Figure legends:

**Fig 1. Characterization of lncRNA expression across tumours and normal tissues. (A)** Principal component analysis of lncRNA expression profiles across 32 tumour types from TCGA. **(B)** Pan-cancer analysis of lncRNA expression compared to protein-coding gene expression, left: all classes of lncRNAs, right: lncRNAs broken down by class. **(C)** The number of cancer types each lncRNA is detected in**.**  **(D)** The number of lncRNAs detected in each cancer type. (**E**) Summarizing the difference in rank for all lncRNAs with available TCGA-GTEx organ matches with barplot summarizing the number of differentially ranked lncRNAs between tumours and normal samples.

**Fig 2. Identification of survival associated lncRNA candidates. (A)** Distribution of significant univariate lncRNA expression profiles divided by favorable and unfavorable hazard ratios and by cancer type. **(B)** Correlation heatmaps showing prognostic lncRNA expression correlation. **(C)** Workflow for integrating machine learning methods to identify the most clinically relevant lncRNAs using cross-validation and regularization. **(D)** Distributions of c-indices per cancer types as obtained from cross-validation with regularization. (cancer types with overall improvement shown here, all others are available in Supplemental figures 2) **(E)** 166 unique lncRNA candidates that were detected in more than 50% of cross-validations ordered by cancer type with increasing overall candidates.

**Fig 3. Copy number aberrations and epigenetic differences in lncRNA defined risk groups. (A)** lncRNA candidates that overlapped copy number segments separated by risk type showing the percentage or risk patients that had an amplification (red, left panel) or deletion (blue, left panel). Right panel shows the correlation between copy number of the region overlapping the lncRNA and the lncRNA’s expression grouped by risk group (red outline) or non-risk group (blue outline). (**B**) lncRNA candidates that overlapped at least one CpG probe in their promoter. Left panel shows proportion of patients with high expression and low promoter methylation (unfavorable lncRNA) or low expression and higher methylation (favorable lncRNA). Right panel shows the correlation between lncRNA expression and promoter methylation outlined by risk group (red outline = risk group and blue outline = non-risk group). (**C**) Summary of significantly (FDR < 0.05) differentially methylated regions per lncRNA-cancer pair. (**D**) Summary of lncRNAs that are overlapped by significantly differentially methylated regions (DMRs). All of these lncRNAs are overlapped by at least 1 DMR while the total number of significant DMRs between lncRNA high and low expression risk group is displayed in the cell as text. (**E**)Visualization of DMR overlapping lncRNA promoter.

**Fig 4. Clinical and molecular features associated with lncRNA expression. (A)** Overview of lncRNAs associated with different clinical or molecular features. (**B**) An example of lncRNA expression being higher in a group of patients that is also defined as high risk by an additional clinical or molecular feature. Here, lncRNA expression is associated with lower risk and is also higher in patients that showed complete remission. **(C)** Kaplan-Miere plot and expression boxplot for those few example lncRNAs that are associated with a clinical feature.

**Fig 5. Identification of lncRNA-mRNA cancer co-expression networks and cancer pathway enrichment. (A)** Number of mRNAs enriched in lncRNA-risk or non-risk groups divided by favorable lncRNAs (HR < 0) and unfavorable lncRNAs (HR > 1). **(B)** Overview of mRNA risk/non-risk group enrichment specificity. Most mRNAs are enriched in only 1-10 lncRNA-cancer pairs. (**C**) Cancer specific co-expression network outlining the predicted associations between lncRNA candidates and mRNAs. mRNAs are colored by whether they are enriched in the risk or non-risk group. mRNAs that have a thicker border define those that are also prognostic within the cancer type. (**D**) Heatmap of most variable mRNAs that are differentially expressed between lncRNA risk and non-risk group for MAPT-AS1 in BRCA. Hortizontal covariate indicates whether mRNA over expressed in the risk group (purple) or less expressed in the risk group (yellow). Vertical covariate indicates risk patient (red), non-risk patient (blue). (**E**) Pathway enrichment map of mRNAs that are down-regulated in the risk groups.

**Fig 6. External validation of lncRNA prognostic candidates.** Kaplan-Meier plots representing patient cohorts split by lncRNA expression with log rank p-value for (A) BRCA, (B) LIHC, (C) LUAD, (D) OV, (E) KIRC & (F) PAAD. Dashed line represents time at which survival probability is 50%.