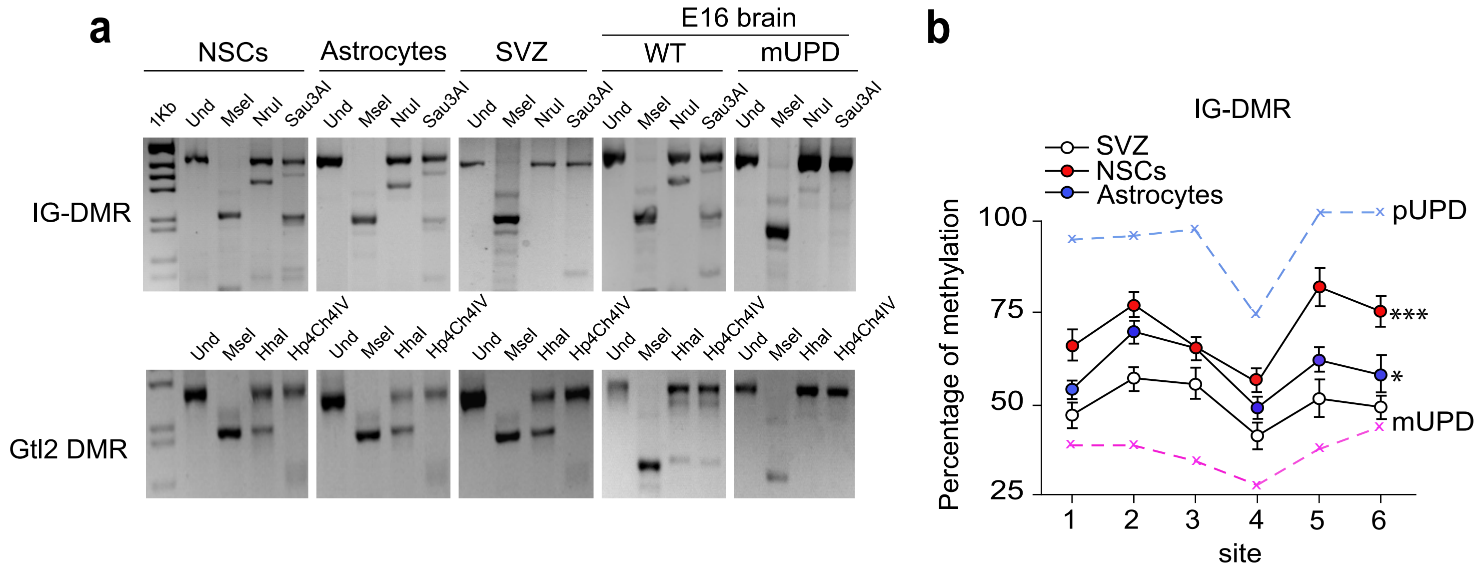
Supplementary Figure 7



Supplementary Figure 7. IG-DMR is hypermethylated in NSCs and niche-astrocytes. (**a**) Overall methylation profiles of the IG-DMR and Gtl2 DMR analyzed by combined bisulfite restriction analysis (COBRA). Bisulfite-treated DNA amplified products were cleaved by restriction enzymes NruI, Sau3AI and MluI for the IG-DMR, HincII and HpyCH4IV for the Gtl2 DMR and HhaI and HpyCH4IV for the Gtl2 DMR. The enzymes only cut the fragments when the specific CpG site was methylated. (**b**) Percentage of IG-DMR methylation determined by pyrosequencing. Maternal and paternal uniparental disomies (mUPD and pUPD) for chromosome 12 were used as controls. *p<0.05, ***p<0.001. Error bars, s.e.m of three independent experiments with three cultures per condition.