



Supplementary Fig. S5.

Bisulfite sequencing indicates that EZH2 wt overexpression but not a mutant lacking the conserved SET domain (EZH2 Δ SET), significantly increases the CpG methylation status of the EZH2-target promoters MYT1 (left panel) and WNT1 (right panel). Each row represents a single sequence cloned and each square is a single CpG. White and black squares represent unmethylated and methylated CpGs, respectively.