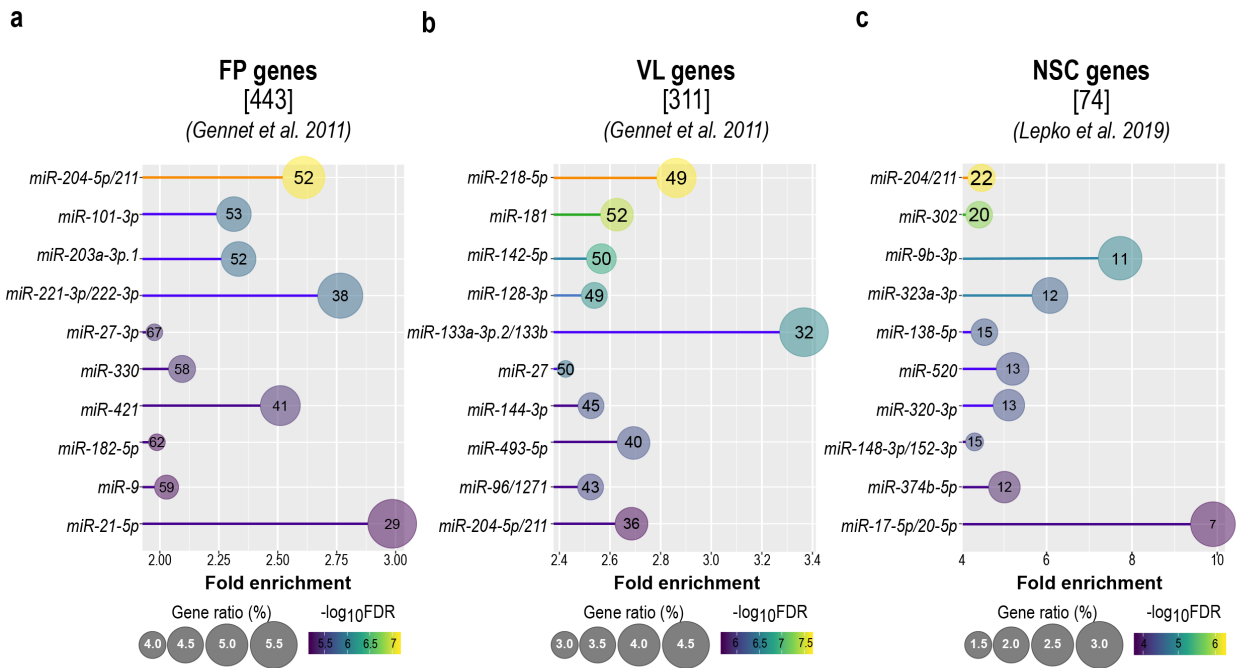


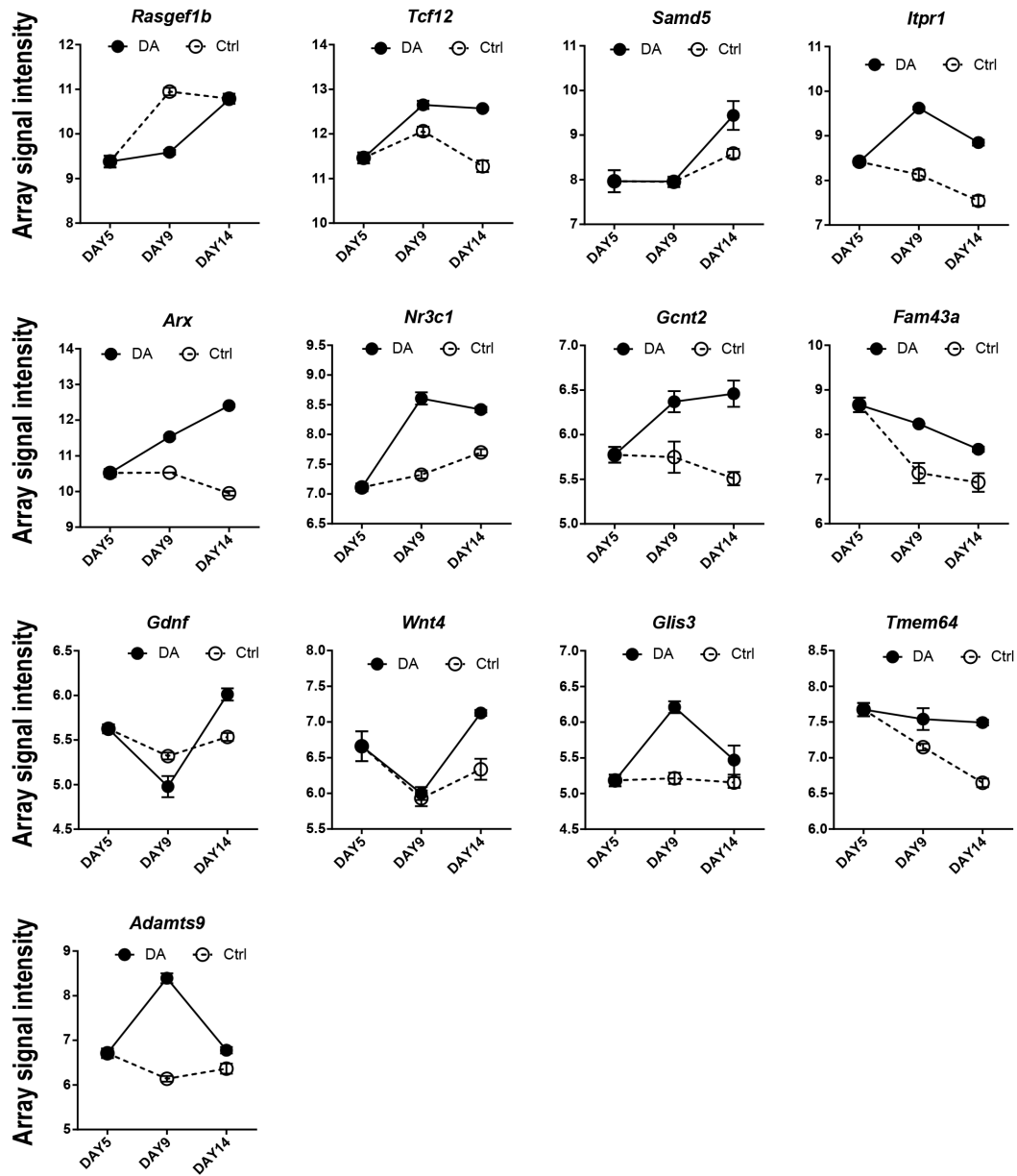
**Figure S1: Lmx1a promotes miR-204/211 expression in human cell lines.**

TaqMan assay for miR-204 on SHSY5Y (a) and HeLa (b) human cell lines. miR-204 values are normalized on the reference sno-202. Data represent the mean  $\pm$  SD of 2-DDCt values from three independent experiments. \* $p < 005$  with respect to Ctrl (one-way ANOVA + Tukey post hoc-test).



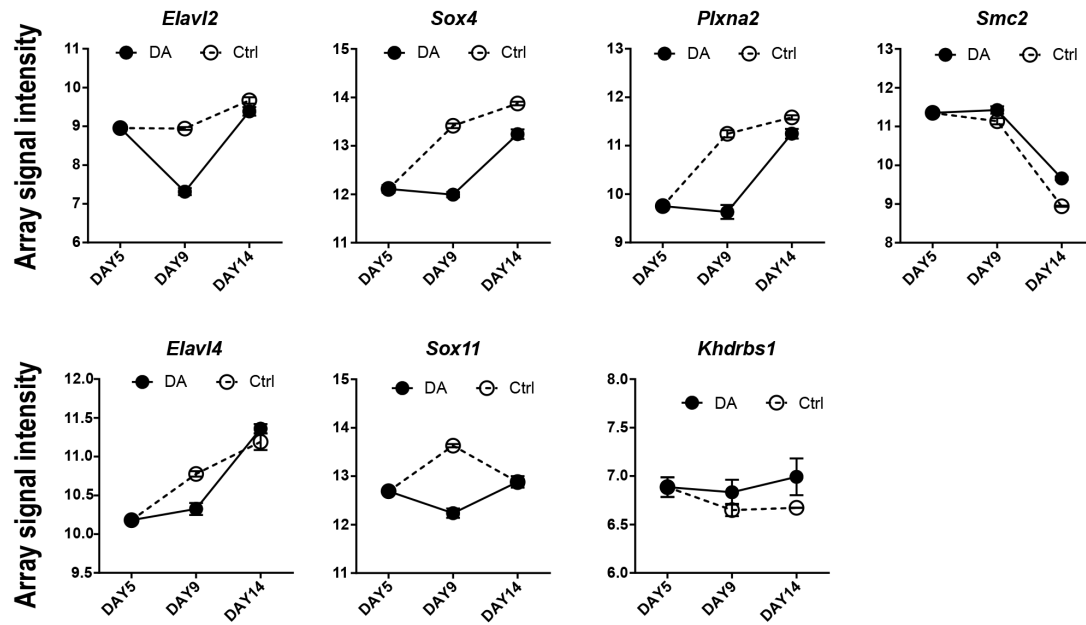
**Figure S2: Genes involved in mid-brain development and highly predicted targets of miR-204/211.**

a-c) miRNAs' binding sites enrichment analysis on floor plate (FP) (a), lateral ventral (LV) (b) and neural stem cell (NSC) (c) specific genes (Gennet et al., 2011; Lepko et al., 2019). Enrichment analysis was performed with TargetScan prediction score using ShinyGO v0741 web-tool (<http://bioinformatics.sdstate.edu/go/>) (Ge et al., 2020). Lollipop-plots representing the fold enrichment for miRNA-target genes on the x-axis, while the bubble-size represent the percentage of predicted genes on the total target for each miRNA. Absolute numbers of predicted genes are included in the bubbles. Enriched miRNAs are ordered for the  $-\log_{10}FDR$  values, represented as color gradient.



**Figure S3: Expression pattern of miR-204/211 target FP genes during in vitro dopaminergic differentiation of mouse epiSCs.**

Array values for selected target genes among the floor plate signature during in vitro DA differentiation of epiSCs (Gennet et al., 2011; De Gregorio et al., 2018). Data represent the mean  $\pm$  SD of array values for triplicate samples.)



**Figure S4: Expression pattern of miR-204/211 target NSC genes during in vitro dopaminergic differentiation of mouse epiSCs.**

Array values for selected target genes among the neural stem cells signature during in vitro DA differentiation of epiSCs (Lepko et al., 2019; De Gregorio et al., 2018). Data represent the mean  $\pm$  SD of array values for triplicate samples)