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Results

Text de presentacio dels resultats...

1.1 Results from the analysis of human brain tissue samples

1.2 Results from the expansion of omics data with biological annotations

Figure 1.1 is an snapshot (F) of one of the heat maps created to show the expanded matrices obtained in (Figures ?? i ?? prèvies, de Methods).

1.3 Results from the analysis of 150 TCGA-BRCA samples

Figure 1.2 contains some of the graphical results of the analysis of the 150 samples from TCGA-BRCA: Heat maps (A, C) and association networks (B, D) resulting from the integration by Regularized Canonical Correlations Analysis with mixomics R package. Performed with the original data sets (A, B) or using data expanded with biological annotations to Gene Ontology (C, D), so adding some GO terms to

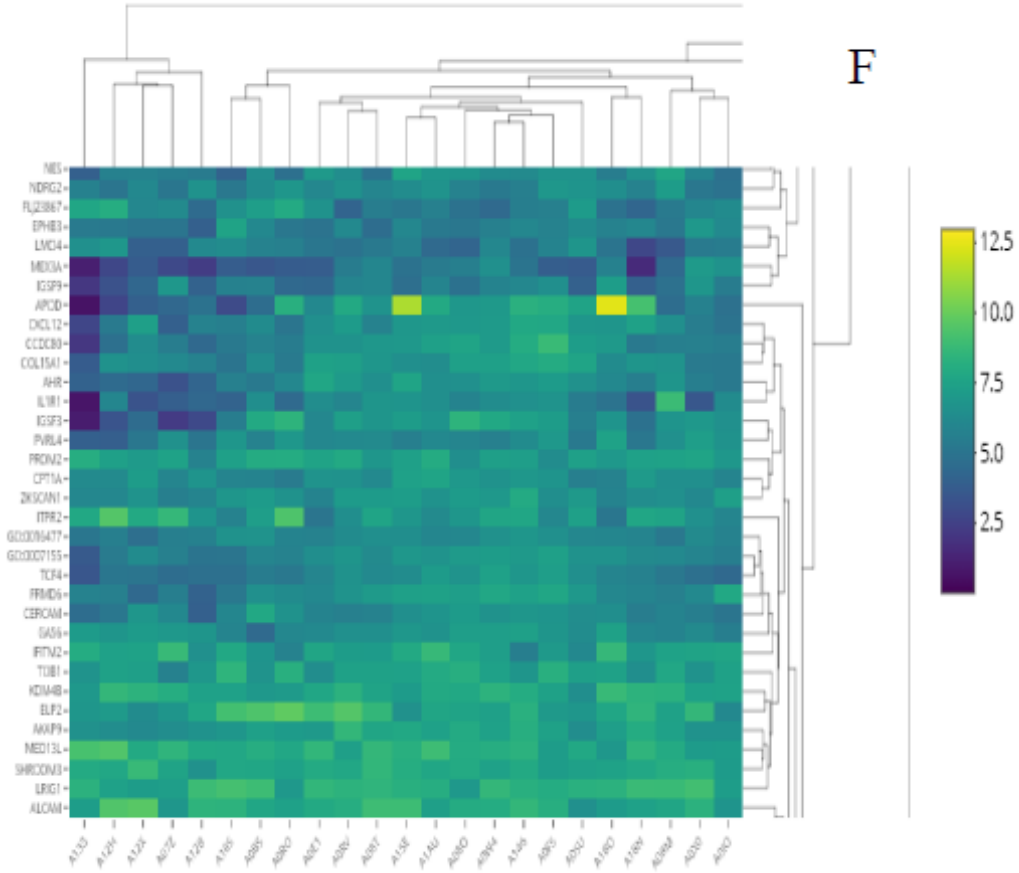


Figure 1.1: Heatmap of an expanded matrix

the features from each source, where the outputs contain higher level of information (higher density in both type of plots).

1.4 Results from the application of MFA on TCGA-BRCA data with, and without, expanded data

Figure 1.3 includes a Correlation Circle (left), with most relevant genes, proteins and added GO annotations. Distribution of samples (right) along the first two plotted dimensions. Both results coming from the application of Multiple Factor Analysis (FactoMineR and factoextra R packages) performed on the same 150 samples (Basal, Her2 and LuminalA conditions) from TCGA-BRCA.

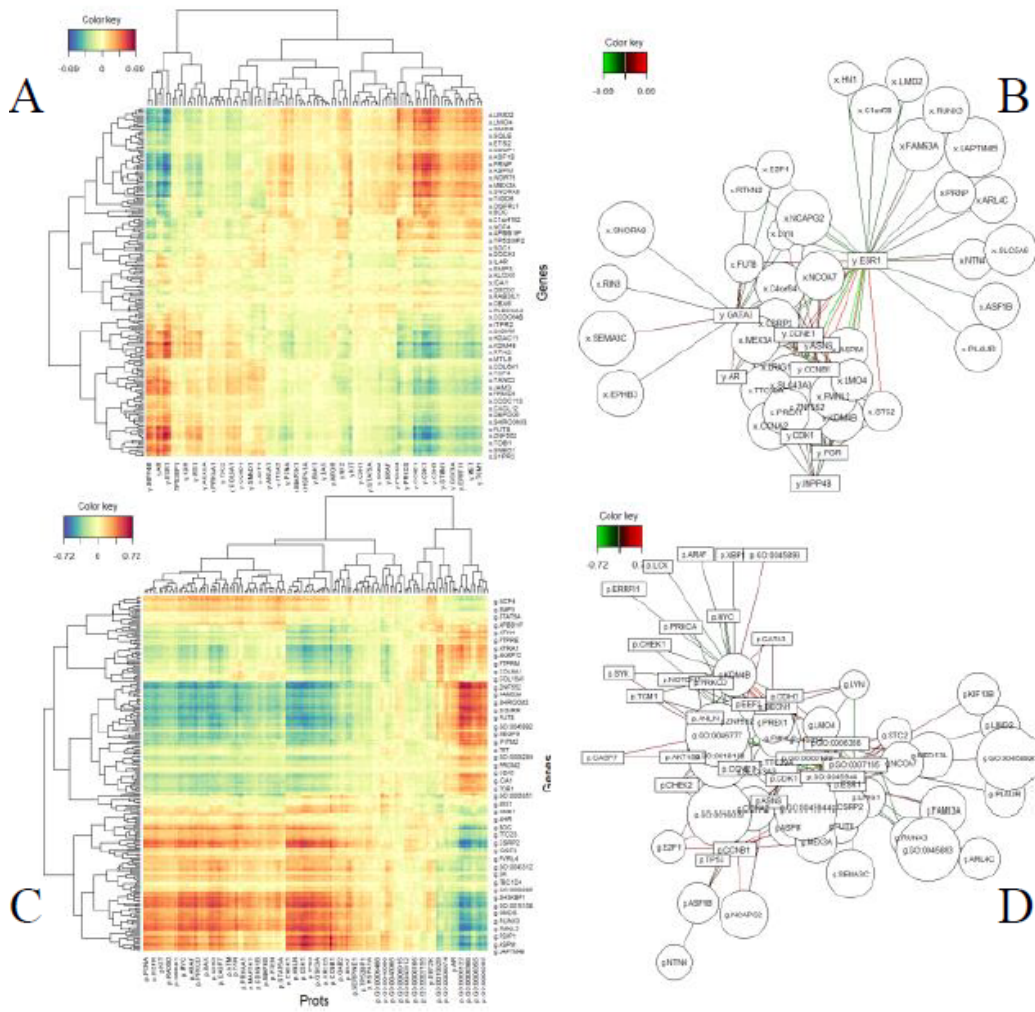


Figure 1.2: BRCA results overview

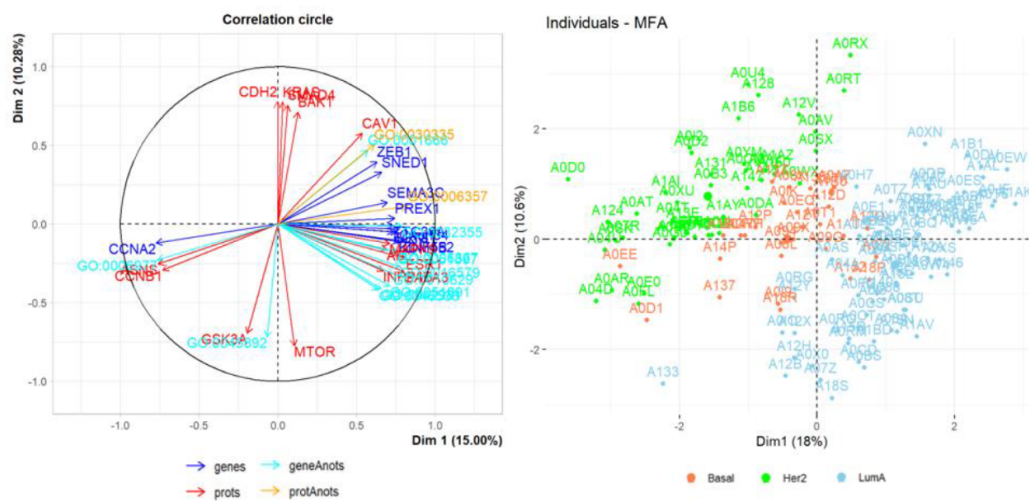


Figure 1.3: BRCA results with MFA