

Pancreatic adenocarcinoma (PAAD)

Calinsky & Harabasz curve

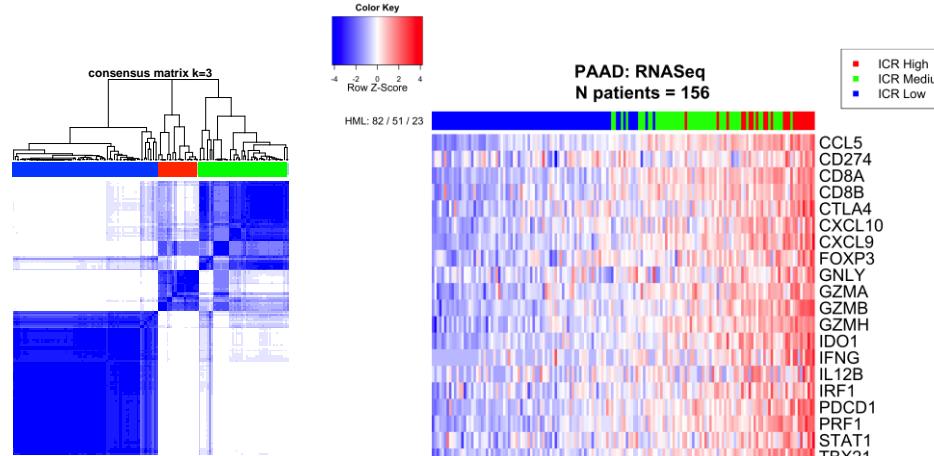
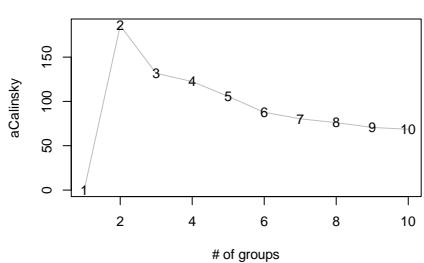
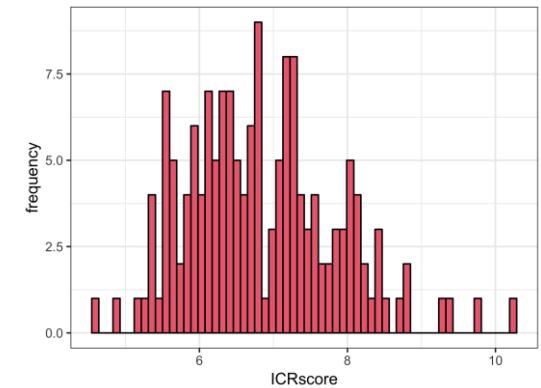


Figure: Gene expression data was obtained from TCGA, pancreas normalized (EDAsed) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is:
none
Resulting in mean ICR scores of 6.08 / 7.37 / 8.37 for Low / Medium / High resp.

Histogram ICRscore in PAAD



Deconvolution immune cell populations



PAAD ssGSEA/Bindea_ORIG signatures



HML ICR clusters

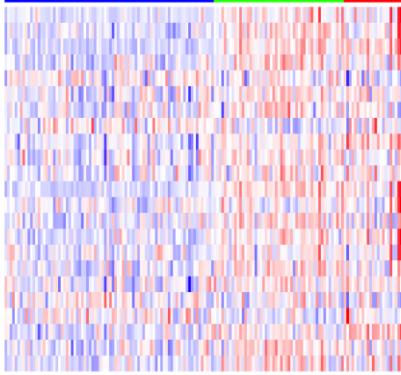
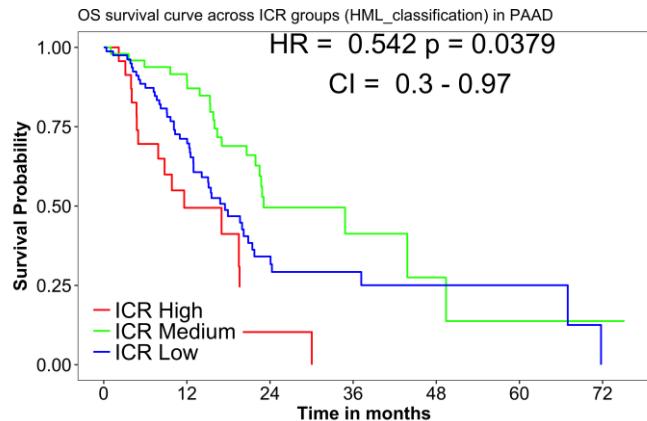


Figure: EDAsed normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Panca_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

Survival analysis



	ICR High	ICR Medium	ICR Low				
ICR High	23	9	1	0	0	0	0
ICR Medium	51	41	11	5	2	1	1
ICR Low	81	49	14	8	4	3	0

Numbers at risk

ssGSEA oncogenic pathways

