

# Head and neck squamous cell carcinoma (HNSC)

## Immune phenotype (ICR) Clustering

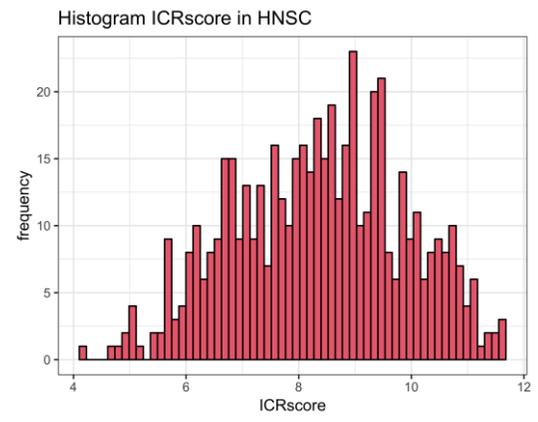
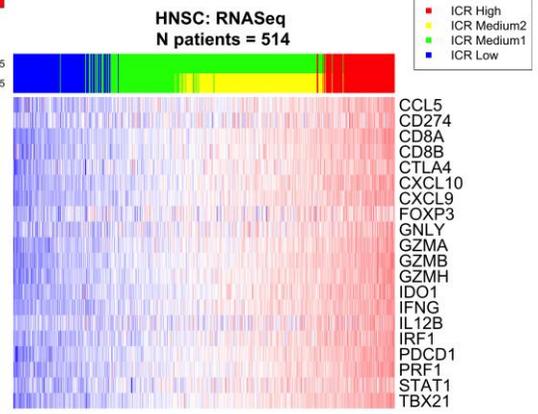
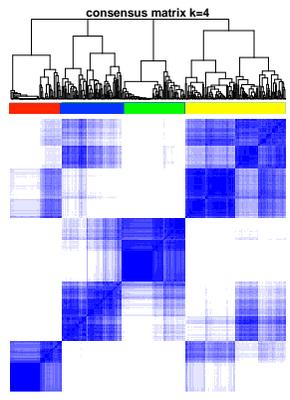
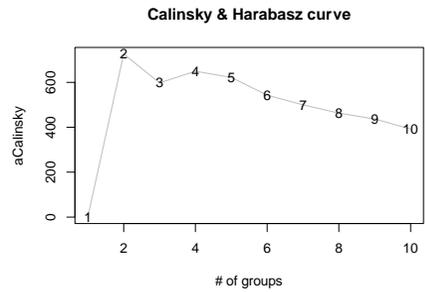


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 4. The combination action performed to reduce to 3 clusters is: Combine clusters ICR2 & ICR3. Resulting in mean ICR scores of 6.32 / 8.49 / 10.5 for Low / Medium / High resp.

## Deconvolution immune cell populations

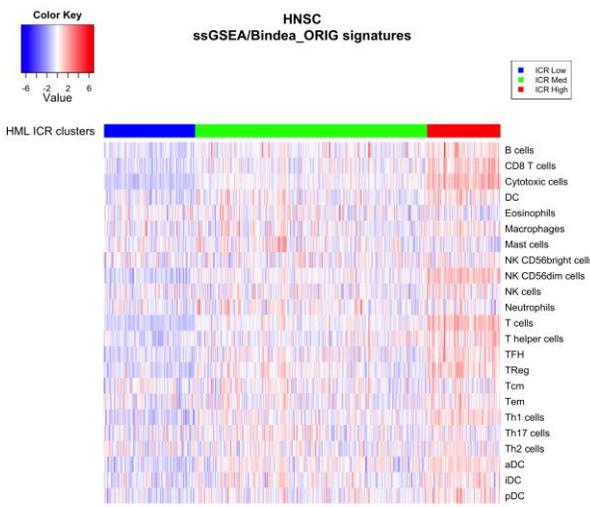
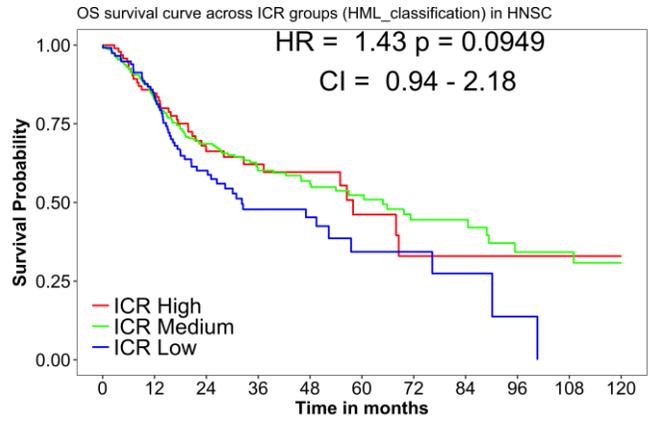


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler\_Panca\_Normalized\_filtered. Bindea\_ORIG enrichment z-scores were used to generate this heatmap.

## Survival analysis



ICR High	94	74	38	25	19	9	4	4	3	3	3
ICR Medium	301	231	146	92	59	37	24	19	12	10	8
ICR Low	118	91	45	26	17	7	6	3	1	0	0

Numbers at risk

## ssGSEA oncogenic pathways

