Mesothelioma (MESO)

TCGA · سدرة للطب Sidra Medicine

Calinsky & Harabasz curve

consensus matrix k=3

Color Key
Row Z-Score

MESO: RNASeq
N patients = 87

- ICR High
- ICR Medium
- ICR Low

HML: 25 / 51 / 11

CCL5, CD274, CD8A, CD8B, CTLA4, CXCL10, CXCL9, FOXP3, GNLY, GZMA, GZMB, GZMH, IDO1, IFNG, IL12B, IRF1, PDCD1, PRF1, STAT1, TBX21
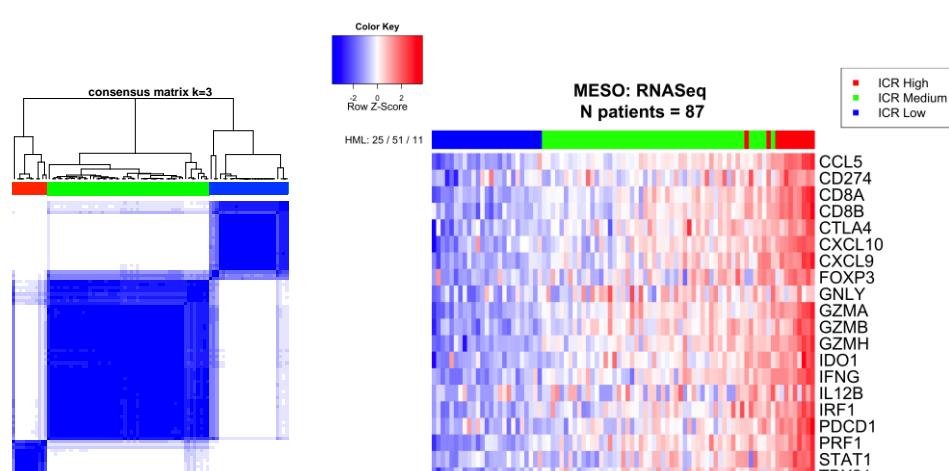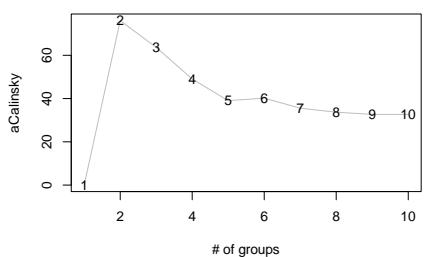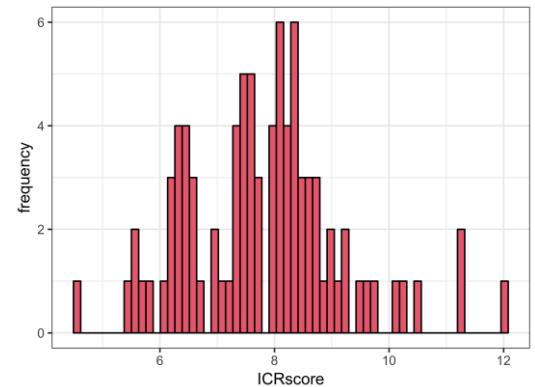
Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is:
none
Resulting in mean ICR scores of 6.23 / 8.08 / 10.19 for Low / Medium / High resp.
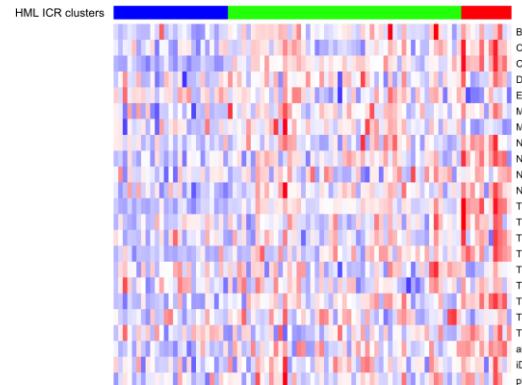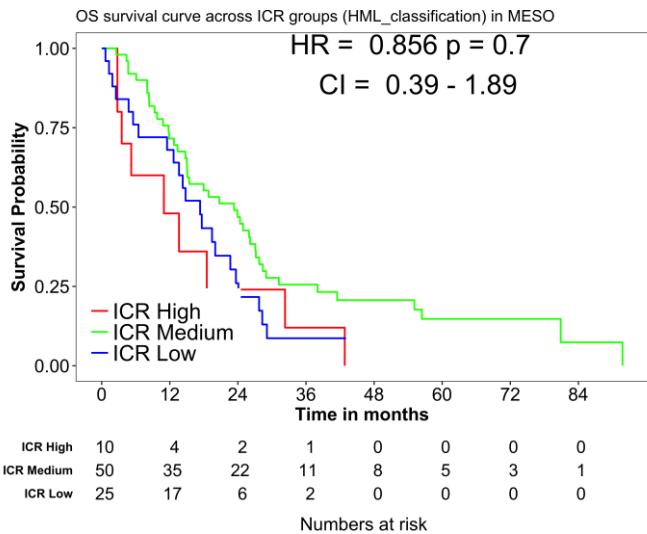
Histogram ICRscore in MESO
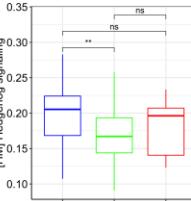
Deconvolution immune cell populations

Color Key
Value

MESO
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 MESO

HR = 0.856 p = 0.7
CI = 0.39 - 1.89

- ICR High
- ICR Medium
- ICR Low

Numbers at risk

	0	12	24	36	48	60	72	84
ICR High	10	4	2	1	0	0	0	0
ICR Medium	50	35	22	11	8	5	3	1
ICR Low	25	17	6	2	0	0	0	0

ssGSEA oncogenic pathways

- ICR High
- ICR Medium
- ICR Low

[HM] Hedgehog signaling