

Supplemental Figures

Figure S1 – Femoral Nerve Axon Diameter and Myelin Thickness XY Plots. A) An XY plot of axon diameter and myelin thickness for the motor branch of the femoral nerve. Slopes differ significantly ($p < 0.0001$). B) An XY plot of axon diameter and myelin thickness for the sensory branch of the femoral nerve. Slopes differ significantly ($p < 0.0001$). Each point indicates one axon. Fifty representative axons were randomly selected from five mice for quantification. Sipa1l2 deletion status is indicated with color. Dots and solid lines indicate mice without the C3-PMP22 transgene while hollow squares and dashed lines indicate transgenic C3-PMP22 mice.

Simple linear regression in GraphPad Prism used to test for difference in slope of regression lines.

Figure S2 – Targeted Investigation of Gene Expression. A) Expression of genes associated with the SOX10/EGR2 co-expression network was investigated directly using TMM normalized counts from RNASeq. None of the selected SOX10/EGR2 genes were identified as differentially expressed between experimental genotypes. B) The overlapping differentially expressed genes between experimental genotypes were visualized using a Venn Diagram. Only three differentially expressed genes are shared between experimental genotypes. C) Representative gene set enrichment analysis enrichment (GSEA) plots for cholesterol-associated pathways in *Sipa1l2*^{-/-} mice depicts negative enrichment or repression in mice with the deletion. D) Representative GSEA leading edge analysis identifies genes associated with cholesterol-associated pathways in *Sipa1l2*^{-/-} mice.

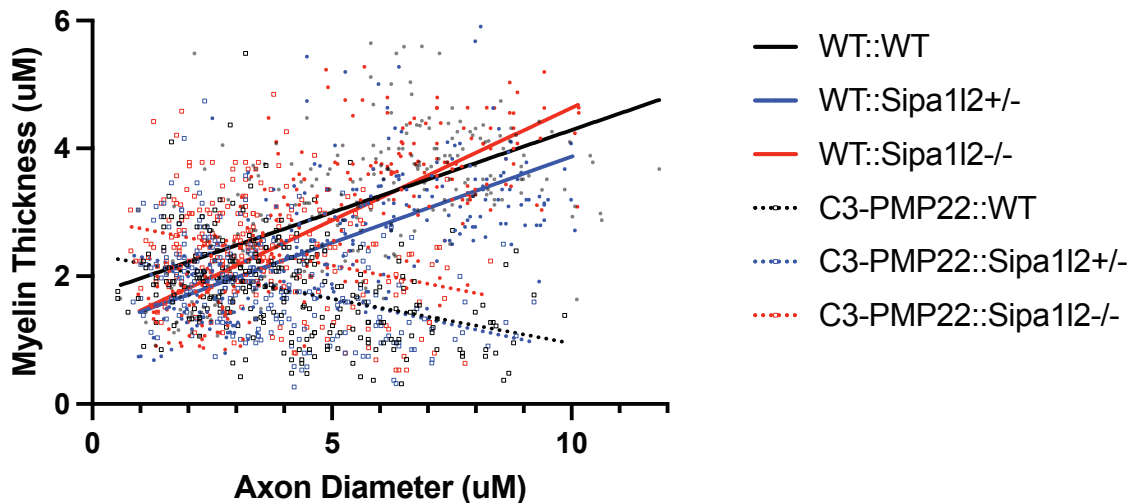
Supplemental Tables

Table S1 – Differential Expression Analysis. Contains the Ensembl identifiers, Log₂Fold-Change, Log₂CPM, p value, false discovery rate, and absolute Log₂Fold-Change for all differentially expressed genes. Each experimental genotype comparison to wild type is contained in a different tab. Filtering can be adjusted to show genes that did not reach FDR or Log₂FC cutoffs.

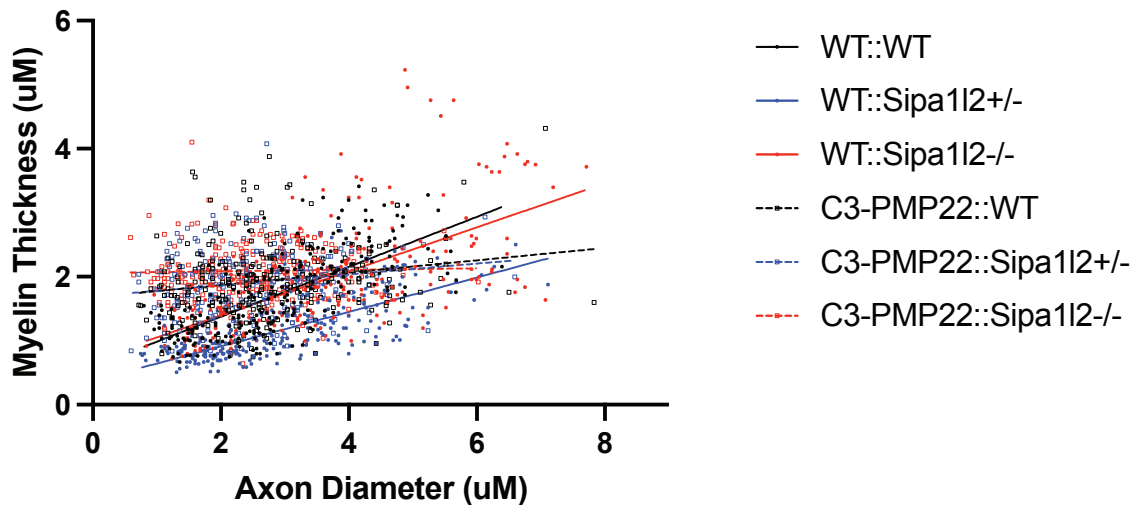
Table S2 – Gene Set Enrichment Analysis. Contains all Reactome pathways returned from gene set enrichment analysis. Gene set size, normalized enrichment score, and family wise error rate are reported for each pathway. Each experimental genotype is included in a different tab.

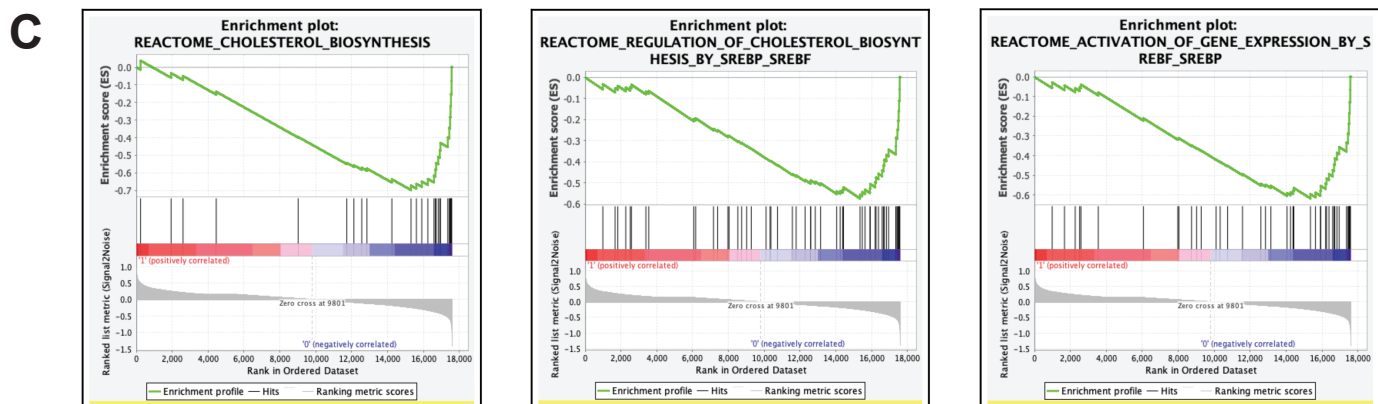
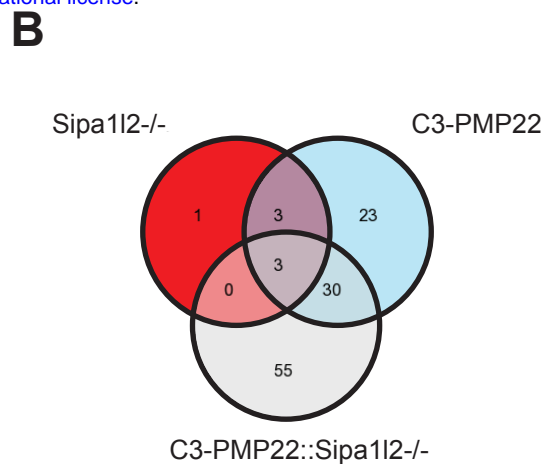
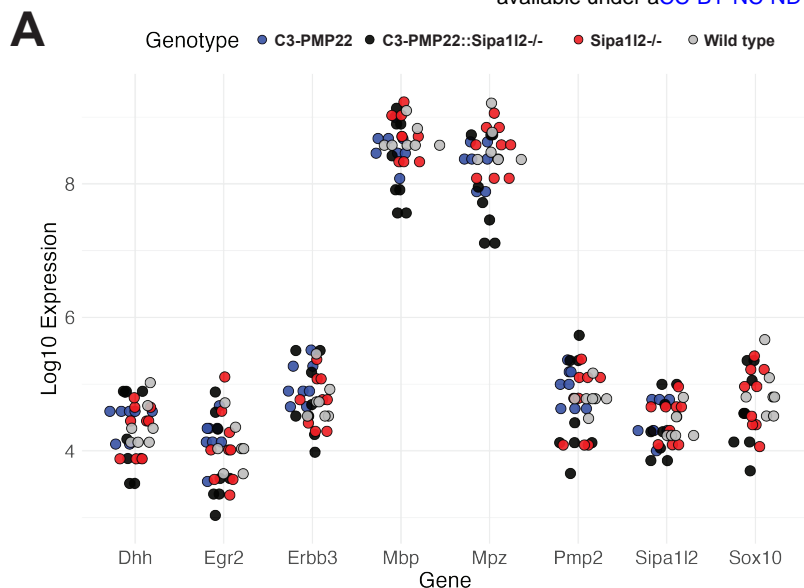
Table S3 – Lead Edge Analysis. Contains all genes returned from leading edge analysis of Reactome pathways related to “cholesterol” with FWER < 0.05. Each experimental genotype is provided in a column.

A XY: Motor Diameter x Myelin Thickness All



B XY: Sensory Diameter x Myelin Thickness All





D Leading edge analysis of Sipa112-/- Gene Expression Data:
 Cholesterol Biosynthesis
 Regulation of Cholesterol Biosynthesis by SREBP / SREBF
 Activation of Gene Expression by SREBF / SREBP

