Breast invasive carcinoma (BRCA)
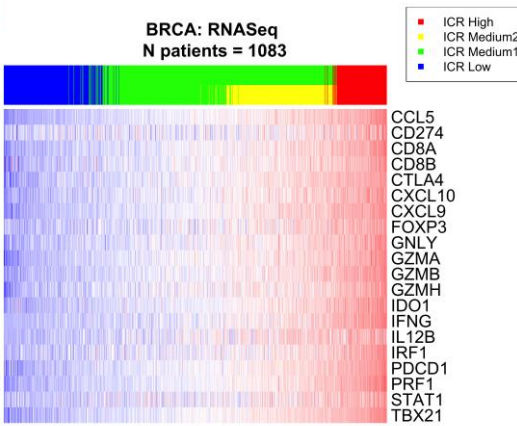
TCGA Sidra Medicine

Calinsky & Harabasz curve

consensus matrix k=4

Color Key
Row Z-Score

**BRCA: RNASeq
N patients = 1083**

- ICR High
- ICR Medium2
- ICR Medium1
- ICR Low

HML: 266 / 665 / 152
k4: 266 / 359 / 306 / 152

CCL5, CD274, CD8A, CD8B, CTLA4, CXCL10, CXCL9, FOXP3, GNLY, GZMA, GZMB, GZMH, IDO1, IFNG, IL12B, IRF1, PDCD1, PRF1, STAT1, TBX21
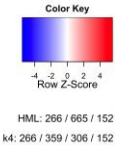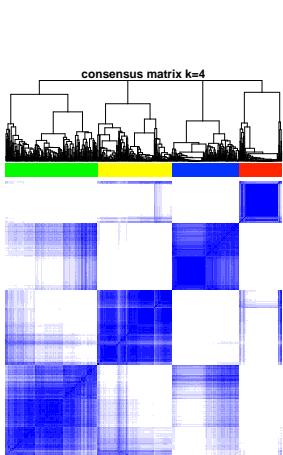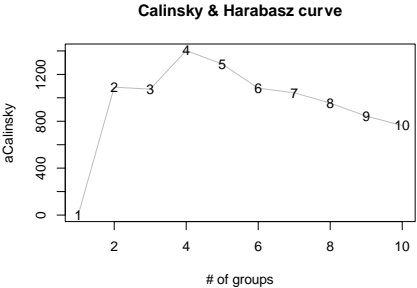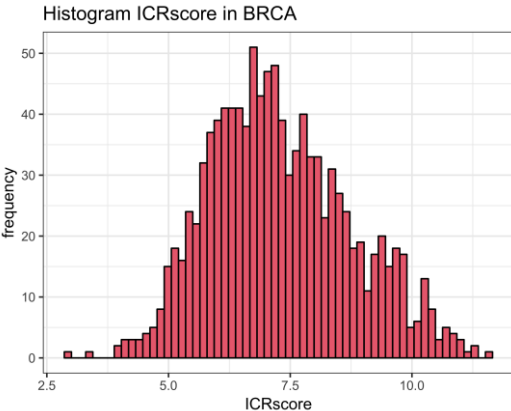
Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 4. The combination action performed to reduce to 3 clusters is: Combine clusters ICR2 & ICR3. Resulting in mean ICR scores of 5.55 / 7.42 / 9.79 for Low / Medium / High resp.

Histogram ICRscore in BRCA

Deconvolution immune cell populations

Color Key
Value

**BRCA
ssGSEA/Bindea_ORIG signatures**

- ICR Low
- ICR Med
- ICR High

HML ICR clusters

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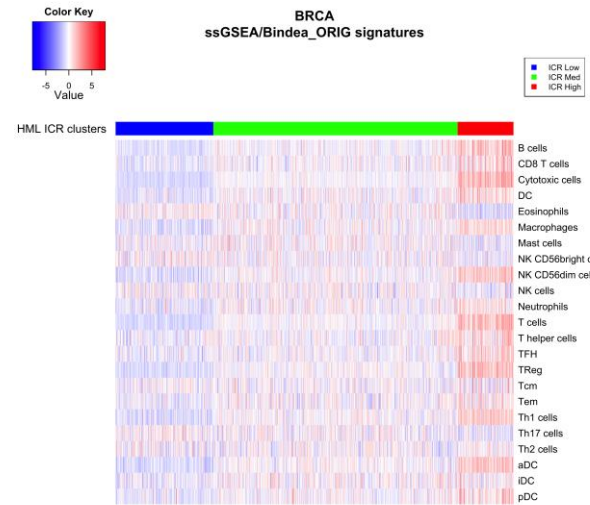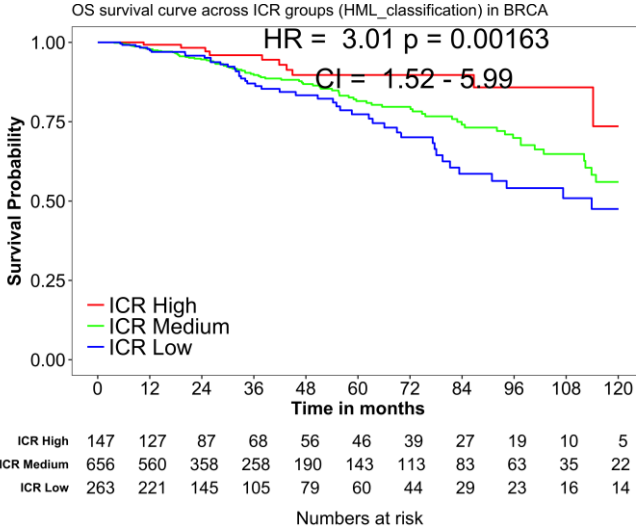
Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Panca_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

Survival analysis

OS survival curve across ICR groups (HML_classification) in BRCA

HR = 3.01 p = 0.00163
CI = 1.52 - 5.99

- ICR High
- ICR Medium
- ICR Low

	0	12	24	36	48	60	72	84	96	108	120
ICR High	147	127	87	68	56	46	39	27	19	10	5
ICR Medium	656	560	358	258	190	143	113	83	63	35	22
ICR Low	263	221	145	105	79	60	44	29	23	16	14

Numbers at risk

ssGSEA oncogenic pathways

- ICR High
- ICR Medium
- ICR Low

[TBI] MAPK up genes
[HM] Estrogen response
[IPA] Telomere Extension by Telomerase
[IPA] AMPK Signaling
[HM] Hedgehog signaling