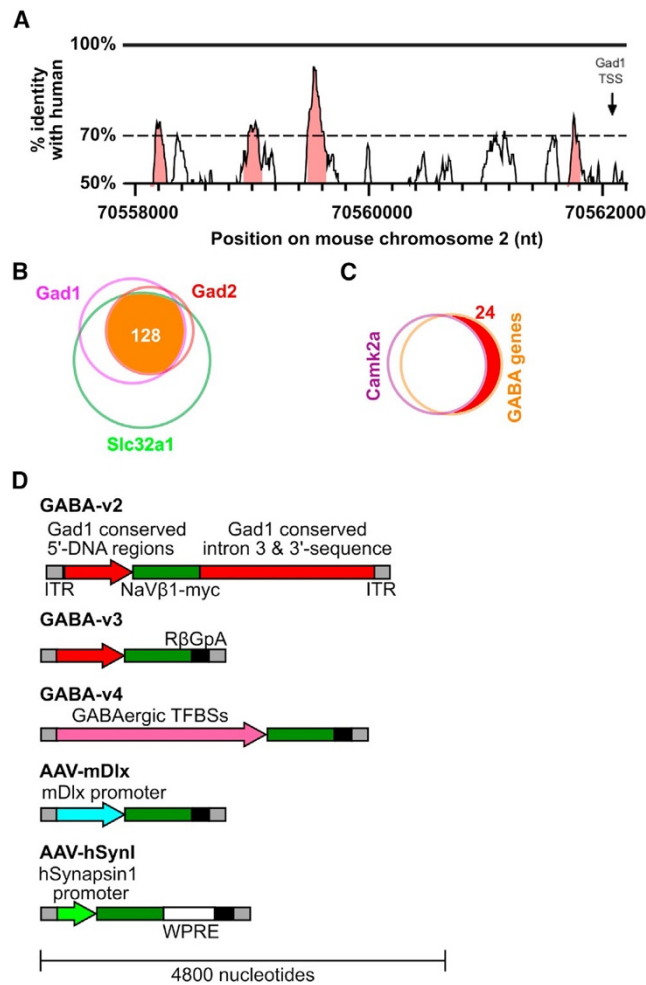




From Y. Niibori et al., 2023.

Figure 1. *In silico* analysis of GABA gene-regulatory elements and the creation of several novel GABA mini-regulatory elements for viral vector gene therapy.

(A) Homology analysis of human and mouse *Gad1* gene sequences from the transcription start site (arrow) to 4 kb upstream in the 5' untranslated region. The homology between *GAD1* on human chromosome 2 and *Gad1* on mouse chromosome 2 is depicted. The red-colored DNA regions indicate sections that are highly conserved between human and mouse. (B) Venn diagram of TFBSs conserved in the *Gad1*, *Gad2*, and *Slc32a1* 5' intergenic sequences. One hundred twenty-eight TFBSs were identified (in orange) that overlap among *Gad1* (magenta), *Gad2* (red), and *Slc32a1* (green). (C) Selection of TFBSs for GABAergic genes. The TFBSs in *Camk2a*, a glutamatergic neuronal marker, were subtracted from the TFBSs of GABA genes, yielding 24 TFBSs as candidate GABA-selective elements.

(D) DNA constructs of rAAV9 vectors. DNA components of GABA-v2 (GABA.v2-NaVb1-myc), GABA-v3 (GABA.v3-NaVb1-myc), GABA-v4 (GABA.v4-

NaVb1-myc), AAV-mDlx (mDlx-NaVb1-myc), and AAV-hSynI (hSynI-NaVb1-myc) are shown. ITR, inverted terminal repeats (gray boxes); 3⁰-downstream region (red boxes); RbGpA, rabbit b-globin polyadenylation region (black boxes); TFBS, transcription factor binding site in GABA-v4; WPRE, woodchuck hepatitis virus posttranslational regulatory element.