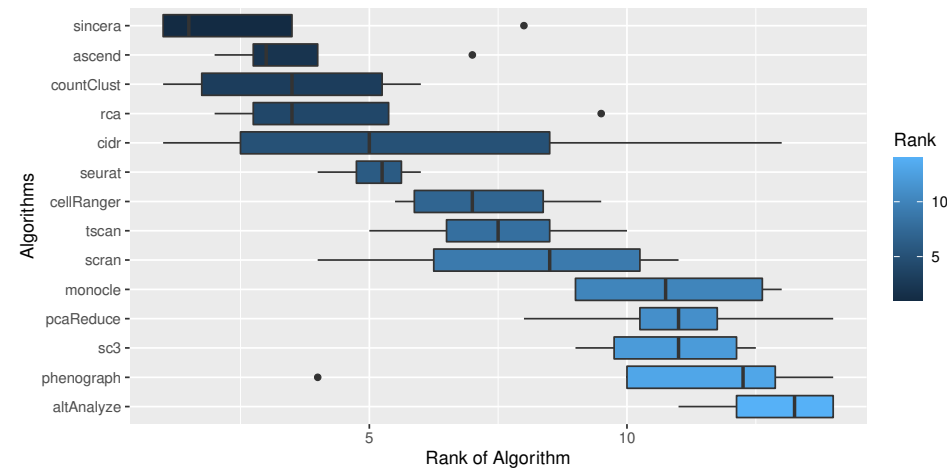
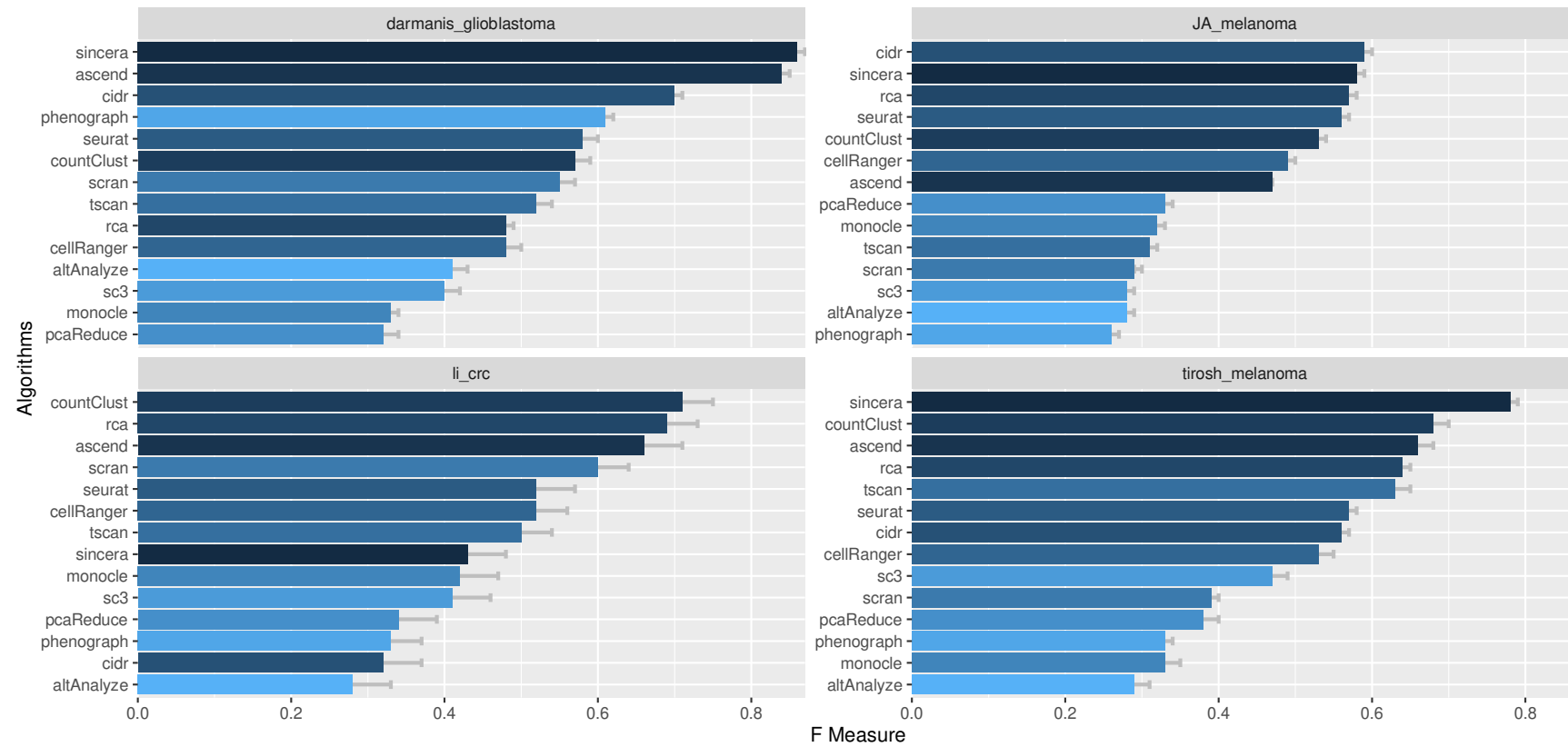


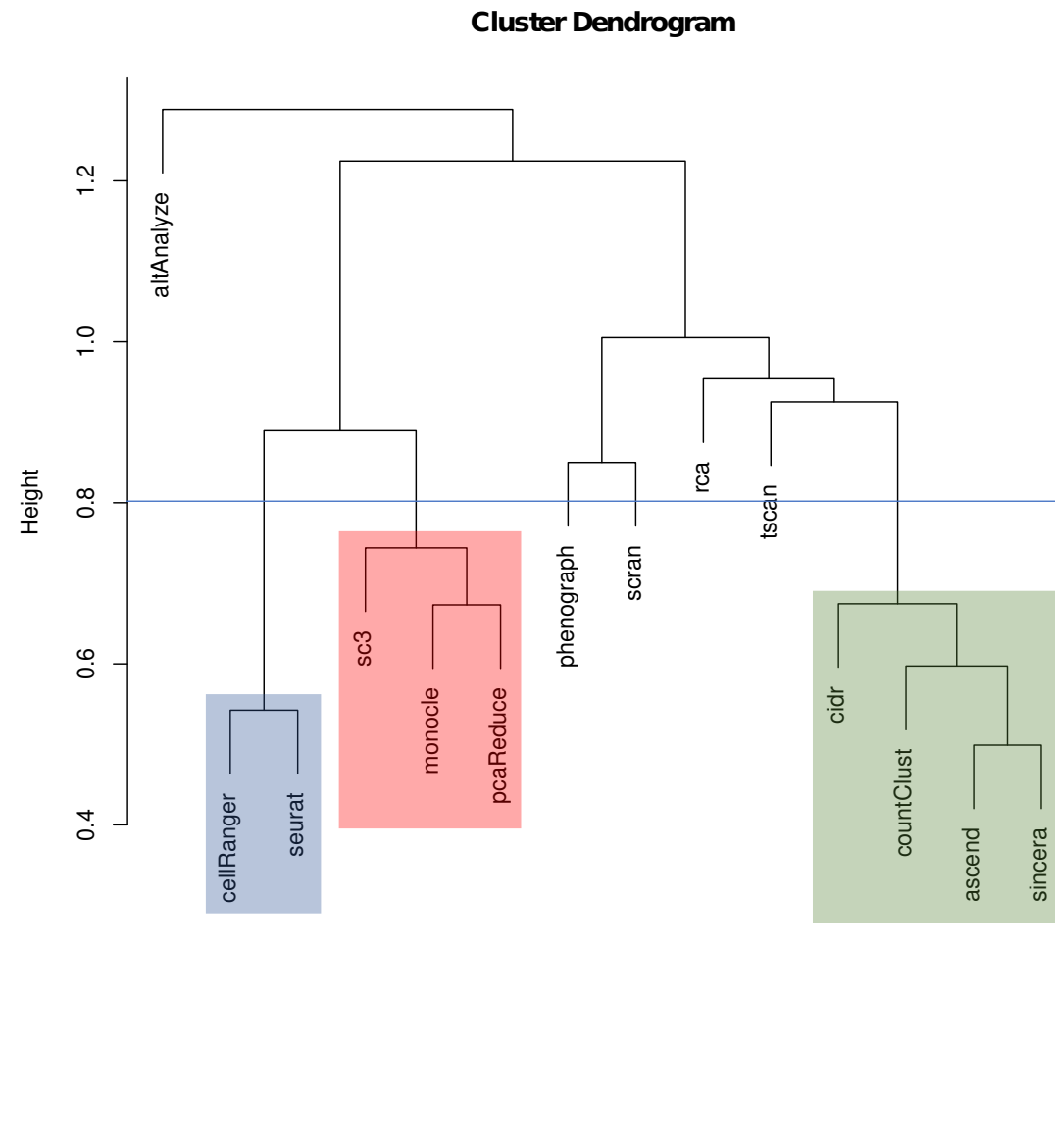
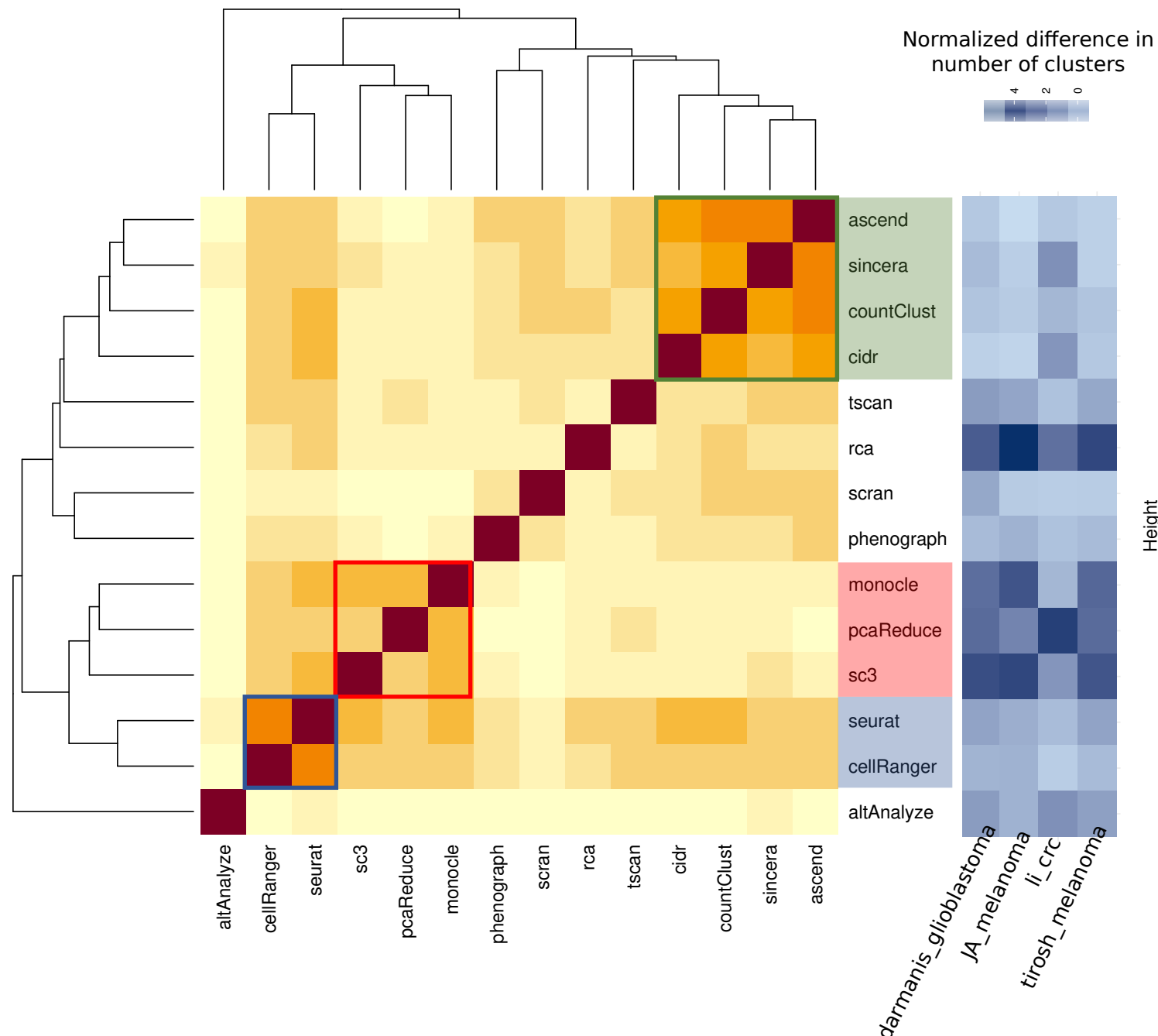
# **Evaluating Performance of Clustering Methods on Cancer Single-Cell RNA-seq Data**

# Datasets

Dataset	Cancer type	Cells	Genes	Tumours	Sequencing technology	Annotation?	Gene signature ?	Accession number
VanGalen_Cell_2019	Acute myeloid leukemia	38,410	27,899	40	Seq-well	No	No	GEO: GSE116256
Chung_Nature_Communications_2017	Primary breast cancer	564	57,915	11	Fluidigm C1	Yes	Yes	GEO: GSE75688
Li_Nature_Genetics_2017	Colorectal cancer	376	57,241	11	Fluidigm C1	Yes	Yes	GEO: GSE81861
Darmanis_Cell_Reports_2017	Primary glioblastoma	3,589	23,368	4	SMART-seq 2	No	No	GEO: GSE84465
Jerby-Arnon_Cell_2018	Melanoma	2,987	23,686	33	SMART-seq 2	Yes	Yes	GEO: GSE115978
Tirosh_Science_2016	Metastatic melanoma	4,645	23,686	19	SMART-seq 2	Yes	Yes	GEO: GSE72056
Lambrechts_Nature_Medicine_2018	Non-small cell lung carcinoma	52,698	22,533	5	10x Genomics	Yes	Yes	AE: E-MTAB-6149, E-MTAB-6653
Peng_Cell_Research_2019	Pancreatic ductal adenocarcinoma	57,530	24,005	24 tumours 11 controls	10x Genomics	Yes	Yes	GSA: CRA001160

What are the top algorithms for each dataset?





What are the top algorithms for each dataset?

