

Figure S1. *St3gal5*<sup>-/-</sup>/*B4galnt1*<sup>-/-</sup> mice exhibit impaired growth and motor function.

(A). A time course body weight from postnatal pups aging from 3 days old to 21 days old. Data are mean ± s.d. of 8-10 animals. Statistical analysis was performed by two-way ANOVA, followed by Sidak's multiple comparisons test. \*\*\*P < 0.001, \*\*\*\*P < 0.0001, ns: not significant. (B). Negative geotaxis successful rate from postnatal pups aging from 9 days old to 15 days old. Data are normalized from 10 animals. (C). Quantification of brain weight from wildtype mice or *St3gal*<sup>+/-</sup>/*B4galnt1*<sup>-/-</sup> mice or *St3gal5*<sup>-/-</sup>/*B4galnt1*<sup>-/-</sup> mice at 1-day old. Data are mean ± s.d. of 4-5 animals. Statistical analysis was performed by one-way ANOVA, followed by Dunnett's multiple comparisons test. \*p<0.05, ns: not significant.

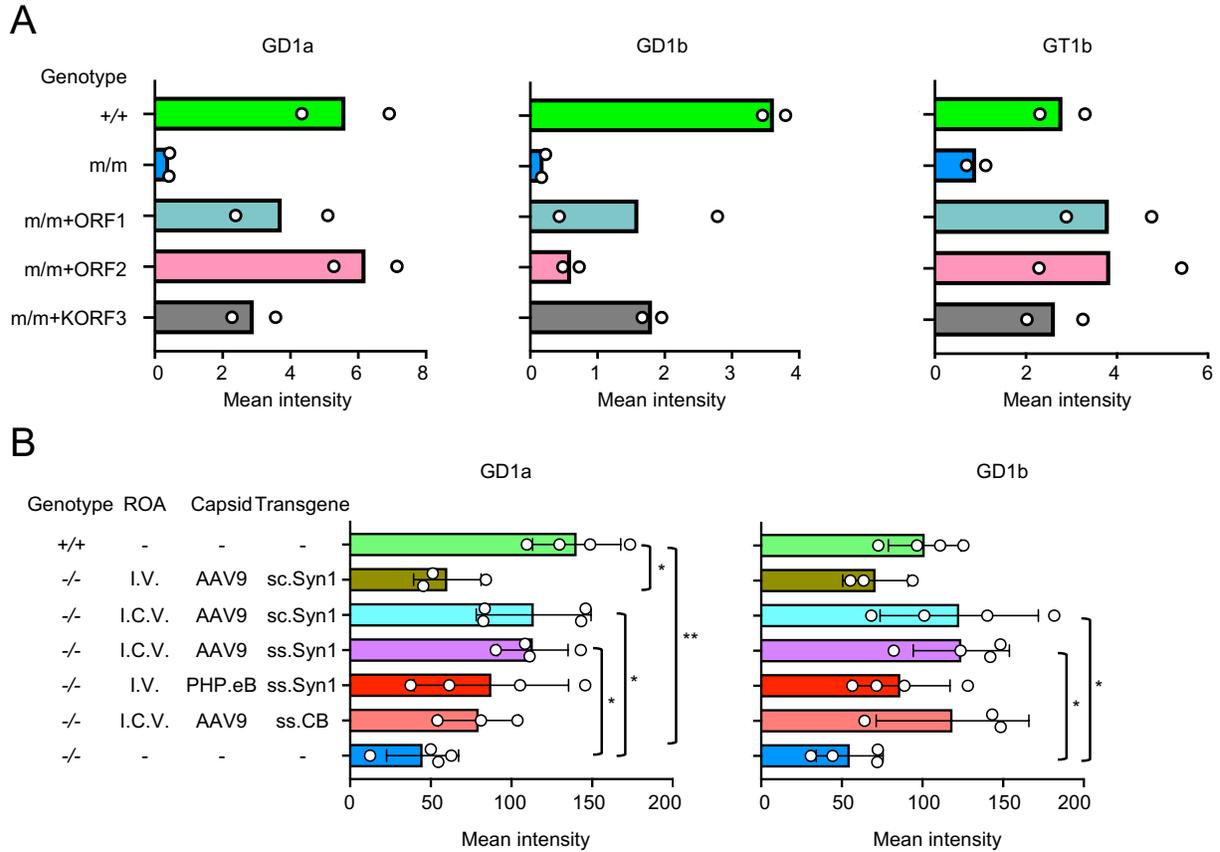


Figure S2. Quantification of gangliosides.

(A). Quantification of mean intensity of GD1a or GD1b or GT1b immunofluorescence from cortical neurons by lentiviral vectors expressing *ST3GAL5* ORFs. +/+, wildtype; *m/m*, *ST3GAL5<sup>mut/mut</sup>*. Data are mean of 2 slides per group. (B). Quantification of mean intensity of GD1a or GD1b immunofluorescence from cortex of *St3gal5<sup>+/+</sup>* and *St3gal5<sup>-/-</sup>* mice, with (+) or without (-) AAV.*ST3GAL5* treatments. ROA, route of administration; sc, self-complimentary vector genome; ss, single-strand vector genome; Syn1, Synapsin1 promoter; CB, chicken-beta actin promoter. Data are mean  $\pm$  s.d. of 3-4 animals per group. Statistical analysis was performed by one-way ANOVA, followed by Sidak's multiple comparisons test. \* $p < 0.05$ , \*\* $p < 0.01$ , ns: not significant.

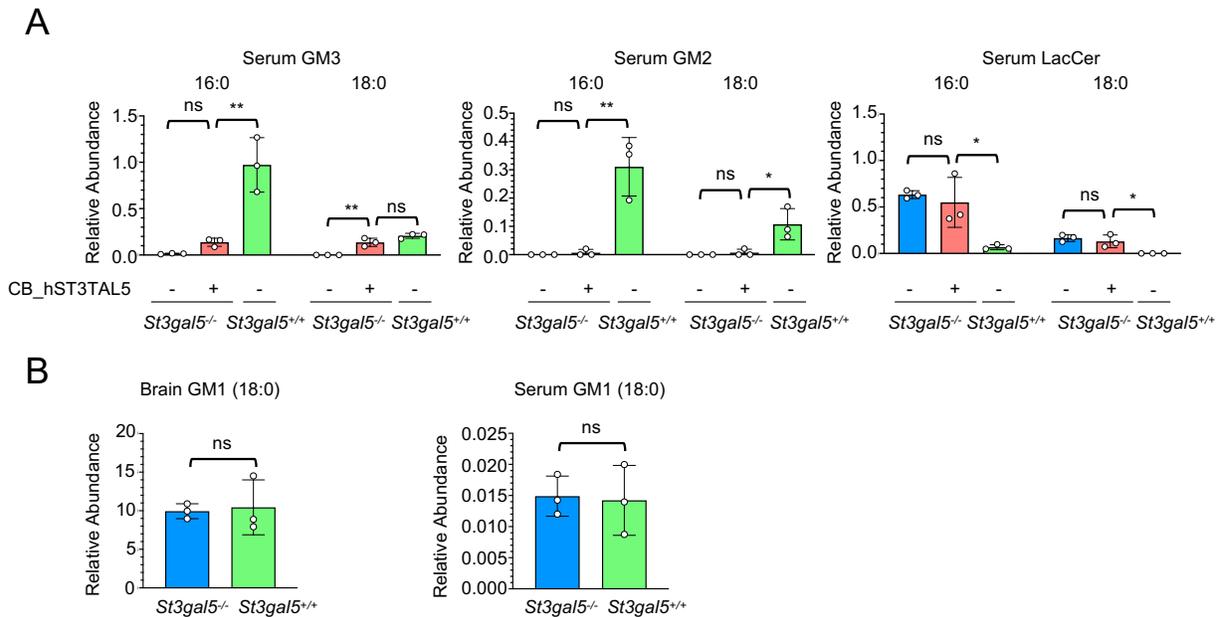


Figure S3. I.C.V. delivery of *ST3GAL5* restores limited peripheral gangliosides production in *St3gal5*<sup>-/-</sup> mouse model.

(A). Mass Spectrometry (MS) quantification of GM3 (16:0, 18:0), GM2 (16:0, 18:0), and LacCer (16:0, 18:0) from serum of *St3gal5*<sup>+/+</sup> and *St3gal5*<sup>-/-</sup> mice, with (+) or without (-) rAAV9.CB.hST3GAL5 treatment. Data are mean  $\pm$  s.d. of 3 animals per group. Statistical analysis was performed by one-way ANOVA, followed by Sidak's multiple comparisons test. \* $p < 0.05$ , \*\* $p < 0.01$ , ns: not significant. (B). Mass Spectrometry (MS) quantification of GM1 (18:0) from brain and serum of *St3gal5*<sup>+/+</sup> and *St3gal5*<sup>-/-</sup> mice. Data are mean  $\pm$  s.d. of 3 animals per group. Statistical analysis was performed by student t-test, ns: not significant.

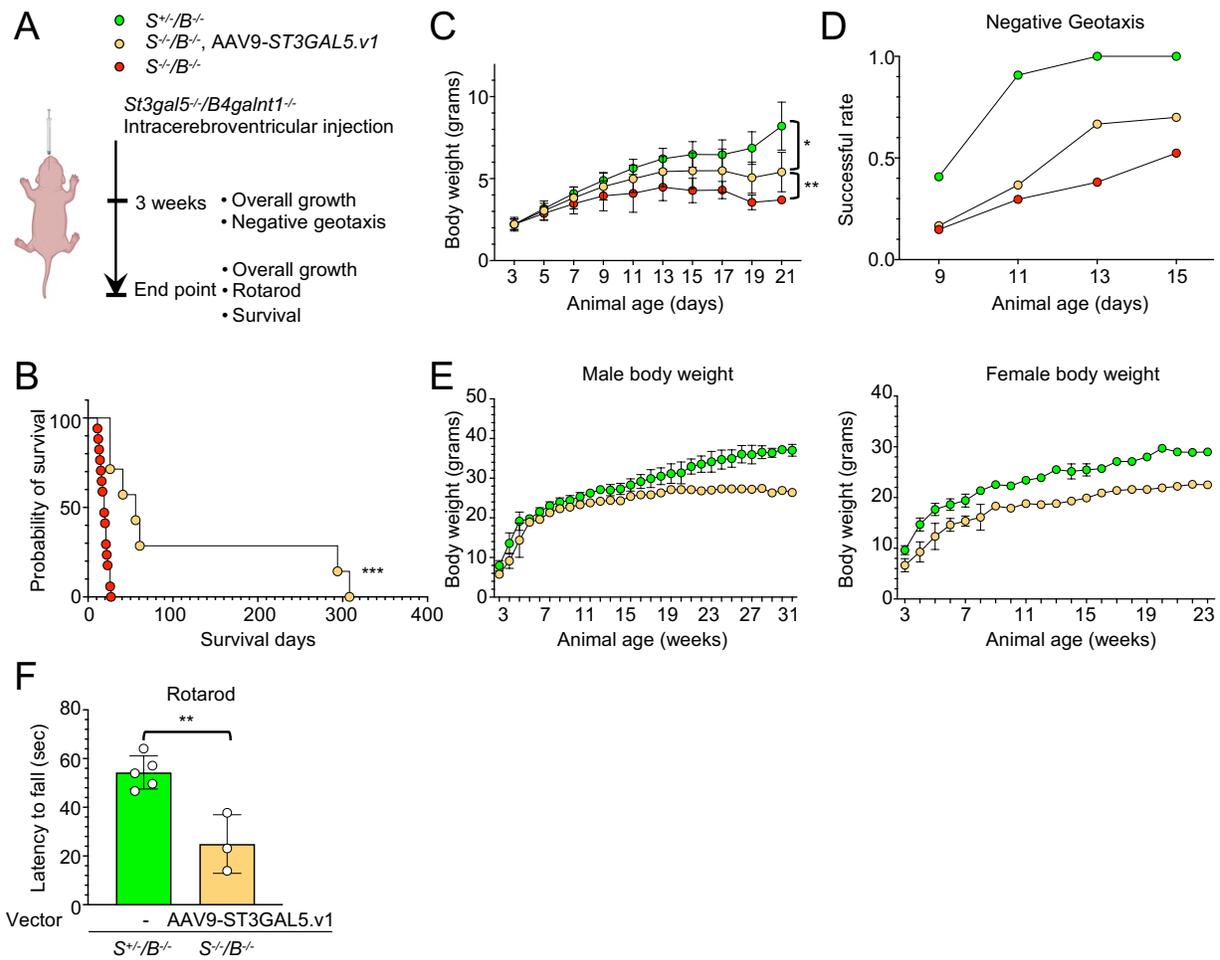


Figure S4. I.C.V. delivery of rAAV9-ST3GAL5.v1 rescues phenotypical changes in *St3gal5<sup>-/-</sup>/B4galnt1<sup>-/-</sup>* mouse model.

(A). Schematic of intracerebroventricular (I.C.V.) delivery of rAAV9-ST3GAL5.v1 in *St3gal5<sup>-/-</sup>/B4galnt1<sup>-/-</sup>* mouse model. (B). Median survival of *St3gal5<sup>-/-</sup>/B4galnt1<sup>-/-</sup>* mice, with or without rAAV9.CB.hST3GAL5 treatment. Data are plotted as probability of survival from 7-17 animals. Statistical analysis was performed by Lon-rank (Mantel-Cox) test. \*\*\* $p < 0.001$ . (C). A time course body weight from postnatal pups aging from 3 days old to 21 days old. Data are mean  $\pm$  s.d. of 8-10 animals. Statistical analysis was performed by two-way ANOVA, followed by Sidak's multiple comparisons test. \* $p < 0.05$ , \*\* $p < 0.01$ . (D). Negative geotaxis successful rate from postnatal pups aging from 9 days old to 15 days old. Data are normalized from 8-10 animals. (E). Body weight of male and female at postweaning stage. Data are represented as mean  $\pm$  s.d. of 3-4 animals. (F). Quantification of rotarod assay for *St3gal5<sup>+/-</sup>/B4galnt1<sup>-/-</sup>* mice and rAAV9-ST3GAL5.v1 treated *St3gal5<sup>-/-</sup>/B4galnt1<sup>-/-</sup>* mice at 6 weeks old. Data are represented as mean  $\pm$  s.d. of 3-5 animals. Statistical analysis was performed by student t-test. \*\* $p < 0.01$ .

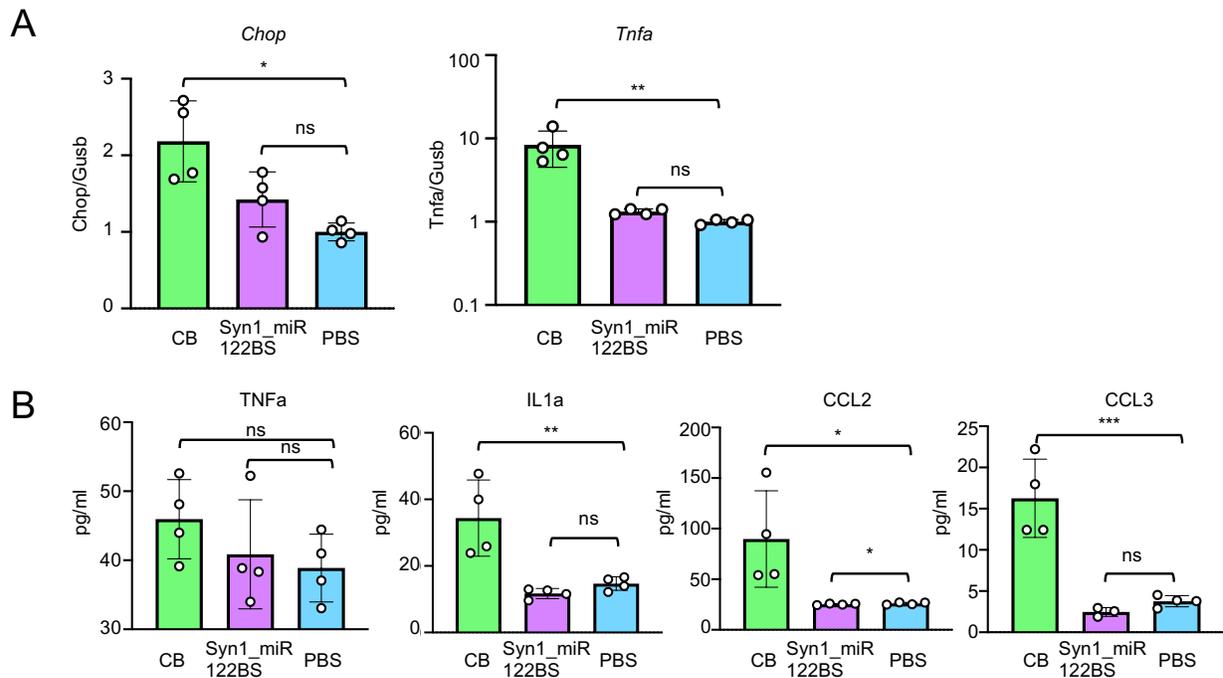


Figure S5. *ST3GAL5* overexpression in liver induces cellular toxicity.

(A). qPCR quantification of *Chop* and *Tnfa* mRNA in the liver of wildtype mice with rAAV9.CB.hST3GAL5 or rAAV9.hSyn1.hST3GAL5.miR122BS or PBS treatments. Data are mean  $\pm$  s.d. of 4 animals per group. Statistical analysis was performed by one-way ANOVA, followed by Sidak's multiple comparisons test. \* $p < 0.05$ , \*\* $p < 0.01$ , ns: not significant. (C). Quantification of enzyme-linked immunosorbent assay (ELISA) of TNFA, IL1a, CCL2, and CCL3 protein in the liver of wildtype mice with rAAV9.CB.hST3GAL5 or rAAV9.hSyn1.hST3GAL5.miR122BS or PBS treatments. Data are mean  $\pm$  s.d. of 4 animals per group. Statistical analysis was performed by one-way ANOVA, followed by Sidak's multiple comparisons test. \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ , ns: not significant.

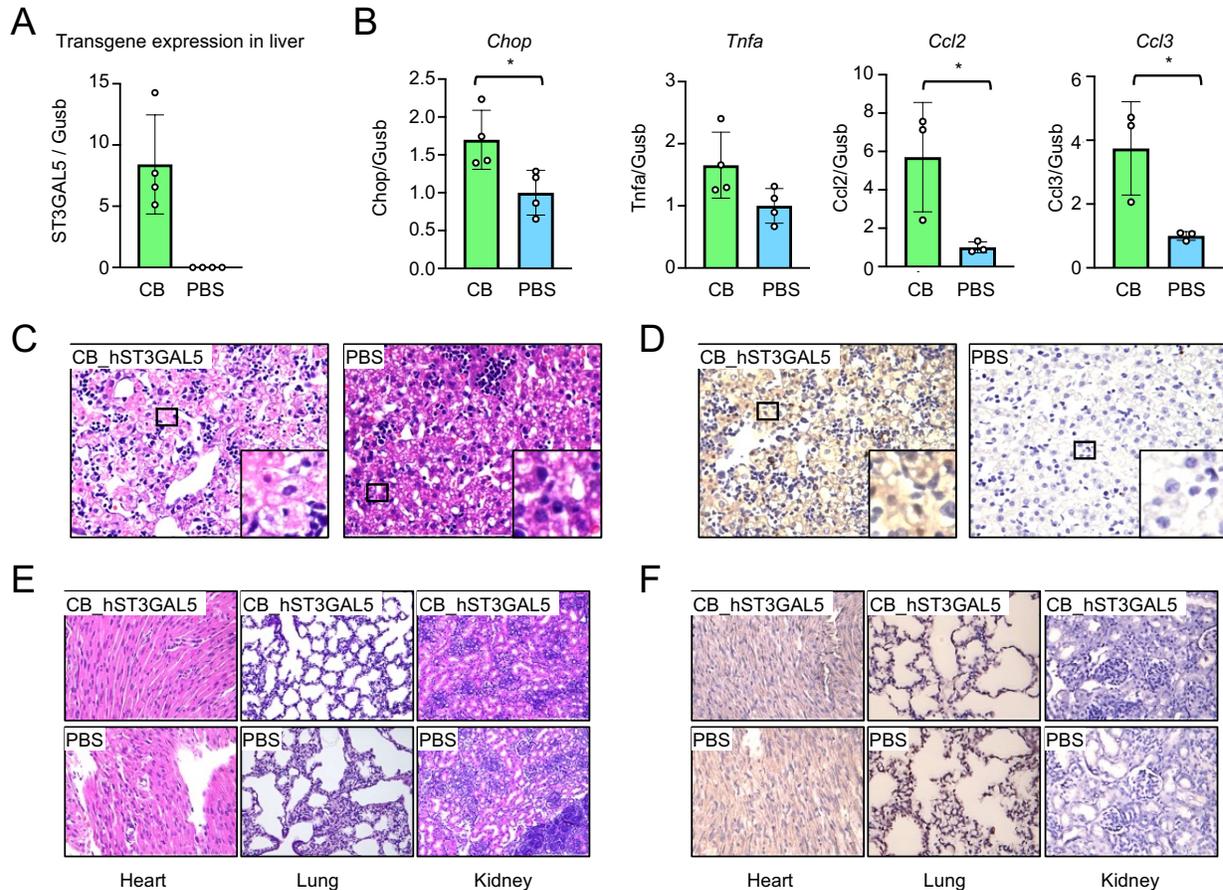


Figure S6. *ST3GAL5* overexpression in liver induces cellular toxicity in *St3gal5*<sup>-/-</sup> mice. (A). ddPCR quantification of *ST3GAL5* mRNA in the liver of *St3gal5*<sup>-/-</sup> mice with rAAV9.CB.hST3GAL5 or PBS treatments. Data are mean ± s.d. of 4 animals per group. (B). ddPCR quantification of *Chop*, *Tnfa*, *CCL2*, and *CCL3* mRNA in the liver of *St3gal5*<sup>-/-</sup> mice with rAAV9.CB.hST3GAL5 or PBS treatments. Data are mean ± s.d. of 3-4 animals per group. Statistical analysis was performed by student t-test. \*p<0.05. (C). Representative images of hematoxylin and eosin (H&E) staining of liver sections from *St3gal5*<sup>-/-</sup> mice injected with rAAV9.CB.hST3GAL5 or PBS. (D). Representative images of terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) staining of liver sections from *St3gal5*<sup>-/-</sup> mice injected with rAAV9.CB.hST3GAL5 or PBS. (E). Representative images of hematoxylin and eosin (H&E) staining of heart, lung, and kidney sections from *St3gal5*<sup>-/-</sup> mice injected with rAAV9.CB.hST3GAL5 or PBS. (F). Representative images of terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) staining of heart, lung, and kidney sections from *St3gal5*<sup>-/-</sup> mice injected with rAAV9.CB.hST3GAL5 or PBS.

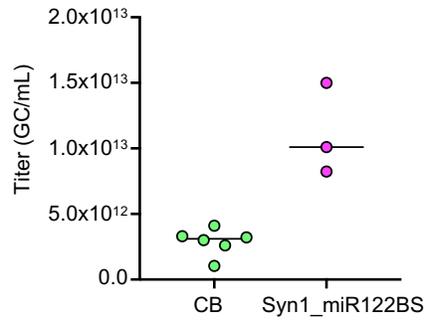


Figure S7. Packaging efficiency of rAAV9.CB.hST3GAL5 and rAAV9.Syn1.hST3GAL5.miR122BS. Quantification of vector titer from AAV9 vector preparation. Data are mean of 3-6 preparations per group.

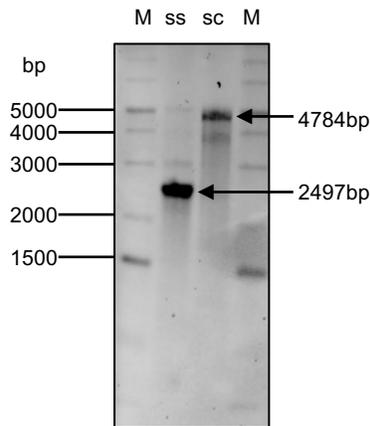


Figure S8. Analysis of genome sizes of ssAAV9.Syn1.hST3GAL5.miR122BS and scAAV9.Syn1.hST3GAL5.miR122BS vectors. Alkaline gel showing the packaged genome sizes of ssAAV9.Syn1.hST3GAL5.miR122BS and scAAV9.Syn1.hST3GAL5.miR122BS vectors. M: DNA ladder; ss: ssAAV9.Syn1.hST3GAL5.miR122BS, expected genome size is 2,497bp; sc: scAAV9.Syn1.hST3GAL5.miR122BS vectors, expected genome size is 4,784bp; bp: basepair

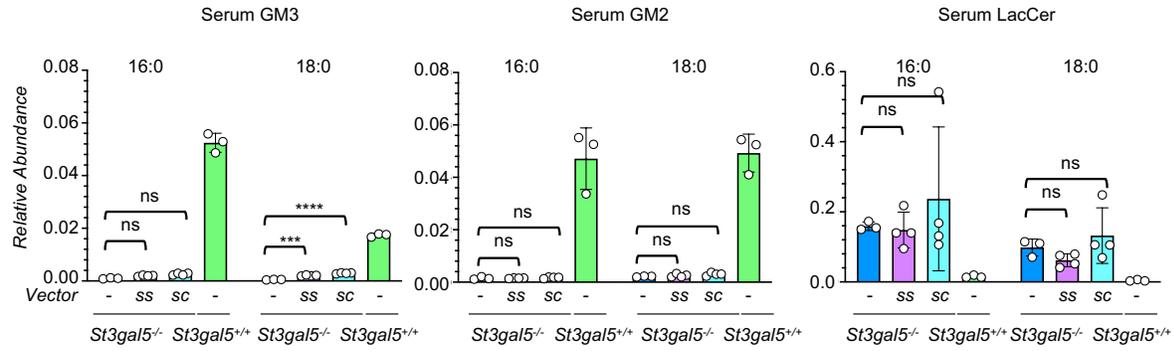


Figure S9. Second generation of *ST3GAL5* replacement vector does not restore peripheral gangliosides production in *St3gal5*<sup>-/-</sup> mouse model.

Mass Spectrometry (MS) quantification of GM3 (16:0, 18:0), GM2 (16:0, 18:0), and LacCer (16:0, 18:0) from serum of *St3gal5*<sup>+/+</sup> and *St3gal5*<sup>-/-</sup> mice, with ssAAV9.ST3GAL5.v2 or scAAV9.ST3GAL5.v2 or no treatment. Data are mean ± s.d. of 3-4 animals per group. Statistical analysis was performed by one-way ANOVA, followed by Sidak's multiple comparisons test. \*p<0.05, \*\*p<0.01, \*\*\*p<0.001, \*\*\*\*p<0.0001, ns: not significant.

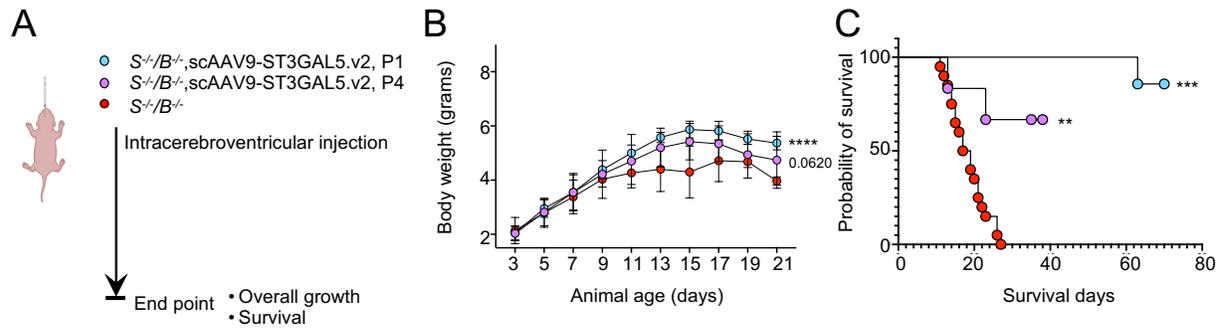


Figure S10. Treatment at a later postnatal stage of scAAV9-ST3GAL5.v2 rescues phenotypical changes in  $St3gal5^{-}/B4galnt1^{-}$  mouse model.

(A). Schematic of intracerebroventricular (I.C.V.) delivery of rAAV9-ST3GAL5.v2 in  $St3gal5^{-}/B4galnt1^{-}$  mouse model. (B). A time course body weight from postnatal pups aging from 3 days old to 21 days old. Data are mean  $\pm$  s.d. of 6-10 animals. Statistical analysis was performed by two-way ANOVA, followed by Sidak's multiple comparisons test. \*\*\*\* $P < 0.0001$ . (C). Median survival of  $St3gal5^{-}/B4galnt1^{-}$  mice, with or without rAAV9-ST3GAL5.v2 treatment. Data are plotted as probability of survival from 6-17 animals. Statistical analysis was performed by Log-rank (Mantel-Cox) test. \*\* $p < 0.01$ , \*\*\*\* $p < 0.0001$ .

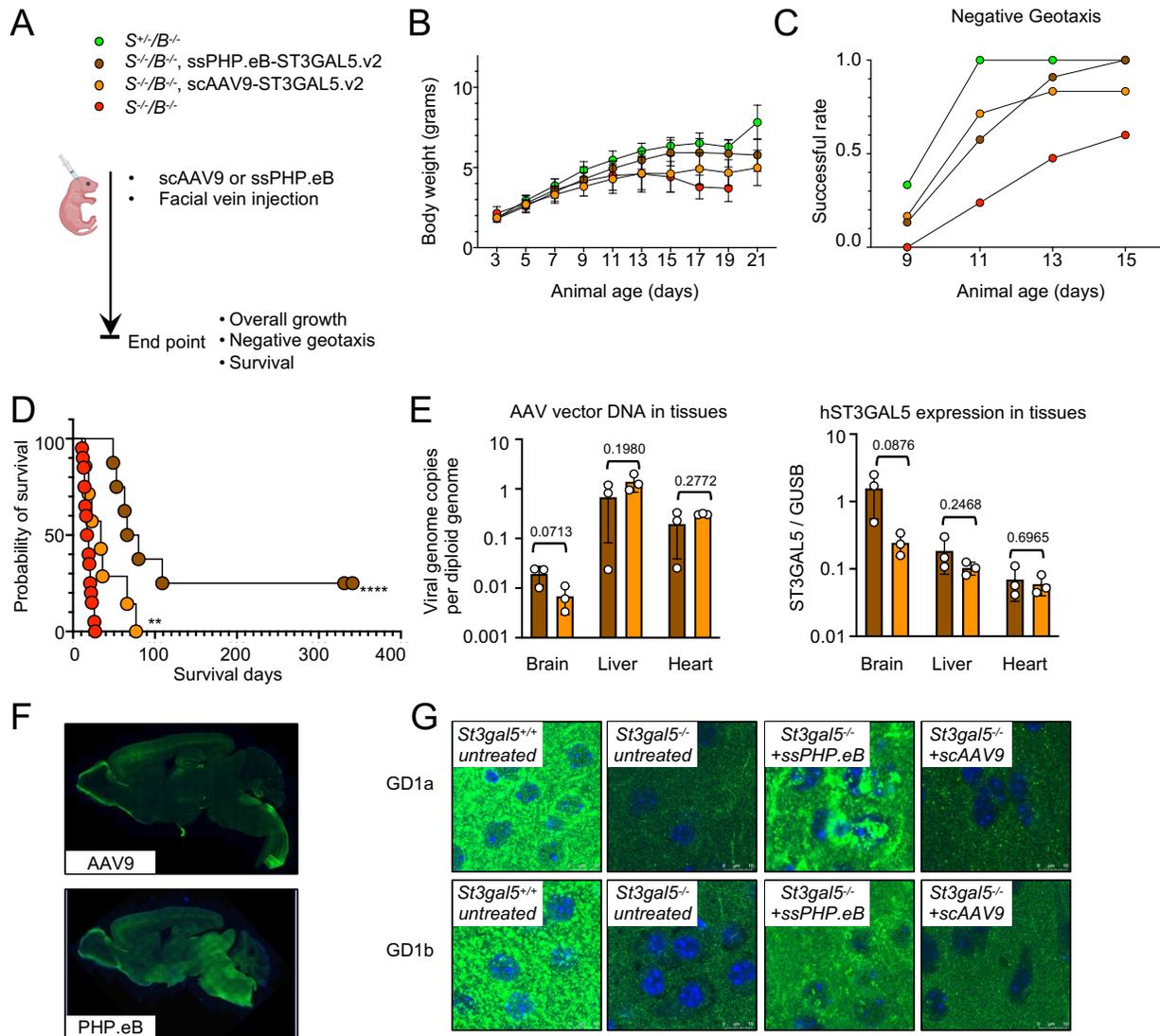


Figure S11. Systematic delivery of second generation *ST3GAL5* vector via AAV PHP.eB rescues GM3SD mouse models.

(A). Schematic of intravenous (I.V.) delivery of rAAV-ST3GAL5.v2 in mouse models. (B). A time course body weight from postnatal pups aging from 3 days old to 21 days old. Data are mean  $\pm$  s.d. of 7-10 animals. (C). Negative geotaxis successful rate from postnatal pups aging from 9 days old to 15 days old. Data are normalized from 8-10 animals. (D). Median survival of  $St3gal5^{-/-}/B4galnt1^{-/-}$  mice, with scAAV9.ST3GAL5.v2 or ssPHP.eB.ST3GAL5.v2 or no treatment. Data are plotted as probability of survival from 7-20 animals. Statistical analysis was performed by Lon-rank (Mantel-Cox) test. \*\*\* $p < 0.001$ . (E). ddPCR quantification of human *ST3GAL5* cDNA and AAV genome in the brain, liver, and heart of AAV9.ST3GAL5.v2 or PHP.eB.ST3GAL5.v2 treated mice. Data are mean  $\pm$  s.d. of 3 animals per group. Statistical analysis was performed by student t-test and P values are marked. (F). Representative images of EGFP staining in the brain with AAV9.Syn1.EGFP.miR122BS or PHP.eB.Syn1.EGFP.miR122BS treatment (G). Representative images of major brain gangliosides in cortex of  $St3gal5^{-/-}$  mice with scAAV9.ST3GAL5.v2 or ssPHP.eB.ST3GAL5.v2 treatment. GD1a, GD1b, green; nuclei, counterstaining in blue. Quantification is in Figure S2.

<b>Oligo name</b>	<b>Oligo sequence 5'-3'</b>
9057mTGU_probe	FAM-TCCAGAGCCACCTTA-MGB
9057mTGU_Fwd	TGGATGCTCAGTCAAAGCCTT
9057mTGU_Rev	GGAAGGCGTTCCGGAGAA
9057mTGD_probe	FAM-CTCAGCGGCGGCA-MGB
9057mTGD_Fwd	GAGACCAAGTTCCTCCTGAAGCT
9057mTGD_Rev	GCCGTGTTCCGAGTTCTCA
15582TU_probe	FAM-CAGGTTGCGGCGGTTGACCTCACT-BHQ-1
15582TU_Fwd	AGCCTTCCCTTGCCCTTTCTG
15582TU_Rev	AAACAGCCCTCAGTCCTCAG
LacZ_probe	FAM-CGATACTGTCGTCCCTCAAAGT-BHQ-1
LacZ_Fwd	GGAGTGCGATCTTCCTGAGG
LacZ_Rev	CGCATCGTAACCGTGCATC

Supplementary Table 1. Primer and probe sequences