Droplet−based cell_line_cluster_purity

Coefficient axis: 0.1, 0.0, −0.1

X-axis labels: salmon_SA, kallisto bustools, scPipe, dropSeqPipe, Cell Ranger, salmon_splici, zUMIs, DESeq2, sctransform_poi, sctransform, scran, linnorm, scone, seurat_slm, seurat_louvain, sc3_SVM, scran_walktrap, scran_louvain, scran_fastgreedy, sc3

Processing steps
- clustering method
- normalization method
- preprocess workflow