

Skin cutaneous melanoma (SKCM)

Immune phenotype (ICR) Clustering

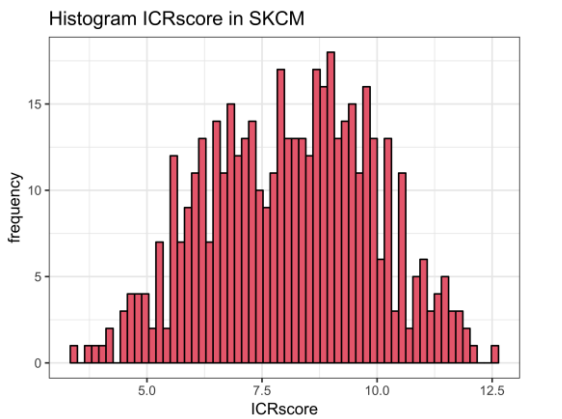
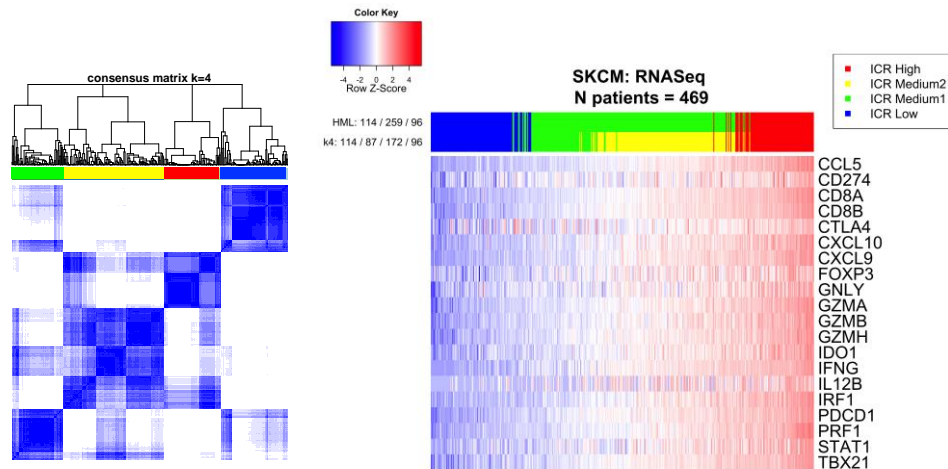
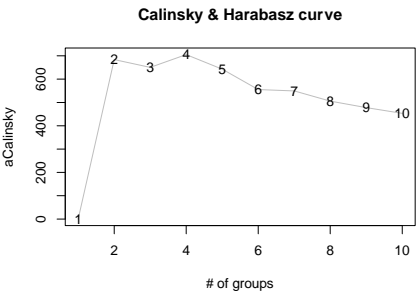


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDaseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 4. The combination action performed to reduce to 3 clusters is: Combine clusters ICR2 & ICR3. Resulting in mean ICR scores of 5.76 / 8.26 / 10.54 for Low / Medium / High resp.

Deconvolution immune cell populations

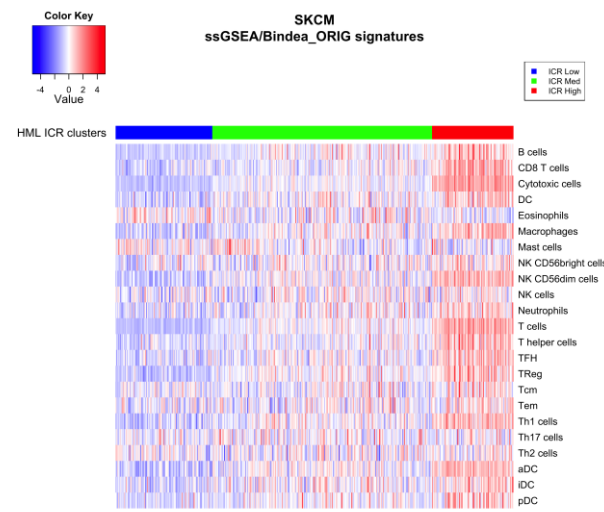
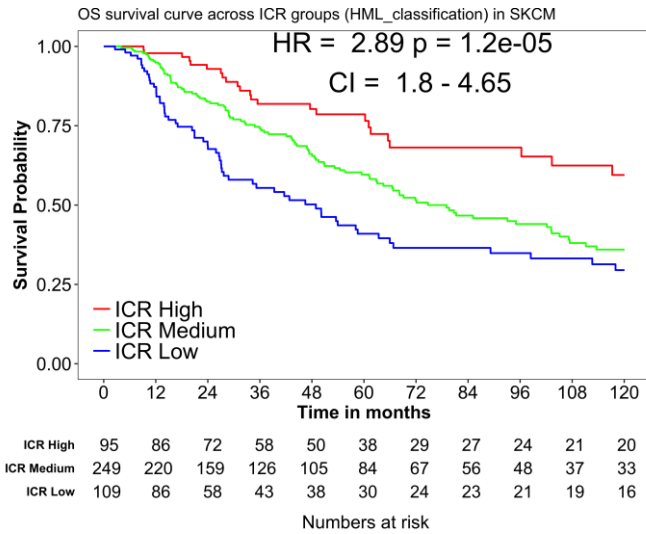


Figure: EDaseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Panca_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

Survival analysis



ssGSEA oncogenic pathways

