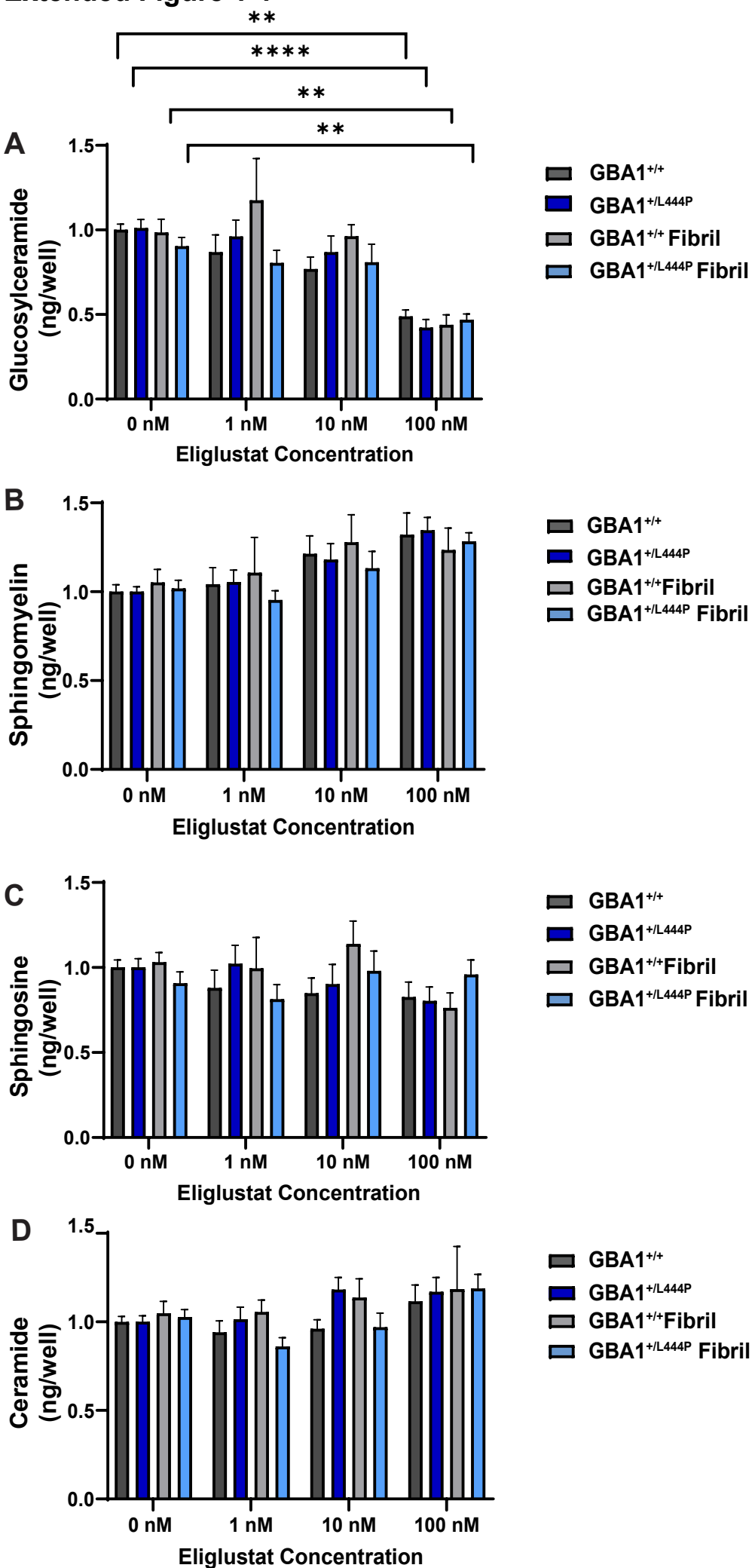


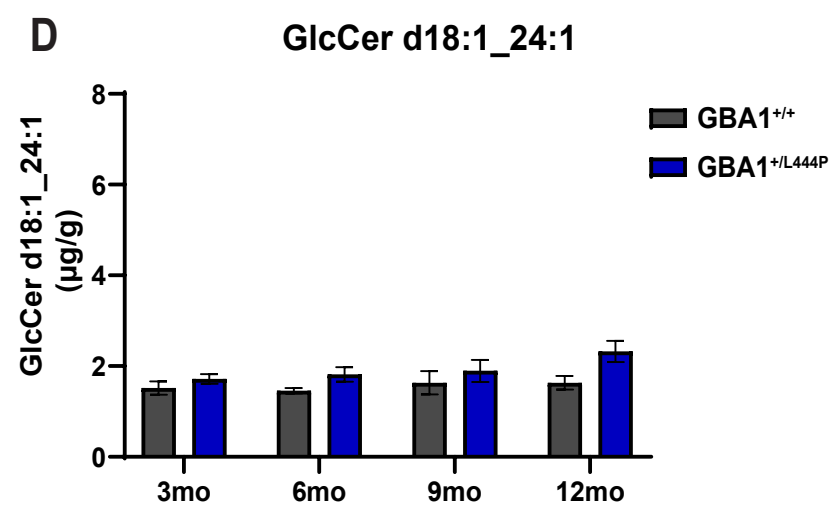
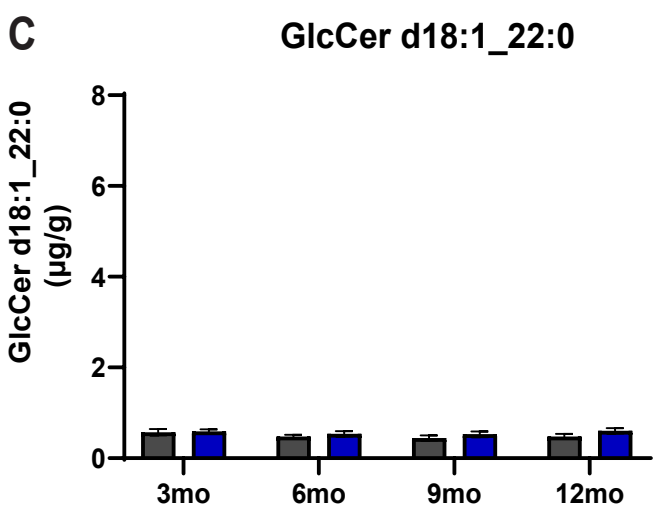
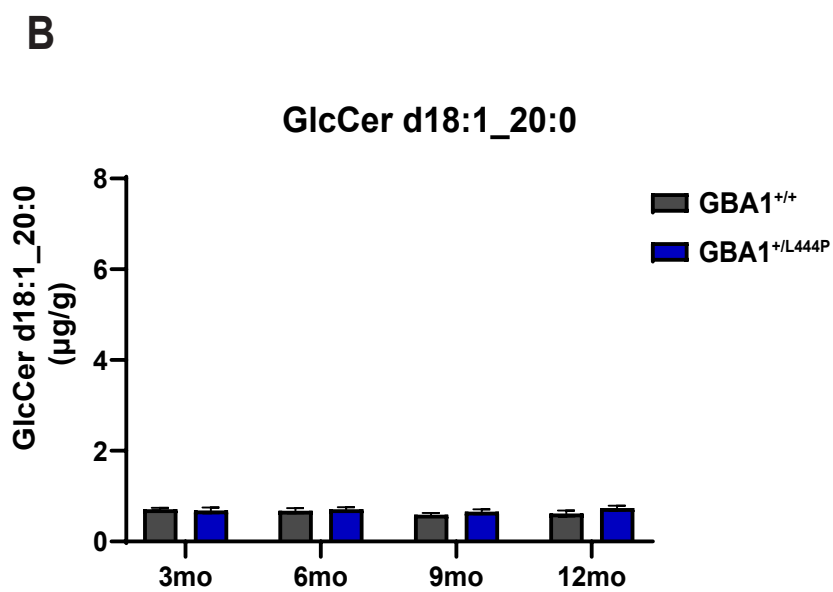
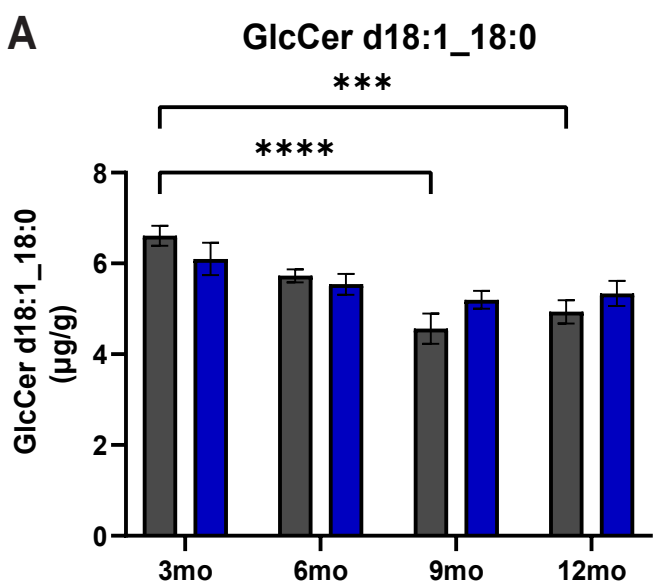
# Extended Figure 1-1



**Extended figure 1-1: Determination of Eliglustat Concentration based on lipid quantification.**

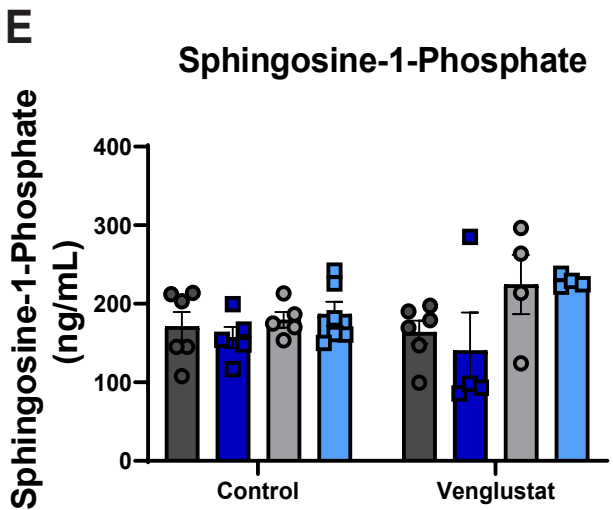
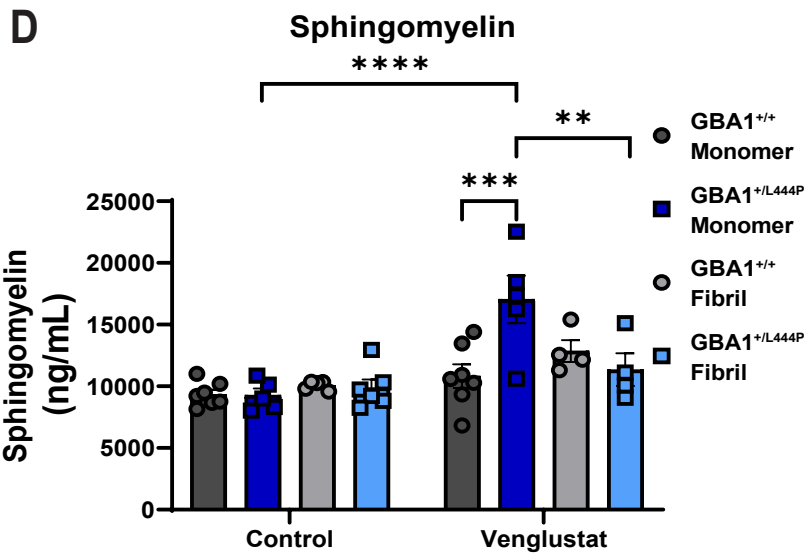
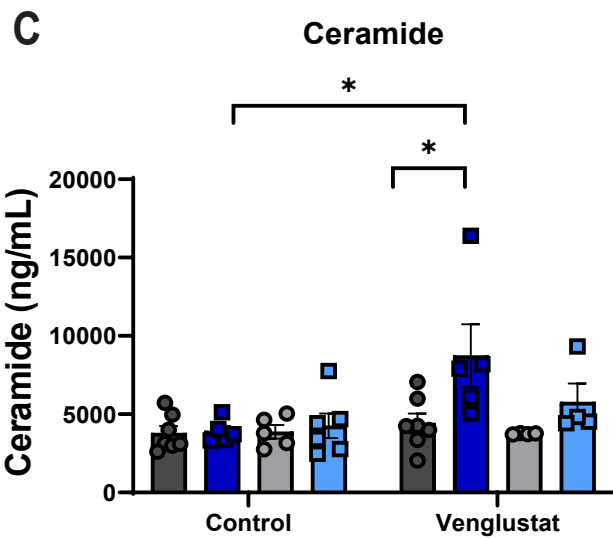
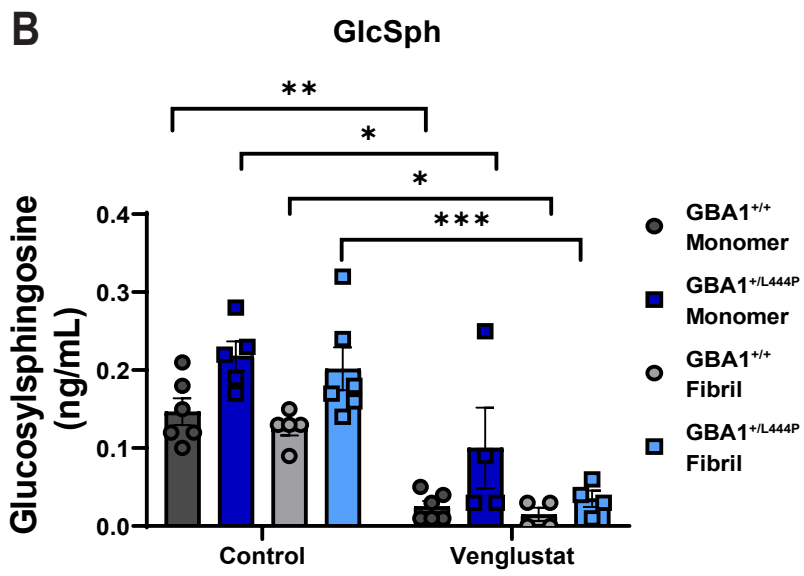
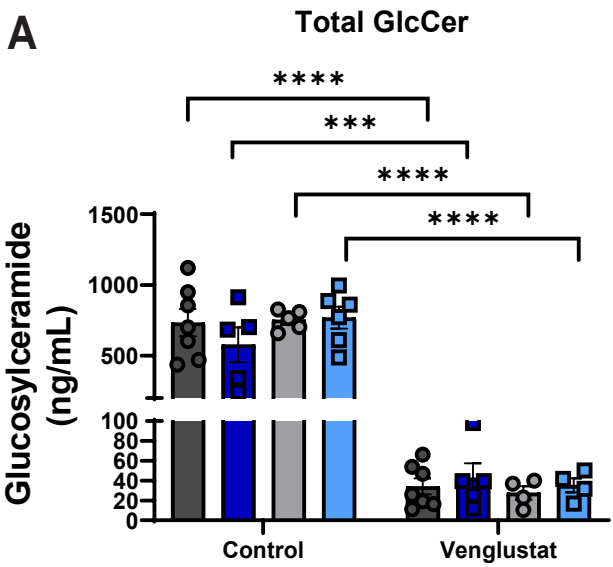
GBA1<sup>+/+</sup> and GBA1<sup>+L444P</sup> Primary cortical neurons were treated at DIV14 with varying concentrations of eliglustat (0, 1, 10, and 100 nM). Neurons were quantified by mass spectrometry for **A.** GlcCer (Three-way ANOVA; *Interaction*:  $F_{(3,151)} = 1.524$ ,  $p = 0.2106$ , *Dose x  $\alpha$ -syn Treatment*:  $F_{(3,151)} = 0.3454$ ,  $p = 0.7926$ , *Dose x Genotype*:  $F_{(3,151)} = 0.7284$ ,  $p = 0.5365$ , *Genotype x  $\alpha$ -syn Treatment*:  $F_{(1,151)} = 3.856$ ,  $p = 0.0514$ , *Dose*:  $F_{(3,151)} = 28.06$ ,  $****p < 0.0001$ ,  *$\alpha$ -syn Treatment*:  $F_{(1,151)} = 1.454$ ,  $p = 0.2299$ , *Genotype*:  $F_{(1,151)} = 0.1898$ ,  $p = 0.6637$ ) and **B.** sphingomyelin (*Interaction*:  $F_{(3,151)} = 0.2265$ ,  $p = 0.8778$ , *Dose x  $\alpha$ -syn Treatment*:  $F_{(3,151)} = 0.3922$ ,  $p = 0.7588$ , *Dose x Genotype*:  $F_{(3,151)} = 0.3684$ ,  $p = 0.7759$ , *Genotype x  $\alpha$ -syn Treatment*:  $F_{(1,151)} = 0.7365$ ,  $p = 0.3921$ , *Dose*:  $F_{(3,151)} = 11.11$ ,  $****p < 0.0001$ ,  *$\alpha$ -syn Treatment*:  $F_{(1,151)} = 0.6928$ ,  $p = 0.4065$ , *Genotype*:  $F_{(1,151)} = 0.08458$ ,  $p = 0.7716$ ,) **C.** sphingosine (*Interaction*:  $F_{(3,157)} = 1.152$ ,  $p = 0.3302$ , *Dose x  $\alpha$ -syn Treatment*:  $F_{(3,157)} = 0.4860$ ,  $p = 0.6925$ , *Dose x Genotype*:  $F_{(3,157)} = 1.166$ ,  $p = 0.3245$ , *Genotype x  $\alpha$ -syn Treatment*:  $F_{(1,157)} = 1.259$ ,  $p = 0.2636$ , *Dose*:  $F_{(3,157)} = 1.922$ ,  $p = 0.1283$ ,  *$\alpha$ -syn Treatment*:  $F_{(1,157)} = 0.05604$ ,  $p = 0.8132$ , *Genotype*:  $F_{(1,157)} = 0.5954$ ,  $p = 0.4415$ ) and **D.** Ceramide (*Interaction*:  $F_{(3,151)} = 1.515$ ,  $p = 0.2128$ , *Dose x  $\alpha$ -syn Treatment*:  $F_{(3,151)} = 0.2502$ ,  $p = 0.8611$ , *Dose x Genotype*:  $F_{(3,151)} = 0.2116$ ,  $p = 0.8882$ , *Genotype x  $\alpha$ -syn Treatment*:  $F_{(1,151)} = 5.610$ ,  $*p = 0.0191$ , *Dose*:  $F_{(3,151)} = 4.115$ ,  $**p = 0.0077$ ,  *$\alpha$ -syn Treatment*:  $F_{(1,151)} = 0.01056$ ,  $p = 0.9183$ , *Genotype*:  $F_{(1,151)} = 0.08041$ ,  $p = 0.7771$ ). Error bars represent SEM. For GlcCer, Sphingomyelin, and Ceramide in control treated neurons, GBA1<sup>+/+</sup> N=18, GBA1<sup>+L444P</sup> N=24, fibril treated GBA1<sup>+/+</sup> N=18, and fibril treated GBA1<sup>+L444P</sup> neurons N=24. To analyze sphingosine for control-treated neurons, GBA1<sup>+/+</sup> fibril-treated neurons N=24. For all lipid quantitation for eliglustat treated neurons (1nM, 10nM, and 100nM), GBA1<sup>+/+</sup> N=6, GBA1<sup>+L444P</sup> N=8, fibril treated GBA1<sup>+/+</sup> N=6, and fibril treated GBA1<sup>+L444P</sup> N=8, apart from fibril treated GBA1<sup>+/+</sup> at 100nM where N=5. All sample sizes depict the number of individual mice. \* $p < 0.05$ , \*\* $p < 0.01$ , and \*\*\*\* $p < 0.0001$ .

# Extended Figure 4-1



**Extended Data 4-1: Evaluation of GlcCer isoform quantification.** Four isoforms of GlcCer **A.** GlcCer C18:0 (Two-way ANOVA; *Interaction*:  $F_{(3,50)} = 2.173$ ,  $p=0.1028$ , *Age*:  $F_{(3,50)} = 12.77$ ,  $****p<0.0001$ , and *Genotype*:  $F_{(1,50)} = 0.2353$ ,  $p=0.6297$ ) **B.** GlcCer C20:0 (*Interaction*:  $F_{(3,48)} = 0.6806$ ,  $p=0.5682$ , *Age*:  $F_{(3,48)} = 0.7990$ ,  $p=0.5005$ , and *Genotype*:  $F_{(1,48)} = 1.619$ ,  $p=0.2094$ ) **C.** GlcCer C22:0 (*Interaction*:  $F_{(3,50)} = 0.3007$ ,  $p=0.8247$ , *Age*:  $F_{(3,50)} = 1.027$ ,  $p=0.3886$ , and *Genotype*:  $F_{(1,50)} = 2.898$ ,  $p=0.0949$ ) and **D.** GlcCer C24:1 (*Interaction*:  $F_{(3,50)} = 0.7606$ ,  $p=0.5215$ , *Age*:  $F_{(3,50)} = 1.821$ ,  $p=0.1554$ , *Genotype*:  $F_{(1,50)} = 9.377$ ,  $***p=0.0035$ ) were examined in the striatum of the same mice groups and time points. Error bars represent SEM. For all lipids, 3mo GBA1<sup>+/+</sup> N= 8, 3mo GBA1<sup>+L444P</sup> N=7 except C18:0 N=5 and C20:0 N=6, 6mo GBA1<sup>+/+</sup> N= 8 except C18=10 and C20 =7, 6mo GBA1<sup>+L444P</sup> N=8, 9mo GBA1<sup>+/+</sup> N= 6, 9mo GBA1<sup>+L444P</sup> N=7, 12mo GBA1<sup>+/+</sup> N= 7, and 12mo GBA1<sup>+L444P</sup> N=7. \* $p<0.05$ , \*\* $p<0.01$ , \*\*\* $p<0.001$ , and \*\*\*\* $p<0.0001$ .

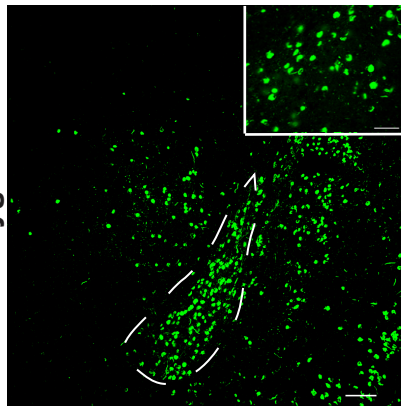
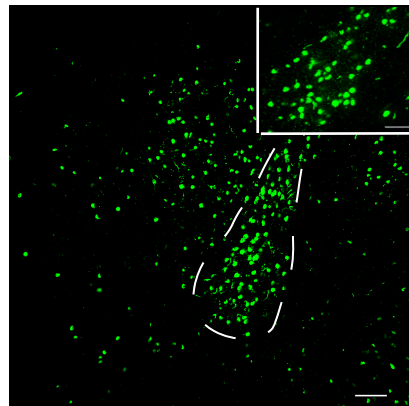
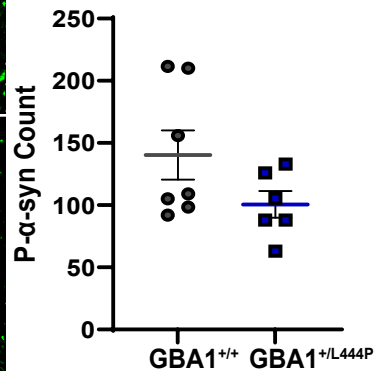
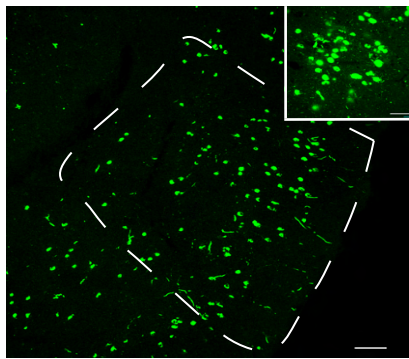
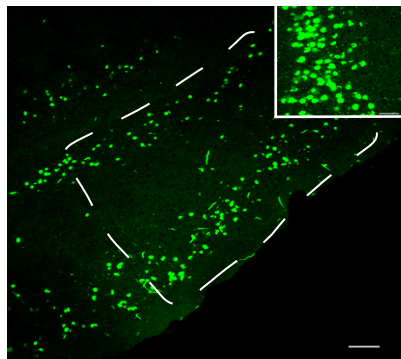
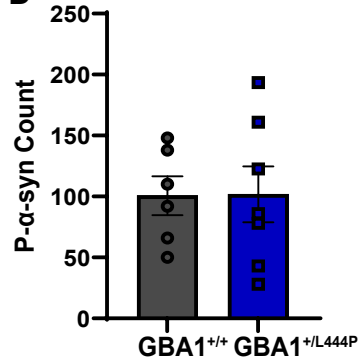
# Extended Figure 5-1



**Extended Data 5-1: Evaluation of lipid plasma concentrations.** Plasma was collected from GBA1<sup>+/+</sup> and GBA1<sup>+L444P</sup> at 10-months post-monomer or fibril injection. Mass Spectrometry was used to quantify

**A.** Total GlcCer levels (Three-way ANOVA; *Interaction*:  $F_{(1,35)} = 0.7606$ ,  $p = 0.3891$ , *Drug Treatment x  $\alpha$ -syn Treatment*:  $F_{(1,35)} = 1.268$ ,  $p = 0.2677$ , *Drug Treatment x Genotype*:  $F_{(1,35)} = 0.6130$ ,  $p = 0.4389$ ,  *$\alpha$ -syn Treatment x Genotype*:  $F_{(1,35)} = 0.7431$ ,  $p = 0.3945$ , *Drug Treatment*:  $F_{(1,35)} = 181.7$ ,  $****P < 0.0001$ ,  *$\alpha$ -syn Treatment*:  $F_{(1,35)} = 0.9673$ ,  $p = 0.3321$ , *Genotype*:  $F_{(1,35)} = 0.3836$ ,  $p = 5394$ ), **B.** GlcSph (*Interaction*:  $F_{(1,35)} = 0.8940$ ,  $p = 0.3515$ , *Drug Treatment x  $\alpha$ -syn Treatment*:  $F_{(1,35)} = 0.3667$ ,  $p = 0.5491$ , *Drug Treatment x Genotype*:  $F_{(1,35)} = 0.6867$ ,  $p = 0.4134$ ,  *$\alpha$ -syn Treatment x Genotype*:  $F_{(1,35)} = 0.6519$ ,  $p = 0.4254$ , *Drug Treatment*:  $F_{(1,35)} = 67.97$ ,  $****p < 0.0001$ ,  *$\alpha$ -syn Treatment*:  $F_{(1,35)} = 3.186$ ,  $p = 0.0838$ , *Genotype*:  $F_{(1,35)} = 14.87$ ,  $***p = 0.0005$ ), **C.** Ceramide (*Interaction*:  $F_{(1,35)} = 0.9955$ ,  $p = 0.3253$ , *Drug Treatment x  $\alpha$ -syn Treatment*:  $F_{(1,35)} = 2.536$ ,  $p = 0.1203$ , *Drug Treatment x Genotype*:  $F_{(1,35)} = 5.255$ ,  $*p = 0.0280$ ,  *$\alpha$ -syn Treatment x Genotype*:  $F_{(1,35)} = 0.6352$ ,  $p = 0.4308$ , *Drug Treatment*:  $F_{(1,35)} = 7.185$ ,  $*p = 0.0111$ ,  *$\alpha$ -syn Treatment*:  $F_{(1,35)} = 1.582$ ,  $p = 0.2168$ , *Genotype*:  $F_{(1,35)} = 7.241$ ,  $*p = 0.0109$ ) **D.** Sphingomyelin (*Interaction*:  $F_{(1,35)} = 7.734$ ,  $**p = 0.0087$ , *Drug Treatment x  $\alpha$ -syn Treatment*:  $F_{(1,35)} = 3.327$ ,  $p = 0.0767$ , *Drug Treatment x Genotype*:  $F_{(1,35)} = 3.289$ ,  $p = 0.0783$ ,  *$\alpha$ -syn Treatment x Genotype*:  $F_{(1,35)} = 8.184$ ,  $**p = 0.0071$ , *Drug Treatment*:  $F_{(1,35)} = 24.29$ ,  $****p < 0.0001$ ,  *$\alpha$ -syn Treatment*:  $F_{(1,35)} = 0.7393$ ,  $p = 0.3957$ , *Genotype*:  $F_{(1,35)} = 2.626$ ,  $p = 1141$ ), and **E.** Sphingosine 1-Phosphate (*Interaction*:  $F_{(1,32)} = 0.008874$ ,  $p = 0.9255$ , *Drug Treatment x  $\alpha$ -syn Treatment*:  $F_{(1,32)} = 3.188$ ,  $p = 0.0836$ , *Drug Treatment x Genotype*:  $F_{(1,32)} = 0.04317$ ,  $p = 0.8367$ ,  *$\alpha$ -syn Treatment x Genotype*:  $F_{(1,32)} = 0.6178$ ,  $p = 0.4376$ , *Drug Treatment*:  $F_{(1,32)} = 1.016$ ,  $p = 0.3209$ ,  *$\alpha$ -syn Treatment*:  $F_{(1,32)} = 9.109$ ,  $**p = 0.0050$ , *Genotype*:  $F_{(1,32)} = 0.1771$ ,  $p = 0.6767$ ). GlcCer, ceramide, and sphingomyelin had GBA1<sup>+/+</sup> N=7, GBA1<sup>+L444P</sup> N=5, fibril treated GBA1<sup>+/+</sup> N=5, and fibril treated GBA1<sup>+L444P</sup> N=6 for control treated groups and GBA1<sup>+/+</sup> N=7, GBA1<sup>+L444P</sup> N=5, fibril treated GBA1<sup>+/+</sup> and GBA1<sup>+L444P</sup> N=4 for venglustat treated groups. GlcSph and sphingosine 1-Phosphate had GBA1<sup>+/+</sup> N=6, GBA1<sup>+L444P</sup> N=4, fibril treated GBA1<sup>+/+</sup> and GBA1<sup>+L444P</sup> N=4 venglustat treated mice. For GlcSph and sphingosine 1-phosphate, GBA1<sup>+/+</sup> N=6, GBA1<sup>+L444P</sup> N=5, and fibril treated GBA1<sup>+/+</sup> N=5. GlcSph had fibril treated GBA1<sup>+L444P</sup> mice N=5, whereas sphingosine 1-phosphate had N=6 for the same group. \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ , and \*\*\*\* $p < 0.0001$ .

# Extended Figure 5-2

**A****GBA1<sup>+/+</sup>****Amygdala****GBA1<sup>+/L444P</sup>****B****Amygdala****C****Entorhinal Cortex****D****ETC**

**Extended Figure 5-2: Aggregate burden in the entorhinal cortex and basolateral amygdala. A.**

Representative images of GBA1<sup>+/+</sup> and GBA1<sup>+L444P</sup> fibril-injected mice of the amygdala were captured using confocal microscopy. Scale bar =100um, zoomed photos scale bar = 50um) **B.** Quantification of p-

$\alpha$ -syn in the amygdala (N=7 for GBA1<sup>+/+</sup>, N=6 for GBA1<sup>+L444P</sup>, Mann-Whitney test: W= 11, p=0.1690).

The amygdala aggregate data failed the test for normality and graphed as a scatter plot without a bar using a Mann-Whitney test. Error bars represent SEM. **C.** Representative images of GBA1<sup>+/+</sup> and GBA1<sup>+L444P</sup>

fibril-injected mice of the entorhinal cortex were captured using confocal microscopy. Scale bar =100um,

zoomed photos scale bar = 50um. **D.** Quantification of p- $\alpha$ -syn in the entorhinal cortex (N=6 for GBA1<sup>+/+</sup>, and N=7 GBA1<sup>+L444P</sup>: Independent t-test:  $t_{(11)} = 0.03628$ ; p=0.9717). Error bars represent SEM.



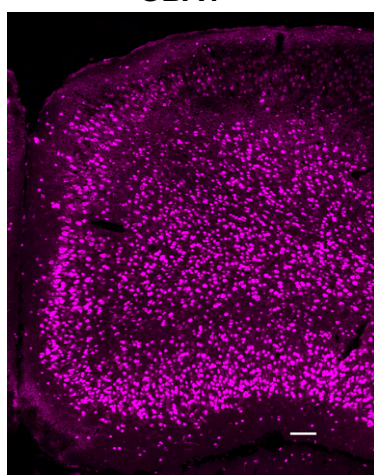
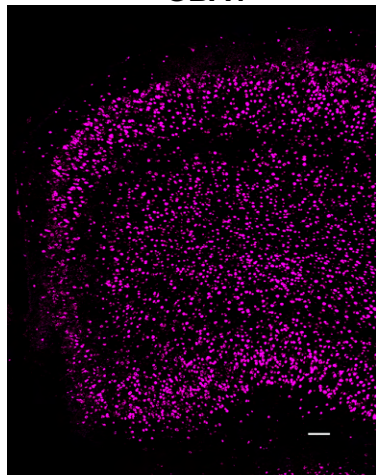
# Extended Figure 5-3

**A**

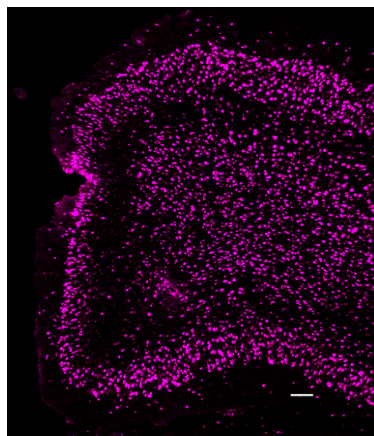
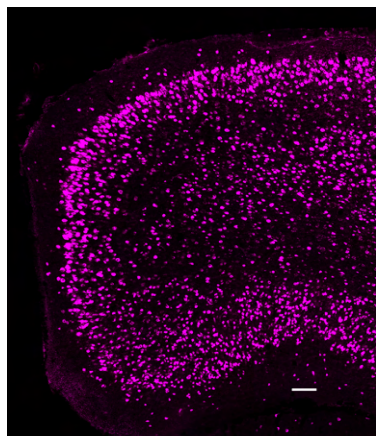
**GBA1<sup>+/+</sup>**

**GBA1<sup>+/-L444P</sup>**

**Control**

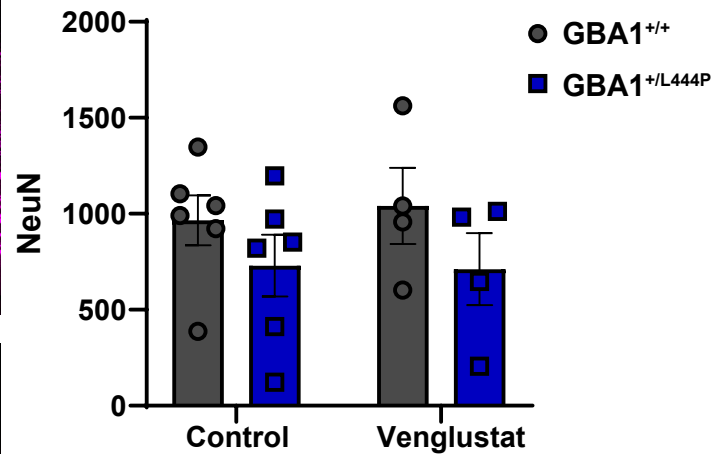


**Venglustat**



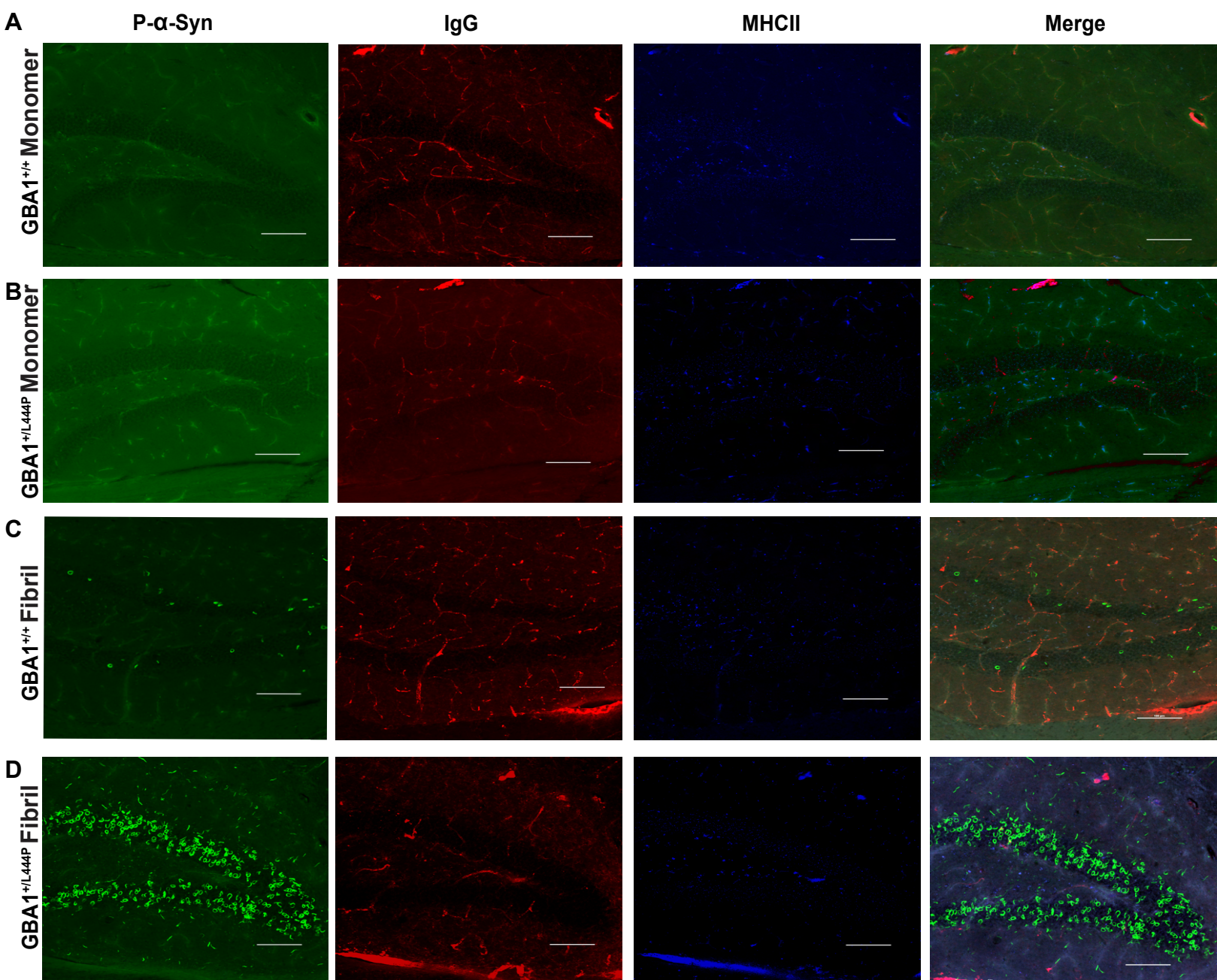
**B**

**Prefrontal Cortex**



**Extended figure 5-3: NeuN analysis of the Prefrontal Cortex. A.** 10-months after bilateral striatal injection, immunofluorescence for NeuN was performed. Representative images of GBA1<sup>+/+</sup> and GBA1<sup>+/L444P</sup> fibril-injected mice fed control or venglustat chow of the dmPFC were captured using confocal microscopy. Scale bar =100um. **B.** Quantification of NeuN in the dmPFC (N=6 for both control chow groups, N=4 for venglustat chow groups, Two-way ANOVA: *Interaction*:  $F_{(1,16)} = 0.07678$ ,  $p=0.7853$ , *Drug Treatment*:  $F_{(1,16)} = 0.02827$ ,  $p=0.8686$ , *Genotype*:  $F_{(1,16)} = 2.821$ ,  $p=0.1124$ ). Error bars represent SEM.

# Extended Figure 5-4



**Extended Figure 5-4: Neuroinflammation of the Granule Cell layer of the dentate gyrus of the hippocampus.** 10-months after bilateral striatal injection, immunofluorescence for p- $\alpha$ -syn, IgG, and MHCII was performed. Representative images of the granule cell layer of the dentate gyrus of the hippocampus of **A.** monomer-injected GBA1<sup>+/+</sup>, **B.** monomer-injected GBA1<sup>+/L444P</sup>, **C.** fibril-injected GBA1<sup>+/+</sup>, and **D.** fibril-injected GBA1<sup>+/L444P</sup> mice were captured using confocal microscopy. Scale bar =100um. N=3 for all groups.