

Kidney renal clear
cell carcinoma
(KIRC)

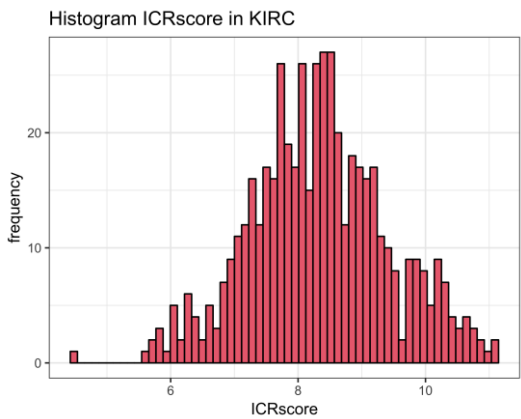
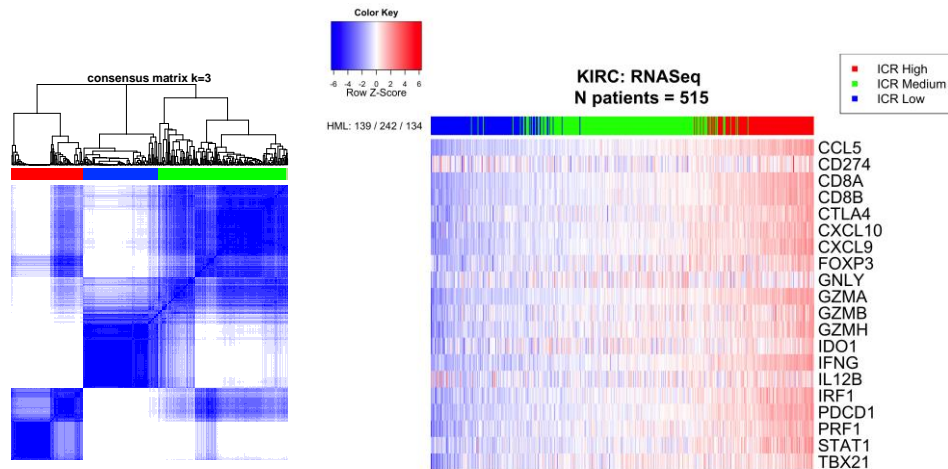
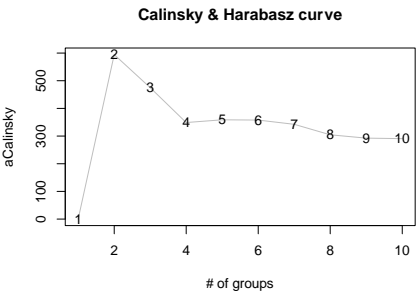


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none Resulting in mean ICR scores of 7.06 / 8.31 / 9.71 for Low / Medium / High resp.

Deconvolution immune
cell populations

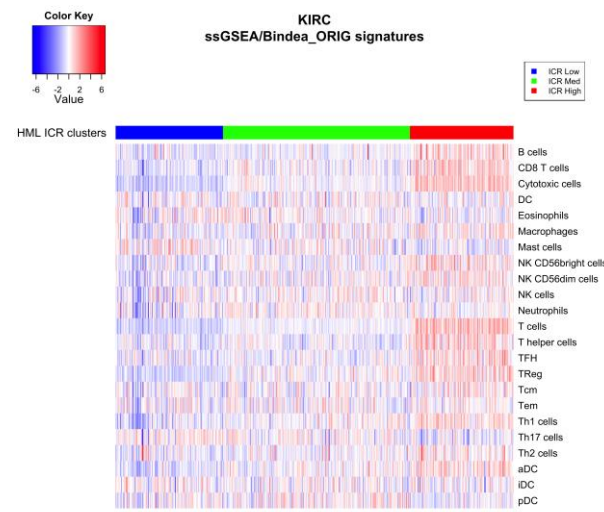
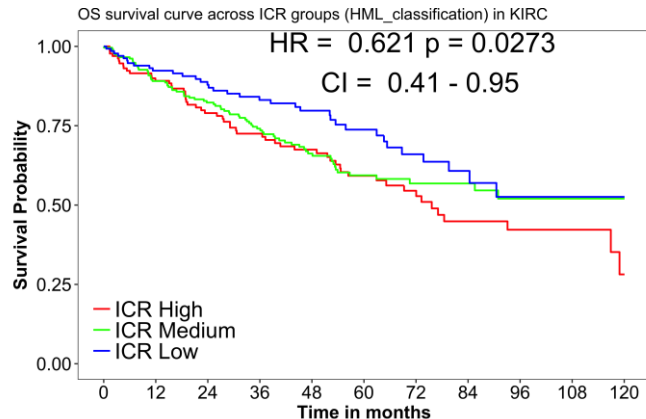


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Pance_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

Survival analysis



ICR High	134	112	89	73	59	45	32	21	14	9	4
ICR Medium	240	198	160	128	92	58	38	26	15	14	7
ICR Low	139	113	96	82	64	45	28	16	10	7	2

Numbers at risk

ssGSEA oncogenic
pathways

