Supplementary tables descriptions

1. List of TCGA cancer types used in study and number of patients in samples in each one with both clinical and RNA-Seq data
2. List of FANTOM lncRNAs analyzed in the study
3. List of tumour types that were compared against GTEx tissues
4. Table 4 results of lncRNA comparison between GTEx and TCGA
5. Table 5 - lncRNAs that were consistently up/down regulated
6. Table 6 - list of 168 lncRNAs identified through elastic net analysis
7. Table 7 - list of 29 lncRNAs evaluated through PCAWG
8. Table 8 - list of lncRNAs potentially influenced by SCNAs
9. Table 9 - list of lncRNAs potentially influenced by methylation
10. Table 10 - list of lncRNAs associated with molecular or clinical subtypes
11. Table 11 - list of differentially expressed PCGs between low and high risk lncRNA groupings
12. Table 12 - list of pathways enriched by genes from above table