

Liver hepatocellular carcinoma (LIHC)

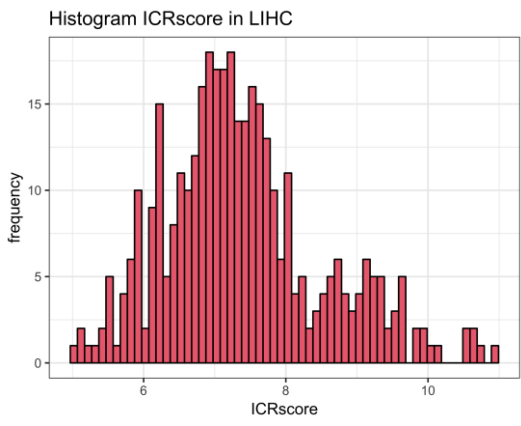
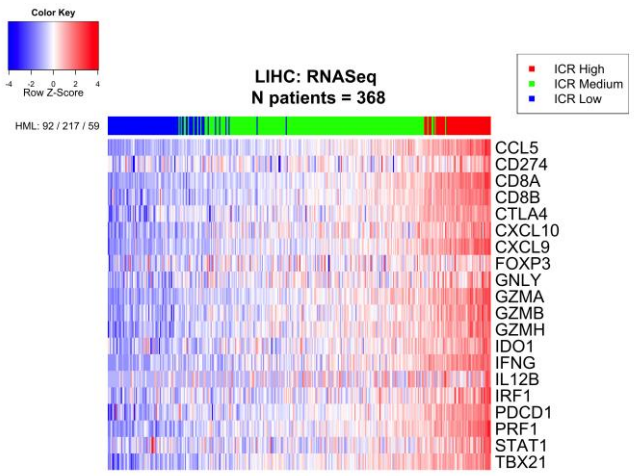
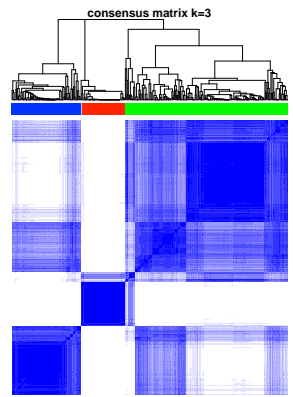
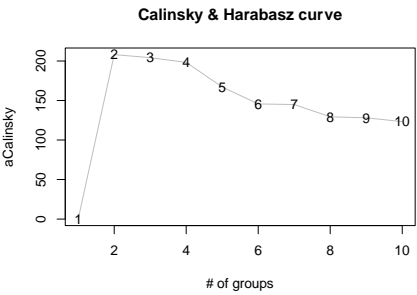


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none Resulting in mean ICR scores of 8.13 / 7.4 / 9.35 for Low / Medium / High resp.

Deconvolution immune cell populations

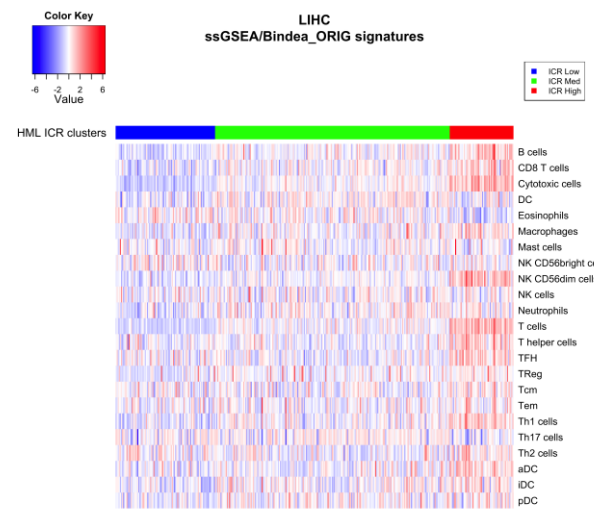
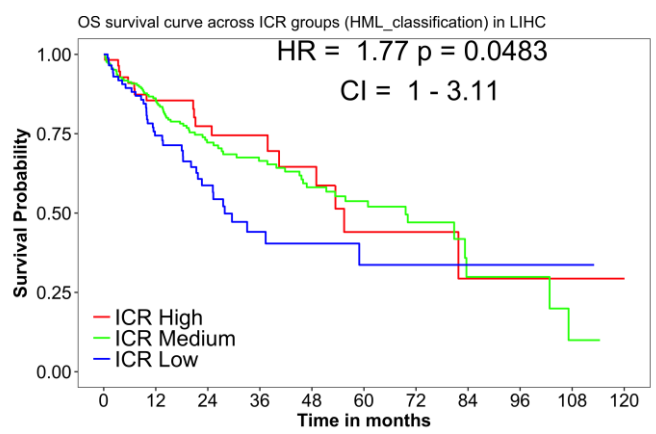


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Pance_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

Survival analysis



ICR High	57	44	28	16	11	5	5	2	1	1	1
ICR Medium	212	161	84	62	44	31	18	5	3	1	0
ICR Low	92	54	27	12	8	4	3	2	2	2	0

Numbers at risk

ssGSEA oncogenic pathways

