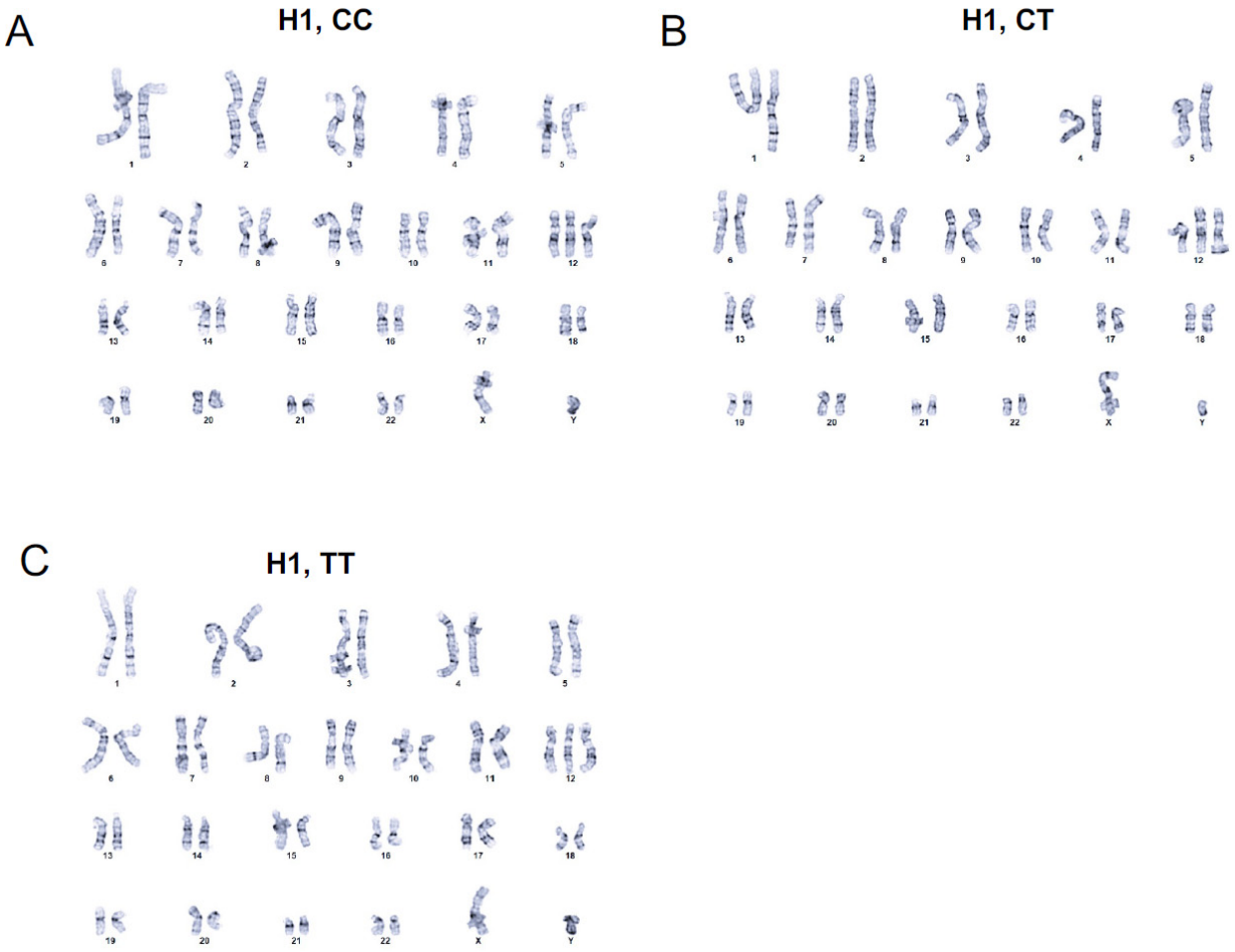
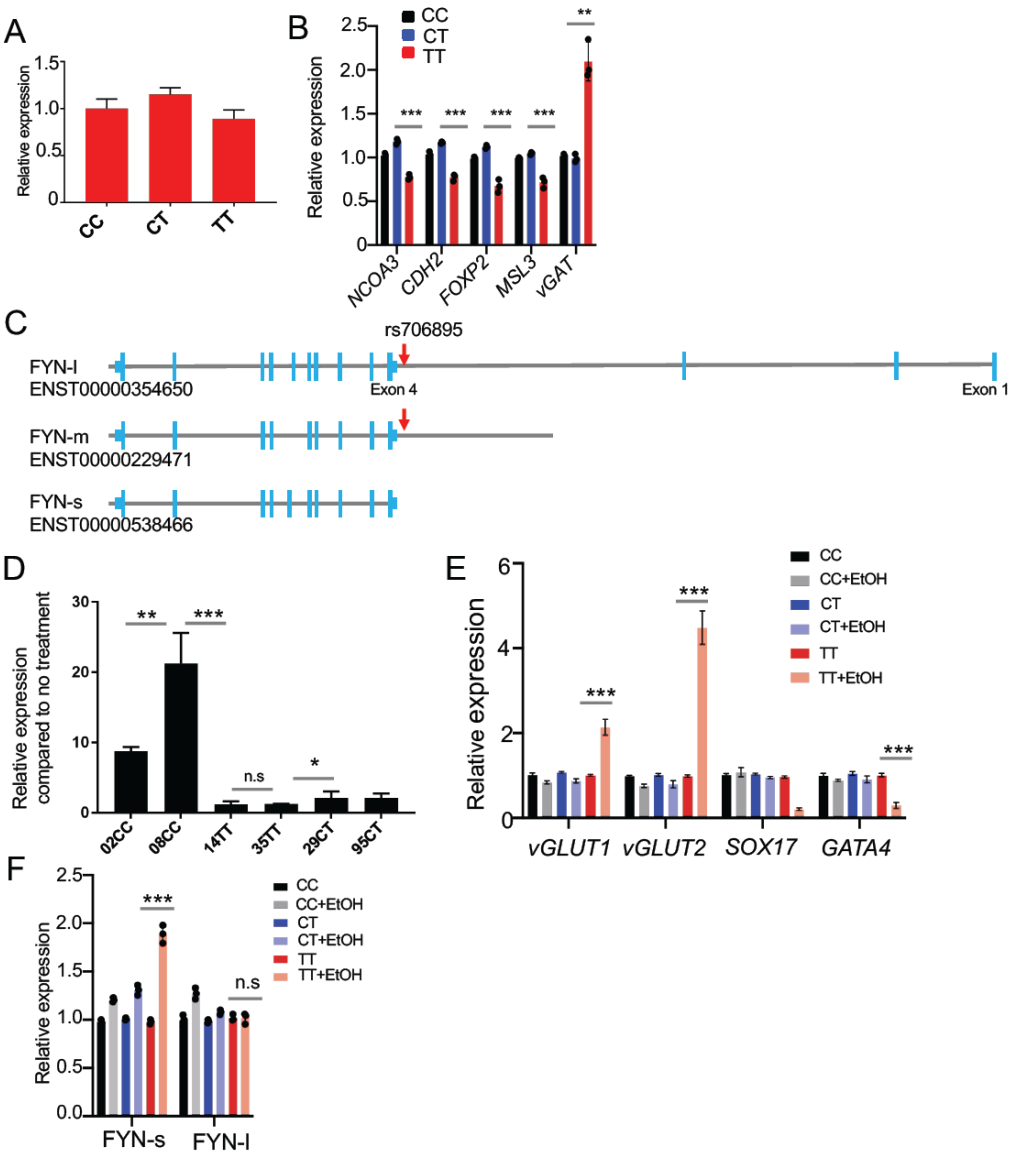


Supplementary Fig. S1. Karyotype analysis of H1 clones, H1-CC (A), H1-CT (B), H1-TT (C) depicting the abnormalities of chromosome 12 (trisomy).



Supplementary Fig. S2. Contribution of *FYN* variants to transcriptome profile of induced neurons. (A) Expression of *FYN* in H1-CC, -CT, and -TT induced neuronal (iN) cells. (B) Expression of differentially down-(*NCOA3*, *CDH2*, *FOXP2*, and *MSL3*) and up-(*vGAT*) regulated genes in H1-TT iNs, identified via RNA-Seq and presented in Fig. 3B. Gene expression was measured relative to H1-iNs and normalized to β-actin. Data represent the mean±SEM (n=3, from independent neural differentiation batches, **p<0.001, ***p<0.0001). (C) Genomic structure of *FYN* showing the location of rs706895, and three major isoforms (*FYN*-l, *FYN*-long, ENST00000354650; *FYN*-m, *FYN*-medium, ENST00000229471; *FYN*-s, *FYN*-short, ENST00000538466). (D) Expression of *FYN* in iNs derived from various human embryonic stem cells (hESCs) clones containing SNPs of *FYN* upon ethanol treatment. Data represent the mean±SEM (n=3, from independent neural differentiation batches, n.s, *p<0.05, **p<0.001, ***p<0.0001). (E) Expression of neuronal genes (*vGLUT1* and *vGLUT2) and stem cell related-genes (SOX17* and *GATA4*) from iNs with and without EtOH treatment. Gene expression was measured relative to H1-iNs without EtOH treatment and normalized to β-actin. Data represent the mean±SEM (n=3, from independent neural differentiation batches, ***p<0.001). (F) Expression levels of *FYN* splicing junctions between CC-, CT- and TT-iNs. *FYN*-s and *FYN*-l levels are detected via primer pairs *FYN-P1* and *FYN-P2*, *FYN-P1* and *FYN-P3*, respectively. Gene expression was measured relative to H1-iNs and normalized to β-actin. Data represent the mean±SEM (n=3, from independent neural differentiation batches, ***p<0.0001). n.s: not significant.