***eLife’s* transparent reporting form**

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see EQUATOR Network), life science research (see the BioSharing Information Resource), or the ARRIVE guidelines for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

If you have any questions, please consult our Journal Policies and/or contact us: editorial@elifesciences.org.

**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
* You should state the statistical method of sample size computation and any required assumptions
* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

1. We did not compute sample-size estimations, and sample-size of biological replicates was determined based on experimental feasibility, sample availability, and the number of

necessary to obtain definitive results; similar to sample sizes used in previous studies to determine defects in myelin development.

2. The exact sample-size (n) used for each experiment can be found in figure legends.

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
* If you encountered any outliers, you should describe how these were handled
* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

1. The number (n) how often an experiment was performed can be found in figure legends.
2. The definition of biological versus technical replication can be found in the Materials and Method sections.
3. The sample sizes (n) provided throughout the manuscript are biological repeats. Technical repeats within the same biological repeat were averaged and subjected to statistical analysis.
4. No outlier was encountered throughout the manuscript.
5. Please find analysis standards of each method that were used in Materials and Method sections.
6. Next-generation sequencing data has been deposited in GEO (GSE145116, token: yjwtqumcnzsjreh; GSE145117, token: irineqsmplsvjcl; GSE144756, szcbyeukfdqlrsz.

**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

1. Statistical analysis methods are described and justified in Materials and Method Section. Specifics on statistical analysis methods used for each experiment can be found in the figure legends.
2. Raw data for each histogram with N <10 were presented in figures as bar graph with individual dots.
3. Statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures can be found in figure legends.
4. Please find the exact *p*-values in the Source data file.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

1. Samples were allocated into groups based on the mouse genotype and when possible, littermate and age pairing. This information can be found in Materials and Method Section.
2. No randomization and blinding events occurred during the experiments.

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

Please find our Source data file.