

Adrenocortical carcinoma (ACC)

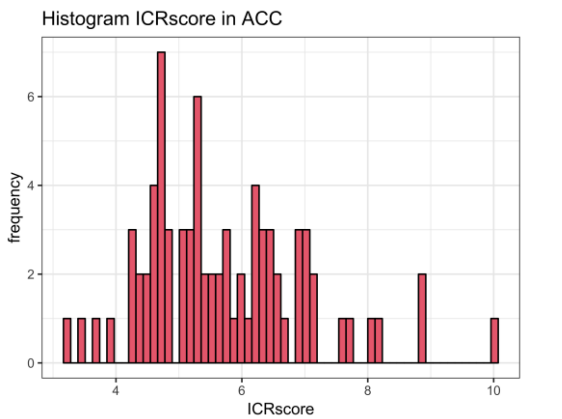
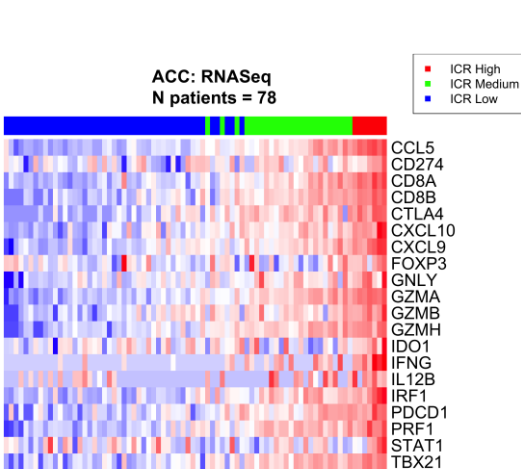
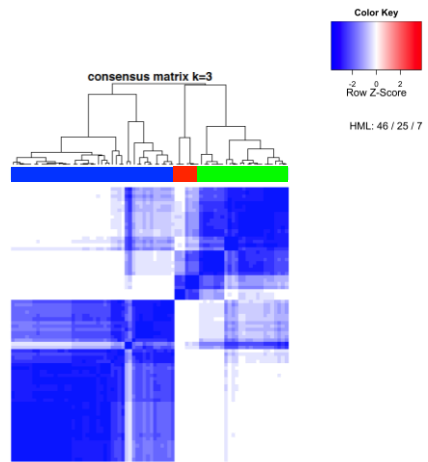
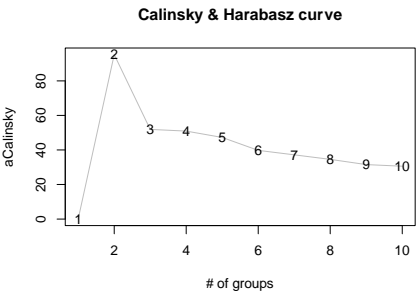


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none Resulting in mean ICR scores of 4.87 / 6.49 / 8.47 for Low / Medium / High resp.

Deconvolution immune cell populations

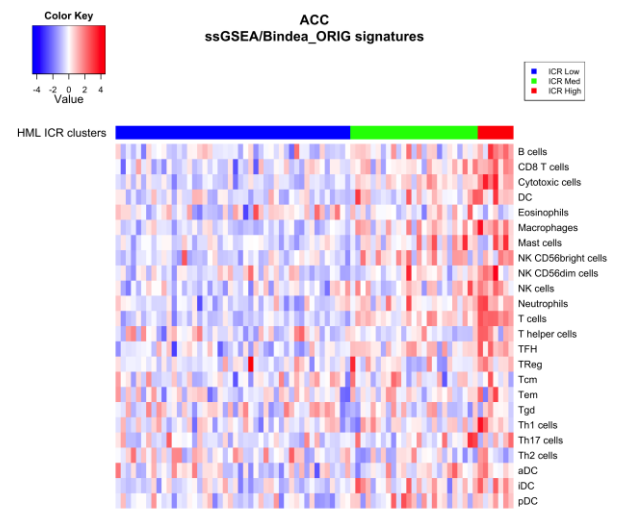
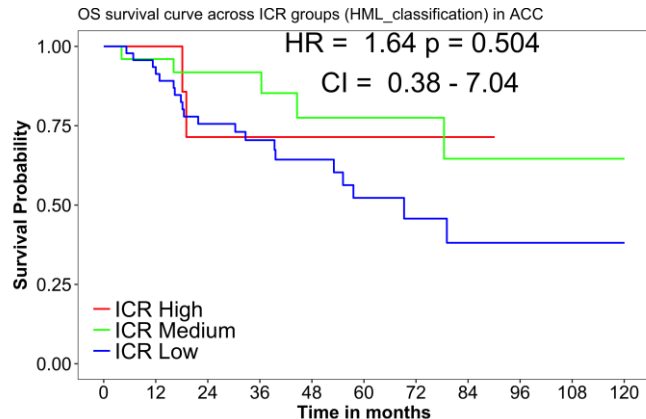


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Panca_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

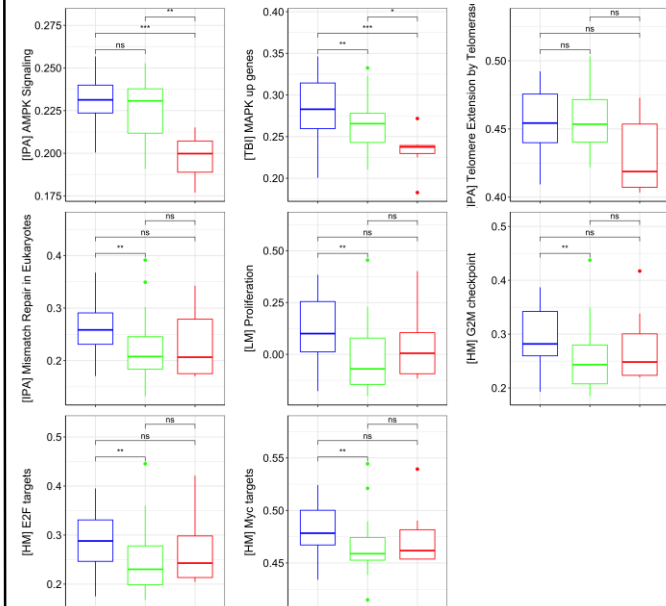
Survival analysis



ICR High	7	7	5	5	3	2	2	1	0	0	0
ICR Medium	25	24	20	14	10	9	7	5	3	2	1
ICR Low	46	43	33	25	17	13	7	5	5	5	3

Numbers at risk

ssGSEA oncogenic pathways



Bladder urothelial carcinoma (BLCA)

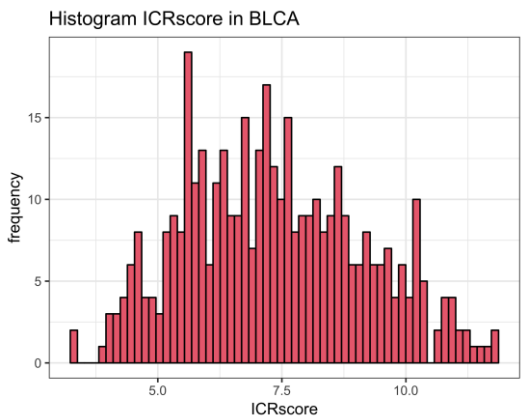
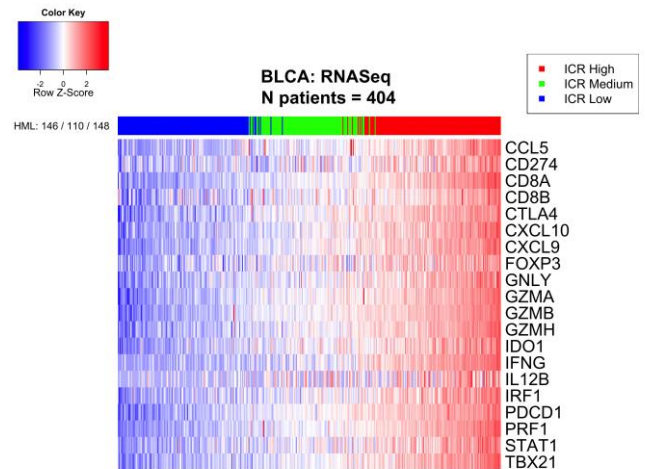
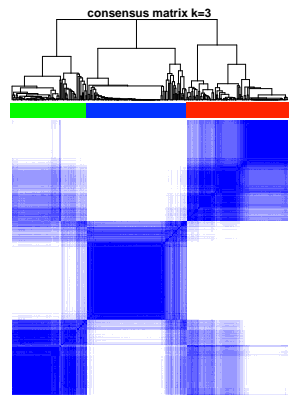
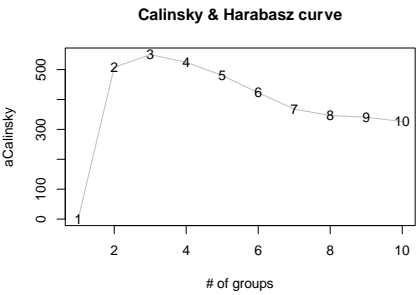


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none Resulting in mean ICR scores of 5.49 / 7.23 / 9.3 for Low / Medium / High resp.

Deconvolution immune cell populations

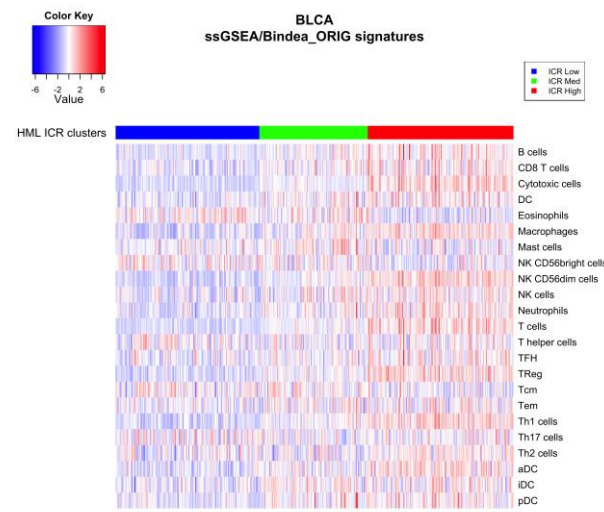
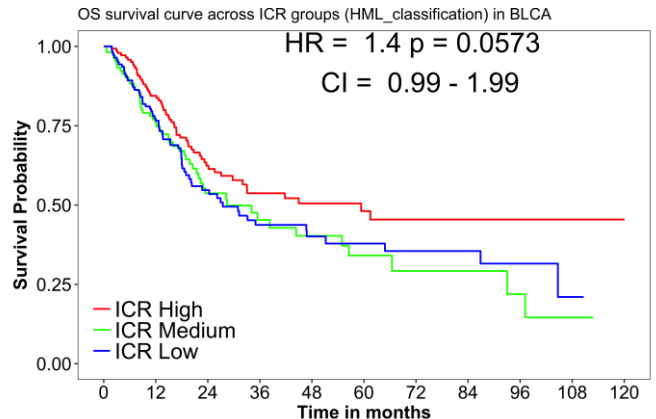


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Pance_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

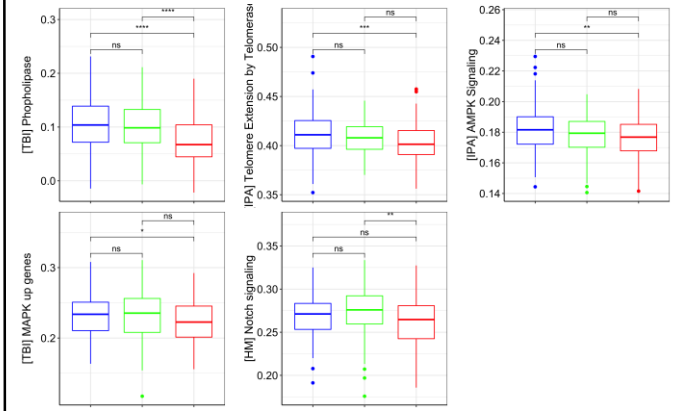
Survival analysis



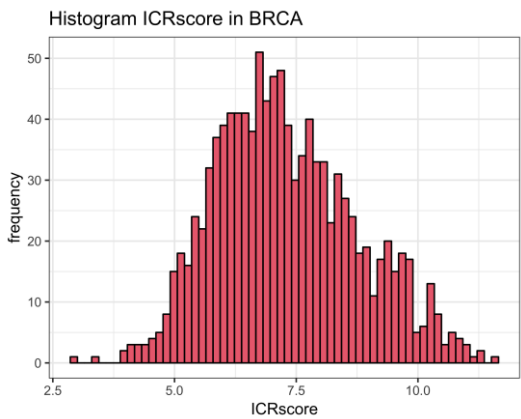
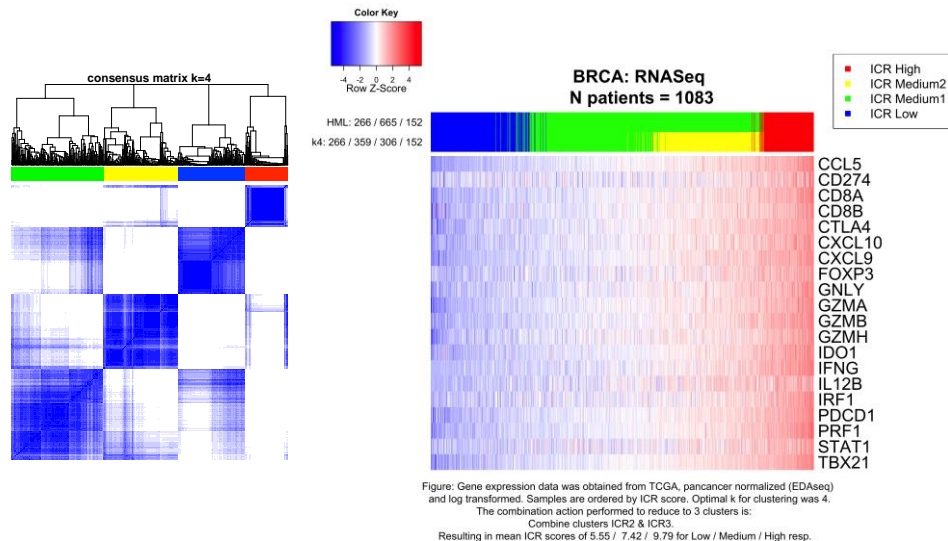
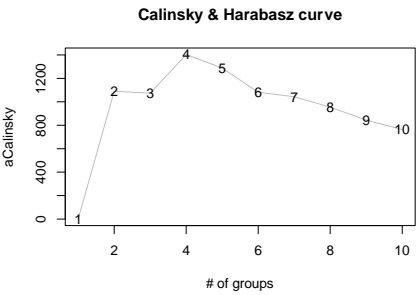
ICR High	147	116	60	37	30	19	10	7	7	6	6
ICR Medium	110	70	33	18	16	11	5	5	3	2	0
ICR Low	145	100	44	30	20	16	12	10	4	2	0

Numbers at risk

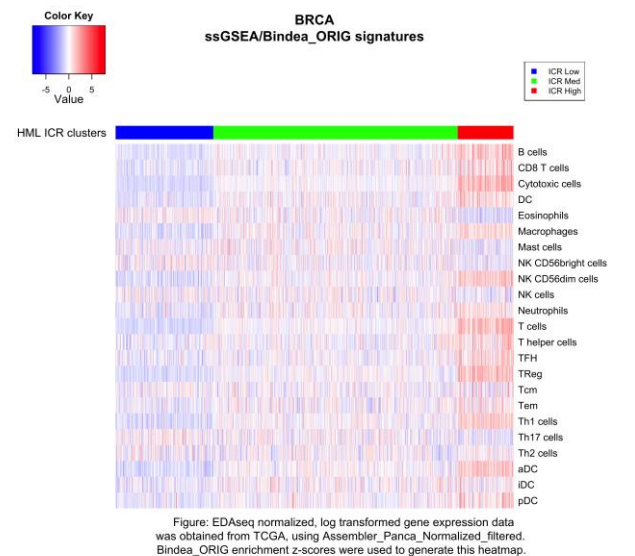
ssGSEA oncogenic pathways



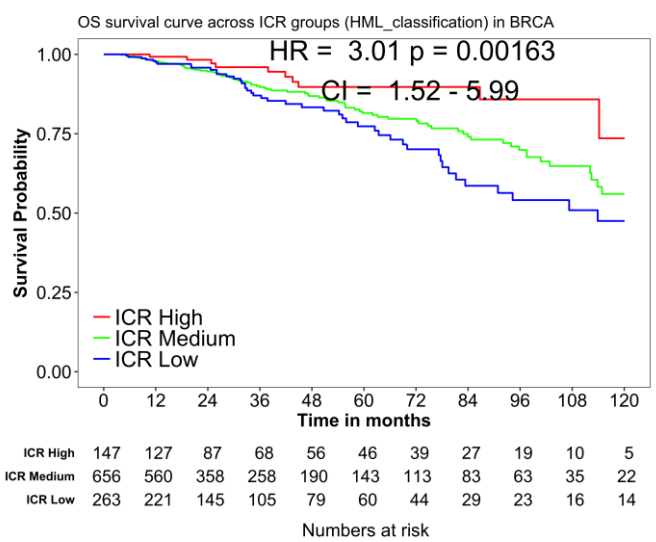
Breast invasive carcinoma (BRCA)



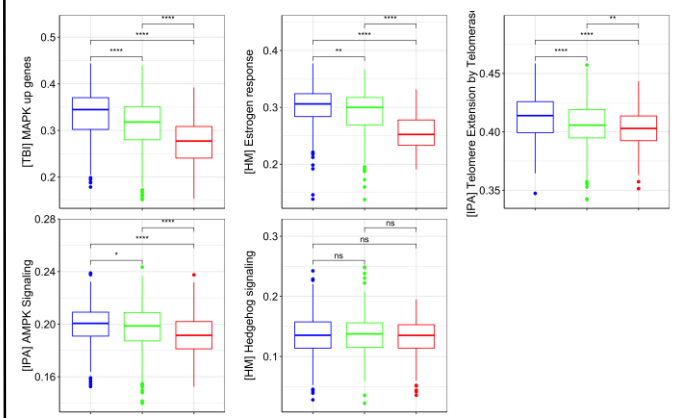
Deconvolution immune cell populations



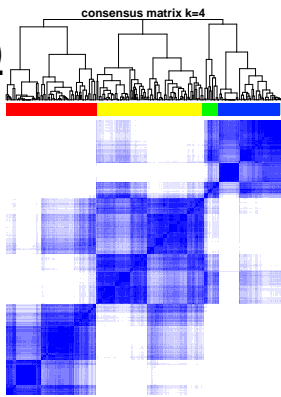
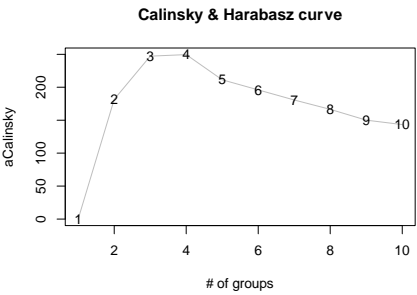
Survival analysis



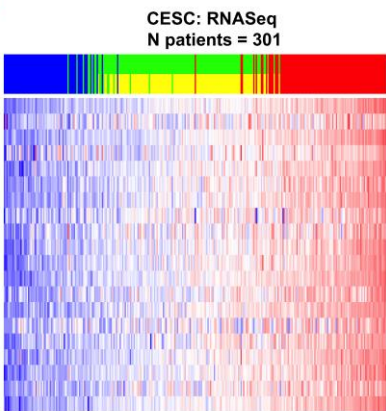
ssGSEA oncogenic pathways



Cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC)



HML: 68 / 134 / 99
k4: 68 / 17 / 117 / 99



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

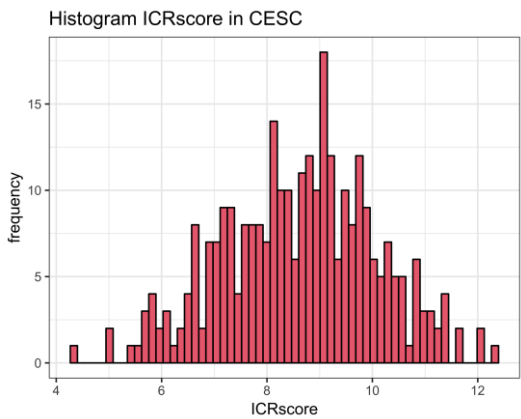


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 4. The combination action performed to reduce to 3 clusters is: Combine clusters ICR2 & ICR3. Resulting in mean ICR scores of 6.65 / 8.46 / 10.19 for Low / Medium / High resp.

Deconvolution immune cell populations

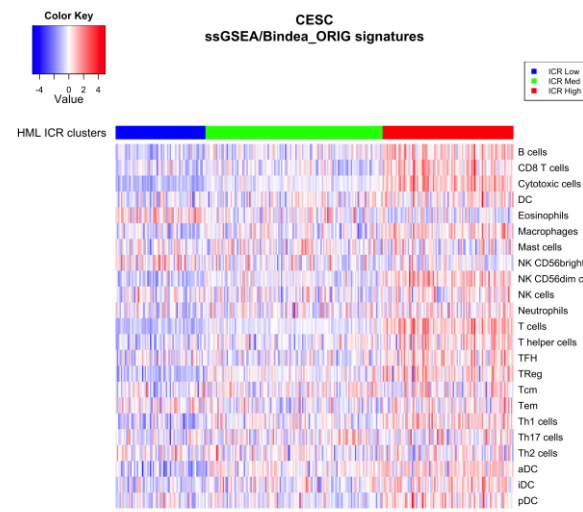
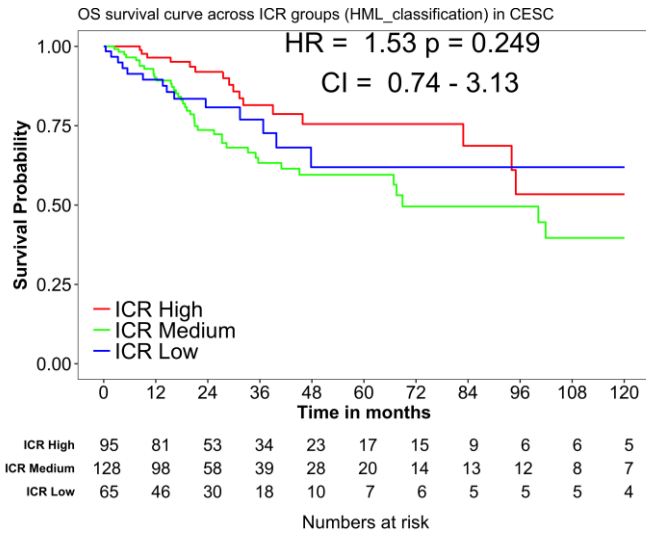
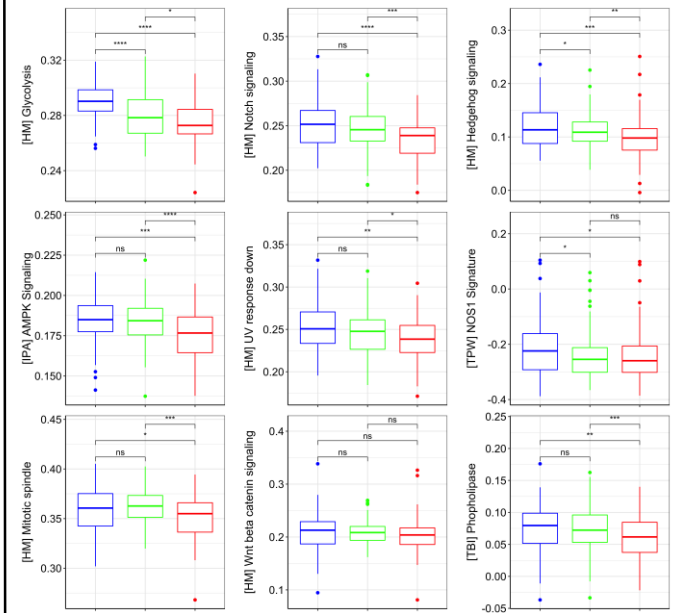


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Panca_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

Survival analysis

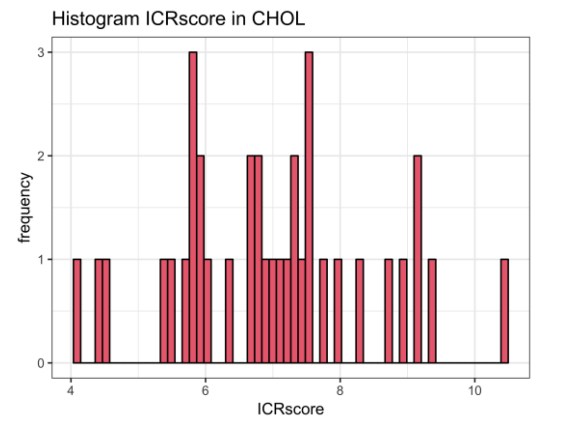
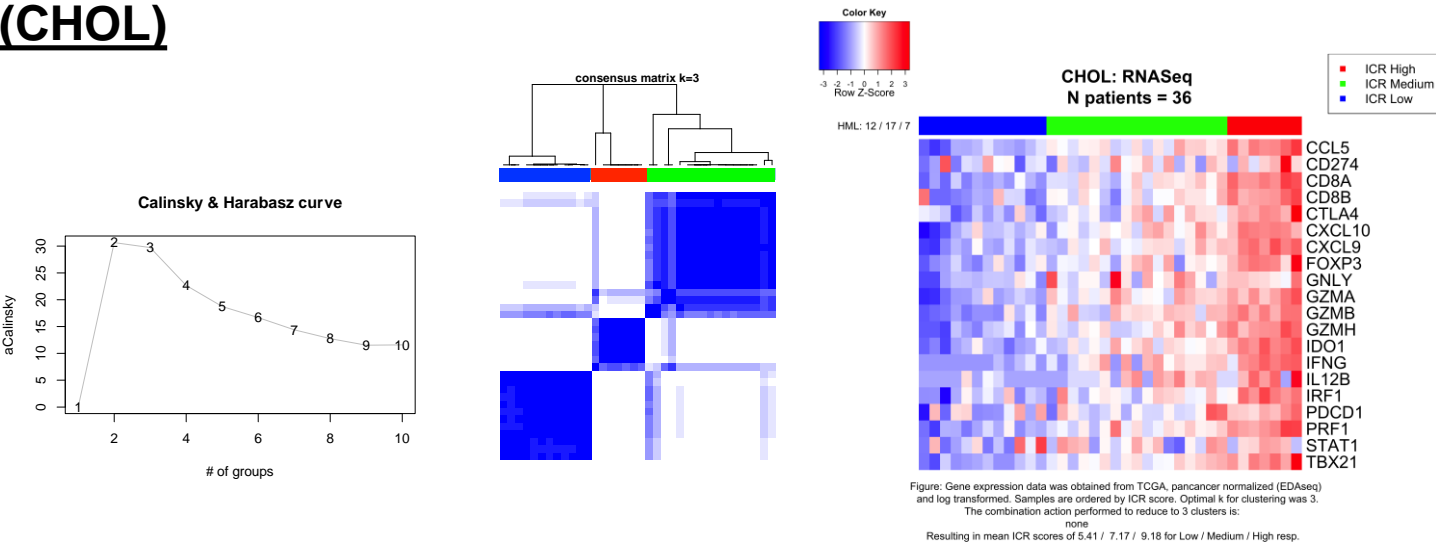


ssGSEA oncogenic pathways

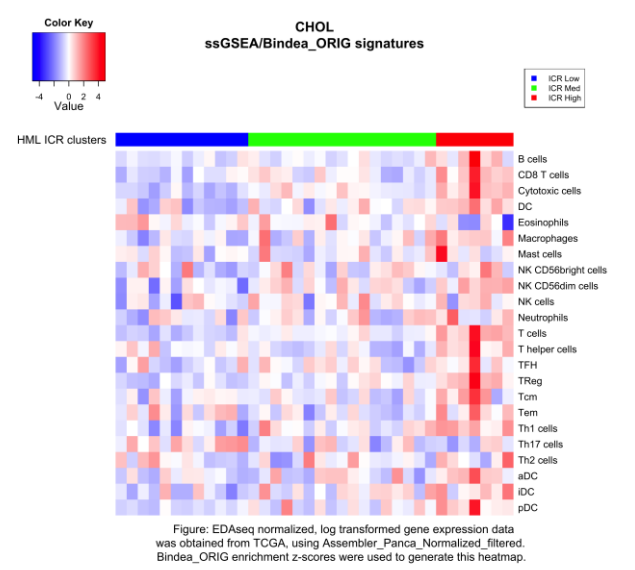


Cholangiocarcinoma (CHOL)

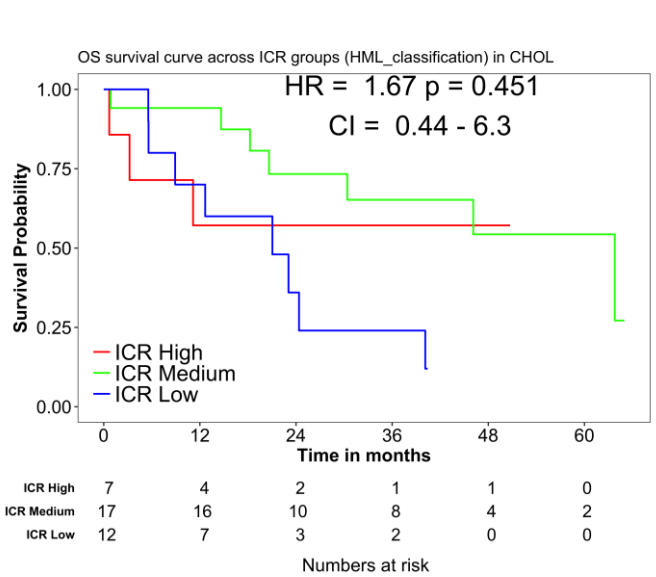
Immune phenotype (ICR) Clustering



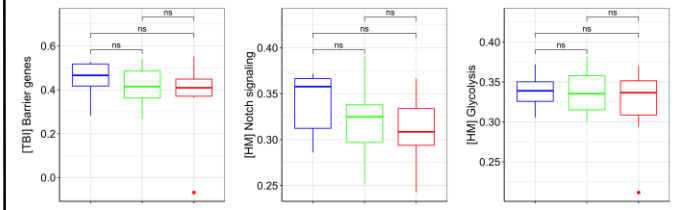
Deconvolution immune cell populations



Survival analysis



ssGSEA oncogenic pathways



Colon adenocarcinoma (COAD)

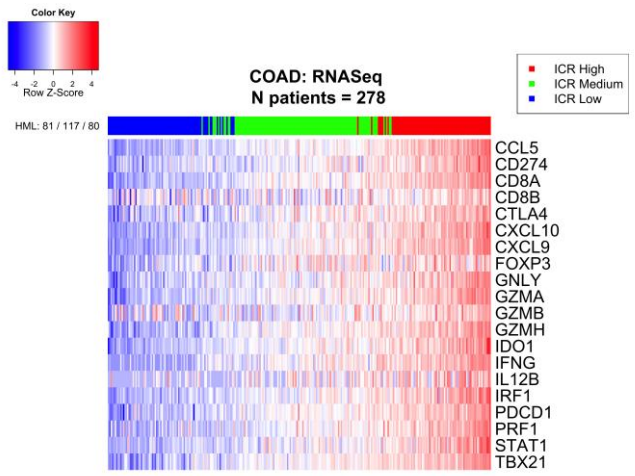
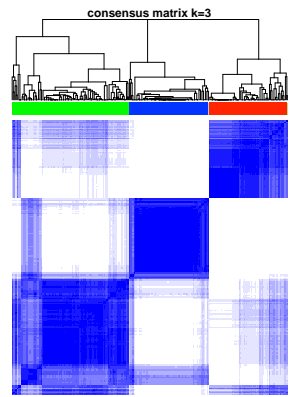
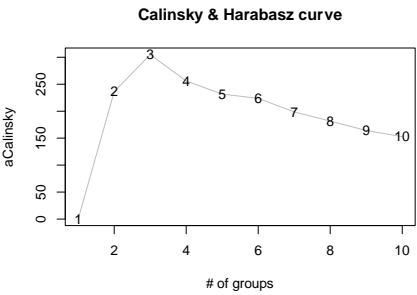
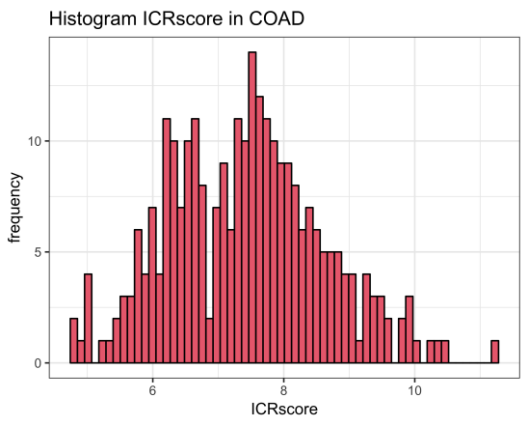


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none. Resulting in mean ICR scores of 8.05 / 7.4 / 8.84 for Low / Medium / High resp.



Deconvolution immune cell populations

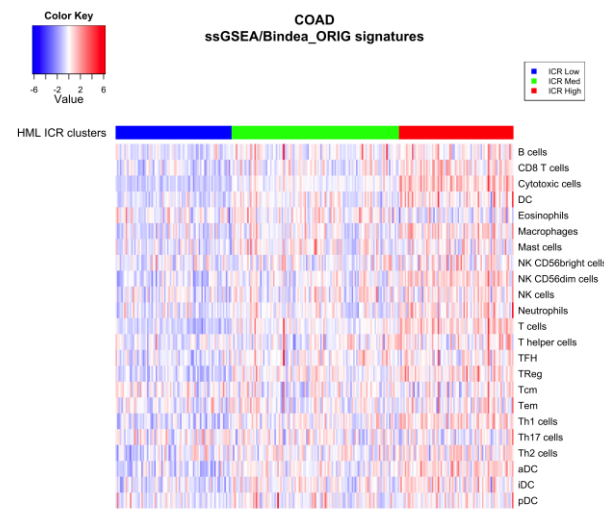
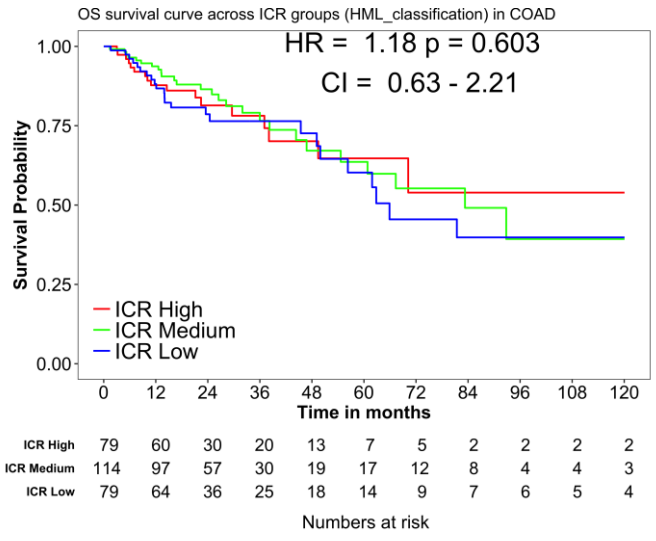
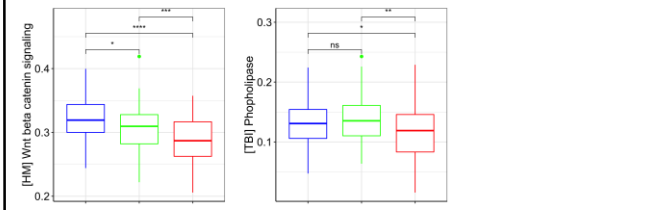


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Pance_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

Survival analysis

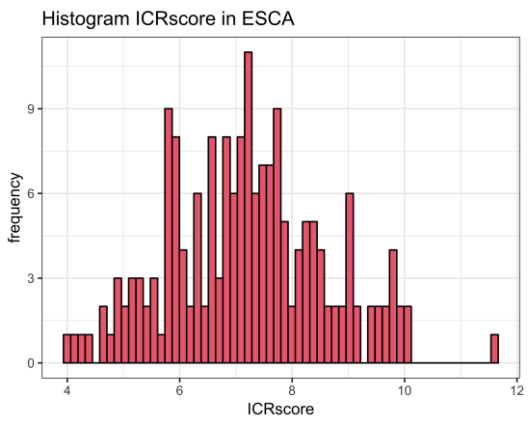
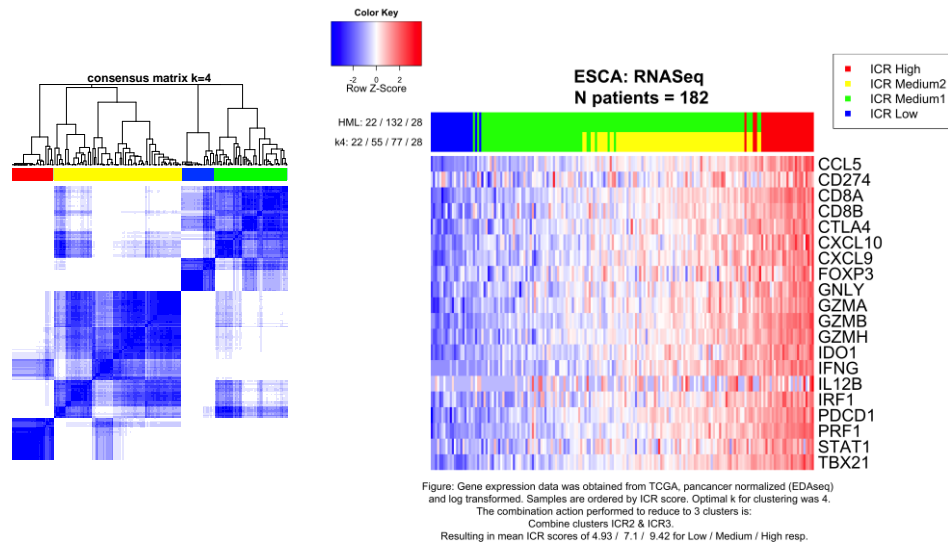
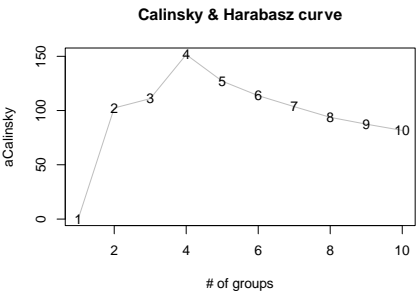


ssGSEA oncogenic pathways

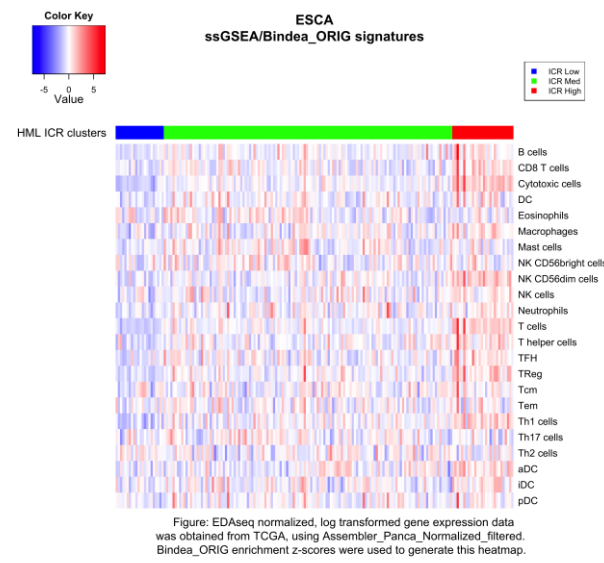


Esophageal carcinoma (ESCA)

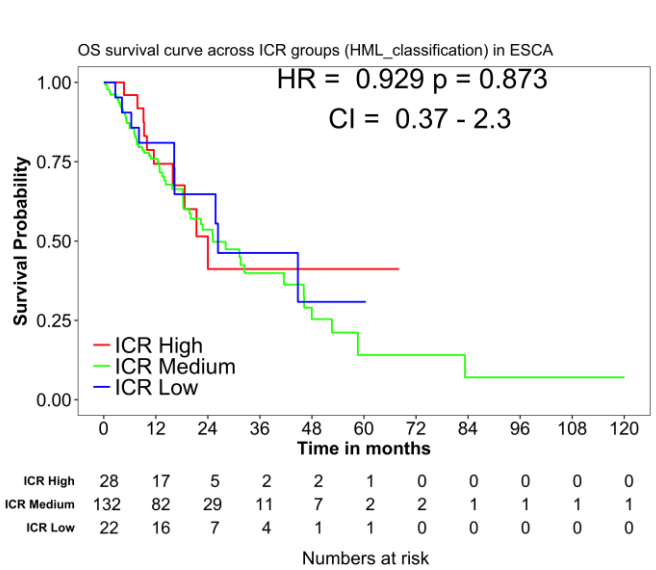
Immune phenotype (ICR) Clustering



Deconvolution immune cell populations



Survival analysis



ssGSEA oncogenic pathways



Glioblastoma multiforme (GBM)

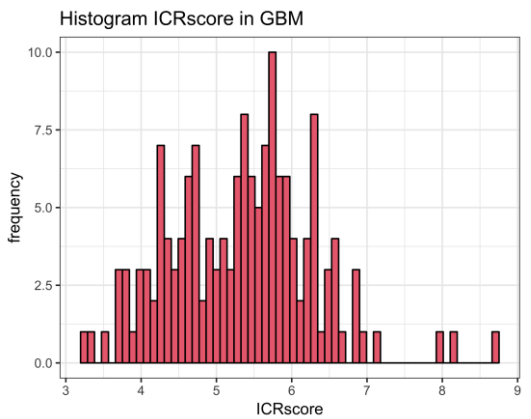
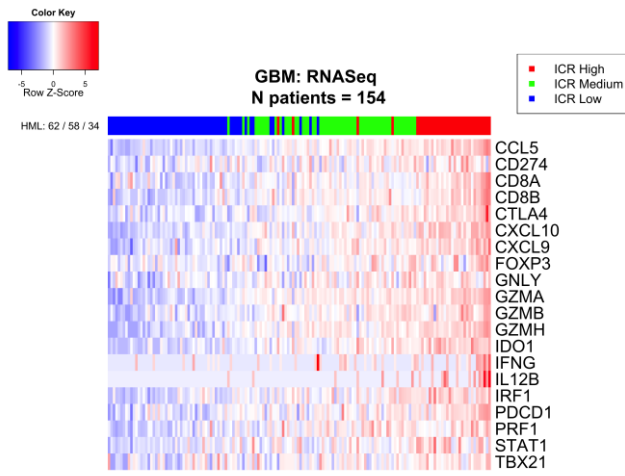
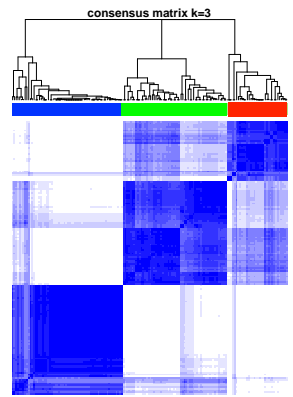
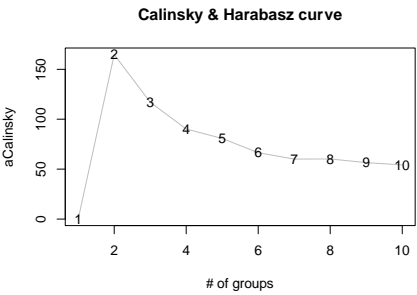


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none Resulting in mean ICR scores of 4.45 / 5.58 / 6.53 for Low / Medium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

Deconvolution immune cell populations

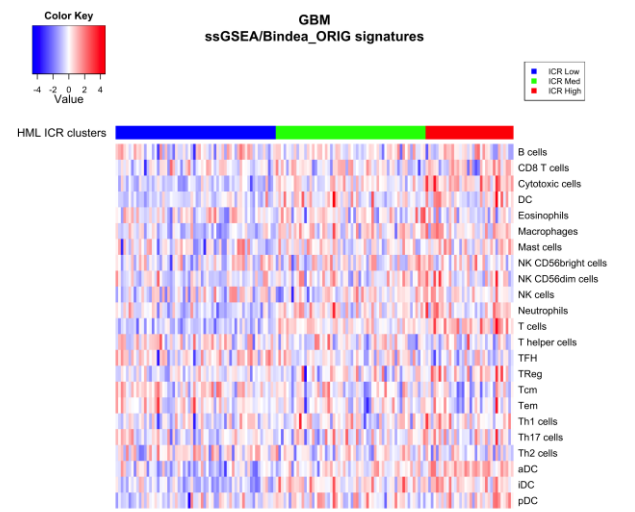
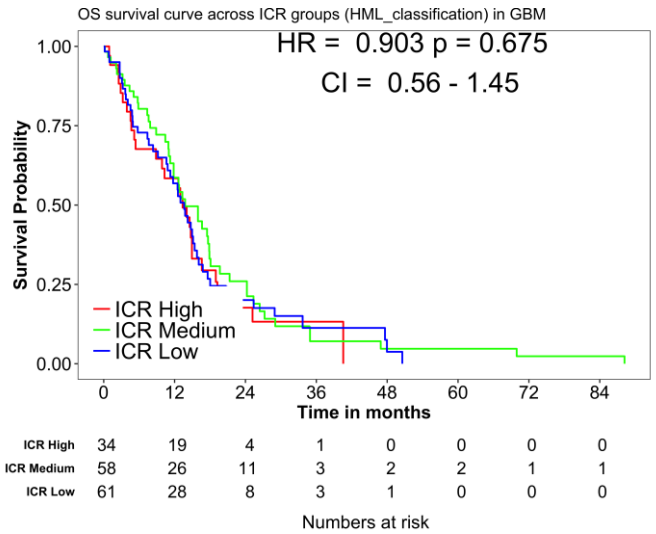
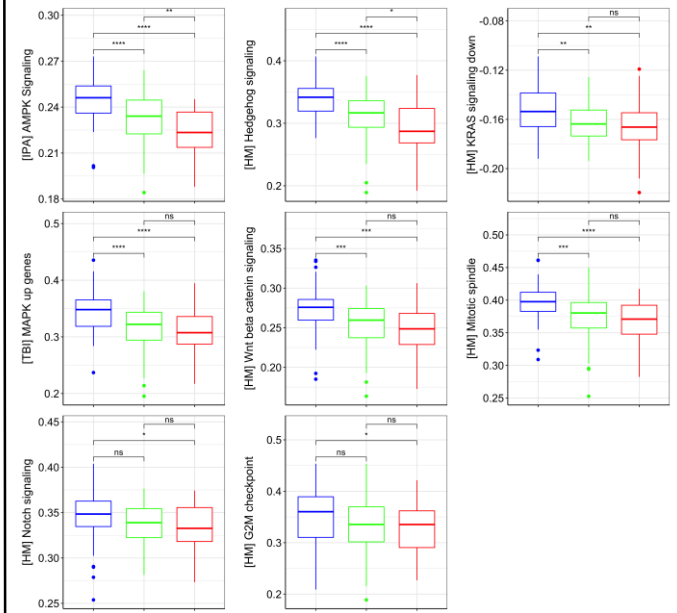


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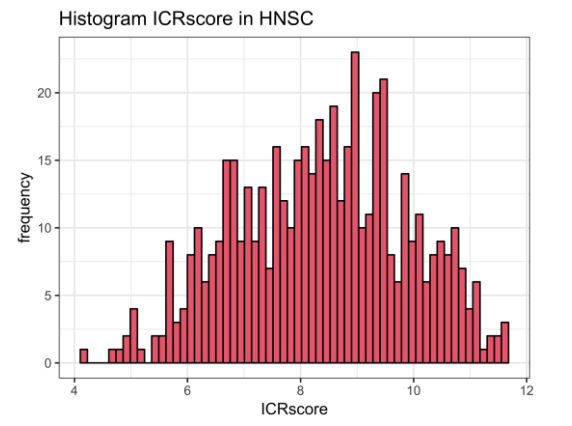
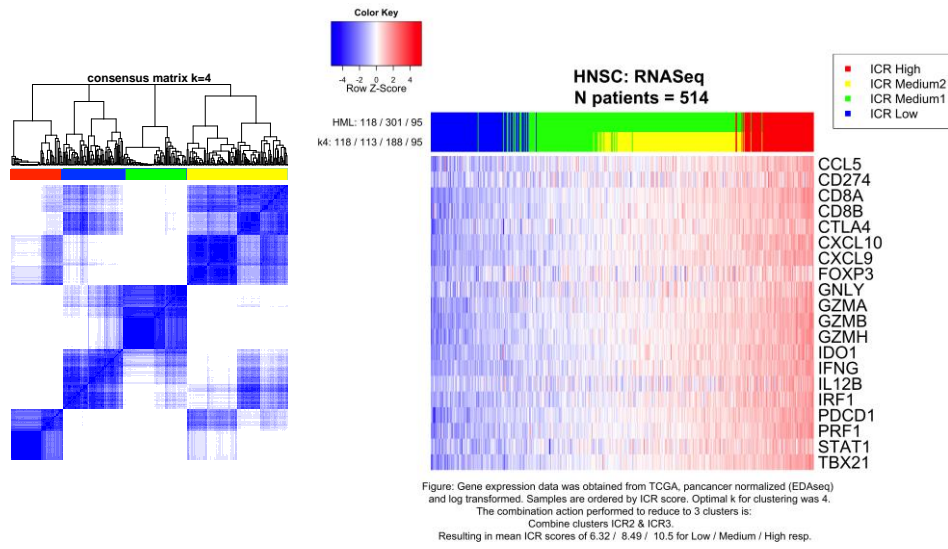
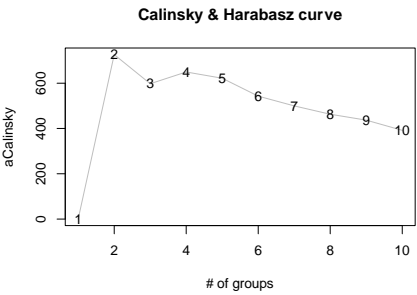
Survival analysis



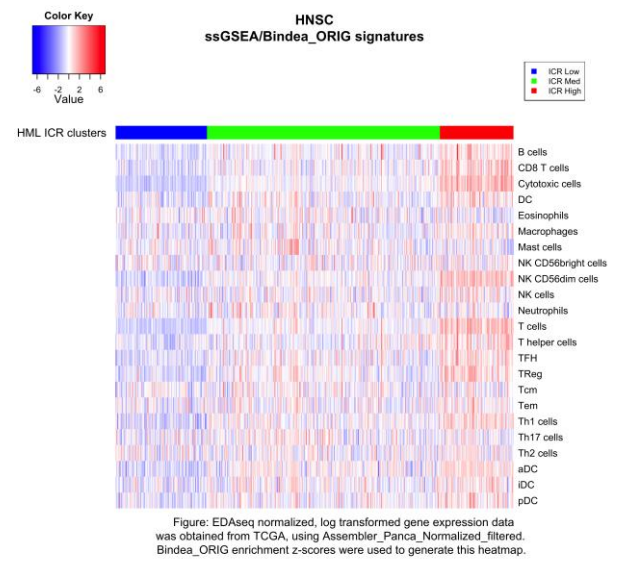
ssGSEA oncogenic pathways



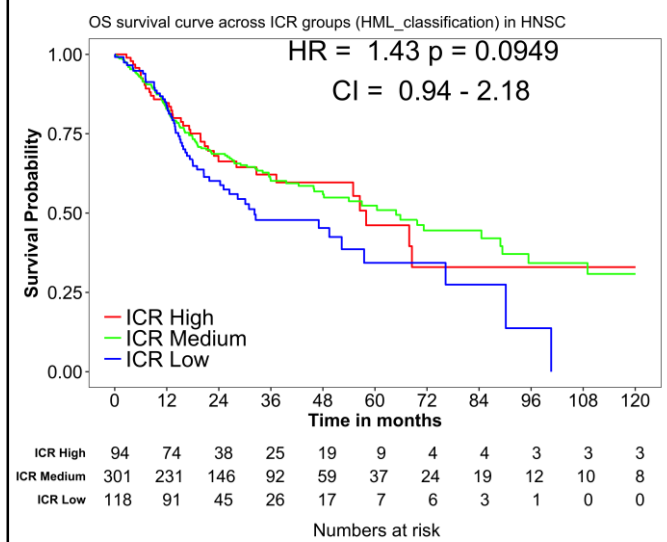
Head and neck squamous cell carcinoma (HNSC)



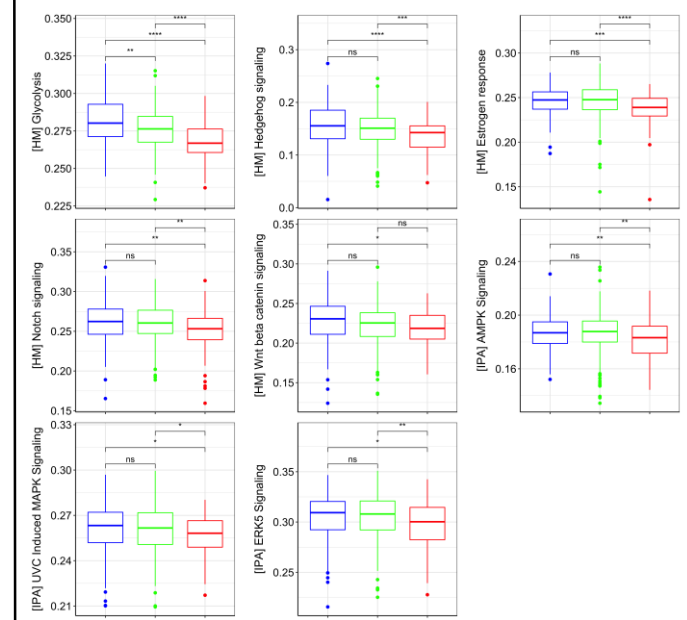
Deconvolution immune cell populations



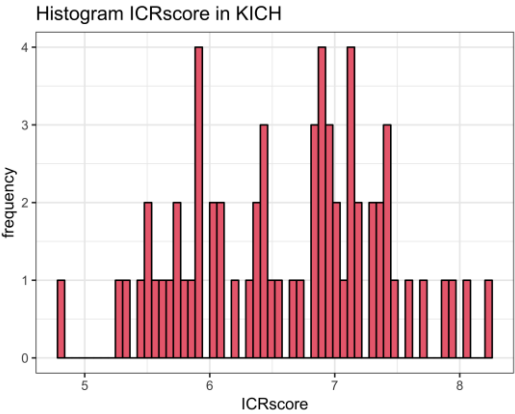
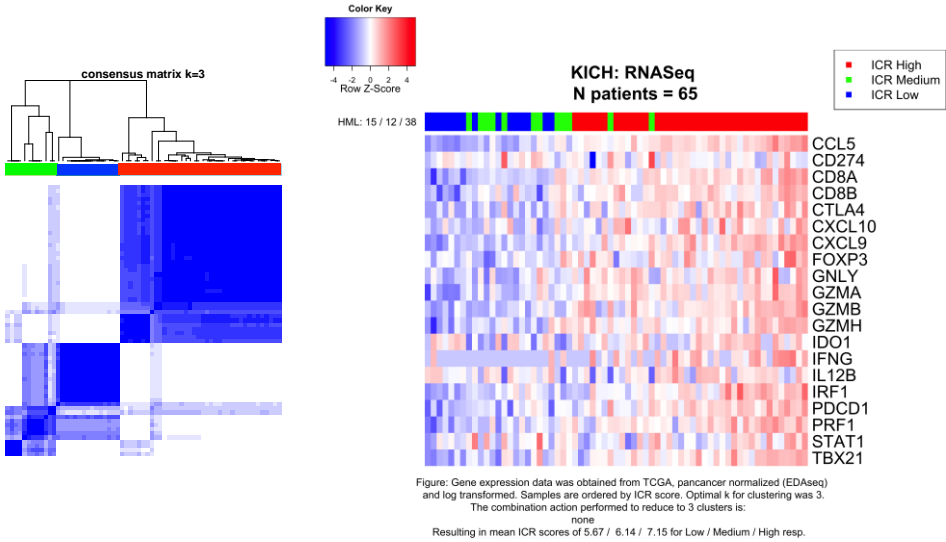
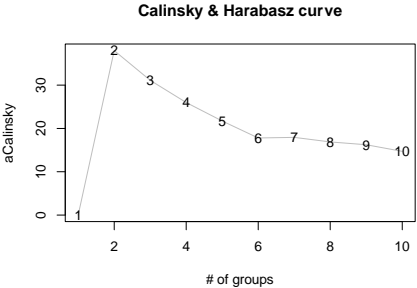
Survival analysis



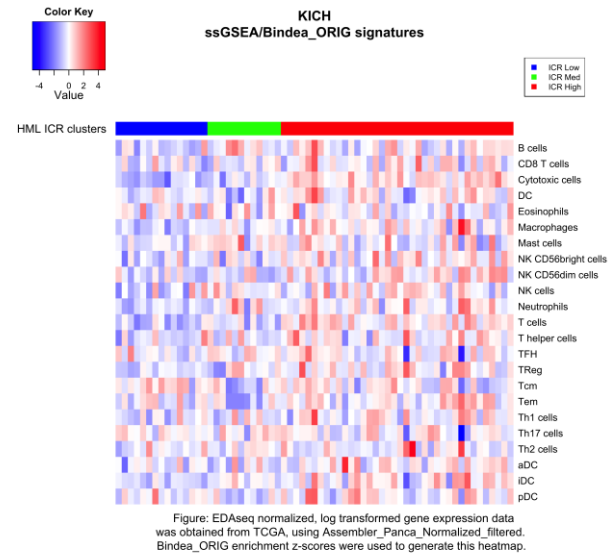
ssGSEA oncogenic pathways



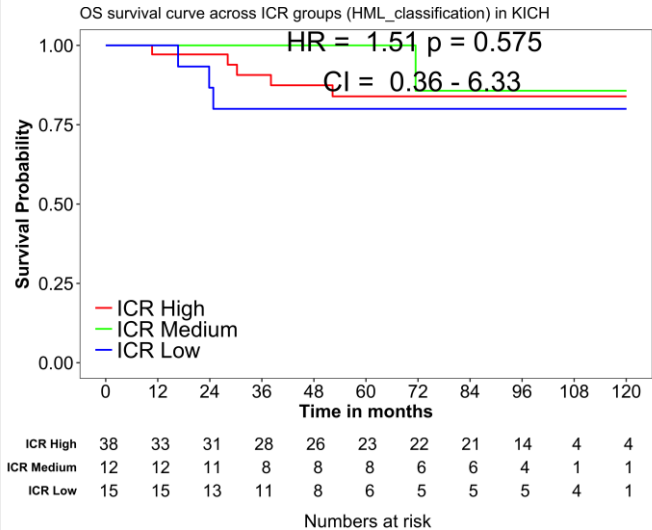
Kidney
chromophobe
(KICH)



Deconvolution immune
cell populations



Survival analysis



ssGSEA oncogenic
pathways

Kidney renal clear
cell carcinoma
(KIRC)

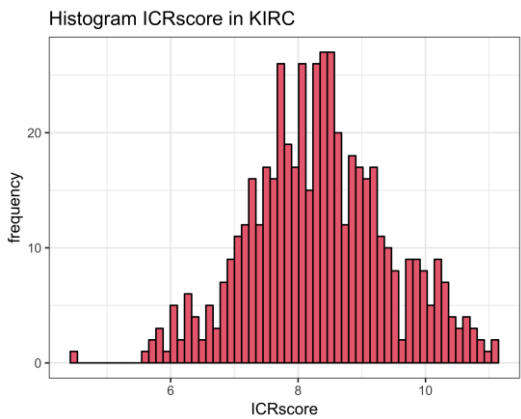
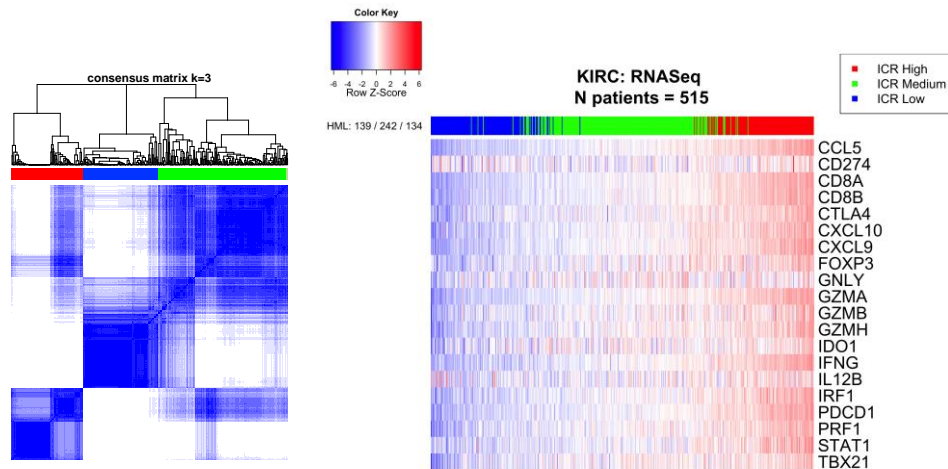
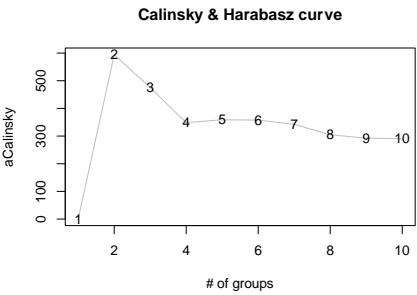


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none Resulting in mean ICR scores of 7.06 / 8.31 / 9.71 for Low / Medium / High resp.

Deconvolution immune
cell populations

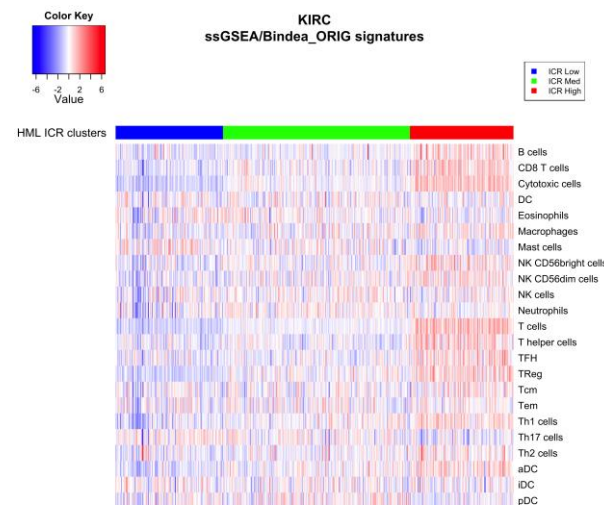
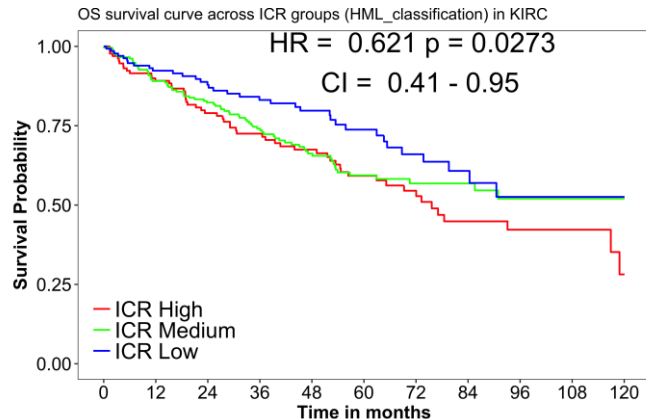


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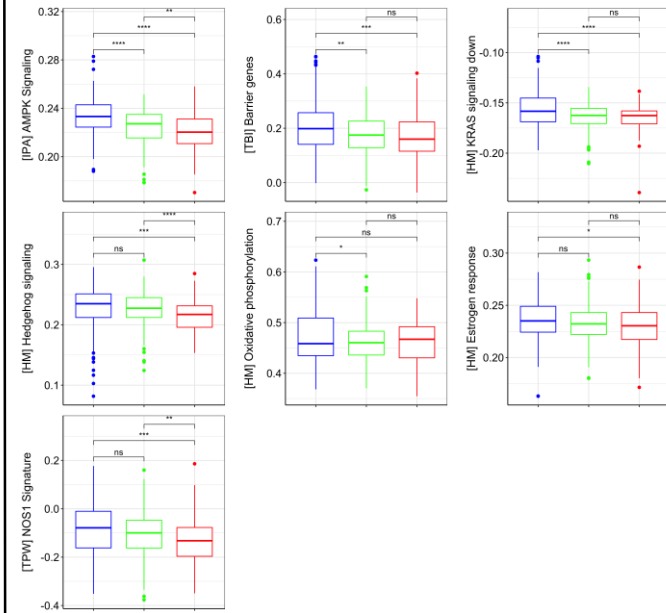
Survival analysis



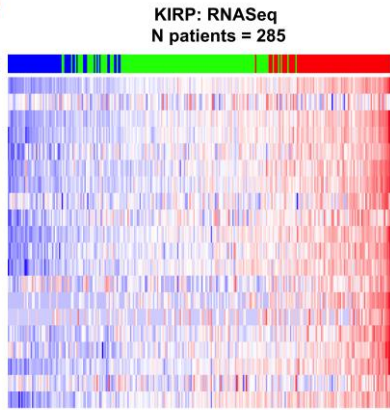
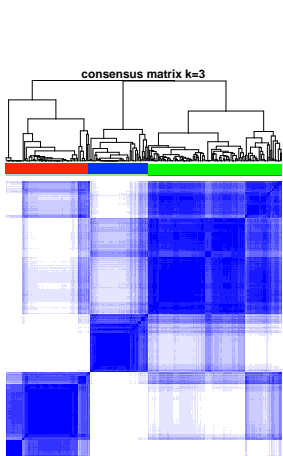
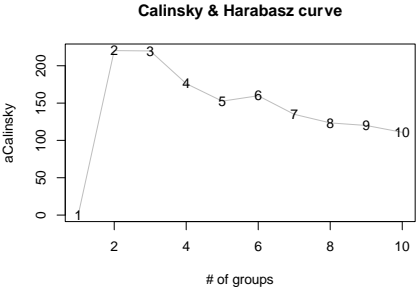
ICR High	134	112	89	73	59	45	32	21	14	9	4
ICR Medium	240	198	160	128	92	58	38	26	15	14	7
ICR Low	139	113	96	82	64	45	28	16	10	7	2

Numbers at risk

ssGSEA oncogenic
pathways

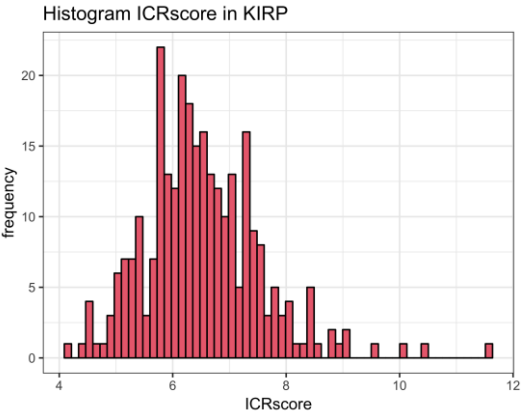


Kidney renal
papillary cell
carcinoma (KIRP)

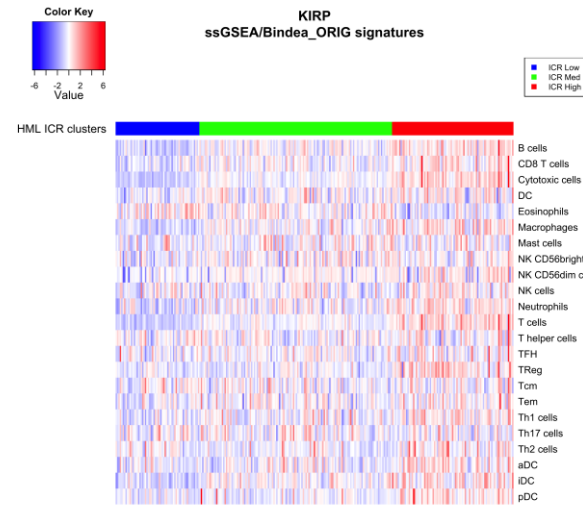


- CCL5
- CD274
- CD8A
- CD8B
- CTLA4
- CXCL10
- CXCL9
- FOXP3
- GNLY
- GZMA
- GZMB
- GZMH
- IDO1
- IFNG
- IL12B
- IRF1
- PDCD1
- PRF1
- STAT1
- TBX21

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 5.3 / 6.31 / 7.7 for Low / Medium / High resp.



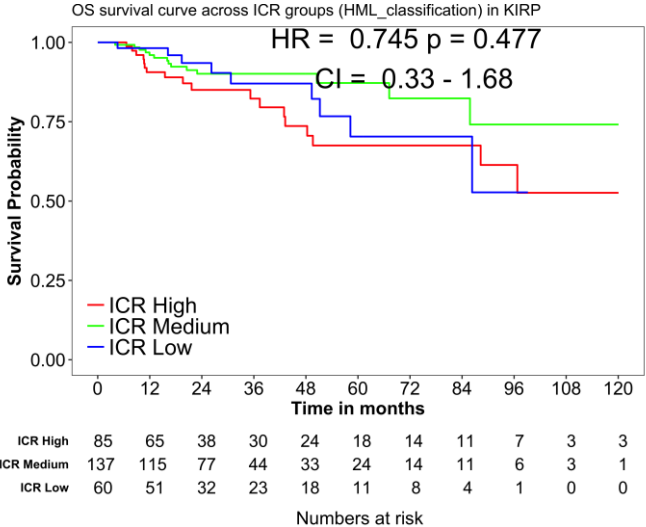
Deconvolution immune
cell populations



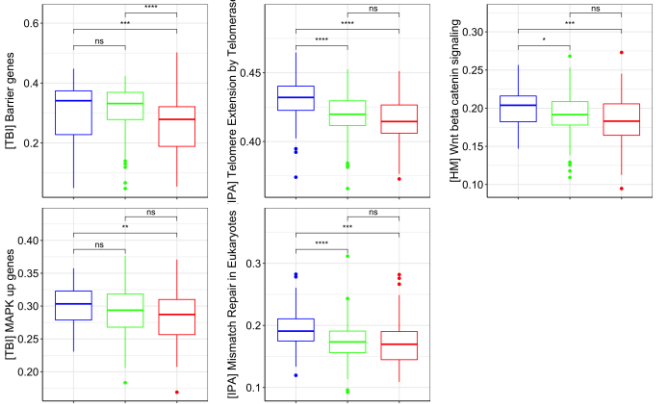
- B cells
- CD8 T cells
- Cytotoxic cells
- DC
- Eosinophils
- Macrophages
- Mast cells
- NK CD56bright cells
- NK CD56dim cells
- NK cells
- Neutrophils
- T cells
- T helper cells
- TFH
- TReg
- Tcm
- Tem
- Th1 cells
- Th17 cells
- Th2 cells
- aDC
- iDC
- pDC

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



Brain lower grade glioma (LGG)

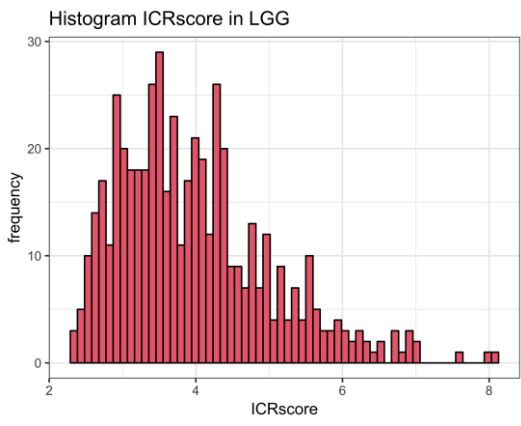
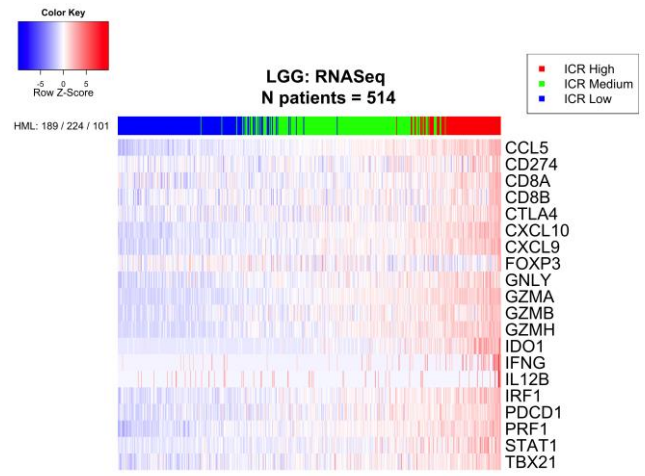
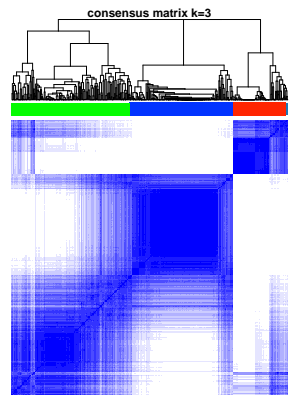
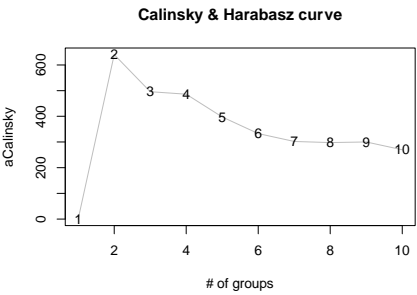


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none Resulting in mean ICR scores of 3.02 / 4.04 / 5.6 for Low / Medium / High resp.

Deconvolution immune cell populations

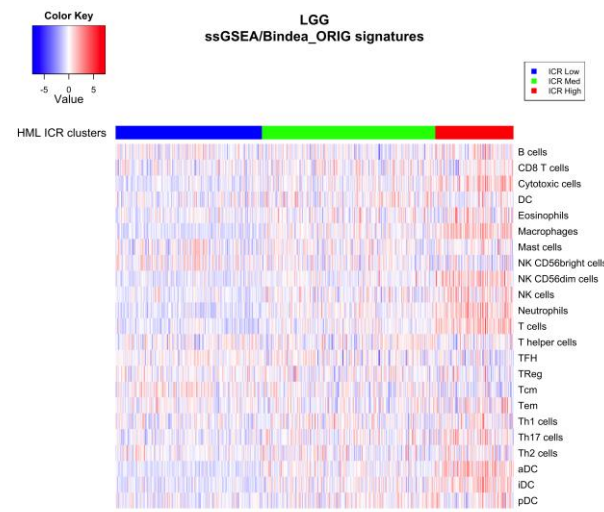
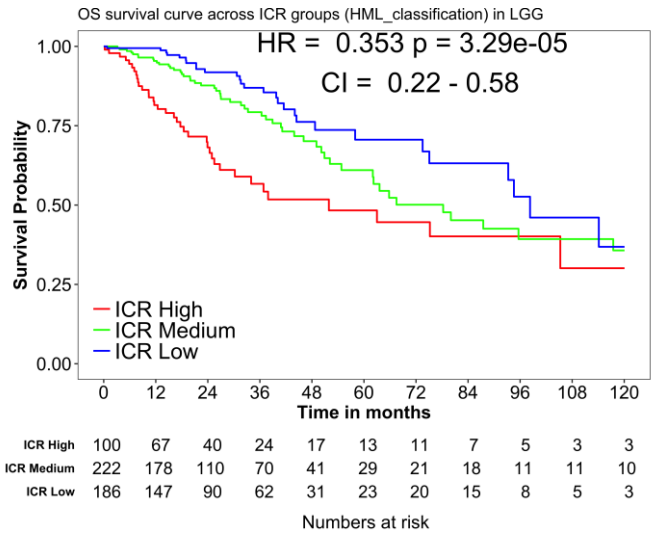
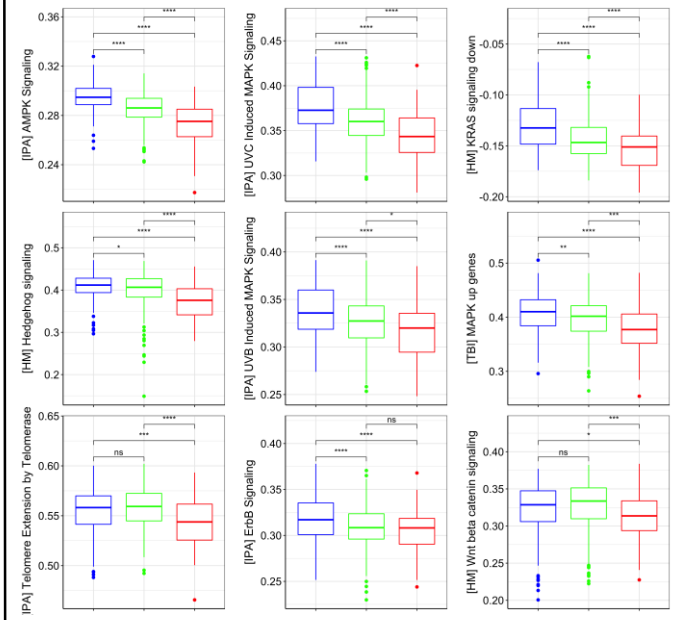


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Pance_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

Survival analysis



ssGSEA oncogenic pathways



Liver hepatocellular carcinoma (LIHC)

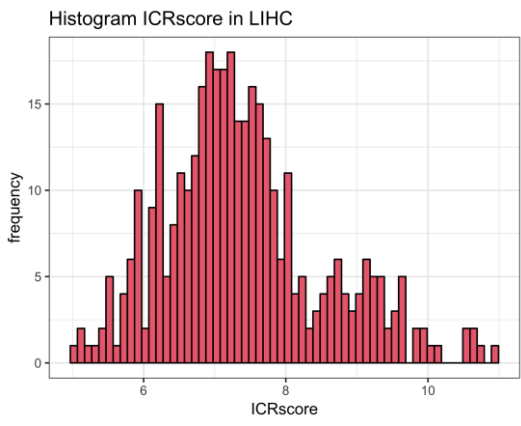
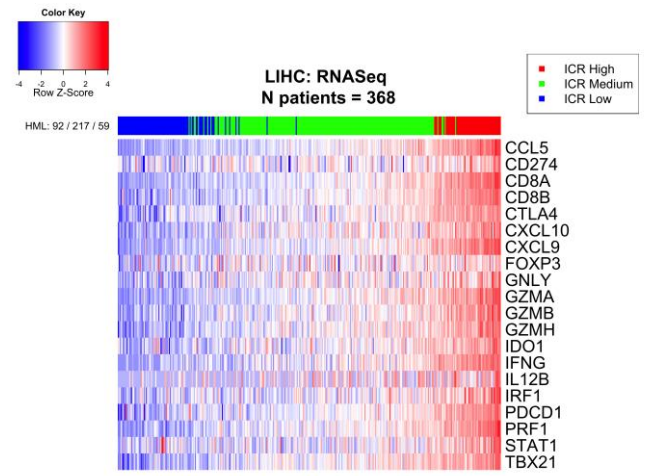
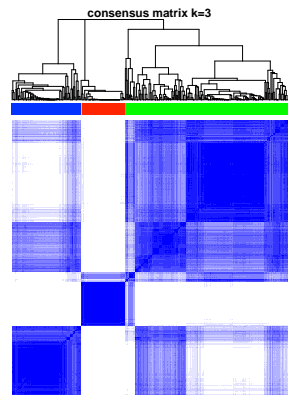
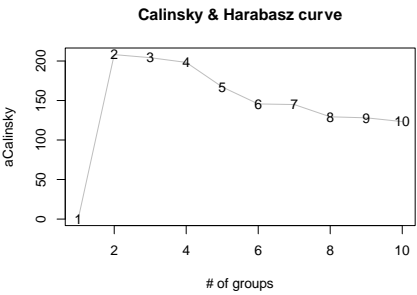


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none Resulting in mean ICR scores of 8.13 / 7.4 / 9.35 for Low / Medium / High resp.

Deconvolution immune cell populations

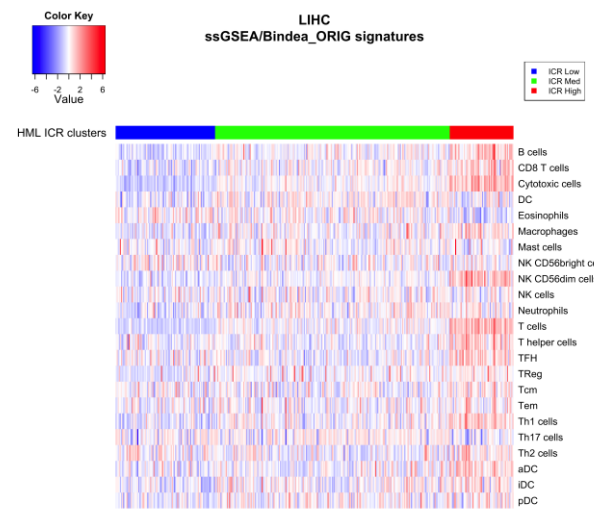
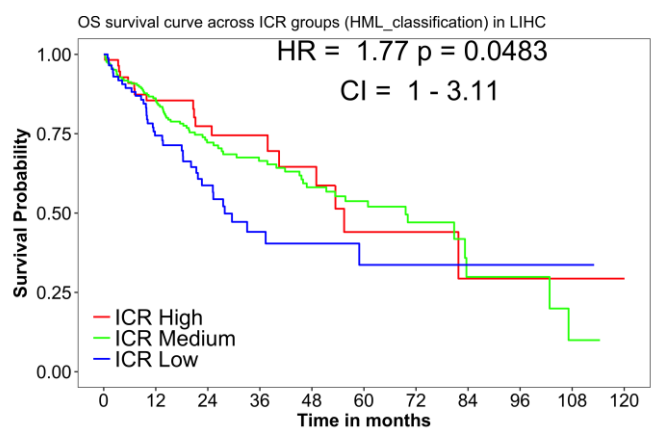


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Pance_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

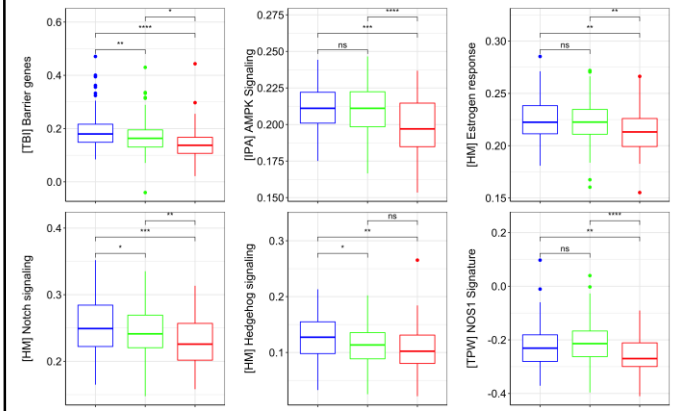
Survival analysis



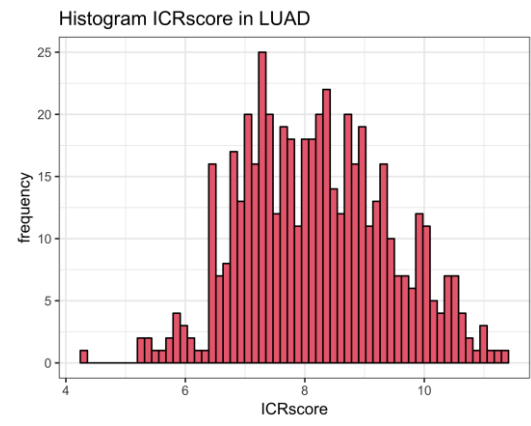
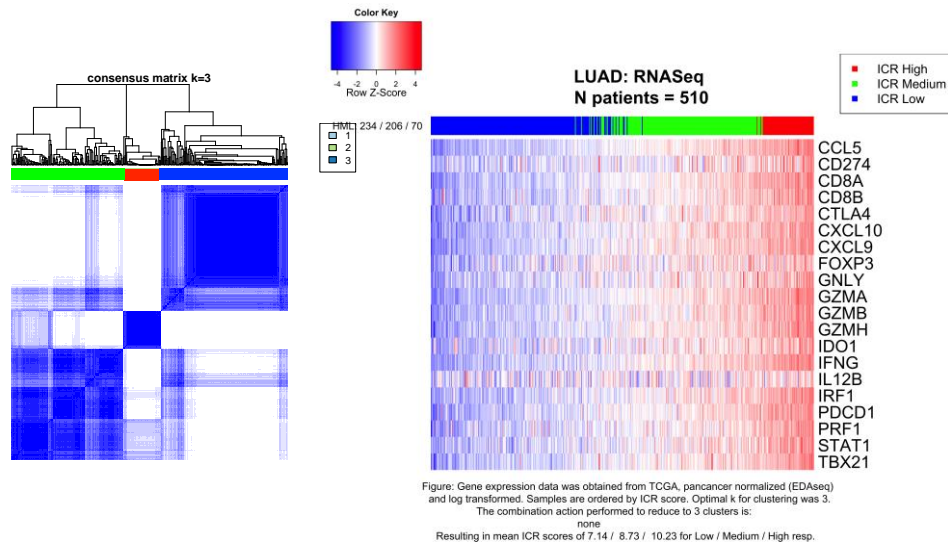
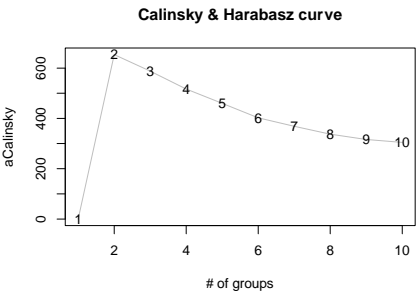
ICR High	57	44	28	16	11	5	5	2	1	1	1
ICR Medium	212	161	84	62	44	31	18	5	3	1	0
ICR Low	92	54	27	12	8	4	3	2	2	2	0

Numbers at risk

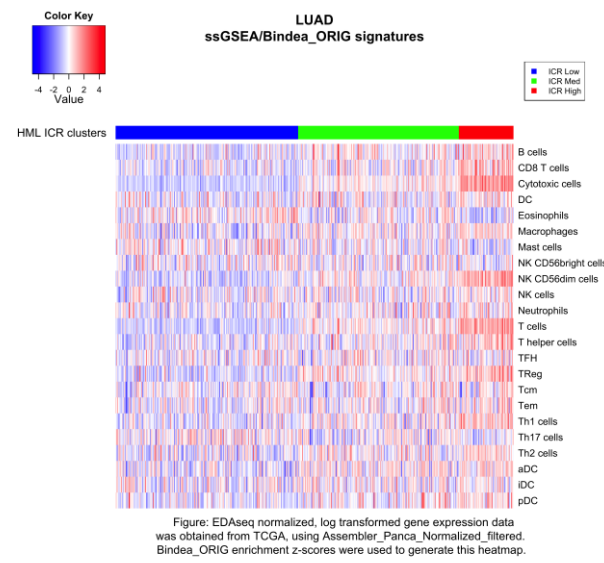
ssGSEA oncogenic pathways



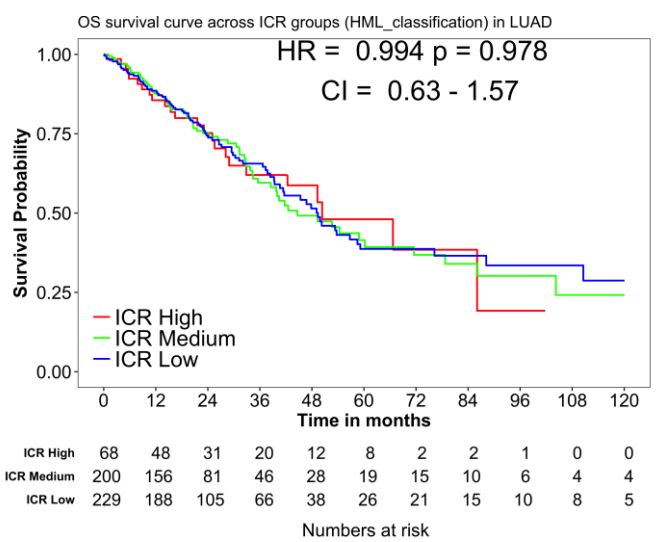
Lung adenocarcinoma (LUAD)



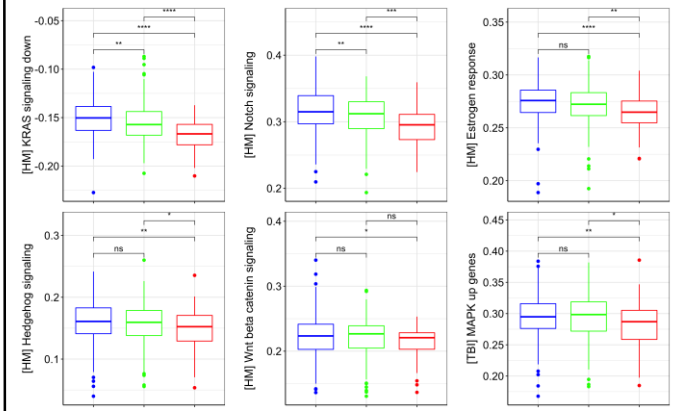
Deconvolution immune cell populations



Survival analysis



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Lung squamous cell carcinoma (LUSC)

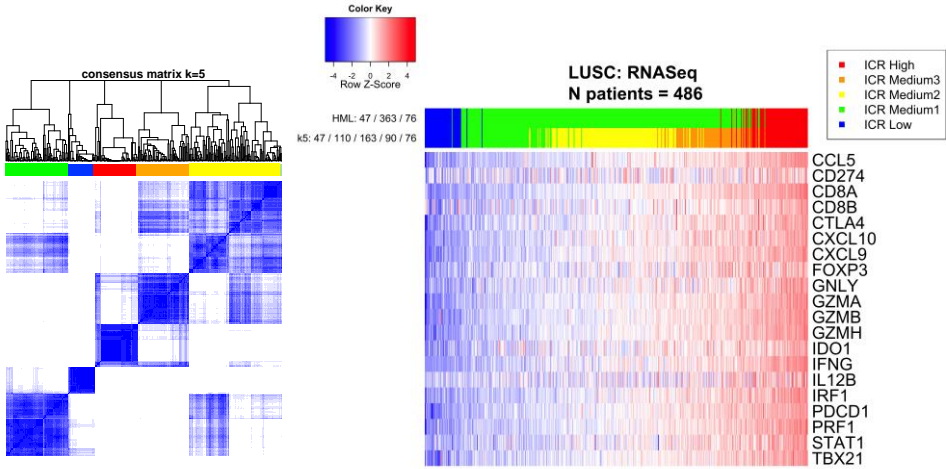
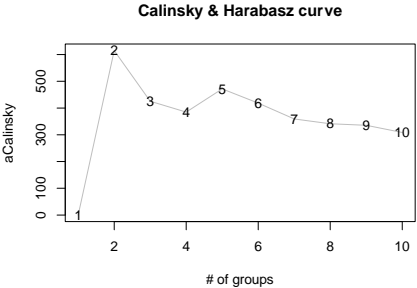
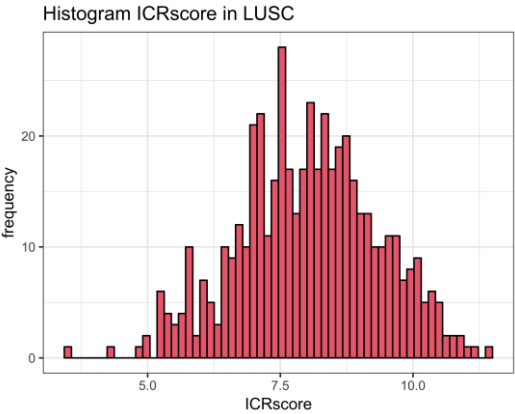


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 5. The combination action performed to reduce to 3 clusters is: Combine clusters ICR2 & ICR3 & ICR4. Resulting in mean ICR scores of 5.63 / 7.92 / 10 for Low / Medium / High resp.



Deconvolution immune cell populations

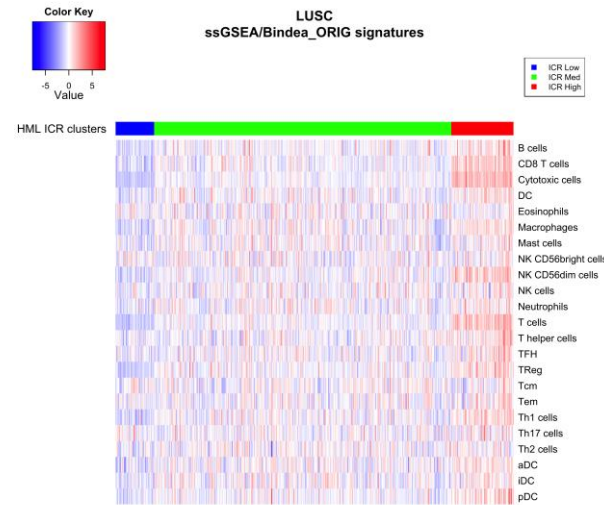
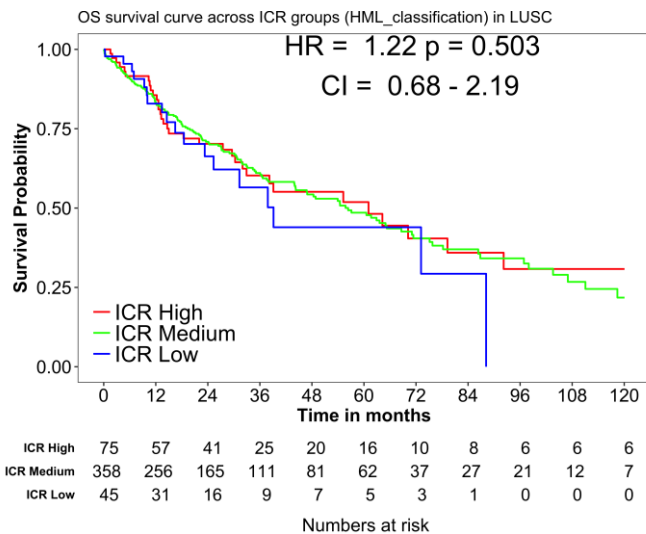
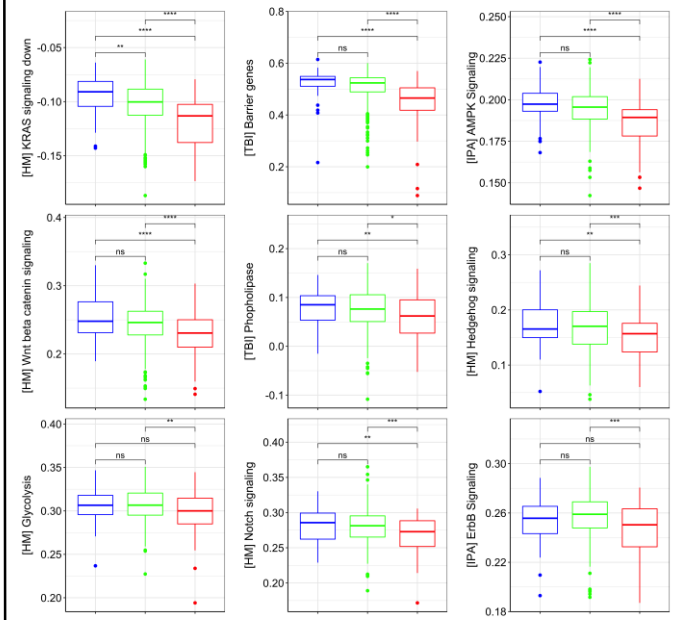


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Pancan_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

Survival analysis

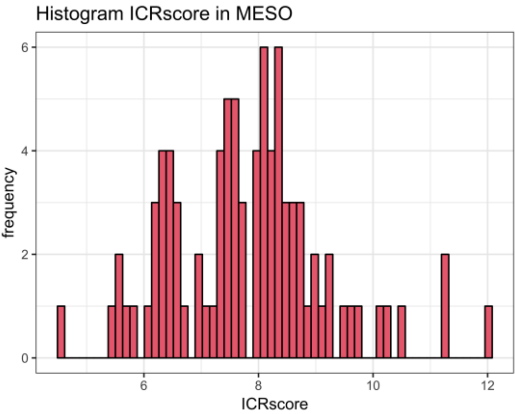
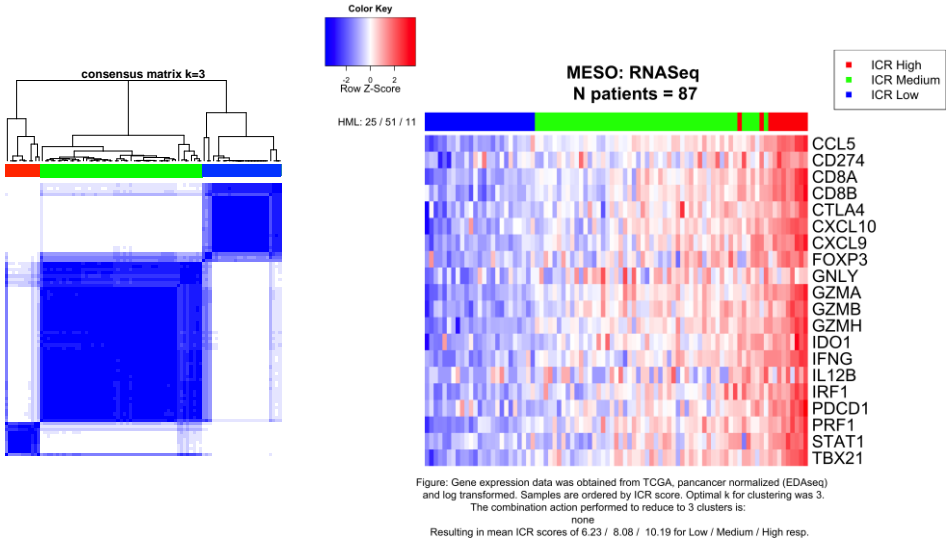
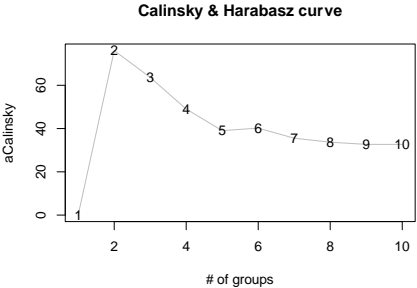


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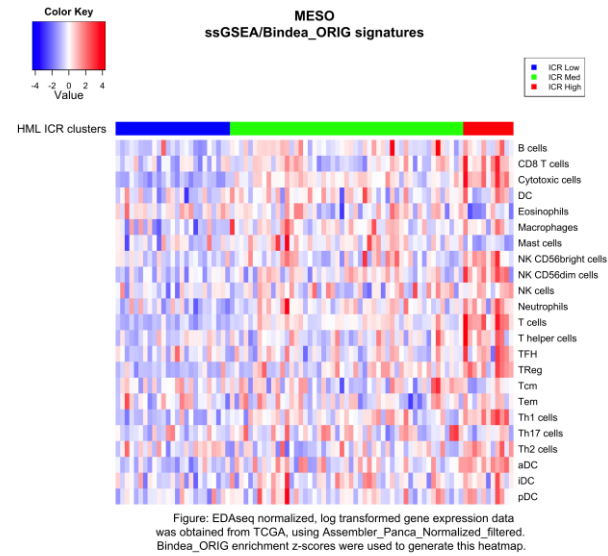


Mesothelioma (MESO)

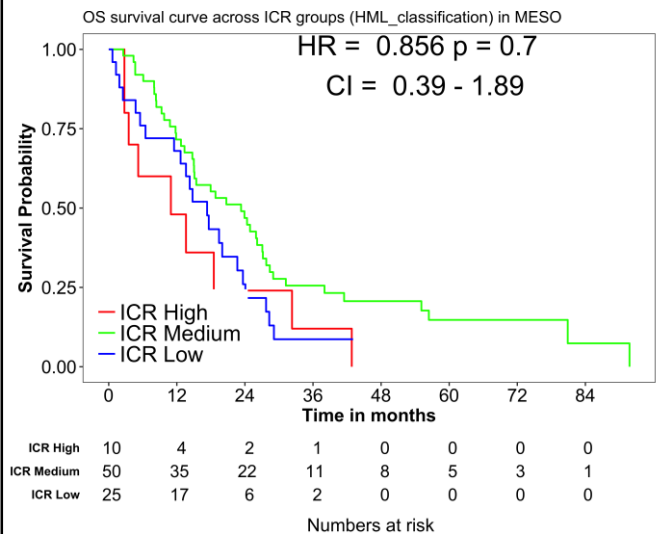
Immune phenotype (ICR) Clustering



Deconvolution immune cell populations



Survival analysis



ssGSEA oncogenic pathways



Ovarian serous cystadenocarcinoma (OV)

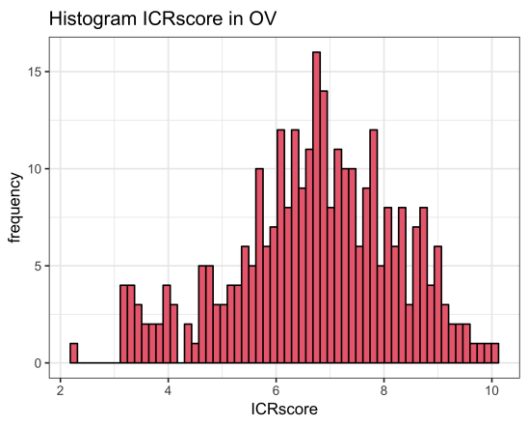
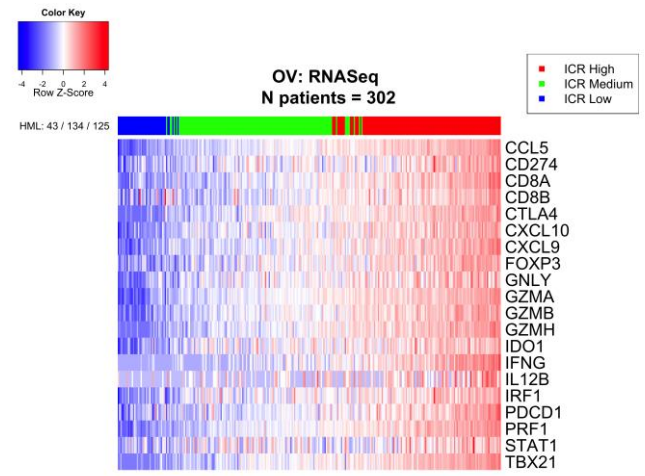
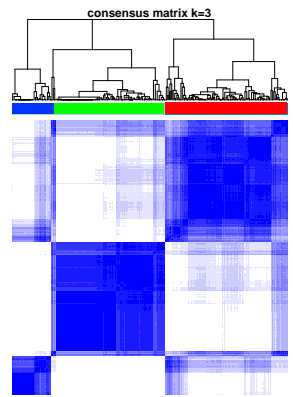
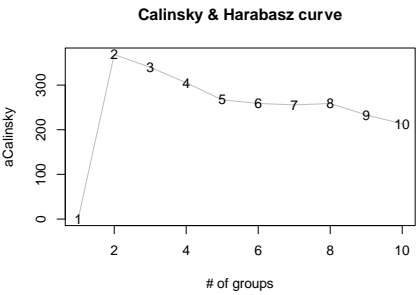


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none. Resulting in mean ICR scores of 4.06 / 6.26 / 8.11 for Low / Medium / High resp.

Deconvolution immune cell populations

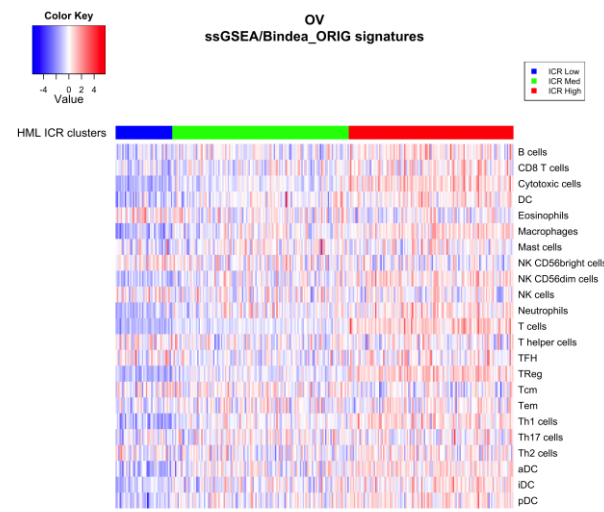
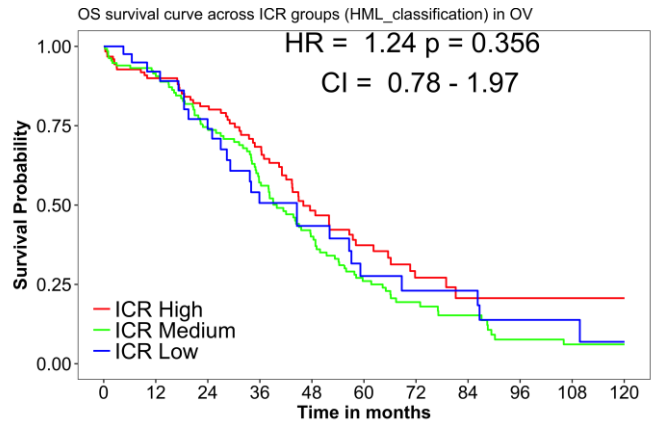


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Panca_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

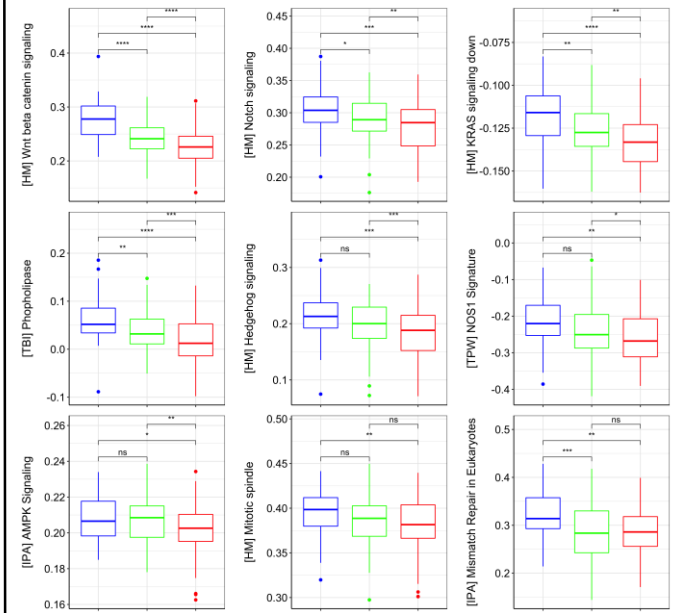
Survival analysis



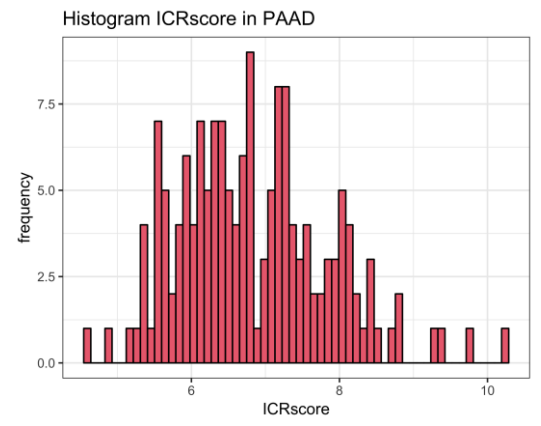
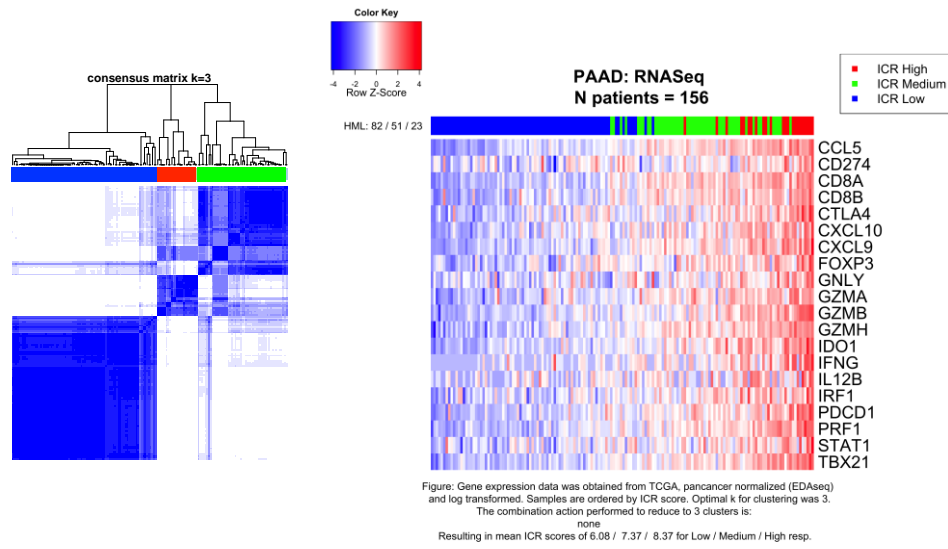
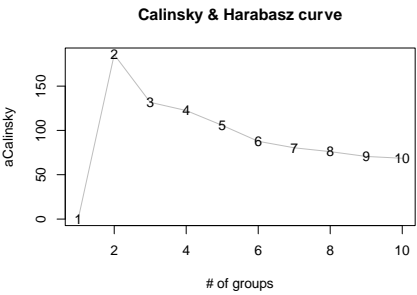
ICR High	124	96	79	54	32	21	12	6	4	3	2
ICR Medium	134	106	81	58	40	26	14	10	5	4	2
ICR Low	43	31	24	15	12	7	5	5	2	2	1

Numbers at risk

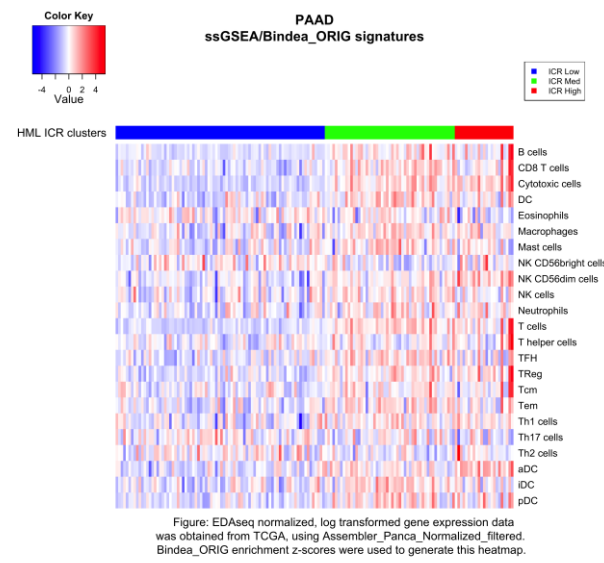
ssGSEA oncogenic pathways



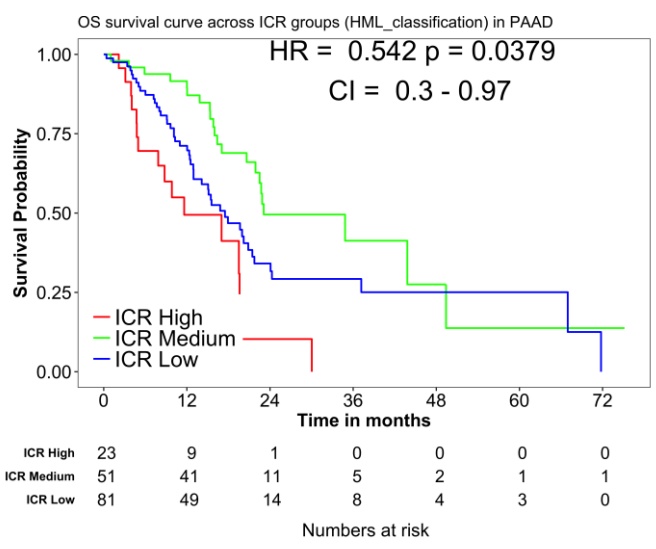
Pancreatic adenocarcinoma (PAAD)



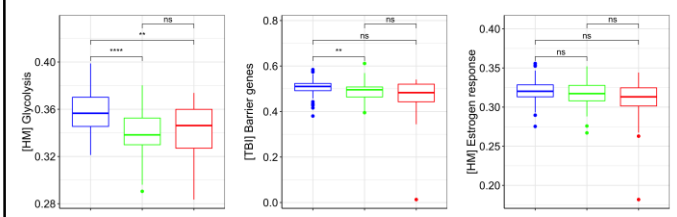
Deconvolution immune cell populations



Survival analysis



ssGSEA oncogenic pathways



Pheochromocytoma and paraganglioma (PCPG)

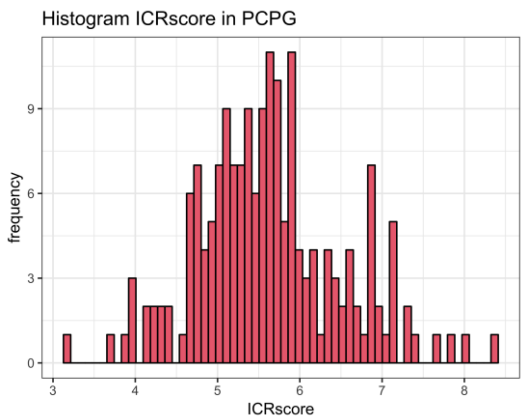
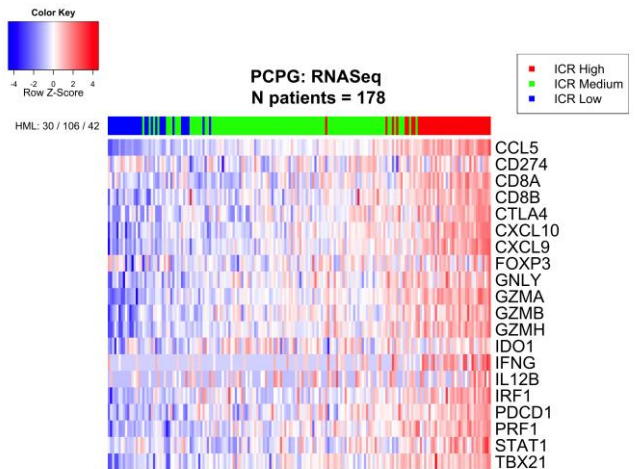
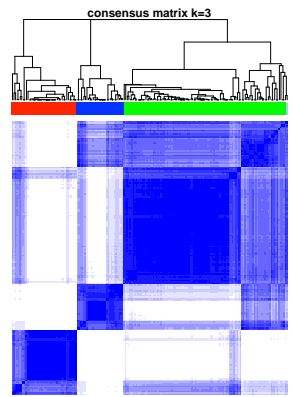
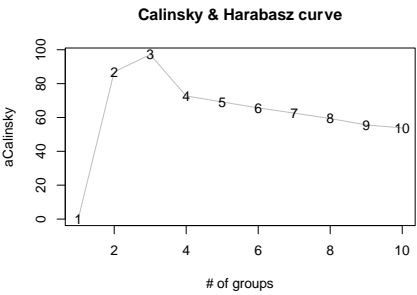


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none Resulting in mean ICR scores of 4.46 / 5.48 / 6.82 for Low / Medium / High resp.

Deconvolution immune cell populations

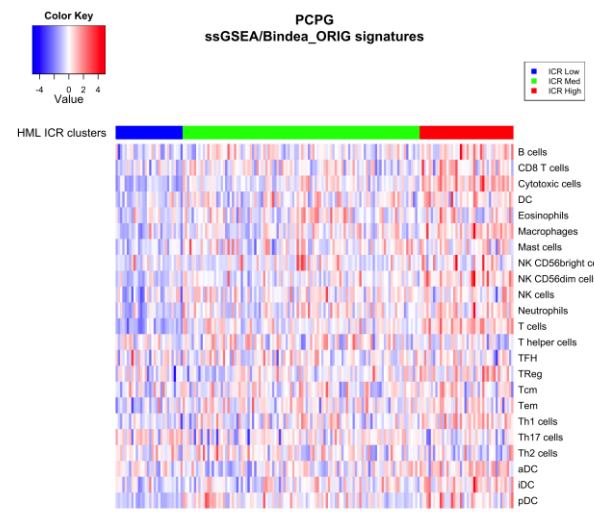
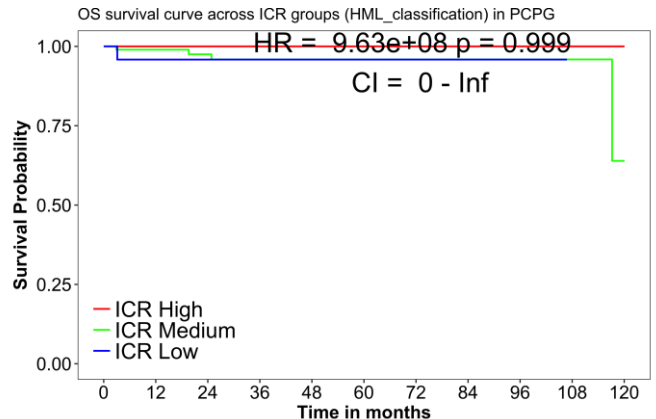


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Panca_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

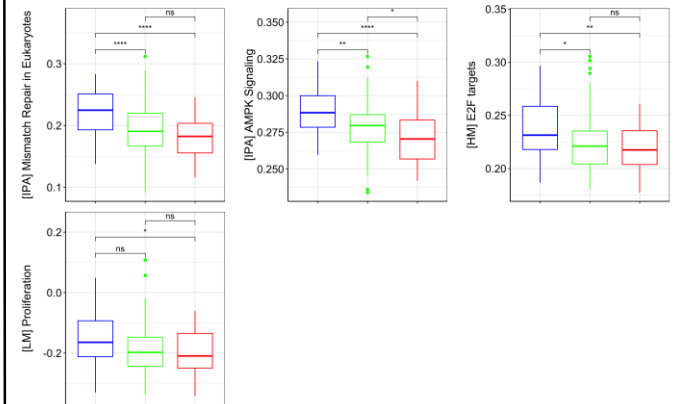
Survival analysis



ICR High	42	29	20	10	8	7	7	5	4	3	2
ICR Medium	106	83	60	45	31	24	19	11	9	9	2
ICR Low	30	20	14	5	1	1	1	1	1	0	0

Numbers at risk

ssGSEA oncogenic pathways



Prostate adenocarcinoma (PRAD)

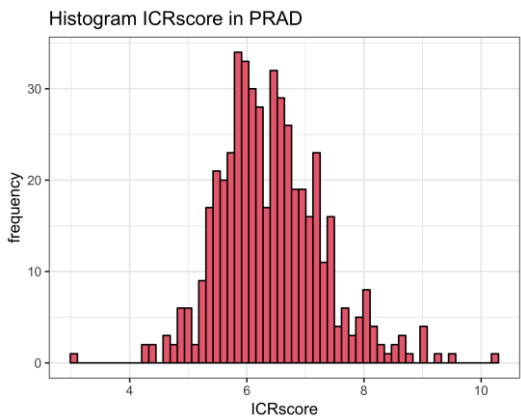
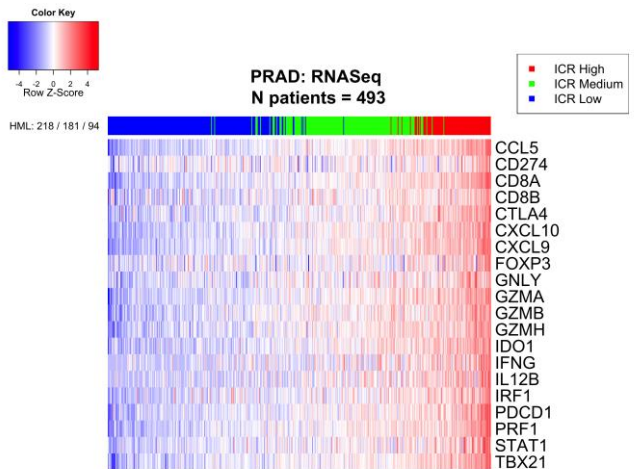
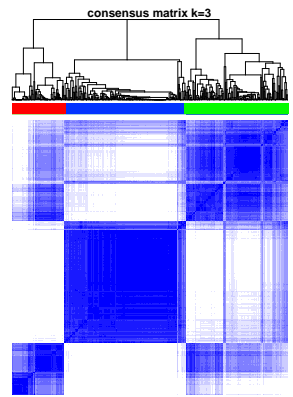
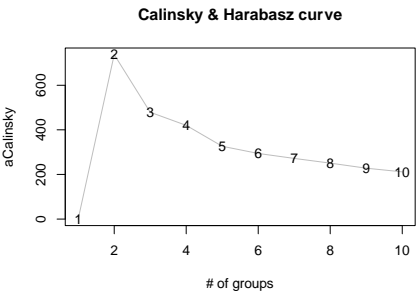


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none Resulting in mean ICR scores of 5.67 / 6.62 / 7.74 for Low / Medium / High resp.

Deconvolution immune cell populations

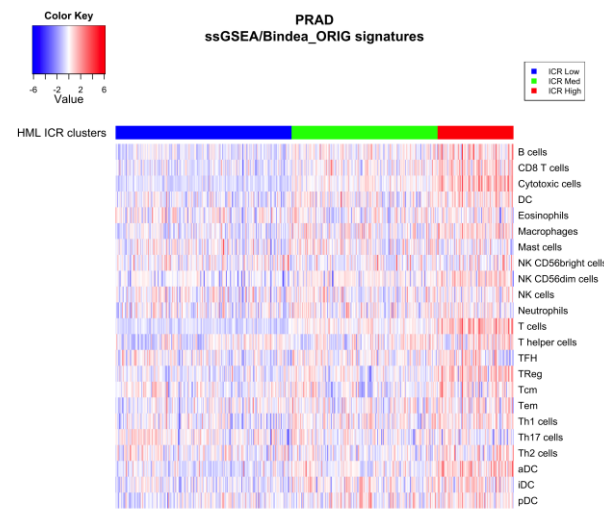
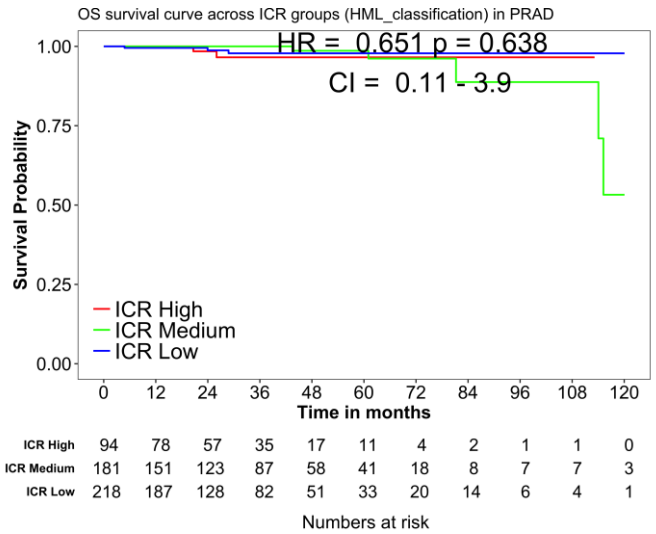
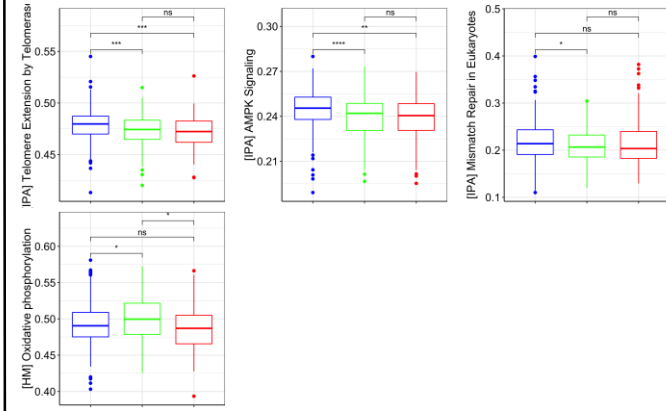


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Panca_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

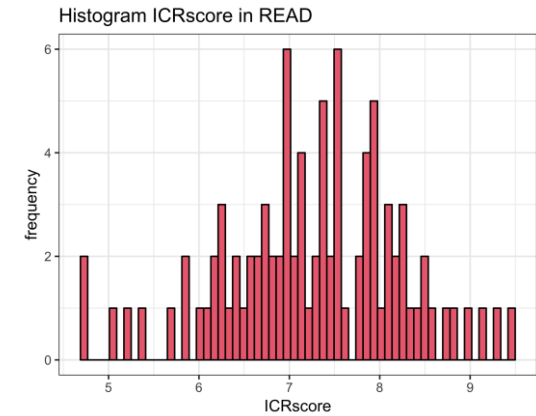
Survival analysis



ssGSEA oncogenic pathways

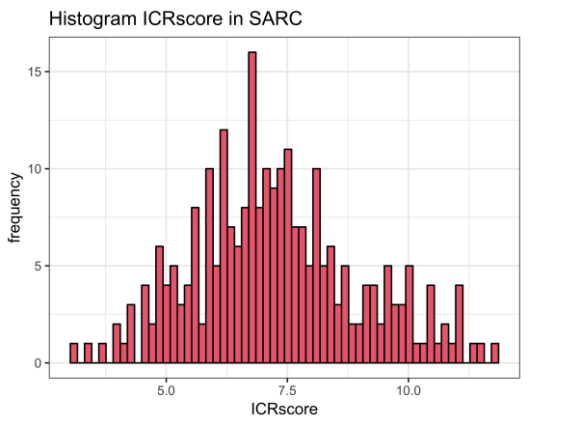
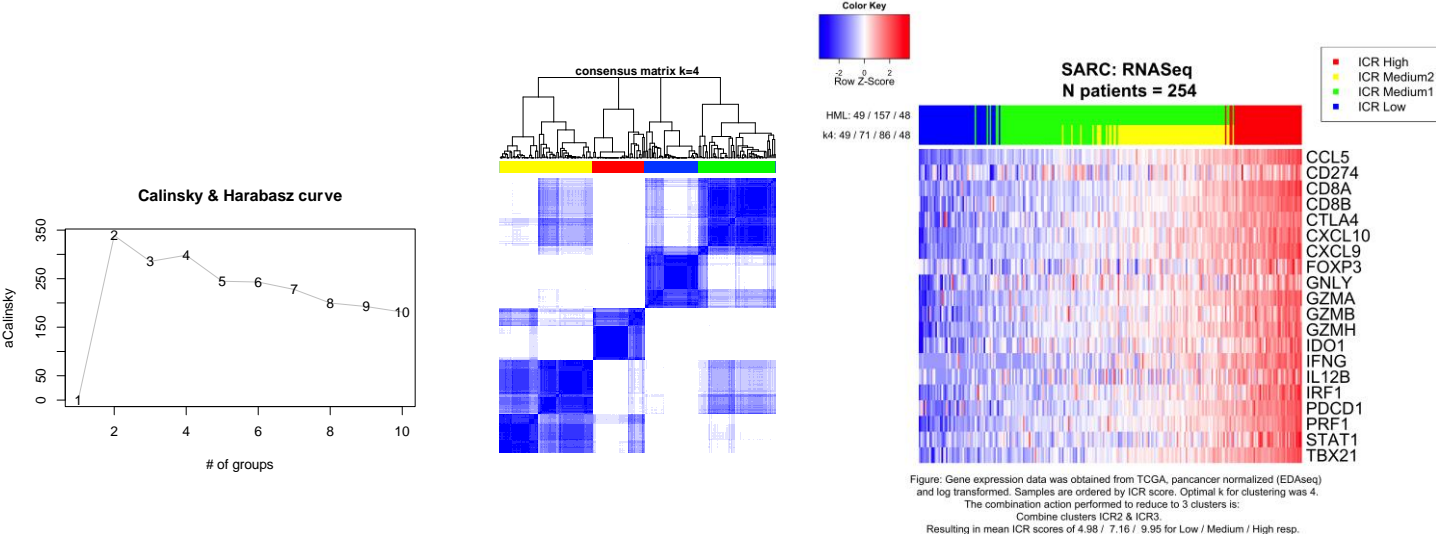


Immune phenotype (ICR) Clustering

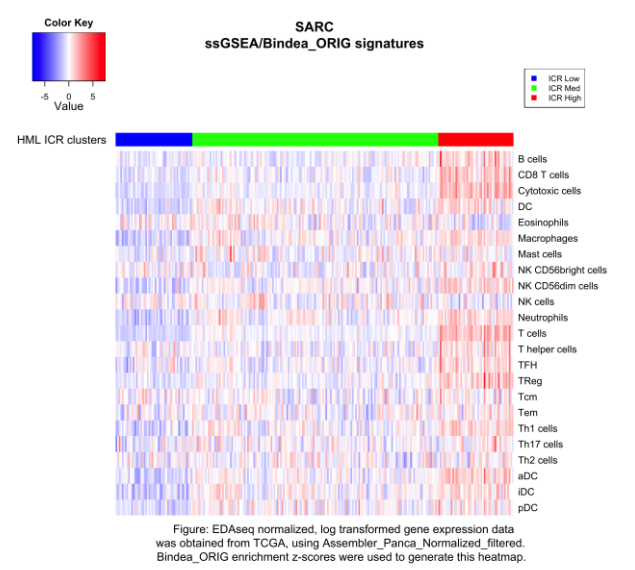


Sarcoma (SARC)

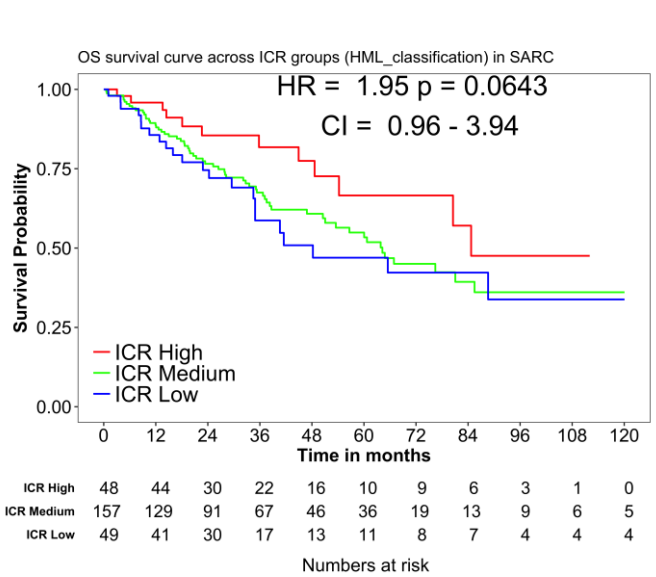
Immune phenotype (ICR) Clustering



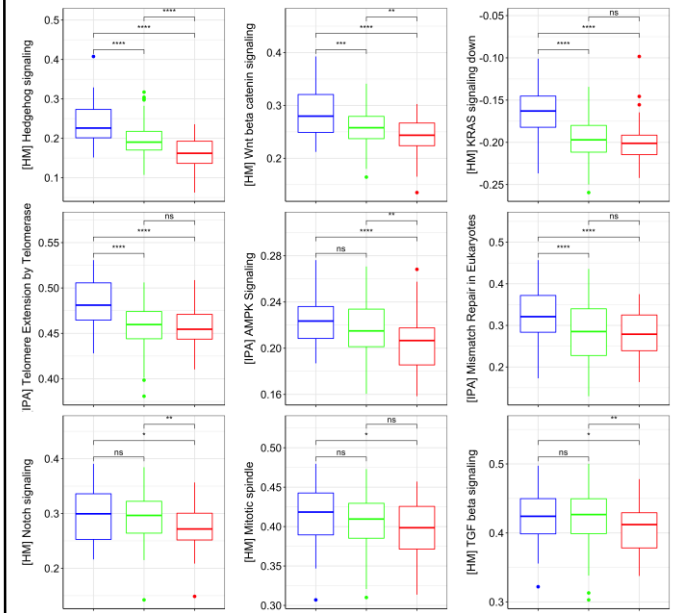
Deconvolution immune cell populations



Survival analysis

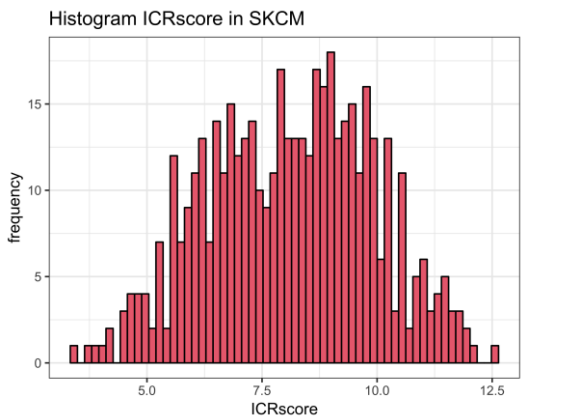
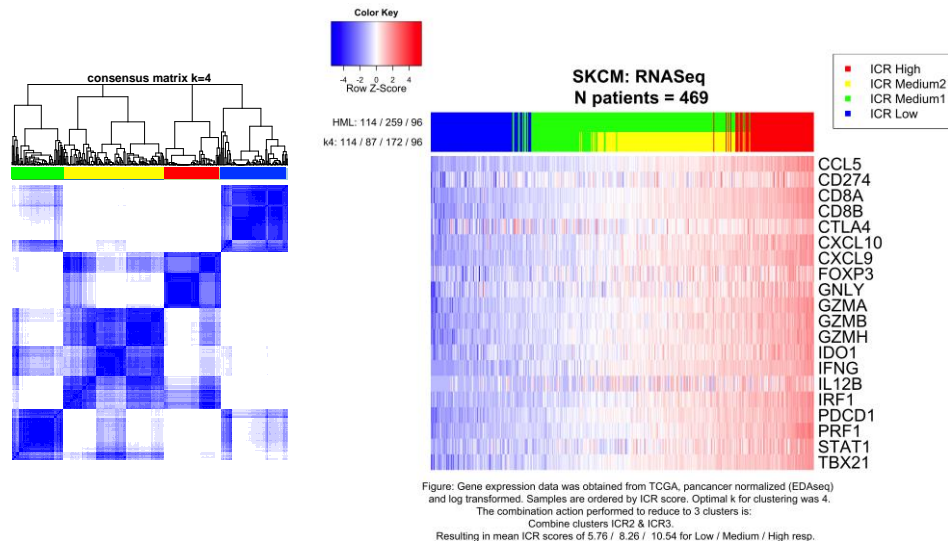
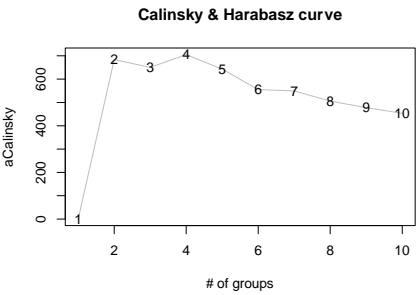


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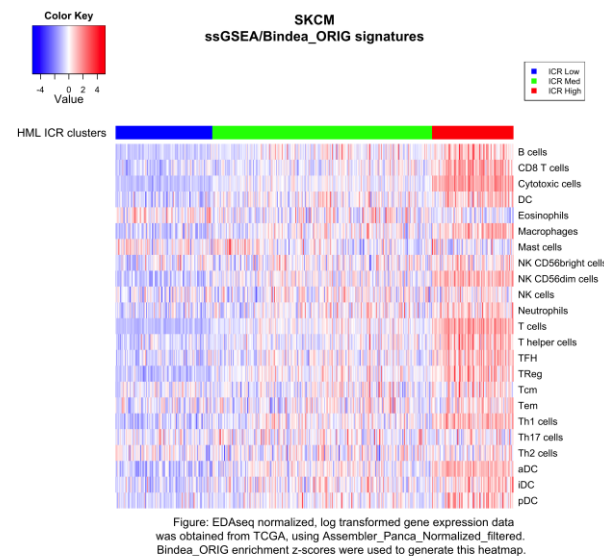


Skin cutaneous melanoma (SKCM)

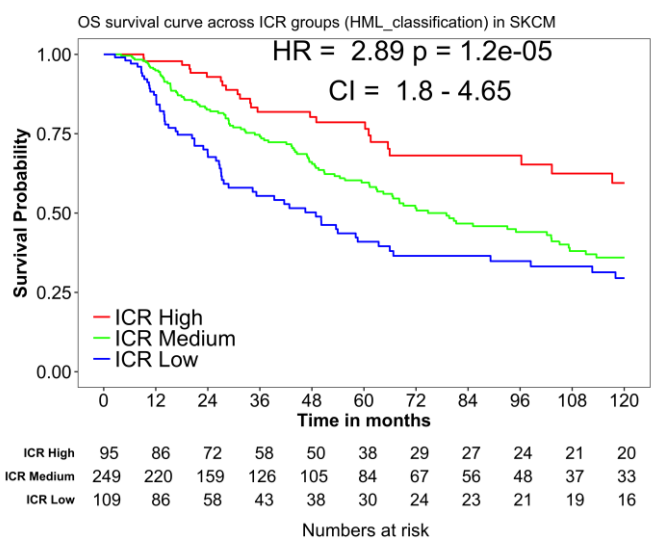
Immune phenotype (ICR) Clustering



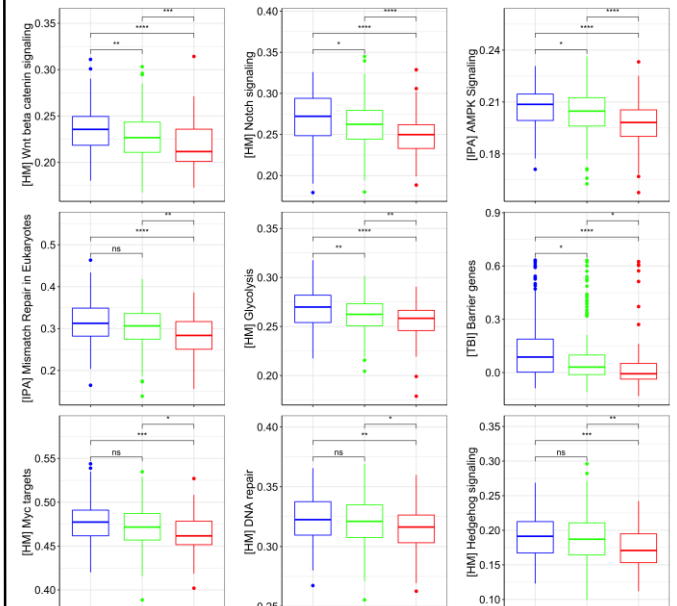
Deconvolution immune cell populations



Survival analysis



ssGSEA oncogenic pathways



Stomach
adenocarcinoma
(STAD)

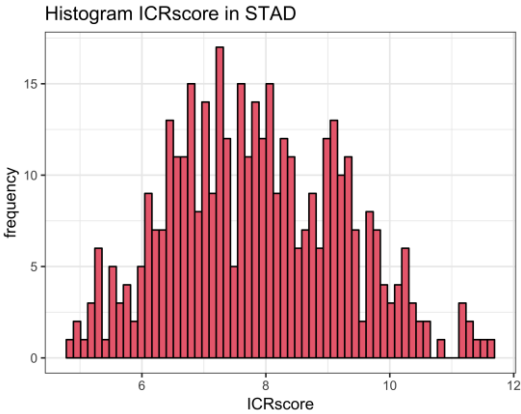
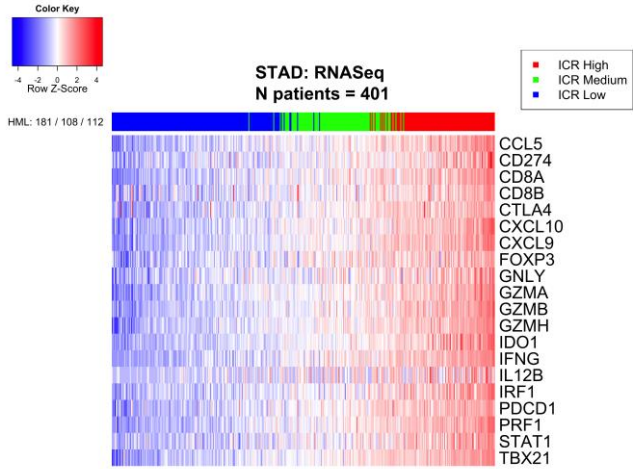
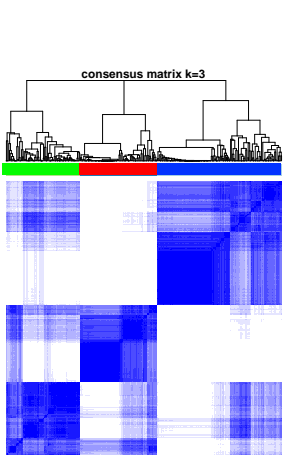
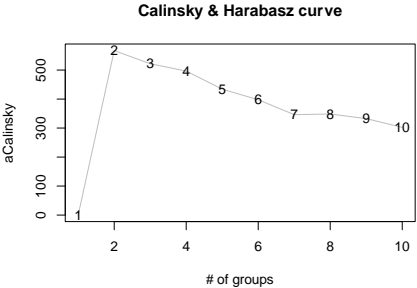


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none Resulting in mean ICR scores of 6.63 / 8.14 / 9.61 for Low / Medium / High resp.

Deconvolution immune
cell populations

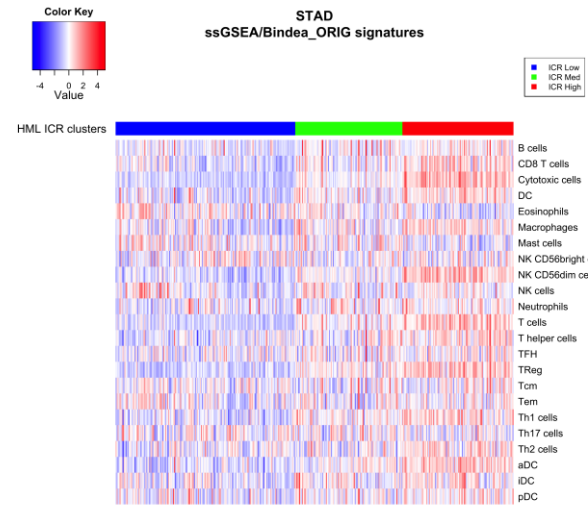
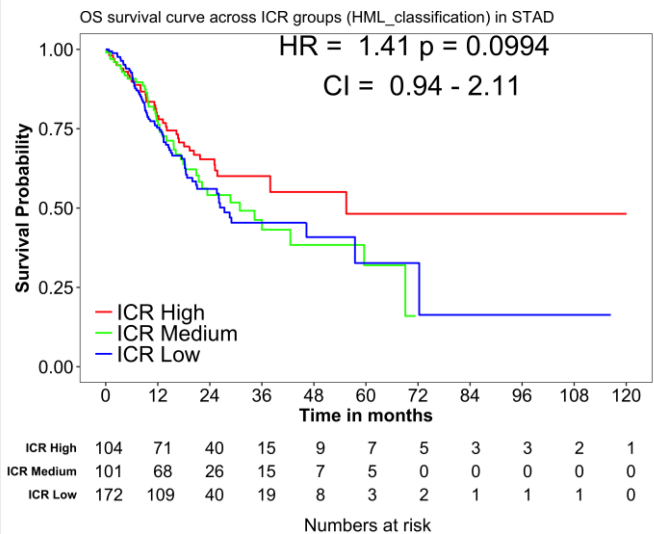
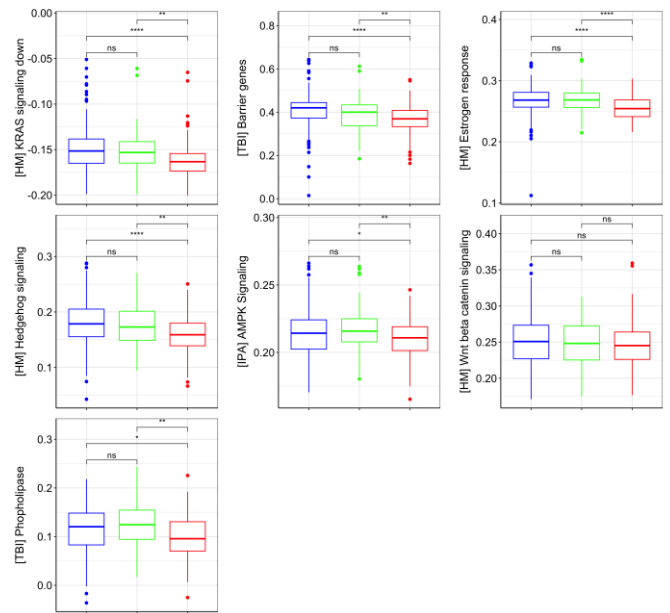


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Pance_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

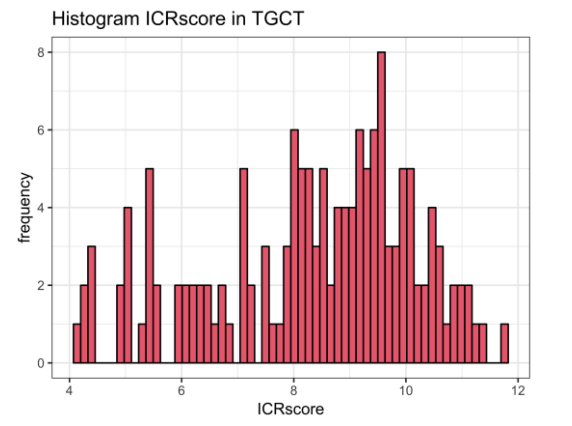
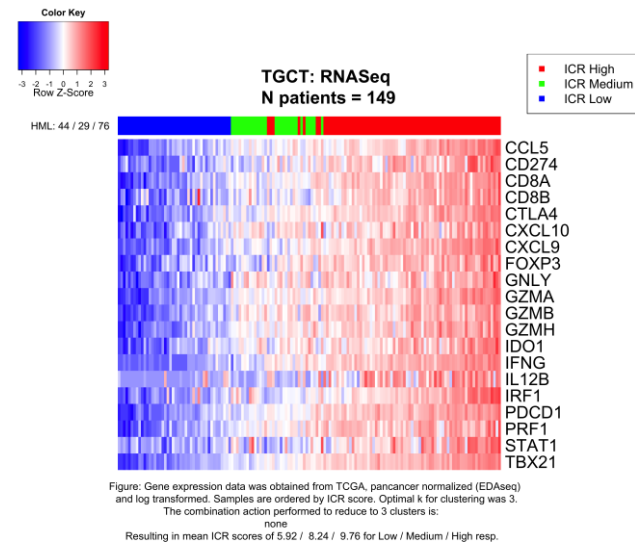
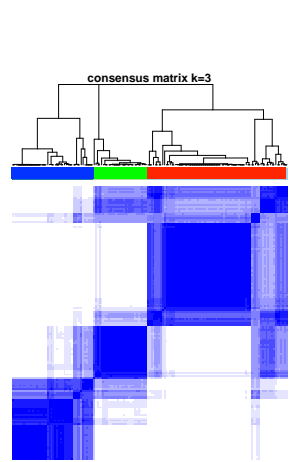
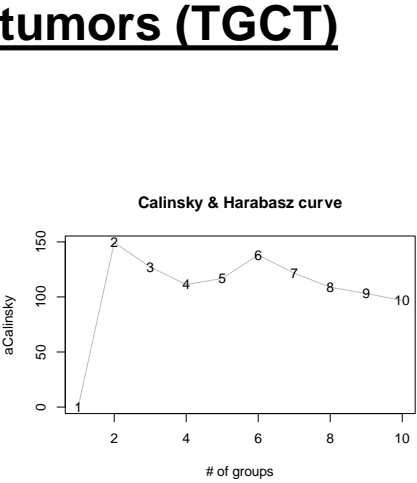
Survival analysis



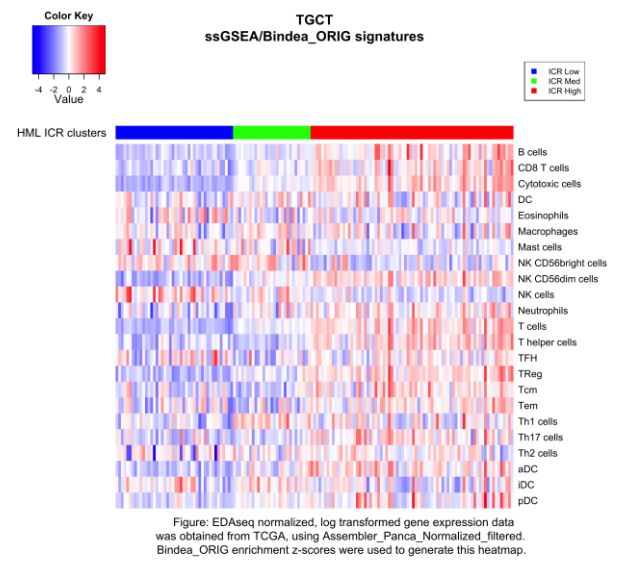
ssGSEA oncogenic
pathways



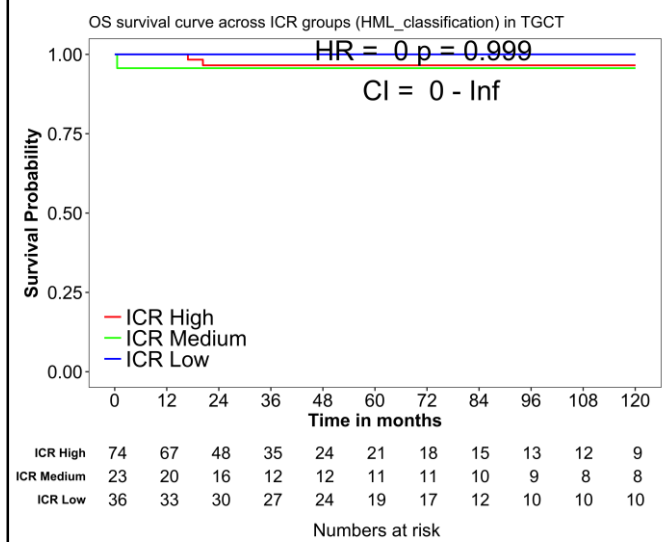
Testicular germ cell tumors (TGCT)



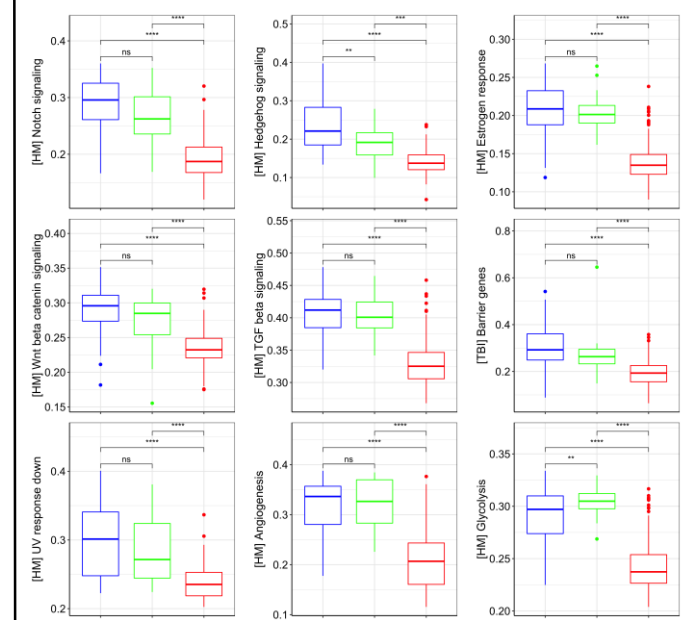
Deconvolution immune cell populations



Survival analysis



ssGSEA oncogenic pathways



Thyroid carcinoma (THCA)

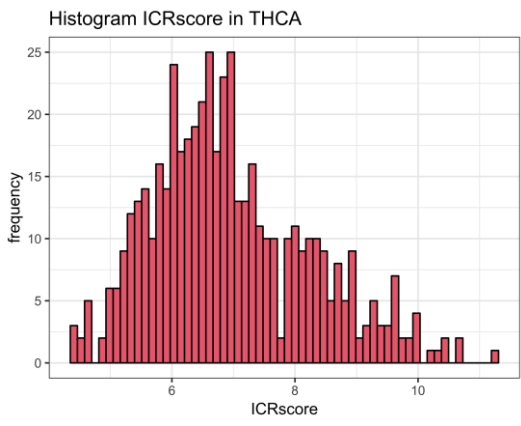
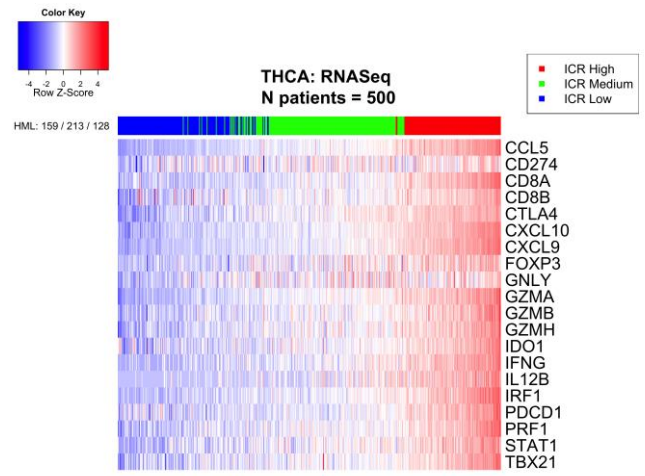
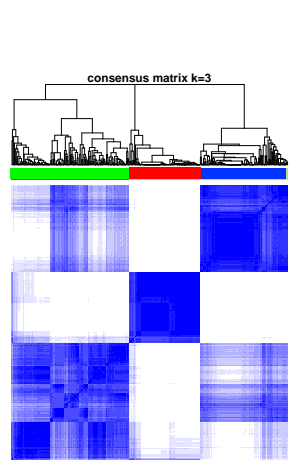
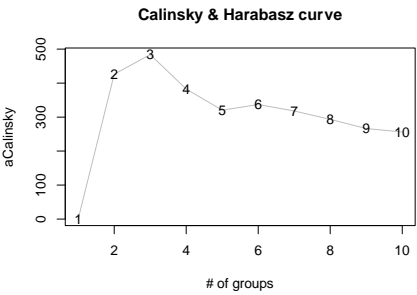


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDaseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none Resulting in mean ICR scores of 5.65 / 6.86 / 8.74 for Low / Medium / High resp.

Deconvolution immune cell populations

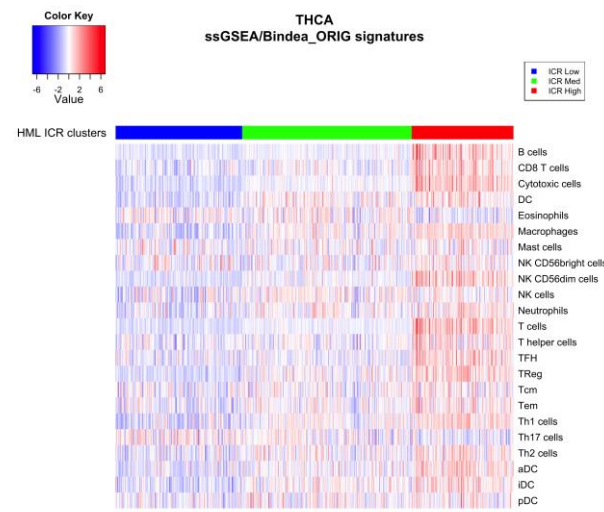
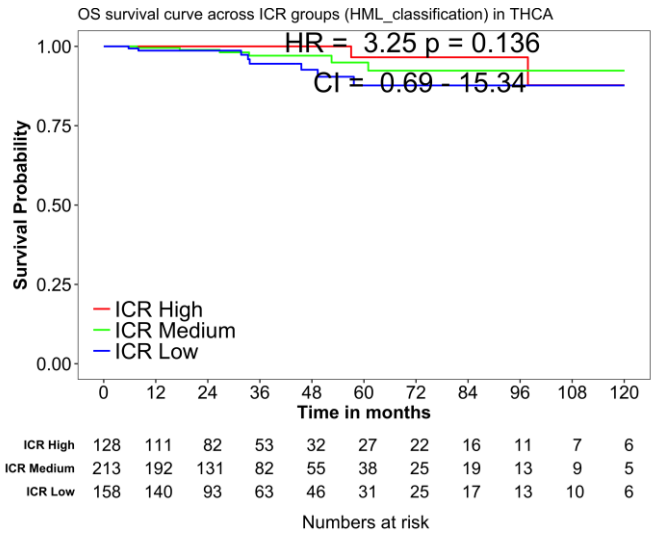
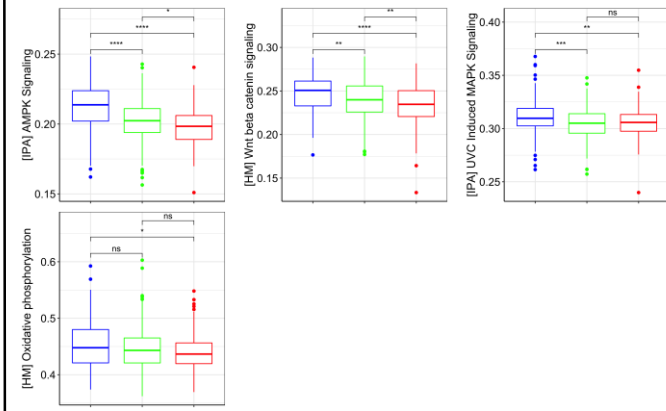


Figure: EDaseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Pance_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

Survival analysis

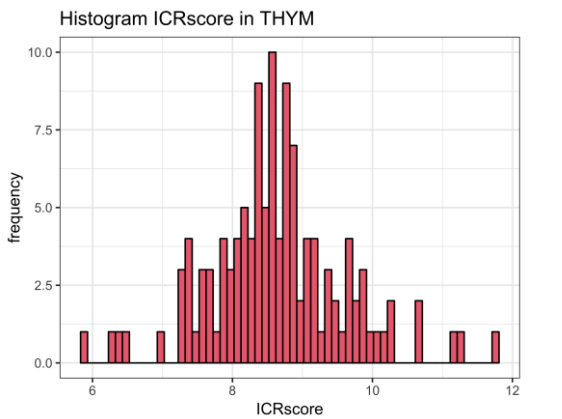
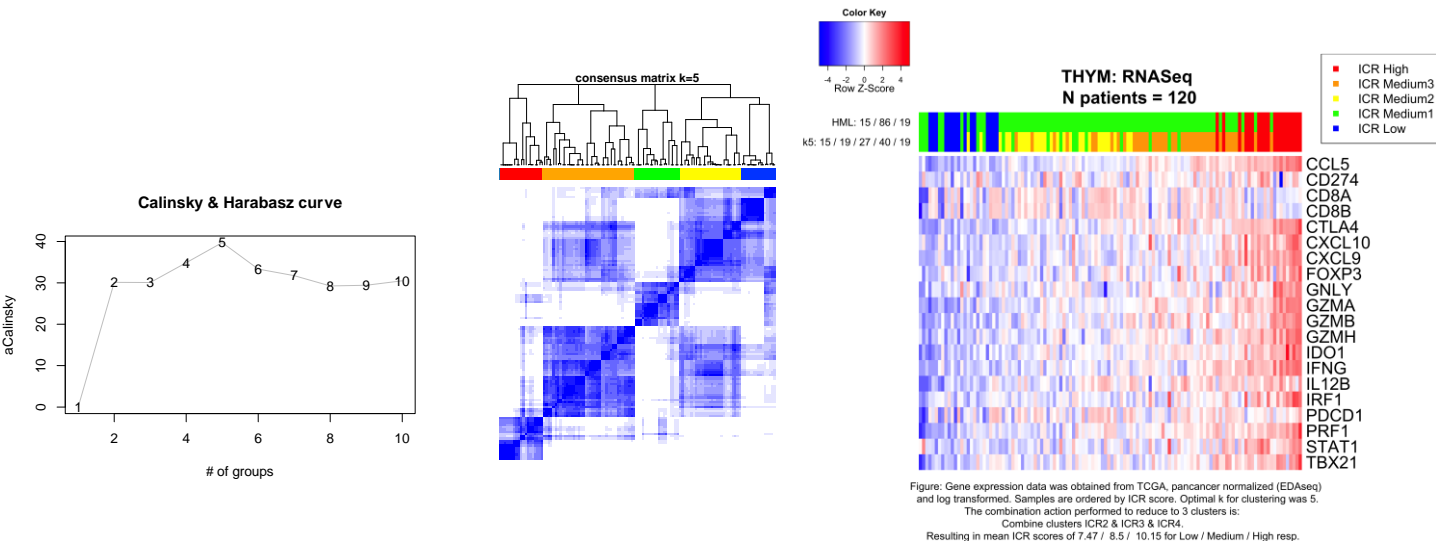


ssGSEA oncogenic pathways

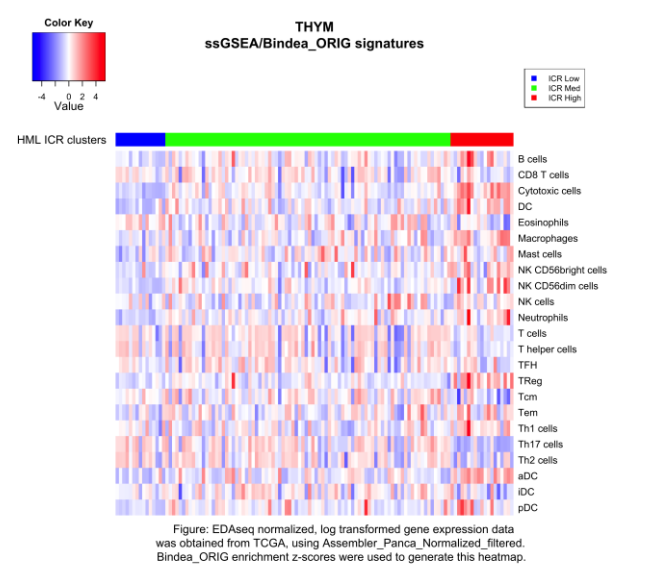


Thymoma (THYM)

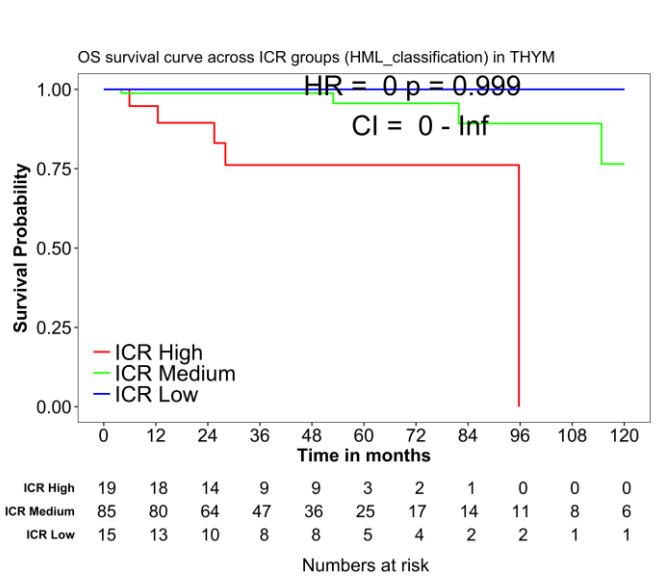
Immune phenotype
(ICR) Clustering



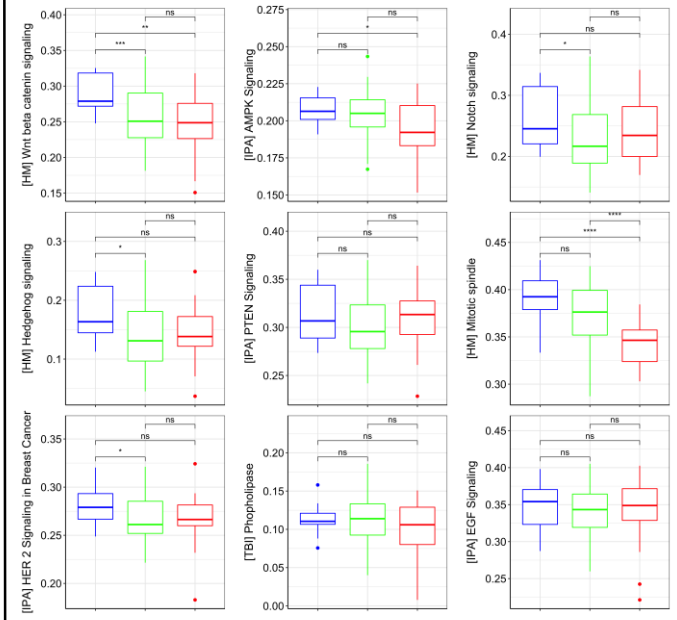
Deconvolution immune
cell populations



Survival analysis



ssGSEA oncogenic
pathways



Uterine corpus endometrial carcinoma (UCEC)

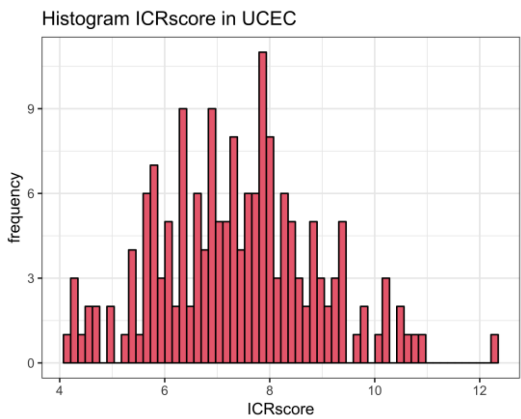
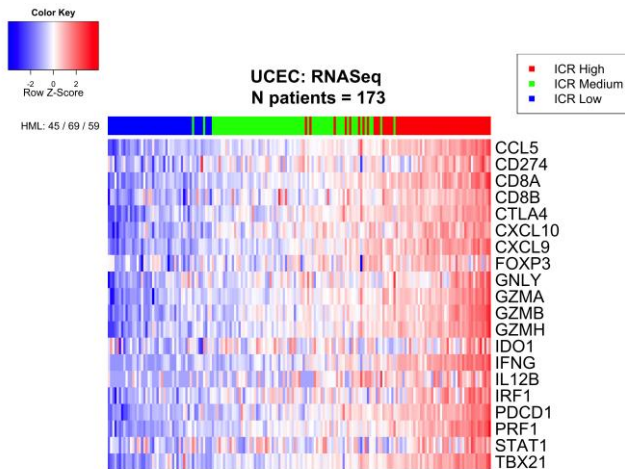
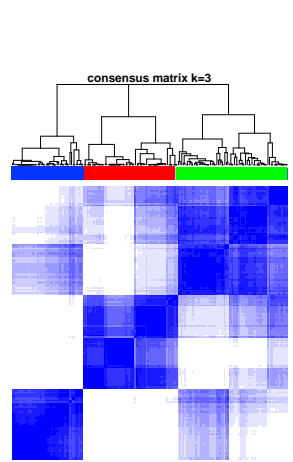
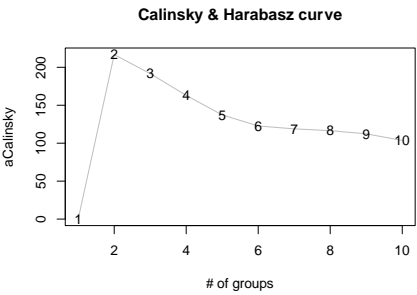


Figure: Gene expression data was obtained from TCGA, pancancer normalized (EDAseq) and log transformed. Samples are ordered by ICR score. Optimal k for clustering was 3. The combination action performed to reduce to 3 clusters is: none Resulting in mean ICR scores of 5.54 / 7.24 / 8.95 for Low / Medium / High resp.

Deconvolution immune cell populations

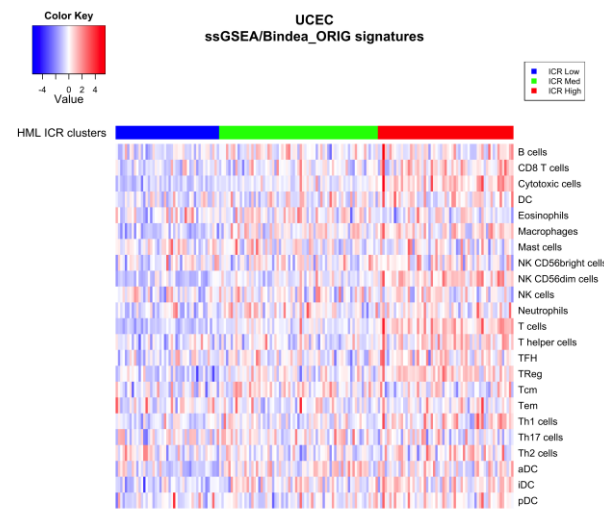
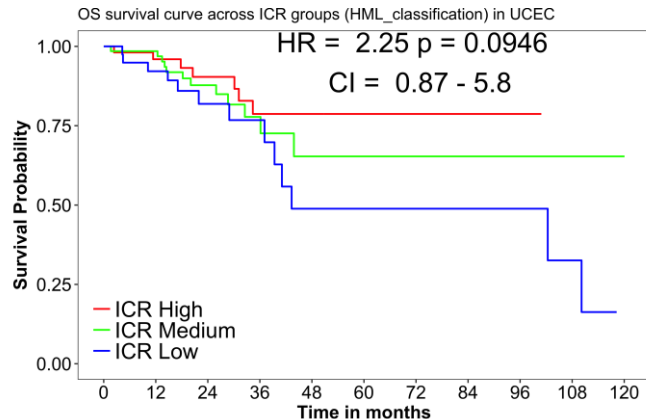


Figure: EDAseq normalized, log transformed gene expression data was obtained from TCGA, using Assembler_Panca_Normalized_filtered. Bindea_ORIG enrichment z-scores were used to generate this heatmap.

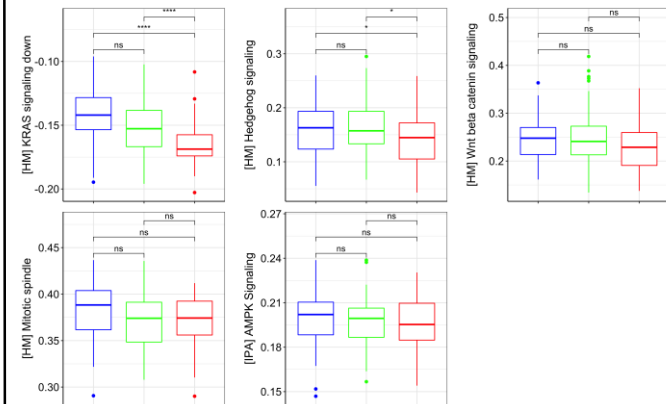
Survival analysis



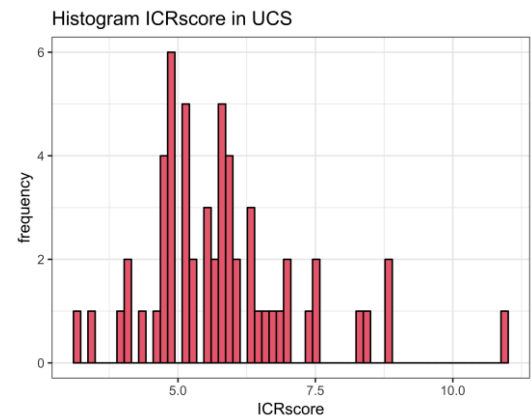
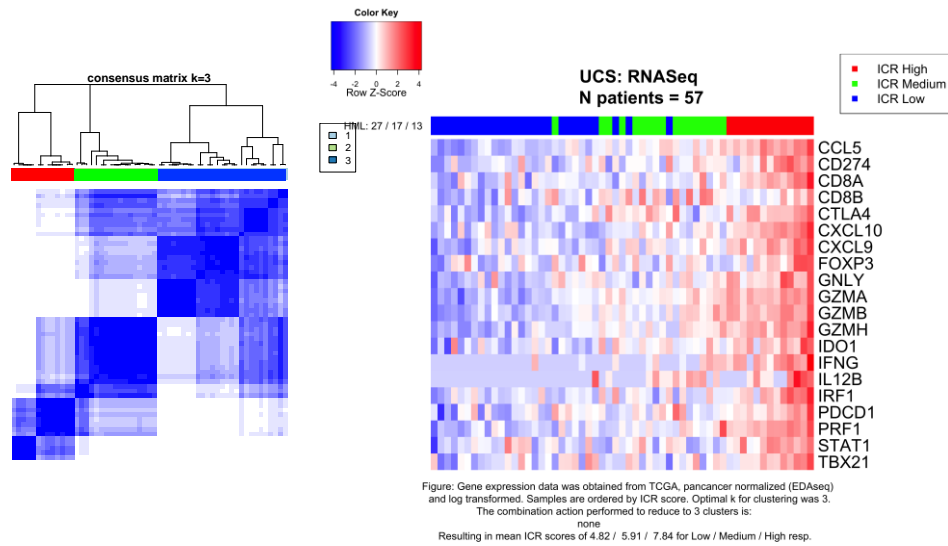
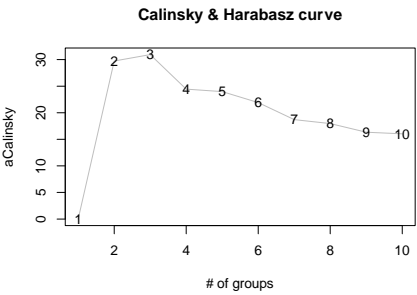
ICR High	58	45	28	17	9	4	2	1	1	0	0
ICR Medium	69	61	32	15	9	8	6	4	2	1	1
ICR Low	44	33	17	12	6	4	4	3	3	2	0

Numbers at risk

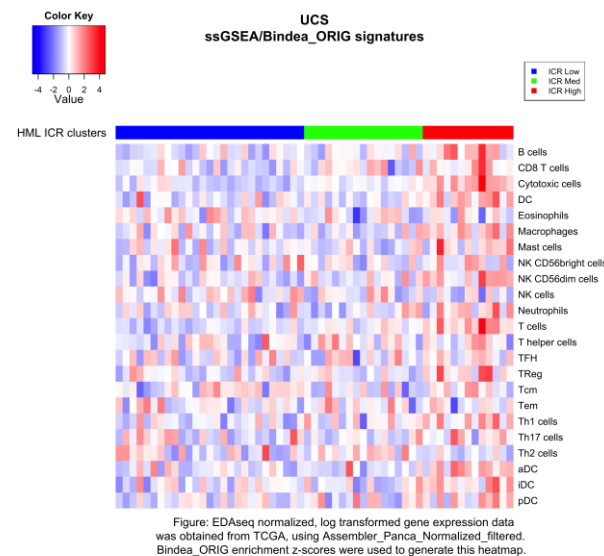
ssGSEA oncogenic pathways



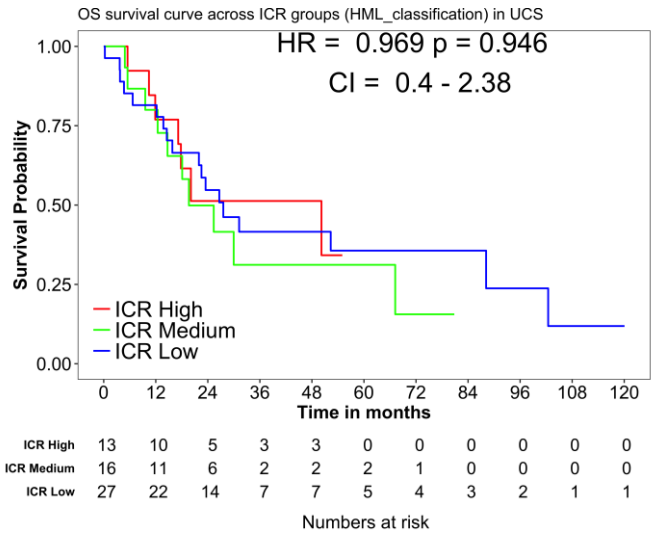
Uterine carcinosarcoma (UCS)



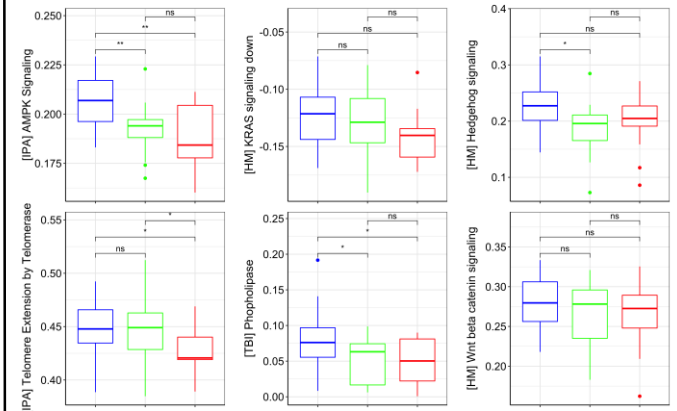
Deconvolution immune cell populations



Survival analysis

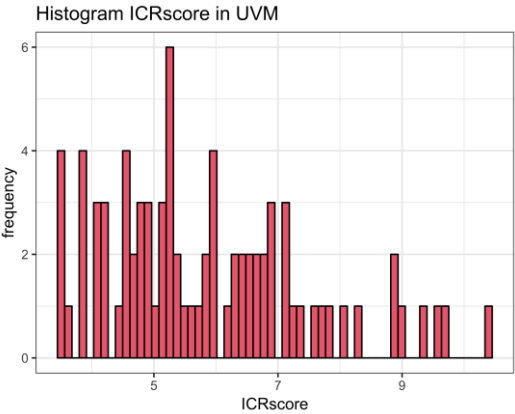
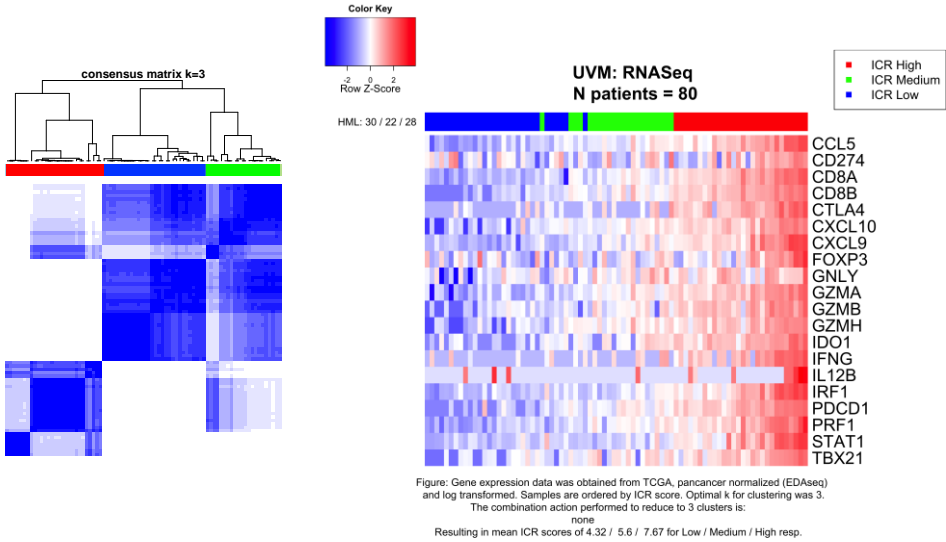
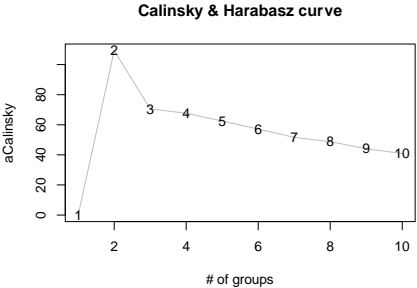


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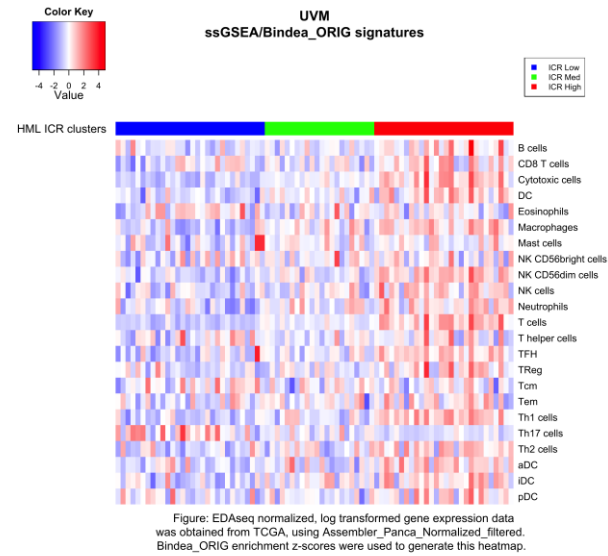


Uveal melanoma (UVM)

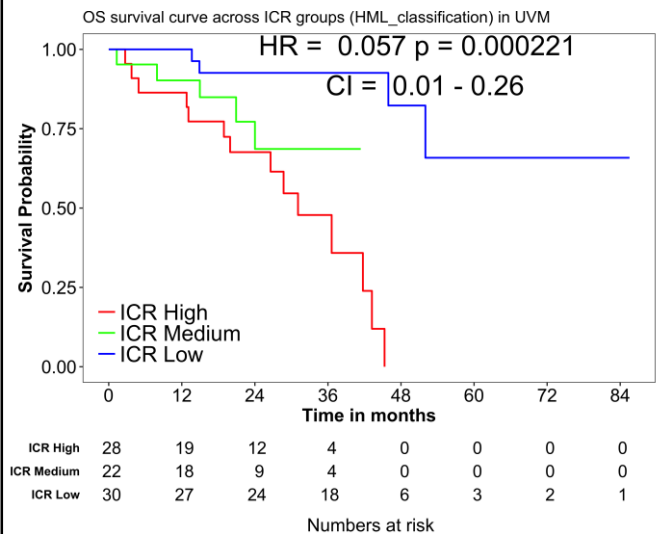
Immune phenotype (ICR) Clustering



Deconvolution immune cell populations



Survival analysis



ssGSEA oncogenic pathways

