

Figure S6

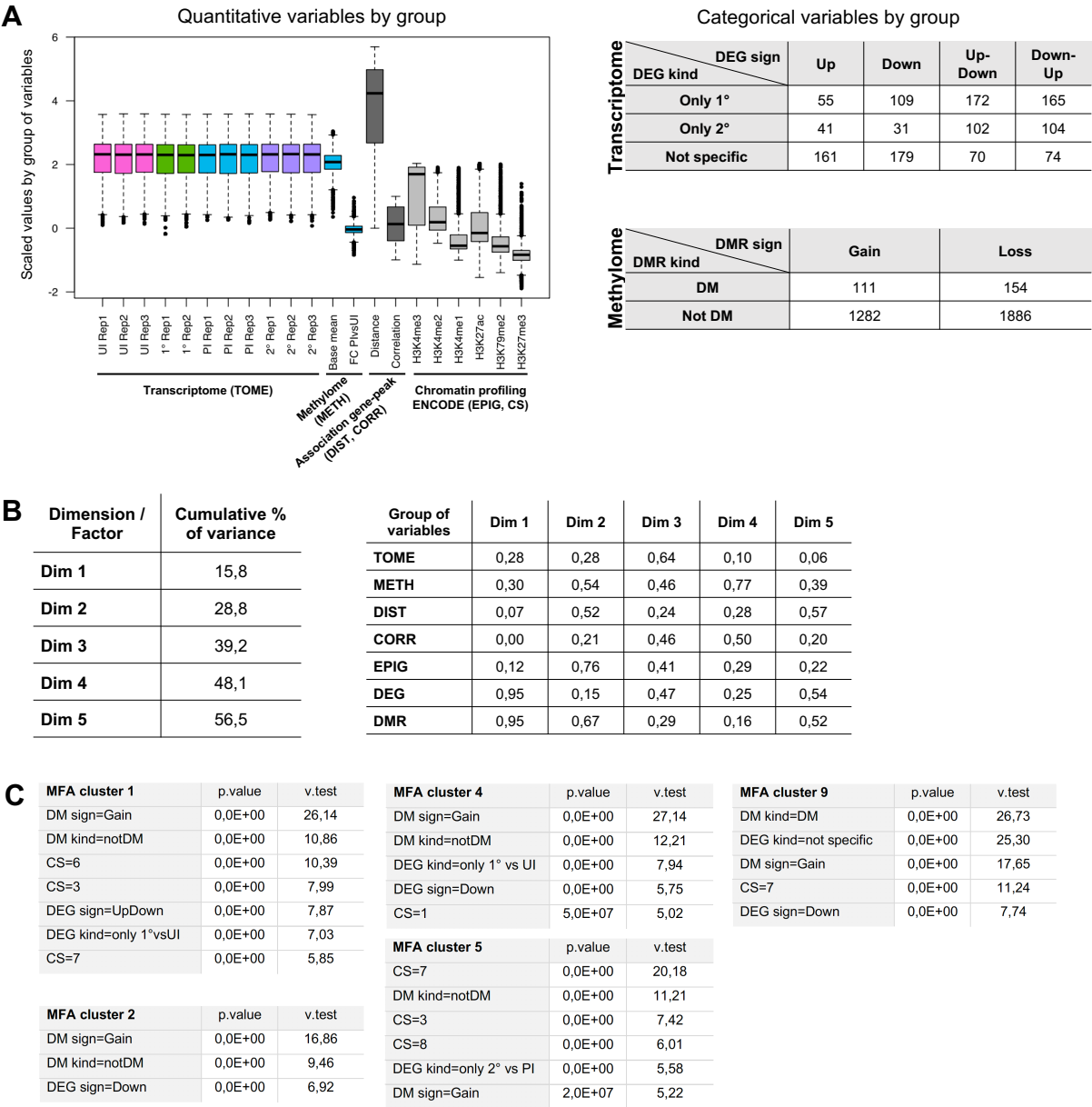


Figure S6: Multiple Factor Analysis (MFA) input data and output metrics

(A) Groups of variables used for MFA. Groups of variables constitute the MFA input matrix and describe the genes (TOME = Transcriptome, DEG = Differentially expressed gene), the H3K4me2 peaks (Methylome = METH, DMR = Differentially methylated region, EPIG = Chromatin profile, CS = Chromatin state) and their association (DIST = distance, CORR = correlation). Box plots of quantitative variables after normalization and scaling (left). Tables with number of genes/peaks classified according to the differential expression/methylation analysis (right). **(B)** Quantitative description of factors/dimensions. Cumulative percentage of input dataset variance explained by first five factors (left). Correlation coefficients of groups with the first five factors (right). **(C)** Description of clusters in terms of significant categorical variables.