

Appendix

Plots

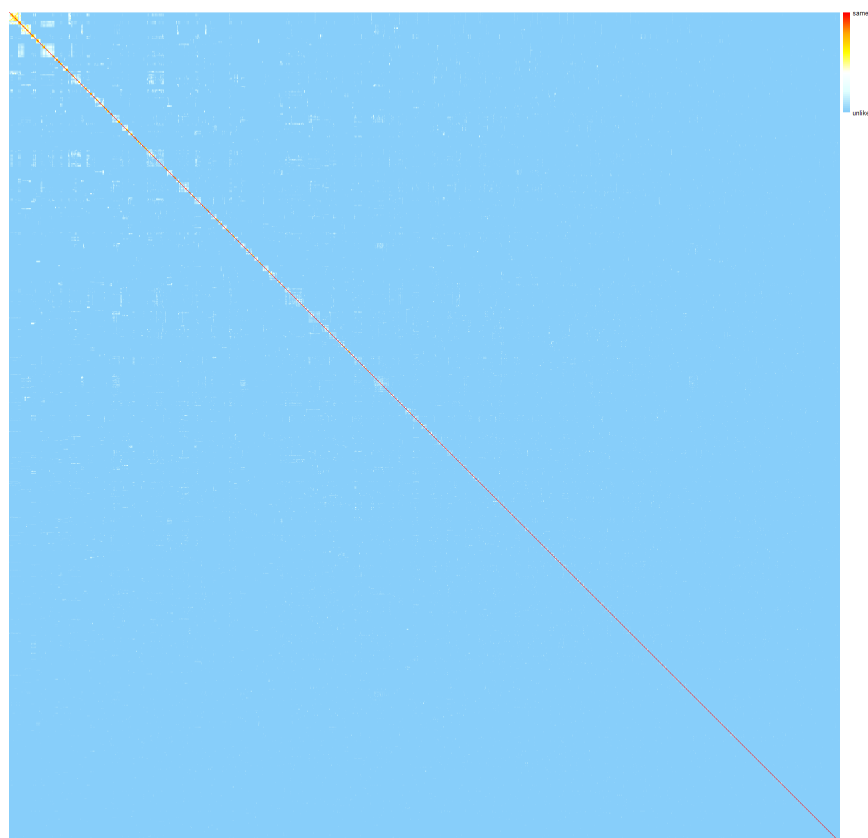


Figure 1: Heatmap, displaying jaccard index obtained by caomparing uncleaned metabolic pathways. Pathways with a high Jaccard index are colored red to white. Pathways without similarity are colored blue.

Packages

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## Warning: Paket 'readxl' wurde unter R Version 4.1.3 erstellt
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Table 1: Packages used in the analysis.

Package	Usage	Authors
biomart	renaming genenames to ensembleIDs	Durinck <i>et al.</i> , 2009
msigdb	downloading canonical pathways and included genes from MSigDB	Bhuva <i>et al.</i> , 2022
dplyr	editing of dataframes	Wickham <i>et al.</i> , 2022

Package	Usage	Authors
ggplot2	creation of plots with detailed options	Wickham <i>et al.</i> , 2022
pheatmap	creation of heatmaps with detailed options	Kolde, 2019
vioplot	creation of violinplots	Kolde, 2019
VennDiagram	creation of VENN-diagrams	Chen, 2022
fgsea	performing a GSEA	Korotkevich <i>et al.</i> , 2019
GSVA	performing a GSVA	Hänzelmann <i>et al.</i> , 2013
ComplexHeatmap	creation of heatmaps with detailed options	Gu <i>et al.</i> , 2016
metaplot	creating of data-driven plots	Bergsma, 2019
gridExtra	implementing of “grid” graphics	Auguie and Antonov, 2017
umap	creating UMAPs	Konopka, 2022
gage	application of GSEA	Luo <i>et al.</i> , 2009
psych	performing an iterative factor analysis	Revelle, 2022
cluster	performing a cluster analysis	Maechler <i>et al.</i> , 2022
MASS	implementing of neural network	Ripley <i>et al.</i> , 2022
neuralnet	training of neural networks	Fritsch <i>et al.</i> , 2019
AnnotationDbi	translating ensemble ids into genenames	Pagès <i>et al.</i> , 2022
org.Hs.eg.db	translating ensemble ids into genenames	Carlson, 2019

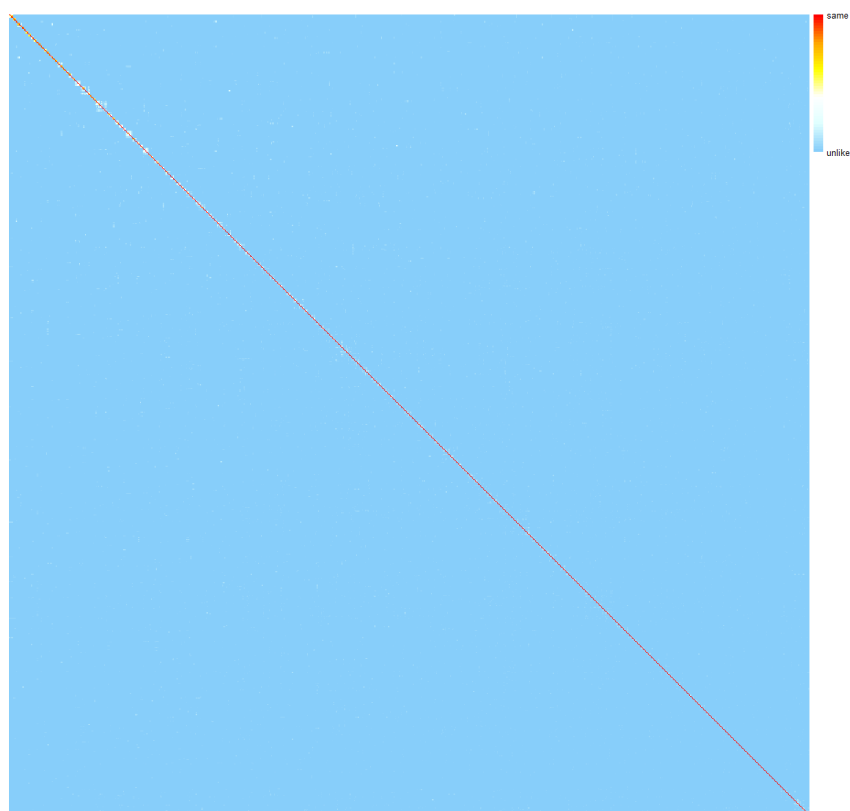


Figure 2: Heatmap, displaying jaccard index obtained by comparing cleaned metabolic pathways. Pathways with a high Jaccard index are colored red to white. Pathways with low similarity are colored blue.

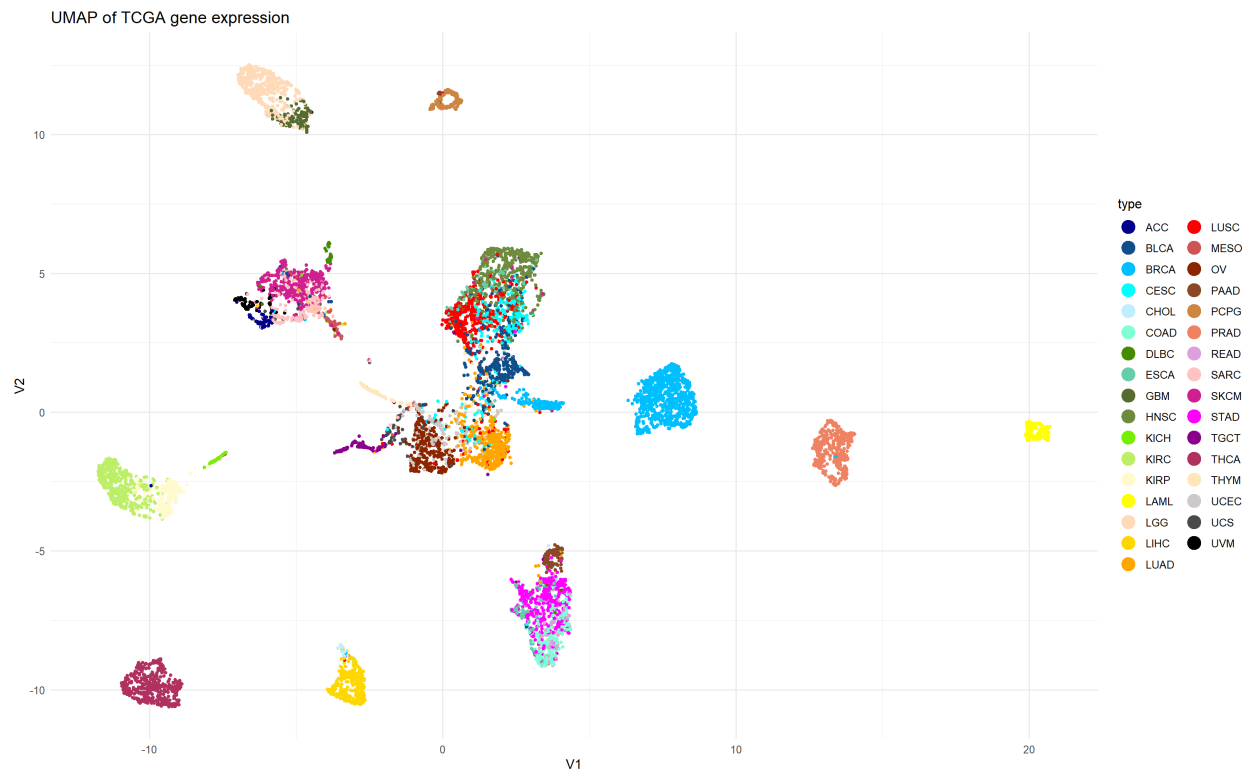


Figure 3: UMAP performed for gene expression data, colored by cancer type

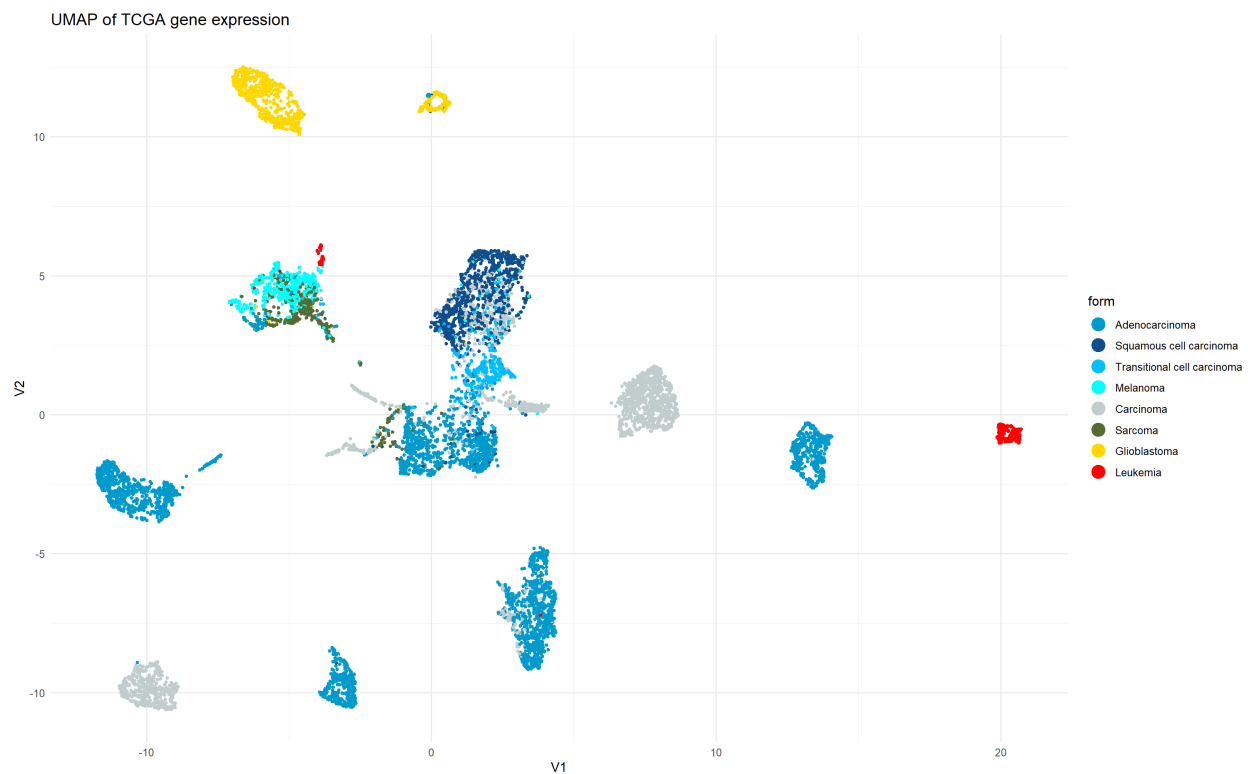


Figure 4: UMAP performed for gene expression data, colored by histological type

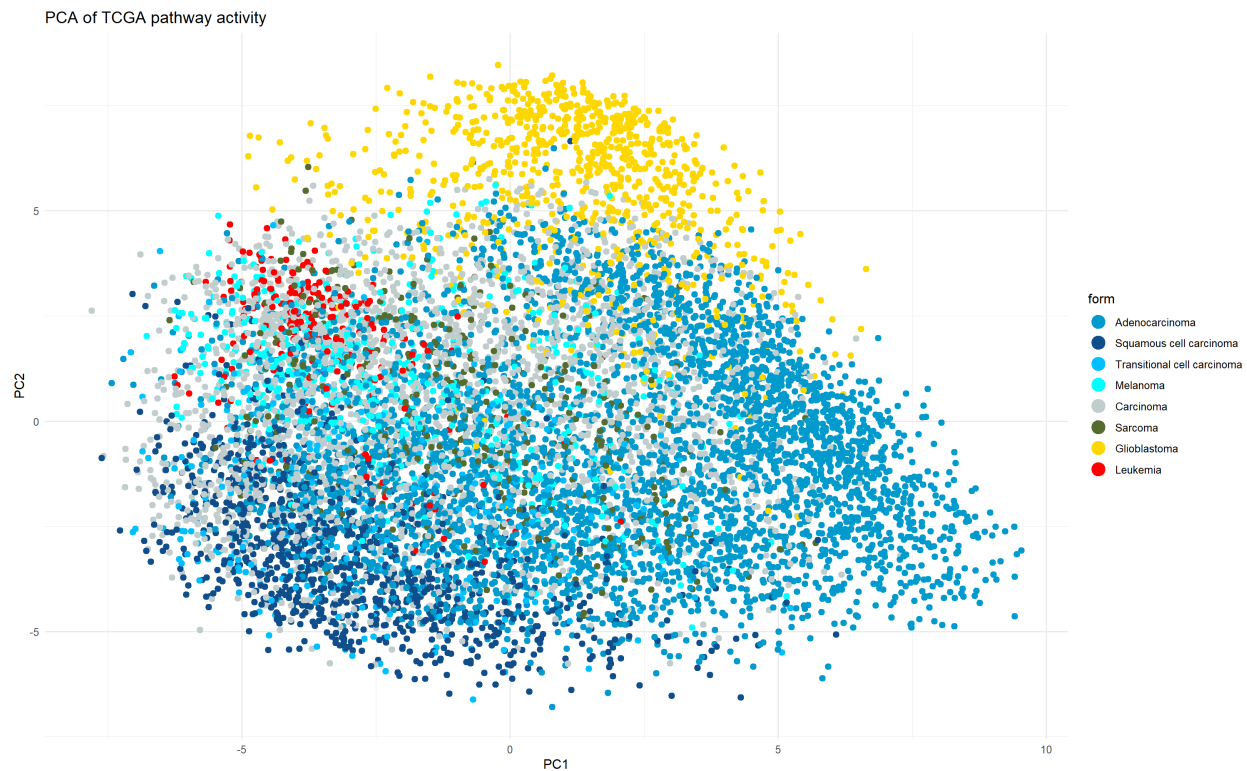


Figure 5: Results of PCA, PC 1 and 2 are shown, samples are colored by histological type.

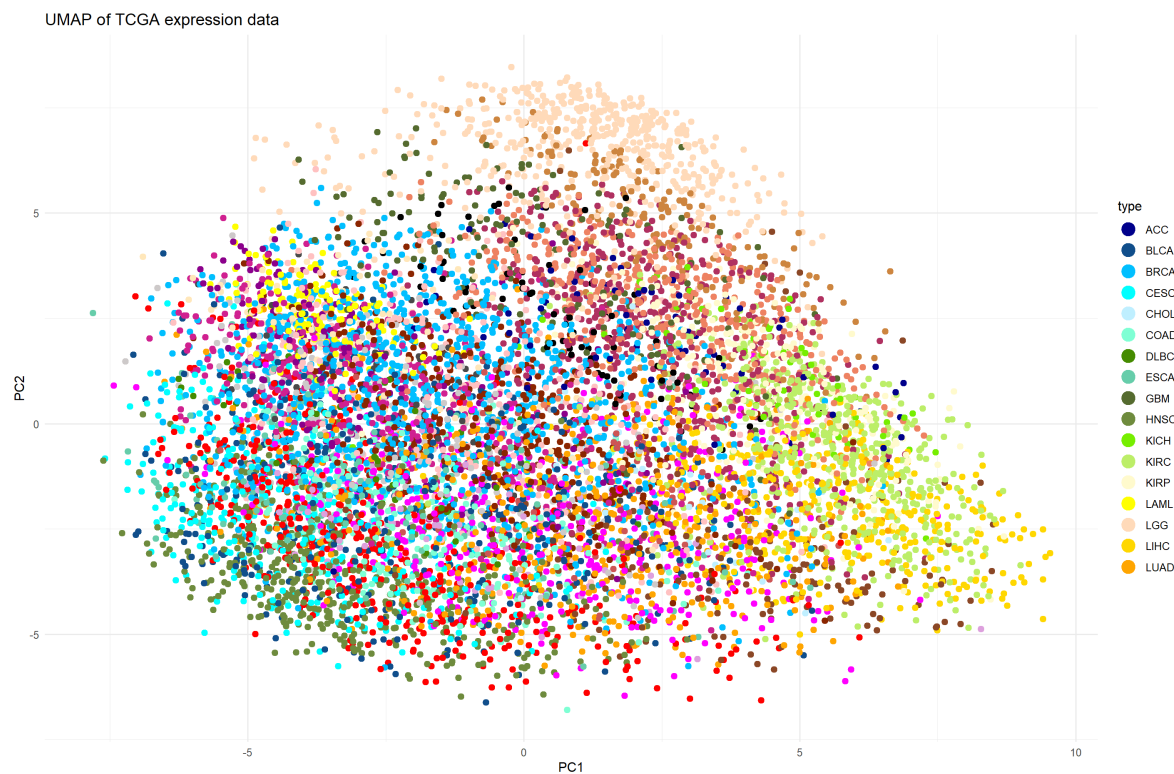


Figure 6: Results of PCA, PC 1 and 2 are shown, samples are colored by cancer type.