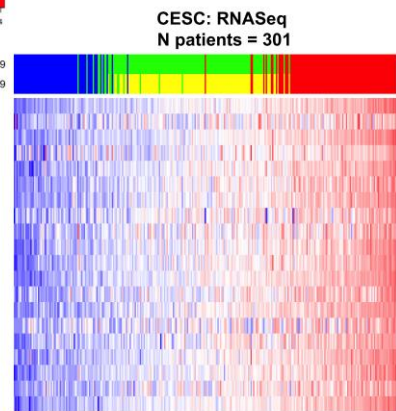
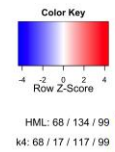
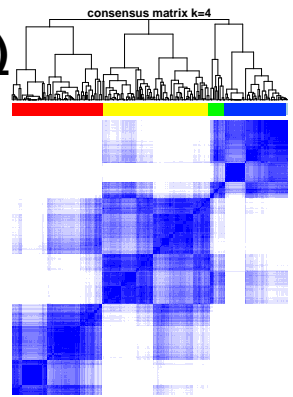
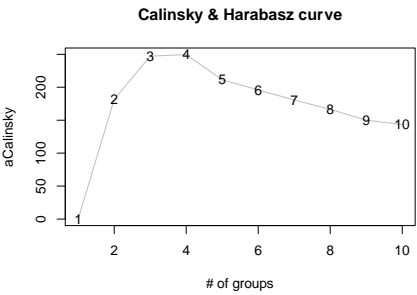


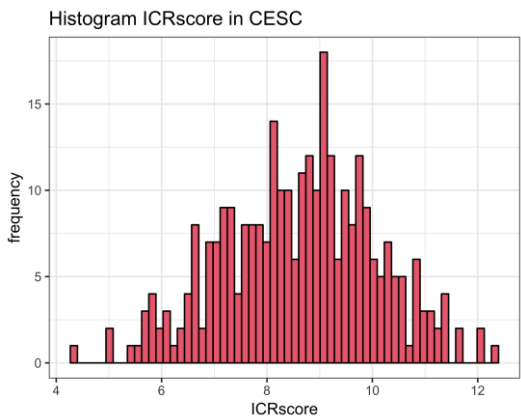
Cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC)



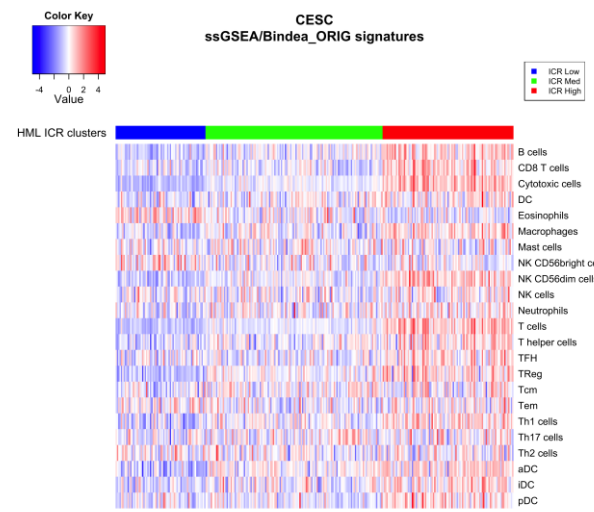
- CCL5
- CD274
- CD8A
- CD8B
- CTLA4
- CXCL10
- CXCL9
- FOXP3
- GNLY
- GZMA
- GZMB
- GZMH
- IDO1
- IFNG
- IL12B
- IRF1
- PDCD1
- PRF1
- STAT1
- TBX21

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 6.65 / 8.46 / 10.19 for Low / Medium / High resp.

Immune phenotype (ICR) Clustering



Deconvolution immune cell populations

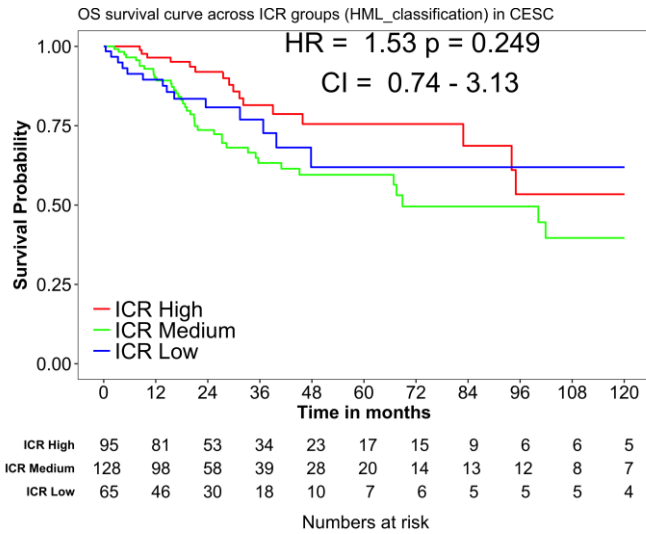


- ICR Low
- ICR Med
- ICR High

- B cells
- CD8 T cells
- Cytotoxic cells
- DC
- Eosinophils
- Macrophages
- Mast cells
- NK CD56bright cells
- NK CD56dim cells
- NK cells
- Neutrophils
- T cells
- T helper cells
- TFH
- TReg
- Tcm
- Tem
- Th1 cells
- Th17 cells
- Th2 cells
- aDC
- iDC
- pDC

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



ssGSEA oncogenic pathways

