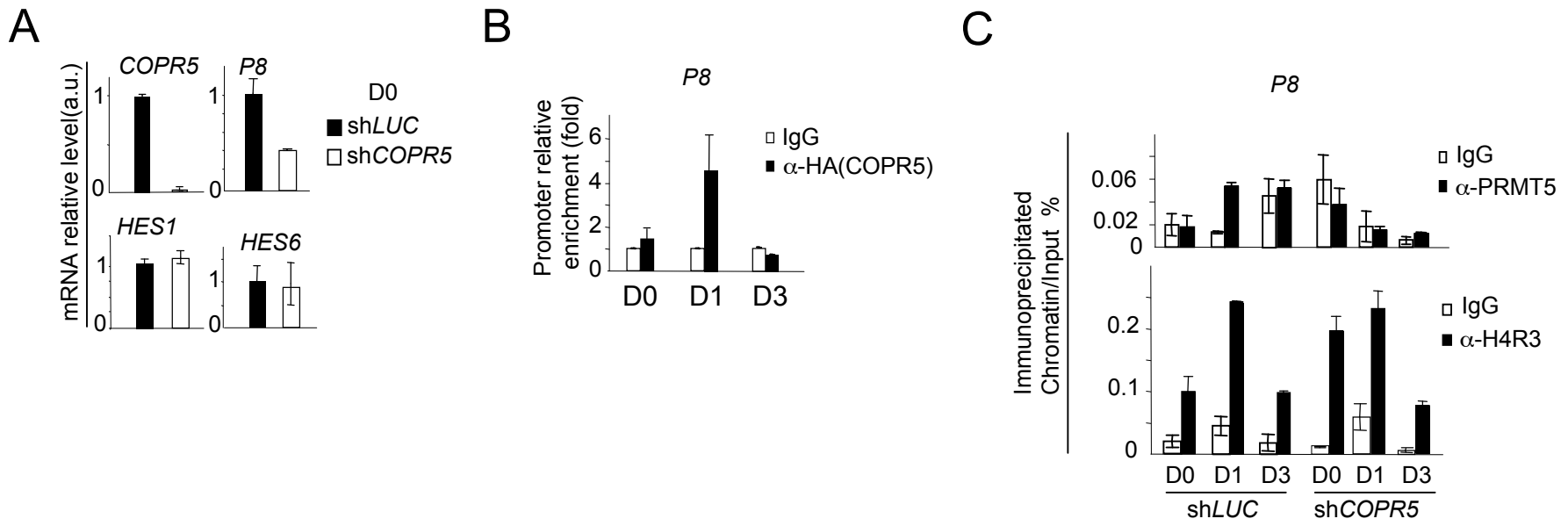
Supplementary figure 3 Paul et al.



Effect of *COPR5* down-regulation on the mRNA expression level of genes expressed in quiescent and G1-arrested cells and on the activation of the *p8* gene promoter activation via PRMT5 recruitment

A) RNA isolated froms from confluent (D0) sh*LUC* or sh*COPR5* C2C12 cells was used to analyse by RT-qPCR the expression of genes involved in cell cycle regulation. Results were normalized to *S26* RNA and values, expressed as a fold change compared to control, represent the means +/- standard deviation of three independent kinetics.

B) Chromatin immunoprecipitation was performed using C2C12 cells that express HA-COPR5 before (D0) and after induction of differentiation, as indicated. The recruitment of COPR5 on the *p8* promoter was analysed. Values express the relative promoter enrichment and correspond to the ratio of immunoprecipitated chromatin compared to control (fold activation). Values represent the means +/- standard deviation of three independent experiments.

C) Chromatin immunoprecipitation was performed using sh*LUC* or sh*COPR5* C2C12 cells before (D0) and after induction of differentiation. Anti-PRMT5 and -H4R3me2s antibodies were used to analyse the recruitment of PRMT5 and the presence of the H4R3 mark to the *p8* gene promoter. Relative values are expressed as a percentage of the immunopreciptated chromatin relative to the input. Values represent the means +/- standard deviation of three independent experiments.