

Pheochromocytoma and paraganglioma (PCPG)

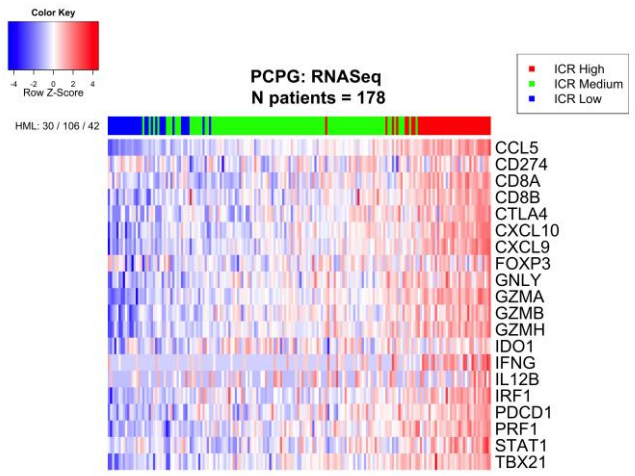
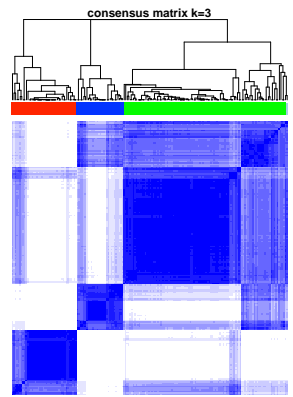
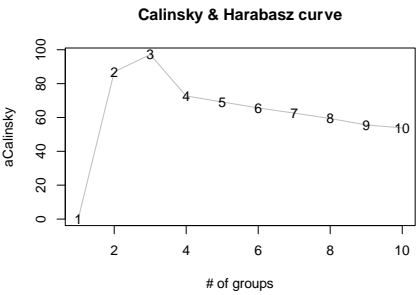
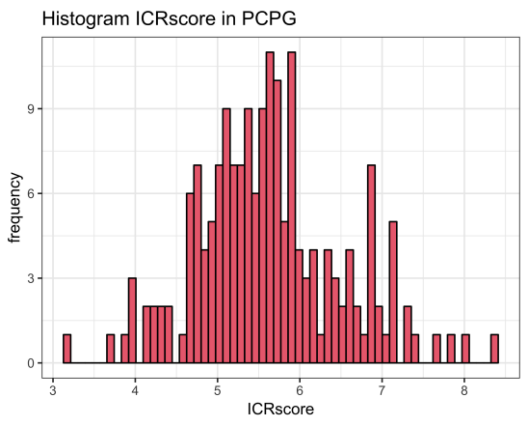


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none Resulting in mean ICR scores of 4.46 / 5.48 / 6.82 for Low / Medium / High resp.



Deconvolution immune cell populations

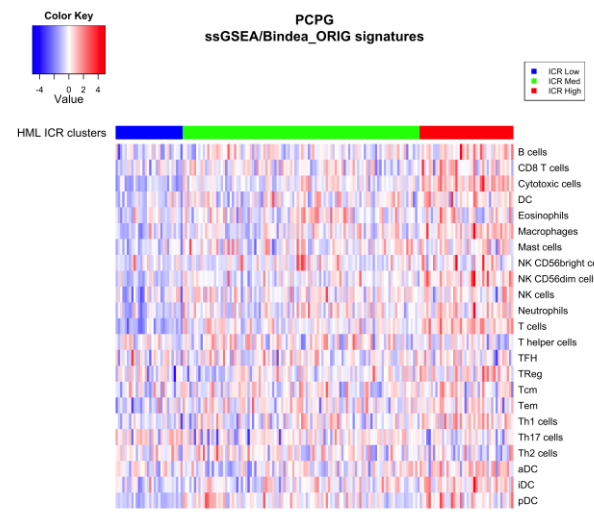
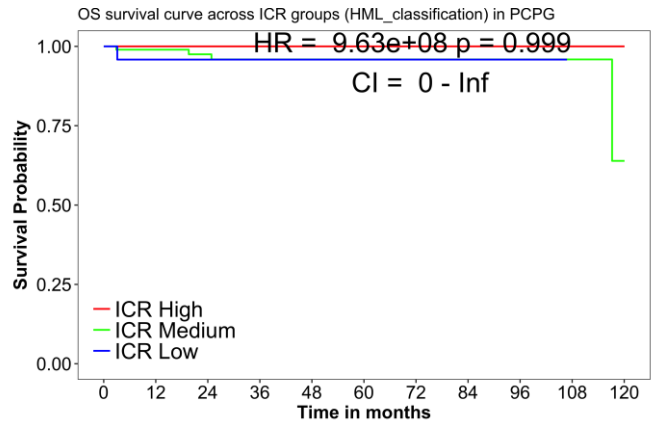


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Panca_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

Survival analysis



ICR High	42	29	20	10	8	7	7	5	4	3	2
ICR Medium	106	83	60	45	31	24	19	11	9	9	2
ICR Low	30	20	14	5	1	1	1	1	1	0	0

Numbers at risk

ssGSEA oncogenic pathways

