

Lung squamous cell carcinoma (LUSC)

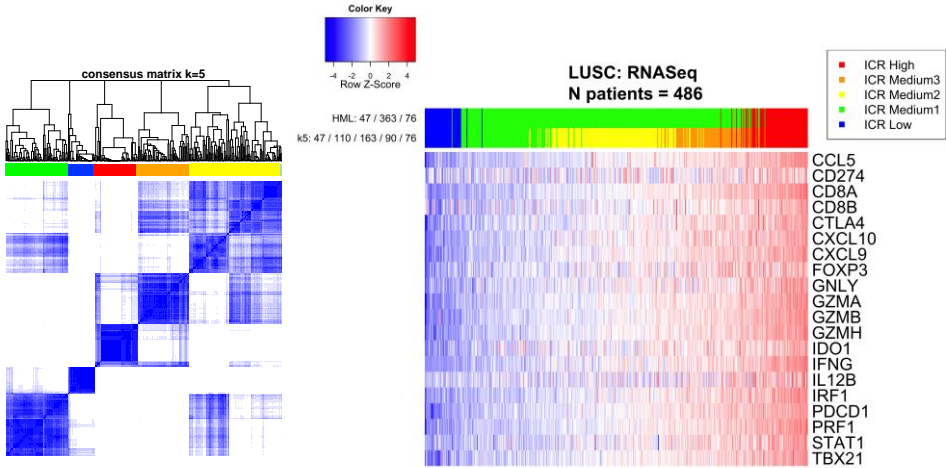
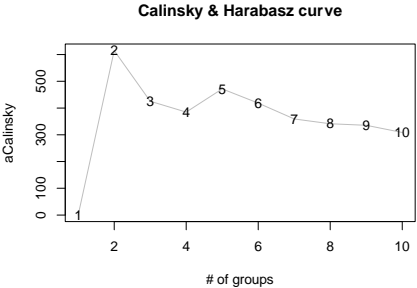
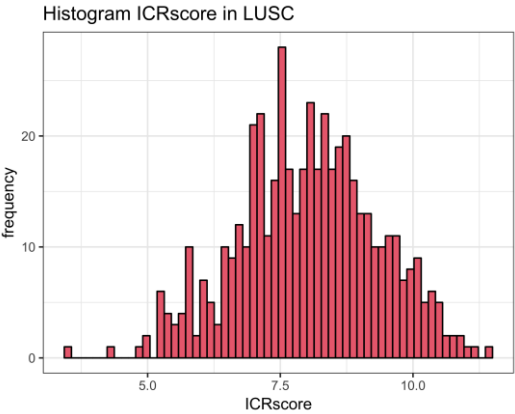


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 5. The combination action performed to reduce to 3 clusters is: Combine clusters ICR2 & ICR3 & ICR4. Resulting in mean ICR scores of 5.63 / 7.92 / 10 for Low / Medium / High resp.



Deconvolution immune cell populations

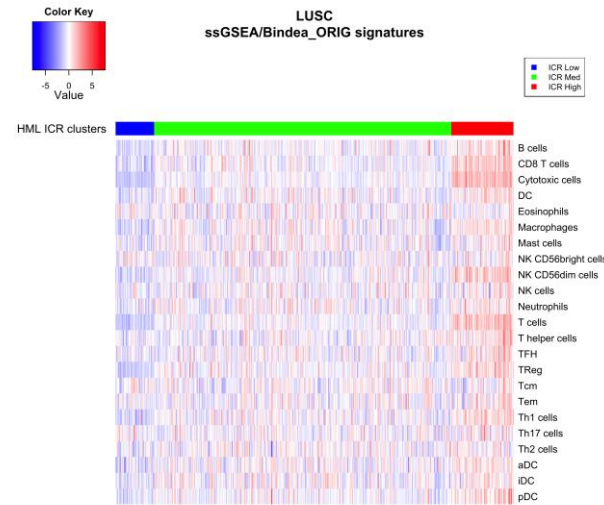
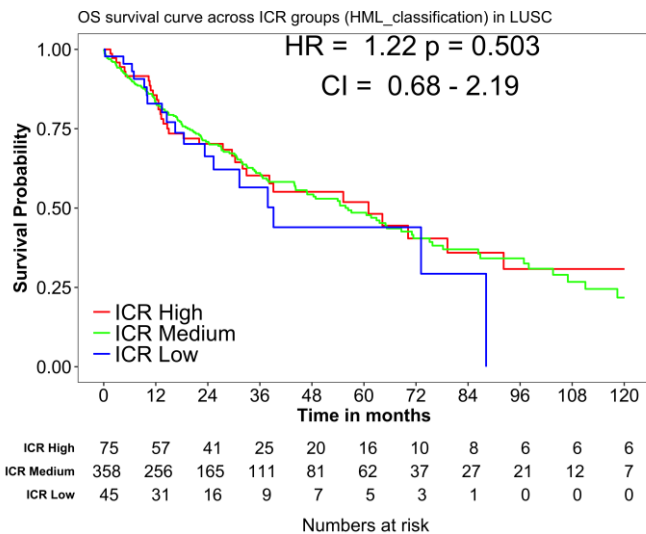


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Panca_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

Survival analysis



ssGSEA oncogenic pathways

