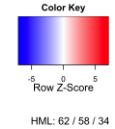
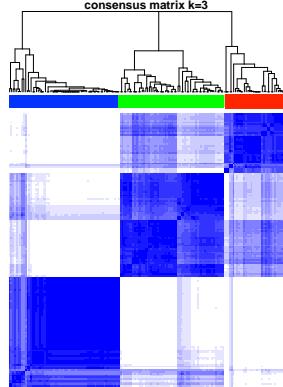
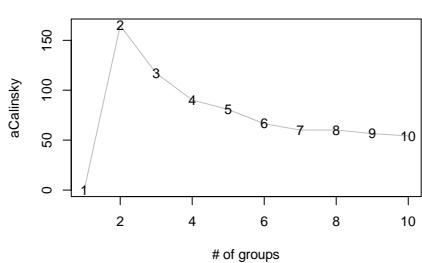


Glioblastoma multiforme (GBM)

Calinsky & Harabasz curve



GBM: RNASeq
N patients = 154

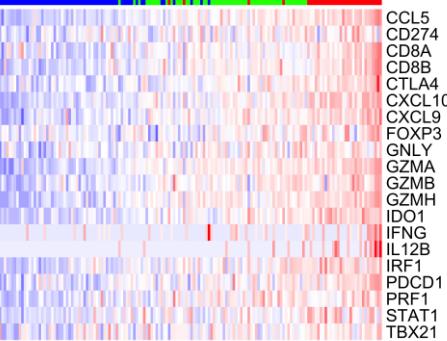
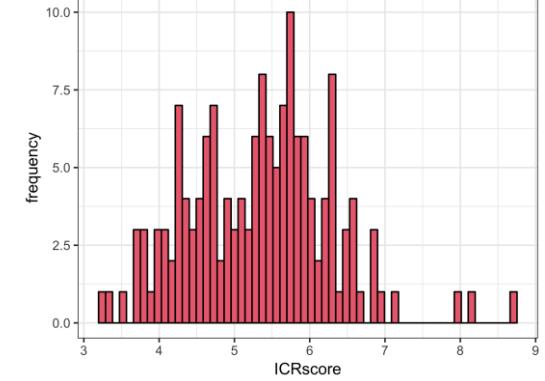


Figure: Gene expression data was obtained from TCGA, panancer normalized (EDAsed) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3.
The combination action performed to reduce to 3 clusters is:
none
Resulting in mean ICR scores of 4.45 / 5.58 / 6.53 for Low / Medium / High resp.

Histogram ICRscore in GBM



Deconvolution immune cell populations



GBM ssGSEA/Bindea_ORIG signatures



HML ICR clusters

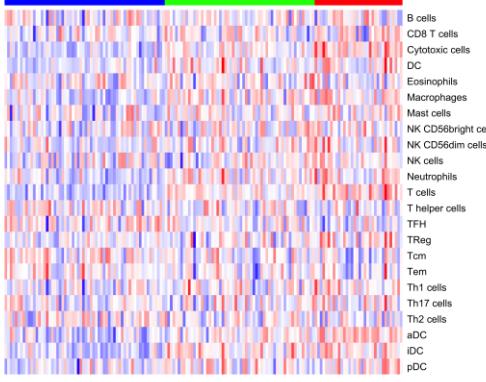
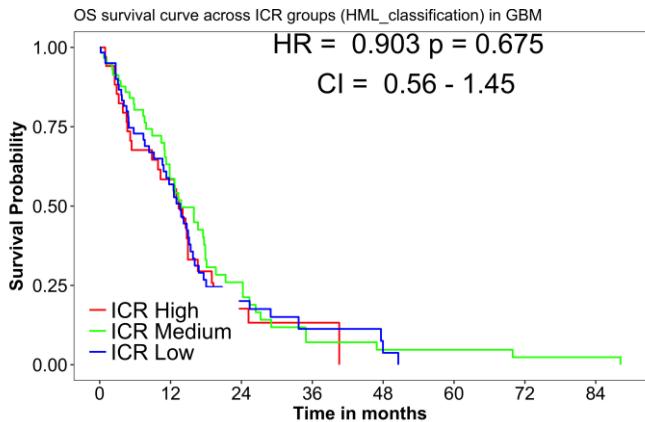


Figure: EDAsed normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Panca_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

Survival analysis



	ICR High	ICR Medium	ICR Low	Numbers at risk
ICR High	34	19	4	1 0 0 0 0 0 0
ICR Medium	58	26	11	3 2 2 1 0 0 0
ICR Low	61	28	8	3 1 0 0 0 0 0

ssGSEA oncogenic pathways

