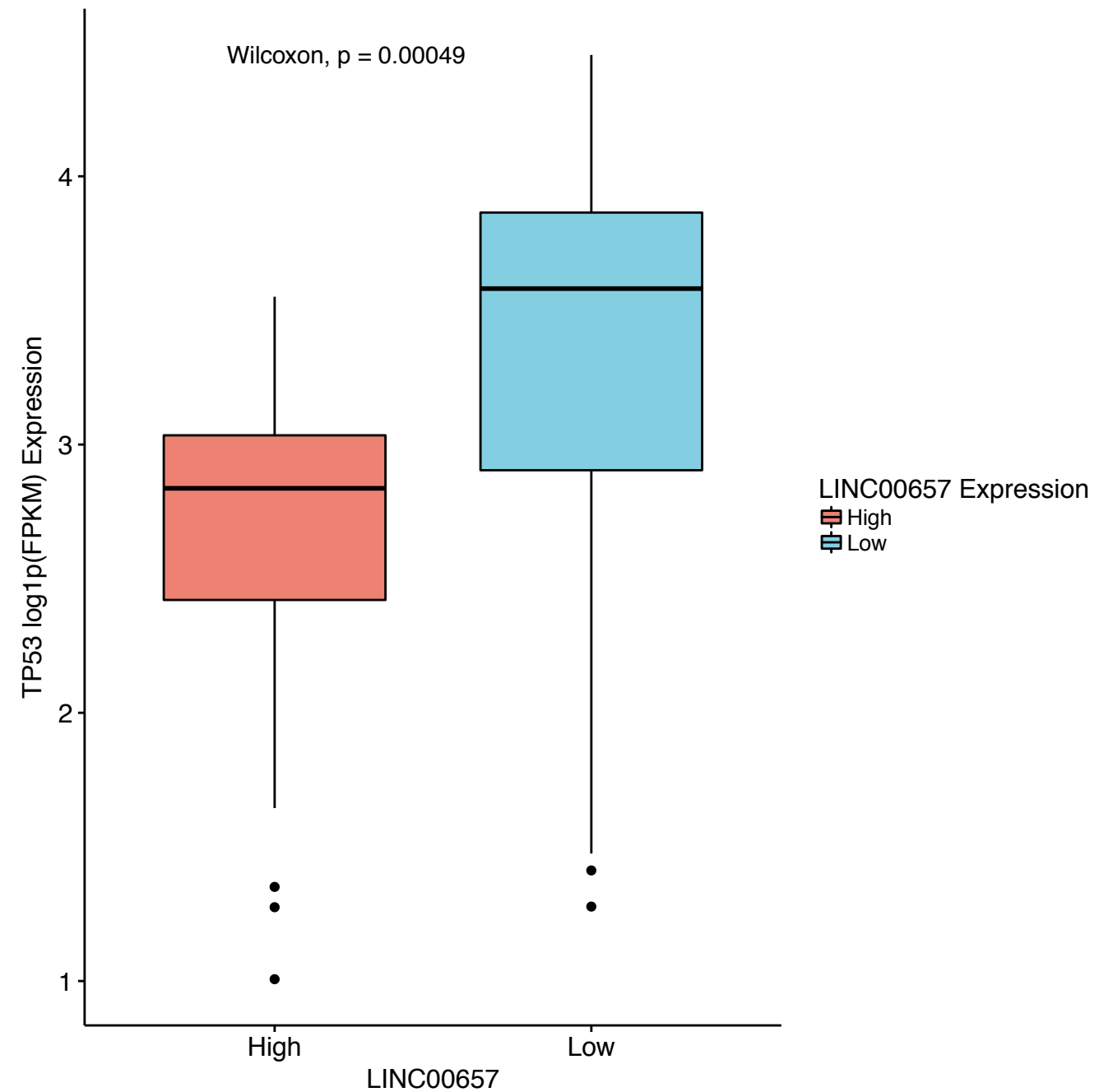
Adj R2 = 0.046223 Intercept = 4.7896 Slope = -0.42657 P = 0.040901



TP53 Relative to NORAD in 97 Normal Ovary Samples

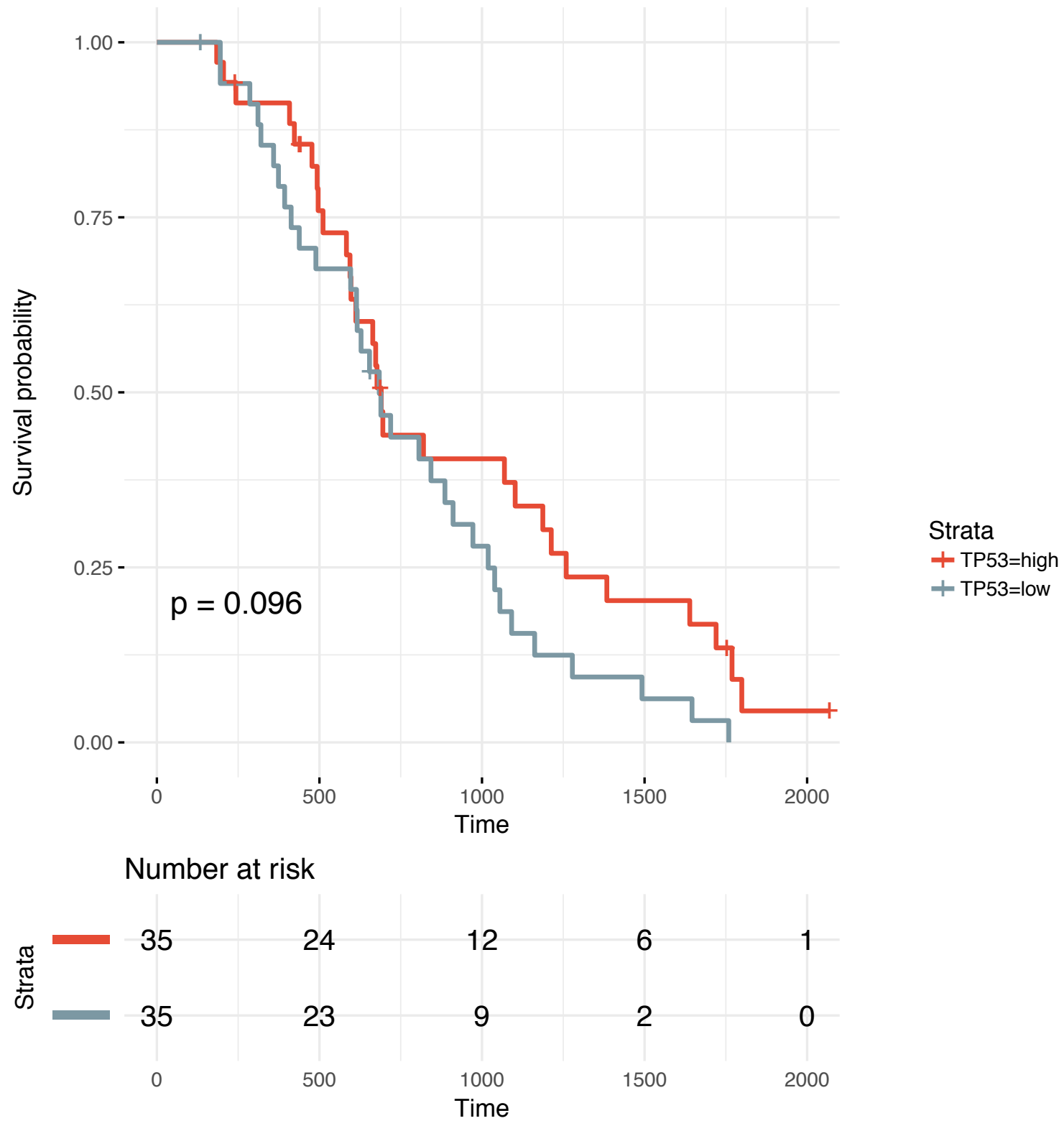


TP53 Relative to NORAD in 70 Tumour Ovary Samples



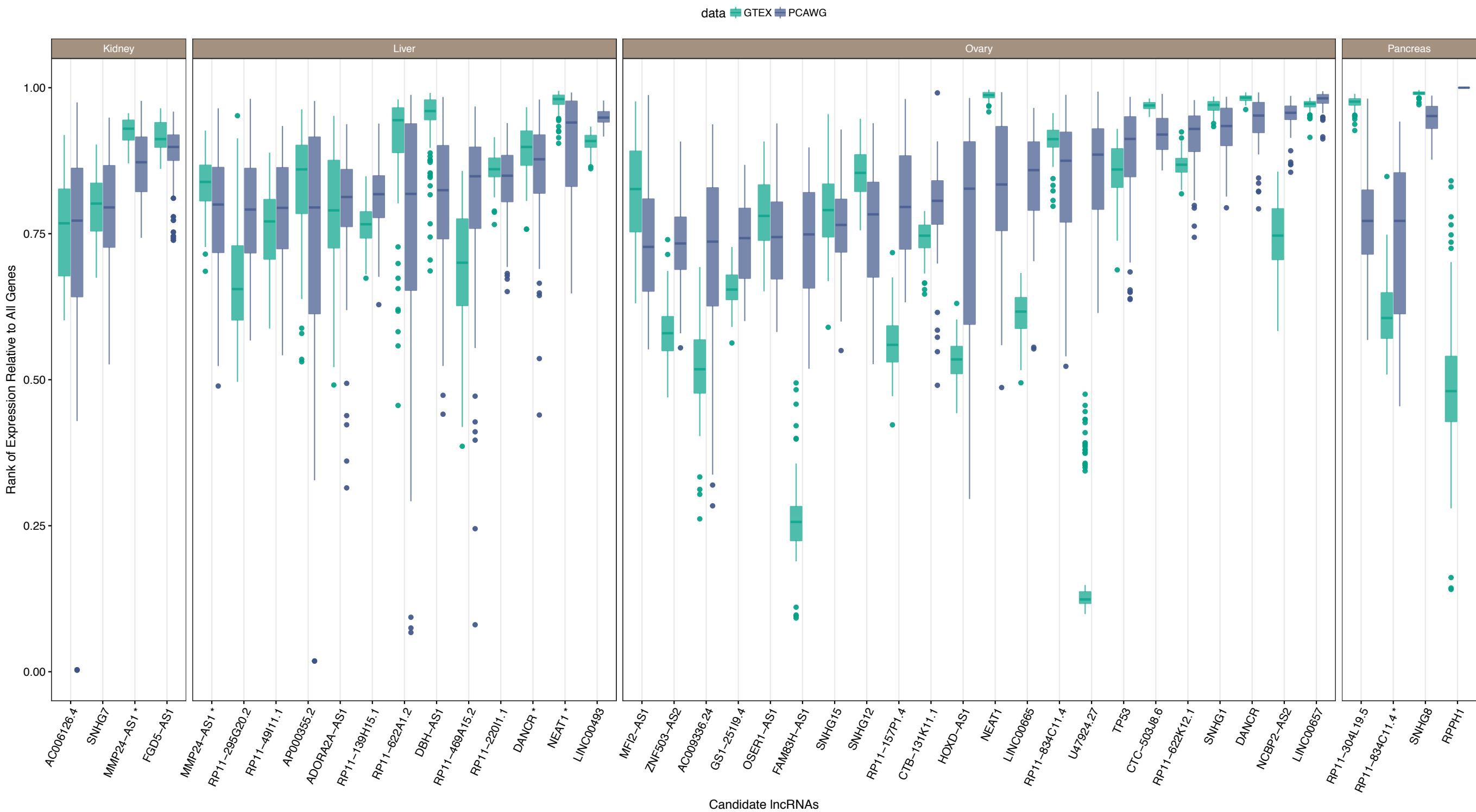
1. NORAD and TP53 negatively correlated in cancer
2. More TP53 expression in those with low LINC00657 expression (low risk group)
 - Less DNA damage in this group? LINC00657 less activated?

Survival analysis using TP53 expression as predictor in 70 Ovarian Cancer Patients



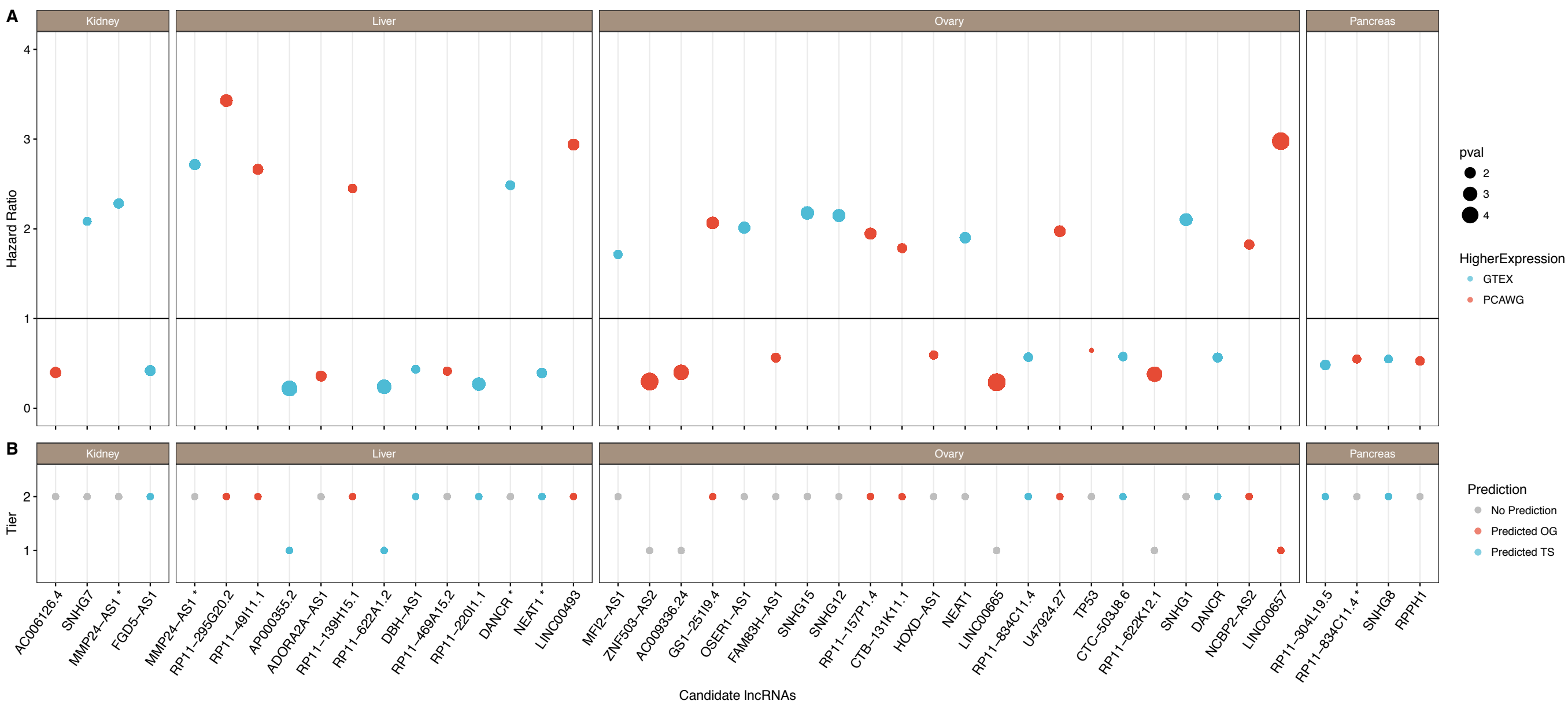
PCAWG-GTEX Workflow

- Will add info on how the analysis was done to obtain direction of change in expression of candidate lncRNAs between GTEX and PCAWG before introducing the figures



Will show one cancer at a time, will hide the other ones so not too busy on the screen just to highlight some of the key messages. These candidates are overall pretty highly expressed in normal tissues but clearly there are still a few that lowly expressed in normal and very highly expressed in cancers. A few also show the opposite pattern. But at the end of the day this analysis is not a perfect comparison since these are two different datasets.

Integrating differential expression analysis between normal and tumour tissues with survival analysis



So if Red and HR > 1 in panel A , predicted oncogene
and if Blue and HR <1 in panel B, predicted tumour suppressor
Ordered by increasing lncRNA expression in PCAWG within each cancer type

Pathway Enrichment Analysis, LINC00657 and LINC00665 Differentially Expressed Genes

