

Figure S5

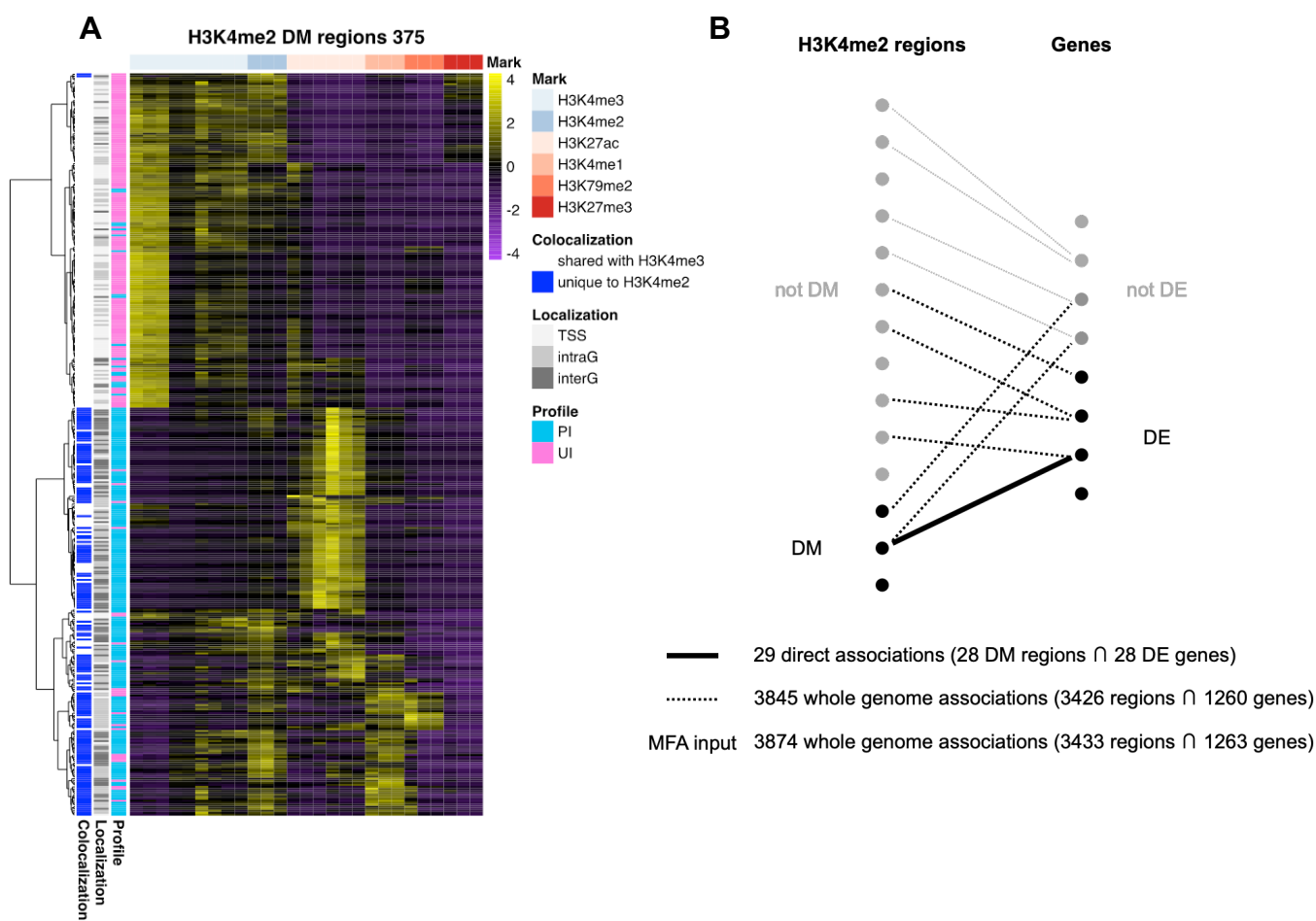


Figure S5: Chromatin profiling over H3K4me2 differentially methylated peaks and regulatory association to genes

(A) Chromatin profiling over the H3K4me2 dynamic peaks. Coverage for key histone modifications recovered from the ENCODE portal for A549 cells is shown for the 375 H3K4me2 dynamic peaks (DM). Histone coverage is normalised by peak length, centred and scaled among samples. Peaks are clustered according to their chromatin state and annotated according to their profile: PI (gain of methylation) or UI (loss of methylation); their localization with respect to the nearest gene (TSS = overlapping the 2 Kb interval centred around the transcription start site; IntraG = located within the gene annotations and outside the TSS interval; InterG = all other peaks); the colocalization with H3K4me3 dynamic peaks (shared or unique). **(B)** Association between methylome and transcriptome. Dots represent H3K4me2 regions or genes and lines are regulatory links predicted by the T-Gene tool of the MEME suite. Black lines show regulatory links where either a DMs and/or a DEs (continuous lines) or either a not DMs and/or a not DEs (dotted lines) are involved. These account for the 3874 (29 + 3845) associations used as input for the multiple factor analysis (MFA). Grey lines represent regulatory links between not DMs and not DEs and are therefore not included in the downstream integrative analysis.